Table S1. Microarray data from D5 WT and PCKO mice.

List of significantly (false discovery rate [FDR]<0.1) altered genes in WT vs. PCKO muscle.

lr.PCKO.WT (mean log2 ratio of KO vs. WT); fc.PCKO.WT (fold change, PCKO vs. WT); lfdr.PCKO.WT (local FDR of changes between PCKO and WT).

Gene	ProbeName	GENE_SYMBOL	GENE_NAME	SystematicName	WT 1	WT 2	WT 3	WT 4	PCKO 1	PCKO 2	PCKO 3	PCKO 4	Average WT	Average PCKO	lr.PCKO.WT	fc.PCKO.WT	lfdr.PCKO.WT
64337	A_51_P149422	Gng13	guanine nucleotide binding p	NM_022422	6.4	2.3	3	4.2	292.3	421.6	410.5	286.6	3.975	352.75	6.55502817	94.0286287	8.17E-05
69101	A_52_P162298	Ydjc	YdjC homolog (bacterial)	NM_026940	4.7	7.1	11.4	10.4	524.6	458.2	546.7	514.3	8.4	510.95	6.00650656	64.289292	4.3551E-05
224022	A_55_P1997400	Slc7a4	solute carrier family 7 (cation	NM_144852	18.5	20.2	11	9.9	817.5	603.8	677.5	657.9	14.9	689.175	5.59155165	48.2197295	4.41E-05
71004	A_55_P2048493	4931440P22Rik	RIKEN cDNA 4931440P22 gen	NR_027955	124	91.7	85	94.1	3813.1	3876.6	4894.2	5756.6	98.7	4585.125	5.53165588	46.2587982	2.86E-06
319642	A_51_P386069	Rab9b	RAB9B, member RAS oncoger	NM_176971	2.6	6.9	4.4	6.7	164.1	222.1	142	196.3	5.15	181.125	5.21834697	37.2287939	0.00059175
17885	A_55_P2120169	Myh8	myosin, heavy polypeptide 8,	ENSMUST00000108685	2.9	2.4	2.9	2.5	93.5	136.7	93.2	75.4	2.675	99.7	5.19086156	36.5262456	5.87E-06
239731	A_66_P128442	Rimbp3	RIMS binding protein 3	NM_001033338	3.1	2.7	2.8	3	385.5	65.2	57.8	66.8	2.9	143.825	5.09913599	34.276217	0.07768692
13982	A_55_P2030883	Esr1	estrogen receptor 1 (alpha)	NM_007956	35.7	19.5	18.6	19.8	995.5	929.5	526.2	697.7	23.4	787.225	5.08440135	33.9279263	0.00021348
94226	A_55_P2075070	S1pr5	sphingosine-1-phosphate rec	NM_053190	7.1	4.4	12.1	3.1	210.5	183.9	169.8	168.3	6.675	183.125	4.96212805	31.1709031	0.00395977
225362	A_52_P125467	Reep2	receptor accessory protein 2	NM_144865	3.2	5.2	3.6	8.2	130.2	140.1	125.6	126.9	5.05	130.7	4.79373384	27.7368844	0.00035497
27356	A_51_P459108	Insl6	insulin-like 6	NM_013754	33.2	30	31.8	26.4	934.9	792.9	796	835.9	30.35	839.925	4.79251293	27.7134215	1.55E-07
19733	A_51_P157462	Rgn	regucalcin	NM_009060	3	3.5	6.6	2.8	96.6	125.6	102.9	88.6	3.975	103.425	4.78019191	27.4777488	0.00031271
16520	A_51_P166740	Kcnj4	potassium inwardly-rectifying	NM_008427	3.7	2.8	8	3	139.2	113	89	86.3	4.375	106.875	4.72257546	26.4020027	0.00224452
78593	A_55_P2000943	Nrip3	nuclear receptor interacting p	NM_020610	7.9	3.9	9	6.5	175.3	189	145.2	176.2	6.825	171.425	4.71080022	26.1873872	0.0001826
109218	A_55_P1995512	Tmem139	transmembrane protein 139	NM_175408	24.5	28.9	18	14	470	541.5	551.5	555.7	21.35	529.675	4.68443166	25.7131001	6.33E-05
20287	A_51_P234359	Sct	secretin	NM_011328	4.6	4.6	7.5	2.7	132.8	117.9	96.4	75.2	4.85	105.575	4.50375888	22.6864486	0.00163491
380684	A_55_P2053181	Nefh	neurofilament, heavy polypep	NM_010904	2.4	1.9	2.5	2.5	62.1	41.4	39.6	52.1	2.325	48.8	4.37645755	20.7704066	1.33E-05
239552	A_51_P115471	Apol8	apolipoprotein L 8	ENSMUST00000070911	3.2	2.2	3	3.1	62.5	62.6	47.1	65.4	2.875	59.4	4.37248569	20.7133026	8.04E-06
107528	A_51_P104430	Magee1	melanoma antigen, family E, 1	NM_053201	2.7	2.9	2.9	2.8	51.5	59.3	58.3	65.2	2.825	58.575	4.36954818	20.6711706	1.30E-07
12447	A_51_P408946	Ccne1	cyclin E1	NM_007633	20.5	43.4	51.8	27.8	749.9	705.7	658	622.3	35.875	683.975	4.34195188	20.2795239	0.00083364
11676	A_55_P2070992	Aldoc	aldolase C, fructose-bisphosp	NM_009657	101.1	86	93.2	61.2	1641.5	1559.8	1928.2	1610.2	85.375	1684.925	4.32259645	20.0092675	1.18E-05
320237	A_51_P247614	Ncrna00086	non-protein coding RNA 86	NR_028086	8.1	4.4	6.2	3.2	94.1	130.6	94.1	89.2	5.475	102	4.28861574	19.5434836	0.00112894
624685	A_66_P103316	Gm6521	predicted gene 6521	XR_035266	3.2	2.2	3.3	3.2	59	35	107.5	42.1	2.975	60.9	4.23493847	18.8297047	0.00529776
56734	A_55_P2054132	Tulp2	tubby-like protein 2	NM_008807	2.9	2.2	2.8	2.5	51.7	53.1	49.1	41.5	2.6	48.85	4.23362788	18.812607	0.00000144
13180	A_51_P139320	Pcbd1	pterin 4 alpha carbinolamine	NM_025273	57.3	33.6	67.5	37.9	913.3	815.7	894.9	770.6	49.075	848.625	4.1676167	17.9712232	0.00019734
74849	A_52_P630687	4930412F12Rik	RIKEN cDNA 4930412F12 gen	XM_001475690	2.9	7.1	2.7	2.9	70.6	70.9	53.1	55.6	3.9	62.55	4.12101968	17.4000516	0.00335554
100126033	A_55_P2170911	Gm10366	predicted gene 10366	ENSMUST00000100571	10.9	8.7	2.7	4.6	96	90.9	88.4	108.6	6.725	95.975	4.02954019	16.3309882	0.03365808
81703	A_51_P254646	Jdp2	Jun dimerization protein 2	NM_030887	292	354.2	250.5	349.2	4953.2	3304	5564.3	6764.3	311.475	5146.45	4.01375776	16.1533083	0.00028884
74589	A_55_P2091120	Kbtbd12	kelch repeat and BTB (POZ) d	NM_001142724	35	45.9	30.7	35.8	603.9	532	568.6	501.1	36.85	551.4	3.9154784	15.0895555	4.94E-06
171282	A_52_P215170	Acot4	acyl-CoA thioesterase 4	NM_134247	2.9	5.3	2.8	3.9	47.4	53.6	63.9	45.4	3.725	52.575	3.85559861	14.4760753	0.00032535
194237	A_52_P69194	Rimkla	ribosomal modification prote	NM_177572	3	2.4	2.9	10.5	54	50.7	53.7	64.7	4.7	55.775	3.85124453	14.432452	0.07832503
272009	A_51_P230347	Srsf12	serine/arginine-rich splicing fa	NM_177774	2.9	3.9	2.7	2.8	45.7	55.4	35.7	39	3.075	43.95	3.83281937	14.2493022	4.80E-05
379043	A_55_P2115955	Raet1e	retinoic acid early transcript 1	NM_198193	4.3	14.3	11.1	11.3	117.3	126.9	148.6	141.4	10.25	133.55	3.82687938	14.1907544	0.01442634
236733	A_51_P315673	Usp11	ubiquitin specific peptidase 1	NM_145628	58.7	66.3	51.5	78.8	842.5	914.6	949.5	828.4	63.825	883.75	3.80697203	13.9962848	7.47E-06
56226	A_66_P108003	Espn	espin	NM_207687	2.8	2	2.7	2.6	38.8	27	40.2	34.2	2.525	35.05	3.7902556	13.8350466	2.98E-05
218518	A_51_P451428	Marveld2	MARVEL (membrane-associat	NM_001038602	8.8	6.6	2.7	7.4	71	100.3	66.8	84.2	6.375	80.575	3.7687488	13.6303321	0.02024494
12683	A_51_P199168	Cidea	cell death-inducing DNA fragr	NM_007702	354	506.9	187.3	499.3	3832.1	4682.7	5132.6	6209.4	386.875	4964.2	3.76415589	13.587008	0.00978041
230603	A_55_P2131238	Ttc39a	tetratricopeptide repeat dom	NM_153392	3.4	2.5	3.1	2.9	44.1	42.3	33.2	36.4	2.975	39	3.71212161	13.1056918	7.07E-06
664788	A_55_P2152165	Gm7339	predicted gene 7339	XM_972614	2.8	1.9	2.6	3.4	33.5	34.2	33.9	35.3	2.675	34.225	3.70783766	13.0668334	4.32E-05
234878	A_52_P629333	BC021891	cDNA sequence BC021891	NM_145608	2.6	1.9	2.6	2.5	34.3	28.9	27	32.9	2.4	30.775	3.68577167	12.8684971	8.29E-06
17190	A_55_P1971124	Mbd1	methyl-CpG binding domain p	NM_013594	922.9	937.9	1032.7	1084.1	11313.2	9146.5	14471.1	17543.6	994.4	13118.6	3.68161481	12.8314723	0.00018214
236900	A_51_P392291	Pdk3	pyruvate dehydrogenase kina	NM_145630	20.1	15.1	15.9	15.2	201.8	238.6	192.2	213.1	16.575	211.425	3.67863235	12.8049734	3.74E-06
16477	A_55_P2011106	Junb	Jun-B oncogene	NM_008416	2.4	5.2	2.5	2.4	67.2	30.1	22.5	43.6	3.125	40.85	3.67342043	12.7587972	0.04654487
232943	A_51_P154753	Klc3	kinesin light chain 3	NM_146182	26.2	26.5	13.1	12	213.2	262.4	261.5	187.3	19.45	231.1	3.65392225	12.5875207	0.00589917
619289	A_55_P2096189	Rfx8	regulatory factor X 8	NM_001145660	2.9	2.4	4	3.2	29.7	44.5	49.7	33.7	3.125	39.4	3.65020397	12.5551205	0.00035981
239435	A_52_P522372	Aard	alanine and arginine rich dom	NM_175503	2.7	1.9	2.6	2.6	32.7	36.5	31.2	21.8	2.45	30.55	3.62869789	12.3693509	0.00013036
68846	A_55_P2035812	Rnf208	ring finger protein 208	NM_176834	8.8	10.2	7.1	9.3	113.9	107	106.8	105.5	8.85	108.3	3.62497686	12.3374887	3.32E-06
73884	A_51_P213725	Zdbf2	zinc finger, DBF-type containi	NM_028673	3.4	2.1	3.8	2.7	32	31	40.2	40.2	3	35.85	3.60439015	12.1626876	0.00023866
332397	A_52_P231232	Nanos1	nanos homolog 1 (Drosophila	NM_178421	3	2	2.7	2.8	34.6	34.1	31.4	26.7	2.625	31.7	3.60312793	12.1520511	2.3513E-05
621427	A_55_P2007467	Gm10244	predicted gene 10244	ENSMUST00000156905	17.2	17.8	14.1	9	170.9	176.2	170.2	163.4	14.525	170.175	3.59893496	12.1167843	0.00036251
100043254	A_55_P2019670	Nps	neuropeptide S	NM_001163611	2.7	6.9	2.7	5.9	47.6	62.2	48.2	44.4	4.55	50.6	3.59548781	12.0878672	0.01755296
279618	A_66_P109012	Gm715	predicted pseudogene 715	XM_205232	3.1	3.7	6.3	3.5	47.3	52.4	52.5	39.6	4.15	47.95	3.57860925	11.9472713	0.00067935
70451	A_55_P2013928	Dhrs13	dehydrogenase/reductase (SD	NM_183286	46	45.3	41.2	40.3	539.9	446.9	492.3	572.7	43.2	512.95	3.56577622	11.8414695	1.25E-06
18476	A_55_P1960074	Pafah1b3	platelet-activating factor acet	NM_008776	75.2	93.7	86.1	59.1	1079.8	868	898.2	783.9	78.525	907.475	3.54196323	11.6476195	5.97E-05
73381	A_51_P317225	Cmtm2a	CKLF-like MARVEL transmemb	NM_027022	2.9	3.1	4.6	2.7	35.3	36	37.5	41.7	3.325	37.625	3.52985027	11.5502347	7.72E-05
20420	A_51_P374818	Shd	src homology 2 domain-conta	NM_009168	20.4	23.2	15.1	8.8	193.1	197.3	170.5	158.8	16.875	179.925	3.50040405	11.3168776	0.00616691
245404	A_55_P2020497	Dcaf12l1	DDB1 and CUL4 associated fa	NM_178739	19.9	22.3	14.3	19.7	209.6	196.9	220.4	218.6	19.05	211.375	3.48930223	11.2301261	1.76E-05
252967	A_55_P2146783	Ropn1l	ropporin 1-like	NM_145852	12.3	9.4	10.3	7.5	119.7	92.2	115.5	106.9	9.875	108.575	3.47428277	11.1138192	5.96E-05
194908	A_51_P155755	Pld6	phospholipase D family, mem	NM_183139	7.5	11	12.5	10.7	150.2	134.6	59.6	131.8	10.425	119.05	3.45325132	10.9529784	0.01249895
230863	A_55_P2003753	Sh2d5	SH2 domain containing 5	NM_001099631	12.6	4.7	5.9	12.4	87.7	98.1	94.7	76.3	8.9	89.2	3.45214852	10.9446091	0.02340902
268480	A_55_P2068066	Rapgefl1	Rap guanine nucleotide excha	NM_001080925	19.9	10.2	13.7	11.4	134.8	147.2	150.1	148.9	13.8	145.25	3.44300774	10.8754843	0.00033434
112415	A_55_P1974612	C030039L03Rik	RIKEN cDNA C030039L03 gen	NM_001112731	24.4	29.3	24.3	42.3	303	297.4	298.1	378.4	30.075	319.225	3.43893687	10.8448401	0.00025161
78373	A_52_P518076	Nudt17	nudix (nucleoside diphosphat	NM_001162925	4.7	4.6	4.3	4.9	43.8	46	48.9	63.6	4.625	50.575	3.43693133	10.8297747	9.16E-06
72640	A_52_P706060	Mex3a	mex3 homolog A (C. elegans)	NM_001029890	2.9	3	4	4.4	41.7	27.8	35.6	50.5	3.575	38.9	3.43312159	10.8012141	0.00070008
105732	A_51_P115666	Fam83h	family with sequence similarit	NM_134087	27.7	39.3	46	43.5	429.3	413.2	439	380.4	39.125	415.475	3.43280311	10.79883	6.56E-05
71003	A_51_P363303	Prss41	protease, serine, 41	NM_027644	11.4	14.5	6.3	5.9	160	69	66.6	113	9.525	102.15	3.43076802	10.7836078	0.08021741
22293	A_55_P2093569	Slc45a2	solute carrier family 45, mem	NM_053077	2.6	2	2.6	2.7	25.6	21.6	30.6	28.4	2.475	26.55	3.42108186	10.7114498	2.58E-05
72168	A_55_P2002849	Aifm3	apoptosis-inducing factor, mit	NM_175178	28.2	25.2	29.4	18.8	337.5	253.6	243.3	245.4	25.4	269.95	3.41683962	10.6799991	0.00011758
243529	A_51_P114843	H1fx	H1 histone family, member X	NM_198622	2.7	2	2.6	2.7	29.7	24.2	29.6	22.8	2.5	26.575	3.41084573	10.6357195	2.19E-05
235048	A_55_P2093679	Zfp599	zinc finger protein 599	NM_181419	2.5	2.9	2.5	3.6	32.9	31.9	24.5	31.2	2.875	30.125	3.39644454	10.5300804	4.27E-05
433470	A_55_P2137049	AA467197	expressed sequence AA46719	NM_001004174	16.1	14.1	21.2	7.3	142.3	157.9	151.4	124.1	14.675	143.925	3.38818476	10.4699653	0.01147958
105833	A_55_P2095603	Ccdc65	coiled-coil domain containing	NM_153518	2.8	3	2.6	2.7	26.1	27.1	23	42	2.775	29.55	3.37505447	10.3751081	0.00019083
22226	A_55_P2150208	Ucn	urocortin	NM_021290	2.6	4.9	2.6	2.4	26.7	22	42.4	36.8	3.125	31.975	3.37324657	10.3621148	0.00883016
26422	A_55_P2250391	Nbea	neurobeachin	NM_030595	2.9	2.8	3.7	2.7	25.7	20.4	67.7	26.1	3.025	34.975	3.36982278	10.3375527	0.04369948
226970	A_51_P260504	Arhgef4	Rho guanine nucleotide excha	NM_183019	4.1	10.3	8.3	2.9	54.3	53.2	72.1	54.7	6.4	58.575	3.36306758	10.2892619	0.09274101
319915	A_66_P117513	A830049F12Rik	RIKEN cDNA A830049F12 gen	AK078028	6.9	9.4	8.9	4.4	78.3	69.6	71.9	71.6	7.4	72.85	3.35779934	10.2517574	0.00140397
56807	A_52_P409731	Scamp5	secretory carrier membrane p	NM_020270	8.7	10.4	13.9	9.6	100.1	127.1	103.2	100.2	10.65	107.65	3.35289546	10.2169697	7.06E-05
382562	A_52_P139629	Pfn4	profilin family, member 4	NM_028376	15.8	18.1	15.6	10.5	155	133.1	154.3	154.5	15	149.225	3.33949661	10.1225202	0.00011011
100038433	A_55_P2203284	9130213A22Rik	RIKEN cDNA 9130213A22 gen	XM_003085417	4	7	4.4	3.3	45.9	55.3	38.6	43.2	4.675	45.75	3.33644843	10.1011555	0.0015774
381633	A_55_P1964965	Gm1673	predicted gene 1673	NM_001033458	37	44.6	42.8	26	378.6	356.9	369.8	370	37.6	368.825	3.32437145	10.0169504	0.00011466
207607	A_51_P490700	Ccdc40	coiled-coil domain containing	NM_175430	3.3	2.7	3.1	2.8	31.2	44.4	22.3	23.9	2.975	30.45	3.30518798	9.88463699	0.00092708
12695	A_66_P100105	Inadl	InaD-like (Drosophila)	NM_172696	16.6	19	16.1	14	138.7	181.8	163	162.2	16.425	161.425	3.29875199	9.84063896	9.76E-06
207686	A_51_P116601	A330021E22Rik	RIKEN cDNA A330021E22 gen	NM_172447	19.2	23.6	21.6	21.1	227.1	206.5	202.6	203.2	21.375	209.85	3.29763724	9.83303815	7.96E-07
18005	A_51_P501018	Nek2	NIMA (never in mitosis gene a	NM_010892	2.7	2	2.6	2.7	27.5	25.4	22.2	21.3	2.5	24.1	3.27223879	9.66144374	2.04E-05
381353	A_55_P2143851	Gm996	predicted gene 996	NM_001005424	10	5.1	5.7	8.8	47.1	90	70.7	66.8	7.4	68.65	3.23350799	9.40552186	0.00806454
106369	A_55_P1961576	Ypel1	yippee-like 1 (Drosophila)	NM_023249	2.7	4.7	2.6	2.6	21.7	29.5	28.4	36.6	3.15	29.05	3.23030339	9.3846529	0.00243831
103784	A_55_P2071952	Wdr92	WD repeat domain 92	NM_178909	5725.5	6964.9	5176.1	5576.9	52031.3	54111.6	47493.9	65040.3	5860.85	54669.275	3.22081824	9.32315491	2.01E-05
29861	A_55_P2067425	Dpf1	D4, zinc and double PHD finge	NM_013874	23.4	29.4	25.9	23.9	231.7	222.7	248.3	247.5	25.65	237.55	3.21557434	9.28932869	1.74E-06
66237	A_52_P374839	Atp6v1g2	ATPase, H+ transporting, lyso	NM_023179	4.6	4.1	5.5	8.9	49.5	42.8	50.1	61.6	5.775	51	3.19749948	9.173673	0.00339759
55994	A_55_P2129696	Smad9	MAD homolog 9 (Drosophila)	NM_019483	4.2	7.7	2.8	3.9	38.5	45.2	36.3	38.8	4.65	39.7	3.19019277	9.12732921	0.01065172
319317	A_55_P2047809	Snhg11	small nucleolar RNA host gen	NM_175692	2.6	2	2.6	2.7	18	24.3	22.9	24.6	2.475	22.45	3.18017222	9.06415301	4.07E-05
75538	A_51_P323531	Fam71e1	family with sequence similarit	NM_028169	110.4	99.9	99.2	124.9	875.5	897.5	1074	1091.7	108.6	984.675	3.17974087	9.06144339	9.37E-06
56191	A_66_P116998	Tro	trophinin	NM_001002272	34.8	26.1	31.3	48.3	362.8	343.6	263.6	275.6	35.125	311.4	3.17180504	9.01173595	0.00075792
74341	A_55_P2045367	G630025P09Rik	RIKEN cDNA G630025P09 gen	NR_027913	29.9	33.9	39.4	62.9	390	347.1	311	346.6	41.525	348.675	3.12600942	8.73016805	0.00193359
14658	A_51_P250797	Glrb	glycine receptor, beta subunit	NM_010298	2.5	3	2.6	6.4	25.2	35.7	26.9	29.6	3.625	29.35	3.12169735	8.7041134	0.02236204
12310	A_52_P154101	Calca	calcitonin/calcitonin-related p	NM_001033954	2.8	2.1	2.7	2.7	26.3	10.5	30.7	29	2.575	24.125	3.12143027	8.7025022	0.05266131
100041639	A_55_P1987196	Gm3448	predicted gene 3448	NM_001123367	12.5	29.8	18.3	19.3	218.4	100.9	147	232.2	19.975	174.625	3.12027765	8.69555224	0.05551028
170461	A_52_P85765	Stard6	StAR-related lipid transfer (ST	NM_029019	6.3	4	3.6	9	48.9	45.8	41.8	47.5	5.725	46	3.10276279	8.59062318	0.01268648
219022	A_51_P441286	Ttc5	tetratricopeptide repeat dom	NM_177625	2.5	3.3	5.1	3.2	35.3	23.5	30.2	29	3.525	29.5	3.09941987	8.57074061	0.00219172
103768	A_55_P2013645	Tubg2	tubulin, gamma 2	NM_134028	176.8	181.8	164.4	199.6	1656.6	1474	1511.3	1463.9	180.65	1526.45	3.0806222	8.45979202	1.20E-06
230587	A_55_P2081373	Glis1	GLIS family zinc finger 1	NM_147221	25.6	18.1	13.6	18.9	148.5	148	191.9	129.7	19.05	154.525	3.04129482	8.2322958	0.00115607
12122	A_52_P574653	Bid	BH3 interacting domain death	NM_007544	17.5	29.4	22.2	11.5	155.6	160.5	179.6	133.8	20.15	157.375	3.03940715	8.22153141	0.01167281
216456	A_51_P169087	Gls2	glutaminase 2 (liver, mitochor	NM_001033264	7.5	5.9	8.1	3.1	46.2	45.8	45.1	52.1	6.15	47.3	3.03189199	8.1788159	0.01871397
635253	A_55_P1959218	Usp51	ubiquitin specific protease 51	NM_001137547	2.7	4.7	2.6	3.7	30.5	22.5	23.5	32.3	3.425	27.2	3.01474612	8.08218918	0.0023672
51960	A_55_P1952634	Kctd18	potassium channel tetrameris	NM_030211	11.2	14.7	9.3	7.4	92.4	94.9	79.2	68.4	10.65	83.725	3.00839575	8.04669167	0.00209669
100503910	A_55_P1973352	Gm19958	predicted gene, 19958	XR_106152	898.1	571.2	481.8	426.2	3767.8	5251.3	4608.5	4821.9	594.325	4612.375	3.00679283	8.03775625	0.00388302
93886	A_51_P159833	Pcdhb15	protocadherin beta 15	NM_053140	7.7	11.8	13.3	4.2	57.5	65.8	77.1	72.1	9.25	68.125	3.00419374	8.02328888	0.08416608
54204	A_55_P2178127	1-Sep	septin 1	NM_017461	16.1	20.1	10.1	21.6	125.8	118.1	128.7	150.3	16.975	130.725	2.99776688	7.98762655	0.00417604
320039	A_55_P2231342	A030010E16Rik	RIKEN cDNA A030010E16 gen	AK042844	8.8	4.9	8.3	2.8	43	48.7	43.1	44.5	6.2	44.825	2.99216015	7.95664452	0.08821643
100038474	A_55_P2392972	K230015D01Rik	RIKEN cDNA K230015D01 gen	AK158572	27.5	35.4	29.2	29.4	238.1	221.8	265.5	236.9	30.375	240.575	2.98914098	7.94001086	5.63E-06
66985	A_51_P521176	Rassf7	Ras association (RalGDS/AF-6	NM_025886	45.4	50.2	47.2	59.4	366.5	501.5	376.6	359.2	50.55	400.95	2.98149154	7.89802286	5.89E-05
432999	A_55_P2043013	A930007A09Rik	RIKEN cDNA A930007A09 gen	AK044312	11.2	17.3	23.1	31.7	124.3	132.4	171.9	189.6	20.825	154.55	2.97108096	7.84123535	0.04547354
67071	A_55_P2020911	Rps6ka6	ribosomal protein S6 kinase p	NM_025949	27.8	40	17.8	37	204.3	253.4	228.6	227.6	30.65	228.475	2.96116417	7.78752111	0.00683255
14198	A_55_P2032714	Fhit	fragile histidine triad gene	NM_010210	15.4	20.2	28.9	11.8	158.9	124.4	166.3	118.3	19.075	141.975	2.95997856	7.78112394	0.01551873
242700	A_52_P621588	Il28ra	interleukin 28 receptor alpha	NM_174851	3.5	2.2	3	3	25.9	21.2	20.1	22.9	2.925	22.525	2.9581221	7.77111762	0.0001499
76856	A_55_P1969962	Catsper3	cation channel, sperm associa	HM179540	2.9	2.2	2.7	4.8	25.4	17.3	32.3	20.5	3.15	23.875	2.94523019	7.70198433	0.01861587
382913	A_55_P2099418	Neil2	nei like 2 (E. coli)	NM_201610	29.8	41	28.5	27.8	241.9	234.2	217.5	274	31.775	241.9	2.94201812	7.68485543	8.61E-05
16772	A_66_P118600	Lama1	laminin, alpha 1	NM_008480	3.9	2.3	2.8	4.9	24.8	25.1	25.9	26.1	3.475	25.475	2.9348563	7.64680085	0.0032383
71017	A_55_P2253284	4933407E14Rik	RIKEN cDNA 4933407E14 gen	AK016717	14.2	19.9	19.4	19.7	115.1	145.1	141.9	141.7	18.3	135.95	2.90061261	7.46743414	7.20E-05
207175	A_55_P2029294	Cetn4	centrin 4	NM_145825	14.1	24.8	18.7	14.8	142.8	124.3	131	128.5	18.1	131.65	2.89804977	7.45418061	0.00059075
14695	A_51_P293862	Gnb3	guanine nucleotide binding p	NM_013530	20.6	12.4	18.2	6.8	95.1	109.3	87.6	103.5	14.5	98.875	2.88540675	7.38914148	0.07662391
75458	A_55_P1989534	Cklf	chemokine-like factor	NM_029295	72.3	72.9	62.3	75.1	487.7	493.9	552.2	532.9	70.65	516.675	2.87225538	7.32208934	2.39E-06
225392	A_55_P2047106	Rell2	RELT-like 2	NM_153793	43.8	47.3	58	32.6	325.8	319.2	317.9	338.2	45.425	325.275	2.86972835	7.30927518	0.00031685
224019	A_51_P165082	Tmem191c	transmembrane protein 191C	NM_177473	39.4	69.2	56.3	76.6	439.7	413.7	374.6	466.3	60.375	423.575	2.8499948	7.20997773	0.00204672
52906	A_51_P112174	Ahi1	Abelson helper integration sit	NM_026203	2.6	4.1	2.7	3.7	22.4	17.5	32.1	22.7	3.275	23.675	2.84730285	7.19653706	0.00405214
53416	A_55_P1953851	Stk39	serine/threonine kinase 39, S	NM_016866	98.2	110.4	124.7	126.3	757.6	855.3	884.9	779.1	114.9	819.225	2.83833465	7.15194009	1.10E-05
15354	A_55_P1992421	Hmgb3	high mobility group box 3	NM_008253	390.1	645.5	515.4	586.2	3949.3	3628	3752.6	3696.8	534.3	3756.675	2.83782618	7.14941985	0.00019652
225655	A_55_P2057035	Slmo1	slowmo homolog 1 (Drosophi	NM_144867	29.6	55.1	27.8	52.8	336.2	321.3	254.5	224.8	41.325	284.2	2.83349712	7.12799892	0.01941083
442803	A_52_P295755	A830005F24Rik	RIKEN cDNA A830005F24 gen	ENSMUST00000065465	2.8	2.9	4	5.6	30.1	26.8	23.1	24.9	3.825	26.225	2.82921023	7.10684989	0.00485012
66536	A_55_P1958349	Nipsnap3b	nipsnap homolog 3B (C. elega	NM_025623	25.8	23.5	24.3	26.4	174.3	192.8	169.6	172.7	25	177.35	2.82631705	7.0926121	1.04E-06

50784	A_55_P2129437	Ppap2c	phosphatidic acid phosphatas	NM_015817	216.8	219.4	232.9	189.4	1517.8	1541.6	1581.5	1432.5	214.625	1518.35	2.825719	7.08967257	2.12E-06
94275	A_51_P174854	Maged1	melanoma antigen, family D,	NM_019791	1008.8	1078.6	948.3	994	7108.5	6665	7117.6	7657.7	1007.425	7137.2	2.82447968	7.08358494	1.01E-06
108832	A_55_P2002768	5430405G05Rik	RIKEN cDNA 5430405G05 gen	NM_001160363	4	7.8	9.9	7.7	42.5	50	45.1	61.4	7.35	49.75	2.81817708	7.05270686	0.0235668
66643	A_55_P2406852	Lix1	limb expression 1 homolog (c	NM_025681	27.9	22.7	20.9	18.9	137	168	176.4	150.1	22.6	157.875	2.81256936	7.0253464	0.00010771
235044	A_51_P427603	BC018242	cDNA sequence BC018242	NM_144935	2.8	3.9	2.7	3.7	21.9	26.5	19.5	23.1	3.275	22.75	2.80665424	6.99660109	0.00025658
22781	A_55_P1979674	Ikzf4	IKAROS family zinc finger 4	NM_011772	51.7	83.3	54.3	61.4	514.5	379.3	427	411.9	62.675	433.175	2.80577035	6.99231582	0.00050288
74443	A_51_P292527	P4htm	prolyl 4-hydroxylase, transme	NM_028944	104.1	106.3	102.5	118	792.2	638	802.6	778.9	107.725	752.925	2.80125449	6.97046302	7.112E-06
19017	A_51_P279038	Ppargc1a	peroxisome proliferative activ	NM_008904	1923.4	1961.6	1637.8	1474.8	10825.6	13189.4	11391.2	12962.6	1749.4	12092.2	2.79396123	6.93531415	3.51E-05
22174	A_55_P2038247	Tyro3	TYRO3 protein tyrosine kinase	NM_019392	113.6	114.5	101.1	79.2	724	678.9	712.8	677.1	102.1	698.2	2.78834732	6.90837941	4.83E-05
234915	A_55_P1991530	AK129341	cDNA sequence AK129341	NM_001045524	12.6	21.1	19.8	16.1	116.5	104.7	118.6	132.3	17.4	118.025	2.78524825	6.89355537	0.00056051
13426	A_55_P2090429	Dync1i1	dynein cytoplasmic 1 interme	NM_010063	25.6	33.7	21.7	21.4	164.2	209	158.1	164.2	25.6	173.875	2.77969068	6.86705099	0.00049823
192734	A_52_P151393	AI646023	expressed sequence AI64602	NM_198860	3.9	10.3	5.5	5.6	37.6	49.5	31.7	44.1	6.325	40.725	2.75955752	6.7718852	0.04365268
212390	A_55_P2111331	Klhl32	kelch-like 32 (Drosophila)	NM_001163020	20.9	11.3	13.2	8.4	98.5	72.6	88.9	84.4	13.45	86.1	2.7501737	6.72798134	0.01978498
60597	A_52_P370392	Mapk8ip2	mitogen-activated protein kin	NM_021921	16	9.9	11.3	8.7	72.9	69.7	85.1	69.7	11.475	74.35	2.72960321	6.63273189	0.00138824
72433	A_55_P1956718	Rab38	RAB38, member of RAS oncog	NM_028238	10.5	20	20	24	108.1	137	109.2	120.4	18.625	118.675	2.72890983	6.62954486	0.01382786
233529	A_55_P1964368	Kctd14	potassium channel tetrameris	NM_001012434	4.3	6.1	7.7	5.5	48.1	32.2	47.3	28.8	5.9	39.1	2.72282075	6.60162298	0.00898613
54561	A_51_P213928	Nap1l3	nucleosome assembly protein	NM_138742	13.5	15.6	12.8	12	75.7	82.9	87.8	110.4	13.475	89.2	2.71921774	6.58515655	0.00012041
66253	A_51_P168203	Aig1	androgen-induced 1	NM_025446	21.8	25.7	25.6	24.5	144.1	178.9	165.4	152.8	24.4	160.3	2.71412946	6.56197209	7.74E-06
208820	A_51_P296878	Gm11818	predicted gene 11818	NM_173746	35.6	41.5	37.7	36.5	295.6	249.8	239.7	212.4	37.825	249.375	2.71317406	6.55762798	2.58E-05
70237	A_55_P2019407	Bhlhb9	basic helix-loop-helix domain	NM_198161	5.2	8.9	10	11.5	64.3	52.2	46.6	61.8	8.9	56.225	2.70667768	6.5281657	0.01441204
74007	A_55_P2082434	Btbd11	BTB (POZ) domain containing	NM_028709	116.3	114	130.6	142.8	705.6	972.7	792.1	815.9	125.925	821.575	2.70222115	6.50803112	5.04E-05
78248	A_55_P2011220	Armcx1	armadillo repeat containing,	NM_001166377	98.5	106	113.5	108.5	683.6	759.4	616.6	705.4	106.625	691.25	2.69453541	6.47345274	4.15E-06
319164	A_55_P2084691	Hist1h2ac	histone cluster 1, H2ac	NM_178189	11.7	14.1	13.4	15.5	103.6	67.9	86.5	97.2	13.675	88.8	2.6883288	6.44566318	0.0002903
69655	A_55_P2181904	Cd164l2	CD164 sialomucin-like 2	NM_027152	2.8	5.7	7.2	5.1	25.7	38.5	31.8	31.7	5.2	31.925	2.68324147	6.42297407	0.04352675
67307	A_51_P165451	Pbld2	phenazine biosynthesis-like p	NM_026085	14.5	25.7	30.5	13.2	111	127	132.6	134.9	20.975	126.375	2.67872581	6.40290148	0.03664766
14570	A_51_P172085	Arhgdig	Rho GDP dissociation inhibito	NM_008113	37	30.2	32.3	31.7	274.4	206.7	172.9	194.8	32.8	212.2	2.67634299	6.39233489	0.00025145
66011	A_51_P413597	Ranbp17	RAN binding protein 17	NM_023146	2.6	2.1	2.5	2.6	16.6	16.6	22.3	9.2	2.45	16.175	2.65937192	6.31757951	0.01902598
171210	A_52_P525183	Acot2	acyl-CoA thioesterase 2	NM_134188	109	131.7	123.4	116	542.5	781.7	1170.3	658.9	120.025	788.35	2.65901338	6.31600967	0.00703666
17761	A_55_P1959903	Mtap7	microtubule-associated prote	NM_008635	22.2	26.7	22.7	25.7	164.9	154.2	145.7	138.4	24.325	150.8	2.63352282	6.20539403	8.49E-06
73061	A_55_P2017561	3110007F17Rik	RIKEN cDNA 3110007F17 gen	NM_028426	11.5	12.8	13.5	7.5	69.8	64.5	72.4	67.1	11.325	68.45	2.62978227	6.18932582	0.00154356
74100	A_52_P38208	Arpp21	cyclic AMP-regulated phosph	NM_028755	13.5	24.5	17.1	19.4	109.8	158.4	87.7	104.9	18.625	115.2	2.62750802	6.17957669	0.01053606
230904	A_55_P2092296	Fbxo2	F-box protein 2	NM_176848	99.5	102.4	80.7	99.4	560	618.9	537.1	633	95.5	587.25	2.62339672	6.16199163	1.75E-05
545652	A_55_P2141724	Gm13275	predicted gene 13275	NM_001085533	3.6	2.1	5.2	4.7	19.5	20.6	21.3	30.9	3.9	23.075	2.62068312	6.15041229	0.07375503
12653	A_51_P191669	Chgb	chromogranin B	NM_007694	13.2	10.4	10.8	9	52.2	52.6	77.2	89.2	10.85	67.8	2.61715187	6.13537647	0.00476126
434128	A_52_P642836	Pnmal2	PNMA-like 2	NM_001099636	2.6	2.1	3.4	2.7	20.4	12.5	17.6	15.5	2.7	16.5	2.60966454	6.10361745	0.00243705
12070	A_55_P2149615	Ngfrap1	nerve growth factor receptor	NM_009750	64.7	52.9	61.5	58.7	369	361.6	343.5	368.3	59.45	360.6	2.60398476	6.07963518	3.21E-06
74542	A_55_P2274134	9030625N01Rik	RIKEN cDNA 9030625N01 gen	AK035942	3.3	3.6	2.7	5.3	21.2	27.6	26.2	15.1	3.725	22.525	2.60278639	6.07458729	0.02649213
666060	A_55_P2039842	Frmpd1	FERM and PDZ domain contai	NM_001081172	18	12.2	10.9	20.5	94.6	79.4	77.6	113.9	15.4	91.375	2.6004754	6.06486443	0.0115207
26757	A_55_P1988413	Dpysl4	dihydropyrimidinase-like 4	NM_011993	24.1	37.4	29.8	36.4	199.2	179.1	184	201	31.925	190.825	2.59956861	6.06105363	0.00029686
50500	A_66_P128446	Ttpa	tocopherol (alpha) transfer pr	NM_015767	2.9	4.4	2.9	2.8	18.8	20.5	20.2	17.7	3.25	19.3	2.59428436	6.03889406	0.00045871
69772	A_55_P2119969	Bdh2	3-hydroxybutyrate dehydroge	NM_001172055	418.3	523.2	498.1	379.8	3098.6	2825.4	2537	2472.8	454.85	2733.45	2.59336932	6.03506502	0.00011001
73112	A_55_P2071271	3110003A17Rik	RIKEN cDNA 3110003A17 gen	NM_028440	201.7	224.7	211.6	194.4	1240.3	1515	1108.7	1179.3	208.1	1260.825	2.59098501	6.02509927	3.27E-05
225875	A_55_P2138878	Lrfn4	leucine rich repeat and fibron	NM_153388	372.8	383.6	321.9	400.2	2399.8	2012	2089.9	2372.1	369.625	2218.45	2.58587932	6.00381416	1.57E-05
20675	A_55_P2163353	Sox3	SRY-box containing gene 3	NM_009237	2.7	2.1	2.6	2.7	16.8	11.8	21.2	12.2	2.525	15.5	2.58277153	5.99089492	0.00407734
66865	A_55_P1992525	Pmpca	peptidase (mitochondrial pro	ENSMUST00000114093	10	9	13	5.6	73.5	44.1	48.3	53.1	9.4	54.75	2.57731267	5.96826946	0.04309933
22154	A_52_P163795	Tubb5	tubulin, beta 5 class I	NM_011655	4988	5286.5	4999.6	4627.9	32662.5	28229.8	27780.3	30221	4975.5	29723.4	2.57730884	5.96825362	3.45E-06
14635	A_51_P243304	Galk1	galactokinase 1	NM_016905	263.9	219.3	211.4	185.3	1449.8	1244.6	1262.3	1254.8	219.975	1302.875	2.57500632	5.95873594	5.87E-05
78255	A_51_P115817	Ralgps2	Ral GEF with PH domain and	NM_023884	9.5	12.4	11.8	13.4	82	69.2	63.1	65.3	11.775	69.9	2.57343989	5.95226966	0.00014302
100503637	A_55_P1954092	Gm19809	predicted gene, 19809	XM_003085330	10768.4	14404.1	12074.7	13872.5	73442.5	70604.7	71582.4	86494.5	12779.925	75531.025	2.56777353	5.92893727	6.04E-05
77411	A_55_P2013143	Esrp2	epithelial splicing regulatory	NM_176838	2.5	2.1	2.5	2.6	18.2	19.3	9.7	12.2	2.425	14.85	2.56260808	5.90774717	0.01059064
226123	A_55_P2058165	Morn4	MORN repeat containing 4	NM_198108	199.3	188.2	196.7	157.4	1079.8	1013.7	1141.4	1131.3	185.4	1091.55	2.56231311	5.90653939	1.22E-05
245020	A_55_P2089020	Tmem22	transmembrane protein 22	NM_001101483	19.5	17.5	17.4	17.6	109.8	131.9	82.7	105.7	18	107.525	2.56061946	5.89960947	0.00022221
20733	A_66_P124011	Spint2	serine protease inhibitor, Kun	NM_011464	103.4	112	113.7	91.3	604.5	613.5	627.6	607.3	105.1	613.225	2.54985162	5.85574048	5.61E-06
15468	A_55_P2083654	Prmt2	protein arginine N-methyltrar	NM_001077638	755.3	953.3	856.6	1217	5170.5	6038.5	5347.1	5106.8	945.55	5415.725	2.5373809	5.80534135	0.00041505
20276	A_51_P213691	Scnn1a	sodium channel, nonvoltage-g	NM_011324	8.5	8.8	8.4	10.8	57.3	51.1	46.2	56.9	9.125	52.875	2.5368943	5.80338364	4.99E-05
213011	A_55_P2113905	Zfp583	zinc finger protein 583	NM_001033249	3	6.2	2.8	4.1	16.5	28.1	26	19.6	4.025	22.55	2.52795809	5.76754794	0.0726218
67547	A_55_P2066309	Slc39a8	solute carrier family 39 (meta	NM_001135150	12.3	16.6	12	13.9	94.5	74.9	62	85.6	13.7	79.25	2.52679955	5.76291825	0.00076161
19652	A_51_P262340	Rbm3	RNA binding motif protein 3	NM_001166409	3412.5	3607.2	3479.3	3806.1	22402.5	19802	19662.2	20572.5	3576.275	20609.8	2.52608528	5.76006577	2.19E-06
319269	A_55_P1973347	A130040M12Rik	RIKEN cDNA A130040M12 ge	NR_002860	357	310.5	305	260.6	1766.2	1602.3	1688.9	1988.7	308.275	1761.525	2.51881282	5.73110299	5.86E-05
320869	A_52_P580533	4732415M23Rik	RIKEN cDNA 4732415M23 ge	NM_177279	7.8	17.1	13	18	72.4	71.3	78.2	83.4	13.975	76.325	2.51876422	5.73090992	0.03182171
18616	A_52_P235861	Peg3	paternally expressed 3	NM_008817	19.8	16.2	19.4	23.6	109.2	115.5	117.3	105.7	19.75	111.925	2.51410468	5.71243039	6.65E-05
18286	A_55_P1952414	Odf2	outer dense fiber of sperm ta	NM_001113214	138.4	160.7	170.4	149.8	877.6	999	951.7	723.5	154.825	887.95	2.51359282	5.71040399	8.56E-05
110877	A_55_P2107432	Slc18a1	solute carrier family 18 (vesic	NM_153054	52.9	41.4	54.3	28.9	160.2	251.7	305.2	292.7	44.375	252.45	2.50838732	5.68983698	0.05206527
69487	A_55_P2133546	2310003L22Rik	RIKEN cDNA 2310003L22 gen	ENSMUST00000028863	2.7	2.2	2.6	2.8	10.8	16.3	13.4	19.2	2.575	14.925	2.5081384	5.68885534	0.00221493
72040	A_52_P523445	Cdhr5	cadherin-related family mem	NM_028069	2.5	2.1	2.5	2.7	16.6	9.7	11.4	20.2	2.45	14.475	2.50778412	5.68745851	0.0158636
70546	A_51_P117226	Zdhhc2	zinc finger, DHHC domain con	ENSMUST00000049389	48.7	56.7	53.1	57.5	331.9	323	252.9	323.2	54	307.75	2.50536127	5.67791508	4.19E-05
66333	A_55_P1995507	Aqp11	aquaporin 11	NM_175105	56.6	65	71.8	61.8	348.8	328.7	372.4	386.4	63.8	359.075	2.4952499	5.63825957	1.54E-05
75404	A_55_P2129261	Arhgap36	Rho GTPase activating protei	NM_001081123	5.3	2.8	2.6	2.7	21.3	17.7	15.8	17.5	3.35	18.075	2.49167611	5.62430997	0.01964939
235300	A_66_P118772	Tmem136	transmembrane protein 136	NM_001034863	171.1	203.6	204.9	207.3	1144.2	1112.8	1035.2	1093.6	196.725	1096.45	2.4820058	5.58673659	6.57E-06
56454	A_51_P215887	Aldh18a1	aldehyde dehydrogenase 18 f	NM_019698	7.5	5.3	8.4	9.8	45.2	38.9	39.4	44.8	7.75	42.075	2.47236141	5.54951391	0.00269026
72852	A_55_P1988899	Mblac2	metallo-beta-lactamase doma	NM_028372	62	52.4	67.4	62.6	346.6	326.1	319.6	348	61.1	335.075	2.46022673	5.50303204	1.26E-05
107815	A_55_P2003803	Scml2	sex comb on midleg-like 2 (Dr	NM_133194	26.7	29.1	17.3	20.2	120.6	129	128.9	123.3	23.325	125.45	2.45768805	5.49335698	0.00124694
71213	A_55_P2185100	Cage1	cancer antigen 1	BC082568	4.5	10.7	6.7	10	43.8	38.1	39.3	43.7	7.975	41.225	2.44876094	5.45947014	0.05431014
319477	A_52_P622244	6030419C18Rik	RIKEN cDNA 6030419C18 gen	NM_176921	13.6	31.4	30.1	21.7	148.1	122.1	125.4	108.2	24.2	125.95	2.44518883	5.44596923	0.05519371
75697	A_51_P415395	C2cd4b	C2 calcium-dependent domai	NM_001081314	12	15.7	11.7	9.9	112.2	58.6	67.4	43.1	12.325	70.325	2.44338249	5.43915483	0.09754568
70857	A_55_P2190152	4921509J17Rik	RIKEN cDNA 4921509J17 gen	AK054449	3.1	7.1	5.4	7	27.6	30.4	30.8	28	5.65	29.2	2.44110189	5.43056346	0.04166326
231093	A_55_P2066750	Agbl5	ATP/GTP binding protein-like	NM_174849	10.7	7.3	11.6	11.6	55.5	55.8	45.2	65	10.3	55.375	2.43942165	5.4242424	0.00252389
432582	A_55_P2100088	E130309D14Rik	RIKEN cDNA E130309D14 gen	NM_001013784	2.6	3.9	3.4	2.6	15.4	19.8	19.1	13.3	3.125	16.9	2.43877748	5.42182099	0.00321349
67917	A_51_P479132	Zcchc3	zinc finger, CCHC domain con	NM_175126	14.9	25.4	14.9	14.9	83.5	83.9	92.2	109.8	17.525	92.35	2.4303136	5.39010585	0.00551428
230751	A_55_P1980601	Oscp1	organic solute carrier partner	NM_172701	290.8	265.6	351.7	267	1714.6	1476.6	1751.4	1372.8	293.775	1578.85	2.42825652	5.38242577	0.00015177
69976	A_55_P1977563	Galk2	galactokinase 2	NM_175154	44.7	42.7	37.9	34.4	240.8	218.3	177.1	223.4	39.925	214.9	2.426734	5.37674852	0.0001574
237052	A_51_P249930	Tceal1	transcription elongation facto	NM_146236	83.3	100.8	74.1	94.6	491.4	433.7	461.2	488.2	88.2	468.625	2.41777963	5.34348005	5.63E-05
230590	A_55_P2026609	Zyg11a	zyg-11 homolog A (C. elegans	NM_001167936	2.6	2.1	2.5	2.8	16.2	12.8	10.5	13.9	2.5	13.35	2.40726709	5.304685	0.00066919
216618	A_55_P2034720	Ccdc104	coiled-coil domain containing	NM_025740	932.1	1062.7	918.2	1020.4	5609.1	4760.3	4872.9	5565.5	983.35	5201.95	2.40195189	5.28517736	1.33E-05
99586	A_51_P473259	Dpyd	dihydropyrimidine dehydroge	NM_170778	95.1	145.8	112.2	97.9	461	567.7	700.1	633	112.75	590.45	2.39317515	5.25312221	0.00277784
627096	A_55_P2206254	LOC627096	uncharacterized LOC627096	AK147870	2.9	2.1	3.3	2.8	14.4	14.9	13.4	14.7	2.775	14.35	2.3882019	5.23504486	0.00035209
22153	A_51_P315795	Tubb4a	tubulin, beta 4A class IVA	NM_009451	89.3	96	123.5	98.2	517.5	478.8	542.6	574.4	101.75	528.325	2.38419561	5.22052758	9.70E-05
50773	A_55_P2038162	Nt5c	5,3-nucleotidase, cytosolic	NM_015807	807.1	875	920.3	906.8	4512.6	4552.8	4422.7	4792.2	877.3	4570.075	2.38228045	5.21360199	2.41E-06
67749	A_55_P2048759	4930583H14Rik	RIKEN cDNA 4930583H14 gen	NM_026358	15.9	22.3	13.8	23.4	115.2	95.9	89.5	84.4	18.85	96.25	2.37737076	5.19588953	0.00579309
67261	A_55_P2075258	2900005J15Rik	RIKEN cDNA 2900005J15 gen	ENSMUST00000128569	2.9	3.5	4.5	4.8	15.1	22.9	23.4	19.5	3.925	20.225	2.37280599	5.17947542	0.00903533
66569	A_52_P75465	Gdpd1	glycerophosphodiester phosp	NM_025638	491.6	463.5	374.1	534.4	2442.4	2135.1	2256.4	2781.3	465.9	2403.8	2.37217487	5.17721013	0.00030586
117109	A_55_P2133431	Pop5	processing of precursor 5, rib	NM_026398	2.7	4	3.9	5.5	15.5	28.6	18.2	20.6	4.025	20.725	2.37167835	5.17542861	0.05054583
12696	A_51_P272106	Cirbp	cold inducible RNA binding pr	NM_007705	2984.8	3420.9	3919.7	4050.5	19315.8	19371.8	18901.8	16410.1	3593.975	18499.875	2.37092651	5.17273222	0.0001037
71746	A_55_P2086825	Rgl3	ral guanine nucleotide dissoci	NM_023622	280.9	316.9	317.3	345.4	1502.7	1518.1	1747.2	1719.2	315.125	1621.8	2.36402962	5.14806269	1.86E-05
66931	A_51_P116687	1700010I14Rik	RIKEN cDNA 1700010I14 gen	NM_025851	6.4	8.2	6.6	7.2	30.1	36.5	35.3	44.9	7.1	36.7	2.3618993	5.14046654	0.00041165
71354	A_55_P2134218	Wdr31	WD repeat domain 31	NM_023597	11.4	8.4	9.4	9.9	59.1	43.3	47.5	50.7	9.775	50.15	2.35842757	5.12811127	0.00023857
224617	A_51_P154679	Tbc1d24	TBC1 domain family, member	NM_173186	10.4	10.3	12.8	15.9	69.4	85.8	50.6	49.3	12.35	63.775	2.35305998	5.10906742	0.01821655
73242	A_52_P480266	Atat1	alpha tubulin acetyltransferas	NM_028476	5.6	9.8	8.1	9	39.7	39.3	37.5	46	8.125	40.625	2.34846242	5.09281185	0.00299334
271813	A_52_P330359	Agbl2	ATP/GTP binding protein-like	NM_178755	2.6	2.2	2.4	3.5	10	17.9	12.4	14.3	2.675	13.65	2.34190569	5.06971867	0.012386
109900	A_51_P174645	Asl	argininosuccinate lyase	NM_133768	99.4	109.9	109.6	85.5	523	489.2	530	497.5	101.1	509.925	2.34104274	5.06668712	2.73E-05
75768	A_55_P2246665	4833422M21Rik	RIKEN cDNA 4833422M21 ge	AK014752	3.6	2.3	3.3	3.3	22.7	17.8	12.8	11.2	3.125	16.125	2.33184041	5.03447176	0.04496184
213121	A_51_P406466	Ankrd35	ankyrin repeat domain 35	NM_001081139	37.3	40.9	34.6	28.3	212	154	168.7	174.1	35.275	177.2	2.33155815	5.03348687	0.0006
245607	A_55_P2004213	Gprasp2	G protein-coupled receptor a	NM_001163015	104.4	165	97.3	196.1	729.1	614.6	694.8	676.4	140.7	678.725	2.33088748	5.03114746	0.0267113
77570	A_55_P1957213	3930401B19Rik	RIKEN cDNA 3930401B19 gen	AK019465	1378.6	1623.1	1402.9	1257.9	6102.3	6669.7	7058.2	8748.4	1415.625	7144.65	2.32847731	5.02274946	0.0003025
100503583	A_55_P2143085	Fsbp	fibrinogen silencer binding pr	ENSMUST00000095145	11	18.7	17.7	26.5	79.1	83.9	103.7	88.1	18.475	88.7	2.32388775	5.00679626	0.04873984
227960	A_51_P188126	Gca	grancalcin	NM_145523	37.4	31	33.4	39.4	151	178.6	182.3	194.6	35.3	176.625	2.32311727	5.00412305	9.19E-05
433809	A_66_P115693	Rnf207	ring finger protein 207	NM_001033489	8.5	9	9.4	10.5	48.5	41.4	47	50	9.35	46.725	2.32188768	4.99985994	2.67E-05
56527	A_55_P2177658	Mast1	microtubule associated serine	NM_019945	13.4	12	12.7	19.6	79.1	58.4	67.6	79.5	14.425	71.15	2.31916865	4.99044564	0.00374895
93887	A_55_P2072522	Pcdhb16	protocadherin beta 16	NM_053141	28	21.8	29.6	28.3	127.3	123.4	148.2	135.4	26.925	133.575	2.31697655	4.98286866	0.00012287
73390	A_55_P2081178	Msl3l2	male-specific lethal 3-like 2 (	NM_001163833	44.1	52.5	45.9	43.5	261.1	246.6	201.2	217.1	46.5	231.5	2.31221801	4.9664604	7.36E-05
72273	A_55_P2031403	2210404O07Rik	RIKEN cDNA 2210404O07 gen	AK030337	27.6	47.2	38	24.3	188.4	135.4	143.9	196.3	34.275	166	2.30661375	4.94720522	0.03205593
23992	A_51_P345836	Prkra	protein kinase, interferon ind	NM_011871	199.7	203.9	206.3	182.2	1063.7	909.3	1005.3	937.7	198.025	979	2.30462337	4.94038466	7.57E-06
668311	A_66_P135435	Gm9099	predicted gene 9099	AK080358	3.5	2.3	3	3.1	15.3	10.7	20.1	13.2	2.975	14.825	2.29509219	4.90785352	0.01504635
216856	A_55_P1960989	Nlgn2	neuroligin 2	NM_198862	389	402.2	409.2	459.9	2091	2072.4	1922.7	2024.1	415.075	2027.55	2.29045315	4.89209747	5.65E-06
269695	A_55_P2028883	Rnft2	ring finger protein, transmem	NM_172998	137.5	112.5	120.7	109.5	616.2	600.5	509.3	619.6	120.05	586.4	2.28942566	4.88861454	5.68E-05
74241	A_55_P2118268	Chpf	chondroitin polymerizing fact	NM_001001565	990.7	1151.4	848.8	905.7	4406.9	4895.2	4441.7	5222.7	974.15	4741.625	2.28913219	4.88762022	0.00011247
76132	A_55_P1997081	6230409E13Rik	RIKEN cDNA 6230409E13 gen	NM_175234	2.8	2.2	2.6	2.9	13.7	18.4	14.2	7.4	2.625	13.425	2.28889682	4.88682289	0.08565319
78282	A_55_P2241488	5330439K02Rik	RIKEN cDNA 5330439K02 gen	AK019939	11.6	6	14.5	10.6	48.5	39.8	55.3	55.8	10.675	49.85	2.28025535	4.85763924	0.09125994
69349	A_55_P2182001	1700008O03Rik	RIKEN cDNA 1700008O03 gen	NM_027049	13.1	10.5	10.2	7	45.4	47.1	45.9	55.7	10.2	48.525	2.28015968	4.85731712	0.00571158
67564	A_51_P171107	Tmem35	transmembrane protein 35	NM_026239	27.5	35	24.4	31	137.5	181.1	110.6	146	29.475	143.8	2.2773286	4.84779469	0.00320725
54646	A_55_P2029622	Ppp1r3f	protein phosphatase 1, regula	NM_138605	41.1	36.1	31.4	43.7	188.4	151.6	199.1	195.4	38.075	183.625	2.27304243	4.83341352	0.0004756
19369	A_55_P2091928	Raet1b	retinoic acid early transcript	NM_009017	13.2	22.2	25.8	28.1	93.8	104.4	102.8	112.1	22.325	103.275	2.26327041	4.80078529	0.0308652
50782	A_55_P2000354	Rgs11	regulator of G-protein signali	NM_001081069	43.9	83.9	66	71.4	301.1	364.4	267.1	308.3	66.3	310.225	2.25597777	4.77657913	0.01222642
76843	A_55_P2164534	Dtl	denticleless homolog (Drosop	NM_029766	3.4	4.8	3.2	2.9	19.9	18.8	17.7	11.9	3.575	17.075	2.25580761	4.77601581	0.01775004
229524	A_55_P2102424	Msto1	misato homolog 1 (Drosophila	NM_144898	404.7	409.4	349.6	387	1871.4	1811	1854.2	1792.9	387.675	1832.375	2.24332652	4.73487559	4.91E-06
243725	A_52_P239536	Ppp1r9a	protein phosphatase 1, regula	NM_181595	169.6	223.7	194	157.3	955.2	849.6	824.6	868.1	186.15	874.375	2.24271639	4.73287359	0.00021164
242681	A_52_P272119	Rab42-ps	RAB42, member RAS oncoger	NM_001081651	28.4	25.5	22.9	22.4	111.6	111.2	114.3	131.3	24.8	117.1	2.242416	4.73188825	5.9215E-05
72029	A_55_P2007636	Cnpy3	canopy 3 homolog (zebrafish)	ENSMUST00000121671	20.5	9	9.1	11.1	55	53.6	59.1	53.6	12.425	55.325	2.2422342	4.731292	0.07615997
207921	A_55_P2081697	A830093I24Rik	RIKEN cDNA A830093I24 gen	NM_175431	22.5	25.8	17.2	18.3	105.1	82.1	124.8	84.5	20.95	99.125	2.24000552	4.72398872	0.00573797
66039	A_55_P1967553	D14Ertd449e	DNA segment, Chr 14, ERATO	NM_026679	35.9	33	37.3	18.7	142	149.1	143.5	134.5	31.225	142.275	2.23746918	4.71569097	0.02141367
106759	A_51_P294020	Ticam1	toll-like receptor adaptor mol	NM_174989	62.4	70.1	50.6	43.4	242	257.8	285	264.5	56.625	262.325	2.23385211	4.70388278	0.00150172
72480	A_51_P257675	Tspyl4	TSPY-like 4	NM_030203	109.4	115.2	100	98.3	490	453.5	489.4	556.1	105.725	497.25	2.23280649	4.70047479	2.52E-05
223918	A_55_P2101862	Spryd3	SPRY domain containing 3	NM_001033277	202.4	199.2	180.9	174.2	976.6	849.4	820.5	910.7	189.175	889.3	2.23258178	4.69974273	1.90E-05
231642	A_55_P2037186	Alkbh2	alkB, alkylation repair homolo	NM_175016	109.3	130.6	125.9	108.6	556.6	533.5	539.2	592	118.6	555.325	2.23094904	4.6944269	1.90E-05
66311	A_52_P609024	Cenpw	centromere protein W	NM_001109747	93.3	94.2	75.9	72.8	435.7	365	401.4	367.6	84.05	392.425	2.22911972	4.68847817	0.00016011
269952	A_52_P443544	D330012F22Rik	RIKEN cDNA D330012F22 gen	NM_178752	12.9	11.8	8.5	8.2	38.3	76.6	42.6	40.9	10.35	49.6	2.22806364	4.6850474	0.08610092
96957	A_66_P113662	Tmem62	transmembrane protein 62	NM_175285	40.4	51.7	55.2	59.2	218.7	214.4	273.3	251.7	51.625	239.525	2.22109404	4.6624687	0.00078513
54651	A_55_P1999691	Usp27x	ubiquitin specific peptidase 2	ENSMUST00000134976	2.9	3.8	2.8	5.8	15.3	14.9	18.3	20.1	3.825	17.15	2.21801587	4.65253133	0.05300863
11983	A_51_P518488	Atpif1	ATPase inhibitory factor 1	NM_007512	5771.4	6698.1	5779.2	5824	28028.1	28598.1	27417.1	27656.4	6018.175	27924.925	2.2169104	4.64896769	5.49E-06
12578	A_55_P2008437	Cdkn2a	cyclin-dependent kinase inhib	NM_009877	6.8	8.9	4.7	8.1	40.9	33.5	34.3	22.8	7.125	32.875	2.21532349	4.64385682	0.06275275
56520	A_51_P164203	Nme4	non-metastatic cells 4, protei	NM_019731	229.6	232.9	291.3	219.8	983.4	1090.5	1275.6	1144.3	243.4	1123.45	2.20916584	4.62407835	0.00022704
232970	A_66_P129622	Phldb3	pleckstrin homology-like dom	NM_001102613	80.6	101.1	95.6	84	440	389	451.2	386.2	90.325	416.6	2.2080526	4.62051161	6.52E-05

50788	A_51_P120254	Fbxl8	F-box and leucine-rich repeat	NM_015821	45.2	57.7	49	48.9	230.1	190.8	220.9	289.3	50.2	232.775	2.20262099	4.60314852	0.00078474
66236	A_51_P407999	1500011B03Rik	RIKEN cDNA 1500011B03 gen	NR_027817	84.6	105.6	114.9	87.4	419.6	450.2	500.4	420.2	98.125	447.6	2.19757883	4.58708876	0.00026601
67416	A_55_P2012221	Armcx2	armadillo repeat containing, X	NM_026139	312.5	375.5	332	458.6	1582.3	2057.2	1662.9	1460.2	369.65	1690.65	2.19729908	4.58619938	0.00169339
21414	A_52_P244702	Tcf7	transcription factor 7, T-cell s	NM_009331	6.4	5.8	6.5	5	20.6	27.8	32.9	28.1	5.925	27.35	2.19440167	4.57699804	0.00205113
78479	A_66_P102265	1700119I11Rik	RIKEN cDNA 1700119I11 gene	AK018965	2.6	2	3.5	3.6	15	11.7	14.5	11.2	2.925	13.1	2.1912179	4.56690854	0.01965582
104362	A_55_P2093705	Meig1	meiosis expressed gene 1	NM_008579	2.5	3.1	2.8	2.7	16.9	12.6	14.4	8.3	2.775	13.05	2.19070722	4.56529225	0.02114182
208691	A_52_P181759	Eif5a2	eukaryotic translation initiatio	NM_177586	77.6	82	69.1	82.9	395.2	367.4	338.6	320.9	77.9	355.525	2.18940359	4.56116887	4.60E-05
102442	A_51_P468240	Dennd4a	DENN/MADD domain contain	NM_001162917	35.8	37.1	34.7	47.8	173.6	171.4	182.9	174.8	38.85	175.675	2.18857041	4.5585355	0.00012743
214158	A_66_P110167	Trim38	tripartite motif-containing 38	NM_001029935	2.8	2.3	2.7	3	8.2	18.4	14.7	9.9	2.7	12.8	2.17936199	4.52953197	0.08499397
666244	A_55_P2008889	Tmsb15b1	thymosin beta 15b1	NM_001080967	588.9	646.9	536.7	573.4	2670	2614.9	2490	2838.4	586.475	2653.325	2.17932709	4.52942242	1.40E-05
213989	A_52_P112110	Tmem82	transmembrane protein 82	NM_145987	29.6	41	25.2	38.4	153.5	136.6	146	160.9	33.55	149.25	2.17807252	4.52548533	0.00275802
18124	A_51_P128397	Nr4a3	nuclear receptor subfamily 4,	NM_015743	3.1	2.6	3.3	3	13.8	15.6	15.3	10.1	3	13.7	2.17590131	4.51867975	0.00189627
269702	A_52_P569794	Mphosph9	M-phase phosphoprotein 9	NM_001081323	13	13.8	18.2	20.5	71.6	80.9	67.7	70.5	16.375	72.675	2.17253403	4.50814536	0.00233421
228550	A_51_P273609	Itpka	inositol 1,4,5-trisphosphate 3	NM_146125	17.3	26.7	34.5	18.3	104.7	114.2	104.4	96.1	24.2	104.85	2.17105368	4.50352192	0.03267457
93878	A_51_P184223	Pcdhb7	protocadherin beta 7	NM_053132	15.6	19.2	25.5	18.4	96.2	80.1	103.3	69.6	19.675	87.3	2.15570986	4.45587839	0.00776183
17087	A_51_P476601	Ly96	lymphocyte antigen 96	NM_016923	257.3	242.6	274.9	247.2	1072.8	1121.6	1163.8	1167.3	255.5	1131.375	2.14751341	4.43063479	5.27E-06
269717	A_55_P2066543	Orai2	ORAI calcium release-activate	NM_178751	77	84	100.3	93.3	479.5	465.4	326.5	319.3	88.65	397.675	2.14658385	4.42778094	0.00432745
17962	A_55_P2063770	Nat3	N-acetyltransferase 3	NM_008674	2.8	3.7	2.7	2.7	17.9	10.9	10.9	13.6	2.975	13.325	2.14526599	4.42373816	0.01022381
623474	A_52_P502771	Rad54b	RAD54 homolog B (S. cerevisi	NM_001039556	3.2	3.5	5.2	4.2	16.6	16.4	19	17.9	4.025	17.475	2.14105567	4.41084684	0.00219929
76787	A_55_P2101367	Ppfia3	protein tyrosine phosphatase	NM_029741	15.4	15.8	19	20.2	82.1	73.8	72.7	79.2	17.6	76.95	2.1363123	4.39636846	0.00013845
67103	A_51_P444437	Ptgr1	prostaglandin reductase 1	NM_025968	192.3	310.9	263.1	268.6	1205.2	1187.8	974.1	1114.6	258.725	1120.425	2.1307662	4.3795001	0.00220211
78889	A_51_P271370	Wsb1	WD repeat and SOCS box-con	NM_001042565	28.6	30.5	37.5	35	140.4	131.5	176.3	128.7	32.9	144.225	2.12882318	4.37360577	0.00072514
67326	A_51_P221632	1700037H04Rik	RIKEN cDNA 1700037H04 gen	NM_026091	568.8	561.7	567.6	532.3	2437.9	2386.5	2428.7	2498.9	557.6	2438	2.12872243	4.37330033	1.93E-06
100038388	A_55_P2183513	Gm10614	predicted gene 10614	ENSMUST00000098354	3.5	6.1	4.7	3.5	17.6	19.8	15.9	23.1	4.45	19.1	2.127382	4.36923894	0.02354267
114679	A_52_P357133	Selm	selenoprotein M	NM_053267	1252.9	1299.8	989.1	1120.7	5765.9	4708.2	4678.3	5179.3	1165.625	5082.925	2.12732839	4.36907658	0.00022203
16156	A_51_P267783	Il11	interleukin 11	NM_008350	20.5	11.1	14.3	16.2	80.4	57.6	61.8	66.9	15.525	66.675	2.1261712	4.36557354	0.01511952
102941	A_51_P513062	B630019K06Rik	novel protein similar to F-box	NM_175327	21.1	32	26.9	24.3	108	124.9	110.4	107.1	26.075	112.6	2.12433461	4.36001956	0.00071673
237339	A_55_P2011116	L3mbtl3	l(3)mbt-like 3 (Drosophila)	NM_172787	127.3	134.7	146.6	127	646.7	568.8	593.1	526.8	133.9	583.85	2.12296323	4.35587704	3.14E-05
69590	A_51_P495232	Gpx8	glutathione peroxidase 8 (put	NM_027127	697.1	749.9	695.6	688.5	2779.3	3166.7	3252.7	3130.7	707.775	3082.35	2.12093969	4.34977171	9.426E-06
52430	A_55_P2142451	Echdc2	enoyl Coenzyme A hydratase	NM_026728	2208.4	2477.9	2467.3	2705.1	10934.9	10572.5	11056.4	10007.7	2464.675	10642.875	2.11305665	4.32606891	1.77E-05
14809	A_51_P428754	Grik5	glutamate receptor, ionotrop	NM_008168	44.8	43.5	49.4	53.2	237.1	209	180.2	200.8	47.725	206.775	2.11290446	4.32561259	0.00015098
16815	A_51_P165602	Lbx2	ladybird homeobox homolog	NM_010692	102	72.9	97.9	78.9	351.2	407.6	400.4	348.6	87.925	376.95	2.1106059	4.31872633	0.00061403
22143	A_55_P2154132	Tuba1b	tubulin, alpha 1B	NM_011654	9939.3	11665.4	9591.1	13403.5	50668.6	48875.7	43377.8	48024.9	11149.825	47736.75	2.10877973	4.31326314	0.00035572
269209	A_55_P2036733	Stk36	serine/threonine kinase 36 (fu	NM_175031	14.4	16.1	18.7	12.5	64.1	66	73	60.5	15.425	65.9	2.10738153	4.30908492	0.0007278
27392	A_52_P275805	Pign	phosphatidylinositol glycan an	NM_013784	3	4.2	2.7	2.9	16.8	13.7	12.2	12	3.2	13.675	2.10397523	4.29892288	0.00527128
67621	A_51_P158018	Bend5	BEN domain containing 5	NM_026279	46.5	67.7	32	52.7	228.8	230.9	177.7	192.7	49.725	207.525	2.10315161	4.29646937	0.04542305
319188	A_66_P101132	Hist1h2bp	histone cluster 1, H2bp	NM_178202	8.5	7.1	8.1	8	38.7	27.6	33.7	36.2	7.925	34.05	2.09506218	4.27244578	0.00033357
17918	A_55_P2006250	Myo5a	myosin VA	NM_010864	497.4	578.6	462.5	472	2285.7	2075.5	2033	2162.4	502.625	2139.15	2.09370949	4.26844174	4.30E-05
69716	A_51_P105709	Trip13	thyroid hormone receptor int	NM_027182	21.4	19.8	20.4	15.6	77.1	83.3	87.3	79.1	19.3	81.7	2.09037007	4.25857298	0.00020147
93892	A_51_P317181	Pcdhb21	protocadherin beta 21	NM_053146	140.8	129.3	172.7	188.9	741.1	608.6	657.3	645.4	157.925	663.1	2.08291193	4.23661471	0.00099797
100049077	A_55_P2256148	LOC100049077	uncharacterized LOC1000490	AK014010	9.4	16.5	13.1	12.9	61.1	54.8	52.5	47.8	12.975	54.05	2.08113494	4.23139961	0.00614714
230157	A_55_P1972575	Tmeff1	transmembrane protein with	NM_021436	26.4	45.1	48.4	52.1	174.4	217.8	163.3	155	43	177.625	2.0807384	4.23023673	0.05521561
13726	A_55_P1984337	Emd	emerin	NM_007927	1932.5	2103.2	1725.6	1484.5	7395.4	5550.9	8304.7	9632.6	1811.45	7720.9	2.07526839	4.21422806	0.0124373
22690	A_55_P2102887	Zfp28	zinc finger protein 28	M36516	52.5	48.4	56.7	51.6	212.7	220.2	223.1	217.7	52.3	218.425	2.06433363	4.1824075	7.21E-06
237411	A_52_P405876	Zfp938	zinc finger protein 938	NM_001105557	30.2	35.7	35	30.6	121.3	158.7	141.4	129.3	32.875	137.675	2.06293481	4.17835425	0.00018117
654803	A_55_P2344943	B130055M24Rik	RIKEN cDNA B130055M24 ger	XR_107952	51	39.9	46.5	45.2	206.1	150.2	209.3	200.4	45.65	191.5	2.06148926	4.17416971	0.00084326
18481	A_55_P2022569	Pak3	p21 protein (Cdc42/Rac)-activ	NM_001195049	15.8	21.9	15.5	17.5	74.7	90.4	71.1	59.3	17.675	73.875	2.06120853	4.17335755	0.00398951
212933	A_55_P2159585	Pm20d1	peptidase M20 domain conta	NM_178079	8.3	12.9	7.5	13.2	41	46.2	36.4	45.5	10.475	42.275	2.05231675	4.14771497	0.03226607
79043	A_52_P65719	Spsb3	splA/ryanodine receptor dom	BC034637	83.2	104.3	93.9	79.3	311.4	372.7	504.5	326.5	90.175	378.775	2.05218415	4.14733375	0.00636097
72495	A_55_P2082418	2610206C17Rik	RIKEN cDNA 2610206C17 gen	ENSMUST00000129059	11.2	8.1	7.1	9.7	33	34	37.1	44.4	9.025	37.125	2.05213488	4.1471921	0.00488022
260305	A_55_P2137586	Nphp4	nephronophthisis 4 (juvenile)	NM_153424	67.9	56.3	57	58.1	260.2	223.9	254.2	252.5	59.825	247.7	2.05159718	4.14564671	4.4068E-05
66515	A_51_P293753	Cul7	cullin 7	NM_025611	1281.6	966	1189.3	1097.4	4452.2	5130.8	4589.1	4493.6	1133.575	4666.425	2.04688546	4.13212947	0.0001388
105727	A_51_P507053	Slc38a1	solute carrier family 38, mem	NM_134086	74.5	88.6	47.7	62.1	254.4	340.5	270.9	239.3	68.225	276.275	2.04147924	4.11667411	0.02843714
228482	A_55_P2103796	Arhgap11a	Rho GTPase activating protein	NM_181416	12.4	8.3	9.6	7.9	35.8	44.5	34.5	39.8	9.55	38.65	2.03264387	4.09153976	0.00416056
22693	A_55_P2008790	Zfp30	zinc finger protein 30	NM_013705	132.5	148.3	122.7	169.8	536.5	492.2	607.6	711.1	143.325	586.85	2.03062862	4.08582842	0.00231608
93888	A_51_P337771	Pcdhb17	protocadherin beta 17	NM_053142	108.6	127.1	97.4	139	433	525.3	440.3	505	118.025	475.9	2.02005304	4.05598702	0.00096618
73447	A_51_P458218	Wdr13	WD repeat domain 13	NM_026137	744.2	867	950.6	919.5	3643.9	3353.6	3361.3	3622.1	870.325	3495.225	2.01083542	4.03015527	7.03E-05
269224	A_51_P223709	Pask	PAS domain containing serine	NM_080850	17.2	14.4	19.3	19.8	78.6	68.9	67.3	68.2	17.675	70.75	2.00920822	4.02561226	0.00041939
241727	A_55_P1984815	Snph	syntaphilin	NM_198214	213.2	181.6	153.7	173.3	776.3	657	668.9	793.2	180.45	723.85	2.00890561	4.02476795	0.00051058
52463	A_55_P2122997	Tet1	tet oncogene 1	NM_027384	51.7	44.5	39.3	42.2	209.1	161.8	157	187.4	44.425	178.825	2.00681516	4.01894033	0.00073731
71846	A_51_P273538	Syce2	synaptonemal complex centra	NM_027954	61.4	68.1	54.3	62.6	256.6	263.5	244.4	222.6	61.6	246.775	2.00393152	4.01091535	7.77E-05
17242	A_55_P1971897	Mdk	midkine	NM_010784	58.1	52.6	48.6	54.3	220.8	234	193.1	208.4	53.4	214.075	2.00253876	4.00704514	5.40E-05
223513	A_66_P132070	Abra	actin-binding Rho activating p	NM_175456	3310.4	4129.5	3572.5	3689	14370.6	14678.3	15576.2	14021.4	3675.35	14661.625	1.99958871	3.99885981	3.83E-05
237253	A_51_P295237	Lrp11	low density lipoprotein recep	NM_172784	62.8	62	64.8	61.4	225.3	246	243.1	293.5	62.75	251.975	1.99896579	3.99713359	6.42E-05
71233	A_51_P131164	Enkur	enkurin, TRPC channel interac	NM_027728	11.1	15.1	18.6	12.3	57.7	49.2	61.2	56.1	14.275	56.05	1.99742322	3.99286204	0.0072509
214345	A_51_P194306	Lrrc1	leucine rich repeat containing	NM_172528	59.4	70.1	68.5	54.3	255.9	249	246	250.4	63.075	250.325	1.9963494	3.98989117	8.98E-05
96935	A_55_P1954393	Susd4	sushi domain containing 4	NM_144796	47.6	46	49.4	52.2	236.6	203.2	161.8	183.9	48.8	196.375	1.99625991	3.98964371	0.00058376
414072	A_55_P2417961	BC031361	cDNA sequence BC031361	NR_033221	35.8	34.1	30.8	21.6	128.4	109.7	105	136.8	30.575	119.975	1.99017142	3.972842	0.01099851
72749	A_51_P497402	Tonsl	tonsoku-like, DNA repair prot	NM_183091	46.4	42.5	36	42.4	185.1	155.1	145.2	179.2	41.825	166.15	1.98879481	3.96905295	0.00037491
214931	A_52_P49457	Fbxl16	F-box and leucine-rich repeat	NM_001164225	314.4	308.2	348	307.7	1264	1151.9	1274.4	1379	319.575	1267.325	1.98652128	3.96280308	2.85E-05
15504	A_55_P1976237	Dnajb3	DnaJ (Hsp40) homolog, subfa	NM_008299	7.8	6.5	7.6	6.2	31.3	29.1	22	29.4	7.025	27.95	1.9865081	3.96276688	0.00144577
56386	A_66_P112816	B4galt6	UDP-Gal:betaGlcNAc beta 1,4	NM_019737	114.3	117.5	91.2	96.2	401.9	433.7	444.7	374.6	104.8	413.725	1.98625416	3.96206942	0.00026288
72205	A_55_P1989921	Eml2	echinoderm microtubule asso	NM_028153	2659.6	2138.7	3100.1	3434.3	12016	10997.6	10519.4	10512	2833.175	11011.25	1.9786683	3.94129106	0.00303742
18227	A_55_P1983508	Nr4a2	nuclear receptor subfamily 4,	NM_013613	41	54.1	44.3	49.6	222.9	185.3	182.4	154	47.25	186.15	1.97377716	3.92795162	0.00155605
216543	A_66_P102076	Cep68	centrosomal protein 68	ENSMUST00000109596	412.4	414.4	466	427.7	1710.5	1507.7	1706.7	1832.5	430.125	1689.35	1.97187627	3.92277956	3.73E-05
108159	A_51_P198137	Ubxn8	UBX domain protein 8	NM_178648	63.6	46.2	65.8	49.5	214.7	224.5	227.2	205.8	56.275	218.05	1.96988003	3.91735541	0.00105985
232875	A_52_P427818	Zscan18	zinc finger and SCAN domain	NM_001017955	50.5	64.5	36.6	60	206.2	211.5	209	183.9	52.9	202.65	1.96811253	3.91255905	0.01196435
239827	A_51_P285669	Pigz	phosphatidylinositol glycan an	NM_172822	54.3	84	72.7	72.8	258.8	284.8	279.6	273.8	70.95	274.25	1.96718765	3.91005162	0.00127515
14163	A_52_P428521	Fgd1	FYVE, RhoGEF and PH domain	NM_008001	10.5	10	10.9	13.6	38	46.1	35.6	57.7	11.25	44.35	1.96322265	3.89932027	0.01089324
19364	A_55_P1982593	Rad51l3	RAD51-like 3 (S. cerevisiae)	NM_011235	29.7	27.9	27.4	26.5	97.8	112.1	107.4	117	27.875	108.575	1.95975281	3.88995324	2.71E-05
80884	A_55_P2093994	Maged2	melanoma antigen, family D,	NM_030700	1632.7	1500.5	1354.8	1225.3	5618	6025.7	5234.6	5192.9	1428.325	5517.8	1.95547181	3.87842745	0.00024586
634012	A_55_P2019118	LOC634012	ubiquitin-conjugating enzyme	XM_003086823	16.2	12.3	10.8	23.1	51.4	64.2	59.7	56.7	15.6	58	1.95296126	3.87168414	0.0977133
241289	A_55_P1999473	Ppp1r26	protein phosphatase 1, regula	NM_001005420	140.9	159.3	112.5	204.9	679.9	455.3	533.2	703.4	154.4	592.95	1.95247482	3.87037893	0.05945582
233280	A_51_P122035	Nipa1	non imprinted in Prader-Willi	NM_153578	311.9	305.7	329.1	379.4	1284.2	1185.4	1211.8	1431.6	331.525	1278.25	1.94832262	3.85925567	0.00014527
240261	A_55_P2181149	Ccdc112	coiled-coil domain containing	NM_001160399	12.4	13.9	12.8	11.4	51.1	51.6	41.9	50.4	12.625	48.75	1.94761642	3.85736703	0.0001436
66190	A_51_P130757	Acer3	alkaline ceramidase 3	NM_025408	82.7	92.6	78.5	89.8	327.4	405.2	298.9	301.1	85.9	333.15	1.94724971	3.85638667	0.00051677
319996	A_55_P1994020	Casc4	cancer susceptibility candidat	NM_177054	151.7	189.9	195	179.1	649.2	818.4	717.4	577.1	178.925	690.525	1.94309194	3.84528876	0.00133709
29809	A_55_P2002819	Rabgap1l	RAB GTPase activating protein	NM_013862	121.2	117.5	101.1	120.2	457.5	389.7	448.3	471.2	115	441.675	1.94141734	3.84082795	0.00010213
57342	A_55_P2130890	Parva	parvin, alpha	NM_020606	49.8	65.2	69.5	67.1	208.9	248.5	280.3	225.9	62.9	240.9	1.94052082	3.83844193	0.00203423
69221	A_66_P111430	2410006H16Rik	RIKEN cDNA 2410006H16 gen	NR_030738	1788.8	1496.1	2492.1	1895.2	7498	6932.3	8310.2	6319.7	1918.05	7265.05	1.93866711	3.83351309	0.00789558
319728	A_55_P2336623	E030042N06Rik	RIKEN cDNA E030042N06 gen	AK087301	34.7	27.6	34.7	30.4	128.6	107.6	128.3	122.6	31.85	121.775	1.93778758	3.83117674	0.00023308
209645	A_52_P50287	Bend7	BEN domain containing 7	NM_178663	9.1	9.4	8.9	7.6	41.5	25	34.6	34.2	8.75	33.825	1.93229703	3.81662391	0.00591456
666938	A_55_P2199118	Bend4	BEN domain containing 4	NM_001164806	54	45.9	44.8	53.8	228.5	180.1	207	147.9	49.625	190.875	1.93009977	3.81081552	0.00351704
207742	A_55_P2079619	Rnf43	ring finger protein 43	NM_172448	27.7	23	28.2	21.1	88.7	92.3	80.9	119.4	25	95.325	1.92616935	3.80044761	0.00424554
68789	A_55_P2007566	Trmt61b	tRNA methyltransferase 61 ho	NR_027952	104.4	104.4	95.3	85.8	304	324.8	404.4	465.2	97.475	374.6	1.92585399	3.79961696	0.00406572
664862	A_55_P2187121	Gpr137b-ps	G protein-coupled receptor 1	NR_003568	109.9	120.6	101.8	122.9	381.9	432.8	392.5	531.7	113.8	434.725	1.92513919	3.79773487	0.00091354
194309	A_55_P2064074	Vps37d	vacuolar protein sorting 37D (	NM_001199677	148.7	136.8	168.7	119.5	517.8	601.3	549.8	497.2	143.425	541.525	1.92431741	3.79557225	0.00071265
106052	A_51_P490257	Fbxo4	F-box protein 4	NM_134099	513.5	603.9	539.4	529.4	2236.7	2121	1892.1	2037.5	546.55	2071.825	1.92255737	3.7909446	4.74E-05
75210	A_55_P2161775	Prr3	proline-rich polypeptide 3	NM_145487	76.4	105	84	78.9	342.3	328.5	274.6	354.1	86.075	324.875	1.92101271	3.78688788	0.00128898
670198	A_55_P2157620	Gm10734	predicted gene 10734	ENSMUST00000099155	93.3	108.8	110.1	106.1	346.6	366.3	437.8	435.7	104.575	396.6	1.91850944	3.78032282	0.00027907
217887	A_51_P370510	BC022687	cDNA sequence BC022687	NM_145450	18.5	18	12	18.3	64.2	65.4	66.9	53.1	16.7	62.4	1.91804544	3.7791072	0.00728829
12530	A_65_P05252	Cdc25a	cell division cycle 25 homolog	NM_007658	472.6	473.8	466.5	489	1973.5	1657.4	1823.6	1744.4	475.475	1799.725	1.91757539	3.77787611	1.8025E-05
66848	A_55_P2102529	Fuca2	fucosidase, alpha-L- 2, plasma	NM_025799	30.9	26.7	30.3	30.9	134.4	121.4	86.8	110.4	29.7	113.25	1.91528746	3.77188963	0.0023852
68813	A_52_P88983	Dock5	dedicator of cytokinesis 5	NM_177780	41.2	50.1	45.4	61.3	185.8	172.3	188.5	192.6	49.5	184.8	1.91513087	3.77148026	0.00106433
71567	A_52_P82660	Mcm9	minichromosome maintenanc	ENSMUST00000075540	11.9	18.2	8.7	12.9	40.1	53.9	51.8	43.9	12.925	47.425	1.91492554	3.77094351	0.08313525
19106	A_52_P559919	Eif2ak2	eukaryotic translation initiatio	NM_011163	95	81.5	94.9	63.2	420.1	276.5	294.9	271.1	83.65	315.65	1.91092884	3.76051132	0.02572506
66049	A_52_P303077	Rogdi	rogdi homolog (Drosophila)	NM_133185	37.2	39.2	39.1	37.3	145.1	136.6	136.8	155.8	38.2	143.575	1.90849508	3.75417287	1.34E-05
329384	A_52_P605812	Ptrh1	peptidyl-tRNA hydrolase 1 ho	NM_178595	316.3	383.9	349.4	336.6	1130.2	1454.6	1302.5	1312	346.55	1299.825	1.90500629	3.74510531	0.00019457
56717	A_52_P67643	Mtor	mechanistic target of rapamy	ENSMUST00000123566	63.9	60.8	82.2	63.3	263.2	250.3	268.9	224.4	67.55	251.7	1.90486036	3.74472652	0.00058762
380712	A_66_P116326	Tlcd2	TLC domain containing 2	AK008522	95.9	128.7	111.1	150.4	447.6	461	466.5	420.7	121.525	448.95	1.90434188	3.74338097	0.00241054
83924	A_55_P2066299	Gpr137b	G protein-coupled receptor 1	NM_031999	55.3	69.6	61.1	71	240.6	231.3	286.9	204.9	64.25	240.925	1.90355601	3.74134242	0.00136188
20646	A_55_P1998194	Snrpn	small nuclear ribonucleoprote	NM_001082962	235	223.8	274	298.4	976.8	948.6	905.9	1002.4	257.8	958.425	1.90307677	3.7400998	0.00028097
110350	A_52_P102783	Dync2h1	dynein cytoplasmic 2 heavy c	NM_029851	144	135.9	123.2	129.7	487.7	481.5	510.4	507.6	133.2	496.8	1.90101379	3.73475548	1.63E-05
494468	A_52_P114282	Armcx5	armadillo repeat containing, X	NM_001009575	260.2	252.7	282.4	304.3	1044.1	1036.4	1077.1	938.7	274.9	1024.075	1.8992901	3.73029597	5.95E-05
79059	A_51_P395111	Nme3	non-metastatic cells 3, protei	NM_019730	1214.6	1036.7	1068.3	1131.4	4225.7	3892.9	4261.8	4194.3	1112.75	4143.675	1.89850573	3.72826842	2.37E-05
69928	A_51_P270519	Apitd1	apoptosis-inducing, TAF9-like	NM_027263	6.2	4.7	4	6.3	21.7	14.9	22.4	19	5.3	19.5	1.88748428	3.69989486	0.03429394
73916	A_51_P511482	Ift57	intraflagellar transport 57 hor	NM_028680	534.7	558.8	681.3	571.4	2169.7	2179.3	2256.6	2025.6	586.55	2157.8	1.88442996	3.69207014	0.00010881
93734	A_51_P352738	Mpv17l	Mpv17 transgene, kidney dise	NM_033564	19.4	19	21.8	25.4	85.1	77.9	83.2	68.6	21.4	78.7	1.88359047	3.68992237	0.00078743
59024	A_55_P2108324	Med12	mediator of RNA polymerase	NM_021521	163.9	140.7	148.3	193.8	616.1	576	570.1	602	161.675	591.05	1.88042162	3.68182644	0.00038092
79565	A_55_P2036538	Wbscr27	Williams Beuren syndrome ch	NM_024479	10.1	12.1	13	8.8	48.1	39.6	39.2	34.4	11	40.325	1.88033754	3.68161186	0.0060579
106014	A_55_P1967325	Fam19a5	family with sequence similarit	NM_134096	132.7	173.2	140.3	202.4	546	578.2	662.1	571.1	162.15	589.35	1.87873262	3.67751855	0.00412625
14226	A_51_P293781	Fkbp1b	FK506 binding protein 1b	NM_016863	35.7	43.9	32.2	29	131.6	150.7	106.9	126.2	35.2	128.85	1.87856661	3.67709541	0.00655604
68385	A_55_P2108599	Tlcd1	TLC domain containing 1	NM_026708	17.9	23.8	30.3	27.6	81.7	96.9	83.6	98.4	24.9	90.15	1.8785217	3.67698093	0.01286251
78267	A_52_P609334	Klhdc8b	kelch domain containing 8B	NM_030075	24.9	26.9	44	33.3	107.4	118.1	108.6	129.5	32.275	115.9	1.87647848	3.6717771	0.02212914
68525	A_55_P2177243	Evc2	Ellis van Creveld syndrome 2	NM_145920	22.5	15.1	17.2	18.6	65.4	64.6	79.6	58.4	18.35	67	1.87434422	3.66634924	0.0041311
384261	A_55_P2183777	Gm5296	predicted gene 5296	ENSMUST00000101177	106.6	107.4	81.7	97.7	430.6	317.7	313.6	382.6	98.35	361.125	1.87218399	3.66086352	0.00279783
97351	A_55_P2340206	E230006M18Rik	RIKEN cDNA E230006M18 ger	AK053951	72.3	56.2	53.5	62.6	201.2	207.5	233	250.1	61.15	222.95	1.87050543	3.65660661	0.00092457
17160	A_51_P311785	Man2b2	mannosidase 2, alpha B2	NM_008550	80.8	86.4	68	58.6	261.2	229.2	266.1	311.5	73.45	267	1.86971324	3.65459933	0.00483623
668661	A_51_P144770	2410002F23Rik	RIKEN cDNA 2410002F23 gen	BC016099	1963.9	2165.6	1815.8	1477.5	6654.5	7202.2	6993.4	6008.4	1855.7	6714.625	1.86587278	3.64488369	0.00153132
93889	A_55_P2184796	Pcdhb18	protocadherin beta 18	NM_053143	51.2	78.4	52.8	88.4	255.9	208.4	241.1	253	67.7	239.6	1.85995877	3.62997288	0.041728
227058	A_55_P2100968	Dnahc7b	dynein, axonemal, heavy chai	NM_001160386	24.6	17	24	16.3	74.4	62.6	79.8	76.4	20.475	73.3	1.85983181	3.62965344	0.01180545
207798	A_55_P2079713	Gramd1c	GRAM domain containing 1C	NM_153528	139	184	141.7	150.2	610.4	583.6	506.6	519.9	153.725	555.125	1.85732521	3.62335262	0.00064875
17159	A_51_P336161	Man2b1	mannosidase 2, alpha B1	NM_010764	970	856.6	928.3	718.6	3142.5	2727.1	3245.3	3408.1	868.375	3130.75	1.85448144	3.61621747	0.00084945
76794	A_55_P2303478	2410133F24Rik	RIKEN cDNA 2410133F24 gen	ENSMUST00000142077	40.9	49.6	45.4	46.7	159.6	157.7	171.1	169.3	45.65	164.425	1.8513054	3.60826526	4.28E-05
20775	A_55_P1975185	Sqle	squalene epoxidase	NM_009270	75.9	90.4	65.3	122.7	289.7	351.1	317.1	286.2	88.575	311.025	1.84788665	3.59972489	0.03884984
68918	A_51_P234044	1190005I06Rik	RIKEN cDNA 1190005I06 gene	NM_197988	46.5	65.3	88	65.3	238.3	227.7	223.7	240.4	66.275	232.525	1.84643189	3.59609688	0.02126427
100502966	A_55_P2009320	LOC100502966	zinc finger protein 717-like	XM_003085405	5.2	7.4	6	6.5	26.9	24.8	18.5	20.3	6.275	22.625	1.84580614	3.59453746	0.00784299
107029	A_51_P490817	Me2	malic enzyme 2, NAD(+)-depe	NM_145494	40.2	38.9	49.2	45.1	163.3	146	152.2	158	43.35	154.875	1.84208676	3.58528241	0.0001462
18807	A_55_P2037513	Pld3	phospholipase D family, mem	NM_011116	350.1	353.7	330	331.8	1319.2	1104.3	1175.5	1305.5	341.4	1226.125	1.84132791	3.58339706	0.0000494
233877	A_51_P398406	Kctd13	potassium channel tetrameris	NM_172747	33.2	49.6	34.9	47.6	159.2	152.5	153.9	120.7	41.325	146.575	1.84126722	3.58324633	0.01251635
16201	A_65_P04980	Ilf3	interleukin enhancer binding	NM_001042708	86.3	111.6	86.5	123.1	411.2	367.2	318.4	350.2	101.875	361.75	1.83976336	3.57951311	0.00455582
59049	A_55_P2028773	Slc22a17	solute carrier family 22 (orgar	NM_021551	431.4	573.8	530.8	606.4	2313.9	1776.5	2000.9	1578.1	535.6	1917.35	1.8369755	3.57260275	0.00674294

654801	A_51_P490955	Zfp784	zinc finger protein 784	NM_001039532	71.9	86.4	67.4	94.1	289.9	273.8	257.7	313.1	79.95	283.625	1.83618495	3.57064561	0.00148795
233040	A_55_P2170847	Fbxo27	F-box protein 27	NM_001163702	68.1	86.5	75.7	95.5	284.7	328.7	263.9	278.8	81.45	289.025	1.83424982	3.5658594	0.0014527
18739	A_55_P1969746	Pitpnm1	phosphatidylinositol transfer	NM_008851	303.8	302.7	293.5	296.8	1063	1053.4	1056.9	1093.8	299.2	1066.775	1.83405826	3.56538597	4.38E-06
108811	A_55_P2074843	Ccdc122	coiled-coil domain containing	NM_175369	61.3	40	60.6	53	202	158.3	209.9	188.8	53.725	189.75	1.83252316	3.56159422	0.01020017
245671	A_52_P206861	Klf8	Kruppel-like factor 8	NM_173780	9.4	11	11.9	15.8	49.5	35	44.4	40.5	12.025	42.35	1.83103568	3.55792396	0.02234547
67145	A_55_P2136757	Tomm34	translocase of outer mitochor	NM_025996	2379	2423	2573.7	2285.8	9075.5	8316.5	9220.5	7697.5	2415.375	8577.5	1.82587396	3.54521705	6.39E-05
73047	A_51_P355151	Camk2n2	calcium/calmodulin-depende	NM_028420	391.5	297.4	282.8	323.2	1117.9	1200.1	1131.3	1107.1	323.725	1139.1	1.82569974	3.54478897	0.00052281
68423	A_55_P2170978	Ankrd13d	ankyrin repeat domain 13 fan	NM_026720	63.1	81.3	60	74.7	275.7	262.4	206.8	242	69.775	246.725	1.82471412	3.54236807	0.00252738
14265	A_55_P2183110	Fmr1	fragile X mental retardation s	NM_008031	53.3	52	60.1	60	211.7	200.9	201.3	183.5	56.35	199.35	1.82409095	3.54083827	6.39E-05
16600	A_55_P2122020	Klf4	Kruppel-like factor 4 (gut)	NM_010637	929.2	1279.4	962.4	1268.1	4737	3501.4	3820.5	3596.8	1109.775	3913.925	1.82386886	3.54029324	0.00688561
72747	A_66_P108059	Ttc39c	tetratricopeptide repeat dom	NM_028341	39.9	62.9	75.1	52.7	215	189.3	208	183.5	57.65	198.95	1.8222556	3.5363366	0.03639362
217578	A_55_P2082203	Baz1a	bromodomain adjacent to zin	NM_013815	97.1	115.5	116.2	115.2	401.3	371.8	395.4	390.9	111	389.85	1.81578339	3.52050743	5.69E-05
71331	A_52_P18854	5430411C19Rik	RIKEN cDNA 5430411C19 gen	AK017294	12.8	8.1	12.5	16.7	47.9	37.7	39.1	46.6	12.525	42.825	1.81204373	3.51139362	0.09964482
66220	A_51_P153224	Zdhhc12	zinc finger, DHHC domain con	NM_025428	146	140.9	128.8	123.3	488.4	457.7	439.1	503.5	134.75	472.175	1.81026536	3.50706789	7.62E-05
12705	A_55_P1979833	Cited1	Cbp/p300-interacting transac	NM_007709	45.5	74.9	61.9	58.7	204.2	209.7	235.6	185.1	60.25	208.65	1.80913359	3.50431774	0.00932802
72997	A_55_P2310898	2900056M20Rik	RIKEN cDNA 2900056M20 gei	AK013346	268.2	348.7	282.1	389.3	1143.4	1054.3	1064.6	1205.4	322.075	1116.925	1.80869171	3.50324458	0.00244239
17254	A_51_P472901	Slc3a2	solute carrier family 3 (activat	NM_008577	2531.4	2421.4	2105.9	2395	8610.4	8001.7	8118.2	8277	2363.425	8251.825	1.80660378	3.4981782	4.1583E-05
68099	A_51_P179498	Fam92a	family with sequence similarit	NM_026558	480	607.7	547	524.8	1969.9	1939.7	1876.5	1747.9	539.875	1883.5	1.80640825	3.49770411	0.00012805
52466	A_55_P2168301	Slc46a1	solute carrier family 46, mem	NM_026740	171.6	172.2	173	207.3	682	585.3	596.3	664.9	181.025	632.125	1.80562422	3.49580381	0.00018722
12660	A_51_P142923	Chka	choline kinase alpha	NM_013490	23.6	27.2	24	27.3	102.9	105.2	77.5	74.7	25.525	90.075	1.80480239	3.49381299	0.00360988
20911	A_51_P134062	Stxbp2	syntaxin binding protein 2	NM_011503	116.6	120.5	90.9	86.4	382.4	390.1	296.9	371.1	103.6	360.125	1.80466382	3.49347742	0.00570365
218138	A_55_P2157814	Gmds	GDP-mannose 4, 6-dehydrata	NM_146041	252.5	263.6	243.2	274.8	798.1	984.6	973.7	865.7	258.525	905.525	1.80457319	3.49325799	0.0001408
69544	A_52_P281711	Wdr5b	WD repeat domain 5B	NM_027113	53.7	58	67.3	71.2	202.3	204.5	234.5	228.2	62.55	217.375	1.80318438	3.48989681	0.00065023
117150	A_52_P594917	Pip4k2c	phosphatidylinositol-5-phosp	NM_054097	1037.2	1015.4	945	893.9	3628.1	3277	3387.5	3253.5	972.875	3386.525	1.80062238	3.48370481	0.00004116
53886	A_51_P236412	Cdkl2	cyclin-dependent kinase-like 2	NM_016912	286	343.3	332.1	323.5	1146.7	1056.6	1123.2	1133.8	321.225	1115.075	1.79813557	3.47770502	0.0000479
14700	A_51_P217047	Gng10	guanine nucleotide binding pr	NM_025277	256.7	275.7	270.4	260.2	923.6	936.3	877.9	948.4	265.75	921.55	1.79397316	3.46768574	9.87E-06
217038	A_52_P350616	Mrm1	mitochondrial rRNA methyltra	NM_145433	1218	1654.5	1199.2	1480.6	4396.3	4411.1	4610.6	5735.2	1388.075	4788.3	1.79076574	3.4599849	0.00426072
70123	A_55_P2042655	2210013O21Rik	RIKEN cDNA 2210013O21 gen	NR_028432	1678.4	1852.1	1773.4	1744.2	5741	6071.6	6447.8	6122.8	1762.025	6095.8	1.79026133	3.45877539	1.76E-05
12566	A_55_P2011852	Cdk2	cyclin-dependent kinase 2	NM_183417	31.4	47.6	51.6	35	149.9	153.4	118.6	141.5	41.4	140.85	1.7898663	3.45782845	0.02895271
69066	A_55_P2102095	1810010H24Rik	RIKEN cDNA 1810010H24 gen	NM_001163473	8	12.4	12.9	10.7	35.9	33.8	36.2	44.3	11	37.55	1.7877274	3.45270578	0.01752993
11841	A_55_P1958653	Arf2	ADP-ribosylation factor 2	NM_007477	2691.2	2824	2571.9	2887.2	10917.9	9831.2	8588.1	8672	2743.575	9502.3	1.78654986	3.44988881	0.00024995
93885	A_51_P240421	Pcdhb14	protocadherin beta 14	NM_053139	91.2	64.2	68.6	114.6	337.6	227.9	286.2	295.8	84.65	286.875	1.78618077	3.44900632	0.09081828
97908	A_55_P2068260	Hist1h3g	histone cluster 1, H3g	NM_145073	28.4	20.6	27.6	34	101.2	76.3	103.6	96.6	27.65	94.425	1.78426436	3.44442786	0.01984162
17750	A_51_P246317	Mt2	metallothionein 2	NM_008630	33718.4	27630.1	22263.4	20825.7	99766.8	85018	84801.5	83961	26109.4	88386.825	1.78183037	3.43862161	0.01253704
216438	A_55_P2011922	9-Mar	membrane-associated ring fir	NM_001033262	172.1	161	168.1	183.2	647.8	539.2	556.9	603.5	171.1	586.85	1.7760235	3.42480893	8.46E-05
13169	A_52_P189957	Dbnl	drebrin-like	NM_013810	73	70.6	75.7	84.9	253.9	261.7	258.7	264.2	76.05	259.625	1.77479368	3.4218907	4.18E-05
70605	A_51_P208870	Zdhhc24	zinc finger, DHHC domain con	NM_027476	43.8	52.7	48.9	46	148.6	175.1	158.9	172.1	47.85	163.675	1.77462241	3.4214845	0.00014038
14628	A_51_P461031	Ostm1	osteopetrosis associated tran	NM_172416	2043	2008.3	1812.2	1850.3	7330.8	6222.1	6026.6	6847.7	1928.45	6606.8	1.77404266	3.42010985	0.00012537
66337	A_52_P651948	1700025K23Rik	RIKEN cDNA 1700025K23 gen	NM_183254	111.8	90.9	87.4	85.9	331.9	282.7	390.7	283.3	94	322.15	1.77217619	3.41568798	0.00401222
383295	A_51_P311694	Ypel5	yippee-like 5 (Drosophila)	NM_027166	40.4	38.7	55.7	45.2	177.6	164	144.4	126.9	45	153.225	1.77077841	3.41238022	0.00852676
72657	A_55_P2010704	2700094K13Rik	RIKEN cDNA 2700094K13 gen	NM_001037279	1398.9	1196	1311.2	1249.6	4605.8	3887.4	4700	4374.1	1288.925	4391.825	1.76725999	3.40406831	0.00013482
14082	A_51_P382925	Fadd	Fas (TNFRSF6)-associated via	NM_010175	82.3	77.1	89.1	59.6	221.6	269.7	300.1	251.7	77.025	260.775	1.76645332	3.40216548	0.00765688
320299	A_66_P132077	Iqcb1	IQ calmodulin-binding motif c	NM_177128	32.5	32.3	36.5	44.1	136.7	127.1	111.3	117	36.35	123.025	1.76625069	3.40168769	0.00171206
330662	A_52_P660922	Dock1	dedicator of cytokinesis 1	NM_001033420	482.4	627.8	536.3	583.8	2320.7	1790.2	1709.1	1763.1	557.575	1895.775	1.76117373	3.3897379	0.00248714
107566	A_51_P396752	Arl2bp	ADP-ribosylation factor-like 2	NM_024191	6492.6	6865.8	7535.7	7561.5	23228.9	24968.7	23833	24214.3	7113.9	24061.225	1.76048391	3.3881175	4.15E-05
18762	A_55_P1987761	Prkcz	protein kinase C, zeta	NM_008860	38.8	35.4	33.2	30.9	106.5	121.8	121.4	116.7	34.575	116.6	1.75676421	3.37939317	0.00018884
53893	A_55_P2070825	Nudt5	nudix (nucleoside diphosphat	NM_016918	135.9	155.9	137.4	137.7	541.4	424.2	456.1	498.6	141.725	480.075	1.7563989	3.37853758	0.00027847
20621	A_52_P295067	Snn	stannin	NM_009223	140.1	192.6	185.5	124.3	640.2	490.4	508.3	507.6	160.625	536.625	1.75613595	3.37792186	0.02005633
106564	A_55_P2166990	Ppcs	phosphopantothenoylcystein	NM_026494	116.4	140.8	120.3	144.7	490.9	322.2	459.7	509	130.55	445.45	1.75482601	3.37485614	0.01536075
20539	A_55_P1973941	Slc7a5	solute carrier family 7 (cation	NM_011404	52.1	47.5	58.7	56.8	169.9	174.5	199.2	180.9	53.775	181.125	1.75414325	3.37325937	0.00021248
192231	A_51_P348397	Hexim1	hexamethylene bis-acetamide	NM_138753	1097.4	989.9	828.4	1057	3845.3	2982.4	3368.4	3173.2	993.175	3342.325	1.75243821	3.36927505	0.0014466
12091	A_51_P327564	Glb1	galactosidase, beta 1	NM_009752	78	91.1	85.2	65.1	289.3	230.7	274.6	276.8	79.85	267.85	1.75200903	3.3682729	0.00219196
329165	A_51_P363556	Abi2	abl-interactor 2	NM_198127	232.7	246.8	242	205.4	803.2	753.4	814.4	741.7	231.725	778.175	1.75012295	3.36387233	8.00E-05
55936	A_55_P2152074	Ctps2	cytidine 5-triphosphate synth	NM_018737	548.1	688.6	611.3	701.2	2200	2216.2	2125.8	1982	637.3	2131	1.74711374	3.35686318	0.00030624
77619	A_51_P480119	Prelid2	PRELI domain containing 2	NM_029942	71.6	57.2	73.6	114.7	262.8	234.7	281.7	252.5	79.275	257.925	1.74686612	3.35628706	0.08148575
106931	A_55_P2069974	Kctd1	potassium channel tetrameris	NM_001142731	42.6	49.2	26.5	41.3	144	113.4	120	148.3	39.9	131.425	1.74627724	3.35491738	0.07709172
29858	A_55_P1972720	Pmm1	phosphomannomutase 1	NM_013872	3585.3	4550.5	3674.1	4029.3	13499.8	13425.8	13013	12939.5	3959.8	13219.525	1.74533873	3.35273562	0.00016073
381644	A_55_P1959515	Cep135	centrosomal protein 135	NM_199032	66.1	67.5	63.5	75.1	210.4	222	238.5	239.7	68.05	227.65	1.74287967	3.34702579	8.43E-05
227620	A_51_P509669	Uap1l1	UDP-N-acteylglucosamine pyr	NM_001033293	210.3	243.8	203.8	185.5	743.3	741.9	660.5	666.3	210.85	703	1.7420449	3.3450897	0.00038952
67704	A_55_P2132207	1810037I17Rik	RIKEN cDNA 1810037I17 gene	NM_024461	127.5	107.4	118.4	107.7	419.2	347.4	377	396.7	115.25	385.075	1.74066771	3.34189801	0.00020082
93891	A_51_P146760	Pcdhb20	protocadherin beta 20	NM_053145	170	137.2	155.3	182.8	597.7	454.4	591.6	513.2	161.325	539.225	1.74009712	3.34057655	0.00258251
208117	A_52_P456750	Aph1b	anterior pharynx defective 1b	NM_177583	106.4	127	107.9	139.4	393.7	415.1	390.8	396.1	120.175	398.925	1.73989968	3.34011942	0.00044208
66487	A_52_P563340	2010107H07Rik	RIKEN cDNA 2010107H07 gen	NR_024069	2649	3028	2579.6	2356.3	9157.6	8021.9	8731.9	9452.6	2653.225	8841	1.73960917	3.3394469	0.00032189
245670	A_52_P599549	Rragb	Ras-related GTP binding B	NM_001004154	22.5	18.7	18	24.4	63.1	69.8	61.8	83.8	20.9	69.625	1.7368957	3.33317185	0.00558721
67513	A_66_P129048	2610002J02Rik	RIKEN cDNA 2610002J02 gene	NM_001190445	744.6	796.2	716.8	763	2402.8	2846.4	2474.1	2363.2	755.15	2521.625	1.73659068	3.33246721	8.89E-05
22590	A_55_P1967867	Xpa	xeroderma pigmentosum, cor	NM_011728	210.3	225.6	212.6	221.4	809.4	720.5	723.6	650.6	217.475	726.025	1.73545044	3.32983443	8.81E-05
12348	A_51_P480013	Car11	carbonic anhydrase 11	NM_009800	116.3	96.7	122.6	126.3	391.1	370.5	392.4	371.9	115.475	381.475	1.73099959	3.3195774	0.00030614
329470	A_52_P625277	Accs	1-aminocyclopropane-1-carbo	NM_183220	243.5	275.5	291	243.7	924.4	811.2	929.9	824.9	263.425	872.6	1.72944256	3.31599667	0.00021657
14231	A_51_P415607	Fkbp7	FK506 binding protein 7	NM_010222	581.7	592.9	548.9	549.8	1995.8	1761.9	1903	1847.7	568.325	1877.1	1.72307583	3.30139516	2.65E-05
67454	A_55_P2115607	Ikbip	IKBKB interacting protein	NM_027078	556.2	668.9	578.5	566.4	2058.2	1873.2	1880.4	1995.9	592.5	1951.925	1.72278675	3.30073371	9.6945E-05
20910	A_55_P2097616	Stxbp1	syntaxin binding protein 1	NM_001113569	17.1	19.5	18.6	25.2	65.2	51.3	73.3	75.2	20.1	66.25	1.72054496	3.29560871	0.02062032
230775	A_55_P1967105	Bai2	brain-specific angiogenesis in	NM_173071	92.3	96.6	133.8	66.7	321.4	333.4	303.6	288.5	97.35	311.725	1.72050818	3.29552469	0.07409336
245857	A_55_P2120615	Ssh3	slingshot homolog 3 (Drosoph	NM_198113	158.4	164.1	159.8	126.4	484.2	494.8	527.6	487.9	152.175	498.625	1.7190168	3.29211971	0.00037519
74246	A_55_P2111855	Gale	galactose-4-epimerase, UDP	NM_178389	50.7	71.5	83.4	60.9	196.1	214.7	203.6	251.8	66.625	216.55	1.71830534	3.29049661	0.0200861
192651	A_52_P664404	Zfp286	zinc finger protein 286	NM_138949	174.1	233.3	160.8	210.8	614.4	703	568.5	654.8	194.75	635.175	1.7169182	3.28733435	0.00467488
665055	A_55_P2021729	Gm7467	predicted gene 7467	ENSMUST00000101096	66.6	75.5	77	77.6	259.3	200.1	256	263.5	74.175	244.725	1.71602215	3.28529325	0.00091694
110417	A_52_P606826	Pigh	phosphatidylinositol glycan ar	NM_029988	27.5	34	24.1	40.8	92.5	101.6	123.8	91.9	31.6	102.45	1.71542937	3.28394364	0.04566419
217265	A_52_P519653	Abca5	ATP-binding cassette, sub-fan	NM_147219	62.3	48.4	50	68.5	213.8	183.6	192.2	159.1	57.3	187.175	1.71520279	3.28342794	0.00777861
67862	A_51_P291819	2310033P09Rik	RIKEN cDNA 2310033P09 gen	NM_024210	211.5	255.7	189.4	190.1	624.7	648	769.2	726.8	211.675	692.175	1.71519246	3.28340442	0.00213186
68166	A_55_P2019203	Spire1	spire homolog 1 (Drosophila)	NM_194355	46.3	36.1	25	41.6	134.3	122.8	110.3	109.4	37.25	119.2	1.70975128	3.27104426	0.06783301
118445	A_51_P215097	Klf16	Kruppel-like factor 16	NM_078477	22.9	22.6	19.8	21	72.5	68.4	63	78.8	21.575	70.675	1.70949116	3.27045454	0.00024634
15452	A_51_P239673	Hprt	hypoxanthine guanine phospl	NM_013556	3048.6	3285.3	3376.8	3542	11352.3	10952.5	10432.3	10527.1	3313.175	10816.05	1.7081824	3.26748905	4.01E-05
70799	A_55_P1979246	Cep192	centrosomal protein 192	ENSMUST00000059254	19.3	28.8	28.9	34	100.4	72.8	81.4	103.7	27.75	89.575	1.70493118	3.2601338	0.08447523
381694	A_66_P106861	B3galtl	beta 1,3-galactosyltransferase	NM_001081204	236.9	257	197	207.5	807.7	714.4	739.3	658.2	224.6	729.9	1.70447101	3.2590941	0.00094055
107823	A_52_P381784	Whsc1	Wolf-Hirschhorn syndrome ca	NM_001177884	265.6	295.1	282	305.8	946.4	997	893.2	892.6	287.125	932.3	1.6995745	3.24805148	5.59E-05
319998	A_55_P1967835	Tmem198	transmembrane protein 198	AK082334	37.1	31.7	28.7	27	101.7	111.5	94.8	92.4	31.125	100.1	1.69202183	3.231092	0.00171857
18846	A_52_P539632	Plxna3	plexin A3	NM_008883	15.4	12.9	15.6	16.6	49.7	63.8	44.2	40	15.125	49.425	1.69195449	3.23094119	0.01607692
69099	A_55_P1975832	1810009N02Rik	RIKEN cDNA 1810009N02 gen	NM_026939	553.5	405.4	482.9	387.7	1376.9	1425.1	1467.5	1578.6	457.375	1462.025	1.68940272	3.2252315	0.00270068
64291	A_55_P2029503	Osbpl1a	oxysterol binding protein-like	NM_207530	13.6	15.4	12.7	11.2	46.4	46.3	34.9	42.8	13.225	42.6	1.68777765	3.22160061	0.00457485
68180	A_55_P2135039	Hyi	hydroxypyruvate isomerase h	NM_026601	650.8	747.4	711	723.8	2400.8	2285.8	2388.7	2054.2	708.25	2282.375	1.68729841	3.22053061	0.00010286
93877	A_51_P403413	Pcdhb6	protocadherin beta 6	NM_053131	29.9	24.7	28.3	32.4	115.6	64.7	92.8	104.8	28.825	94.475	1.68676861	3.21934816	0.06238477
12890	A_51_P485161	Cplx2	complexin 2	NM_009946	67.6	75	82.3	72.9	238.1	255.6	244.9	218.7	74.45	239.325	1.68589719	3.21740419	0.00016743
213582	A_55_P1997931	Mtap9	microtubule-associated prote	NM_001081230	103.1	136.4	121.2	123.5	405	363.5	365.5	416.8	121.05	387.7	1.68382881	3.21279473	0.00062361
71519	A_66_P101879	Cyp2u1	cytochrome P450, family 2, su	ENSMUST00000090250	12.7	19.1	14.9	16	52.6	45.2	47.5	54.4	15.675	49.925	1.68278359	3.21046794	0.0048914
68949	A_52_P598309	1500012F01Rik	RIKEN cDNA 1500012F01 gen	NM_001081005	2486.6	2577.6	3179	2295	8532.8	7438.2	9203.4	8503.8	2634.55	8419.55	1.68274434	3.21038059	0.00197661
67826	A_55_P2029151	Snap47	synaptosomal-associated pro	NM_144521	124.5	136.7	118.2	109.3	381.2	419.5	383	379	122.175	390.675	1.68051969	3.20543396	0.00017871
16504	A_52_P337326	Kcnc3	potassium voltage gated char	NM_008422	62.2	41.6	38.1	34.9	151.2	132	133.5	136.2	44.2	138.225	1.68018969	3.20470084	0.04384478
193452	A_55_P2074246	Zfp184	zinc finger protein 184 (Krupp	NM_183014	37	35.1	31.5	46.1	126.6	121.1	116.7	110.2	37.425	118.65	1.67700064	3.19762474	0.00252853
72091	A_52_P199776	Snhg7	small nucleolar RNA host gen	NR_024068	164.8	195.7	206	150.2	539.4	496.1	635.9	606	179.175	569.35	1.67280376	3.18833618	0.00436052
654788	A_55_P2168791	4732440D04Rik	RIKEN cDNA 4732440D04 gen	AK161112	151.3	127.7	96.9	102	380.8	314.4	398.9	411	119.475	376.275	1.67087299	3.18407208	0.02414391
56464	A_52_P660945	Ctsf	cathepsin F	NM_019861	499.6	507.2	462.8	407	1523	1213.3	1507.6	1759.2	469.15	1500.775	1.67049799	3.18324454	0.00410625
83965	A_55_P2021704	Enpp5	ectonucleotide pyrophosphat	ENSMUST00000087066	120.9	131.1	125.1	122.6	380	364.7	434.4	412.4	124.925	397.875	1.66856384	3.17897978	8.29E-05
69215	A_55_P2047345	Sat2	spermidine/spermine N1-acet	NM_026991	351.9	333.7	412.8	302.6	995.7	1154.3	1257	1034.7	350.25	1110.425	1.66778467	3.17726333	0.00236207
68977	A_51_P292073	Haghl	hydroxyacylglutathione hydro	NM_026897	1569.9	1341.8	1572.8	1292.8	4329.3	4490.3	4679.8	4733	1444.325	4558.1	1.66286769	3.16645306	0.00024461
27414	A_51_P507787	Sergef	secretion regulating guanine	NM_013789	83.8	83.7	94.3	84.2	234.3	303.1	266.1	295.7	86.5	274.8	1.66217752	3.16493861	0.00057934
232670	A_55_P2086664	Tspan33	tetraspanin 33	NM_146173	549.8	524.1	447	683.7	1634	1839.1	1647.2	1782.2	551.15	1725.625	1.661602	3.16367631	0.00453715
230903	A_55_P2054350	Fbxo44	F-box protein 44	NM_173401	337.2	299.8	306.3	214	945.9	855	826.6	990.2	289.325	904.425	1.66059008	3.16145806	0.01262502
103406	A_55_P2053320	Zfr2	zinc finger RNA binding prote	NM_001034895	304.8	257.2	344.5	303.5	952.1	892.1	1015	949.7	302.5	952.225	1.66056104	3.16139443	0.00058125
170753	A_51_P399853	Zfp704	zinc finger protein 704	NM_133218	278.5	378.8	372.4	462.1	1273.4	1077.7	1085.2	1214.6	372.95	1162.725	1.65965602	3.15941187	0.0165774
216825	A_52_P413623	Usp22	ubiquitin specific peptidase 2	NM_001004143	12.6	13.8	9.1	16.6	38.5	37	36.7	49.7	13.025	40.475	1.65704898	3.15370777	0.0925971
74901	A_52_P570240	Kbtbd11	kelch repeat and BTB (POZ) d	NM_029116	192	203.2	171.2	200.6	617.2	523.4	606.1	676	191.75	605.675	1.65655501	3.15262815	0.00060516
15194	A_55_P2088530	Htt	huntingtin	NM_010414	1583.4	1330.6	1703	1304.6	4380.4	4636.9	4668.4	4860.9	1480.4	4636.65	1.65539655	3.15009765	0.00078248
226856	A_51_P453351	Lpgat1	lysophosphatidylglycerol acyl	NM_172266	1025.1	1031.9	1011.8	962	3456.7	2857.6	3163.4	3239.5	1007.7	3179.3	1.65483644	3.1488749	8.38E-05
20401	A_51_P342906	Sh3bp1	SH3-domain binding protein 1	NM_009164	58.4	70.7	75	65.9	203.6	219.4	203.2	213.4	67.5	209.9	1.6421566	3.12132071	0.0003094
320655	A_55_P2018492	Pgap3	post-GPI attachment to prote	NM_001033537	258	236.2	215.4	228.8	745.5	762.5	721.5	688.4	234.6	729.475	1.63867671	3.11380093	9.97E-05
110173	A_51_P454103	Manba	mannosidase, beta A, lysoson	NM_027288	142.4	186.6	205.8	157.8	562.6	566.8	530.2	478.9	173.15	534.625	1.63799302	3.11232566	0.00470677
27965	A_52_P219966	Spg21	spastic paraplegia 21 homolo	NM_138584	45.8	41.2	65.4	53.1	161.9	166.5	135	168.6	51.375	158	1.63722676	3.11067304	0.0190597
74008	A_55_P2043122	Arsg	arylsulfatase G	NM_028710	54.5	45.2	55.8	56.5	156	158.3	175	168.1	53	164.35	1.63687483	3.10991431	0.00036907
22751	A_51_P448814	Zfp90	zinc finger protein 90	NM_011764	125.5	145.6	122.9	138.8	412.6	420.7	414.9	404.3	133.2	413.125	1.63638382	3.10885607	8.19E-05
60364	A_55_P1981739	Donson	downstream neighbor of SON	NM_021720	136.2	161.3	130.3	195	516.9	415.4	461.6	522.2	155.7	479.025	1.63371194	3.10310376	0.01308609
72284	A_51_P244504	Oraov1	oral cancer overexpressed 1	NM_028184	480.7	510.5	497.6	462	1654	1421.5	1553	1419.8	487.7	1512.075	1.63047604	3.09615144	9.76E-05
215708	A_55_P2052862	Fam73a	family with sequence similarit	NM_174868	928.3	843	846	1033	2807.7	2927.3	2743.2	2783.6	912.575	2815.45	1.62998343	3.09509445	0.00017969
75690	A_55_P2120777	Vsig10l	ZV-set and immunoglobulin d	XM_355890	11.9	10.1	14.1	11.9	41.7	40.1	31.7	34.7	12	37.05	1.62777363	3.09035726	0.00567475
66279	A_51_P331207	Tmem218	transmembrane protein 218	NM_025464	433.6	516.4	427.9	481.5	1382.6	1429.5	1378.6	1540.2	464.85	1432.725	1.6268163	3.08830728	0.00021029
52028	A_55_P1955472	Bbs1	Bardet-Biedl syndrome 1 (hur	NM_001033128	160.8	129.7	134.6	114.9	379.2	381.7	436.2	460.2	135	414.325	1.62328645	3.08076033	0.00315506
333789	A_55_P2452914	N4bp2	NEDD4 binding protein 2	NM_001024917	176.1	166.8	135.4	148.3	486.6	439.7	473.1	519.4	156.65	479.7	1.61949662	3.07267807	0.00090033
71710	A_55_P2064917	Lrrcc1	leucine rich repeat and coiled	NM_028915	153.8	187.2	176.4	205	617.9	449.9	630.7	529.3	180.6	556.95	1.61947673	3.07263571	0.00874337
234683	A_52_P114620	Elmo3	engulfment and cell motility 3	NM_172760	193.3	187	205.8	204	612.3	583.5	635.1	596.1	197.525	606.75	1.61945436	3.07258806	3.28E-05
68603	A_55_P2076533	Pmvk	phosphomevalonate kinase	NM_026784	3315.3	4043.9	3249.6	3601.2	11345	9491.5	11484.2	11222.7	3552.5	10885.85	1.61673014	3.06679161	0.00081768
13555	A_55_P2317665	E2f1	E2F transcription factor 1	NM_007891	21	23.6	21.6	15.9	61.1	73.4	59.3	56.5	20.525	62.575	1.61600029	3.06524053	0.01133266
214601	A_55_P2067513	Slc10a3	solute carrier family 10 (sodiu	NM_145406	319	351.6	347.6	350.5	960.6	1037.9	1041.1	1161.4	342.175	1050.25	1.61575678	3.0647232	0.00012987
17427	A_51_P100174	Mns1	meiosis-specific nuclear struc	NM_008613	63.6	75.1	59	63.7	206.7	187.6	199.8	204.4	65.35	199.625	1.61575359	3.06471644	0.0003071
53883	A_52_P360515	Celsr2	cadherin, EGF LAG seven-pass	NM_017392	178.8	181.2	174.8	151.7	571.3	492.8	478.1	551.7	171.625	523.475	1.6083978	3.0491303	0.000453
67477	A_51_P386503	Abhd15	abhydrolase domain containi	NM_026185	17.4	27.5	27.3	22.5	70.3	82.8	72.5	60.1	23.675	71.425	1.60778914	3.04784417	0.04663052
621580	A_55_P2068731	Gm13308	predicted gene 13308	NM_001177580	417.1	434.7	357.2	352.3	1172.7	1214.9	1189.3	1159.9	390.325	1184.2	1.60713677	3.04646628	0.00029545
235504	A_55_P2153923	Slc17a5	solute carrier family 17 (anior	NM_172773	35.4	32.7	33	25.6	110.1	93.1	98.8	81.8	31.675	95.95	1.60112145	3.03379047	0.00685869
381201	A_55_P2168549	Gm962	predicted gene 962	NM_001033448	150.6	109.6	121.4	150	392.7	370.2	433.9	402.9	132.9	399.925	1.6004541	3.03238745	0.00381693
140859	A_52_P491073	Nek8	NIMA (never in mitosis gene a	NM_080849	50.2	60	50.2	42.4	135.5	166.4	142.6	168.3	50.7	153.2	1.59981708	3.03104881	0.00500765
227545	A_51_P474169	5430407P10Rik	RIKEN cDNA 5430407P10 gen	NM_144883	61.2	77.6	54.8	54.9	191.5	186.5	169.4	199.2	62.125	186.65	1.59957839	3.03054737	0.00476479
104383	A_55_P2118784	Rcor2	REST corepressor 2	NM_054048	95.7	97.8	127.7	134.7	361.1	326.7	314.1	362.1	113.975	341	1.59524285	3.02145374	0.007851
56174	A_55_P1959238	Nagk	N-acetylglucosamine kinase	NM_019542	85.5	91.3	95.2	90.3	238.7	250.5	265.8	350.1	90.575	276.275	1.59340072	3.0175982	0.00480488
73668	A_55_P2098734	Ttc21b	tetratricopeptide repeat dom	NM_001047604	267	311.7	292.4	337.6	1012.4	871.1	813.4	947.9	302.175	911.2	1.5927474	3.016232	0.00108595

71780	A_51_P228658	Isyna1	myo-inositol 1-phosphate syn	NM_023627	285.2	229.2	227.4	232.2	702	745.9	726.3	750	243.5	731.05	1.59218205	3.01505025	0.00038113
12338	A_52_P474089	Capn6	calpain 6	NM_007603	42.8	43.2	43.3	44.7	116.8	136.2	137.5	135	43.5	131.375	1.5916466	3.01393145	9.02E-05
353170	A_52_P556337	Txlng	taxilin gamma	AK078477	26.6	37.5	30.9	26.2	91.9	83	97.6	89	30.3	90.375	1.58959305	3.00964442	0.00545897
213575	A_51_P472481	Dync2li1	dynein cytoplasmic 2 light int	NM_172256	83.3	141.9	129.3	132.4	325.1	378	366.6	367.5	121.725	359.3	1.58858311	3.0075383	0.05011842
97031	A_55_P2096777	Tprn	taperin	NM_175286	111.2	101.2	118.8	118	372.6	311.9	321.9	339.3	112.3	336.425	1.58254937	2.99498622	0.00031748
11443	A_51_P475342	Chrnb1	cholinergic receptor, nicotinic	NM_009601	104.5	125.2	125.4	161.8	430.3	431.2	311.4	368.5	129.225	385.35	1.58141178	2.99262556	0.03508232
237412	A_55_P2062593	Gm4924	predicted gene 4924	ENSMUST00000105311	64.1	73.5	70.3	62.1	195.3	193.4	203.3	214.6	67.5	201.65	1.58101646	2.99180566	0.00016057
244962	A_52_P274555	Snx14	sorting nexin 14	NM_172926	545.3	644.6	657.5	722	2044.3	1797.8	1698.8	2127.9	642.35	1917.2	1.57876353	2.98713726	0.00254401
76561	A_55_P2059957	Snx7	sorting nexin 7	NM_029655	69.8	80.1	60.2	67.6	227.6	250.9	166.1	190.9	69.425	208.875	1.57859464	2.98678759	0.02015084
192166	A_66_P121480	Sardh	sarcosine dehydrogenase	NM_138665	24.6	22.2	19.8	27.8	65.9	78.1	63	73.7	23.6	70.175	1.57820354	2.98597801	0.00491015
52837	A_51_P319379	Tmx4	thioredoxin-related transmen	NM_029148	486.1	619.5	598.7	666.5	1693.6	1934.7	1636.1	1781.2	592.7	1761.4	1.57805758	2.98567592	0.00218609
76222	A_55_P2043207	Magef1	melanoma antigen family F, 1	AK018285	214.4	263	265.6	293.8	820	785	701.2	767.6	259.2	768.45	1.57476001	2.97885935	0.00175509
240660	A_55_P1959828	Tmem20	transmembrane protein 20	NM_175507	271.9	316.4	230.6	295.3	922.9	790.6	806.3	781.9	278.55	825.425	1.57375587	2.97678675	0.00249421
16210	A_51_P483220	Impact	imprinted and ancient	NM_008378	1490.1	1836.4	1829.6	2005.6	5527.3	4677.3	5442.1	5586.7	1790.425	5308.35	1.57263976	2.97448471	0.00202641
52118	A_52_P628590	Pvr	poliovirus receptor	NM_027514	101.2	81.4	132.7	84	281	339.2	311.5	242	99.825	293.425	1.57250148	2.97419962	0.08035647
13537	A_52_P399934	Dusp2	dual specificity phosphatase 2	NM_010090	405.7	419.9	456.6	398.5	1423.1	1537.7	1018.2	1086.6	420.175	1266.4	1.57184893	2.97285466	0.01635651
552912	A_55_P2398264	LOC552912	uncharacterized LOC552912	AK049060	158.2	133.3	175.8	129.5	391.9	474.5	447.1	449.1	149.2	440.65	1.57030359	2.969672	0.00362468
72720	A_55_P2021231	Zfp248	zinc finger protein 248	NM_028335	23.5	30.7	27.2	36.7	87	76.6	80.4	103.5	29.525	86.875	1.56670701	2.96227794	0.03104872
228602	A_55_P2070406	4930402H24Rik	RIKEN cDNA 4930402H24 gen	ENSMUST00000110243	40.1	36	34.2	41	103.7	117.1	110.1	116	37.825	111.725	1.56489731	2.95856443	0.00028632
72341	A_51_P311905	2610002I17Rik	RIKEN cDNA 2610002I17	NM_001081381	87.4	90.1	71.5	84.9	254	242.3	241.5	245.3	83.475	245.775	1.56325938	2.95520739	0.00032915
338365	A_51_P219505	Slc41a2	solute carrier family 41, mem	NM_177388	23.9	27.8	20.2	19.2	58	65.4	76.2	67.8	22.775	66.85	1.56221568	2.95307025	0.01350977
192192	A_51_P134972	Shkbp1	Sh3kbp1 binding protein 1	NM_138676	249.5	200.5	213.8	202.1	622.5	652	669.3	603	216.475	636.7	1.5609459	2.95047227	0.00042345
20365	A_51_P254986	Serf1	small EDRK-rich factor 1	NM_011353	1911.6	2027.5	1788.6	1774.7	5821.3	5088.4	5710	5510.8	1875.6	5532.625	1.56085436	2.95028506	0.00014086
27078	A_55_P1958140	B9d1	B9 protein domain 1	NM_013717	239.5	291	278.8	247.6	771.1	822.6	782.6	734.1	264.225	777.6	1.56076852	2.95010953	0.00030862
210035	A_55_P2003129	Tmem194	transmembrane protein 194	NM_001113211	58.7	49.2	45.6	50.9	163.8	149	155	134.2	51.1	150.5	1.56072366	2.95001781	0.0011435
77106	A_55_P2021099	Tmem181a	transmembrane protein 181A	NM_001033178	473.1	483.4	457.7	540.7	1422.7	1471.1	1454.6	1403	488.725	1437.85	1.55944585	2.94740609	8.89E-05
17874	A_52_P282762	Myd88	myeloid differentiation prima	NM_010851	204.4	196.5	196.3	179.9	554.2	538.4	656.2	546.3	194.275	573.775	1.55918357	2.94687031	0.00035049
103711	A_55_P1952220	Pnpo	pyridoxine 5-phosphate oxida	NM_134021	1723.2	1959.9	1847.4	1755.4	5022.5	5291.8	5355.4	5799.6	1821.475	5367.325	1.55898641	2.94646762	0.00012284
18516	A_55_P2107367	Pbx3	pre B-cell leukemia transcript	ENSMUST00000040638	386	414.2	393.9	415.9	1377.6	1156.5	1132.7	1091.6	402.5	1189.6	1.55821257	2.94488761	0.00039712
319845	A_55_P2121491	Bbs9	Bardet-Biedl syndrome 9 (hur	NM_178415	538.2	688.6	716.9	640.4	1847.9	1936.2	1897.4	1884	646.025	1891.375	1.55802402	2.94450276	0.00086925
56213	A_51_P225224	Htra1	HtrA serine peptidase 1	NM_019564	7137.7	6062.6	5572.6	6294.7	19185.6	14584	18528.2	21932	6266.9	18557.45	1.55674968	2.941903	0.01224435
93893	A_51_P515649	Pcdhb22	protocadherin beta 22	NM_053147	40.5	38.1	39.2	48.2	141.5	115.1	101.4	131.6	41.5	122.4	1.55500493	2.9383473	0.00686045
214552	A_55_P2091368	Cep164	centrosomal protein 164	NM_001081373	118.6	105.7	99.8	110.3	306.7	319.5	327	320.5	108.6	318.425	1.5544088	2.93713341	9.99E-05
101543	A_52_P481686	Wtip	WT1-interacting protein	NM_207212	1039.3	1141.6	1172.3	1308.7	3635.7	3774.8	3320.8	2945.1	1165.475	3419.1	1.5510838	2.93037196	0.00183017
56876	A_55_P2045802	Nelf	nasal embryonic LHRH factor	NM_001039386	2267.5	2305.6	2366.2	2162.6	6785.2	6920.2	6345.1	6596.1	2275.475	6661.65	1.5497194	2.92760192	3.87E-05
67672	A_52_P27075	0610040B10Rik	RIKEN cDNA 0610040B10 gen	NR_027874	8.4	14.1	11.7	10.4	27.2	34.1	38.1	29.9	11.15	32.325	1.5490166	2.92617612	0.0796182
20340	A_51_P260548	Glg1	golgi apparatus protein 1	NM_009149	4226.1	3789.6	4028.3	4122.2	12553.5	10726.1	11473.9	12573.1	4041.55	11831.65	1.54766644	2.92343891	0.0001772
50524	A_51_P137094	Sall2	sal-like 2 (Drosophila)	NM_015772	46.1	38.5	57.9	47.5	120.8	155.7	131.5	144.1	47.5	138.025	1.54752971	2.92316186	0.01348141
100041576	A_55_P1992413	Gm3414	predicted gene 3414	NR_027993	11.6	10.6	10.5	16.8	37.3	30.5	40.5	34.1	12.375	35.6	1.54465972	2.91735251	0.06348401
68157	A_55_P2160253	6720475J19Rik	RIKEN cDNA 6720475J19 gen	AK020160	122.2	110.1	89.2	137.2	328.7	338.7	297.1	359.3	114.675	330.95	1.54336553	2.91473664	0.01345338
320152	A_55_P2196185	4930412C18Rik	RIKEN cDNA 4930412C18 gen	NR_030693	24.9	37	28.8	27.8	101.1	83	80.8	78.2	29.625	85.775	1.54188041	2.91173771	0.015411
231997	A_55_P1981259	Fkbp14	FK506 binding protein 14	NM_153573	830.3	1009.8	816.3	1123.7	2869.5	2878.2	2374.3	2812.5	945.025	2733.625	1.54102977	2.91002141	0.00718413
109241	A_55_P1963585	Mbd5	methyl-CpG binding domain p	NM_029924	360.7	375.3	410.2	414.1	1010.3	1126	1077.4	1341.5	390.075	1138.8	1.53998839	2.90792164	0.00148896
17688	A_51_P405565	Msh6	mutS homolog 6 (E. coli)	NM_010830	541.9	683.1	649.6	682.5	1759.7	1857.4	1893.1	1894.4	639.275	1851.15	1.53957848	2.90709552	0.00055161
233532	A_55_P2132805	Rsf1	remodeling and spacing facto	NM_001081267	29.5	26.4	32.6	32.7	97.6	79.2	88.7	86.2	30.3	87.925	1.53839702	2.9047158	0.00117568
214585	A_51_P289414	Spg11	spastic paraplegia 11	NM_145531	560.7	667.6	629.6	773.7	2014.4	1693	1825.4	2075.3	657.9	1902.025	1.53668856	2.90127804	0.00389911
382620	A_52_P324767	Tmed8	transmembrane emp24 doma	NM_001033475	182.1	164.8	150.1	174	509.1	493	482.8	456.6	167.75	485.375	1.5353587	2.89860491	0.00023416
19075	A_51_P168632	Prim1	DNA primase, p49 subunit	NM_008921	144.1	135.4	128.8	146.8	383.4	407.8	416.1	400	138.775	401.825	1.53508994	2.89806498	7.82E-05
69894	A_51_P308029	2010107G23Rik	RIKEN cDNA 2010107G23 gen	NM_027251	90.9	103	113.1	108.5	305.1	308.4	302.2	281	103.875	299.175	1.52996706	2.88779245	0.00035501
67951	A_51_P421140	Tubb6	tubulin, beta 6 class V	NM_026473	2295.9	2400.6	2370	2216.1	6091.4	7171.7	6659.3	6915.3	2320.65	6709.425	1.52972162	2.88730121	0.00011942
235047	A_55_P2047614	Zfp809	zinc finger protein 809	NM_172763	55.4	67.2	52.7	68.9	179.9	173.1	179.3	168.1	61.05	175.1	1.52938859	2.88663478	0.00156434
77015	A_52_P408025	Mpped2	metallophosphoesterase dom	NM_001143683	133.2	129.5	88.2	138.6	386.1	386.1	303	323.7	122.375	349.725	1.52890007	2.88565748	0.05415224
69863	A_65_P16231	Ttc39b	tetratricopeptide repeat dom	NM_027238	10.9	7.4	6.8	8.5	27.5	21.6	25	21.7	8.4	23.95	1.52775484	2.88336772	0.04570196
68106	A_55_P2156464	Nt5c3l	5-nucleotidase, cytosolic III-lik	NM_001102650	75.9	68.8	72.8	79.5	198	221.8	201.2	236.2	74.25	214.3	1.52742742	2.88271342	0.00035737
70779	A_55_P2060097	Prdm5	PR domain containing 5	NM_027547	231.8	257.5	265	249.8	678.1	777.5	749.1	690.1	251.025	723.7	1.52702141	2.88190227	0.00017451
116871	A_55_P2022094	Mta3	metastasis associated 3	NM_001171053	147.5	155.8	139.3	149.1	432.2	423.7	396.7	453.1	147.925	426.425	1.5269336	2.88172686	9.08E-05
76809	A_51_P227108	Bri3bp	Bri3 binding protein	NM_029752	675.8	702.5	661	678.4	2132.1	1786.4	1940.2	1980.1	679.425	1959.7	1.52573507	2.87933385	0.00011348
71591	A_65_P15340	Zfp251	zinc finger protein 251	NM_001007568	275.6	239.2	285.9	253.9	695.2	801.1	780	755.1	263.65	757.85	1.52474699	2.87736251	0.00032724
80291	A_51_P344399	Rilpl2	Rab interacting lysosomal pro	NM_030259	140.2	143.9	152.8	133.5	422.9	437.7	419.4	362.4	142.6	410.6	1.52378288	2.8754403	0.00032191
19038	A_51_P161086	Ppic	peptidylprolyl isomerase C	NM_008908	2955.1	3687.6	3995.5	3166.8	10012.7	9762.4	9827.4	9769.9	3451.25	9843.1	1.52221441	2.87231588	0.00160347
244745	A_55_P2045549	Dpy19l1	dpy-19-like 1 (C. elegans)	NM_172920	88.4	110.6	92.1	111.7	301	265.7	280.2	303.3	100.7	287.55	1.51959807	2.86711161	0.00152306
15370	A_51_P239654	Nr4a1	nuclear receptor subfamily 4,	NM_010444	26478.6	27065	35118.9	35043.5	96543	85805.7	82258.9	87440.9	30926.5	88012.125	1.51951885	2.86695419	0.00558211
67217	A_51_P408989	2810055F11Rik	RIKEN cDNA 2810055F11 gen	NM_026038	64.2	107.3	97.5	72.2	241.5	246	231.8	235.3	85.3	238.65	1.51555581	2.85908956	0.05895062
70281	A_55_P2377693	2310068J16Rik	RIKEN cDNA 2310068J16 gen	NR_028124	99.3	95.5	106.7	92.9	307.3	266.4	265.7	287.6	98.6	281.75	1.5140887	2.85618357	0.00023081
71876	A_55_P1988373	Mlf1ip	myeloid leukemia factor 1 int	NM_027973	7.4	8.6	9.7	7.1	24.2	28.1	20.7	20.7	8.2	23.425	1.51372135	2.85545638	0.01875431
72938	A_55_P2024749	Hspb11	heat shock protein family B (s	NM_028394	696.6	715.2	847	709.4	2141	2037.2	2261.1	2017.9	742.05	2114.3	1.51370644	2.85542688	0.000408
104401	A_55_P2000384	Pcnxl3	pecanex-like 3 (Drosophila)	NM_144868	2274.9	2418.6	2213.8	2243.7	6533.4	7069.5	5868.4	6668.6	2287.75	6534.975	1.51185332	2.85176148	0.0001886
244329	A_51_P477676	Mcph1	microcephaly, primary autoso	NM_173189	105.8	94.2	100.5	95.9	292.8	270.8	280	285.9	99.1	282.375	1.51153598	2.85113427	6.50E-05
54151	A_52_P134083	Cyhr1	cysteine and histidine rich 1	NM_180962	836	949.2	929.7	763.1	2564.2	2380.4	2422.1	2510	869.5	2469.175	1.51062964	2.84934367	0.00044569
23991	A_55_P1982683	Cib1	calcium and integrin binding 1	NM_011870	1402.6	1642.4	1594	1381.2	4352.4	4241	4312.2	4167.3	1505.05	4268.225	1.50781741	2.84379489	0.00021987
27223	A_66_P139355	Trp53bp1	transformation related protei	NM_013735	26.1	25.7	30.8	35	74.9	86.2	86.7	83.5	29.4	82.825	1.50358959	2.83547333	0.00439242
14775	A_52_P684378	Gpx1	glutathione peroxidase 1	NM_008160	7336.2	6891.7	7150	6332.4	20066.8	20035.8	18895.8	19235	6927.575	19558.35	1.4990785	2.82662108	0.00010118
26931	A_55_P2105873	Ppp2r5c	protein phosphatase 2, regula	NM_001135001	124.9	154	141.2	149.5	448.5	375.9	370	414.2	142.4	402.15	1.49793008	2.82437192	0.00124082
170833	A_55_P2065621	Hook2	hook homolog 2 (Drosophila)	NM_133255	439.1	474.4	471.2	571	1544.4	1219.7	1507.3	1244.6	488.925	1379	1.49461252	2.81788458	0.00569381
225888	A_55_P2144456	Suv420h1	suppressor of variegation 4-2	NM_001167884	100.7	97.4	109.8	138.6	304.9	280.1	321.5	341.5	111.625	312	1.49327994	2.81528298	0.00902619
75739	A_52_P17098	Mpp7	membrane protein, palmitoyl	NM_001161620	68	63.9	51.7	73.3	164.9	175.7	165.1	215.6	64.225	180.325	1.49219678	2.81317008	0.01593435
68628	A_51_P357561	Fbxw9	F-box and WD-40 domain pro	NM_026791	38.7	38.8	46.5	43.1	132.9	124.9	134.8	83.6	41.775	119.05	1.48947838	2.80787435	0.06466256
234086	A_55_P2038972	Erich1	glutamate-rich 1	NM_001034862	26.6	21.3	30	20	75.2	60.2	59.7	78.1	24.475	68.3	1.48907686	2.807093	0.05528786
53375	A_52_P86158	Mtx2	metaxin 2	NM_016804	2519.1	2485	2291.2	1938.6	6096.1	6355	6239.3	7136.4	2308.475	6456.7	1.48877164	2.80649918	0.0019873
107166	A_55_P2287269	AI415730	expressed sequence AI41573	AK138764	312.6	322.8	288	365.9	915	841.9	841.1	1011	322.325	902.25	1.48623312	2.80156529	0.00151071
66713	A_51_P303906	Actr2	ARP2 actin-related protein 2	NM_146243	2218.7	2152	2750.7	3017.7	8188.2	7487.1	7251.7	5487.1	2534.775	7103.525	1.4859189	2.80095518	0.05839658
208884	A_55_P1960960	Zdhhc9	zinc finger, DHHC domain con	NM_172465	1736.7	1895.2	1748.9	1942.8	4726.1	4811	5622.3	5354.2	1830.9	5128.4	1.48388364	2.79700657	0.00040458
110147	A_55_P2001143	Ehmt2	euchromatic histone lysine N-	NM_145830	7968.4	7106.4	9190	9001	24596.2	22041.8	23680.1	22300.7	8316.45	23154.7	1.48339873	2.79606661	0.00139479
433466	A_51_P288549	Jmjd7	jumonji domain containing 7	NM_001114637	110	154.2	130.6	134.5	347.5	366.4	426.7	334.3	132.325	368.725	1.48243265	2.79419489	0.00812153
100042071	A_55_P2044592	Gm15432	uncharacterized protein C4or	XM_001472378	2734.5	2721.2	2955.5	2791	7012	8440.5	8495.1	7377.1	2800.55	7831.175	1.4792837	2.78810268	0.00046605
66874	A_51_P101660	1200014J11Rik	RIKEN cDNA 1200014J11 gen	NM_025818	25.9	27	26.1	30.5	80.6	79.1	67.1	78.5	27.375	76.325	1.4786731	2.78692292	0.00072111
12418	A_51_P133582	Cbx4	chromobox homolog 4 (Droso	NM_007625	230.2	222.2	231.5	173.1	643.7	567	544.8	621.5	214.25	594.25	1.47846343	2.78651792	0.00456186
67856	A_55_P2131190	Echdc3	enoyl Coenzyme A hydratase	ENSMUST00000114941	155.3	158.7	158.5	126.8	432	390.6	386.4	457.5	149.825	416.625	1.47804814	2.78571591	0.00183601
67263	A_55_P2002752	Zswim6	zinc finger, SWIM domain cor	NM_145456	54.3	54.4	55.2	53.4	155.9	139.1	153.4	157.5	54.325	151.475	1.4777598	2.7851592	6.92E-05
12368	A_51_P215922	Casp6	caspase 6	NM_009811	168.6	205.2	204.7	210.7	511.1	583.6	534.4	560.5	197.3	547.4	1.47597079	2.78170763	0.00088071
230991	A_55_P2170732	B930041F14Rik	RIKEN cDNA B930041F14 gen	NM_178699	311.7	254	363.2	275.6	935.3	711.1	867.2	821.3	301.125	833.725	1.47535724	2.78052487	0.01612218
319468	A_55_P2074591	Ppm1h	protein phosphatase 1H (PP2	NM_001110218	51.8	49.2	39.7	43.9	139.4	140.5	103.8	130.3	46.15	128.5	1.47454656	2.77896287	0.01190017
18415	A_55_P2173737	Hspa4l	heat shock protein 4 like	NM_011020	243.7	244	252.2	295.2	672.7	777.3	699.4	719.5	258.775	717.225	1.47332472	2.77661031	0.00062999
94214	A_52_P221756	Spock2	sparc/osteonectin, cwcv and	NM_052994	118	112.9	86.8	82.3	269	262.6	275.6	289.8	100	274.25	1.47238574	2.77480374	0.01287271
433022	A_55_P2045755	Plcxd2	phosphatidylinositol-specific	NM_001134480	32.2	36.9	36.9	29.7	103.1	112.6	87.2	75.8	33.925	94.675	1.47021702	2.77063568	0.02448009
50887	A_55_P1982451	Hmgn5	high-mobility group nucleoso	NM_016710	521	443.9	470.7	555.9	1259.6	1261.8	1574.8	1417.8	497.875	1378.5	1.46845816	2.76725992	0.00302788
71949	A_55_P2099930	Lass5	LAG1 homolog, ceramide syn	NM_028015	1073.8	1319.2	1151.5	1187.3	3190.5	3509.3	3200.5	3163	1182.95	3265.825	1.46774229	2.76588713	0.00039573
674810	A_55_P2021515	LOC674810	60S ribosomal protein L3-like	XM_977204	13842.4	15694.7	15434.9	16000	44664.8	42811.9	38513.5	42615	15243	42151.3	1.46755904	2.76553583	0.00027746
74471	A_51_P300054	4933440N22Rik	RIKEN cDNA 4933440N22 gen	AK017138	81.4	79.8	83.3	62	220.6	185.5	241.1	198.8	76.625	211.5	1.46737788	2.76518859	0.01028374
380614	A_52_P177373	Intu	inturned planar cell polarity e	NM_175515	32.2	32.3	36.6	35	93.4	95.1	107	81.9	34.025	94.35	1.4671192	2.76469284	0.00130679
11836	A_51_P301259	Araf	v-raf murine sarcoma 3611 vi	NM_009703	1582.9	1621.5	1860.3	2366.1	5195	4881.7	5089.8	5107.1	1857.7	5068.4	1.4666688	2.76382984	0.01296612
56297	A_66_P139974	Arl6	ADP-ribosylation factor-like 6	NM_019665	195.4	206.9	187.2	185.3	590.2	488.4	520.5	544.7	193.7	535.95	1.46620493	2.76294134	0.00032947
65972	A_51_P490305	Ifi30	interferon gamma inducible p	NM_023065	293.1	239.6	235.3	203.1	728.6	562	656	723.8	242.775	667.6	1.4640679	2.75885169	0.01674717
242642	A_51_P317214	Hpdl	4-hydroxyphenylpyruvate dio	NM_146256	257	289.9	210	228.8	612.6	588.3	735.1	781	246.425	679.25	1.4632401	2.75726915	0.01867014
223658	A_55_P2210011	Heatr7a	HEAT repeat containing 7A	ENSMUST00000162204	46.8	33.5	44.1	39.8	114.5	94.5	109.5	133.8	41.05	113.075	1.46205962	2.75501395	0.02450216
27367	A_55_P2030802	Rpl3	ribosomal protein L3	NM_013762	5381.4	5440.9	5016.4	5058.9	14558.6	14994.9	13521.1	14433.6	5224.4	14377.05	1.46034916	2.75174953	8.13E-05
66441	A_51_P187018	Magohb	mago-nashi homolog B (Droso	NM_025564	437.6	455.1	423.6	417.6	1160.1	1281.2	1271.7	1065.7	433.475	1194.675	1.45934909	2.7498427	0.00035529
67702	A_55_P2141699	Rnf149	ring finger protein 149	NM_001033135	641.9	689.4	619.3	638.5	1816.9	1744.6	1818.7	1730.9	647.275	1777.775	1.45837568	2.74798796	6.07E-05
100504423	A_55_P2372902	LOC100504423	uncharacterized LOC1005044	XR_105384	315.8	322.9	282.4	328.6	830	882.1	879.2	837.9	312.425	857.3	1.45821296	2.74767803	0.00015178
110074	A_52_P480360	Dut	deoxyuridine triphosphatase	NM_023595	197.2	170.3	186.7	189.5	499	476.9	519.7	544.5	185.925	510.025	1.45616999	2.74378985	0.00022388
100503849	A_55_P2166745	1700011J10Rik	RIKEN cDNA 1700011J10 gen	ENSMUST00000146195	530.3	510.3	457.9	599.3	1403.8	1321.7	1528.1	1468.5	524.45	1430.525	1.45226536	2.73637387	0.00148755
22750	A_52_P372013	Zfp9	zinc finger protein 9	NM_011763	33	36.2	36.7	35.9	93.2	106.8	92.3	96	35.45	97.075	1.45207878	2.73602001	0.00021366
72514	A_55_P2044385	Fgfbp3	fibroblast growth factor bindi	NM_028263	203.3	219.5	197.1	229.3	638.4	527.7	530	632.1	212.3	582.05	1.45158213	2.73507829	0.0014482
56199	A_55_P1963529	Abcb10	ATP-binding cassette, sub-fan	NM_019552	1203.7	1232.9	1155.4	1254.2	3370.3	3016.8	3070.8	3844.1	1211.55	3325.5	1.45061625	2.73324778	0.00095025
234875	A_55_P1996573	Ttc13	tetratricopeptide repeat dom	NM_145607	4861.8	5223.2	5435.3	6634.7	15356.5	14403.9	15118.4	15273.8	5538.75	15038.15	1.4503926	2.7328241	0.00217899
243983	A_55_P2126552	Zdhhc13	zinc finger, DHHC domain con	NM_028031	276.2	350.2	332.3	371.2	952.6	838.6	875.6	950.7	332.475	904.375	1.45013502	2.73233622	0.00281105
74270	A_51_P122085	Usp20	ubiquitin specific peptidase 2	NM_028846	1487	1529.9	1742.4	1671.9	4589.8	4252.5	4360.3	4332.4	1607.8	4383.75	1.44948249	2.73110066	0.00020538
12633	A_55_P1983468	Cflar	CASP8 and FADD-like apoptos	NM_009805	79.9	89	79.1	103.4	237.4	234.7	248.7	233.2	87.85	238.5	1.44899541	2.73017875	0.00155568
381356	A_55_P2053516	5930434B04Rik	RIKEN cDNA 5930434B04 gen	NM_029862	9209	9115.7	9205.5	10413.4	26691.9	23950.1	26270.6	26567.6	9485.9	25870.05	1.44824995	2.7287684	0.00021009
224143	A_51_P248444	Poglut1	protein O-glucosyltransferase	NM_172380	153.8	160	169.6	160.7	399.4	432.6	446.5	480.6	161.025	439.775	1.44718283	2.72675075	0.00026343
67623	A_52_P405206	Tm7sf3	transmembrane 7 superfamil	NM_026281	767.7	925.6	745	886.7	2292.6	2290.8	2166.8	2278.5	831.25	2257.175	1.44689523	2.72620722	0.00072854
101023	A_55_P2077535	Zfp513	zinc finger protein 513	NM_175311	884.3	895.9	970.6	726.3	2251.1	2223.1	2510.8	2450.7	869.275	2358.925	1.44623508	2.72496006	0.00232202
215090	A_55_P1953266	Maneal	mannosidase, endo-alpha-like	NM_001007573	56.5	59.4	53	64.3	152.1	127.5	211.8	153.5	58.3	161.225	1.44616153	2.72482114	0.05135274
65945	A_55_P2075592	Clstn1	calsyntenin 1	NM_023051	102.2	96	81	81.6	251.6	253.4	226.3	247.7	90.2	244.75	1.44606063	2.72463057	0.00159119
12972	A_51_P435198	Cryz	crystallin, zeta	NM_009968	2508.6	1955.3	2055.6	2084.6	5880.2	5695.9	5768.4	5980.6	2151.025	5831.275	1.44516198	2.72293394	0.00077937
12228	A_55_P1972322	Btg3	B-cell translocation gene 3	NM_009770	1418.3	1870.3	1562.4	1687.8	4318.6	5400.5	4158.1	3952.8	1634.7	4457.5	1.44402896	2.72079633	0.0121997
52357	A_51_P300378	Wwc2	WW, C2 and coiled-coil doma	NM_133791	1491.6	1860.9	1575.3	1902.5	4970.7	4763.4	4322	4445.6	1707.575	4625.425	1.44328342	2.71939065	0.00228998
241950	A_55_P1973553	Bbs12	Bardet-Biedl syndrome 12 (hu	NM_001008502	64	66.6	58	76.4	174	161.5	173.3	211.6	66.25	180.1	1.44243138	2.71778509	0.00641993
56068	A_52_P305995	Ammecr1	Alport syndrome, mental reta	NM_019496	189.2	140.5	167.8	134.7	409.5	380.3	493.2	424.7	158.05	426.925	1.44066088	2.71445182	0.01831321
12626	A_51_P229105	Cetn3	centrin 3	NM_007684	663.3	702.9	704.6	695.9	1919.1	1782.9	1908.5	1900.6	691.675	1877.775	1.44064918	2.71442981	5.08E-05
104732	A_55_P2063336	4930427A07Rik	RIKEN cDNA 4930427A07 gen	NM_134041	11	13.1	14.3	12.7	33	42	31.1	32.8	12.775	34.725	1.43888794	2.71111807	0.00946256
217864	A_52_P535052	Rcor1	REST corepressor 1	NM_198023	19.2	14.8	14.5	17	45.6	42.6	43.8	44.4	16.375	44.1	1.43827167	2.70996021	0.0021332
319475	A_55_P1954266	Zfp672	zinc finger protein 672	NM_178761	1035.4	1038.6	962.7	1138.3	2906.7	2489.1	2682.7	3228.5	1043.75	2826.75	1.43317219	2.70039825	0.00192036
66423	A_51_P357422	2410022L05Rik	RIKEN cDNA 2410022L05 gen	NM_025556	254.6	278.4	289.6	250.9	692.6	715	721.4	765.6	268.375	723.65	1.43269754	2.69950997	0.00022463
17748	A_66_P111660	Mt1	metallothionein 1	NM_013602	34047.5	29644.8	28202.3	25813.3	75956.1	84612.8	76204.6	79086.1	29426.975	78964.9	1.43002216	2.69450855	0.00160522
216829	A_55_P2133225	Mmgt2	membrane magnesium transp	NM_175002	189.4	188.5	202.6	176.9	503.4	470.1	523.3	540.6	189.35	509.35	1.4273259	2.68947746	0.00023921
98170	A_55_P2113081	Tmem132a	transmembrane protein 132A	NM_133804	897.4	877.8	936.2	983.7	2405.6	2559.4	2493	2467.6	923.775	2481.4	1.4265569	2.68804427	8.42E-05
69709	A_55_P2135621	2410017P09Rik	RIKEN cDNA 2410017P09 gen	BC067010	16.6	17.9	14.2	13.8	38.6	45.6	42.7	40.4	15.625	41.825	1.426131	2.68725085	0.0033851
77032	A_51_P358243	2610029I01Rik	RIKEN cDNA 2610029I01 gen	NM_029840	646	745.7	544.4	543.2	1567.7	1804.9	1638.2	1601.5	619.825	1653.075	1.42588401	2.68679083	0.00756591
69445	A_55_P2049831	1700023D09Rik	RIKEN cDNA 1700023D09 gen	AK043475	30.5	22.2	27.4	24.8	62.4	66.2	82.1	69.7	26.225	70.1	1.4207583	2.67726194	0.01343798
114654	A_55_P2052145	Ly6g6d	lymphocyte antigen 6 comple	NM_033478	101.5	96.4	107.5	71.2	230.6	247.1	261.1	258	94.15	249.2	1.41989762	2.67566522	0.02045236
14693	A_55_P1987264	Gnb2	guanine nucleotide binding pr	NM_010312	16080.8	18535.3	14993.4	16026.5	46897.9	46685	38418.4	43401.9	16409	43850.8	1.41790911	2.67197981	0.00193576

78369	A_51_P235726	Icam4	intercellular adhesion molecu	NM_023892	115.4	93.2	112.8	90.3	302.7	268.1	262.1	262	102.925	273.725	1.4171835	2.67063628	0.00365501
238799	A_52_P480939	Tnpo1	transportin 1	NM_178716	617.4	682.9	676.1	764.6	1908.8	1696.5	1851.1	1832.5	685.25	1822.225	1.41382853	2.66443296	0.00059762
22654	A_55_P1990217	Zfp13	zinc finger protein 13	NM_011747	34.6	25.3	29	26.6	80.9	73.9	71.4	79.6	28.875	76.45	1.4132545	2.66337302	0.00461304
71086	A_55_P2213828	4933412E12Rik	RIKEN cDNA 4933412E12 gen	XR_105385	38.2	50.4	33.8	33.4	102.9	106.7	109.7	89.5	38.95	102.2	1.40804273	2.65376888	0.04034563
67211	A_55_P2011132	Armc10	armadillo repeat containing 1	NM_026034	284.9	326.4	308.3	360.7	821.6	877.5	859.6	823.9	320.075	845.65	1.40643476	2.65081274	0.00072534
68556	A_51_P198387	Uckl1	uridine-cytidine kinase 1-like	NM_026765	303.4	344	393	450.4	941.5	941	988.5	1041.3	372.7	978.075	1.40633621	2.65063168	0.01312315
66391	A_52_P638513	2310061J03Rik	RIKEN cDNA 2310061J03 gene	NR_027965	196.7	184.5	211.4	210.7	509.1	478.4	624.1	524.7	200.825	534.075	1.40616325	2.65031391	0.00224729
16593	A_55_P2044119	Klc1	kinesin light chain 1	NM_008450	140.7	123.8	130.3	123.9	317.4	380.3	306.9	374.3	129.675	344.725	1.40593921	2.64990238	0.00182552
791294	A_66_P107536	Gm9958	predicted gene 9958	ENSMUST00000068250	45.8	54	59.6	73.4	140.6	134.9	161.3	172.2	58.2	152.25	1.40140788	2.6415924	0.06733836
53415	A_52_P515036	Htatip2	HIV-1 tat interactive protein 2	NM_016865	106.2	145.3	146	153	458.5	335.6	321.5	338.1	137.625	363.425	1.40015368	2.63929695	0.08026846
232664	A_51_P135732	Ccdc136	coiled-coil domain containing	NM_001201378	272.7	244.7	263	269.9	759.3	679.4	648.7	683	262.575	692.6	1.39813792	2.63561185	0.00029314
19893	A_55_P1968833	Rpgr	retinitis pigmentosa GTPase r	NM_001177950	144.9	126.6	145.3	154.3	394.1	357.5	385.7	364.8	142.775	375.525	1.39774553	2.6348951	0.00051376
13859	A_52_P528963	Eps15l1	epidermal growth factor rece	NM_001122832	116.3	78.8	78.3	103.7	230.9	245.1	248.1	255	94.275	244.775	1.39710973	2.63373415	0.03340537
71910	A_51_P281593	Ppapdc1b	phosphatidic acid phosphatas	NM_028000	178.7	209.3	230.9	221	527	545.9	574	554.9	209.975	550.45	1.39632293	2.63229819	0.00134824
19158	A_66_P105843	Cyth2	cytohesin 2	NM_011181	2874.9	2923.8	2716.7	2488.1	6867.1	7967.4	6958.3	7143.1	2750.875	7233.975	1.39520976	2.63026792	0.00061901
22294	A_55_P2112589	Uxt	ubiquitously expressed transc	BC082294	1225.4	1175.1	1035.6	959	3013.3	2889.4	2981.8	2621.9	1098.775	2876.6	1.39320113	2.62660841	0.00229173
22248	A_55_P1957378	Unc119	unc-119 homolog (C. elegans)	NM_011676	653.7	613.9	797.2	705.3	1849.2	1826.2	1779.3	1787.1	692.525	1810.45	1.39314436	2.62650506	0.00117993
72151	A_51_P246339	Rfc5	replication factor C (activator	NM_028128	242	282.3	209.5	275.1	720.5	672.6	629.9	613.4	252.225	659.1	1.39288891	2.62604003	0.00624076
68857	A_52_P349143	Dtwd2	DTW domain containing 2	NM_026854	95.4	86.4	84.1	91.6	262.8	226.5	225.2	224.4	89.375	234.725	1.39149856	2.62351049	0.00053993
75731	A_52_P335609	5133401N09Rik	RIKEN cDNA 5133401N09 gen	NM_198004	278.8	265.1	215	219.8	670.3	614.7	652.3	615.5	244.675	638.2	1.39142216	2.62337156	0.00326564
54366	A_52_P372151	Ctnnal1	catenin (cadherin associated	NM_018761	503.9	511	560	518.8	1363.2	1227.7	1492.3	1410.1	523.425	1373.325	1.38923418	2.61939599	0.00052249
75221	A_51_P147373	Dpp3	dipeptidylpeptidase 3	NM_133803	1627.4	1382.7	1454.8	983.7	3770.8	3406.9	3591	3283.6	1362.15	3513.075	1.38895652	2.61889191	0.06639271
68876	A_55_P2093023	Xrcc6bp1	XRCC6 binding protein 1	NM_026858	25.2	21.1	32.7	25	71.5	61.1	71.2	65	26	67.2	1.38488678	2.61151462	0.02834022
69697	A_55_P2067722	Camsap3	calmodulin regulated spectrin	NM_001163749	140	108.2	111.7	87.8	320.8	299.2	276.3	258.7	111.925	288.75	1.38231264	2.60685917	0.04811978
12575	A_51_P363947	Cdkn1a	cyclin-dependent kinase inhib	NM_007669	570.4	490.4	452.2	422.4	1577.5	1040	1241.6	1201.3	483.85	1265.1	1.37930727	2.60143429	0.05359019
76889	A_55_P1998761	Adck4	aarF domain containing kinas	NM_133770	234.4	220.9	212.9	218.7	645.6	556.8	523	586	221.725	577.85	1.37850406	2.59998637	0.00064091
56354	A_55_P2111950	Dnajc7	DnaJ (Hsp40) homolog, subfa	NM_019795	7964.8	6993.3	7444.8	8308.9	22180.9	19236.3	18174.2	20187.9	7677.95	19944.825	1.37643555	2.59626123	0.00127739
108902	A_51_P305320	B3gnt1	UDP-GlcNAc:betaGal beta-1,3	NM_175383	1873.1	1898.2	2134.9	1961	4729.4	4768.1	5482.3	5449.6	1966.8	5107.35	1.37504633	2.5937624	0.00073001
15185	A_55_P2009792	Hdac6	histone deacetylase 6	NM_010413	1340.6	1377.7	1380.1	1322.1	3544.8	3457.4	3498	3548.8	1355.125	3512.25	1.37412715	2.59211037	4.23E-05
73991	A_52_P526396	Atl1	atlastin GTPase 1	NM_178628	46.9	49.1	44.9	56	121.7	137.4	129.5	120.6	49.225	127.3	1.37378808	2.59150124	0.00128518
66949	A_55_P2030938	Trim59	tripartite motif-containing 59	NM_025863	47.1	41.9	48	50	143.6	127	116.6	100.4	46.75	121.9	1.37357097	2.59111127	0.01168272
26447	A_55_P2053497	Poli	polymerase (DNA directed), io	NM_011972	86.6	104.4	90.9	81.8	231.5	183.9	238.1	298.1	90.925	237.9	1.37255302	2.58928365	0.06895061
19090	A_51_P241667	Prkdc	protein kinase, DNA activated	NM_011159	151.8	133.3	160.4	157.7	414.5	332	425.9	389.6	150.8	390.5	1.36983959	2.5844183	0.0039427
98541	A_55_P2330822	AU019278	expressed sequence AU01927	AK044967	53	60.5	43.5	51.8	168.9	113.2	129.9	129.6	52.2	135.4	1.36933195	2.58350908	0.05595251
545861	A_55_P2055762	Gm5878	predicted gene 5878	NM_001034902	27.7	26	27.8	29.8	72.4	72.2	67.1	75.2	27.825	71.725	1.36655979	2.57854958	0.00023722
30045	A_51_P442284	Dnajc12	DnaJ (Hsp40) homolog, subfa	NM_013888	1531.1	1461	1599.7	1624.8	4084.4	3878.4	4248.2	3782	1554.15	3998.25	1.36299965	2.57219435	0.0002169
58193	A_55_P1955568	Extl2	exostoses (multiple)-like 2	NM_021388	720.1	751.3	637.4	748.3	1968.3	1763.3	1696.5	1916.7	714.275	1836.2	1.36268107	2.5716264	0.00091162
11566	A_52_P206613	Adss	adenylosuccinate synthetase,	NM_007422	252	236.6	294.3	218.4	557.1	620	699.2	693.9	250.325	642.55	1.36262582	2.57152792	0.01132459
105525	A_55_P2278093	AI480461	expressed sequence AI48046	AK148445	33.6	32.6	41	38.9	92	89.2	97.3	95.6	36.525	93.525	1.36235018	2.57103666	0.00168081
619331	A_52_P500077	Zfp551	zinc fingr protein 551	NM_001033820	88.1	90.4	95.2	96.2	231.2	192.8	265.2	267.6	92.475	239.2	1.35966362	2.56625337	0.00895103
218734	A_51_P278427	3830406C13Rik	RIKEN cDNA 3830406C13 gen	NM_146051	195.8	214	220.7	191.1	473.5	513.8	591.4	531.1	205.4	527.45	1.35857078	2.56431018	0.00152835
67588	A_52_P123738	Rnf41	ring finger protein 41	NM_001164237	28	33.9	39.1	36.4	84.5	81.9	77	109.6	34.35	88.25	1.35850749	2.56419769	0.05326898
110006	A_51_P211491	Gusb	glucuronidase, beta	NM_010368	399.1	399.6	376.6	371.2	1009.3	1009.2	960.7	984	386.625	990.8	1.35815777	2.56357618	8.32E-05
66684	A_55_P2004452	Tceal8	transcription elongation facto	NM_025703	71.8	78.3	95.9	83.2	199.6	219.3	205.4	214.7	82.3	209.75	1.35684445	2.56124355	0.00277125
235330	A_55_P2186352	Ttc12	tetratricopeptide repeat dom	NM_172770	503.3	447.4	429.7	537.5	1176.6	1246.4	1291.9	1180.7	479.475	1223.9	1.35666548	2.56092585	0.00140524
232440	A_55_P2099540	H2afj	H2A histone family, member	NM_177688	103.7	111.7	101.5	83.7	274.8	253.2	223.2	272.4	100.15	255.9	1.3564747	2.56058722	0.00817296
330064	A_55_P2000182	Slc5a6	solute carrier family 5 (sodiun	NM_001177621	649.6	836.5	745.8	871.9	2159	1756.8	1987.6	2009.5	775.95	1978.225	1.35550524	2.55886713	0.00858939
20585	A_52_P532033	Hltf	helicase-like transcription fac	NM_009210	169.6	146.9	182	147.7	419.3	419.2	408.2	400.1	161.55	411.7	1.35541988	2.55871574	0.00115551
76123	A_51_P108252	Gpsm2	G-protein signalling modulato	NM_029522	81.6	101.9	93.2	89.8	250	245.2	237.5	204.4	91.625	234.275	1.35455637	2.5571847	0.0028887
14697	A_55_P2000643	Gnb5	guanine nucleotide binding pr	ENSMUST00000098556	776.9	788.6	595.6	810	2204	1721.6	1664.6	2001	742.775	1897.8	1.35454875	2.5571712	0.03179292
320560	A_55_P2081585	Dennd5b	DENN/MADD domain contain	NM_177192	497.9	661.8	539.8	725.6	1435.6	1472.5	1623.2	1606	606.275	1534.325	1.35402394	2.55624115	0.02366902
73490	A_52_P470869	Mipol1	mirror-image polydactyly gen	NM_001164370	56.7	51.7	64.2	62.2	172.4	132.2	140.2	156.4	58.7	150.3	1.35398007	2.55616342	0.00736989
407824	A_55_P2333580	BC020402	cDNA sequence BC020402	NR_033219	42.9	36.2	37.8	53.2	109.9	93.5	104.8	123.7	42.525	107.975	1.35366161	2.55559922	0.04895045
234740	A_51_P432779	Tmem231	transmembrane protein 231	NM_001033321	13.4	15.5	17.3	15.4	37.1	51.2	35.2	35.3	15.4	39.7	1.35365075	2.55557999	0.04891338
22051	A_52_P382914	Trip6	thyroid hormone receptor int	NM_011639	717	930.2	840.8	849.8	1825.7	2237.4	2589.2	1916.4	834.45	2142.175	1.35262259	2.55375937	0.02970322
407786	A_55_P2244722	Taf9b	TAF9B RNA polymerase II, TA	NM_001001176	108	106.6	111.3	109.3	259.9	279.6	311.2	263.4	108.8	278.525	1.35260816	2.55373383	0.00040986
100039042	A_55_P2055168	Gm2016	predicted gene 2016	NM_001122662	105.8	153.5	140.6	162.6	367.6	376.7	305.7	370.9	140.625	355.225	1.35054937	2.55009213	0.06034237
67706	A_52_P228031	Tmem179b	transmembrane protein 179B	NM_026325	348.3	352.4	315.3	284	767	800.2	891.3	849.2	325	826.925	1.35036055	2.54975839	0.00200518
19165	A_55_P2036280	Psen2	presenilin 2	NM_001128605	800.1	826.7	977.2	905.2	2276.8	2088	2214.8	2337.2	877.3	2229.2	1.34859115	2.54663316	0.00094462
386655	A_52_P659762	Eid2	EP300 interacting inhibitor of	NM_198425	109.7	109.4	151.5	112.3	284.4	314.8	315.8	303.3	120.725	304.575	1.34806542	2.54570531	0.01228894
66704	A_66_P136259	Rbm4b	RNA binding motif protein 4B	NM_025717	45.4	53.3	51.7	54.1	124	131.1	129.8	134.7	51.125	129.9	1.34803493	2.5456515	0.00047839
66144	A_55_P1973486	Atp6v1f	ATPase, H+ transporting, lyso	NM_025381	12671	13376.7	12903.3	12496.9	30437	35078.3	33080.7	32486.1	12861.975	32770.525	1.34791358	2.5454374	0.0001908
56378	A_55_P2023953	Arpc3	actin related protein 2/3 com	NM_019824	5699	5416.3	6393.6	5638.6	14630.5	13617.2	14984.6	15639	5786.875	14717.825	1.34769211	2.54504667	0.00059208
14590	A_55_P2119463	Ggh	gamma-glutamyl hydrolase	NM_010281	1556.8	1828.1	1824.2	1769.1	4183.6	4433.2	4551.1	4534.4	1744.55	4425.575	1.34525305	2.54074758	0.00045303
16322	A_52_P401484	Inha	inhibin alpha	NM_010564	71.2	77.5	82.3	77.3	181	175.3	217.4	211.7	77.075	196.35	1.34461672	2.53962718	0.00241366
72320	A_52_P45606	2510003E04Rik	RIKEN cDNA 2510003E04 gen	NM_028197	36.7	37.4	30.9	32.7	85.7	83.3	91.5	88	34.425	87.125	1.34329279	2.53729768	0.00087166
11785	A_51_P344249	Apbb1	amyloid beta (A4) precursor p	NM_009685	24.5	21.7	28.7	31.5	64.9	73.4	68.7	60.8	26.6	66.95	1.34287515	2.53656328	0.02408277
54126	A_52_P26357	Arhgef7	Rho guanine nucleotide excha	NM_001113517	19.1	25.1	23.2	18.6	59.2	55.2	55.9	46.8	21.5	54.275	1.34223371	2.53543573	0.01974281
68763	A_52_P31814	1110038B12Rik	RIKEN cDNA 1110038B12 gen	NR_027943	1059.6	1087.5	1513.2	1178.1	2728.4	2797.6	3756.3	2944.6	1209.6	3056.725	1.34025725	2.53196462	0.07221492
18759	A_55_P2064578	Prkci	protein kinase C, iota	NM_008857	955.6	1067.5	910.2	1067.7	2757.4	2724	2290.4	2365.6	1000.25	2534.35	1.33984108	2.53123435	0.00257812
12330	A_52_P337679	Canx	calnexin	NM_007597	6270.8	6612.1	6444.1	7044	16705.7	17691.4	16418.5	15835	6592.75	16662.65	1.3378521	2.52774704	0.00022419
100504166	A_52_P68223	4933421O10Rik	RIKEN cDNA 4933421O10 gen	NR_036602	42.8	40.4	31	36.2	96.1	85.5	97.5	98.7	37.6	94.45	1.33717229	2.52655623	0.00933524
104831	A_55_P2172989	Ptpn23	protein tyrosine phosphatase	NM_001081043	991.1	958.5	1176.2	1148.2	3111.5	2410.2	2559	2706.9	1068.5	2696.9	1.33488116	2.52254701	0.00737191
98417	A_55_P1976017	Cnih4	cornichon homolog 4 (Drosop	NM_030131	5238.5	4646.2	4700.5	5461	12384.4	13202.6	11820.4	13083	5011.55	12622.6	1.33471157	2.5222505	0.00073924
217700	A_51_P191354	Acot6	acyl-CoA thioesterase 6	ENSMUST00000056822	210.8	244.3	204.4	216.1	544.2	504.3	604.9	552.9	218.9	551.575	1.33362785	2.52035657	0.00131084
13872	A_51_P366024	Ercc3	excision repair cross-complen	NM_133658	209.5	187.7	212.8	198.4	498.3	544.2	486	506.4	202.1	508.725	1.33227404	2.5179926	0.00031197
20467	A_52_P57526	Sin3b	transcriptional regulator, SIN3	NM_001113248	4961.6	5259.2	5281.7	5979.5	13205	14605.1	13726.3	12438	5370.5	13493.6	1.33007256	2.51415319	0.00110016
18010	A_52_P58524	Neu1	neuraminidase 1	NM_010893	2322.4	2602.2	2423.6	2408.7	6136.5	6245.3	5838.3	6289	2439.225	6127.275	1.32945281	2.5130734	0.00015964
56613	A_51_P482633	Rps6ka4	ribosomal protein S6 kinase,	NM_019924	432.8	352.1	384.4	299.3	929.4	883.5	954	888.4	367.15	913.825	1.32771052	2.51004029	0.01106763
19691	A_55_P1990490	Recql	RecQ protein-like	NM_023042	101	121.6	98.2	105.1	271	265	237.9	294	106.475	266.975	1.32710013	2.50897854	0.00332175
52808	A_52_P270035	Tspyl2	TSPY-like 2	NM_029836	321.5	264.8	292.5	289.9	852.9	639.3	708	733.8	292.175	733.5	1.32357304	2.50285209	0.00606613
22712	A_55_P2017075	Zfp54	zinc finger protein 54	NM_011760	22.4	24.9	27.5	27.3	65.1	55.4	69.7	65	25.525	63.8	1.32154121	2.49932967	0.00472975
50505	A_51_P210082	Ercc4	excision repair cross-complen	NM_015769	545.7	666.4	681.7	629.3	1461.6	1567.3	1624	1623.3	630.775	1569.05	1.31866055	2.49434418	0.00167431
56433	A_55_P2044197	Vps29	vacuolar protein sorting 29 (S	NM_019780	1852.5	1838.2	1699.2	1843.3	4131.8	4901.4	4368.8	4658.7	1808.3	4515.175	1.31805374	2.49329526	0.00053003
108012	A_51_P435321	Ap1s2	adaptor-related protein comp	NM_026887	37.9	36.6	37.4	34	91.5	91.8	87.8	92.4	36.475	90.875	1.31794129	2.49310094	0.00014404
235461	A_55_P2295786	Fam63b	family with sequence similarit	NM_172772	38.4	49.7	34.1	42.2	94.4	100.1	95	118	41.1	101.875	1.31735812	2.49209337	0.03430516
12752	A_55_P1977917	Cln3	ceroid lipofuscinosis, neurona	NM_001146311	347.2	414.2	373.6	332.6	930.9	841.7	914.1	956.1	366.9	910.7	1.31501718	2.48805293	0.00164382
70088	A_55_P2085664	Meaf6	MYST/Esa1-associated factor	NM_027310	911.5	1070	916.2	1066.9	2502.5	2335.5	2541.4	2457.3	991.15	2459.175	1.31467855	2.487469	0.00092808
20926	A_55_P2030204	Supt6h	suppressor of Ty 6 homolog (S	NM_009297	2480.8	2131.6	1903.5	2274.9	5873.1	5291.7	5239.9	5378.1	2197.7	5445.7	1.31432237	2.48685496	0.00282046
66958	A_55_P2052495	Tmx2	thioredoxin-related transmen	NM_025868	2755.1	2388.4	2135.3	2163.9	6067.5	5485.2	5272.3	6625.9	2360.675	5862.725	1.31424339	2.48671882	0.01062122
77110	A_55_P1985040	Gpbp1l1	GC-rich promoter binding pro	NM_029868	108	90.8	83.2	72.5	237.5	201.8	225.7	209	88.625	218.5	1.3140648	2.48641101	0.02709225
72322	A_52_P201232	Xpo5	exportin 5	NM_028198	100	99.8	107.8	98.9	260.3	243.7	259	247.1	101.625	252.525	1.31345434	2.48535914	0.00013877
97387	A_51_P234833	Strn4	striatin, calmodulin binding p	NM_133789	482	516.1	426.8	534.4	1315.5	1238	1091.3	1211.9	489.825	1214.175	1.31162235	2.48220514	0.0032294
228858	A_66_P123666	Gdap1l1	ganglioside-induced different	NM_144891	27.7	23.3	23.9	25.9	61.6	67.7	57	63.7	25.2	62.5	1.31104071	2.4812046	0.00141103
75746	A_55_P2078710	Morc4	microrchidia 4	NM_029413	304.3	380.8	327.7	404.2	883.4	976.4	846.9	795.5	354.25	875.55	1.31065497	2.48054129	0.01109129
26378	A_51_P443293	Decr2	2-4-dienoyl-Coenzyme A redu	NM_011933	138.4	124.6	123.8	139.7	342.2	311.1	290.6	364.6	131.625	327.125	1.31026902	2.47987778	0.00251028
74340	A_52_P162509	Ahcyl2	S-adenosylhomocysteine hyd	NM_021414	53	46.8	51.4	43.5	118.6	110.1	130.5	122.7	48.675	120.475	1.30913282	2.47792551	0.00202378
72144	A_51_P122740	Slc37a3	solute carrier family 37 (glyce	NM_028123	324.5	316.3	298.9	325.4	795.4	766.7	771.4	798.1	316.275	782.9	1.30825056	2.47641063	0.00010989
67422	A_51_P384618	Dhdds	dehydrodolichyl diphosphate	NM_026144	289.3	274.2	299.6	283.8	675.5	660.5	788.8	719.7	286.725	711.125	1.30771561	2.47549255	0.0006318
319160	A_55_P2091145	Hist1h4k	histone cluster 1, H4k	NM_178211	6242.2	5139.6	5879.6	6013.3	15757.9	12592.3	14182.1	15103.6	5818.675	14408.975	1.30692688	2.47413955	0.00379253
68053	A_51_P359293	Ubxn2b	UBX domain protein 2B	NM_026534	81	81.8	70.7	74.1	203.9	193	151.4	218	76.9	191.575	1.30641546	2.47326265	0.02107093
18570	A_51_P431903	Pdcd6	programmed cell death 6	NM_011051	2539	2848.3	2593.2	2368.1	6027.4	6447.4	6447.8	6604.6	2587.15	6381.8	1.30492663	2.47071161	0.0005908
75029	A_55_P1989871	Purg	purine-rich element binding p	NM_152821	19.7	19.8	21.6	27.7	54.9	55.6	49.4	57.5	22.2	54.35	1.30383767	2.46884741	0.02066526
72075	A_55_P1956827	Ogfr	opioid growth factor receptor	NM_031373	6688.9	6033.7	6709	6416.8	16059.4	16115.8	15197.8	16372.2	6462.1	15936.3	1.30298829	2.46739432	0.00019526
70508	A_51_P322542	Bbx	bobby sox homolog (Drosoph	NM_027444	212.5	232	219	257.5	597.6	573.9	563.8	532.7	230.25	567	1.30284883	2.46715582	0.00098573
66863	A_55_P2102175	Lztr1	leucine-zipper-like transcripti	NM_025808	1929	1873.6	2202.5	2166	5186.2	4402.6	5350	5227.1	2042.775	5041.475	1.30268547	2.46687646	0.00274186
237246	A_55_P2032633	BC022960	cDNA sequence BC022960	XM_001477798	27.6	23.5	25	30.7	61.9	63.6	64.9	71.8	26.7	65.55	1.30091818	2.46385641	0.00474671
26419	A_52_P558382	Mapk8	mitogen-activated protein kin	NM_016700	45.5	46.2	39.6	47.2	109.4	115.6	106.9	106.1	44.625	109.5	1.29752658	2.45807099	0.00069712
68737	A_51_P112237	Angel1	angel homolog 1 (Drosophila)	NM_144524	387.7	380.9	427.5	396.6	987.4	898	1012.2	1017.5	398.175	978.775	1.29719183	2.45750071	0.00042705
17161	A_55_P2055257	Maoa	monoamine oxidase A	NM_173740	169.8	166.2	162.3	157.8	404.2	376.1	456.5	379.2	164.025	404	1.2965606	2.4564257	0.0009279
214063	A_52_P533083	Dnajc16	DnaJ (Hsp40) homolog, subfa	NM_172338	193.1	226.1	209.3	194.6	510	497.3	502	508	205.775	504.325	1.29618409	2.45578471	0.00038519
69786	A_55_P1964213	Tprkb	Tp53rk binding protein	NM_001170488	191.5	254.3	206.6	233.8	543.1	510.5	578.9	532.8	221.55	541.325	1.29601151	2.45549095	0.00551925
107932	A_55_P2020373	Chd4	chromodomain helicase DNA	NM_145979	4073.1	3773.3	3962.4	4075.9	10400.3	8224.8	10311.7	10182.8	3971.175	9779.9	1.29433983	2.45264738	0.00260749
67455	A_55_P2111770	Klhl13	kelch-like 13 (Drosophila)	NM_026167	578.7	679.5	748.6	801.7	1719	1895.8	1577.2	1658	702.125	1712.5	1.2935879	2.4513694	0.01452192
19089	A_55_P2035892	Prkcsh	protein kinase C substrate 80	NM_008925	3891.9	3958.3	3974.4	3526.9	8679	9264.5	9454.8	10176.5	3837.875	9393.7	1.29074127	2.44653729	0.00066438
12727	A_55_P1962731	Clcn4-2	chloride channel 4-2	NM_011334	6853.2	7801.9	6868.8	7241.2	18107.8	16912.2	17230.2	18049.7	7191.275	17574.975	1.29060303	2.44630287	0.00032417
276852	A_66_P134878	D11Wsu47e	DNA segment, Chr 11, Wayne	NM_177777	919.5	944.9	1016.4	1189.1	2483.1	2403.6	2512.5	2505.1	1017.475	2476.075	1.2902094	2.44563551	0.00253537
72672	A_52_P676623	Zfp518a	zinc finger protein 518A	NM_028319	58.2	66.5	66.1	66.6	165.5	147.9	159.7	155.8	64.35	157.225	1.28991981	2.44514465	0.00053108
214899	A_52_P374669	Kdm5a	lysine (K)-specific demethylas	NM_145997	220.3	171.5	206.5	199	487.1	417.7	521.5	520.6	199.325	486.725	1.28823485	2.44229057	0.00933849
76850	A_55_P2113071	Eif2c4	eukaryotic translation initiatio	NM_153177	447.3	455.1	388.2	451	1081.8	962.3	1065.7	1136.2	435.4	1061.5	1.28609227	2.43866616	0.00140039
74552	A_55_P2109257	Nipal3	NIPA-like domain containing 3	NM_028995	264.3	289.7	285.6	274.5	682.7	601.5	672.3	763.4	278.525	679.975	1.28345565	2.43421339	0.00163345
16568	A_55_P1978441	Kif3a	kinesin family member 3A	NM_008443	428.5	444.3	423.2	502.2	1057.5	918.3	1136	1286.7	449.55	1099.625	1.28315376	2.43370409	0.01535042
66953	A_55_P2012498	Cdca7	cell division cycle associated 7	NM_025866	25.8	32.4	35.5	29.1	74.3	70.6	75.6	76.3	30.7	74.2	1.28272416	2.43297949	0.00741327
22700	A_55_P1966908	Zfp40	zinc finger protein 40	NM_009555	41.7	39.4	46.8	43.9	90.5	89	124.4	118	42.95	105.475	1.28259505	2.43276176	0.04128615
74025	A_51_P382347	Nphp3	nephronophthisis 3 (adolesce	NM_172460	67.6	44.8	47.7	53.7	135.1	133.2	140.3	107.3	53.45	128.975	1.28151647	2.43094368	0.09762827
74044	A_55_P2062836	Ttf2	transcription termination fact	NM_001013026	757.8	955.3	1019.4	820.1	2132.6	2093.1	2273.7	2081.6	888.15	2145.25	1.28137065	2.43069798	0.00750377
18641	A_51_P310896	Pfkl	phosphofructokinase, liver, B	NM_008826	89.2	88.7	88.1	74.9	193.6	216.6	203.6	211.8	85.225	206.4	1.27854479	2.42594155	0.00118307
319719	A_55_P1992403	4732471D19Rik	RIKEN cDNA 4732471D19 gen	NM_176987	253.9	346.8	301.3	344.5	788.8	684.7	699.4	836.3	311.625	752.3	1.27780024	2.42468989	0.02616558
53902	A_52_P283524	Rcan3	regulator of calcineurin 3	NM_022980	43.8	56.6	45.3	52.3	101.5	129.5	115	133	49.5	119.75	1.27428735	2.41879307	0.02480171
78943	A_51_P516705	Ern1	endoplasmic reticulum (ER) to	NM_023913	132.7	101.8	108.2	96	325.5	239.4	264.2	232.5	109.675	265.4	1.27305728	2.41673164	0.07575637
67030	A_55_P2135880	Fancl	Fanconi anemia, complement	NM_025923	403.9	445.4	410.9	419.6	991.6	1029	1058.9	977.9	419.95	1014.35	1.27255226	2.41588579	0.00020769
27368	A_52_P109304	Tbl2	transducin (beta)-like 2	NM_013763	27.9	32.6	32.2	24.2	83.9	67.7	67.8	62.6	29.225	70.5	1.27201744	2.41499037	0.04220403
212326	A_51_P195215	Fam149a	family with sequence similarit	NM_153535	118	105	134.2	111.9	281.4	314	277.2	258.3	117.275	282.725	1.27189772	2.41478999	0.00526022
54650	A_55_P2006940	Sfmbt1	Scm-like with four mbt domai	NM_001166532	687.6	623.8	700.5	814.7	1761.5	1725.7	1747	1566.6	706.65	1700.2	1.27172699	2.41450423	0.00366455
55988	A_52_P209311	Snx12	sorting nexin 12	NM_001110310	2561.1	2785.7	2797	2943.8	6872.2	7269.2	6225.9	6418.3	2771.9	6696.4	1.27166971	2.41440837	0.00089059
17766	A_55_P2091681	Nudt1	nudix (nucleoside diphosphat	NM_008637	376.7	362.6	302.5	298.6	842.5	773.1	822.7	780.6	335.1	804.725	1.27083434	2.41301075	0.0044153
67911	A_52_P196743	Zfp169	zinc finger protein 169	NM_026450	32.3	30.8	30.3	38	76.7	70.1	80	90.1	32.85	79.225	1.2700966	2.41177714	0.00970629
319817	A_51_P158400	Rc3h2	ring finger and CCCH-type zin	NM_001100591	2150	1867.5	1780.3	1629	5033	3973.1	4214.4	4673	1856.7	4473.375	1.26995203	2.41153547	0.01415789
216560	A_52_P129443	Wdpcp	WD repeat containing planar	NM_145425	169.5	147.4	144.3	144.4	373.6	372.6	380.9	330.7	151.4	364.45	1.26847341	2.40906514	0.00143809
66078	A_55_P2062029	Tsen34	tRNA splicing endonuclease 3	NM_001164204	10921.5	11451.7	10947.4	12710.3	28871.8	30172.2	25501.8	26324.9	11507.725	27717.675	1.26764723	2.40768596	0.00179435
23830	A_51_P370252	Capn10	calpain 10	NM_011796	279.9	331.2	319.4	234.8	711.2	636.6	770.6	663.6	291.325	695.5	1.26438192	2.40224271	0.03014298
110920	A_52_P140789	Hspa13	heat shock protein 70 family,	NM_030201	471.7	614.3	522.9	489.3	1306	1239.8	1170.7	1298.2	524.55	1253.675	1.26319786	2.40027193	0.00462798

71787	A_55_P2131607	Trnau1ap	tRNA selenocysteine 1 associa	NM_027925	319.9	329.1	380	388.1	839.9	794.7	860.2	897.3	354.275	848.025	1.2630789	2.40007401	0.00228273
100121	A_55_P1999213	Tdrd7	tudor domain containing 7	NM_146142	1516.5	1858.6	1656.3	1940	4519.7	4012.2	3999.2	4139.9	1742.85	4167.75	1.26273636	2.39950423	0.00429439
13637	A_55_P2049687	Efna2	ephrin A2	NM_007909	19.5	20.5	22.9	18.5	53.8	40.6	44.6	57.6	20.35	49.15	1.26255688	2.39920574	0.04149891
68961	A_55_P2108579	Phkg2	phosphorylase kinase, gamma	NM_026888	1679.3	1670.7	1554.9	1470.3	3947.5	3639.4	3719.6	3972	1593.8	3819.625	1.26210199	2.39844938	0.0005265
269401	A_55_P2044252	Znf512b	zinc finger protein 512B	NM_001164597	1714.7	1359	1574.1	1570.7	4329.3	3469.4	3293.4	3851.6	1554.625	3735.925	1.26185477	2.39803842	0.01382039
66262	A_52_P264229	Ing5	inhibitor of growth family, me	NM_025454	126.7	145.9	136	141.7	372.9	264.3	327.4	364.3	137.575	332.225	1.26107593	2.39674418	0.02310942
70317	A_55_P2182810	Arl16	ADP-ribosylation factor-like 1	NM_197995	138.9	194.3	149.8	170.2	371	401.5	379.8	401.1	163.3	388.35	1.26085497	2.39637713	0.01292234
13590	A_51_P354706	Lefty1	left right determination facto	NM_010094	27.2	26.5	27.4	24.6	53.2	79.1	57.4	66.2	26.425	63.975	1.26013817	2.39518679	0.0361777
72477	A_55_P2122260	Tmem87b	transmembrane protein 87B	NM_028248	130.4	185.8	208.2	188	420.1	452.3	396.7	413.9	178.1	420.75	1.25998658	2.39493513	0.09205948
75712	A_51_P422893	Tmem14a	transmembrane protein 14A	NM_029398	454.3	538	490.4	569.3	1310.6	1260.7	1151	1176.4	513	1224.675	1.25875795	2.39289642	0.00302201
51800	A_66_P124052	Bok	BCL2-related ovarian killer pr	NM_016778	159.4	203.4	209.9	170.1	443.8	498.1	431.8	396.6	185.7	442.575	1.2578341	2.39136458	0.01999963
15331	A_55_P1993789	Hmgn2	high mobility group nucleoso	NM_016957	1411.9	1589.3	1495.6	1495.1	3318.5	3990.1	3636.2	3405.7	1497.975	3587.625	1.25758584	2.39095311	0.00121361
434825	A_55_P2350372	LOC434825	uncharacterized LOC434825	AK148969	141.9	120.8	135.2	164.6	363.1	308.1	370	301	140.625	335.55	1.25737496	2.39060365	0.02271707
12028	A_55_P2137406	Bax	BCL2-associated X protein	NM_007527	1708.1	2042.4	1820.3	1646.3	3959.1	4960.1	4188.1	4145.2	1804.275	4313.125	1.25680448	2.38965854	0.00705944
213673	A_55_P2009477	9530068E07Rik	RIKEN cDNA 9530068E07 gen	NM_153117	10726	10432.4	11781.9	12403.8	26586.7	26264.6	26944.9	28336.6	11336.025	27033.2	1.2567414	2.38955405	0.00085892
224440	A_55_P2052425	Setd4	SET domain containing 4	NM_145482	693.4	683.8	714	758.6	1709.5	1802.5	1768.3	1531.8	712.45	1703.025	1.25558784	2.38764415	0.00082012
19672	A_51_P305437	Rcn1	reticulocalbin 1	NM_009037	820.5	875.4	943.9	782.6	2093.3	2097.1	2010.7	1946.1	855.6	2036.8	1.25420399	2.385355	0.00093525
320351	A_52_P8903	D230037D09Rik	RIKEN cDNA D230037D09 ger	NM_177140	379.6	483.9	427.1	460.9	1093.6	1033.2	1004.9	1028.4	437.875	1040.025	1.25328848	2.38384178	0.00254573
20492	A_55_P2071799	Slbp	stem-loop binding protein	NM_009193	128.9	166.3	145.1	161.6	386.2	365.2	295.9	388.8	150.475	359.025	1.25316442	2.3836368	0.0280474
14828	A_55_P2076772	Hspa5	heat shock protein 5	NM_022310	16944.7	19316.1	17858.7	17486.5	39753.8	47807.7	41619	41698.9	17901.5	42719.85	1.25302021	2.38339854	0.0013669
54324	A_51_P313157	Arhgef5	Rho guanine nucleotide excha	NM_133674	302.6	256.9	307	295.7	659.4	708.2	718	678.4	290.55	691	1.25260974	2.38272052	0.00102739
56517	A_51_P407774	Slc22a21	solute carrier family 22 (orgar	NM_019723	45.8	59.4	48.5	45.1	129.6	128	109	105	49.7	117.9	1.24892917	2.37664952	0.02345493
69534	A_55_P2120254	Avpi1	arginine vasopressin-induced	NM_027106	5048.9	5198.6	4909.7	4713.8	11424.2	12628.9	11268.2	11877.1	4967.75	11799.6	1.24758913	2.37444301	0.00036487
12408	A_66_P108152	Cbr1	carbonyl reductase 1	NM_007620	1581.1	1678.8	1654	1693.6	3585.4	3660.1	4271	4208.1	1651.875	3931.15	1.24683716	2.37320571	0.00136213
100040631	A_55_P2151138	Dynlt1e	dynein light chain Tctex-type	NM_001199948	6391.2	7456.4	7568.1	6896.1	18371.9	15406.8	14794.5	18798.2	7077.95	16842.85	1.2460395	2.37189393	0.01026039
235180	A_66_P102903	Fez1	fasciculation and elongation p	NM_183171	17.1	12	16	17.8	33.8	37.7	35.7	40.6	15.725	36.95	1.24550292	2.37101193	0.06056639
64113	A_51_P475291	Moap1	modulator of apoptosis 1	NM_022323	112.1	103.3	95.4	99	246.1	254.6	221.4	249.1	102.45	242.8	1.2454173	2.37087121	0.00119284
106672	A_66_P112855	AI413582	expressed sequence AI41358	NM_001002895	838.1	870.8	855.3	975.5	2307.3	2093.3	1774.3	2244.4	884.925	2104.825	1.24531016	2.37069515	0.00740706
269831	A_55_P2011061	Tspan12	tetraspanin 12	NM_173007	924.4	1175.3	916.1	1061.8	2233.4	2771.4	2078.1	2584.1	1019.4	2416.75	1.24376908	2.36816415	0.03545355
69234	A_55_P2010966	Zfp688	zinc finger protein 688	NM_026999	81.4	111.8	96.3	88.1	231.4	209.5	218.1	228.5	94.4	221.875	1.24192013	2.36513106	0.01017847
69109	A_55_P2013598	Fam58b	family with sequence similari	NM_197989	1296.7	1095	1277.3	1119.1	2886.5	2292.4	3125.2	3065.3	1197.025	2842.35	1.24123621	2.36401012	0.02501451
57370	A_55_P2184364	B4galt3	UDP-Gal:betaGlcNAc beta 1,4	NM_020579	4191.7	4719.9	4733.5	4828	9862	11346.6	10591.9	11880.3	4618.275	10920.2	1.24020813	2.3623261	0.00196617
74766	A_55_P2170474	Yipf2	Yip1 domain family, member	NM_138303	340.5	363.4	343.5	351.9	859	833.4	793.5	819.8	349.825	826.425	1.24012015	2.36218205	0.00016709
214685	A_55_P2036220	Chadl	chondroadherin-like	NM_001164320	670.4	718.9	702.2	687.5	1686.3	1468.1	1560.2	1872.9	694.75	1646.875	1.23961843	2.3613607	0.00250607
171095	A_55_P2185332	Il17rc	interleukin 17 receptor C	NM_134159	834.4	763.6	785	805.5	2089.4	1948.5	1849.3	1644.1	797.125	1882.825	1.23532721	2.3543474	0.00243118
22346	A_66_P106593	Vhl	von Hippel-Lindau tumor sup	NM_009507	770	899.2	901.9	935.8	2275.9	2004.4	2045.8	1908.1	876.725	2058.55	1.23236342	2.34951573	0.00323905
65107	A_51_P430357	Lrp10	low-density lipoprotein recep	NM_022993	517.3	449.1	402.4	394.2	974.7	980.3	997.1	1178.7	440.75	1032.7	1.23236211	2.34951359	0.01635041
216136	A_51_P117109	Ilvbl	ilvB (bacterial acetolactate sy	NM_173751	251.8	229.2	203.1	219.6	560.7	458.1	498.9	611.6	225.925	532.325	1.23206927	2.34903673	0.01727981
69071	A_55_P2048110	Tmem97	transmembrane protein 97	NM_133706	111.5	109.4	99.9	104.6	243.3	251.6	271.8	232.7	106.35	249.85	1.23119726	2.34761732	0.0008017
213452	A_52_P355095	Dstyk	dual serine/threonine and tyr	NM_172516	52.1	62.7	60.1	55.9	136.5	138.4	125	140.7	57.7	135.15	1.2300114	2.34568844	0.00157911
16765	A_55_P2068663	Stmn1	stathmin 1	NM_019641	419.2	568.6	445.3	527.9	1233.5	1264.1	1108	980.1	490.25	1146.425	1.22936108	2.34463132	0.04753886
76952	A_52_P391983	Nt5c2	5-nucleotidase, cytosolic II	NM_029810	82.5	113.2	91.2	103.3	235.8	224.8	241	208.1	97.55	227.425	1.22930747	2.3445442	0.01611737
216831	A_55_P1970309	Arhgap44	Rho GTPase activating protei	NM_175003	745.1	613.9	748	756.5	1704.6	1702	1612.7	1666.2	715.875	1671.375	1.22815006	2.34266402	0.00210531
70449	A_55_P2216531	2610209C05Rik	RIKEN cDNA 2610209C05 gen	AK085917	13.4	17.6	14.3	12	36.4	31.3	30.5	35	14.325	33.3	1.22735182	2.34136819	0.04563606
67978	A_66_P137943	Tctn2	tectonic family member 2	NM_026486	177.9	237.4	242.2	219	511.7	440.6	530.2	561.6	219.125	511.025	1.22633279	2.33971497	0.03588
13664	A_66_P112853	Eif1a	eukaryotic translation initiati	NM_010120	1034.5	1184.1	1024.6	1190.8	2454.9	2727.1	2445.9	2720.8	1108.5	2587.175	1.22442792	2.33662777	0.00208234
66411	A_66_P124788	Tbcb	tubulin folding cofactor B	NM_025548	891.6	940.8	934.9	855.8	2074.3	2086.3	2338.6	1976.3	905.775	2118.875	1.22434006	2.33648546	0.0009206
75597	A_52_P2947	Ndufaf2	NADH dehydrogenase (ubiqu	NM_001127346	1397.7	1287.9	1365.4	1209.9	2999.3	2898.2	3157	3225.2	1315.225	3069.925	1.22385977	2.33570775	0.00080187
67453	A_52_P600304	Slc25a46	solute carrier family 25, mem	NM_026165	84.4	70.8	86.9	102.8	216.4	179	184	222.9	86.225	200.575	1.22383949	2.33567491	0.05786735
26425	A_51_P123077	Nubp1	nucleotide binding protein 1	NM_011955	701.4	699.9	690	709	1719.8	1655.4	1577.2	1588.9	700.075	1635.325	1.22318969	2.33462315	0.00017221
67732	A_52_P507305	Iah1	isoamyl acetate-hydrolyzing e	NM_026347	31.8	28	27.7	28.7	76.1	70.1	72.5	54.2	29.05	68.225	1.22204861	2.33277734	0.02533823
382118	A_55_P2034270	Zfp167	zinc finger protein 167	NM_001177505	32.7	26.3	22	24	65.8	52.6	58.6	66.3	26.25	60.825	1.22204214	2.33276687	0.08815757
18114	A_55_P2144436	Rrp1	ribosomal RNA processing 1 h	NM_010925	1000.3	933.5	993.4	1113.3	2385.6	2244.5	2458.9	2318.8	1010.125	2351.95	1.2214235	2.33176677	0.00089345
14854	A_52_P358860	Gss	glutathione synthetase	NM_008180	100.2	87.8	90.2	113.3	213.2	286.2	219.3	198.2	97.875	229.225	1.22064283	2.33050536	0.07771747
11546	A_52_P227445	Parp2	poly (ADP-ribose) polymerase	NM_009632	45.4	52.6	69.6	60.5	141.1	133.1	122.4	128.8	57.025	131.35	1.21997489	2.32942662	0.0670691
269338	A_66_P114449	Vps39	vacuolar protein sorting 39 (y	NM_147153	124.1	123.3	136.9	140	259.2	340.6	322.4	301.7	131.075	305.975	1.21797135	2.32619389	0.00853929
106740	A_55_P2189571	LOC106740	uncharacterized LOC106740	NR_027905	2220.8	2715.7	2622.6	2829.6	6523.7	6589.9	5373.8	5666	2597.175	6038.35	1.21755519	2.32552296	0.01382562
230866	A_52_P306537	C230096C10Rik	RIKEN cDNA C230096C10 gen	NM_146157	191.3	183.3	177.2	170.4	434.9	390.9	423.6	429.9	180.55	419.825	1.21745985	2.32536929	0.00050436
26448	A_55_P2065529	Stk30	serine/threonine kinase 30	NM_011973	76.6	63.3	83.2	74	172	150.9	190.3	176.7	74.275	172.475	1.21740817	2.32528599	0.01528707
58231	A_52_P474636	Stk4	serine/threonine kinase 4	NM_021420	7.1	5.5	7.5	5.8	14.4	15	15.1	15.2	6.475	14.925	1.21679236	2.32429366	0.01735153
20523	A_55_P1972187	Slc25a14	solute carrier family 25 (mito	NM_011398	544.2	660.9	644.9	699.5	1564.6	1486.2	1363.6	1490.4	637.375	1476.2	1.21607153	2.32313265	0.00508196
387524	A_66_P111798	Znrf2	zinc and ring finger 2	NM_199143	106.9	100.9	110.2	78.6	227.6	243.1	218.5	224.6	99.15	228.45	1.21528205	2.32186171	0.02275894
382245	A_52_P475870	Tmem29	transmembrane protein 29	NM_001164686	112.3	124.6	145.8	118.8	273.5	308.6	319.3	261.3	125.375	290.675	1.21517776	2.32169387	0.01410002
11777	A_55_P2088637	Ap3s1	adaptor-related protein comp	NM_009681	39	30.5	36.2	34.6	87.5	75.7	79.8	81.7	35.075	81.175	1.21431401	2.32030428	0.00455774
67397	A_55_P2049383	Erp29	endoplasmic reticulum protei	NM_026129	7539.9	8229.1	8952	8488	17756.8	18788.1	22675.8	18052.7	8302.25	19318.35	1.21408913	2.31994263	0.00823597
13681	A_55_P2046398	Eif4a1	eukaryotic translation initiati	NM_144958	5693.2	7723	5696.3	6023.2	15067	14490.5	13389.6	14934.4	6283.925	14470.375	1.21375191	2.31940042	0.01900592
229363	A_52_P47255	Gmps	guanine monophosphate synt	NM_001033300	146.6	169.6	188.3	180.2	430	393.7	386.4	372.5	171.175	395.65	1.2130289	2.31823835	0.00583191
83704	A_52_P307752	Slc12a9	solute carrier family 12 (potas	NM_031406	84.4	71.8	75.1	66	160.8	165.3	169.3	192.7	74.325	172.025	1.21287482	2.31799077	0.00719023
17685	A_51_P283708	Msh2	mutS homolog 2 (E. coli)	NM_008628	2966.9	2890	3127.6	3382.9	7501.6	6880.5	7172.2	7063.4	3091.85	7154.425	1.21228698	2.31704647	0.00078012
15382	A_55_P2066041	Hnrnpa1	heterogeneous nuclear ribon	NM_010447	309.4	293.9	424.4	312.3	770.9	837.8	766.5	701.6	335	769.2	1.21223209	2.31695832	0.04990673
68177	A_55_P2173702	Ebpl	emopamil binding protein-like	NM_026598	1411.1	1556.7	1538.9	1676.1	3194.4	3760	3770.7	3595.7	1545.7	3580.2	1.21126595	2.31540722	0.00250219
66241	A_51_P359237	Tmem9	transmembrane protein 9	NM_025439	417.2	540.1	413	541.8	1020.1	1170.5	1131.6	1070.7	478.025	1098.225	1.2106496	2.31441825	0.02749521
76281	A_55_P2046158	Tax1bp3	Tax1 (human T-cell leukemia	BC008166	1680.3	1775.4	1999.9	2071.1	4297.3	4853.2	4265.7	3981.5	1881.675	4349.425	1.21031834	2.31388689	0.006793
319149	A_55_P2127139	Hist1h3d	histone cluster 1, H3d	NM_178204	2566.2	2938.5	3101.5	2815.3	7222.7	6683.4	6852.7	5702	2855.375	6615.2	1.21007318	2.31349372	0.00715448
68268	A_51_P228254	Zdhhc21	zinc finger, DHHC domain con	NM_026647	923.2	826.1	939.5	859.6	1951.6	1895.2	1945.7	2434.2	887.1	2056.675	1.20748464	2.30934648	0.00784339
68212	A_51_P368713	Tmbim4	transmembrane BAX inhibitor	NM_026617	1994.4	1978.1	1989.8	1838.4	4710.3	4137.4	4696.8	4478	1950.175	4505.625	1.20698295	2.30854355	0.00061873
11844	A_55_P2160716	Arf5	ADP-ribosylation factor 5	ENSMUST00000020717	15172	14798.8	16117.9	17030.3	37302.5	37054.7	34245.9	36924.6	15779.75	36381.925	1.20644583	2.30768424	0.00069512
83767	A_55_P1978642	Wasf1	WASP family 1	NM_031877	69.4	56.8	64.7	58.4	143.1	144.1	170.5	120	62.325	144.425	1.20601296	2.30699194	0.03528008
67763	A_55_P2069832	Prpsap1	phosphoribosyl pyrophosphat	NM_026364	2870	2983	2966.7	3124.1	6358.3	7027.6	6734.5	7469	2985.95	6897.35	1.20601118	2.30698908	0.00074978
72795	A_51_P107808	Ttc19	tetratricopeptide repeat dom	NM_028360	409	437.5	424.1	374	932	908	993.5	954.9	411.15	947.1	1.20551632	2.3061979	0.00080048
56794	A_66_P128918	Hacl1	2-hydroxyacyl-CoA lyase 1	NM_019975	678.2	794.4	844.7	826.6	1886.4	1750.7	1803.6	1785.6	785.975	1806.575	1.20534085	2.30591743	0.00252167
108755	A_52_P75146	Lyrm2	LYR motif containing 2	NM_175364	456.6	424.8	449.7	396.6	867.4	929.5	1179.7	1027.9	431.925	1001.125	1.20519156	2.30567883	0.01545957
16469	A_52_P505143	Jrk	jerky	NM_008415	22.8	21.4	17.7	18.7	46.6	47.5	41.3	49.9	20.15	46.325	1.2050017	2.30537542	0.01223626
320683	A_55_P1977478	Zfp629	zinc finger protein 629	NM_177226	1669.5	1808.7	1466.5	2147.6	4014.6	3590.4	4201.3	4416.8	1773.075	4055.775	1.20344163	2.30288383	0.05309406
107513	A_55_P1962831	Ssr1	signal sequence receptor, alp	NM_025965	995.7	1214.2	1038.6	1172.2	2321.7	2855.3	2541.9	2451	1105.175	2542.475	1.20261342	2.30156218	0.00741
319262	A_52_P456158	Fchsd1	FCH and double SH3 domains	NM_175684	60.8	51.2	45.2	65.1	132.7	141.3	115.2	118.9	55.575	127.025	1.20233405	2.30111654	0.06977741
21778	A_55_P1973783	Tex9	testis expressed gene 9	NM_009359	127.7	99.3	111.3	109.7	279.1	239.4	259.9	249.6	112	257	1.20178464	2.3002404	0.0056204
404634	A_66_P125560	H2afy2	H2A histone family, member	NM_207000	302	326.1	286.1	287.8	657.2	719.8	693.3	692	300.5	690.575	1.20168283	2.30007806	0.00061507
100039968	A_55_P2019909	Gm12942	predicted gene 12942	NM_001099319	152.4	160.2	148.2	131.6	349.6	305.4	318.7	391.6	148.1	341.325	1.20163576	2.30000303	0.01078387
223649	A_51_P296036	Nrbp2	nuclear receptor binding prot	NM_144847	894.5	1277	1006	1167.4	2471.6	2363.5	2495.2	2567.1	1086.225	2474.35	1.20045598	2.29812294	0.02622746
319347	A_55_P2220342	C230094B09Rik	RIKEN cDNA C230094B09 gen	AK082713	27.4	27.9	26.7	36.4	63.7	68.4	69	68.8	29.6	67.475	1.19976885	2.29702866	0.01685763
435965	A_52_P178866	Lrp3	low density lipoprotein recep	NM_001024707	125.5	139.5	151.1	120.5	327.7	287.7	292.7	320.8	134.15	307.225	1.19888712	2.29562521	0.00552318
252876	A_52_P392509	Gin1	gypsy retrotransposon integr	AK018404	347.4	429.5	326.5	408.4	880.2	862.8	833.5	871.5	377.95	862	1.19830467	2.29469859	0.00862363
244891	A_55_P2426272	Scaper	S phase cyclin A-associated pr	NM_001081341	102.6	109.5	136	108	295.1	228.5	264.7	256.2	114.025	261.125	1.1981068	2.29438389	0.02840542
11778	A_55_P2088630	Ap3s2	adaptor-related protein comp	NM_009682	1855.8	1646.1	1687.7	1873.6	4551	3718.9	4066.6	3877	1765.8	4053.375	1.19696467	2.29256823	0.00331097
52712	A_55_P2084741	Zkscan6	zinc finger with KRAB and SCA	NM_026107	441.7	515.1	537.6	493.9	1193	1088.3	1092.9	1173.7	497.075	1136.975	1.19623409	2.29140756	0.00195614
66196	A_51_P434171	Myo19	myosin XIX	NM_025414	111.7	118.1	103.1	105.9	225.3	226.5	263	295.3	109.7	252.525	1.19555436	2.29032822	0.01373578
67511	A_51_P262878	Tmed9	transmembrane emp24 prote	NM_026211	11701.1	12223.9	12094.3	12745.6	28037.9	29103.7	26083.4	28416.5	12191.225	27910.375	1.19444158	2.28856232	0.00039152
12724	A_51_P332141	Clcn2	chloride channel 2	NM_009900	85.1	83.3	72.8	83.1	195.3	181	187.6	177.1	81.075	185.25	1.19383888	2.28760645	0.00109265
66061	A_55_P1961690	Tctex1d2	Tctex1 domain containing 2	NM_025329	795.9	767.5	811.5	779.8	1806.6	1699.5	1956.3	1759.4	788.675	1805.45	1.19321546	2.28661813	0.00049697
75320	A_51_P229599	Etnk1	ethanolamine kinase 1	NM_029250	137.9	146.6	127.1	120.4	305.3	289.4	316.4	301.9	133	303.25	1.19245147	2.28540757	0.00180392
66961	A_51_P234692	Neat1	nuclear paraspeckle assembly	NR_003513	39092.2	51469.2	48736.4	51161.1	105359.5	106421.2	104693.7	116507.6	47614.725	108245.5	1.19219499	2.2850013	0.0118725
20818	A_52_P131559	Srprb	signal recognition particle rec	NM_009275	38.4	34.6	43.7	42	92.8	92.9	90.1	85.1	39.675	90.225	1.19014717	2.28176018	0.00386088
381196	A_55_P2164609	Gm960	predicted gene 960	ENSMUST00000096325	17.6	12.9	16.6	14	28.6	35.8	37.5	37.1	15.275	34.75	1.18868199	2.27944403	0.080902
14299	A_51_P114062	Ncs1	neuronal calcium sensor 1	NM_019681	33.9	39.6	42.9	39.8	87	101.7	88.7	78.6	39.05	89	1.1875487	2.27765416	0.0154075
66361	A_51_P329322	Zfand1	zinc finger, AN1-type domain	NM_025512	881.8	948.7	929	1190	2256.2	2183.3	2134.5	2365.7	987.375	2234.925	1.18732783	2.27730548	0.01267011
74498	A_55_P2125972	Gorasp1	golgi reassembly stacking pro	NM_028976	437.7	452.9	506.5	507.4	1023.1	1005.9	1166.5	1137.6	476.125	1083.275	1.18612635	2.27540972	0.00318685
224671	A_55_P1968553	Btbd9	BTB (POZ) domain containing	NM_027060	896.1	824.8	850.3	881.3	2078.3	1877.9	1955	1944.9	863.125	1964.025	1.18594798	2.27512842	0.00037222
70823	A_55_P2045476	Hmgxb4	HMG box domain containing	NM_178017	335.7	300.1	310.7	305.8	715.5	751.4	651	729.3	313.075	711.8	1.18424408	2.27244296	0.00097667
14593	A_51_P469902	Ggps1	geranylgeranyl diphosphate s	AK046876	135.1	136.1	129.9	126.4	308.3	291	316.3	283.3	131.875	299.725	1.18372139	2.2716198	0.00046714
669389	A_66_P136489	Gm9456	predicted gene 9456	AK085185	127.2	105.5	113.1	141.6	310.6	270	236.9	287.9	121.85	276.35	1.18352534	2.27131112	0.04436886
15227	A_55_P2059765	Foxf1a	forkhead box F1a	ENSMUST00000098351	41.5	44.5	44.2	47.5	126	86.5	108.3	87.4	44.425	102.05	1.18343901	2.27117521	0.07541846
78808	A_55_P1984596	Stxbp5	syntaxin binding protein 5 (to	NM_001081344	35.7	41	47.2	48.1	89.1	91	95.9	113.1	43	97.275	1.18149452	2.26811615	0.04928568
14567	A_51_P391276	Gdi1	guanosine diphosphate (GDP)	NM_010273	68.5	77	75.7	94.2	159.7	198.7	177	176.2	78.85	177.9	1.17941226	2.26484491	0.02928834
319953	A_51_P199608	Ttll1	tubulin tyrosine ligase-like 1	NM_178869	74.4	70	60.4	85.7	152.9	154.3	160.1	187.3	72.625	163.65	1.17846544	2.26335901	0.04544773
435684	A_55_P2098354	Shf	Src homology 2 domain conta	NM_001013829	110.7	86.1	90.4	94.2	208.3	200.7	235.8	215.9	95.35	215.175	1.1781741	2.26290199	0.00866729
319740	A_51_P353095	Zfyve27	zinc finger, FYVE domain cont	NM_177319	1287.8	1187.8	1309.5	1105.8	2771.6	2671.2	2766.3	2827.2	1222.725	2759.075	1.1770579	2.26115188	0.00114352
74239	A_55_P2004084	Iqce	IQ motif containing E	NM_028833	162.2	158.9	160.3	166.4	356	344.1	359.6	406.4	161.95	366.525	1.17566894	2.25897599	0.00088248
23917	A_52_P183038	Impdh1	inosine 5-phosphate dehydro	NM_011829	488.9	437.2	524	461.9	967.5	1069	1248.9	1042.4	478	1081.95	1.17547365	2.25867023	0.01017229
67883	A_55_P2047225	Uxs1	UDP-glucuronate decarboxyla	NM_026430	60.2	66.7	73.1	54.2	140.4	155.1	136.9	138.8	63.55	142.8	1.17524238	2.25830818	0.01440646
101943	A_55_P2056300	Sf3b3	splicing factor 3b, subunit 3	NM_133953	1972.7	2247.2	1984.1	2266.2	4804.6	4897.6	4366.4	5004.8	2117.55	4768.35	1.17229699	2.25370235	0.00231697
212503	A_55_P2019751	Paox	polyamine oxidase (exo-N4-a	BC082783	1266.8	1126.7	1145.4	1191.2	2786	2580	2627.8	2649.3	1182.525	2660.775	1.17086841	2.25147181	0.00051296
18148	A_55_P2117243	Npm1	nucleophosmin 1	ENSMUST00000109354	103.3	113.9	118.6	137.3	266.4	262.3	277.3	253.9	118.275	264.975	1.17061907	2.25108271	0.00735311
22201	A_55_P1971966	Uba1	ubiquitin-like modifier activat	NM_001136085	8109.2	7196.2	7376.9	7615.1	16467.6	16165.5	17971.9	17582	7574.35	17046.75	1.1703576	2.25067478	0.00080857
105446	A_51_P430327	Gmpr2	guanosine monophosphate re	NM_177992	117.9	108.2	104.7	105.3	229.6	273.7	240.9	238.2	109.025	245.6	1.1700737	2.25023191	0.00207494
320124	A_55_P2266744	B930095M22Rik	RIKEN cDNA B930095M22 ge	AK047590	28.1	24.8	26.1	27.3	67.8	62.2	49.6	60.8	26.575	60.1	1.16968757	2.24962974	0.01620693
20392	A_55_P1958160	Sgce	sarcoglycan, epsilon	NM_001130188	384.8	434.2	422.9	398	895.5	876.2	900.5	1017.4	409.975	922.4	1.16898538	2.24853505	0.00154686
216440	A_51_P109171	Os9	amplified in osteosarcoma	NM_177614	1051.3	1003	993.5	958.7	2196.5	2154.6	2283.7	2374	1001.625	2252.2	1.1687701	2.24819956	0.00044046
13866	A_52_P49250	Erbb2	v-erb-b2 erythroblastic leuke	NM_001003817	70.1	75.4	72.2	69.6	157.8	180.8	156.3	151.9	71.825	161.7	1.1681447	2.24722519	0.00145828
231050	A_55_P1989703	Galnt11	UDP-N-acetyl-alpha-D-galacto	NM_144908	115.2	113.4	127.1	120.9	285.2	239	234.6	320	119.15	269.7	1.16797997	2.24696861	0.02781155
231130	A_66_P125734	Tnip2	TNFAIP3 interacting protein 2	NM_139064	180.8	201.1	166.2	177.6	400.8	383.8	446.4	398.1	181.425	407.275	1.16771135	2.24655028	0.00301925
74244	A_66_P119999	Atg7	autophagy-related 7 (yeast)	NM_028835	638	700.9	642.1	615.6	1533.6	1406.3	1433.9	1455.4	649.15	1457.3	1.16758572	2.24635465	0.00064018
56150	A_55_P2133255	Mad2l1	MAD2 mitotic arrest deficient	NM_019499	117.5	133.1	111.9	117.5	264.4	291	266.1	254.5	120	269	1.16583334	2.24362777	0.00206537
227700	A_55_P1971849	Sh3glb2	SH3-domain GRB2-like endop	NM_139302	4729.2	5464	5842	5358.1	11728.8	12105.6	12206.5	11816.9	5348.325	11964.45	1.16555152	2.24318953	0.00180803
208968	A_55_P2052261	Zfp280c	zinc finger protein 280C	NM_153532	268.3	340	280.8	360.7	700.5	699.9	686	692.4	312.45	694.7	1.163906	2.24063243	0.01758118
110524	A_52_P494380	Dgkq	diacylglycerol kinase, theta	NM_199011	265.2	298.9	273	309	516.9	654.9	662.4	751.4	286.525	646.4	1.16379804	2.24046477	0.04848454
268470	A_66_P102581	Ube2z	ubiquitin-conjugating enzyme	NM_172300	998	999.8	1053.6	1138.7	2570.4	2314	2006.4	2526.5	1047.525	2354.325	1.16364827	2.24023219	0.00962628
223666	A_55_P2105242	Arhgap39	Rho GTPase activating protei	NM_001168288	561.1	568.6	523.5	617.4	1183.7	1214.6	1296.5	1392.9	567.65	1271.925	1.163536	2.24005787	0.00273253
74126	A_55_P2015734	Syvn1	synovial apoptosis inhibitor 1	NM_028769	6257.8	5840.2	5770.8	5160.7	12626.2	12600.2	13265.1	12962.6	5757.375	12863.525	1.16288969	2.23905457	0.00136622
69920	A_55_P2135601	Polr2i	polymerase (RNA) II (DNA dire	NM_027259	388.1	342.6	332.9	396.8	903.8	767.9	809.7	785	365.1	816.6	1.16263691	2.2386623	0.00513278
99982	A_55_P1993820	Kdm1a	lysine (K)-specific demethylas	NM_133872	2863	3386.3	3510.5	3626.8	7754.3	8008.8	6486.2	7641.9	3346.65	7472.8	1.16006909	2.23468129	0.01605765
233405	A_55_P2024260	Vps33b	vacuolar protein sorting 33B (	NM_178070	134.2	154.3	177.9	163.7	376.1	330.1	315.5	383.6	157.525	351.325	1.15975465	2.23419429	0.02501657

320234	A_52_P562769	Ccdc66	coiled-coil domain containing	NM_177111	141	130.6	147.7	163.2	318.7	290.2	345.9	345.7	145.625	325.125	1.1597403	2.23417207	0.00838724
78309	A_55_P2099980	Cul9	cullin 9	NM_001081335	548	478.5	656.4	629.4	1342.3	1198.5	1297.8	1292	578.075	1282.65	1.15951909	2.23382952	0.02361788
67169	A_51_P405227	Nradd	neurotrophin receptor associ	NM_026012	30.5	31	23.2	28.8	62	68.2	59.1	62.9	28.375	63.05	1.15924676	2.23340789	0.01968632
68777	A_55_P2024337	Tmem53	transmembrane protein 53	NM_026837	577	822.6	725.9	696	1583.2	1521.8	1513.5	1635.9	705.375	1563.6	1.15917185	2.23329193	0.02379943
76467	A_51_P464911	Msrb2	methionine sulfoxide reducta	NM_029619	1870.5	1744.7	1738.2	1681.8	4213	3695.3	3702.3	4100.6	1758.8	3927.8	1.15769826	2.23101198	0.00130786
328801	A_51_P503542	Zfp414	zinc finger protein 414	NM_026712	440.2	408.9	411	434.4	799.9	1006.4	953.5	1032.5	423.625	948.075	1.15604617	2.22845862	0.00726943
68948	A_51_P252784	1500011H22Rik	RIKEN cDNA 1500011H22 gen	NM_026883	648.4	769.9	627.6	713.7	1483.8	1562.9	1495.6	1581.5	689.9	1530.95	1.15413354	2.22550622	0.00277604
30934	A_55_P1972406	Tor1b	torsin family 1, member B	NM_133673	585.5	523.6	523.2	499	1270.7	1019.8	1194	1264.3	532.825	1187.2	1.15280678	2.22346051	0.00811429
73836	A_55_P2086094	Slc35b2	solute carrier family 35, mem	NM_028662	2339.7	2434.5	2357.6	2512.9	5579.1	4917	5618	5347.2	2411.175	5365.325	1.15250744	2.22299921	0.00080671
59052	A_51_P259861	Mettl9	methyltransferase like 9	NM_021554	1488.4	1700.1	1662	1467.6	3258.6	3854.6	3593.6	3339.2	1579.525	3511.5	1.15250117	2.22298955	0.00407717
638532	A_52_P73559	Gm7241	predicted pseudogene 7241	XM_987328	71.9	83.9	68.7	98.5	178	164.4	172.4	197.2	80.75	178	1.15178071	2.22187971	0.0694352
228061	A_55_P2050088	Agps	alkylglycerone phosphate syn	ENSMUST00000111952	42.5	44.3	47.6	36.6	111.9	92.3	84.4	91.5	42.75	95.025	1.15097719	2.22064256	0.03860579
103266	A_52_P545643	AI597468	expressed sequence AI59746	NM_001013028	933.5	760.7	923.9	858.1	1803.9	1997.4	1927	1971.2	869.05	1924.875	1.15088141	2.22049513	0.00375353
15193	A_51_P400773	Hdgfrp2	hepatoma-derived growth fac	NM_008233	2210.9	1979.1	2088.8	2039.5	4824.4	4209.6	4638	4810.7	2079.575	4620.675	1.15085355	2.22045225	0.00123217
74349	A_55_P2049080	Fam160a2	family with sequence similarit	NM_199009	1466.8	1631.5	1609.6	1652.5	3548.5	3481.9	3551.1	3523.5	1590.1	3526.25	1.15053391	2.21996035	0.00045497
71946	A_51_P505823	Endod1	endonuclease domain contair	NM_028013	365.1	442.7	360.1	476.6	940	895.2	883.1	905.6	411.125	905.975	1.15013099	2.21934045	0.01803636
101351	A_55_P2046793	A130022J15Rik	RIKEN cDNA A130022J15 gen	NM_175313	54.7	42.8	56.9	49.9	109.6	110.9	107.2	123.7	51.075	112.85	1.14993746	2.21904275	0.01750571
98682	A_55_P2169445	Mfsd6	major facilitator superfamily	NM_133829	913.6	1136.9	969.6	1249.8	2417.9	2572.9	2150.8	2269.1	1067.475	2352.675	1.14806119	2.21615869	0.03983698
384214	A_55_P2074694	Ephx4	epoxide hydrolase 4	NM_001001804	74.3	81	83.8	88.8	191.5	190.6	154.4	190.1	81.975	181.65	1.14506053	2.2115541	0.01107075
106489	A_55_P1974671	Sft2d1	SFT2 domain containing 1	NM_134114	64.3	75.4	90.1	76.4	174.2	174	165.2	158.3	76.55	167.925	1.14248406	2.20760807	0.02120854
101240	A_66_P119884	Wdr91	WD repeat domain 91	NM_001013366	343.3	254.9	305.5	281.7	626.8	622.7	706.3	648.5	296.35	651.075	1.14229924	2.20732527	0.01644277
52592	A_55_P1986958	Brms1l	breast cancer metastasis-sup	NM_001037756	2034.4	2188.2	1935.3	2023.7	5135.1	4374.2	4420.3	4164.9	2045.4	4523.625	1.14198427	2.20684341	0.00383981
319391	A_55_P2403874	D230014I24Rik	RIKEN cDNA D230014I24 gen	AK051876	44.7	34	37.4	46.9	91.4	79.1	97.7	89.5	40.75	89.425	1.14192058	2.206746	0.06081051
18146	A_55_P1974650	Npdc1	neural proliferation, different	NM_008721	2378.2	3180.6	3117.9	3359.3	6304.5	6268.6	6720	7072.8	3009	6591.475	1.14184091	2.20662414	0.04333849
142682	A_51_P496054	Zcchc14	zinc finger, CCHC domain con	NM_080855	381.8	466.8	391.2	431.6	1082.8	868.1	845.1	897.6	417.85	923.4	1.14163199	2.20630462	0.02145983
53627	A_55_P2077666	Porcn	porcupine homolog (Drosoph	NM_023638	562.5	714.2	646.4	636.5	1360.1	1438.7	1381.6	1446.1	639.9	1406.625	1.14098232	2.20531129	0.00366043
52521	A_66_P122087	Zfp622	zinc finger protein 622	NM_144523	14773.7	15986.9	16183.3	16388.2	31874.9	37982.3	35479.2	34371	15833.025	34926.85	1.13970719	2.20336299	0.00183862
26921	A_51_P439876	Map4k4	mitogen-activated protein kin	NM_008696	1875.6	1806.4	1735.6	1493.5	4054.9	3871.1	3739.2	3524.2	1727.775	3797.35	1.13945851	2.20298323	0.00662703
56317	A_55_P2075523	Anapc7	anaphase promoting complex	NM_019805	9.3	10.5	12.7	9.8	22.3	25.6	21.6	23.2	10.575	23.175	1.13924238	2.20265323	0.03107611
66711	A_51_P466875	Sbds	Shwachman-Bodian-Diamond	NM_023248	1887.9	2222.2	2008	2272.5	4406.2	4725.1	4622.8	4678.2	2097.65	4608.075	1.13894744	2.20220296	0.00238974
68187	A_55_P1997282	Fam135a	family with sequence similarit	NM_026604	319.9	307.9	320.1	308.4	663.7	657.6	725.3	721.3	314.075	691.975	1.13837764	2.20133336	0.00053425
72611	A_55_P2153580	Zfp655	zinc finger protein 655	NM_001083958	120.1	97.7	98	91	232.9	228.5	230.6	199.1	101.7	222.775	1.13633295	2.19821569	0.01842237
53418	A_52_P399990	B4galt2	UDP-Gal:betaGlcNAc beta 1,4	NM_017377	111.9	110.2	116.4	102.3	220.6	258.1	243.8	245.8	110.2	242.075	1.13457863	2.19554427	0.0018031
223527	A_52_P653902	Eny2	enhancer of yellow 2 homolo	NM_175009	650.4	566.3	610.7	608.1	1419.1	1315.2	1373.3	1239.8	608.875	1336.85	1.13451471	2.19544701	0.00152472
54196	A_55_P2064442	Pabpn1	poly(A) binding protein, nucle	NM_019402	4755.5	5265.3	4957.9	4508.9	11977.9	10421.3	9902.6	10498.3	4871.9	10700.025	1.13376004	2.19429888	0.0041824
65247	A_51_P111757	Asb1	ankyrin repeat and SOCS box-	NM_001039126	771.5	803.7	751.6	785.5	1763.1	1680.2	1651.4	1726.6	778.075	1705.325	1.13204589	2.19169325	0.00031173
227613	A_55_P2153292	Tubb4b	tubulin, beta 4B class IVB	NM_146116	22418.2	21574.4	25038.3	19195.6	48537.5	47143.7	45881.8	51061.3	22056.625	48156.075	1.13185348	2.19140096	0.00785218
242474	A_55_P2444965	D730040F13Rik	RIKEN cDNA D730040F13 gen	NM_175518	354.2	337.5	315.5	314.2	742.9	724.5	729.2	694.8	330.35	722.85	1.13107278	2.19021543	0.00075354
14272	A_55_P1990225	Fnta	farnesyltransferase, CAAX bo	NM_008033	7725.3	7889.7	8494.2	9304	18069	18405.7	17985.7	18290.6	8353.3	18187.75	1.12636095	2.18307387	0.00188201
56360	A_52_P392674	Acot9	acyl-CoA thioesterase 9	NM_019736	735.1	647.2	732.8	774.1	1463	1922.2	1453.6	1494.5	722.3	1583.325	1.12515056	2.18124309	0.03374428
73373	A_51_P351413	Phospho2	phosphatase, orphan 2	NM_028521	143.4	154.2	126.2	131.6	309.8	253.7	286.9	368.4	138.85	304.7	1.12489063	2.18085012	0.08056212
67201	A_55_P1979252	Glod4	glyoxalase domain containing	NM_026029	1965.6	2196.7	1936.2	2313.8	4949.2	4486.1	4546.9	4320.7	2103.075	4575.725	1.12375142	2.17912873	0.00436898
76983	A_55_P2083954	Scfd1	Sec1 family domain containin	NM_029825	146.4	134.2	125.9	137.9	296.4	300	292.4	293.4	136.1	295.55	1.12077979	2.17464483	0.00079614
66257	A_52_P94845	Nicn1	nicolin 1	NM_025449	146.1	174.5	188.3	153.9	369.6	332.5	380.5	353.2	165.7	358.95	1.12062286	2.17440829	0.01343041
241075	A_55_P2152956	Plekhm3	pleckstrin homology domain	NM_001039493	166.4	161.2	164.5	223.5	402.5	377.9	393.8	367.8	178.9	385.5	1.12037708	2.17403788	0.043148
26562	A_55_P1998545	Ncdn	neurochondrin	NM_011986	1654.6	1449.9	1607.4	1466	3418	3097.2	3726.8	3200.9	1544.475	3360.725	1.12037049	2.17402796	0.00472264
76359	A_55_P2410325	2610028D06Rik	RIKEN cDNA 2610028D06 gen	AK011582	46	40	42.5	50.1	97	100.2	100.9	88.7	44.65	96.7	1.1181691	2.17071317	0.00715093
17035	A_51_P487813	Lxn	latexin	NM_016753	148.4	184	160.5	167.8	341.5	379.2	328.5	383.5	165.175	358.175	1.1178629	2.1702525	0.00841263
210973	A_55_P1964852	Kbtbd2	kelch repeat and BTB (POZ) d	NM_145958	3764.3	4072.2	3691	3750.6	7797.8	8704.1	7873.9	8807.5	3819.525	8295.825	1.11781252	2.1701767	0.0014905
67797	A_51_P249867	Snrnp48	small nuclear ribonucleoprote	NM_026382	224	191.2	206	202.8	451.1	387.5	469.5	482.5	206	447.65	1.11700361	2.16896025	0.00832761
66549	A_55_P2049577	Aggf1	angiogenic factor with G patc	NM_025630	3862.5	5031.9	3829.8	4452.5	10046.3	8337.6	8868.4	9869.7	4294.175	9280.5	1.11684544	2.16872246	0.03941162
269529	A_52_P358093	Fbxo10	F-box protein 10	NM_001024142	236.9	284.7	268.3	307.7	579.7	610.5	620	560.6	274.4	592.7	1.11636139	2.16799494	0.0091135
240087	A_55_P1995165	Mdc1	mediator of DNA damage che	NM_001010833	195.7	160.9	155.6	217.6	403	388.1	371.9	404.9	182.45	391.975	1.11633999	2.16796278	0.05147662
12569	A_55_P2173183	Cdk5r1	cyclin-dependent kinase 5, re	NM_009871	30.9	31.4	39.8	36.8	85.7	78.3	69.9	66.9	34.725	75.2	1.11619015	2.16773762	0.05490199
67072	A_51_P446315	Cdc37l1	cell division cycle 37 homolog	NM_025950	1319.6	1559.8	1272.9	1499.7	3398.6	2722.3	2748.4	3410.8	1413	3070.025	1.11605351	2.16753232	0.04373498
73744	A_52_P517896	Man2c1	mannosidase, alpha, class 2C,	NM_028636	1996.5	2449.8	2039.4	2512.1	4487.8	4719.9	4597.2	5677	2249.45	4870.475	1.11586829	2.16725406	0.0450974
100040563	A_55_P2151143	Dynlt1c	dynein light chain Tctex-type	NM_001166630	7651.3	7176.9	8012	7674.8	17577.2	15018.2	15054.8	18740.4	7628.75	16597.65	1.11578689	2.16713179	0.00950002
227099	A_52_P235278	Pms1	postmeiotic segregation incre	NM_153556	86.1	71.5	80.1	105.2	188.1	178.6	177.2	192.1	85.725	184	1.11558973	2.16683564	0.05599454
228071	A_55_P1988760	Sestd1	SEC14 and spectrin domains 1	NM_175465	155.9	158.2	150.7	140.7	307.6	348.2	318.3	335.7	151.375	327.45	1.11296478	2.16289673	0.00141005
546663	A_55_P2079729	Gm5963	predicted pseudogene 5963	XM_001002128	18892.6	19795.3	20154.6	22501.1	45074.3	40133.3	43292.9	47154	20335.9	43913.625	1.1111329	2.1601521	0.00422451
109889	A_55_P2048096	Mzf1	myeloid zinc finger 1	NM_145819	42	56.7	56.3	56	117.7	112.2	112.3	110.2	52.75	113.1	1.11102043	2.15998371	0.0309533
17939	A_51_P117130	Naga	N-acetyl galactosaminidase, a	NM_008669	48.4	44	57.1	48.7	108.7	122.9	91.1	105.7	49.55	107.1	1.11028112	2.15887711	0.05172661
209011	A_51_P352264	Sirt7	sirtuin 7 (silent mating type ir	NM_153056	867.2	987.6	964.9	973	1904.1	2171.7	1969.6	2134.4	948.175	2044.95	1.10856721	2.15631391	0.00232407
13194	A_55_P1989901	Ddb1	damage specific DNA binding	NM_015735	19403.9	20304.2	20680.3	22452.4	46304.8	43971.4	42850.1	45201.5	20710.2	44581.95	1.10753621	2.15477347	0.00112409
218232	A_55_P2007871	Ptpdc1	protein tyrosine phosphatase	NM_207232	772.3	951.2	673.3	912.7	1743.7	1639	1834.7	1854.9	827.375	1768.075	1.10731635	2.15444512	0.06295902
433931	A_55_P1962026	Pigg	phosphatidylinositol glycan ar	NM_001081234	61.8	78	75.6	74.6	161.3	153	157.5	150.6	72.5	155.6	1.10710531	2.15412999	0.00639859
77305	A_51_P118603	Wdr82	WD repeat domain containing	NM_029896	992.7	1049.2	1022.9	1064.4	2225.4	2039.4	2167.3	2482.1	1032.3	2228.55	1.10706115	2.15406406	0.0024514
99349	A_66_P129747	Dnajc24	DnaJ (Hsp40) homolog, subfa	NM_026992	267.7	280.5	258.2	251.1	568.9	565.8	540	602.7	264.375	569.35	1.10687445	2.15378531	0.00095919
76524	A_52_P163939	Cln6	ceroid-lipofuscinosis, neurona	NM_001033175	300.8	254.3	299.5	293.1	651.4	619.4	610.4	586.5	286.925	616.925	1.10675404	2.15360557	0.00281521
732482	A_55_P1964375	Gm9731	Fam58a pseudogene	NR_003107	1128.3	1198.8	1194.5	1201.5	2787.2	2097.7	2681.6	2659.1	1180.775	2556.4	1.10616795	2.15273084	0.01683425
27103	A_55_P1998396	Eif2ak4	eukaryotic translation initiatio	NM_013719	675.8	720.7	790.5	885.8	1626.7	1696.1	1569	1688.5	768.2	1645.075	1.10543192	2.15163286	0.01136291
241944	A_51_P511386	D3Ertd254e	DNA segment, Chr 3, ERATO D	NM_001101478	29.7	29.3	35.1	23.8	58.4	59.9	62.8	70.9	29.475	63	1.10531959	2.15146533	0.09417112
22222	A_51_P107938	Ubr1	ubiquitin protein ligase E3 co	NM_009461	160.5	150.3	165.1	192.5	341.8	364.1	372.2	353.4	167.1	357.875	1.10406259	2.1495916	0.00693962
74245	A_55_P2092391	Ctbs	chitobiase, di-N-acetyl-	NM_028836	155.3	129.4	144.3	121	271.4	272.2	346.8	291.8	137.5	295.55	1.10329944	2.14845483	0.04761547
72096	A_55_P2131393	Mettl10	methyltransferase like 10	NM_028095	588.5	598.7	590.7	677	1362.6	1181.3	1346.9	1382.6	613.725	1318.35	1.10275483	2.14764395	0.00412132
15267	A_55_P1962084	Hist2h2aa1	histone cluster 2, H2aa1	NM_013549	16236.6	14650.3	17772.7	12847.6	31866.5	33904.5	35316.2	30282.3	15376.8	32842.375	1.10274518	2.14762958	0.04011471
14020	A_55_P2095794	Evi5	ecotropic viral integration site	NM_007964	1297.7	1496.6	1523.5	1446.6	3208.3	3168.4	2857.1	3133.9	1441.1	3091.925	1.10259327	2.14740345	0.00271447
15270	A_51_P245275	H2afx	H2A histone family, member	NM_010436	1719	1930	1650.3	1980.3	4029.2	3500.2	3822.1	4274.8	1819.9	3906.575	1.10238388	2.14709181	0.01128378
100683	A_55_P2024654	Trrap	transformation/transcription	NM_001081362	1399.6	1773.1	1706.4	2021.9	4012.6	3860.6	3395	3452.4	1725.25	3680.15	1.10160441	2.14593207	0.07511064
12522	A_51_P199135	Cd83	CD83 antigen	NM_009856	78	102	72.8	80.6	176.6	197.9	174.1	161.9	83.35	177.625	1.09982472	2.1432865	0.06505455
67803	A_52_P78023	Limd2	LIM domain containing 2	NM_172397	702.9	687.5	670.7	871.9	1584.5	1552.3	1698.5	1423.5	733.25	1564.7	1.09883543	2.14181731	0.02435823
67711	A_51_P173022	Nsmce1	non-SMC element 1 homolog	NM_026330	776	891.3	800.2	710	1713.2	1689	1745.4	1636	794.375	1695.9	1.09853958	2.14137814	0.00405496
75612	A_52_P585751	Gns	glucosamine (N-acetyl)-6-sulf	NM_029364	1446.2	1521.7	1562	1434.8	2783.8	3241.7	3641.1	3154.8	1491.175	3205.35	1.09838348	2.14114645	0.00946206
76482	A_66_P124445	3110002H16Rik	RIKEN cDNA 3110002H16 gen	NM_029623	111	110.3	131.1	119.8	246.1	237.8	237.2	290.8	118.05	252.975	1.09795915	2.14051678	0.0135435
320165	A_52_P117420	Tacc1	transforming, acidic coiled-co	NM_177089	186.9	179.6	193.1	172.9	372.5	393.6	415.3	386.3	183.125	391.925	1.09787656	2.14039425	0.00103821
23939	A_55_P1952502	Mapk7	mitogen-activated protein kin	NM_011841	608.2	586.3	600.7	605.6	1271	1374.9	1231.8	1263.4	600.2	1285.275	1.09747197	2.13979408	0.00056074
68591	A_51_P140321	Mocos	molybdenum cofactor sulfura	NM_026779	533.9	614.4	516	567.9	1226.5	966.8	1371.1	1237	558.05	1200.35	1.09674314	2.13871336	0.06260935
74159	A_55_P2125633	Acbd5	acyl-Coenzyme A binding dom	NM_001102438	78.7	75.1	77.4	74.9	168.2	155.7	154.5	176.9	76.525	163.825	1.09618102	2.13788022	0.00119689
103743	A_51_P368496	Tmem98	transmembrane protein 98	NM_029537	52.8	51.9	56	42.2	105.9	113.7	94	118	50.725	107.9	1.09155611	2.1310377	0.04966359
77134	A_66_P118233	Hnrnpa0	heterogeneous nuclear ribon	NM_029872	2679.9	2975.9	2692	3085	5714.5	6582.7	5836	6214.5	2858.2	6086.925	1.0911177	2.13039021	0.00392492
213573	A_55_P2367843	Efcab4a	EF-hand calcium binding dom	AK140493	39.3	31	31.8	35.5	61.3	70.2	77.5	84.9	34.4	73.475	1.09091891	2.13009668	0.09165377
20524	A_52_P72654	Slc25a17	solute carrier family 25 (mito	NM_011399	1859.9	2572.7	2007.6	2524.3	4319.4	4880.4	4882.9	4847.9	2241.125	4732.65	1.09076624	2.12987128	0.08240064
240442	A_52_P179583	Adnp2	ADNP homeobox 2	NM_175028	35.7	45.8	45.2	44.2	97.6	88.3	82.8	94.1	42.725	90.7	1.09036982	2.12928611	0.02296369
74570	A_55_P1980411	Zkscan1	zinc finger with KRAB and SC	NM_133906	1211.3	1127.7	1133.9	1230.2	2587.1	2311.6	2470.4	2646.8	1175.775	2503.975	1.0897739	2.12840678	0.0015844
319156	A_55_P2158701	Hist1h4d	histone cluster 1, H4d	NM_175654	3062.6	2482	2925.2	3301.8	7286.9	5805.4	5880.8	6020.5	2942.9	6248.4	1.08763708	2.12525666	0.05504002
26384	A_55_P1965892	Gnpda1	glucosamine-6-phosphate de	NM_011937	1310.5	1694.5	1592.6	1790.4	3444.8	3239.8	3156.2	3661.4	1597	3375.55	1.08706653	2.12441633	0.03907954
97122	A_55_P1973349	Hist2h4	histone cluster 2, H4	NM_033596	4999.4	4318.3	4573.3	4580	12527.2	8621.1	9226.4	9224.4	4617.75	9899.775	1.08632134	2.12331931	0.09692658
269198	A_55_P2208071	Nbeal1	neurobeachin like 1	AK010199	750.9	697.9	727.4	682.7	1526	1433.6	1582.5	1524.8	714.725	1516.725	1.0855734	2.12221879	0.00085803
13360	A_55_P2022337	Dhcr7	7-dehydrocholesterol reducta	NM_007856	25.5	29	25.2	32.3	57.5	60.1	55.4	63.5	28	59.125	1.08401537	2.11992815	0.01853963
17221	A_55_P2058230	Cd46	CD46 antigen, complement re	ENSMUST00000110814	36.7	29.7	28.3	27.3	68.7	55.2	63.7	70.4	30.5	64.5	1.08397529	2.11986926	0.08122736
74097	A_55_P2047698	Pop7	processing of precursor 7, rib	NM_028753	3815	4330.8	3822	3804.4	7887.6	8462.7	8042.9	9034.6	3943.05	8356.95	1.0838919	2.11974673	0.00294172
100993	A_55_P2274378	AW549542	expressed sequence AW5495	XR_106114	35.2	40.3	48.7	40.9	84.3	89.9	90.8	82.8	41.275	86.95	1.08344973	2.11909715	0.02705256
54138	A_66_P120901	Atxn10	ataxin 10	NM_016843	1217.9	1167.9	1278.5	1110.1	2356.5	2576.6	2753.3	2435	1193.6	2530.35	1.0834359	2.11907684	0.00338164
56368	A_51_P103509	Cyb561d2	cytochrome b-561 domain co	NM_019720	324.9	375.7	350	298.2	707.4	703.8	715.9	719.3	337.2	711.6	1.08270784	2.11800771	0.00496573
15423	A_55_P2074688	Hoxc4	homeobox C4	NM_013553	636.9	624	556.8	673.6	1303.1	1421.8	1268.1	1275.3	622.825	1317.075	1.08230491	2.11741626	0.00423146
246277	A_51_P268529	Csad	cysteine sulfinic acid decarbo	NM_144942	236	229	230.8	236.2	469.2	448.6	538.4	522.5	233	494.675	1.08223886	2.11731931	0.00299368
67006	A_51_P333965	Cisd2	CDGSH iron sulfur domain 2	NM_025902	368.2	338.5	380.9	395.7	810	772.8	778.2	774.4	370.825	783.85	1.08194303	2.1168852	0.00139166
231834	A_52_P77245	Snx8	sorting nexin 8	NM_172277	937.6	952.1	904.2	956.5	2130.3	1841.2	1973.5	1998.4	937.6	1985.85	1.08113117	2.11569428	0.00112855
56530	A_51_P342082	Cnpy2	canopy 2 homolog (zebrafish)	NM_019953	2158.2	2292.4	2145.8	1946.8	4421.7	4253.1	5060.3	4343.3	2135.8	4519.6	1.0804557	2.11470394	0.00598481
15239	A_55_P2103856	Hgs	HGF-regulated tyrosine kinas	NM_001159328	4724.1	5008.4	4997.9	5435.6	11388.5	9928	11349.8	9964.9	5041.5	10657.8	1.07857716	2.11195216	0.00444206
237107	A_66_P131045	Gnl3l	guanine nucleotide binding p	NM_198110	44.4	38.8	38.1	30	82.7	77.3	80.3	75.9	37.825	79.05	1.07662145	2.10909115	0.07392608
78779	A_51_P250807	Spata2l	spermatogenesis associated 2	NM_030176	77.9	77.4	69.3	85.3	164.2	150.5	184.8	154.2	77.475	163.425	1.07608488	2.10830689	0.01527035
241062	A_55_P1963184	Pgap1	post-GPI attachment to prote	ENSMUST00000097739	42.4	43.6	45.6	55.5	91	87.8	108.2	106.9	46.775	98.475	1.07599801	2.10817994	0.06286685
434156	A_55_P2133845	Eid2b	EP300 interacting inhibitor of	NM_001177427	229.3	215	218.5	204.6	488.1	403.8	459	480.2	216.85	457.775	1.0752337	2.10706336	0.00485461
20740	A_55_P2072985	Spna2	spectrin alpha 2	NM_001076554	2515.5	2904.4	2582	2776.2	5234.4	6004.3	5939.3	5505.1	2694.525	5670.775	1.07359902	2.10467725	0.00390984
78914	A_51_P140350	Nadsyn1	NAD synthetase 1	NM_030221	227.4	241.3	239.2	236.3	451.4	434.9	512.9	604.4	236.05	500.9	1.07359354	2.10466927	0.04244746
19286	A_52_P177021	Pts	6-pyruvoyl-tetrahydropterin s	NM_011220	306.2	351.7	340.7	346.1	743.1	632.6	724.4	731.3	336.175	707.85	1.07339733	2.10438305	0.00478063
22245	A_55_P2078285	Uck1	uridine-cytidine kinase 1	NM_011675	3176.3	3663.2	3181.3	3258.9	6746.5	6986	6850.2	7299.4	3319.925	6970.525	1.07201918	2.10237377	0.00191553
170823	A_66_P133520	Glmn	glomulin, FKBP associated pro	NM_133248	251.4	269	274.3	316	570.7	582.6	598.7	575	277.675	581.75	1.07184087	2.10211394	0.00508835
109785	A_52_P341449	Pgm3	phosphoglucomutase 3	NM_028352	141.9	149.5	138.7	174.2	306.1	324.1	327.8	307.1	151.075	316.275	1.07105849	2.10097426	0.0079455
52696	A_51_P163378	Zwint	ZW10 interactor	ENSMUST00000020081	6391.7	7480.2	7064.9	7558.1	15699.6	15151.3	14987.5	13903.8	7123.725	14935.55	1.06978787	2.09912469	0.0039556
230784	A_51_P161354	Sesn2	sestrin 2	NM_144907	114.6	111.5	122.1	95.9	228.7	227.6	256.6	217.4	111.025	232.575	1.06962834	2.09889259	0.01554729
76295	A_51_P146505	Atp11b	ATPase, class VI, type 11B	NM_029570	218.9	234.6	222.8	263.6	473.5	541.5	460.5	495.5	234.975	492.75	1.06945935	2.09864675	0.00844624
72053	A_55_P1968998	Tmub2	transmembrane and ubiquitir	NM_028076	384.5	354.5	355.1	277.7	734.2	660	730.2	734.9	342.95	714.825	1.06848925	2.09723605	0.04334416
67759	A_51_P351238	5033414D02Rik	RIKEN cDNA 5033414D02 gen	NM_026362	1784.4	1858	1910.9	1938.8	3856.6	3790.6	4200.3	3868.5	1873.025	3929	1.06835414	2.09703965	0.00096418
72486	A_51_P135939	Rnf219	ring finger protein 219	NM_026047	10.3	12	11.3	13.4	25.8	26.8	23.2	22.5	11.75	24.575	1.06735484	2.09558761	0.02761787
73689	A_55_P1984825	Bloc1s2	biogenesis of lysosome-relate	NM_028607	1705	1955.5	1832.1	1898.5	3591.8	4101.4	3885.7	3906.6	1847.775	3871.375	1.067311	2.09552394	0.00243603
70616	A_51_P341789	Sugp1	SURP and G patch domain co	NM_027481	4591.7	4719.4	4430.4	5042.2	10084.9	9494.2	10315.8	9427.5	4695.925	9830.6	1.06642705	2.09424039	0.00158759
71742	A_51_P208020	Ulk3	unc-51-like kinase 3 (C. elegar	NM_027895	360.8	408.3	384.2	454.2	771.7	855.7	777.2	960.2	401.875	841.2	1.06518798	2.0924425	0.03190603
99311	A_55_P2063366	Commd7	COMM domain containing 7	NM_001195390	2133.9	2045	2279.4	2663.4	4383.3	4834.9	4794.6	4995.4	2280.425	4752.05	1.06499937	2.09216897	0.0191557
104625	A_51_P449911	Cnot6	CCR4-NOT transcription comp	ENSMUST00000145353	989.4	881	895.5	993.5	1990.9	1886.2	2086.3	1893.8	939.85	1964.3	1.06448427	2.09142211	0.00238044
20509	A_51_P502152	Slc19a1	solute carrier family 19 (sodiu	NM_031196	382.9	391.5	339.4	414.4	763.7	716.8	843.6	872.9	382.05	799.25	1.0642404	2.09106861	0.01562473
21371	A_55_P2056315	Tbca	tubulin cofactor A	NM_009321	4208.2	4704.3	4590.1	4750.4	9747.3	9506.7	9867	9001.1	4563.25	9530.525	1.06322555	2.08959818	0.00150165
319688	A_55_P2115696	5930422O12Rik	RIKEN cDNA 5930422O12 gen	ENSMUST00000059351	46.4	40.9	39	41.8	81.1	82.7	95.4	92.1	42.025	87.825	1.06289424	2.08911837	0.00834283
434402	A_55_P2183894	Gm5617	predicted gene 5617	NM_001004191	1022.7	940.4	775.8	819.6	1972	1724.2	1906.1	1796.4	889.625	1849.675	1.06271027	2.088852	0.03015998
327951	A_52_P264647	Cyb5d1	cytochrome b5 domain conta	ENSMUST00000134903	189.5	228	214.8	199.5	388.5	457.2	437.1	453.5	207.95	434.075	1.06229788	2.08825498	0.00930654
69683	A_55_P2070657	2310044H10Rik	RIKEN cDNA 2310044H10 gen	NM_197991	98.3	88.6	85.9	70.9	184.9	177.7	160.4	191	85.925	178.5	1.06155155	2.08717497	0.05541672
51875	A_51_P348183	Tmem141	transmembrane protein 141	NM_001040130	3043.3	2921.2	3181.8	3113.2	6700.4	6665.5	6103.4	6109.5	3064.875	6394.7	1.06029717	2.08536102	0.00125182
94184	A_52_P542290	Pdxdc1	pyridoxal-dependent decarbo	NM_053181	274.3	294.9	306.5	300.2	640.9	607.7	599.4	602.6	293.975	612.65	1.06009671	2.08507128	0.00097076
21767	A_51_P274504	Tex264	testis expressed gene 264	NM_011573	2258.8	2172.2	2311.5	2019.7	4435.5	4390.7	4515.7	4921.1	2190.55	4565.75	1.05994858	2.08485722	0.00236967
67157	A_55_P2429432	2610301B20Rik	RIKEN cDNA 2610301B20 gen	NM_026005	77.5	81.2	80.9	69.3	156.7	154.3	166	165.8	77.225	160.7	1.05935294	2.08399663	0.00287774
12499	A_55_P1998656	Entpd5	ectonucleoside triphosphate	NM_001026214	89	97.9	106.3	119.3	221.8	205.8	199.7	228.6	103.125	213.975	1.05929211	2.08390875	0.03054415

229055	A_52_P495553	Zbtb10	zinc finger and BTB domain co	NM_177660	123.9	105.1	129.3	107.3	256.8	200	267	248.2	116.4	243	1.05891921	2.08337019	0.07780948
321006	A_55_P2026783	Vprbp	Vpr (HIV-1) binding protein	ENSMUST00000045973	40.7	46.9	37.6	45.9	90.3	91.7	76.5	97.9	42.775	89.1	1.0586432	2.08297164	0.04201672
232236	A_55_P2135261	C130022K22Rik	RIKEN cDNA C130022K22 gen	NM_172730	1527.1	1612.8	1537.3	1574.2	3389.5	3130.9	3273	3228.7	1562.85	3255.525	1.05845931	2.08270616	0.00055104
11984	A_55_P1979053	Atp6v0c	ATPase, H+ transporting, lyso	NM_009729	2449.1	2037.6	2080.3	1911.5	4401.3	4326.8	4607.4	4246.7	2119.625	4395.55	1.05772646	2.08164848	0.00978651
69723	A_55_P2143261	Rpain	RPA interacting protein	NM_027186	997.5	1219.1	1239.7	1201.2	2370	2536.9	2554.7	2213.6	1164.375	2418.8	1.05770738	2.08162094	0.01520597
27973	A_51_P395555	Vkorc1	vitamin K epoxide reductase c	NM_178600	1466.1	1597.3	1304.1	1379	2730.3	3129.4	3211.7	2880	1436.625	2987.85	1.05751393	2.08134184	0.01141159
78885	A_51_P323878	Coro7	coronin 7	NM_030205	1313.2	1248.1	1234.9	1184.5	2744.2	2440	2583.8	2591.6	1245.175	2589.9	1.05627791	2.07955942	0.00131219
72865	A_55_P2133266	Cxx1c	CAAX box 1 homolog C (huma	NM_028375	3731	3902.6	3804.8	3766.6	7708.7	7751.9	8224.7	7929.6	3801.25	7903.725	1.05579182	2.07885887	0.00046773
109275	A_52_P594049	Actr5	ARP5 actin-related protein 5 h	NM_175419	379.1	504.3	435.6	473.1	884.5	969.1	881.2	973.3	448.025	927.025	1.05546298	2.07838509	0.02639008
74775	A_55_P2085641	Lmbr1l	limb region 1 like	NM_029098	2212.3	2071.3	2129.1	1949.8	4368.7	4076.2	4309.7	4621.4	2090.625	4344	1.05517322	2.07796768	0.00201227
544678	A_55_P2009066	2010015L04Rik	RIKEN cDNA 2010015L04 gen	NM_001166029	12041.7	10064.1	12334.2	12184	25023.2	22927.7	24776.8	23871.3	11656	24149.75	1.05492893	2.07761585	0.00739626
77891	A_55_P1957168	Ube2s	ubiquitin-conjugating enzyme	NM_133777	2853.3	2674.8	3005.3	2674.2	5742.2	5373.2	6138	6026.2	2801.9	5819.9	1.05443087	2.07689873	0.00284758
68642	A_55_P2075268	Tmem216	transmembrane protein 216	NM_026798	379.9	453.2	386.4	463.4	748	864.1	876.5	1010.3	420.725	874.725	1.05364544	2.07576834	0.06948851
237500	A_51_P151835	Tmtc3	transmembrane and tetratric	NM_001110013	227.1	200.8	196.9	192.2	441.2	414.1	386.6	453.2	204.25	423.775	1.05331077	2.07528686	0.00705905
66400	A_55_P2016682	Alkbh7	alkB, alkylation repair homolo	NM_025538	5399.5	5469.3	4815.1	4644.8	10178.9	9634.3	10474.4	11925.1	5082.175	10553.175	1.05326263	2.07521761	0.01589808
67988	A_55_P2064230	Tmx3	thioredoxin-related transmen	NM_198295	295.9	366.1	318.2	365.9	696	722.2	648.7	715.4	336.525	695.575	1.05226414	2.07378185	0.01283999
57896	A_55_P2063646	Krcc1	lysine-rich coiled-coil 1	NM_145568	4068.5	5061.1	4481	5151.1	10084.9	10047.6	9489.7	9135.6	4690.425	9689.45	1.05202916	2.0734441	0.01517385
68832	A_51_P492446	1110057K04Rik	RIKEN cDNA 1110057K04 gen	NM_172401	803.9	815	739.4	734.1	1488	1617.7	1627.9	1676.3	773.1	1602.475	1.05179392	2.07310605	0.00214162
226026	A_55_P2062632	Smc5	structural maintenance of chr	NM_153808	958.6	1073	1196.1	1237.6	2221.9	2521.4	2445.9	2050.8	1116.325	2310	1.05150927	2.07269706	0.04627874
101739	A_55_P1993054	Psip1	PC4 and SFRS1 interacting pro	NM_133948	121.8	124.8	157.7	118.7	257.5	287.4	285.4	248.4	130.75	269.675	1.05116209	2.07219832	0.04827846
19300	A_51_P138760	Abcd4	ATP-binding cassette, sub-fan	NM_008992	365.9	407.3	410.6	370.1	735.3	712.2	874.5	911.4	388.475	808.35	1.05099205	2.0719541	0.03006186
107885	A_55_P2061319	Mthfs	5, 10-methenyltetrahydrofola	NM_026829	60.9	57.9	72.6	71.6	128.7	123.9	144.7	146.4	65.75	135.925	1.0509866	2.07194628	0.03495909
320678	A_55_P2009187	Iffo1	intermediate filament family	NM_001039669	205.4	213.1	176.5	215.7	413.6	402.9	414.2	443	202.675	418.425	1.04940778	2.06968007	0.0067498
78795	A_52_P215418	Armc9	armadillo repeat containing 9	NM_027456	29.1	27.9	28.7	27.6	54.9	61.3	62.3	56.2	28.325	58.675	1.04887306	2.06891311	0.00158885
223752	A_55_P1983152	Gramd4	GRAM domain containing 4	NM_172611	938.4	847.9	1006	996.9	1965.2	1870.8	2081.6	1903.4	947.3	1955.25	1.04755279	2.06702064	0.00456901
67418	A_51_P388374	Ppil4	peptidylprolyl isomerase (cyc	NM_026141	941.4	956.1	949.1	807.7	1908.6	1794.9	1825.6	2006.2	913.575	1883.825	1.04615444	2.06501811	0.00532656
75291	A_51_P169880	Zbtb3	zinc finger and BTB domain co	NM_133759	32	35.7	34.7	29.3	56.3	69	69.8	77.7	32.925	68.2	1.04526015	2.06373847	0.07423621
76742	A_55_P2018944	Snx27	sorting nexin family member	NM_001082484	223.8	225.5	223.2	229.1	519	460.3	441	442.3	225.4	465.65	1.04361523	2.06138679	0.00252297
11746	A_55_P2092859	Anxa4	annexin A4	NM_013471	1141.7	1463	1276.7	1345	2570.1	3189.9	2534.4	2489.7	1306.6	2696.025	1.04320318	2.06079812	0.06277767
108903	A_51_P392244	Tbcd	tubulin-specific chaperone d	NM_029878	566.5	462.7	646.6	540.7	1021.4	1170	1219.3	1133.6	554.125	1136.075	1.04296969	2.06046462	0.06638578
224020	A_52_P454994	Pi4ka	phosphatidylinositol 4-kinase	NM_001001983	3733.2	3492.6	3637.7	4469.8	7776.6	8263.2	7381	8049.6	3833.325	7867.6	1.04265561	2.06001609	0.01551153
140629	A_52_P224358	Ubox5	U box domain containing 5	NM_080562	140.9	110.3	124.8	132.8	282	223	253.3	291.1	127.2	262.35	1.04253083	2.05983793	0.07184677
103012	A_52_P223508	6720401G13Rik	RIKEN cDNA 6720401G13 gen	NR_026976	141.1	123.5	127.2	137.8	268.9	273	270.8	275.9	132.4	272.15	1.04161008	2.05852373	0.00149416
75146	A_51_P345792	Tmem180	transmembrane protein 180	NM_029186	79.1	77.5	76.8	74.1	150.7	143.9	176	163.8	76.875	158.6	1.04087883	2.0574806	0.00518468
381510	A_55_P2006990	Dpy19l4	dpy-19-like 4 (C. elegans)	NM_001081201	25.2	31.2	32.2	24.4	58.6	56.7	56.5	58.9	28.25	57.675	1.04046408	2.05688919	0.04248977
223646	A_51_P414115	Naprt1	nicotinate phosphoribosyltran	NM_172607	872.8	1019.1	800.9	843.5	1738.5	1679.6	1934.3	1898.8	884.075	1812.8	1.03942191	2.05540389	0.01927068
56347	A_52_P18807	Eif3c	eukaryotic translation initiatio	NM_146200	9241.5	8905.9	8638.7	9397	18876.5	18135.7	19017.4	18314.2	9045.775	18585.95	1.03937897	2.05534271	0.00070544
23885	A_55_P1984878	Gmcl1	germ cell-less homolog 1 (Dro	ENSMUST00000113679	27.1	26.9	25.1	23.4	48.9	54.6	48.3	59.1	25.625	52.725	1.03845545	2.05402744	0.01507111
72351	A_51_P168981	Ptar1	protein prenyltransferase alp	NM_028208	71.1	73.7	67.9	79.6	151.9	147.4	141.9	158.4	73.075	149.9	1.03783088	2.0531384	0.00320093
76721	A_55_P2083824	1700085B13Rik	RIKEN cDNA 1700085B13 gen	AK007003	72.6	64.1	68	70.9	155.5	124.6	138.9	148.1	68.9	141.775	1.03773375	2.05300017	0.01096358
217370	A_55_P2084448	BC017643	cDNA sequence BC017643	NM_144832	393.4	455.9	446.1	404.4	881.7	842.3	890.8	867.7	424.95	870.625	1.03726385	2.0523316	0.00255152
67980	A_55_P2098499	Gnpda2	glucosamine-6-phosphate dea	NM_001038015	209.5	253.9	246.3	229.7	489.2	451.6	492.7	487.9	234.85	480.35	1.03534668	2.04960611	0.00573128
319653	A_51_P329490	Slc25a40	solute carrier family 25, mem	NM_178766	57.8	76.9	77.6	69.1	135.4	138.6	151.6	147.7	70.35	143.325	1.03500288	2.04911773	0.04814292
553127	A_55_P1980262	Cxx1b	CAAX box 1 homolog B (huma	NM_001018063	4900.5	4922	4607.8	4484.9	9703.3	9418.9	9972.1	9640.8	4728.8	9683.775	1.03493919	2.04902727	0.00095322
53858	A_51_P371255	Rwdd2b	RWD domain containing 2B	NM_016924	98.8	80.7	93.7	86.4	178.5	192	171.1	193.5	89.9	183.775	1.033939	2.04760723	0.00985539
77573	A_51_P102507	Vps33a	vacuolar protein sorting 33A (	NM_029929	842.6	895.5	893.2	891.4	1787.5	1732.4	1800.8	1892.7	880.675	1803.35	1.03372846	2.04730843	0.00081094
17283	A_66_P137048	Men1	multiple endocrine neoplasia	NM_008583	723.4	718.1	650.8	693.6	1493.1	1253.9	1413	1547.2	696.475	1426.8	1.03139253	2.04399622	0.00878707
67230	A_52_P270145	Zfp329	zinc finger protein 329	NM_026046	672	686.8	526.5	674.6	1301.8	1225.1	1287.8	1392.8	639.975	1301.875	1.03129981	2.04386487	0.03443332
11651	A_55_P2066384	Akt1	thymoma viral proto-oncogen	NM_009652	2602.6	2737.4	2744.3	2922.1	5674.1	5768	5361.9	5677.6	2751.6	5620.4	1.03107116	2.04354096	0.00121629
69806	A_55_P2028788	Slc39a11	solute carrier family 39 (meta	NM_001166503	543.9	595.5	506.9	533.9	1191.5	1043.7	1030	1186.9	545.05	1113.025	1.02908187	2.04072513	0.00898385
63872	A_55_P2011026	Zfp296	zinc finger protein 296	NM_022409	60.6	60.6	60.8	71.4	138.5	120.4	118.1	140.2	63.35	129.3	1.02857452	2.04000759	0.01900605
320528	A_55_P1954403	Vps13c	vacuolar protein sorting 13C (	NM_177184	28.4	38.6	31.8	38.1	72.6	72.1	65.6	66.7	34.225	69.25	1.02701046	2.03779717	0.07356237
52666	A_51_P451516	Arhgef25	Rho guanine nucleotide excha	NM_028027	4102.1	4483.1	4337.3	4878.6	9062	9495.3	8700.5	8963	4450.275	9055.2	1.02699983	2.03778215	0.00339609
72612	A_51_P450518	2700029M09Rik	RIKEN cDNA 2700029M09 ge	NM_028299	3359.1	4083.1	3265.5	4241.4	8000.1	7658.1	7094.2	7531.6	3737.275	7571	1.0267542	2.03743524	0.04308673
12445	A_55_P2041075	Ccnd3	cyclin D3	NM_001081636	2676	2443.8	2873.6	2304.7	4911.6	5216.9	5382.1	5388.9	2574.525	5224.875	1.02522583	2.03527794	0.01041146
320506	A_51_P375078	Lmbrd2	LMBR1 domain containing 2	NM_177178	159.7	132.7	126.9	141.7	314.3	273.6	308.6	246.4	140.25	285.725	1.02522158	2.03527195	0.06077543
231999	A_52_P138205	Plekha8	pleckstrin homology domain c	NM_001164361	45.1	49.7	43.2	50.2	97.4	84.6	92.8	108.9	47.05	95.925	1.02463608	2.03444613	0.02558038
66044	A_55_P2029549	Dtd1	D-tyrosyl-tRNA deacylase 1 h	NM_025314	2040.7	1929.4	2273.1	2632.4	4437.6	4673.7	4371.2	4445.8	2218.9	4482.075	1.02414023	2.03374702	0.04018733
18038	A_55_P2050697	Nfkbil1	nuclear factor of kappa light p	NM_010909	1351.3	1537.6	1558.9	1527.2	2977.2	3002.6	3096.6	3050.6	1493.75	3031.75	1.02337522	2.03266887	0.00204589
75472	A_51_P430259	1700009P17Rik	RIKEN cDNA 1700009P17 gen	NM_001081275	542.6	483.2	575.7	533.8	1065.9	961.8	1312.9	1021.7	533.825	1090.575	1.02329899	2.03256148	0.06646267
103677	A_55_P2061021	Smg6	Smg-6 homolog, nonsense me	NM_001002764	3749.6	3693.8	4195.2	3988.5	8079.4	7893.9	7720.6	8015	3906.775	7927.225	1.02249339	2.03142682	0.00157242
80280	A_51_P288257	Cdk5rap3	CDK5 regulatory subunit asso	NM_030248	2832.9	2610	2516.5	2634.2	5835.2	4977.6	5354.6	5344.2	2648.4	5377.9	1.02096806	2.02928017	0.00367177
76108	A_52_P336290	Rap2a	RAS related protein 2a	NM_029519	336.9	338.8	334.8	310	677	633.7	674.1	694.4	330.125	669.8	1.02084084	2.02910123	0.0013098
328417	A_51_P343913	Parp4	poly (ADP-ribose) polymerase	NM_001145978	151.9	139.6	130	152.7	248.9	268.2	339.4	314.4	143.55	292.725	1.02020769	2.02821092	0.08952748
69672	A_51_P276039	Txndc15	thioredoxin domain containin	NM_175150	6445.5	7613	7314.4	8348.5	15124.1	14005.1	15201.4	15657.7	7430.35	14997.075	1.01814414	2.02531196	0.01725093
66799	A_52_P182592	Ube2w	ubiquitin-conjugating enzyme	NM_025773	297.9	370.2	345.5	372	726.5	711.7	628.4	733.6	346.4	700.05	1.01794688	2.02503505	0.02459704
74479	A_55_P2120466	Snx11	sorting nexin 11	NM_028965	441.3	389.6	387.8	485	859.3	786	886.9	907.3	425.925	859.875	1.01774783	2.02475568	0.02336789
16475	A_52_P131548	Jub	ajuba	NM_010590	56.7	57.2	55.1	56.2	99.7	132.4	109.1	117.2	56.3	114.6	1.01772956	2.02473004	0.01994937
268291	A_55_P2128577	Rnf217	ring finger protein 217	NM_001146349	78.8	82.2	100.2	83.9	151.3	176.9	167.5	203	86.275	174.675	1.01572095	2.02191304	0.09343677
320727	A_55_P2064233	Ipo8	importin 8	NM_001081113	340.2	427	355.8	392.2	784.4	691.8	705.2	883.8	378.8	766.3	1.01510542	2.02105058	0.06647423
319757	A_51_P258766	Smo	smoothened homolog (Droso	NM_176996	798.3	850.5	662.9	787.7	1534.7	1663.6	1454.5	1584.6	774.85	1559.35	1.01323497	2.01843198	0.02046911
338363	A_55_P2157927	6030446N20Rik	RIKEN cDNA 6030446N20 gen	NM_178801	105.5	112.2	113.8	130	225.9	268.7	219.9	217.6	115.375	233.025	1.01296972	2.01806092	0.03257639
433759	A_55_P2077608	Hdac1	histone deacetylase 1	NM_008228	136.4	140.1	147.1	121.5	281.2	266.9	249	302.3	136.275	274.85	1.01199212	2.01669389	0.01663751
320615	A_52_P260787	Dopey1	dopey family member 1	NM_177208	25	24.4	27.9	22.3	49	46.5	60.7	45.3	24.9	50.375	1.01127549	2.01569239	0.09590031
81535	A_55_P2058903	Sgpp1	sphingosine-1-phosphate pho	NM_030750	4535.7	4621.4	4258.7	5016.1	9213.9	9236.8	9031	9616.6	4607.975	9274.575	1.01124583	2.01565095	0.00265608
117197	A_55_P2098428	Cno	cappuccino	NM_133724	292.4	286	268.4	231	595.5	511.8	537	522.8	269.45	541.775	1.01115673	2.01552646	0.02554
68533	A_51_P453010	Mphosph6	M phase phosphoprotein 6	NM_026758	369	378.2	334.6	389.1	818.2	680.1	739.4	728.4	367.725	741.525	1.01098445	2.0152858	0.00897117
228880	A_52_P214927	Zmynd8	zinc finger, MYND-type conta	ENSMUST00000109262	286.6	245.8	241.1	259.8	543.9	523.2	548.9	465.5	258.325	520.375	1.01061797	2.01477393	0.01256291
68839	A_52_P253230	Ankrd46	ankyrin repeat domain 46	NM_175134	876.7	1002.3	924.3	919.8	1998.1	1838.8	1768.7	1886.6	930.775	1873.05	1.00914414	2.01271673	0.00307705
77582	A_51_P144868	Mboat7	membrane bound O-acyltrans	NM_029934	462	400.6	429.7	434.1	876.6	787.1	921.5	886.6	431.6	867.95	1.00733017	2.01018763	0.00566403
74352	A_51_P128775	Zfp84	zinc finger protein 84	NM_023750	289.7	322.7	261.7	301.6	584.1	601	613.4	558.5	293.925	589.25	1.00666555	2.0092618	0.00781847
232853	A_51_P294778	Zfp954	zinc finger protein 954	NM_172738	528.4	529.4	483.5	543.4	1121.6	955.9	1039.5	1073.7	521.175	1047.675	1.00629096	2.00874016	0.0046758
52710	A_51_P288828	Gpr172b	G protein-coupled receptor 1	NM_029643	242.8	198	219.6	194.9	429.1	404.5	473.4	407.5	213.825	428.625	1.00610809	2.00848557	0.02608127
17319	A_55_P2052848	Mif	macrophage migration inhibit	NM_010798	15340.3	16279.5	14048.9	14788.6	29542.8	31909.1	30219.4	29584.8	15114.325	30314.025	1.00544498	2.0075626	0.00270268
22320	A_52_P279152	Vamp8	vesicle-associated membrane	NM_016794	1702.6	1987.4	1644.4	1471.9	3587.8	3589.9	3210.3	3206.4	1701.575	3398.6	1.00421073	2.00584584	0.04676137
192173	A_55_P1985079	Fam195b	family with sequence similarit	NM_001033231	4066.6	4440.2	4363	4312.4	9108	8836.3	8408.4	8120.6	4295.55	8618.325	1.00393377	2.00546081	0.00195853
73067	A_55_P2003951	Tmem192	transmembrane protein 192	NM_028427	4383	3957.9	4351.2	3607.7	8186.7	7613.6	8124	8677.8	4074.95	8150.525	1.00305846	2.00424442	0.01215507
75805	A_65_P19149	Nln	neurolysin (metallopeptidase	NM_029447	133.6	122.2	120.3	108.1	269.4	234.9	225.7	239.1	121.05	242.275	1.00191241	2.00265293	0.01810736
230082	A_52_P489119	Nol6	nucleolar protein family 6 (RN	NM_139236	602.4	592.9	686.6	532.4	1155.3	1131.6	1253.7	1279	603.575	1204.9	1.00126536	2.00175493	0.02220547
268512	A_51_P113403	Slc26a11	solute carrier family 26, mem	NM_178743	521.3	554	615	571.1	1098.2	1136.2	1110.5	1175.1	565.35	1130	1.00118332	2.00164111	0.00320401
233064	A_55_P2105808	Wdr62	WD repeat domain 62	NM_146186	184.3	197.4	206.9	155.3	395	394.7	340	354	185.975	370.925	1.00118094	2.0016378	0.06226651
80907	A_55_P1981544	Lactb	lactamase, beta	NM_030717	1367.3	1646.6	1597.3	1476	3207.6	2806.6	3173.4	2979.8	1521.8	3041.85	1.00085365	2.00118377	0.01123387
269941	A_55_P2059904	Chsy1	chondroitin sulfate synthase 1	NM_001081163	201.2	193.5	181.5	227.2	419.9	382.7	415.3	385.2	200.85	400.775	1.00028125	2.00038994	0.01250001
74347	A_51_P472329	4632415K11Rik	RIKEN cDNA 4632415K11 gen	NM_028883	79.7	85.3	87.1	77.7	159.2	152.4	177.8	170.3	82.45	164.925	0.99925915	1.99897323	0.00559997
381760	A_55_P2155021	Ssbp1	single-stranded DNA binding p	NM_028358	59.3	59.7	50.1	60.9	121.1	118.5	103.8	115.7	57.5	114.775	0.99899444	1.99860648	0.01705712
97761	A_55_P1982201	Sgsm2	small G protein signaling mod	NM_197943	454.1	576.2	514.4	518.1	1040.6	1171.9	973	934.5	515.7	1030	0.9977637	1.99690224	0.0472624
13448	A_51_P275976	Dok1	docking protein 1	NM_010070	133.2	132	109.4	123.2	237.4	259.7	249.9	244	124.45	247.75	0.99691275	1.99572474	0.00917433
211007	A_55_P1962339	Trim41	tripartite motif-containing 41	NM_145377	7096.9	8957.9	7632.1	8467.5	15661.7	17334.5	15597	15389.3	8038.6	15995.625	0.99685747	1.99564828	0.02069048
224656	A_55_P2113359	Zfp523	zinc finger protein 523	NM_172617	2304.2	2167.2	2402.6	2392.4	5011.7	4679.7	4388.4	4420.2	2316.6	4625	0.99659236	1.99528158	0.00378137
21376	A_55_P2021555	Tbrg1	transforming growth factor be	NM_025289	11680.6	12018.1	12194.7	12008.3	23289.6	24732	24374.9	23151.3	11975.425	23886.95	0.99573622	1.99409787	0.00080574
70533	A_55_P2111429	Btf3l4	basic transcription factor 3-lik	NM_027453	666.8	618.5	644.1	626.2	1279.1	1224.7	1359.5	1231.6	638.9	1273.725	0.99473596	1.99271579	0.00171578
71890	A_55_P1966863	Mad2l2	MAD2 mitotic arrest deficient	NM_027985	2985.6	2451.8	2926.3	2411.3	5189.8	5402.5	5373.4	5401.4	2693.75	5341.775	0.99443093	1.99229451	0.01871832
75758	A_52_P495031	9130401M01Rik	RIKEN cDNA 9130401M01 ge	NM_029418	3635.8	3940.7	3756.1	3986	7760.1	8061.5	7803	6908.7	3829.65	7633.325	0.99366619	1.99123872	0.00421719
77805	A_55_P2060747	Esco1	establishment of cohesion 1 h	NM_001081222	1005.7	1088.7	1077.1	1153.4	2433.9	1968.9	2101	2122.9	1081.225	2156.675	0.99348018	1.990982	0.01263716
208111	A_55_P2089118	9830147E19Rik	RIKEN cDNA 9830147E19 gen	NM_001034857	266.1	291.8	260.8	315.1	551.1	590.5	535.6	575.2	283.45	563.1	0.9934422	1.99092959	0.00910114
99412	A_55_P2002379	Golga2	golgi autoantigen, golgin subf	NM_133852	8437.1	8419.1	9535.3	9513.2	17255.5	18767.2	17997.3	17357.6	8976.175	17844.4	0.99317695	1.99056357	0.00434877
75871	A_52_P367774	Zfp821	zinc finger protein 821	NM_029468	197.1	189.1	198.6	219.6	424.4	438.8	357.2	383.3	201.1	400.925	0.99284336	1.99010336	0.01804705
216292	A_66_P134412	BC067068	cDNA sequence BC067068	NM_207522	588.1	594.7	543.7	573.4	1242	1127	1105	1100.3	574.975	1143.575	0.99105802	1.98764212	0.00275965
234463	A_55_P2102295	Tmem184c	transmembrane protein 184C	NM_145599	577	524	581.6	539	1125.9	1026.2	1169.5	1094.7	555.4	1104.075	0.99101994	1.98758965	0.00352414
12453	A_52_P91235	Ccni	cyclin I	NM_017367	2851	3098.9	2991.9	3471.5	6170.4	6074.9	6029.6	6332	3103.325	6151.725	0.99077572	1.98725322	0.00575108
50760	A_55_P2010936	Fbxo17	F-box protein 17	NM_015796	540.8	457	643.8	533.3	1055.5	1024	1131	1081.9	543.725	1073.1	0.99054288	1.98693253	0.06546734
73833	A_55_P1953796	Fam98c	family with sequence similarit	NM_001146023	3060.5	2717	2820.2	2909.8	5489.8	5936.9	5882.4	5545.4	2876.875	5713.625	0.9904151	1.98675655	0.00224612
217558	A_55_P2457154	G2e3	G2/M-phase specific E3 ubiqu	NM_001167964	32	27	27.5	25.9	61.4	49.4	58.2	54.3	28.1	55.825	0.9903265	1.98663455	0.03799192
56470	A_55_P2183692	Rgs19	regulator of G-protein signali	NM_026446	35.6	41.5	44.9	48.1	82.1	87.1	77.8	89.3	42.525	84.075	0.99018609	1.9864412	0.05893933
64685	A_55_P2034705	Nmi	N-myc (and STAT) interactor	NM_001141949	380.5	410.9	433.4	437.1	789.7	934.1	766.5	815.1	415.475	826.35	0.98994956	1.98611555	0.01464157
100503842	A_51_P191893	2410022M11Rik	RIKEN cDNA 2410022M11 ge	ENSMUST00000095785	1005.7	824	1012.9	1023.8	1893.3	1871.8	2107.1	1786.5	966.6	1914.675	0.98909553	1.98494017	0.02980103
84095	A_55_P1965902	Pi4k2a	phosphatidylinositol 4-kinase	NM_145501	233.1	203.7	233.1	180.4	465.9	406.7	424	385.6	212.575	420.55	0.98890283	1.98467507	0.06786551
71990	A_55_P1986406	Ddx54	DEAD (Asp-Glu-Ala-Asp) box p	NM_028041	1710.3	1611.5	1576.9	1376.8	3023.9	2974.4	3259.2	3162.6	1568.875	3105.025	0.98839358	1.98397463	0.0108148
72023	A_55_P2071087	Cyb561d1	cytochrome b-561 domain co	NM_001081320	32.9	39.8	37.4	40.3	68.6	70	74.8	85.1	37.6	74.625	0.98827169	1.98380702	0.04296265
18193	A_55_P2016877	Nsd1	nuclear receptor-binding SET-	NM_008739	2120.4	1993.7	2110.9	2275.5	4503.9	3625.5	4014.6	4784.5	2125.125	4232.125	0.98728814	1.98245504	0.04341841
232210	A_55_P2100963	8430410A17Rik	RIKEN cDNA 8430410A17 gen	NM_173737	855.2	974.9	1064.3	1029.1	2003.4	1959.7	1905.8	1883.8	980.875	1938.175	0.98704447	1.98212023	0.01064495
56289	A_55_P2092909	Rassf1	Ras association (RalGDS/AF-6	NM_019713	2186.9	2174.6	2604.3	2178.9	4309.7	4575	4656.4	4530.2	2286.175	4517.825	0.986504	1.98137781	0.00854714
100910	A_65_P15875	Chpf2	chondroitin polymerizing fact	NM_133913	740.1	691.9	820.9	624.4	1370.3	1475.8	1573.1	1270.1	719.325	1422.325	0.98607327	1.98078634	0.07092527
67846	A_51_P415519	Tmem39a	transmembrane protein 39a	NM_026407	248.9	301	276.6	287	490.5	578.8	569.4	566.3	278.375	551.25	0.98603637	1.98073567	0.01744463
69757	A_52_P152952	Leng1	leukocyte receptor cluster (LR	NM_027203	270	269.6	244.6	230.9	476.5	534	493.1	503.4	253.775	501.75	0.98535724	1.97980349	0.00715698
105501	A_51_P406020	Abhd4	abhydrolase domain containi	NM_134076	7277.6	7670.3	7875.2	6832.4	14217.2	14585.6	15231.1	14607.5	7413.875	14660.35	0.98529228	1.97971435	0.00282905
76781	A_55_P2225082	Mettl4	methyltransferase like 4	AK010837	81.1	76.3	84.7	83.8	160.7	148.8	161.2	175	81.475	161.425	0.98524158	1.97964478	0.00477742
66627	A_55_P1977353	Ogfod2	2-oxoglutarate and iron-depe	NM_025671	1626.6	1683.2	1671.6	1718.1	3370.1	3306.8	3200.8	3384.5	1674.875	3315.55	0.98512316	1.97948229	0.00079498
13644	A_51_P412914	Efs	embryonal Fyn-associated sul	NM_010112	146.2	201.2	173.2	170.6	341.3	363	317.6	339	172.8	340.225	0.98496899	1.97927077	0.05731352
272589	A_52_P244723	Tbcel	tubulin folding cofactor E-like	NM_173038	676.8	699.2	704.2	616.1	1385.8	1314.5	1266.7	1359.6	674.075	1331.65	0.98340455	1.97712564	0.00342872
19697	A_55_P1974288	Rela	v-rel reticuloendotheliosis vir	NM_009045	5816.6	6200.1	6171.9	6881.5	11851.7	12416.5	12912.6	12317.2	6267.525	12374.5	0.98340337	1.97712402	0.00426467
75965	A_55_P2033084	Zdhhc20	zinc finger, DHHC domain con	NM_029492	77	94.1	92.4	89.4	160.5	182.6	173.2	180.1	88.225	174.1	0.98324718	1.97690998	0.01536875
68631	A_51_P336952	Cryl1	crystallin, lambda 1	NM_030004	488.2	498	457.2	461.5	881	998.2	970.4	917.9	476.225	941.875	0.98315334	1.9767814	0.00299862
235043	A_51_P503654	Tmem205	transmembrane protein 205	NM_178577	317	349.9	348.9	357.3	719.1	669.4	659.6	664.9	343.275	678.25	0.98310368	1.97671336	0.00262396
319493	A_55_P2108983	A430078G23Rik	RIKEN cDNA A430078G23 ger	NM_001033378	34668.3	29952.7	30639.7	32302.9	70546.4	60225.6	63651.1	57982.5	31890.9	63101.4	0.98284582	1.97636009	0.01489358
319192	A_55_P2131438	Hist2h2aa2	histone cluster 2, H2aa2	NM_178212	10453	9778.6	9682.8	8053	17850.8	19490.7	19989.8	17440.3	9491.85	18692.9	0.98193805	1.97511691	0.03796694
207565	A_55_P2329923	Camkk2	calcium/calmodulin-depende	NM_001199676	1142.5	1085.6	943.7	1140.3	2083.7	2176	2128.4	2094	1078.025	2120.525	0.98008911	1.97258725	0.00794779
12055	A_51_P114028	Bcl7c	B-cell CLL/lymphoma 7C	NM_009746	299.8	270.2	319.3	305.6	566.8	637.8	575.3	575.4	298.725	588.825	0.9800596	1.97254689	0.00707391
54006	A_55_P2077872	Deaf1	deformed epidermal autoregu	NM_016874	586.2	573	592.9	587	1089.8	1066.6	1336.5	1139.2	584.775	1158.025	0.98004962	1.97253325	0.01274554
329679	A_52_P494930	Fnip2	folliculin interacting protein 2	NM_001162999	137	120.6	151	156.2	311.3	253.1	273.6	273.2	141.2	277.8	0.9794225	1.971676	0.06626657
68606	A_51_P224564	Ppm1f	protein phosphatase 1F (PP2C	NM_176833	1882.1	1570.6	1615.9	1788.5	3194	3557	3330.2	3407	1714.275	3372.05	0.97884723	1.97088997	0.00957322
70235	A_55_P2053258	Poc1a	POC1 centriolar protein homo	NM_027354	338	263.3	256.3	294.1	593.3	538	521.6	607.8	287.925	565.175	0.97875937	1.97076993	0.07097142

21981	A_55_P1973965	Ppp1r13b	protein phosphatase 1, regula	NM_011625	1653.3	1397.4	1410.8	1462.1	3099.2	2730.6	2946.9	2872.5	1480.9	2912.3	0.97749245	1.96904004	0.0087291
17984	A_52_P451644	Ndn	necdin	NM_010882	56.5	51.4	52.1	56.8	118.5	107.4	97.4	104.1	54.2	106.85	0.97709091	1.96849209	0.01012408
30046	A_51_P275591	Zfp292	zinc finger protein 292	NM_013889	214.7	240.2	180.7	219.1	463.9	381.5	404.5	427.1	213.675	419.25	0.97611654	1.96716305	0.06959685
16976	A_51_P513941	Lrpap1	low density lipoprotein recep	NM_013587	1715.2	1760.1	1583.2	1521.1	3581.9	3055.2	3370.2	2951.3	1644.9	3239.65	0.97604599	1.96706685	0.0192538
114863	A_52_P188425	Prosc	proline synthetase co-transcr	NM_001039077	362	344	355.2	341.5	678.9	700.4	684.5	692.3	350.675	689.025	0.97472766	1.96527017	0.0007891
100226	A_51_P252363	Stx12	syntaxin 12	NM_133887	1658.7	1890.5	1854	2192.1	3981.3	3488.1	3744.4	3655.2	1898.825	3717.25	0.97464755	1.96516105	0.03593573
12015	A_55_P1962234	Bad	BCL2-associated agonist of ce	NM_007522	1835.2	1899.6	1996	1736.2	3689.9	3628.9	3787.3	3548.7	1866.75	3663.7	0.97422413	1.96458437	0.00261266
15587	A_51_P284577	Hyal2	hyaluronoglucosaminidase 2	NM_010489	3009.2	3022.8	3394.4	3325.7	5898	5880.5	6342.8	6949.1	3188.025	6267.6	0.97400763	1.96428957	0.0121301
77045	A_55_P2185870	Bcl7a	B-cell CLL/lymphoma 7A	NM_029850	242.4	226.6	246.2	263.2	442.5	503.5	512.5	463.9	244.6	480.6	0.97387682	1.96411148	0.00855526
98732	A_51_P244558	Rab3gap2	RAB3 GTPase activating prote	NM_001163754	1099	1027.4	1121.3	1019.6	2246.4	2070.5	1962.8	2098	1066.825	2094.425	0.97278923	1.96263138	0.00376013
320129	A_51_P108581	Adrbk2	adrenergic receptor kinase, b	NM_177078	230.6	210.8	212.6	249	472.1	446	420.7	431	225.75	442.45	0.97276529	1.96259881	0.0087317
100041677	A_55_P2008722	Gm13157	predicted gene 13157	NM_001127189	111.7	96.2	91.1	92.3	163.8	191	206.5	207.4	97.825	192.175	0.97260054	1.96237471	0.07048588
269593	A_55_P2043987	Luzp1	leucine zipper protein 1	NM_024452	1538.3	1646	1395.8	1767.2	3245.8	3094	3053.7	3013.2	1586.825	3101.675	0.97176082	1.96123284	0.01521553
100310809	A_55_P2010992	Gm10509	zinc finger protein 51 pseudo	ENSMUST00000072133	34.4	40	35.9	36.9	77.4	64.6	66.5	81.1	36.8	72.4	0.97172769	1.9611878	0.03888272
71041	A_52_P412321	Pcgf6	polycomb group ring finger 6	NM_027654	239.9	239.3	263.2	223.7	467	470.8	523.6	433.6	241.525	473.75	0.97109711	1.96033077	0.01336993
18648	A_51_P342669	Pgam1	phosphoglycerate mutase 1	NM_023418	1299.1	1543.1	1285	1240.2	2485.4	2303.6	2841.4	2885.6	1341.85	2629	0.96928909	1.95787558	0.07559378
109754	A_51_P153170	Cyb5r3	cytochrome b5 reductase 3	NM_029787	868.5	827.1	953.4	813	1664.8	1913.6	1464.1	1744.9	865.5	1696.85	0.9673961	1.9553083	0.04669617
212880	A_55_P2078008	Ddx46	DEAD (Asp-Glu-Ala-Asp) box p	NM_145975	1205.1	1019.3	1117	1226.6	2158.6	2202.9	2257.5	2290	1142	2227.25	0.96713697	1.95495713	0.00756337
67500	A_55_P1962419	Ccar1	cell division cycle and apopto	NM_026201	688.2	800.9	751.8	761.9	1575.5	1375.1	1421.1	1492.4	750.7	1466.025	0.96582511	1.95318027	0.00709425
106957	A_51_P259214	Slc39a6	solute carrier family 39 (meta	NM_139143	213.4	201.1	182.6	207.3	356	404.5	427	383.4	201.1	392.725	0.9648058	1.95180078	0.01443191
191578	A_55_P2131128	Helq	helicase, POLQ-like	NM_001081107	168.3	174.3	159.9	191.6	377	300.9	308.4	372.7	173.525	339.75	0.96469774	1.95165459	0.06909247
270627	A_51_P139400	Taf1	TAF1 RNA polymerase II, TAT	NM_001081008	125.7	133.9	144.6	155.5	247.2	280.3	274.8	288.3	139.925	272.65	0.96462015	1.95154962	0.0231432
105785	A_52_P473966	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endop	NM_134090	51.1	50.8	42.3	45.1	95.3	89.7	94.8	88.3	47.325	92.025	0.96323695	1.94967946	0.01310977
52174	A_55_P1959600	Tmem222	transmembrane protein 222	NM_025667	2049.9	1972.3	1884.8	2121.7	4023.8	3714.2	3848.6	4055	2007.175	3910.4	0.96264527	1.94888001	0.00295152
434179	A_52_P235102	Gm5595	predicted gene 5595	NM_001008427	279.6	327.8	321.4	334	643.2	589.7	536.6	696.1	315.7	616.4	0.961998	1.94800583	0.06058584
217869	A_52_P533304	Eif5	eukaryotic translation initiatio	NM_173363	5228.5	5136	5459.2	5135.9	10590.4	10038.6	10663.9	9553	5239.9	10211.475	0.96160987	1.94748184	0.00229773
70361	A_52_P10781	Lman1	lectin, mannose-binding, 1	NM_001172062	195.5	203.7	201.2	185.2	410.1	363.8	375.8	380.6	196.4	382.575	0.96150823	1.94734464	0.00306268
223723	A_51_P286373	Ttll12	tubulin tyrosine ligase-like far	NM_183017	292	265.2	292.7	259.5	515	525.1	630.9	495.4	277.35	541.6	0.96124085	1.94698377	0.03627546
320244	A_51_P512629	Ttll5	tubulin tyrosine ligase-like far	NM_001081423	102.4	104.8	94.4	82.7	179.9	163.5	210.5	193.7	96.075	186.9	0.95986439	1.94512705	0.09904283
320057	A_55_P2326507	A630057N01Rik	RIKEN cDNA A630057N01 ger	AK079103	60.7	56.4	48.4	60.8	112.6	100.3	112.2	113.7	56.575	109.7	0.95951892	1.94466133	0.03356807
23984	A_51_P419017	Pde10a	phosphodiesterase 10A	NM_011866	30.8	32.3	28.9	24.2	60.3	55.7	52.7	56.1	29.05	56.2	0.9587745	1.94365815	0.06148378
80744	A_66_P128586	Cwc22	CWC22 spliceosome-associat	NM_030560	393.6	362	408.4	386.9	770.7	750.8	707.1	783.2	387.725	752.95	0.95780739	1.94235565	0.00336315
140500	A_55_P2077009	Acap3	ArfGAP with coiled-coil, ankyr	NM_207223	645.8	563.3	582.8	530.5	1266.7	1079.7	1092.9	1069.9	580.6	1127.3	0.95742765	1.94184446	0.02506255
64652	A_51_P355413	Nisch	nischarin	NM_022656	16096.7	17325.9	16297.4	20063.1	32862.8	34238.3	33531.3	34260.7	17445.775	33723.275	0.95631198	1.94034337	0.01548312
94219	A_55_P2167451	Cnnm2	cyclin M2	NM_033569	296.9	311.2	277.3	330.8	583.2	591.7	581.2	598.8	304.05	588.725	0.95618488	1.94017244	0.00483179
20480	A_55_P2054842	Clpb	ClpB caseinolytic peptidase B	NM_009191	4703.8	3847.6	3646.6	3985.9	7473	7782.9	8518.6	7522.6	4045.975	7824.275	0.95615001	1.94012555	0.03865697
68240	A_66_P106090	Rpa3	replication protein A3	NM_026632	569	678.5	514.7	548.1	1041.1	1062.3	1212.8	1146	577.575	1115.55	0.95475315	1.93824796	0.06295937
11305	A_52_P485007	Abca2	ATP-binding cassette, sub-fan	NM_007379	232.4	201.7	250.6	206	424.4	413.2	427.6	454.8	222.675	430	0.95422678	1.93754092	0.02142201
66155	A_55_P1975011	Ufc1	ubiquitin-fold modifier conjug	NM_025388	15039.6	16588.5	16810.9	15070.3	31224	30681.5	31028.7	29844.4	15877.325	30694.65	0.95275829	1.93556974	0.00295376
237400	A_55_P2058737	Mex3d	mex3 homolog D (C. elegans)	NM_198615	344	399.8	407.1	365.1	688.2	825.3	743.5	679.2	379	734.05	0.95263845	1.93540897	0.03151527
72282	A_55_P1979335	1810062G17Rik	RIKEN cDNA 1810062G17 gen	ENSMUST00000029268	17.1	22.9	20	21.6	37.7	44.3	37.3	38.1	20.4	39.35	0.95261565	1.93537838	0.09971715
105787	A_51_P158922	Prkaa1	protein kinase, AMP-activated	NM_001013367	786.4	810.2	773.2	849.2	1477.2	1742.4	1482	1536.6	804.75	1559.55	0.95211327	1.93470456	0.00834602
12751	A_55_P1987043	Tpp1	tripeptidyl peptidase I	NM_009906	458.3	405.6	448.3	385	793.9	800.2	832.8	849.6	424.3	819.125	0.95209972	1.93468638	0.00866198
66309	A_55_P2166011	Tmem128	transmembrane protein 128	ENSMUST00000119047	151.1	154.9	185.9	152.7	299.4	317.4	346.3	281.9	161.15	311.25	0.95087864	1.93304958	0.05169756
211286	A_51_P320888	Cln5	ceroid-lipofuscinosis, neurona	NM_001033242	1527.6	1568.5	1544.6	1501.4	2915.9	3069	2917.7	2966.9	1535.525	2967.375	0.95032593	1.93230915	0.00096263
620986	A_55_P2071028	Gm6195	predicted pseudogene 6195	XM_885368	410.6	449.5	364.6	423.3	706.5	762.8	887.1	830.4	412	796.7	0.95021195	1.93215649	0.05388841
12808	A_51_P302167	Cobl	cordon-bleu	NM_172496	122.1	136.3	150.4	152.6	290.3	262.2	260.2	268.2	140.35	270.225	0.94943354	1.93111428	0.02678092
272027	A_55_P2003643	Tstd2	thiosulfate sulfurtransferase (	NM_173033	268.1	274.9	293.9	344.8	515.4	571.1	594.6	592.3	295.425	568.35	0.94873005	1.93017286	0.05187084
51810	A_52_P73369	Hnrnpu	heterogeneous nuclear ribonu	NM_016805	1474.4	1705.9	1527.2	1700	3318.5	3024.3	2773.8	3254	1601.875	3092.65	0.94853144	1.92990714	0.02244991
13043	A_55_P2037677	Cttn	cortactin	NM_007803	1789.1	1970.2	1913.6	2050.4	3620.7	4336.9	3335	3661.8	1930.825	3738.6	0.94835045	1.92966505	0.0396599
67345	A_55_P2005190	Herc4	hect domain and RLD 4	NM_030114	1514.5	1700.2	1647.8	2026.3	3284.1	3281.1	3072.4	3600.7	1722.2	3309.575	0.94834653	1.92965981	0.06845663
381560	A_55_P2053032	Xkr8	X Kell blood group precursor r	NM_201368	33.2	41.9	35.9	33.1	77	70.8	66.7	63	36.025	69.375	0.94817446	1.92942968	0.07152187
55927	A_51_P429366	Hes6	hairy and enhancer of split 6 (	NM_019479	544.6	483.7	466.1	428	1017.3	862.5	896.8	920.2	480.6	924.2	0.94609291	1.92664786	0.03732097
17975	A_51_P134007	Ncl	nucleolin	NM_010880	5704.4	5596.9	6479.2	6504.2	12404.1	11088.4	11117.8	12110.7	6071.175	11680.25	0.94571095	1.92613784	0.01438856
56703	A_55_P2042202	Pigo	phosphatidylinositol glycan ar	NM_020035	1607.7	1359.9	1302.2	1488.6	3064.7	2572.6	2607.6	2830.1	1439.6	2768.75	0.94478566	1.92490289	0.04077184
72825	A_51_P268903	Mon1a	MON1 homolog A (yeast)	NM_028369	995.9	994.6	906.4	766.2	1816.6	1595.6	1842.6	1766.4	915.775	1755.3	0.94440525	1.92439539	0.07243022
71960	A_55_P2090070	Myh14	myosin, heavy polypeptide 14	NM_028021	4899.4	4488.1	5592	5196.1	10574.9	8608.2	10401.8	9213.9	5043.9	9699.7	0.94283837	1.92230649	0.06373868
109054	A_55_P1959628	Pfdn4	prefoldin 4	NM_001110152	97.5	111.1	106.7	102.5	192.6	170.8	231.8	212.1	104.45	201.825	0.94275596	1.92219668	0.08182052
235606	A_52_P420394	Apeh	acylpeptide hydrolase	NM_146226	2505.2	2432.6	2469.8	1933	4295	4159.4	4872.5	4557	2335.15	4470.975	0.94227984	1.92156242	0.07894527
66365	A_55_P2144975	Ccdc90b	coiled-coil domain containing	NM_001162918	186.8	241.6	227.5	236.4	431.8	417.3	386	475.2	223.075	427.575	0.94184309	1.92098079	0.09267091
15312	A_55_P1989102	Hmgn1	high mobility group nucleoso	NM_008251	660.2	652.3	598.2	727.9	1217.7	1312.1	1221.8	1307.6	659.65	1264.8	0.94171782	1.920814	0.01016064
110208	A_52_P84096	Pgd	phosphogluconate dehydroge	NM_001081274	466.7	480.9	524.6	435.7	806.7	931.7	980.6	945.9	476.975	916.225	0.94111622	1.92001318	0.02926979
22377	A_51_P160372	Wbp1	WW domain binding protein 1	NM_016757	6568.5	6937	6197.3	6140.3	12518.6	11856.5	11949.6	13275.6	6460.775	12400.075	0.9408446	1.91965174	0.00577919
104771	A_55_P2003123	Jkamp	JNK1/MAPK8-associated mem	NM_024205	2943.7	3084.2	2821.6	2773.7	5100.7	6019	5550	5659.1	2905.8	5582.2	0.94060682	1.91933536	0.00756562
19338	A_55_P1968235	Rab33b	RAB33B, member of RAS onco	NM_016858	986.1	1197.6	1088.9	1238.9	2058.4	2281.9	2132.8	2157.5	1127.875	2157.65	0.94049624	1.91918827	0.02493662
70093	A_51_P348119	Ube2q1	ubiquitin-conjugating enzyme	NM_027315	661.9	610.3	686.6	694.3	1366.8	1135.6	1189.4	1414	663.275	1276.45	0.94020612	1.91880237	0.03721079
20397	A_55_P1984730	Sgpl1	sphingosine phosphate lyase	NM_009163	414.6	437.6	479	526.5	858.4	952.9	910.4	832.8	464.425	888.625	0.94016337	1.9187455	0.03713097
56442	A_51_P358225	Serinc1	serine incorporator 1	NM_019760	13043.7	15576.6	13792.6	16423.6	30206.3	28013.1	26097.8	28224.6	14709.125	28135.45	0.93985852	1.91834011	0.03879227
17237	A_55_P2045026	Mgrn1	mahogunin, ring finger 1	NM_029657	9036.3	8628.6	8356.3	8746.4	18427.9	16299.8	15145.3	16943.3	8691.9	16704.075	0.93940777	1.91774084	0.00935112
73852	A_55_P2035539	D3Ertd751e	DNA segment, Chr 3, ERATO D	NM_028667	175.1	161	164	154.1	310.8	284.8	327.2	332.7	163.55	313.875	0.93938195	1.91770652	0.00930075
227102	A_51_P382121	Ormdl1	ORM1-like 1 (S. cerevisiae)	NM_145517	511.3	521	498.1	494.9	934.2	914.9	1032.1	1002.8	506.325	971	0.93794813	1.91580155	0.00316404
93871	A_51_P181538	Brwd1	bromodomain and WD repea	NM_145125	621.2	576.2	700.6	560.4	1115.5	1139.1	1179.8	1262	614.6	1174.1	0.93771902	1.91549734	0.02803613
103199	A_51_P405985	Fig4	FIG4 homolog (S. cerevisiae)	NM_133999	225.9	217.6	259.8	216.6	480.9	443.3	419.5	416.4	229.975	440.025	0.93771592	1.91549322	0.02242794
98956	A_55_P1999172	Nat10	N-acetyltransferase 10	NM_153126	1490.8	1561.8	1474.7	1516.7	2900.8	2970	2844.9	2859.5	1511	2893.8	0.93760023	1.91533962	0.00111333
102545	A_55_P2080870	Cmtm7	CKLF-like MARVEL transmemb	NM_133978	867.4	892.6	995.1	749.4	1761.2	1687.7	1545.1	1690.4	876.125	1671.1	0.93727644	1.9149098	0.05244274
72108	A_52_P269461	Ddhd2	DDHD domain containing 2	NM_028102	83.2	94.5	91.6	101.3	178.7	166	180.6	183.1	92.65	177.1	0.9372643	1.9148937	0.01172882
53381	A_55_P1979457	Prdx4	peroxiredoxin 4	NM_016764	371.1	378.2	331.1	372.5	715.9	602.6	732.9	736	363.225	696.85	0.93720402	1.91481368	0.02809825
110175	A_52_P641758	Ggct	gamma-glutamyl cyclotransfe	NM_026637	1070.8	1336.8	1117.8	1282.6	2034.6	2481	2472.2	2210.4	1202	2299.55	0.93714094	1.91472997	0.08790767
245666	A_55_P1991964	Iqsec2	IQ motif and Sec7 domain 2	NM_001114664	385.9	387.4	402.9	394.2	691.9	789.5	784.9	743.3	392.6	752.4	0.93663892	1.91406381	0.00353949
14923	A_51_P235878	Guk1	guanylate kinase 1	NM_008193	1638.3	1472.4	1497.4	1537.1	3035.9	2836.7	3055.9	2831.5	1536.3	2940	0.93661545	1.91403267	0.0033124
73692	A_55_P2067772	2410089E03Rik	RIKEN cDNA 2410089E03 gen	NM_001162906	226.7	212	200.6	237.5	429	403.3	426.5	416.3	219.2	418.775	0.93647564	1.91384719	0.00664703
13424	A_51_P354698	Dync1h1	dynein cytoplasmic 1 heavy c	NM_030238	7399.9	6169.1	7259.4	6600.5	12546.4	13174.8	13569.1	13078.9	6857.225	13092.3	0.93633543	1.91366119	0.01093132
245174	A_55_P2057720	Zfp937	zinc finger protein 937	NM_001142411	63.5	65.6	63	58.7	111.9	113.5	117.9	137.9	62.7	120.3	0.93615904	1.91342723	0.0214721
70999	A_55_P2155062	Naa40	N(alpha)-acetyltransferase 40	NM_027643	608.5	597.1	648	604.4	1260	1165.5	1248	1040.1	614.5	1178.4	0.9359245	1.91311619	0.01345704
56397	A_55_P1969882	Morf4l2	mortality factor 4 like 2	NM_019768	12671	15188.7	14614.8	15505	28070.9	31851.1	24161	27042.9	14494.875	27781.475	0.93591404	1.91310233	0.09682225
27029	A_55_P2028571	Sgsh	N-sulfoglucosamine sulfohydr	NM_018822	490.9	447.7	531	493.2	934.2	932.7	955.1	920	490.7	935.5	0.93339602	1.90976618	0.00490859
67451	A_51_P225427	Pkp2	plakophilin 2	NM_026163	361.9	366.1	339.9	307.3	689.9	588.7	640.5	707.6	343.8	656.675	0.93336637	1.90972694	0.03117005
223827	A_55_P2019776	Gxylt1	glucoside xylosyltransferase 1	NM_001033275	36.9	38.2	34.9	28.9	62.9	71	67.3	62.9	34.725	66.025	0.9332639	1.9095913	0.07377684
22123	A_51_P130427	Psmd3	proteasome (prosome, macro	NM_009439	24421.4	27023.6	27077.1	28739.2	48529.9	52861.2	49496.1	53708.6	26815.325	51148.95	0.93277303	1.90894168	0.00825307
21411	A_52_P621567	Tcf20	transcription factor 20	NM_001114140	846.5	953.7	978.7	1066.9	1774.7	1944.8	1784.7	1810.2	961.45	1828.6	0.93136867	1.90708437	0.0203348
223753	A_55_P2146177	Cerk	ceramide kinase	NM_145475	1327.6	1235.3	1320.6	1498.8	2638.4	2586.4	2563.8	2453.4	1345.575	2560.5	0.93124787	1.90692469	0.00931527
27681	A_55_P2083382	Snf8	SNF8, ESCRT-II complex subur	NM_033568	6649.7	6738.2	6585.5	6477.7	13295.5	11936.1	12221.5	13027.9	6612.775	12620.25	0.93114518	1.90678896	0.00244689
50793	A_55_P1965554	Orc3	origin recognition complex, su	NM_015824	2377.3	2833.4	2913.1	2919	4940.6	5303.5	5633.6	5118.4	2760.7	5249.025	0.93037334	1.90576911	0.02930128
67153	A_51_P474454	Rnaseh2b	ribonuclease H2, subunit B	NM_026001	204.1	244.1	203.8	185.2	409.5	380.4	387.9	409.7	209.3	396.875	0.92966168	1.90482926	0.04105656
58810	A_51_P327295	Akr1a1	aldo-keto reductase family 1,	NM_021473	4592.8	4104.6	4928.1	4314.9	8130.7	8632.4	9365.2	8011	4485.1	8534.825	0.92886479	1.90377739	0.02235001
67939	A_55_P2102574	Prorsd1	prolyl-tRNA synthetase doma	NM_001163454	1211.5	1333.7	1493.5	1345.2	2558	2398.5	2609	2661.8	1345.975	2556.825	0.92857533	1.90339545	0.01497689
74919	A_52_P679205	4930471M23Rik	RIKEN cDNA 4930471M23 ger	NM_175675	565.1	488.5	512.6	437.4	978.9	893.8	909.5	1017.2	500.9	949.85	0.9272668	1.90166984	0.04421402
72826	A_51_P104125	Fam76b	family with sequence similarit	NM_176836	630.2	564.2	571.5	513.9	1101.7	1087.4	1096.4	1039.6	569.95	1081.275	0.92721793	1.90160544	0.01025207
16653	A_51_P509489	Kras	v-Ki-ras2 Kirsten rat sarcoma	NM_021284	663.3	669	640.7	667.6	1251	1194	1254	1324.4	660.15	1255.85	0.92704315	1.90137507	0.00197236
73124	A_55_P1994348	Golim4	golgi integral membrane prot	NM_175193	383.8	385.2	358.5	395.1	758.7	717.4	705	712.1	380.65	723.3	0.92646425	1.90061228	0.00247589
52585	A_51_P293901	Dhrs1	dehydrogenase/reductase (SD	NM_026819	256.1	238.4	260.5	258.9	462	517	442.8	507.3	253.475	482.275	0.92594542	1.89992889	0.00919509
69684	A_55_P2046453	Aarsd1	alanyl-tRNA synthetase doma	NM_144829	7960.4	8116.5	7456.8	7744.9	14632	14091.9	15310.5	15292.9	7819.65	14831.825	0.92339675	1.89657542	0.00265456
66366	A_55_P1990319	Ergic3	ERGIC and golgi 3	NM_025516	1635.7	1478.8	1481	1387.6	3062.7	2626.3	2730.5	2926	1495.775	2836.375	0.92310805	1.89619594	0.01570093
233824	A_51_P212560	Cog7	component of oligomeric golg	NM_001033318	486.3	530.4	472.6	487.2	966.7	846.1	987.9	946.9	494.125	936.9	0.9218531	1.89454722	0.00965777
268936	A_55_P2025463	Brpf3	bromodomain and PHD finger	NM_001081315	543.4	515	625.1	676.8	1161.1	1105.7	1146.5	1034.7	590.075	1112	0.92130248	1.89382429	0.07607366
28193	A_55_P2175692	Reep3	receptor accessory protein 3	NM_178606	262.9	314	331.5	278.1	574.5	588	526.2	550.3	296.625	559.75	0.92101533	1.89344738	0.03792139
69582	A_55_P1995012	Plekhm2	pleckstrin homology domain c	NM_001033150	10337.4	8796.8	11184.8	10272.7	19390.2	20211.6	17964.4	19065.6	10147.925	19157.95	0.92083623	1.89321234	0.03006025
27225	A_55_P1958007	Ddx24	DEAD (Asp-Glu-Ala-Asp) box p	NM_001159502	13177.4	13273.9	13571.7	16412.1	28031	24131.7	26417.4	27940.2	14108.775	26630.075	0.91994106	1.892038	0.05263437
55944	A_55_P2016346	Eif3d	eukaryotic translation initiatio	NM_018749	9080.2	10092.5	9471.5	10313.6	17310.1	18484.3	19334.2	18531.1	9739.45	18414.925	0.91968142	1.89169751	0.00615881
17961	A_51_P124606	Nat2	N-acetyltransferase 2 (arylam	NM_010874	53.5	51	58.2	47.3	101.6	96.6	101	96.7	52.5	98.975	0.91843887	1.89006896	0.01285227
100039707	A_55_P2062707	Gm2382	predicted gene 2382	NM_001128601	374.2	381.2	380.1	405.6	670.7	712.3	762.4	770.3	385.275	728.925	0.9183317	1.88992855	0.00612664
77766	A_55_P2023441	Elp4	elongation protein 4 homolog	NM_023876	214.7	215.5	198.5	197.3	371.8	363.9	432.1	395.2	206.5	390.75	0.91811924	1.88965026	0.01273126
12050	A_55_P2132507	Bcl2l2	BCL2-like 2	NM_007537	546.6	536.9	592	527.5	1071.7	957.9	1075.7	1056.6	550.75	1040.475	0.9175896	1.88895666	0.00648148
108138	A_55_P1981205	Xrcc4	X-ray repair complementing d	NM_028012	360.8	347.5	427.5	343.5	738.6	672.3	729.9	645	369.825	696.45	0.91661239	1.88767761	0.04445367
70432	A_55_P2020472	Rufy2	RUN and FYVE domain-contai	NM_027425	131.4	139	135.2	142.6	258.2	249.6	257.3	269.2	137.05	258.575	0.91602938	1.88691492	0.00217848
54616	A_55_P1955562	Extl3	exostoses (multiple)-like 3	NM_018788	3384.3	3391.3	3751.7	3776	6052	6764.4	7081.4	7095.4	3575.825	6748.3	0.91529837	1.88595908	0.0164535
69151	A_51_P125446	Lzic	leucine zipper and CTNNBIP1	NM_026963	185.6	168.6	168.9	189.7	312.3	382.4	330.2	321.4	178.2	336.575	0.91500872	1.88558047	0.02853662
66881	A_55_P2156293	Pcyox1	prenylcysteine oxidase 1	NM_025823	1043.1	1225.8	1122.2	1112.5	2203.4	2077.6	2172.6	2022.3	1125.9	2118.975	0.91383318	1.88404468	0.00741563
54399	A_52_P630016	Bet1l	blocked early in transport 1 h	NM_018742	313.1	302.9	292.3	262.4	569.7	518.4	555.8	554.7	292.675	549.65	0.91146476	1.88095425	0.01131798
66979	A_51_P450924	Pole4	polymerase (DNA-directed), e	NM_025882	41.3	35.6	35.9	36.2	65.2	74.1	72.1	68.6	37.25	70	0.91114019	1.88053114	0.0132092
66612	A_55_P2059347	Ormdl3	ORM1-like 3 (S. cerevisiae)	NM_025661	4075.5	4873.3	4617.7	4181.9	8579.2	8399	8141.7	8163.8	4437.1	8320.925	0.91060562	1.87983446	0.01178231
216578	A_51_P478003	Papolg	poly(A) polymerase gamma	NM_172555	226.7	239.8	223.1	207.6	416.6	398.8	459.9	409	224.3	421.075	0.90840907	1.87697453	0.01135955
53334	A_52_P313071	Gosr1	golgi SNAP receptor complex	NM_016810	1074.8	1259.5	1161.4	1251	2124.7	2226.6	2209.6	2330.1	1186.675	2222.75	0.90760314	1.87592629	0.01017947
72569	A_55_P2073885	Bbs5	Bardet-Biedl syndrome 5 (hur	NM_028284	177.2	200.9	201.3	206	397.9	327.8	363.1	385.1	196.35	368.475	0.90674353	1.87480888	0.03030081
12617	A_51_P277718	Cenpc1	centromere protein C1	NM_007683	107.4	107.2	104.4	117.8	198.9	196.1	206.1	217.5	109.2	204.65	0.90655814	1.87456798	0.00585597
68796	A_55_P1998097	Tmem214	transmembrane protein 214	NM_144525	196.6	171.9	195	170.1	347	333.6	354.6	337	183.4	343.05	0.90632649	1.874267	0.01018368
66055	A_51_P424781	0610009D07Rik	RIKEN cDNA 0610009D07 gen	NM_025323	2390.8	2483.1	2652.5	2852.3	4475.3	4965.7	5025.4	4951.3	2594.675	4854.425	0.90547825	1.87316534	0.01660897
28036	A_51_P211934	Larp7	La ribonucleoprotein domain	NM_138593	306.4	340.4	282.6	290.3	580	585.7	512.3	604.7	304.925	570.675	0.90511747	1.87269698	0.03178291
67226	A_51_P392090	Tmem19	transmembrane protein 19	NM_133683	971.9	1009.2	899.7	940.8	1725.6	1807.2	1736.4	1885.6	955.4	1788.7	0.90510236	1.87267736	0.00455588
77963	A_52_P535623	Hook1	hook homolog 1 (Drosophila)	NM_030014	180.7	199.8	195.7	205.4	343.7	351.7	392.3	375.9	195.4	365.9	0.9046421	1.87208002	0.00981731
57869	A_52_P222967	Adck2	aarF domain containing kinas	NM_178873	142.7	176.3	155.8	161.5	280.7	273.8	312.3	323.2	159.075	297.5	0.90381602	1.87100838	0.04632371
71609	A_51_P288505	Tradd	TNFRSF1A-associated via dea	NM_001033161	415.2	411.2	382.6	429.7	737.3	834	739.6	754.5	409.675	766.35	0.90293798	1.86987001	0.00770342
170644	A_55_P1960431	Ubn1	ubinuclein 1	NM_026666	3550.5	3614.3	3574.8	3621.1	6792.4	6717	6480.4	6856.9	3590.175	6711.675	0.9023372	1.8690915	0.00133776
227619	A_55_P2020796	Man1b1	mannosidase, alpha, class 1B,	NM_001029983	1504	1416	1430.5	1365.5	2804.2	2510.7	2689.2	2677.6	1429	2670.425	0.90180544	1.86840271	0.00413133
56187	A_51_P481832	Rabggta	Rab geranylgeranyl transferas	NM_019519	457.9	353	461.1	419.7	796.6	725.6	803.2	820.6	422.925	786.5	0.90158237	1.86811384	0.08871541
76022	A_55_P2059532	Gon4l	gon-4-like (C.elegans)	NM_027389	61.4	62.3	65.2	58.3	107.7	108.6	123	122.9	61.8	115.55	0.90101482	1.86737908	0.01272544
69754	A_55_P2018949	Fbxo7	F-box protein 7	NM_153195	2790.1	2999.6	2851.1	3473.1	5736.3	5656.3	5561.5	5574.7	3028.475	5632.2	0.90037945	1.86655684	0.02162508
23837	A_51_P446978	Cfdp1	craniofacial development pro	NM_011801	1885.3	1689.8	1792.3	1711	3134.8	3275.4	3421.5	3371.9	1769.6	3300.9	0.89998417	1.86604551	0.00462188
68011	A_55_P1990081	Snrpg	small nuclear ribonucleoprote	NM_026506	5986.6	6035	5625.8	6470.8	10037.2	12087	12115.6	10786.9	6029.55	11256.675	0.89789466	1.86334479	0.03177672
272322	A_55_P2114799	Arntl2	aryl hydrocarbon receptor nu	ENSMUST00000111639	252.4	282.9	250.9	278.5	533	500	436.4	514.2	266.175	495.9	0.89581261	1.86065763	0.03179642
67495	A_55_P2072288	Tmem167b	transmembrane protein 167B	NM_026198	678.7	659.9	663.6	585.4	1206.3	1235.9	1140.1	1226.3	646.9	1202.15	0.89564435	1.86044063	0.00822857
217353	A_51_P354038	Tmc6	transmembrane channel-like	NM_145439	465.9	429.9	434	433.8	774.6	839.3	829.8	836.3	440.9	820	0.89516894	1.85982766	0.00329885

71069	A_51_P441970	Stox2	storkhead box 2	NM_175162	82.9	67.3	74.3	68.7	140.7	136.4	125.8	140.9	73.3	135.95	0.89458274	1.85907213	0.03275659
56447	A_55_P1953485	Copz1	coatomer protein complex, su	NM_019817	3412.8	3177.9	3314.8	2782.1	5890.5	5753.4	6080.3	5797.3	3171.9	5880.375	0.89455071	1.85903084	0.01760192
56371	A_55_P2132681	Fzr1	fizzy/cell division cycle 20 rela	NM_019757	216.7	181.5	227	230.8	392.6	384.1	439.2	371.5	214	396.85	0.89444454	1.85889405	0.08182417
75339	A_55_P2077746	Mphosph8	M-phase phosphoprotein 8	NM_023773	1505.6	1507.1	1548	1623.2	2811	2733.1	3026.1	2920.2	1545.975	2872.6	0.89344716	1.85760937	0.00382692
14651	A_55_P2154536	Hagh	hydroxyacyl glutathione hydro	NM_001159626	2943	2652	2780.7	2339	4752.1	4734.6	5353.8	5016.9	2678.675	4964.35	0.89336472	1.85750323	0.04069894
66609	A_55_P2183288	Cryzl1	crystallin, zeta (quinone redu	NM_133679	702.4	818.7	725.6	871.2	1549.9	1350.4	1478.4	1398.2	779.475	1444.225	0.89326889	1.85737986	0.04873514
14977	A_51_P174016	Slc39a7	solute carrier family 39 (zinc t	NM_008202	9638.6	9783.2	8801.8	8954.2	17426.7	18153.3	16098.5	17342	9294.45	17255.125	0.89273675	1.85669488	0.00733702
68966	A_51_P131025	Ngdn	neuroguidin, EIF4E binding pr	NM_026890	5211.8	6298.5	5909.2	5972.5	10351.3	10845.9	11275.3	10850.5	5848	10830.75	0.89187842	1.85559057	0.01393126
319965	A_55_P2102050	Cc2d1b	coiled-coil and C2 domain cor	NM_177045	5854.6	5498.2	6383.4	6667.8	10772.8	11955.8	11226.6	11199.3	6101	11288.625	0.89077002	1.8541655	0.02071592
76804	A_55_P2053206	Kdm4c	lysine (K)-specific demethylas	NM_144787	367.2	386.3	373.1	360.8	756.2	644.8	692.4	667.1	371.85	690.125	0.89001973	1.85320147	0.00815164
83435	A_55_P2319370	Plekha3	pleckstrin homology domain-(	NM_031256	883.8	885.4	856	815.9	1789.2	1498.8	1465.1	1634.5	860.275	1596.9	0.88865775	1.85145277	0.02308691
56440	A_51_P159673	Snx1	sorting nexin 1	NM_019727	1621.1	1787.6	1582.4	1917.5	3166	3320.4	2940.9	3335.2	1727.15	3190.625	0.88792784	1.8505163	0.03202556
20383	A_55_P2177614	Srsf3	serine/arginine-rich splicing fa	NM_013663	736.9	659.5	606.2	794.6	1273.3	1234.8	1392.4	1250.1	699.3	1287.65	0.8868288	1.84910712	0.08486978
231670	A_51_P193490	Fbxo21	F-box protein 21	NM_145564	1248.3	1203.4	1397.2	1301.5	2315.2	2537.8	2320.4	2341.9	1287.6	2378.825	0.88674335	1.84899759	0.00959181
100756	A_55_P2026089	Usp30	ubiquitin specific peptidase 3(	NM_001033202	757.5	945.6	969.1	779.4	1571.1	1523.1	1624.6	1625.4	862.9	1586.05	0.886473	1.84865114	0.08617227
218100	A_51_P328968	Zfp322a	zinc finger protein 322A	NM_172586	1127.6	1022.8	992.4	1095.6	1835.9	1896.3	2001.9	2100.4	1059.6	1958.625	0.88630361	1.8484341	0.01254432
50873	A_55_P1978226	Park2	Parkinson disease (autosomal	NM_016694	757.3	758	839.6	862.8	1651.1	1394.1	1531.2	1373.5	804.425	1487.475	0.88530061	1.84714947	0.03753488
12512	A_55_P2000224	Cd63	CD63 antigen	NM_001042580	25185.1	28652.1	29584.9	29055.3	56078.6	56322.5	47025.4	48617	28119.35	52010.875	0.88529727	1.84714519	0.05514989
106021	A_51_P267346	Topors	topoisomerase I binding, argi	NM_134097	526.1	682.8	566.5	601	1149.1	1083.7	1045.1	1090.6	594.1	1092.125	0.88417604	1.84571019	0.05047721
226151	A_52_P426870	Fam178a	family with sequence similarit	NM_001081225	354.7	423	364.5	388.8	690.8	719	623.6	796.4	382.75	707.45	0.88404249	1.84553934	0.07696491
14670	A_55_P2177173	Gnl1	guanine nucleotide binding pr	NM_008136	2499	2416.7	2901.7	3021.5	4765.4	4774.1	5116.3	5274	2709.725	4982.45	0.88381798	1.84525216	0.05907098
68299	A_55_P1961260	Vps53	vacuolar protein sorting 53 (y	NM_026664	56.2	56.2	55.8	61.9	104.7	116.6	101.5	101.8	57.525	106.15	0.88285353	1.84401901	0.01190665
20320	A_55_P2171463	Nptn	neuroplastin	NM_009145	9231.5	10190.1	10859.3	11115.7	19304.3	18828.9	18600.4	19295.8	10349.15	19007.35	0.88053909	1.84106312	0.01391037
20658	A_55_P1952788	Son	Son DNA binding protein	ENSMUST00000119368	177	168.5	185.8	177.7	321.7	307.3	352.3	324.3	177.25	326.4	0.87995127	1.84031314	0.00725066
13014	A_51_P114910	Cstb	cystatin B	NM_007793	453	532.9	437.5	439.6	917.4	866.9	878.2	762	465.75	856.125	0.87972668	1.84002668	0.06575015
77113	A_51_P398164	Klhl2	kelch-like 2, Mayven (Drosopl	NM_178633	153.6	167.1	181	175.1	340.6	319.6	264.3	324.1	169.2	312.15	0.87972564	1.84002535	0.09295039
21982	A_51_P328932	Tmem165	transmembrane protein 165	NM_011626	877.3	823	877.3	795.5	1626.3	1517.7	1594	1464.5	843.275	1550.625	0.87883934	1.8388953	0.00687832
56404	A_55_P2088640	Trip4	thyroid hormone receptor int	NM_019797	372	360.4	348	370.5	650.8	575.4	730.9	719.7	362.725	669.2	0.87759667	1.83731204	0.0487102
70031	A_51_P308048	Cmtm8	CKLF-like MARVEL transmemb	NM_027294	554	643.2	596.5	623.5	1041.8	1115.2	1124	1152.1	604.3	1108.275	0.87623402	1.83557749	0.01060363
11974	A_51_P336874	Atp6v0e	ATPase, H+ transporting, lyso	NM_025272	2839.7	3102.8	2957.5	2571.5	4929.8	5822	5347.8	4945.2	2867.875	5261.2	0.8754302	1.83455505	0.04485456
21452	A_55_P2088425	Tcn2	transcobalamin 2	NM_015749	3916.8	4209.2	4260.7	3592.5	7265.4	7099.8	7016.6	7885.5	3994.8	7316.825	0.8748737	1.83384754	0.02188479
230119	A_55_P2178803	Zbtb5	zinc finger and BTB domain co	NM_001163284	460.3	435.9	445.7	480.4	796.5	794.2	871.1	881.3	455.575	835.775	0.87469188	1.83361643	0.0078297
207965	A_55_P1971854	Mettl21d	methyltransferase like 21D	NM_001033236	331.6	353.3	337.9	318	552.2	614.6	679.8	616.4	335.2	615.75	0.87446375	1.83332651	0.02283125
80911	A_52_P745	Acox3	acyl-Coenzyme A oxidase 3, p	NM_030721	1019	939.2	972.2	881.9	1641	1654.6	1799.7	1890.2	953.075	1746.375	0.87317067	1.83168404	0.01940928
105246	A_66_P109049	Brd9	bromodomain containing 9	NM_001024508	319.4	365	322.6	387.6	569	671.2	654.2	654.5	348.65	637.225	0.87193013	1.83010971	0.06540919
21855	A_55_P2172299	Timm17b	translocase of inner mitochor	BC008275	4852.2	5070.2	5092.9	4925.3	9939.9	8668.1	8719.1	9204.8	4985.15	9132.975	0.87153302	1.82960602	0.0072424
21672	A_55_P1979432	Prdx2	peroxiredoxin 2	NM_011563	6976.1	6658.6	6660	6749.6	13824.2	10596.3	12954	12313.2	6761.075	12421.925	0.87102715	1.82896459	0.05297238
109674	A_51_P479769	Ampd2	adenosine monophosphate d	NM_028779	375.4	302.2	380.1	326.6	654.2	650.8	578.5	638.8	346.075	630.575	0.87044779	1.82823027	0.07764158
22187	A_55_P1965827	Ubb	ubiquitin B	NM_011664	64770.8	57691.4	72068.8	63253.6	117910.1	111727.9	117287.5	122986.2	64446.15	117477.925	0.86992816	1.82757189	0.02817352
233011	A_51_P507622	Itpkc	inositol 1,4,5-trisphosphate 3	NM_181593	277.1	234.1	246.3	247.7	424	456.5	456.9	496.3	251.3	458.425	0.86780697	1.82488679	0.02466132
80286	A_55_P2175245	Tusc3	tumor suppressor candidate 3	NM_030254	183.2	179.1	187.3	210.9	382.1	341	346.8	317.8	190.125	346.925	0.86746255	1.82445118	0.03638263
76205	A_51_P172688	Stard3nl	STARD3 N-terminal like	NM_024270	504.9	518.8	499.5	505.6	945	1044.5	874.9	848	507.2	928.1	0.867145	1.82404965	0.02314981
68617	A_55_P1996963	1110012J17Rik	RIKEN cDNA 1110012J17 gene	NM_001114098	181.4	213	181.4	215.1	381	368.5	356.7	332.3	197.725	359.625	0.86611081	1.82274256	0.04856631
72726	A_51_P388801	Tbcc	tubulin-specific chaperone C	NM_178385	2130.9	2469.2	2238.6	2564.6	3946.1	4619.4	4408.9	4145.6	2350.825	4280	0.86582387	1.82238007	0.04486166
108707	A_55_P2090708	1810008A18Rik	RIKEN cDNA 1810008A18 gen	NM_133998	2272.5	2813.4	2725.8	2617.8	4398.6	4772.5	5120.7	4670.3	2607.375	4740.525	0.86500408	1.82134481	0.05131116
69834	A_65_P09032	Rab43	RAB43, member RAS oncoger	NM_001039394	1246.7	1316.8	1282.9	1253	2211.2	2506.9	2371.4	2203.5	1274.85	2323.25	0.86408105	1.8201799	0.00745821
76497	A_66_P110791	Ppp1r11	protein phosphatase 1, regula	NM_029632	2657.7	2720.8	2544.5	2808.6	4774.1	4823	5322.1	4615.1	2682.9	4883.575	0.86301865	1.81884001	0.01022486
12807	A_51_P496934	Hps3	Hermansky-Pudlak syndrome	NM_080634	107.5	125.9	124.9	129.8	234.1	218	213	220.8	122.025	221.475	0.86284197	1.81861728	0.02331382
64658	A_55_P2101426	Mrps25	mitochondrial ribosomal prot	NM_025578	4953.7	5464.7	4607.3	4979.7	9725.8	8466.2	9505.9	8665.8	5001.35	9090.925	0.86226462	1.81788964	0.02784415
76799	A_55_P2020831	2510006D16Rik	RIKEN cDNA 2510006D16 gen	ENSMUST00000071840	2858.3	2836.4	2688.4	2351.3	5262.2	4781.7	4799.2	4604.8	2683.6	4861.975	0.85992434	1.81494312	0.04130042
15441	A_55_P1974362	Hp1bp3	heterochromatin protein 1, b	NM_001122897	8865.3	10450.3	9438.9	11063.7	19094.5	17902.5	17290.3	17738.8	9954.55	18006.525	0.85946981	1.8143714	0.04396927
319168	A_55_P2084656	Hist1h2ah	histone cluster 1, H2ah	NM_175659	8473.3	8541.6	9710.2	7546.8	16059.3	14909.4	16039.5	14963.5	8567.975	15492.925	0.85940602	1.81429119	0.04951089
268822	A_55_P2027496	Adck5	aarF domain containing kinas	NM_172960	2676.6	2735.8	2836.6	2860.5	4889.9	5214.6	5116	4910.6	2777.375	5032.775	0.85762068	1.81204739	0.00338299
23989	A_51_P370286	Med24	mediator complex subunit 24	NM_011869	1905.3	1714	1744.3	1570.3	2945.6	3186.4	3108.2	3304.2	1733.475	3136.1	0.8574489	1.81183163	0.02377883
207212	A_55_P1963863	Arhgef17	Rho guanine nucleotide excha	NM_001081116	1684.8	1523.2	1820.5	1828	3167	2844.9	3121	3259.5	1714.125	3098.1	0.85596758	1.80997225	0.03813906
66964	A_51_P152826	Golt1b	golgi transport 1 homolog B (S	NM_025872	559.3	439.4	537.5	546.6	908.3	977	912.2	957.2	520.7	938.675	0.85594765	1.80994725	0.06451296
64451	A_55_P1999361	Dip2a	DIP2 disco-interacting protein	NM_001081419	350.3	348.2	348.4	378.1	688.2	605.8	612	675.3	356.25	645.325	0.8556775	1.80960837	0.01246351
100038641	A_55_P2229351	Gm10452	predicted gene 10452	XM_003086845	42	45.7	45.3	41	79.9	72.1	82.2	80.7	43.5	78.725	0.85554584	1.80944323	0.01412973
192232	A_55_P2073218	Hps4	Hermansky-Pudlak syndrome	NM_138646	1137.3	1167.7	1171.1	1261	2225.4	1918.5	2217.7	2211.6	1184.275	2143.3	0.85412076	1.80765676	0.01771604
105670	A_52_P630632	Rcbtb2	regulator of chromosome con	NM_134083	401	368.2	415.7	346.6	636.7	723.9	737.7	666.5	382.875	691.2	0.85328426	1.80660894	0.04551826
140483	A_55_P2043509	Hnmt	histamine N-methyltransferas	NM_080462	89.6	89.3	92.3	104.3	162.1	181.7	165.4	168.3	93.875	169.375	0.85299812	1.80625067	0.0206576
76594	A_52_P271	Dnajc18	DnaJ (Hsp40) homolog, subfa	NM_029669	732.7	929.4	840.2	887.2	1634	1439.7	1446.4	1585.3	847.375	1526.35	0.85239916	1.80550092	0.07835815
104318	A_55_P1970229	Csnk1d	casein kinase 1, delta	NM_027874	7107.2	6653.7	7030.1	8184.3	13061	13021.7	12884.6	13166.9	7243.825	13033.55	0.85165416	1.80456882	0.02107627
170750	A_55_P1997275	Xpnpep1	X-prolyl aminopeptidase (ami	NM_133216	3601.5	4180.3	3729.9	3727.2	6407.5	6507.8	7374	7204.6	3809.725	6873.475	0.85096592	1.80370814	0.02906256
19712	A_55_P2143306	Rest	RE1-silencing transcription fa	NM_011263	231.5	201.9	223.9	207.9	380.4	392.8	411.1	374.3	216.3	389.65	0.8503998	1.80300051	0.01239245
208718	A_55_P2151797	Dis3l2	DIS3 mitotic control homolog	NM_001172157	3216.9	3451.6	3553.6	3597.8	6650.3	5719.7	6538.5	6027.5	3454.975	6234	0.85013642	1.80267138	0.01961403
56541	A_51_P269078	Habp4	hyaluronic acid binding prote	NM_019986	301.5	322.7	312.8	275	606	521.9	519.2	537.8	303	546.225	0.84985691	1.80232215	0.03452878
73728	A_51_P251205	Psd	pleckstrin and Sec7 domain co	NM_028627	30.2	32.7	30.9	32.3	56.1	55	52	64.7	31.525	56.95	0.84918238	1.80147969	0.0348858
116848	A_52_P4046	Baz2a	bromodomain adjacent to zin	NM_054078	137	113.8	137.4	132.7	226.4	222.2	230.2	258.5	130.225	234.325	0.84913952	1.80142616	0.05708927
67207	A_51_P206655	Lsm1	LSM1 homolog, U6 small nucl	NM_026032	848	945.2	920.9	927.9	1587.9	1642.4	1671.1	1654.2	910.5	1638.9	0.848968	1.801212	0.00501279
24051	A_66_P108345	Sgcb	sarcoglycan, beta (dystrophin	NM_011890	3086.7	3132.9	3216.9	3542.6	5842.3	5787.3	5498.6	6225.6	3244.775	5838.45	0.84816511	1.80020987	0.01522605
13877	A_55_P1966124	Erh	enhancer of rudimentary hom	NM_007951	6654.5	6807.7	6638.7	6696	12602.3	11670.9	13290.3	10778	6699.225	12085.375	0.8467701	1.79847001	0.02549093
77862	A_51_P323620	Thyn1	thymocyte nuclear protein 1	NM_144543	5433.4	6023.6	4722.2	5152.8	9426.2	10330	8976.8	9433.9	5333	9541.725	0.84305081	1.79383949	0.07325002
67067	A_55_P2114467	Romo1	reactive oxygen species modu	NM_001164217	19687.5	20662.5	19662	19640.7	37157.6	34497.6	34596.1	36675	19913.175	35731.575	0.84300213	1.79377897	0.0041241
319176	A_66_P129188	Hist2h2ac	histone cluster 2, H2ac	NM_175662	6755.2	6711.1	6754.5	5556.1	12195.2	10989.5	12043.3	10910.8	6444.225	11534.7	0.84291748	1.79367372	0.06212975
67389	A_51_P425824	Fam132a	family with sequence similarit	NM_026125	2519.4	2420.5	2768.7	2300.7	4476.9	4439.5	4550.4	4442.2	2502.325	4477.25	0.84262453	1.79330954	0.01537517
70057	A_55_P2031611	2210008F06Rik	RIKEN cDNA 2210008F06 gen	XR_106204	69	63.4	73.9	63.6	130	118.2	107.9	128.2	67.475	121.075	0.84246621	1.79311275	0.06190498
67371	A_55_P1963777	Gtf3c6	general transcription factor II	NM_026113	1921.3	1870.9	2013.4	1833.9	3376.1	3341.2	3736.8	3254.9	1909.875	3427.25	0.84244413	1.79308531	0.01177978
104184	A_51_P480904	Blmh	bleomycin hydrolase	NM_178645	1060.7	1018.4	1134.4	1030.3	2056.3	1831.1	1908.2	1809.1	1060.95	1901.175	0.84098274	1.79126991	0.01330469
20016	A_51_P112557	Polr1c	polymerase (RNA) I polypepti	NM_009085	1153.3	1140.6	1138.7	1161.4	2146.1	1928.8	2101.7	2057.4	1148.5	2058.5	0.84074662	1.79097677	0.00439286
76547	A_51_P365656	Tmem101	transmembrane protein 101	NM_029649	957	859.4	927.6	819.9	1613.2	1439.4	1619.6	1711.1	890.975	1595.825	0.84071685	1.79093981	0.03935814
107986	A_55_P2092904	Ddb2	damage specific DNA binding	NM_028119	183.1	180	185.9	193.7	325.9	349	317.1	338.5	185.675	332.625	0.84069267	1.79090979	0.00533525
75416	A_51_P246705	Nop14	NOP14 nucleolar protein hom	NM_029278	266.4	280.4	298.8	328	479.2	583.7	513.7	524	293.4	525.15	0.84059787	1.79079211	0.08634556
68607	A_52_P560728	Serhl	serine hydrolase-like	NM_023475	888.7	950.9	933.9	869.9	1583.5	1548	1595.2	1805.6	910.85	1633.075	0.84058565	1.79077694	0.01683507
67466	A_66_P104312	Pdcl	phosducin-like	NM_026176	125.2	117.7	133.9	108.6	213.1	194.7	225.8	234.7	121.35	217.075	0.83977946	1.78977653	0.08501228
105689	A_51_P473919	Mycbp2	MYC binding protein 2	NM_207215	805.5	759.6	764.6	874.7	1468.5	1390.1	1490.5	1377.6	801.1	1431.675	0.83914494	1.78898952	0.01394149
20529	A_55_P2028655	Slc31a1	solute carrier family 31, mem	NM_175090	794.9	899.7	773.7	923.2	1487.5	1474.9	1504.3	1584.9	847.875	1512.9	0.8390171	1.78883101	0.02938514
53598	A_51_P298178	Dctn3	dynactin 3	NM_016890	8052	8280	9457.6	8900.4	15054.3	16192.8	16317	14415.6	8672.5	15494.925	0.83823124	1.78785686	0.02976108
94245	A_55_P2024580	Dtnbp1	dystrobrevin binding protein	NM_025772	10267.4	9941.9	10936.9	10456.9	19028.5	17837	18577	18901	10400.775	18585.875	0.83792286	1.78747475	0.00487142
99334	A_52_P249920	Zscan29	zinc finger SCAN domains 29	ENSMUST00000052770	55	60.7	59.6	56.4	96.8	106.1	103.6	107.5	57.925	103.5	0.83736026	1.78677783	0.00921082
68146	A_55_P1960748	Arl13b	ADP-ribosylation factor-like 1	NM_026577	190.8	203	209.1	201.8	383.2	357.5	380	319.3	201.175	360	0.83657316	1.78580327	0.0283663
232944	A_55_P2142580	Mark4	MAP/microtubule affinity-reg	ENSMUST00000085715	1174.3	1092.1	1204.1	1175.4	2294.8	1823.7	2033.3	2167.5	1161.475	2079.825	0.83626973	1.78542772	0.05205426
74343	A_55_P2024515	Crtc2	CREB regulated transcription	NM_028881	1311.5	1238.8	1297.8	1369	2268.2	2157.4	2294.4	2611.5	1304.275	2332.875	0.83612139	1.78524415	0.02703841
69305	A_51_P275953	Dcps	decapping enzyme, scavenger	NM_027030	602.1	626.2	586.8	702.8	1079.8	1233	1087.3	1090.9	629.475	1122.75	0.83607713	1.78518938	0.04226053
22027	A_52_P624149	Hsp90b1	heat shock protein 90, beta (C	NM_011631	7025.5	8374.1	7846.1	7239.3	12838.4	13788.8	12775.2	14971.6	7621.25	13593.5	0.835222	1.78413156	0.05632599
54122	A_55_P2086770	Uevld	UEV and lactate/malate dehy	NM_001040695	72.3	68.8	74	72.7	150	116.1	124.6	124.7	71.95	128.85	0.83448088	1.78321528	0.06914199
68427	A_55_P1973668	Slc39a13	solute carrier family 39 (meta	NM_026721	1569.1	1524.7	1723.6	1643.3	2679.5	2595.2	3025.5	3251.6	1615.175	2887.95	0.83391233	1.78251267	0.08135196
104348	A_51_P476261	Zfp120	zinc finger protein 120	NM_181266	348.3	298.3	345.9	334.7	597.4	558.4	587.3	617.5	331.8	590.15	0.83255373	1.78083485	0.0199944
74895	A_51_P190437	4930455F23Rik	RIKEN cDNA 4930455F23 gen	NM_029115	2869.9	2769.4	2929.5	3441.9	5072.6	5094	5925.6	5246.7	3002.675	5334.725	0.83136559	1.77936884	0.09166292
140559	A_55_P2026218	Igsf8	immunoglobulin superfamily,	NM_080419	754.3	826.3	747.4	894.2	1528	1449.3	1414.2	1332.1	805.55	1430.9	0.83102988	1.77895483	0.04420386
102774	A_51_P193000	Bbs4	Bardet-Biedl syndrome 4 (hur	NM_175325	453.5	516.7	534	502.1	955.6	836.7	815.3	962.8	501.575	892.6	0.83011014	1.77782108	0.06669433
30791	A_55_P2098558	Slc39a1	solute carrier family 39 (zinc t	NM_013901	3807.3	3639.1	3803.8	3297.3	6675.6	6687.6	6223.8	6246.7	3636.875	6458.425	0.83004988	1.77774683	0.01683637
269180	A_55_P2002727	Inpp4a	inositol polyphosphate-4-pho	NM_172971	244.2	242.8	250.1	288.2	452.3	450.3	460.9	454	256.325	454.375	0.82947638	1.77704028	0.01915383
269704	A_55_P2039038	Zfp664	zinc finger protein 664	NM_001081750	536.3	420.5	458.9	476.3	830.3	821.7	860.2	836	473	837.05	0.82880578	1.77621446	0.04661778
20641	A_55_P1971448	Snrpd1	small nuclear ribonucleoprote	NM_009226	1937.6	1819.6	2055.7	2017.3	3055.9	3759	3535.4	3568.9	1957.55	3479.8	0.82733792	1.77440818	0.04960538
55935	A_51_P509808	Fnbp4	formin binding protein 4	NM_018828	73.4	73.4	83.5	73.1	134.8	135.5	138.2	129	75.85	134.375	0.82693667	1.77391474	0.01286957
52822	A_55_P2169839	Rufy3	RUN and FYVE domain contai	ENSMUST00000101048	683.8	592.9	621.3	659.3	1069.8	1087.9	1287.1	1096.5	639.325	1135.325	0.82651026	1.77339051	0.05604352
66276	A_55_P1968035	1810009A15Rik	RIKEN cDNA 1810009A15 gen	NM_025463	3112.9	3296.6	3115.4	3419.7	5630.7	5539.3	5735	6027.2	3236.15	5733.05	0.82544353	1.77207975	0.00784463
78521	A_52_P75384	B230219D22Rik	RIKEN cDNA B230219D22 gen	NM_181278	2426.9	2022.7	2158.9	2086.6	4257.7	3430.4	3924.7	3792.6	2173.775	3851.35	0.8243433	1.77072884	0.0938718
21886	A_55_P2185543	Tle2	transducin-like enhancer of sp	ENSMUST00000051853	1012.7	954.1	993.6	1036.2	1827.8	1652.6	1683	1922.8	999.15	1771.55	0.82415772	1.77050107	0.01829754
20586	A_55_P2154684	Smarca4	SWI/SNF related, matrix assoc	NM_001174078	8519.9	8083	8825.6	8547	15660.9	14381.4	15403.3	14685.5	8493.875	15032.775	0.82346891	1.76965596	0.00667271
66513	A_51_P121466	Tab1	TGF-beta activated kinase 1/N	NM_025609	2462.6	2227.8	2055.7	1998.1	4181.4	3509.2	3782.5	3981.3	2186.05	3863.6	0.82341184	1.76958595	0.09544134
23854	A_55_P1986188	Def8	differentially expressed in FD(	NM_054046	5210.5	4593.3	4923.2	5140.1	9887.3	7971.9	8608.4	8739.8	4966.775	8801.85	0.822875	1.7689276	0.05529249
30957	A_55_P2059019	Mapk8ip3	mitogen-activated protein kin	NM_001163447	3498.8	3518.2	3213.5	3659.4	6586.6	5865.2	5728.4	6393.5	3472.475	6143.425	0.82225053	1.76816208	0.02534645
229584	A_51_P513449	Pogz	pogo transposable element w	NM_172683	302.4	272.7	337.9	346.9	547.6	556.7	536.8	576.5	314.975	554.4	0.82170969	1.76749936	0.07888998
28042	A_51_P104891	Ept1	ethanolaminephosphotransfe	NM_027652	473.3	501.4	511.4	534	956.6	846.9	833.7	936.2	505.025	893.35	0.82161093	1.76737836	0.02461378
224139	A_55_P2051859	Golgb1	golgi autoantigen, golgin subf	NM_030035	2043.6	2207.4	2575.2	2350.3	3857.8	4187.4	4062.2	4049.4	2294.125	4039.2	0.82070305	1.76626651	0.05192638
28077	A_55_P2108334	Med10	mediator of RNA polymerase	NM_138596	367.6	387.3	367	357	675.4	639.2	661.6	634.9	369.725	652.775	0.82030145	1.76577491	0.00494847
12748	A_55_P2060072	Clk2	CDC-like kinase 2	NM_007712	552.4	451.4	493.8	486.8	932.8	831	887.2	843.3	496.1	873.575	0.81858646	1.76367711	0.04307389
231717	A_51_P466829	Fam109a	family with sequence similarit	NM_175474	2019.6	2273.4	1947.7	2087.3	3757.2	3597.8	3682.4	3627.6	2082	3666.25	0.81852602	1.76360322	0.01255386
319173	A_55_P2084666	Hist1h2af	histone cluster 1, H2af	NM_175661	8443.8	7442	8058.4	6799.5	14017.2	12970.2	13901.1	13143.5	7685.925	13508	0.81753874	1.76239675	0.05171178
20312	A_51_P196925	Cx3cl1	chemokine (C-X3-C motif) liga	NM_009142	127.5	143	131.6	124.1	258.4	238.2	211.3	220.7	131.55	232.15	0.81724597	1.76203914	0.06326884
114143	A_51_P404236	Atp6v0b	ATPase, H+ transporting, lyso	NM_033617	1954.5	1966.7	1882.8	1653.4	3223.7	3362.6	2979.7	3569.9	1864.35	3283.975	0.81711334	1.76187716	0.07148901
67091	A_55_P2106250	Trappc6a	trafficking protein particle co	NM_025960	921.2	1059.3	1136	1163	1886.5	1824.3	2016.9	1785.1	1069.875	1878.2	0.81617202	1.76072795	0.09304622
22289	A_52_P551707	Kdm6a	lysine (K)-specific demethylas	NM_009483	89	94.9	86.5	85.2	156.3	136.6	172.7	162.2	88.9	156.95	0.81606564	1.76059813	0.06971787
20384	A_55_P2157872	Srsf5	serine/arginine-rich splicing fa	NM_001079695	4415.6	4123.4	4869.5	4384.1	8715	7907.8	7277	7440.1	4448.15	7834.975	0.81573615	1.76019609	0.0598162
73166	A_52_P35064	Tm7sf2	transmembrane 7 superfamily	NM_028454	810.2	782.6	858.9	787.1	1343.1	1383.7	1396.9	1580.4	809.7	1426.025	0.81468462	1.7589136	0.02401075
24045	A_66_P132510	Scamp3	secretory carrier membrane p	NM_011886	4990.9	5129.6	5248.8	5291.4	9530	8795.5	9067.2	8933.9	5165.175	9081.65	0.8138514	1.75789804	0.00505203
213990	A_55_P2274233	Agap3	ArfGAP with GTPase domain,	NM_139153	6342.1	5952.2	6581.2	6464.9	10068.3	11254.3	12382.7	10914.6	6335.1	11154.975	0.81330791	1.75723594	0.040962
69038	A_52_P119117	1810006K21Rik	RIKEN cDNA 1810006K21 gen	NM_001163431	2395.9	2440.3	2621.1	2342.9	4235.8	4200.8	4641.9	4139.9	2450.05	4304.6	0.81287899	1.75671358	0.01454516
15356	A_51_P308961	Hmgcl	3-hydroxy-3-methylglutaryl-C	NM_008254	4181.5	4793.9	4020.8	4437.6	7592.1	7328.6	7314.3	8355.1	4358.45	7647.525	0.81223273	1.75592683	0.04621574
21745	A_51_P506755	Tep1	telomerase associated protei	NM_009351	1283.3	1290.1	1261.9	1337.4	2253.9	2158.6	2270.3	2404.3	1293.175	2271.775	0.81216233	1.75584115	0.0065769
101489	A_51_P265406	Ric8	resistance to inhibitors of cho	NM_053194	1004.5	859.7	1058.4	1051	1614.7	1795	1744.5	1801.5	993.4	1738.925	0.81130796	1.75480164	0.07117499
53380	A_66_P139393	Psmd10	proteasome (prosome, macro	NM_016883	366.9	353.3	353.2	318.2	656.8	556.1	594.4	635.4	347.9	610.675	0.81079946	1.75418324	0.04170825
76577	A_51_P255193	Faf2	Fas associated factor family m	NM_178397	225.2	197.3	214	235.9	380.8	368.8	382.2	394.8	218.1	381.65	0.80998448	1.75319258	0.02306018
380840	A_52_P498355	Lyrm4	LYR motif containing 4	NM_201358	435.3	375.5	377.6	352.2	714.3	624.7	704.1	652	385.15	673.775	0.80906734	1.75207841	0.07346625
234358	A_55_P1959076	Zfp930	zinc finger protein 930	NM_001013379	46.6	42.4	47.1	48.6	81.1	73.5	80.5	88.8	46.175	80.975	0.80897926	1.75197144	0.04447599
11987	A_66_P106661	Slc7a1	solute carrier family 7 (cation	NM_007513	503.1	538.7	507.9	573.3	932	1028.7	945.8	819.4	530.75	931.475	0.80875535	1.75169955	0.07952785
53610	A_55_P1957927	Nono	non-POU-domain-containing,	NM_023144	4167.4	4560.9	4635.3	5214.3	7856.5	8089.7	8121.1	8353.2	4644.475	8105.125	0.80759367	1.75028962	0.04212637
217119	A_55_P1952269	Xylt2	xylosyltransferase II	NM_145828	589.9	622.1	571	599.7	910.4	1118.4	1096.1	1056	595.675	1045.225	0.80734043	1.74998243	0.05011789
22644	A_55_P1988273	Rnf103	ring finger protein 103	NM_009543	1885.4	2115.4	2116.1	2088.3	3421.9	3560.4	3628.5	3738	2051.3	3587.2	0.80723472	1.7498542	0.01301971
67475	A_52_P424462	Ero1lb	ERO1-like beta (S. cerevisiae)	NM_026184	75.4	83.3	77.9	88.3	142.3	137.8	153	134.9	81.225	142	0.80693204	1.74948711	0.03308481

14109	A_55_P2027225	Fau	Finkel-Biskis-Reilly murine sar	NM_001190436	67364.8	73249.1	66974.2	75923.2	128732.8	126924.4	126629.9	113462.1	70877.825	123937.3	0.80648446	1.74894445	0.02808862
52335	A_51_P129866	Atxn1l	ataxin 1-like	NM_001080930	982.4	820.7	913.6	884.9	1710.9	1516.5	1578.9	1486.7	900.4	1573.25	0.80600102	1.74835848	0.04574037
12018	A_55_P2013113	Bak1	BCL2-antagonist/killer 1	NM_007523	977.6	1023.1	1124.3	1005.7	1731.9	1743.9	1821.4	1914.8	1032.675	1803	0.80485601	1.74697142	0.01956348
54411	A_51_P447988	Atp6ap1	ATPase, H+ transporting, lyso	NM_018794	391.5	355.7	426.4	401.8	742.9	658.8	645	703.2	393.85	687.475	0.80447113	1.74650543	0.05048028
104263	A_55_P1982578	Kdm3a	lysine (K)-specific demethylas	NM_173001	548.2	551.3	602	566	996.9	955.7	944	1063.6	566.875	990.05	0.80389294	1.74580563	0.0145156
74257	A_55_P2067453	Tspan17	tetraspanin 17	NM_028841	4300	4254.4	5189.7	4189.5	7933.8	8036.3	7738.8	7486.6	4483.4	7798.875	0.80381061	1.745706	0.06521866
270201	A_55_P1965391	Klhl18	kelch-like 18 (Drosophila)	NM_177771	506.9	433.6	464.5	480.2	782.3	805.1	923.3	782.2	471.3	823.225	0.80346176	1.74528394	0.05875141
234854	A_52_P328497	Cdk10	cyclin-dependent kinase 10	NM_194446	684.5	661.9	683.9	709.5	1230.8	1098.2	1273.1	1185.1	684.95	1196.8	0.80338805	1.74519476	0.01501419
50755	A_55_P2139640	Fbxo18	F-box protein 18	NM_015792	297.3	316.6	273.3	269.9	467.9	491.6	496.1	564.3	289.275	504.975	0.80332182	1.74511465	0.07717606
56486	A_55_P2010223	Gabarap	gamma-aminobutyric acid rec	NM_019749	11170.7	9389.5	10294.1	9667.1	18186.8	16260.5	18019.3	18154.2	10130.35	17655.2	0.80307426	1.74481523	0.04172636
71853	A_51_P297968	Pdia6	protein disulfide isomerase as	NM_027959	323	307.2	339.6	309.2	565.2	595.5	567.9	504.8	319.75	558.35	0.80278066	1.74446017	0.02757094
69171	A_51_P101075	1810031K17Rik	RIKEN cDNA 1810031K17 gen	NM_026977	5834.7	5377.1	5634.2	5719.7	10177.2	9571.1	9404.5	10213.8	5641.425	9841.65	0.80252889	1.74415576	0.00842178
71968	A_52_P526265	Wdr73	WD repeat domain 73	NM_028026	1046.1	995.9	1145.6	1166.5	1823.5	1953.4	1978	1827.7	1088.525	1895.65	0.80234651	1.74393529	0.03057284
12913	A_52_P135707	Creb3	cAMP responsive element bin	NM_013497	1323.7	1331.7	1377.4	1187.6	2193.1	2417	2222.2	2264	1305.1	2274.075	0.80230245	1.74388204	0.02103378
18571	A_66_P133498	Pdcd6ip	programmed cell death 6 inte	NM_001164677	418	391.7	396.7	330.6	667.7	663.5	650.3	687.3	384.25	667.2	0.80123867	1.74259665	0.06371386
227622	A_55_P2085806	BC029214	cDNA sequence BC029214	NM_153557	2119.6	1912	1900.3	2041	3660.3	3820.9	3300	3139.5	1993.225	3480.175	0.80112433	1.74245854	0.06546456
83486	A_51_P234025	Rbm5	RNA binding motif protein 5	NM_148930	5297	5687.2	5893.8	6056.5	9733.3	10082	10270.4	9823	5733.625	9977.175	0.80066167	1.74189984	0.01184195
26465	A_55_P1969530	Zfp146	zinc finger protein 146	NM_011980	116.8	115	98.6	115.2	203.5	173.5	208.2	191	111.4	194.05	0.80050819	1.74171454	0.09449831
399510	A_55_P2006634	Map4k5	mitogen-activated protein kin	NM_201519	2600.8	2621.4	2830.9	2979.9	4686.1	4643.2	4725	5130.4	2758.25	4796.175	0.79926878	1.74021889	0.02376178
544971	A_51_P163797	Bdp1	B double prime 1, subunit of I	NM_001081061	144.2	138.4	129.5	124.7	237.3	211.4	246.7	238.6	134.2	233.5	0.79892764	1.73980744	0.04277762
71514	A_55_P2128451	Sfpq	splicing factor proline/glutam	NM_023603	1446	1430.6	1326	1628.4	2443.5	2452	2714	2505.9	1457.75	2528.85	0.79735846	1.73791613	0.05152871
108155	A_52_P656545	Ogt	O-linked N-acetylglucosamine	NM_139144	172.1	189.1	203.9	185.6	294.6	321.1	349.4	338.4	187.675	325.875	0.79573358	1.73595985	0.06134432
26611	A_66_P117389	Rcn2	reticulocalbin 2	NM_011992	310.7	256.4	316.2	299.3	523.8	502.5	515.5	504.2	295.65	511.5	0.79544001	1.73560664	0.05140338
66181	A_52_P490863	Nop10	NOP10 ribonucleoprotein hor	NM_025403	7507.7	7686.4	7912.6	7311.4	13559.8	12640.3	12775.6	13800.7	7604.525	13194.1	0.79455823	1.73454615	0.00920272
20637	A_55_P1990573	Snrnp70	small nuclear ribonucleoprote	NM_009224	8805.3	9081.4	8923.9	9195.8	15159.5	16525.8	14385.4	16451.1	9001.6	15630.45	0.79387693	1.73372723	0.01671491
18081	A_55_P2142830	Ninj1	ninjurin 1	NM_013610	4033.8	4099.5	4564	3878.8	6965.7	7393.8	7415.5	6869.9	4144.025	7161.225	0.79098018	1.73024961	0.02626881
72807	A_51_P142989	Zfp429	zinc finger protein 429	NM_001080941	141.9	154.7	153.6	136	232.4	234	274.4	274.5	146.55	253.825	0.78976814	1.7287966	0.09885412
74653	A_51_P496715	4930444A02Rik	RIKEN cDNA 4930444A02 gen	NM_029037	397	366.7	319.7	336.3	590.2	641.3	576.3	638.9	354.925	611.675	0.78860167	1.72739938	0.08957732
101358	A_51_P113722	Fbxl14	F-box and leucine-rich repeat	NM_133940	798	778.7	834.8	704.8	1445.8	1367.2	1294.1	1270.4	779.075	1344.375	0.78798393	1.72665988	0.0448148
14390	A_52_P152283	Gabpa	GA repeat binding protein, alp	NM_008065	205.2	209	197.3	215.3	394.2	331.8	332.3	372.4	206.7	357.675	0.78782702	1.7264721	0.04659012
117171	A_51_P121447	1110038F14Rik	RIKEN cDNA 1110038F14 gen	NM_054099	3761.7	4241.2	3868.3	4043.7	6738.5	7091	6983.3	6622.1	3978.725	6858.725	0.78659534	1.72499878	0.01274196
100039220	A_55_P2167512	Gm12751	predicted gene 12751	XM_001472479	4166.7	4270.6	4570.1	4629.1	7731.2	7820.6	7059.7	7800.6	4409.125	7603.025	0.78621554	1.72454472	0.01887867
19943	A_55_P2044109	Rpl28	ribosomal protein L28	BC024395	32242.3	30589.1	31538.3	32782	59567	50133.1	56722.1	52813.6	31787.925	54808.95	0.78327902	1.72103808	0.03047609
218460	A_52_P293556	Wdr41	WD repeat domain 41	NM_172590	479.3	474.3	481.4	505.4	776.6	817.4	865.5	878.2	485.1	834.425	0.78122667	1.71859151	0.01443481
67045	A_51_P255329	Riok2	RIO kinase 2 (yeast)	NM_025934	1483.7	1638.1	1476.2	1451.1	2704.5	2470.1	2505	2710.2	1512.275	2597.45	0.78072082	1.71798903	0.02236321
64294	A_51_P267370	Itm2c	integral membrane protein 2C	NM_022417	359.3	336.9	346.7	332.8	578.5	570.5	574.9	641.1	343.925	591.25	0.78063791	1.7178903	0.01553487
269999	A_55_P2182690	Orai3	ORAI calcium release-activate	NM_198424	2190.7	2313.4	2477.9	2359.2	3838	3949.4	4195.7	4055.9	2335.3	4009.75	0.78052486	1.71775569	0.01484471
78937	A_52_P480402	Avl9	AVL9 homolog (S. cerevisiase)	NM_030235	149	173	145.3	142.1	279.7	253.8	249.6	261.2	152.35	261.075	0.78007988	1.71722595	0.0712921
71448	A_55_P1960298	Tmem80	transmembrane protein 80	NM_027797	894.8	930.9	918.5	1056.9	1577.7	1678.3	1615.3	1641.2	950.275	1628.125	0.77946274	1.71649153	0.02765365
74585	A_52_P480301	Sppl3	signal peptide peptidase 3	NM_029012	107	91.3	100.3	99.7	164.9	180.9	161.6	175.1	99.575	170.625	0.77777638	1.7144863	0.03451144
11771	A_55_P2116105	Ap2a1	adaptor protein complex AP-2	NM_007458	1805.8	1629.6	1841.2	1804.8	3088.4	2757.5	2906.4	3394.8	1770.35	3036.775	0.77578476	1.71212111	0.08295388
213498	A_55_P1975041	Arhgef11	Rho guanine nucleotide excha	NM_001003912	171	158.5	163.6	161.3	310.7	255.1	259.3	298.2	163.6	280.825	0.77477231	1.71092001	0.080999
20170	A_51_P113274	Hps6	Hermansky-Pudlak syndrome	NM_176785	920.2	919.4	908.8	871	1421.9	1518.7	1583.9	1675.1	904.85	1549.9	0.77420552	1.71024798	0.02396323
14470	A_55_P1955227	Rabac1	Rab acceptor 1 (prenylated)	NM_010261	26753.2	28662.8	26156.1	29481	46213.3	46386.5	48684.2	48421.1	27763.275	47426.275	0.77381967	1.70979063	0.01541261
233812	A_52_P108089	BC030336	cDNA sequence BC030336	NM_001164580	1442	1550.4	1316.1	1483.1	2753	2284.1	2449.8	2419.8	1447.9	2476.675	0.7736464	1.70958528	0.08299291
13244	A_51_P498890	Degs1	degenerative spermatocyte h	NM_007853	1969.9	1949.5	1845.9	1716.4	3154.5	3056	3221.5	3336.7	1870.425	3192.175	0.77256843	1.70830838	0.02367074
20932	A_51_P115326	Surf4	surfeit gene 4	NM_011512	6147.1	6387.7	5992.3	6695.8	11497.7	10793.1	9768.5	11051.1	6305.725	10777.6	0.77199927	1.70763457	0.03816023
72831	A_51_P426283	Dhx30	DEAH (Asp-Glu-Ala-His) box p	NM_133347	5631	5306.6	4647.7	5595.3	8982.8	8545	8894.5	9656.9	5295.15	9019.8	0.77120199	1.70669113	0.07905027
72727	A_52_P506344	B3gat3	beta-1,3-glucuronyltransferas	NM_024256	192.5	179.3	188.1	161.4	301.2	310.6	296.9	319.3	180.325	307	0.77032372	1.70565247	0.03891826
72129	A_55_P2140516	Pex13	peroxisomal biogenesis factor	NM_023651	1746.6	2057.9	1885.1	2015.1	3032.3	3195.2	3396.1	3505.5	1926.175	3282.275	0.76965082	1.7048571	0.06745282
217365	A_55_P2164111	Nploc4	nuclear protein localization 4	NM_001195023	4023.1	3952.8	4388.7	4106.1	7708.5	6193.8	7093.7	7144.9	4117.675	7035.225	0.76949553	1.7046736	0.07800522
19340	A_52_P432919	Rab3d	RAB3D, member RAS oncoger	NM_031874	75.3	93.3	89.6	78.6	144.8	145.5	142.9	138.5	84.2	142.925	0.76878251	1.70383131	0.0883337
71904	A_51_P430973	Paqr7	progestin and adipoQ recepto	NM_027995	224	202.8	222.6	234.1	404.8	364.6	340	396.7	220.875	376.525	0.76799302	1.70289918	0.07510365
15384	A_52_P20966	Hnrnpab	heterogeneous nuclear ribonu	NM_010448	5790.3	5686.2	5846.6	5958.8	10432.6	10250.4	9410.8	9578.9	5820.475	9918.175	0.76777246	1.70263886	0.01170901
72323	A_51_P478610	Asb6	ankyrin repeat and SOCS box-	NM_133346	697.1	688.2	687.5	643.1	1183.6	1132.1	1100.8	1203	678.975	1154.875	0.76612202	1.70069215	0.01217643
22764	A_52_P248483	Zfx	zinc finger protein X-linked	NM_001044386	65.2	65.2	61.9	61.3	103.7	101.7	117.9	108.5	63.4	107.95	0.76603408	1.70058849	0.02576556
107476	A_55_P2084706	Acaca	acetyl-Coenzyme A carboxyla	BC023946	1361.1	1380.8	1268.9	1180.6	2302.1	2104.9	2119.8	2291.1	1297.85	2204.475	0.76582368	1.7003405	0.04431614
64933	A_51_P467837	Ap3m2	adaptor-related protein comp	NM_029505	59.9	68.5	64.6	65.5	104	107.9	104.2	124	64.625	110.025	0.76549928	1.69995821	0.07590285
74778	A_55_P1952537	Rrp7a	ribosomal RNA processing 7 h	NM_029101	3169.1	2900.3	2916.6	3103.4	5337.8	5015.4	4953.6	5237	3022.35	5135.95	0.76535387	1.69978688	0.01329411
18099	A_55_P2008687	Nlk	nemo like kinase	NM_008702	1100.9	1131.4	1214	1183.2	1771	1998.1	2086.4	2021.4	1157.375	1969.225	0.76507718	1.69946091	0.04017106
70349	A_51_P160113	Copb1	coatomer protein complex, su	NM_033370	829.8	858.5	814.6	934.1	1333.2	1460.3	1640.4	1415.2	859.25	1462.275	0.76491834	1.69927382	0.09601545
68273	A_55_P2033160	Pomgnt1	protein O-linked mannose be	NM_026651	5982.3	6411	6679.3	6869.5	11291.8	10665.7	11318.5	10747.5	6485.525	11005.875	0.76437468	1.69863359	0.02080413
20924	A_51_P429983	Supt5h	suppressor of Ty 5 homolog (S	NM_013676	6058.6	5575.4	5705.1	5261.2	9205.3	8675.4	10364.7	10127.4	5650.075	9593.2	0.76187239	1.69568994	0.08278717
12460	A_52_P400224	Ccs	copper chaperone for supero:	NM_016892	3661	4171.7	3604.3	4103.5	6458.6	6773.3	6344.7	6722.7	3885.125	6574.825	0.76155646	1.69531865	0.03802906
108652	A_51_P151254	Slc35b3	solute carrier family 35, mem	NM_134060	240.4	292.1	279.7	254.6	461.1	443.7	454.2	444.5	266.7	450.875	0.76154085	1.6953003	0.05328709
230088	A_55_P1987261	B230312A22Rik	RIKEN cDNA B230312A22 gen	NM_172691	1364.8	1310.9	1404	1224.2	2292.4	2147.7	2136.3	2413.9	1325.975	2247.575	0.76137552	1.69510603	0.03991412
51797	A_51_P251357	Ctps	cytidine 5-triphosphate synth	NM_016748	2627.8	2830.7	2656.1	3196.1	4848.5	4947.5	4566.6	4735.9	2827.675	4774.625	0.75959022	1.69300968	0.06891753
20018	A_55_P1972923	Polr1d	polymerase (RNA) I polypepti	NM_181730	5012.5	5366	5106.5	5361.9	9431.9	8323.2	8539.2	8993.8	5211.725	8822.025	0.75831549	1.69151443	0.02016067
381629	A_55_P1991552	0610007C21Rik	RIKEN cDNA 0610007C21 gen	NM_027855	3167	3548.2	3424.3	3463.5	5928.9	5883.8	5652.8	5530.2	3400.75	5748.925	0.7581415	1.69131045	0.0157879
104570	A_55_P2058152	Smek2	SMEK homolog 2, suppressor	NM_134034	231.2	237.3	197.9	239.9	368.6	381.4	407.7	371.8	226.575	382.375	0.75808434	1.69124345	0.08262731
56295	A_55_P1958867	Higd1a	HIG1 domain family, member	NM_001112668	24311.7	27928	25905.7	23569.5	45679	43115.4	40480.1	42462.8	25428.725	42934.325	0.75739823	1.69043932	0.05502063
18749	A_55_P2024075	Prkacb	protein kinase, cAMP depend	NM_011100	4440.9	4269.9	3765.1	3837.3	7097.1	6929.6	6856.3	6627.5	4078.3	6877.625	0.75701565	1.6899911	0.04566657
77626	A_51_P159814	Smpd4	sphingomyelin phosphodieste	NM_029945	292.4	308.1	283.4	264.3	462.2	474.3	478.6	523.5	287.05	484.65	0.75624222	1.68908534	0.04343769
65103	A_52_P453624	Arl6ip6	ADP-ribosylation factor-like 6	NM_022989	119.3	107.4	115.6	124.1	186.4	184.5	211.4	205.3	116.6	196.9	0.75537478	1.68807006	0.05999184
209416	A_55_P2045602	Gpkow	G patch domain and KOW mo	NM_173747	313.5	288.4	277.5	282.6	490.3	476.2	480.6	509.5	290.5	489.15	0.75284133	1.68510832	0.01833666
75914	A_55_P1997415	Exoc6b	exocyst complex component (	NM_177077	892.6	838.2	911.1	864.7	1475	1404.2	1593.2	1438.6	876.65	1477.75	0.75241281	1.68460787	0.02169324
67772	A_51_P212630	Chd8	chromodomain helicase DNA	NM_201637	2311.2	2190.7	2044.2	2154.1	3437.7	3454.6	3799.6	3978	2175.05	3667.475	0.75229938	1.68447543	0.05345214
15108	A_55_P2042698	Hsd17b10	hydroxysteroid (17-beta) deh	NM_016763	11513.9	11847.3	10586.9	10946.2	19147.5	19591.2	18172.3	18573.7	11223.575	18871.175	0.75042971	1.68229383	0.01781909
11637	A_55_P1957613	Ak2	adenylate kinase 2	NM_016895	2554.7	2563.3	2549.4	2478.2	4338.6	4520.1	4289.4	3936.5	2536.4	4271.15	0.75016675	1.68198723	0.01777718
23947	A_55_P2275279	Mid2	midline 2	NM_011845	37.2	37.9	32.5	34.5	56.4	61.4	58.9	62	35.525	59.675	0.74998328	1.68177334	0.04466924
81601	A_55_P2017714	Kat5	K(lysine) acetyltransferase 5	NM_178637	2991	3090.5	2767.9	2667.2	5191.5	4873.1	4602.5	4681.4	2879.15	4837.125	0.74944076	1.68114103	0.05159827
230700	A_55_P2118931	Foxj3	forkhead box J3	NM_172699	5428.7	4831.9	5718.6	5789.8	8985.5	8819.9	9302.2	9379.7	5442.25	9121.825	0.74827549	1.67978372	0.0541937
212555	A_55_P2078073	Pqlc2	PQ loop repeat containing 2	NM_145384	676.2	725.6	758.5	751.8	1224	1240.6	1325.9	1102	728.025	1223.125	0.7468319	1.67810373	0.06759963
50884	A_55_P1962966	Nckap1	NCK-associated protein 1	ENSMUST00000111760	4116.5	3736.2	4436.7	3824.3	6644	6608.6	6908.7	6816.3	4028.425	6744.4	0.74653181	1.67775471	0.0417976
19173	A_55_P2144850	Psmb5	proteasome (prosome, macro	NM_011186	49283.1	58705.2	57072.7	59789.2	97434.8	95769	88537	94674.1	56212.55	94103.725	0.74649478	1.67771166	0.08173499
319322	A_51_P280158	Sf3b2	splicing factor 3b, subunit 2	NM_030109	3261.8	3042.3	3157.5	3348.3	5499.8	5441.3	5819.3	4765.1	3202.475	5381.375	0.74591009	1.67703185	0.07261325
66083	A_51_P342271	Setd6	SET domain containing 6	NM_001035123	1900.3	2097.3	1977.8	2014.2	3588.6	3119.2	3535.4	3170.8	1997.4	3353.5	0.7456134	1.676687	0.04698986
216964	A_55_P2121372	Trp53i13	transformation related protei	NM_001024920	1309.7	1416.4	1353.8	1350.3	2258.7	2387.2	2309.5	2150.8	1357.55	2276.55	0.74537658	1.67641179	0.01502678
319169	A_55_P2084652	Hist1h2ak	histone cluster 1, H2ak	NM_178183	5840.9	5797.3	5998.2	4937.3	9851.2	9132	9576.4	9186.6	5643.425	9436.55	0.74510525	1.67609654	0.07672552
319177	A_51_P180140	Hist1h2ba	histone cluster 1, H2ba	NM_175663	890.9	994.9	1047.9	977.2	1709.6	1612.9	1610.8	1610	977.725	1635.825	0.74449205	1.67538429	0.03258328
56529	A_55_P2002562	Sec11a	SEC11 homolog A (S. cerevisia	NM_019951	664	754.2	731.8	829.4	1243	1228.4	1271.2	1230.5	744.85	1243.275	0.74352673	1.67426365	0.07079748
67118	A_55_P2047967	Bfar	bifunctional apoptosis regulat	NM_025976	8711.6	8637.5	8431	9020.3	13195.1	14175.8	14672.6	16335	8700.1	14594.625	0.74245128	1.67301604	0.07208106
233887	A_55_P2060498	Zfp553	zinc finger protein 553	NM_146201	339.5	314.9	312.8	319.1	549.3	485	564.5	555.5	321.575	538.575	0.74219627	1.67272035	0.04103576
109658	A_55_P2003891	Txlna	taxilin alpha	NM_001005506	694.7	692.6	647.5	751.3	1296.6	1096.5	1102.1	1164.9	696.525	1165.025	0.74078278	1.6710823	0.09103915
102182	A_55_P1996374	Prmt10	protein arginine methyltransf	NM_001081240	1722.6	2003.3	1911.9	2060.8	2996.9	3159	3448.8	3242.8	1924.65	3211.875	0.7402739	1.67049296	0.08886496
72587	A_55_P2086258	Pan3	PAN3 polyA specific ribonucle	NM_028291	838.8	840.2	859.4	924.4	1375.6	1368.7	1547.9	1495.9	865.7	1447.025	0.74024975	1.67046499	0.0377762
68250	A_51_P327530	Fam96a	family with sequence similarit	NM_026635	2300.3	2385.6	2240.6	2030.1	3767.5	3690.2	3561.5	3905.1	2239.15	3731.075	0.73838523	1.6683075	0.04289973
71999	A_55_P2065819	Fbxo22	F-box protein 22	NM_028049	1830	1999.2	1910.6	1965.9	3182.1	3341.1	3111.1	3217.6	1926.425	3212.975	0.73830748	1.6682176	0.01325597
228368	A_51_P443723	Slc35c1	solute carrier family 35, mem	NM_211358	1295.9	1340.4	1172.8	1358	1999.4	2191.3	2070.1	2357.7	1291.775	2154.625	0.73759407	1.66739287	0.09089061
67068	A_55_P2069949	Dynlrb1	dynein light chain roadblock-t	NM_025947	6396.2	7485.2	6746.5	6849	11875.4	11320.7	11609.3	10928.7	6869.225	11433.525	0.73669148	1.66635003	0.03603195
66795	A_51_P378858	Atg10	autophagy-related 10 (yeast)	NM_025770	191.7	191.7	168.5	175.2	308.2	286.3	297.3	318.4	181.775	302.55	0.73617557	1.66575425	0.04486816
70381	A_51_P240693	Tecpr1	tectonin beta-propeller repea	NM_027410	3280.4	2948.1	3431.2	3047.8	5025.9	5153.3	5290.1	5674.2	3176.875	5285.875	0.73561297	1.66510479	0.05935539
53869	A_52_P444162	Rab11a	RAB11a, member RAS oncoge	NM_017382	594.8	591.3	661.1	615.1	1056.3	1014.3	1073.3	954.9	615.575	1024.7	0.73517674	1.66460138	0.03477647
20318	A_52_P649332	Sdf4	stromal cell derived factor 4	NM_011341	1615.3	1598.6	1464.3	1577.1	2632.8	2533.8	2644.6	2578.9	1563.825	2597.525	0.73290238	1.66197926	0.01396479
52206	A_51_P434198	Anapc4	anaphase promoting complex	NM_024213	7307.1	8124.3	8204.7	8318.2	12729.8	13830.1	13265.1	13140.7	7988.575	13241.425	0.73028675	1.65896879	0.03047648
11518	A_55_P1990336	Add1	adducin 1 (alpha)	NM_001102444	7901.7	8033.1	8154.7	8954.6	14181.9	13477.8	13028.1	14048.4	8261.025	13684.05	0.72900001	1.65748983	0.03074989
56407	A_55_P2019257	Trpc4ap	transient receptor potential c	NM_001163452	17470.9	17830.2	19392.8	18236.1	30153.3	27470.6	31341.7	31815.7	18232.5	30195.325	0.72660787	1.6547438	0.05005687
16150	A_52_P64364	Ikbkb	inhibitor of kappaB kinase bet	NM_010546	112.2	131.7	133.5	134.4	219.1	211.6	208.1	205.5	127.95	211.075	0.72566089	1.653658	0.07684661
436081	A_55_P1958103	Gm5745	predicted gene 5745	ENSMUST00000085344	24835.6	23970.4	21398.2	23176.8	41120.6	39248.7	37410.2	36476.4	23345.25	38563.975	0.7247667	1.65263336	0.05729723
213539	A_51_P204913	Bag2	BCL2-associated athanogene	NM_145392	522.4	610.9	541.9	536.3	942.7	940.2	871.2	891.9	552.875	911.5	0.72312357	1.6507522	0.05155818
232196	A_55_P2104583	C87436	expressed sequence C87436	NM_146170	447.2	482.3	455.1	438.7	726.1	713.4	805	765.5	455.825	752.5	0.72250033	1.65003924	0.03278525
71881	A_51_P277295	2310001A20Rik	RIKEN cDNA 2310001A20 gen	NM_027977	863.8	918.5	929.1	862.1	1400.7	1546	1431.8	1513.8	893.375	1473.075	0.72118479	1.64853531	0.02495349
78796	A_66_P119943	Zcchc4	zinc finger, CCHC domain con	NM_030185	17.9	19.4	18.2	17.9	31.3	31	27.9	30.7	18.35	30.225	0.71925509	1.64633176	0.0305487
57354	A_52_P126825	Cramp1l	Crm, cramped-like (Drosophil	NM_020608	927.7	819.1	881.1	902.9	1381.1	1442.7	1536.6	1441.8	882.7	1450.55	0.71708607	1.64385845	0.03605691
27058	A_55_P2112947	Srp9	signal recognition particle 9	NM_012058	1221.7	1393.2	1351.9	1327.8	2251.2	2286.9	2107.9	2053.3	1323.65	2174.825	0.71662991	1.64333876	0.04813177
14678	A_55_P2004137	Gnai2	guanine nucleotide binding pr	NM_008138	934	958.1	928.8	1009.9	1483.8	1471.5	1635.3	1708	957.7	1574.65	0.71526314	1.64178264	0.06280566
19045	A_55_P2039439	Ppp1ca	protein phosphatase 1, cataly	NM_031868	20813.2	21514.8	20832.9	22917	36879.3	35005.8	33652.3	35642.9	21519.475	35295.075	0.71415375	1.64052064	0.02515135
73062	A_55_P1991618	Ppp1r16a	protein phosphatase 1, regula	NM_033371	3778	3729	3849.5	3352.4	6177.7	5922.6	5794.6	6187.8	3677.225	6020.675	0.71278981	1.63897041	0.0390141
17524	A_51_P124568	Mpp1	membrane protein, palmitoyl	NM_008621	640.1	676	692.8	627.4	986.2	1082.9	1155.6	1099	659.075	1080.925	0.71256326	1.63871306	0.05972731
16784	A_52_P483280	Lamp2	lysosomal-associated membra	NM_010685	4395.1	4926.2	4457.8	4894.5	8086.1	7486.1	7754.8	7234.2	4668.4	7640.3	0.71142921	1.63742544	0.05186155
20316	A_51_P148196	Sdf2	stromal cell derived factor 2	NM_009143	11055.3	12455.1	11829.9	11233.5	17576	18723.6	20675.9	19324	11643.45	19074.875	0.71127209	1.63724712	0.07595183
76709	A_55_P1980831	Arpc2	actin related protein 2/3 com	NM_029711	10839.9	12161.2	10945.4	11201.4	18657.6	19323.6	18303.7	17528.6	11286.975	18453.375	0.70983316	1.63561495	0.03465466
67040	A_51_P381321	Ddx17	DEAD (Asp-Glu-Ala-Asp) box p	NM_199080	10421.9	10723.8	11852	11450.4	17898.3	18426.1	17237.5	19085.3	11112.025	18161.8	0.70965567	1.63541374	0.04555328
78455	A_66_P139568	Helz	helicase with zinc finger doma	NM_198298	758.5	661.7	730.5	790.8	1164.2	1143.9	1261.5	1232.5	735.375	1200.525	0.70905412	1.63473198	0.08593173
19255	A_55_P2080850	Ptpn2	protein tyrosine phosphatase	NM_001127177	1387.4	1401	1499.1	1548.9	2419.6	2352.3	2447.3	2312.5	1459.1	2382.925	0.7088259	1.6344734	0.02669519
67945	A_55_P2027819	Rpl41	ribosomal protein L41	NM_018860	47568.8	56986.1	47401.4	50467.8	80323.3	82296.5	82679.9	83836.4	50606.025	82284.025	0.70521112	1.63038323	0.08497519
245866	A_51_P486091	Ift52	intraflagellar transport 52 hor	NM_172150	472	490.4	495.4	553.8	806.1	799	847.9	819.9	502.9	818.225	0.70444791	1.62952096	0.0489892
16969	A_55_P2159890	Zbtb7a	zinc finger and BTB domain co	NM_010731	381.2	362.6	400.8	350.1	603.5	565	605.5	661.9	373.675	608.975	0.70419206	1.62923201	0.08574751
14148	A_55_P2059890	Fdx1	ferredoxin 1	NM_007996	5090.8	5841.1	5167.6	5101.9	8641.4	8623.7	8616.5	8565.1	5300.35	8611.675	0.70262065	1.62745839	0.03765411
269997	A_55_P2002465	Zfp747	zinc finger protein 747	NM_175560	875.9	930.9	823.1	988.7	1457	1438.7	1433	1549.1	904.65	1469.45	0.70248875	1.6273096	0.083937
19082	A_51_P121818	Prkag1	protein kinase, AMP-activated	NM_016781	1854.7	1797.1	1713.8	1793.2	2690.7	2890.8	3093.7	2982.3	1789.7	2914.375	0.70215434	1.62693243	0.03975215
65961	A_51_P325485	Utp3	UTP3, small subunit (SSU) pro	NM_023054	4804.7	5766.3	5446.3	5372	8821.6	8505.3	8838	8563.5	5347.325	8682.1	0.70212374	1.62689793	0.06193164
50767	A_55_P1985219	Pnpla6	patatin-like phospholipase do	NM_001122818	508.4	542	482.2	511.8	805.3	802.7	876.7	840.3	511.1	831.25	0.70197657	1.62673198	0.03378952
75083	A_55_P2020248	Usp50	ubiquitin specific peptidase 5(	ENSMUST00000136319	18029.9	18536.5	18906.8	17400.8	32160.6	28259.8	30407.5	27853.4	18218.5	29670.325	0.70187678	1.62661946	0.05554323
22134	A_52_P143477	Tgoln1	trans-golgi network protein	NM_009443	3064.7	3442.7	2965.9	3077	5175.1	5222	4846.9	5142.6	3137.575	5096.65	0.70161718	1.6263268	0.05007051
72834	A_55_P2425938	2810468N07Rik	RIKEN cDNA 2810468N07 gen	XR_105883	142.9	156.7	155.4	171.6	254.6	264.8	255.8	241.7	156.65	254.225	0.70083053	1.62544026	0.07597605
244216	A_55_P2014269	Zfp771	zinc finger protein 771	NM_177362	7543.6	7808.5	7802.3	6925.9	12283.6	12655.4	12147.7	11751.8	7520.075	12209.625	0.70039105	1.62494519	0.03552205
56462	A_55_P2019397	Mtch1	mitochondrial carrier homolo	NM_019880	15301.3	15887.5	14319.2	16647.6	25246.4	25935.3	23399.4	26344.9	15538.9	25231.5	0.70004463	1.62455505	0.07313282
80743	A_55_P1963483	Vps16	vacuolar protein sorting 16 (y	NM_030559	2774.5	2680.5	2974.5	3137.3	4442.9	4592.1	4923.7	4801.5	2891.7	4690.05	0.69924579	1.62365576	0.07802695
64213	A_55_P2011991	St7	suppression of tumorigenicity	NM_022332	831.6	871.8	938.9	881.7	1352.6	1403.7	1472.1	1487	881	1428.85	0.69795407	1.62220266	0.03998644
229782	A_52_P514317	Slc35a3	solute carrier family 35 (UDP-	NM_144902	75.4	78.9	68.6	81	120.9	129.3	121.8	119.8	75.975	122.95	0.69666766	1.62075684	0.07067582
71131	A_55_P1963563	Zfp689	zinc finger protein 689	NM_175163	149.5	157.4	150.2	139.3	235.4	235.9	238.8	255.7	149.1	241.45	0.69597091	1.61997428	0.03672253

80877	A_55_P2100305	Lrba	LPS-responsive beige-like anc	NM_030695	3673.8	3630.4	3475.8	3670.7	6208.6	5320.9	6162.9	5742.9	3612.675	5858.825	0.6951313	1.61903178	0.06117945
67247	A_52_P661722	Mosc2	MOCO sulphurase C-terminal	NM_133684	14742.9	14306.9	15625.6	14227.6	24539.8	24420	23858.1	22372.9	14725.75	23797.7	0.69252069	1.61610473	0.03357764
11773	A_55_P1969857	Ap2m1	adaptor protein complex AP-2	NM_009679	5284.3	5302.2	5060.2	5153.1	8140.5	8580.9	8576.9	8314.3	5199.95	8403.15	0.69233976	1.61590206	0.01377928
224250	A_51_P446477	Cldnd1	claudin domain containing 1	NM_171826	1247	1418.2	1217.3	1280.4	2052.1	2054.1	2213.7	2013.4	1290.725	2083.325	0.6922248	1.6157733	0.06964076
74043	A_55_P1969660	Pex26	peroxisomal biogenesis factor	NM_028730	592.6	687.2	661.8	642.7	1067.1	1005	1044	1053.4	646.075	1042.375	0.69186223	1.61536729	0.04517306
56844	A_51_P179241	Tssc4	tumor-suppressing subchrom	NM_020285	940.8	1054.9	986.6	927.4	1663.2	1549.4	1472.4	1605.6	977.425	1572.65	0.68652161	1.60939852	0.07054718
57813	A_51_P310398	Tk2	thymidine kinase 2, mitochon	NM_021028	96.2	108.8	99.4	94.9	163.7	155.3	159.6	162.6	99.825	160.3	0.68507874	1.60778973	0.04486171
65113	A_55_P1963873	Ndfip1	Nedd4 family interacting prot	ENSMUST00000025293	11207.6	11120.6	12138.8	11696.7	17913.2	19596.6	18447.4	18224.2	11540.925	18545.35	0.68436502	1.60699453	0.03162481
52635	A_66_P100349	Esyt2	extended synaptotagmin-like	NM_028731	867.7	907.3	954.4	844.7	1367.3	1446.4	1447.3	1476.8	893.525	1434.45	0.68388454	1.60645942	0.04064174
27632	A_52_P110270	Rdbp	RD RNA-binding protein	NM_001045864	424.7	395.2	407.1	414.7	665.2	622.3	726.3	626.1	410.425	659.975	0.68296969	1.60544105	0.07315614
11843	A_51_P295625	Arf4	ADP-ribosylation factor 4	NM_007479	888.8	850.4	888.1	837.5	1397.6	1401.4	1347.2	1408.1	866.2	1388.575	0.6811087	1.60337146	0.01689959
68294	A_55_P2023747	Mfsd10	major facilitator superfamily d	NM_026660	268.4	287.7	247.9	254.3	401.1	441.9	425.9	426.1	264.575	423.75	0.68103726	1.60329207	0.07246119
66272	A_55_P1997747	Cox16	COX16 cytochrome c oxidase	NM_025461	5402.5	6058	6103.1	6071.1	9868.8	9346	9670.2	8951.6	5908.675	9459.15	0.67973652	1.60184719	0.06209093
77031	A_55_P1997741	Slc9a8	solute carrier family 9 (sodiun	NM_148929	6124.7	5154.3	5609.6	5453.6	9186.3	8600.8	8678.9	9216.3	5585.55	8920.575	0.67753304	1.59940249	0.08615376
67106	A_55_P2032238	Zbtb8os	zinc finger and BTB domain co	NM_025970	527.6	453.3	519.6	513.3	780	786.2	808.9	841.4	503.45	804.125	0.67750231	1.59936843	0.0767278
11758	A_55_P2103561	Prdx6	peroxiredoxin 6	NM_007453	13346.6	13491.7	14350.4	13866.5	20871	22019.5	23331.3	21855.7	13763.8	22019.375	0.67732967	1.59917704	0.03378589
94112	A_55_P1955722	Med15	mediator complex subunit 15	NM_033609	1383.8	1433.5	1528.4	1507.4	2424.2	2386.1	2385.1	2160.9	1463.275	2339.075	0.67639587	1.5981423	0.05757609
170707	A_55_P1984497	Usp48	ubiquitin specific peptidase 4	NM_130879	628.5	640.9	673.1	666.2	1046.3	1066.9	1015.5	1036.1	652.175	1041.2	0.67524979	1.59687324	0.01904285
19336	A_51_P320401	Rab24	RAB24, member RAS oncogen	NM_009000	2439.7	2614.2	2588.5	2320.8	3865.6	3841.4	4178.1	4002.7	2490.8	3971.95	0.67408332	1.59558263	0.05416509
56358	A_51_P230904	Copz2	coatomer protein complex, su	NM_019877	377.6	386.5	381.6	348.3	637.8	600.3	568	575.3	373.5	595.35	0.67231859	1.59363207	0.06119427
76846	A_55_P2047571	Rps9	ribosomal protein S9	NM_029767	30776.5	30733.7	30667.3	30126.8	48757	45679	50706.3	49848	30576.075	48747.575	0.67186046	1.59312609	0.02600988
11426	A_55_P2017684	Macf1	microtubule-actin crosslinking	NM_001199136	1960.7	2045.9	2190.1	2072.9	3502.3	3406.5	3097.6	3168.9	2067.4	3293.825	0.67124354	1.59244499	0.07123661
210766	A_51_P373461	Brcc3	BRCA1/BRCA2-containing com	NM_145956	2041.4	1994.2	1763.2	1955.3	3089.4	3000.1	3228.4	3012.1	1938.525	3082.5	0.67074279	1.59189236	0.06877942
71722	A_55_P1952950	Cic	capicua homolog (Drosophila)	NM_001110132	6773.8	6437.6	6062.1	6697.7	10875.4	9961.5	10646.3	9852.6	6492.8	10333.95	0.67054313	1.59167207	0.06147406
69860	A_55_P2052081	Eif1ad	eukaryotic translation initiatio	NM_027236	1750.7	1753.9	1882.5	1644.8	2779.7	2889.2	2948.2	2577	1757.975	2798.525	0.67051645	1.59164263	0.09399882
319887	A_55_P2150283	E030030I06Rik	RIKEN cDNA E030030I06 gene	ENSMUST00000069372	675.8	658.4	615.5	669.8	1104	964.5	1017.6	1083.9	654.875	1042.5	0.6696645	1.59070301	0.07493279
13885	A_55_P1988158	Esd	esterase D/formylglutathione	NM_016903	8110.1	8041.6	8818.7	8398.4	14106.8	12627.9	13150.2	13179.6	8342.2	13266.125	0.66905661	1.59003289	0.0466284
56457	A_51_P332799	Clptm1	cleft lip and palate associated	NM_019649	2312.4	2275.6	2102.8	2240.3	3601.8	3458.3	3713.3	3403.1	2232.775	3544.125	0.66667274	1.58740774	0.04011201
69878	A_55_P1952877	Snrpf	small nuclear ribonucleoprote	NM_027246	3004.2	3444.4	3413.7	3209.5	5090.9	5296.9	4956.4	5288.1	3267.95	5158.075	0.66004817	1.58013538	0.072204
100038969	A_55_P1955287	Gm14958	predicted gene 14958	XM_001472037	31271.8	34155.8	31439.6	32403.5	53927.3	49185.5	52880.9	48199.7	32317.675	51048.35	0.6588236	1.57879472	0.06494311
625730	A_55_P2010469	Gm6616	small nuclear ribonucleoprote	ENSMUST00000100667	2603.2	2486.3	2467.6	2750	3818.5	4074.6	4100.7	4254.2	2576.775	4062	0.65689895	1.57668991	0.06457569
19188	A_55_P1996862	Psme2	proteasome (prosome, macro	NM_011190	6356.1	6404.6	6917.7	6859.9	10957.5	10209.6	10500.3	10161.8	6634.575	10457.3	0.65685341	1.57664014	0.04330785
11821	A_52_P594768	Aprt	adenine phosphoribosyl trans	NM_009698	3221.8	3020.6	3362.8	3225.1	5069.3	5002.5	5251.2	4891.6	3207.575	5053.65	0.65642011	1.57616668	0.03901496
71743	A_55_P2117843	Coasy	Coenzyme A synthase	NM_027896	2792	3088.6	3220.8	3225.3	5029.9	4811.4	4702.7	4841.8	3081.675	4846.45	0.65522871	1.57486559	0.08269775
21761	A_55_P2018559	Morf4l1	mortality factor 4 like 1	NM_001039147	5663.8	5434.8	5940.5	6047.5	9482.6	8952.9	9205.4	8701.1	5771.65	9085.5	0.65509887	1.57472386	0.05181018
11774	A_51_P119597	Ap3b1	adaptor-related protein comp	NM_009680	2635.8	2509.8	2887.4	2837.9	4295	4191	4155.5	4447.7	2717.725	4272.3	0.65440654	1.57396836	0.07980763
66111	A_51_P284244	Tmed3	transmembrane emp24 doma	NM_025360	5726.6	5583.5	5462.8	5595.1	8506.7	8781.7	8912.7	8973.2	5592	8793.575	0.65298296	1.57241601	0.02008817
13660	A_51_P469008	Ehd1	EH-domain containing 1	NM_010119	5439.8	5435.9	5487.4	5787.1	8853.3	9186.4	8553.3	8157.8	5537.55	8687.7	0.64883509	1.56790167	0.05179225
67840	A_52_P528707	Mrp63	mitochondrial ribosomal prot	NM_026401	14036	13929.6	13447.1	13942.8	21379.6	21222	22086.8	22058.3	13838.875	21686.675	0.64805011	1.5670488	0.02021555
54383	A_55_P2027067	Phc2	polyhomeotic-like 2 (Drosoph	NM_001195130	3684.8	3740.8	3843.4	3717.6	6434.9	5856.1	5433.3	5791	3746.65	5878.825	0.64745282	1.56640017	0.08626865
20226	A_55_P1972257	Sars	seryl-aminoacyl-tRNA synthet	NM_011319	7193.7	7229.4	7265.2	6691.1	11334.4	10600.5	10740.4	11699.2	7094.85	11093.625	0.64453862	1.56323928	0.05774312
54131	A_55_P2083939	Irf3	interferon regulatory factor 3	NM_016849	4658.4	4960.6	4814.8	4971.1	7149.1	7537.2	7542	8119.1	4851.225	7586.85	0.64416678	1.56283642	0.05834639
224619	A_55_P2056035	Traf7	TNF receptor-associated facto	NM_153792	4077.7	3984.5	3938.3	3859.1	6354.8	6477.7	5767.4	6186.3	3964.9	6196.55	0.64308362	1.5616635	0.04978496
13595	A_51_P429682	Ebp	phenylalkylamine Ca2+ antag	NM_007898	3877.3	3786.4	3781.2	3543.7	5425.4	5936.1	5849.2	6192.2	3747.15	5850.725	0.64198912	1.56047919	0.07672602
228005	A_51_P265008	Ppig	peptidyl-prolyl isomerase G (c	NM_001081086	1694.5	1786.3	1792.2	1828.3	2908.1	2733.7	2633.7	2788.6	1775.325	2766.025	0.63937384	1.55765295	0.04632881
80886	A_55_P2070054	Senp3	SUMO/sentrin specific peptid	NM_030702	3711.2	3715.3	3655.8	3925.4	5911.2	5883.2	5821.7	5747.5	3751.925	5840.9	0.63900897	1.55725907	0.02577054
54217	A_55_P2071326	Rpl36	ribosomal protein L36	NM_018730	22589.4	22339.6	20502.5	21001.5	33571	32682.6	34110	34001.3	21608.25	33591.225	0.63749535	1.55562611	0.04483058
329015	A_52_P478729	Atg2a	ATG2 autophagy related 2 ho	NM_194348	428	403.6	413.4	393	627.2	638.7	639.3	641.1	409.5	636.575	0.63712546	1.55522731	0.02944612
53890	A_51_P212023	Sart3	squamous cell carcinoma anti	NM_016926	1856.8	1919	1775.2	1866.4	2963.2	2841.5	2837	2880.4	1854.35	2880.525	0.63575778	1.55375365	0.03031011
72736	A_52_P651034	Tmx1	thioredoxin-related transmen	NM_028339	301.2	297.4	300.5	272.4	474	444.2	446.1	454.8	292.875	454.775	0.63561944	1.55360466	0.05565471
98828	A_51_P113072	Cdc123	cell division cycle 123 homolo	NM_133837	3379.2	3482.3	3403.5	3600.2	5292.5	5402.5	5253.6	5588.5	3466.3	5384.275	0.6353814	1.55334835	0.03201913
622404	A_66_P100565	Ccdc107	coiled-coil domain containing	NM_001037913	9643.6	9451.6	9106.2	10360.6	15431.7	15005.3	14706.1	14538.4	9640.5	14920.375	0.63133739	1.54900027	0.06688731
76788	A_55_P2037221	Klhdc10	kelch domain containing 10	NM_029742	5071.6	4816.9	4689	4957.2	8096.2	7527.9	7286.8	7327.5	4883.675	7559.6	0.62968679	1.54722905	0.06588079
15353	A_55_P2112295	Hmg20b	high mobility group 20 B	NM_010440	2998.5	3022.6	3068.8	2915.5	4488.8	4521.4	4823.1	4725.9	3001.35	4639.8	0.62805005	1.54547472	0.03613402
53379	A_55_P2017082	Hnrnpa2b1	heterogeneous nuclear ribonu	NM_182650	4827.4	5362.3	4876.1	5480.5	7785	7992.5	8037.2	7863.4	5136.575	7919.525	0.62676414	1.54409781	0.08838031
76223	A_52_P675617	Agbl3	ATP/GTP binding protein-like	ENSMUST00000115014	44.4	41.5	42.4	45.7	69.6	64	65.6	69.4	43.5	67.15	0.62646531	1.54377801	0.07128108
67382	A_55_P2037897	Brd3	bromodomain containing 3	NM_023336	2701.5	2684.6	2877.6	2910.6	4445.6	4339.4	4143.8	4308.4	2793.575	4309.3	0.62583245	1.54310096	0.05174228
69367	A_55_P2095384	Glrx2	glutaredoxin 2 (thioltransfera	NM_001038592	2099.6	1953.4	2211.4	2259.1	3191.4	3309.7	3339.8	3258.7	2130.875	3274.9	0.62203453	1.53904405	0.09756367
69372	A_51_P146813	Mocs3	molybdenum cofactor synthe	NM_001160330	472.5	490.6	450.6	490.1	737.3	708.4	773.3	708.7	475.95	731.925	0.62080855	1.53773676	0.06932815
107686	A_55_P2177968	Snrpd2	small nuclear ribonucleoprote	NM_026943	11559.7	12208.4	12942.6	13114.5	19315.5	18567.6	19183.1	18952	12456.3	19004.55	0.611116	1.5274403	0.08571735
68436	A_55_P2024358	Rpl34	ribosomal protein L34	NM_001005859	19428.7	19495.7	17869.9	18044.9	26794.6	29279.1	28949.2	29193.7	18709.8	28554.15	0.6101315	1.52639833	0.09434007
107767	A_51_P217336	Scamp1	secretory carrier membrane p	NM_029153	2206.1	2232	2290.5	2205.4	3429.2	3574.8	3300	3309.7	2233.5	3403.425	0.60709073	1.52318453	0.0477272
18432	A_55_P2152926	Mybbp1a	MYB binding protein (P160) 1	NM_016776	5467.7	5652.1	5575.5	5522.8	8381.6	7881.9	9020.3	8569	5554.525	8463.2	0.60596231	1.52199362	0.08233027
75475	A_51_P378550	Oplah	5-oxoprolinase (ATP-hydrolys	NM_153122	1687	1704.6	1638.6	1513.2	2459	2452.3	2432.4	2597.2	1635.85	2485.225	0.6043963	1.52034243	0.09646495
73192	A_51_P292566	Xpot	exportin, tRNA (nuclear expor	NM_001081056	847.9	779.8	764.5	764.9	1174.9	1152.6	1219.4	1249.8	789.275	1199.175	0.60405626	1.51998413	0.09543237
20416	A_55_P1979082	Shc1	src homology 2 domain-conta	NM_001113331	1178.3	1171.7	1130.8	1192.1	1664.7	1852.9	1775	1803.2	1168.225	1773.95	0.60181662	1.51762634	0.06868738
235682	A_51_P446583	Zfp445	zinc finger protein 445	NM_173364	476.2	503.7	451.4	461.1	708.2	697.3	717.7	742.4	473.1	716.4	0.59947388	1.51516392	0.08037329
69216	A_55_P2155002	Ccdc23	coiled-coil domain containing	NM_001038998	1485	1418.8	1436.7	1527.6	2172.2	2205.7	2187.7	2285.9	1467.025	2212.875	0.59335272	1.50874891	0.05484556
54127	A_55_P1972841	Rps28	ribosomal protein S28	NM_016844	37076	35468.6	34971.4	37602.7	52836.1	53974	54808.6	56468.8	36279.675	54521.875	0.58790126	1.50305861	0.06673694
109093	A_55_P1972699	Rars2	arginyl-tRNA synthetase 2, mi	NM_181406	1826.7	1815.7	1911.7	1982	2778.3	2743.3	2786.6	2843.8	1884.025	2788	0.56621551	1.48063446	0.08575816
53356	A_51_P489229	Eif3g	eukaryotic translation initiatio	NM_016876	17709.9	17612.6	17786.7	17138.2	25625.3	25201.6	26105	26492.3	17561.85	25856.05	0.55795126	1.47217713	0.06229799
217715	A_51_P229816	Eif2b2	eukaryotic translation initiatio	NM_145445	9484	8912.9	9248.5	9280	6443.4	6212.4	6495.1	6309	9231.35	6364.975	-0.5362497	-1.4501978	0.09376701
108124	A_55_P2013716	Napa	N-ethylmaleimide sensitive fu	NM_025898	12740.2	11922	13410	12551.7	8299	7992.6	8571.2	8339.6	12655.975	8300.6	-0.6077102	-1.5238387	0.07696632
216795	A_55_P2032147	Wnt9a	wingless-type MMTV integrat	NM_139298	1054.7	999.7	1024.5	1065.3	693.7	649.1	680.9	688	1036.05	677.925	-0.611922	-1.5282938	0.04493995
14712	A_51_P224575	Gnpat	glyceronephosphate O-acyltra	NM_010322	13423.8	12973.2	12984.4	13198.3	9172.7	8185.9	8315.7	8757.8	13144.925	8608.025	-0.6120694	-1.5284501	0.06811572
30795	A_52_P531175	Fkbp3	FK506 binding protein 3	NM_013902	11696.4	12308.6	11586.4	11530.3	7907.1	7804.2	7621.3	7379.8	11780.425	7678.1	-0.6175719	-1.5342908	0.04355549
75705	A_55_P1974554	Eif4b	eukaryotic translation initiatio	NM_145625	3279.2	3174.1	2981.7	3228.9	2002.5	2026.2	2060.2	2153.7	3165.975	2060.65	-0.6191722	-1.5359936	0.05893816
110119	A_51_P393897	Mpi	mannose phosphate isomeras	NM_025837	1090.9	1075.3	1061	1075.8	717.8	664.4	720.7	694	1075.75	699.225	-0.6222091	-1.5392303	0.03723701
54364	A_66_P131530	Rpp30	ribonuclease P/MRP 30 subur	NM_019428	59.6	68	66.7	67.7	43.9	41.6	43	41.1	65.5	42.4	-0.6258525	-1.5431224	0.09949971
381820	A_51_P313337	2700089E24Rik	RIKEN cDNA 2700089E24 gen	NM_001163445	3283.6	3480.3	3021.5	3328.9	2156.9	2038.7	2108.7	2155.6	3278.575	2114.975	-0.6309371	-1.5485705	0.07912122
208922	A_55_P1957835	Cpeb3	cytoplasmic polyadenylation e	NM_198300	9198.7	8944.6	8686.2	8498.9	5709.5	5335.3	5676.1	6053.7	8832.1	5693.65	-0.6341993	-1.5520761	0.06927717
12041	A_51_P404413	Bckdk	branched chain ketoacid dehy	NM_009739	2761.8	2426.9	2566.9	2415.6	1709.1	1580.4	1657.1	1599.1	2542.8	1636.425	-0.6344212	-1.5523148	0.09888784
235041	A_55_P2167112	Kank2	KN motif and ankyrin repeat d	NM_145611	2300.4	2315.5	2247.1	2571	1589.8	1455.7	1490.5	1520.9	2358.5	1514.225	-0.6380806	-1.5562573	0.0903586
432768	A_55_P1995447	Gm5451	predicted gene 5451	XM_003086172	2288	2243.9	1997.7	2165.1	1420.3	1345.2	1346.1	1440.8	2173.675	1388.1	-0.6457992	-1.5646058	0.08064921
13854	A_55_P2007733	Epn1	epsin 1	NM_010147	34913.6	36551.9	34051.3	35621.8	22331.4	23458.2	21656.6	21954.7	35284.65	22350.225	-0.6589258	-1.5789066	0.02951626
665211	A_55_P1955715	Gm14326	predicted gene 14326	NM_001190302	1454.1	1541.4	1402.3	1659.9	957.2	974.4	930.7	964.4	1514.425	956.675	-0.6599223	-1.5799975	0.08786687
544717	A_52_P598634	1190007I07Rik	RIKEN cDNA 1190007I07 gene	NM_001135567	4119.5	4575.5	4043.5	4160	2492.8	2712.4	2714.9	2708.2	4224.625	2657.075	-0.6682541	-1.5891487	0.06202548
13819	A_55_P2053988	Epas1	endothelial PAS domain prote	NM_010137	367.9	328.4	375.2	383.4	239.5	230.2	223.6	220.7	363.725	228.5	-0.6688394	-1.5897935	0.08520925
19328	A_55_P1953414	Rab12	RAB12, member RAS oncogen	NM_024448	20100.8	18905.5	19948.2	19351.7	12699.4	12079.1	12754	11669.9	19576.55	12300.6	-0.6709406	-1.5921107	0.03045592
66048	A_51_P177518	Tmem93	transmembrane protein 93	NM_025318	4935.6	5212.8	5277.8	5724	3169.7	3272.5	3255.5	3567.5	5287.55	3316.3	-0.6724281	-1.593753	0.08804886
71452	A_55_P2047290	Ankrd40	ankyrin repeat domain 40	NM_146024	425	492.7	476.8	472.8	300.2	285.6	297.8	285.7	466.825	292.325	-0.6735055	-1.5949437	0.05832601
228714	A_55_P1991802	Csrp2bp	cysteine and glycine-rich prot	NM_181417	1315.2	1468	1420	1516.7	882.2	876.1	884.8	936.4	1429.975	894.875	-0.6747489	-1.5963189	0.0554219
97820	A_55_P2139043	4833439L19Rik	RIKEN cDNA 4833439L19 gen	NM_133797	17832.4	18276.4	18239.7	19009.4	11791.9	10429.9	11800.3	11795.9	18339.475	11454.5	-0.6806618	-1.6028749	0.04924898
93684	A_55_P2111237	15-Sep	selenoprotein	NM_053102	5133.3	5272.9	5149.8	5748.6	3386.3	3378.1	3159.9	3329.1	5326.15	3313.35	-0.6838193	-1.6063868	0.03926093
73327	A_55_P2040416	1700040I03Rik	RIKEN cDNA 1700040I03 gene	NM_001163427	570.5	559.9	566.6	535.2	308.5	352.4	359.5	370.9	558.05	347.825	-0.6850746	-1.6077851	0.09773708
67417	A_52_P512749	Ears2	glutamyl-tRNA synthetase 2 (	NM_026140	212	215.5	211.5	210.2	138.1	126.7	143.7	120.3	212.3	132.2	-0.6868365	-1.6097498	0.08028426
223881	A_51_P111164	Rnd1	Rho family GTPase 1	NM_172612	371.2	438.6	374.6	411.4	248.3	249.5	238	253.3	398.95	247.275	-0.6870156	-1.6099497	0.08871394
26367	A_55_P2386236	Ceacam2	carcinoembryonic antigen-rel	NM_001113368	191.3	157.2	177.8	173	106	111.1	108.8	105.8	174.825	107.925	-0.692631	-1.6162284	0.08495598
69577	A_55_P2132237	Fastkd3	FAST kinase domains 3	NM_027123	785.9	844.8	724.2	862.3	497.7	489.2	501.7	494.4	804.3	495.75	-0.6948323	-1.6186963	0.0694582
237403	A_51_P436491	Lingo3	leucine rich repeat and Ig dom	NM_001013758	446.1	360.4	404.9	396.8	250.2	247.8	251.2	240.6	402.05	247.45	-0.6963032	-1.6203474	0.0996105
231327	A_51_P296905	Ppat	phosphoribosyl pyrophosphat	NM_172146	916.1	900.6	899.8	983	591.8	598.2	529.3	564.2	924.875	570.875	-0.6967894	-1.6208936	0.04587458
24109	A_66_P112886	Ubl3	ubiquitin-like 3	NM_011908	3203.8	3232.5	3462.1	3171.8	1988.4	2005.8	2041	2016.2	3267.55	2012.85	-0.6981707	-1.6224463	0.01600922
11992	A_51_P372473	Auh	AU RNA binding protein/enoy	NM_016709	5194.8	5838.4	5553.6	5103.7	3406.2	3331.8	3495.4	3124	5422.625	3339.35	-0.6985728	-1.6228985	0.06322962
66521	A_55_P1965935	Rwdd1	RWD domain containing 1	NM_025614	851.8	748.2	806.8	823.3	537.6	483.8	490.6	476.1	807.525	497.025	-0.7002031	-1.6247335	0.05950276
229228	A_55_P1999324	Nudt6	nudix (nucleoside diphosphat	NM_153561	2708.9	3115	2806.2	2812.5	1742	1847.6	1732.3	1696.8	2860.65	1754.675	-0.703877	-1.6288762	0.04361294
21987	A_51_P482503	Tpd52l1	tumor protein D52-like 1	NM_009413	1442.9	1544.9	1470.6	1698.4	922.9	951.4	976.9	918	1539.2	942.3	-0.7054617	-1.6306665	0.05872137
14660	A_55_P2452259	Gls	glutaminase	NM_001113383	1205.5	1348.3	1267.2	1302.5	777.2	845	761.7	756.2	1280.875	785.025	-0.7065463	-1.6318928	0.04100292
109624	A_51_P357573	Cald1	caldesmon 1	NM_145575	226.3	244.5	239.7	227.6	148.6	142	146.3	132.7	234.525	142.4	-0.7203446	-1.6475755	0.02731006
99138	A_55_P1988433	Stard7	START domain containing 7	NM_139308	14825.8	16091.4	14206.2	14004.8	8655.7	8970.8	8774.5	9439.7	14782.05	8960.175	-0.7209023	-1.6482125	0.04048644
16553	A_55_P2011887	Kif13a	kinesin family member 13A	NM_010617	4441.6	4513.7	4766.1	4443.1	2684.1	2832.6	2667.5	2817	4541.125	2750.3	-0.7233882	-1.651055	0.01407963
18242	A_51_P141535	Oat	ornithine aminotransferase	NM_016978	5511.6	5611.5	6135.9	5823.4	3528	3563.2	3395.1	3480.7	5770.6	3491.75	-0.7237847	-1.6515088	0.01726222
20259	A_51_P335460	Scin	scinderin	NM_009132	187.4	211.6	177.4	183.8	122.4	107.8	117.9	111.4	190.05	114.875	-0.7248324	-1.6527086	0.09310793
11749	A_55_P2076792	Anxa6	annexin A6	NM_013472	10587.5	10217.8	10663.9	9923.1	5987.1	6038.3	6673.7	6348.4	10348.075	6261.875	-0.7254693	-1.6534384	0.0233072
12491	A_51_P375146	Cd36	CD36 antigen	NM_007643	3302.5	3222.2	2830.4	3100.8	1839.7	1895.3	1881.2	1903.4	3113.975	1879.9	-0.7257806	-1.6537952	0.03307361
67938	A_55_P2139407	Myl12b	myosin, light chain 12B, regul	NM_023402	2486.6	2764.2	2572.3	2507.7	1476.8	1702.5	1568.2	1492.3	2582.7	1559.95	-0.7284209	-1.6568247	0.05071466
74144	A_55_P2036026	Robo4	roundabout homolog 4 (Dros	NM_028783	4296.8	4609.7	4590.4	4262.5	2631.4	2849.7	2669.1	2545.4	4439.85	2673.9	-0.7318422	-1.6607584	0.02433758
76429	A_51_P286946	Lhpp	phospholysine phosphohistid	NM_029609	2581.4	2586.4	2456	2367.1	1543.9	1377.7	1526.7	1544.3	2497.725	1498.15	-0.7380799	-1.6679545	0.02970968
101437	A_55_P1991920	Dhx32	DEAH (Asp-Glu-Ala-His) box p	NM_133941	791.3	686.4	709.8	738.6	464.7	408.4	444.1	434.6	731.525	437.95	-0.7396562	-1.6697779	0.04631387
320790	A_55_P2129920	Chd7	chromodomain helicase DNA	NM_001081417	9024.2	10457.7	10701.3	10428.7	6093.8	5615.5	6520.3	6063.7	10152.975	6073.325	-0.7401502	-1.6703498	0.09246051
75991	A_52_P366572	Slain2	SLAIN motif family, member 2	NM_153567	318	347.7	387.1	345.2	197.6	213.5	218.3	204.3	349.5	208.425	-0.7432971	-1.6739971	0.06870864
225341	A_55_P2174203	Lims2	LIM and senescent cell antige	NM_144862	6960.9	6537.6	6781.2	6719.4	3679.6	4364.6	4152.5	3938.4	6749.775	4033.775	-0.7452299	-1.6762414	0.03757385
14479	A_55_P2099785	Usp15	ubiquitin specific peptidase 1	NM_027604	4952.1	5147.7	5036	5815.3	3103.2	3056.4	3283.5	3021.3	5237.775	3116.1	-0.7470266	-1.6783302	0.04344455
68275	A_51_P333159	Rpa1	replication protein A1	BC019119	3541	3254	3752.9	3703	2040.9	1941.6	2289.2	2213.1	3562.725	2121.2	-0.748927	-1.6805424	0.08459003
11906	A_55_P2106459	Zfhx3	zinc finger homeobox 3	NM_007496	1007.4	978.6	976.4	1069.8	658.1	588.9	591.7	560.2	1008.05	599.725	-0.750722	-1.6826347	0.03916954
78830	A_51_P430620	Slc25a12	solute carrier family 25 (mitoc	NM_172436	16188.1	15818.5	14654.7	15346	9903.9	8784.5	8419.6	9804.3	15501.825	9228.075	-0.7508404	-1.6827728	0.06169221
67391	A_52_P168338	Fundc2	FUN14 domain containing 2	NM_026126	583.5	535.5	555.9	548.8	339.8	319	320.7	339.3	555.925	329.7	-0.7536743	-1.6860815	0.01172392
67698	A_55_P2172599	Fam174a	family with sequence similarit	NM_026321	4425.3	5041.8	4695.8	4624.6	2884.3	2899.4	2710.5	2640.6	4696.875	2783.7	-0.7542533	-1.6867584	0.02643629
208650	A_65_P14951	Cblb	Casitas B-lineage lymphoma b	NM_001033238	466.3	482.5	426.4	408.6	262.7	277.1	250.9	261	445.95	262.925	-0.7599247	-1.6934022	0.04789545
12549	A_52_P400999	Arhgap31	Rho GTPase activating protein	NM_020260	1537.7	1362	1413.6	1513.3	874.9	903.7	870.3	786.4	1456.65	858.825	-0.7623867	-1.6962946	0.03930473
56198	A_52_P337259	Heyl	hairy/enhancer-of-split relate	NM_013905	577.9	654.9	701.9	644.9	388	363.9	388	376.7	644.9	379.15	-0.763341	-1.697417	0.04408381
14154	A_51_P285770	Fem1a	feminization 1 homolog a (C.	NM_010192	48909	50321.4	51507.7	46551.7	29040.1	28356.3	30553.4	27896.6	49322.45	28961.6	-0.767939	-1.7028354	0.01407893
77056	A_55_P2180944	Tmco4	transmembrane and coiled-co	NM_029857	3088.4	2870.5	2881.5	2568.3	1739.2	1618.2	1573.1	1748.9	2852.175	1669.85	-0.7707309	-1.7061339	0.053702
16468	A_52_P370203	Jarid2	jumonji, AT rich interactive do	NM_021878	791.5	762.3	793.2	684.9	421.9	445.1	458.9	446.7	757.975	443.15	-0.7725024	-1.7082302	0.02818378
50780	A_55_P2027102	Rgs3	regulator of G-protein signalir	NM_134257	914.1	1088.3	1095.9	987.5	613.6	620.7	552.2	600.4	1021.45	596.725	-0.772968	-1.7087816	0.07386953
14256	A_55_P2145506	Flt3l	FMS-like tyrosine kinase 3 liga	ENSMUST00000123381	85	93.9	94.9	91.2	48.3	57.8	53	54.6	91.25	53.425	-0.774011	-1.7100174	0.04651013
382030	A_55_P2097126	Tmem188	transmembrane protein 188	NM_029074	1961	2006.1	2053.8	2070.2	1263.1	1171.1	1131.3	1162.7	2022.775	1182.05	-0.7759388	-1.712304	0.01042651
14359	A_51_P372463	Fxr1	fragile X mental retardation g	NM_008053	12273.4	13309.2	13642	14003.6	8354	7941.7	7516.4	7246.6	13307.05	7764.675	-0.7775658	-1.714236	0.03596885
654472	A_55_P1955747	Gm12070	glyceraldehyde-3-phosphate d	NR_002890	99344	90301.8	99539.2	90005.1	54839.6	50748.6	59033.6	56528.6	94797.525	55287.6	-0.7783389	-1.715155	0.0368048
233103	A_55_P2098210	4931406P16Rik	RIKEN cDNA 4931406P16 gen	NM_172741	3224.9	3167.7	3253.5	3392.4	2030	1884.9	1863.6	1826.4	3259.625	1901.225	-0.7784816	-1.7153245	0.0106734
66790	A_51_P109144	Grtp1	GH regulated TBC protein 1	NM_025768	230.8	217.2	187.9	219.8	126.4	132.1	124.6	113.6	213.925	124.175	-0.7827325	-1.7203862	0.09041892
225020	A_55_P1966209	Fez2	fasciculation and elongation p	NM_199448	6551.3	7435.1	7468.3	7426.5	4076.4	4416	4020.4	4233.5	7220.3	4186.575	-0.7850925	-1.7232028	0.02399325
17064	A_51_P238722	Cd93	CD93 antigen	NM_010740	4065.6	3465.3	4084.1	3860.2	2031.5	2382.2	2199.3	2364.6	3868.8	2244.4	-0.7854155	-1.7235886	0.08087826

18442	A_52_P587738	P2ry2	purinergic receptor P2Y, G-pr	NM_008773	1944.4	2288.5	1904.3	2025.9	1210.9	1160.5	1283.3	1077	2040.775	1182.925	-0.785962	-1.7242417	0.09310217
69556	A_51_P317272	Bod1	biorientation of chromosome	NM_001024919	13608.7	16429.1	14529.7	13832.4	8729.7	8862.5	7916.7	8274	14599.975	8445.725	-0.7871054	-1.7256087	0.06063161
18514	A_55_P2051701	Pbx1	pre B-cell leukemia transcript	NM_183355	913.2	864.7	822.6	876.3	487.7	554.7	462	511.1	869.2	503.875	-0.7888866	-1.7277405	0.03815262
217258	A_55_P2102769	Abca8a	ATP-binding cassette, sub-fan	NM_153145	373.4	298.7	318	348.9	197.9	189	203.7	181.6	334.75	193.05	-0.7902229	-1.7293416	0.09107072
77219	A_51_P146655	Ptgr2	prostaglandin reductase 2	NM_029880	2005.7	2237.5	1916.6	2059	1236	1102.9	1130.8	1283.5	2054.7	1188.3	-0.7905197	-1.7296974	0.05258392
11652	A_55_P2066518	Akt2	thymoma viral proto-oncoger	NM_001110208	19325.6	20103.3	19633.1	18732.2	11638.8	11241.1	10440.3	11247.6	19448.55	11141.95	-0.804312	-1.7463128	0.00823815
11512	A_51_P243134	Adcy6	adenylate cyclase 6	NM_007405	846.1	786.8	845.6	808.6	467.7	487.9	444.3	482	821.775	470.475	-0.8048726	-1.7469916	0.00829173
68292	A_52_P67200	Stt3b	STT3, subunit of the oligosacc	NM_024222	1749.6	1831.5	2004	1733.5	928.7	1078.5	1040.8	1145.8	1829.65	1048.45	-0.8050656	-1.7472252	0.07833544
224860	A_51_P219444	Plcl2	phospholipase C-like 2	NM_013880	5812.2	5934.3	6834	6710.3	3517.1	3566.4	3646.3	3705	6322.7	3608.7	-0.805627	-1.7479053	0.02927425
73431	A_51_P134262	1700052K11Rik	RIKEN cDNA 1700052K11 gen	NR_027956	1043.4	985.6	1022.9	1184.8	600.1	562.3	629.4	627.6	1059.175	604.85	-0.8062555	-1.7486669	0.04317205
56695	A_51_P372141	Pnkd	paroxysmal nonkinesiogenic	NM_001039509	63.9	53.6	66.1	60.8	34	34	34.5	36.7	61.1	34.8	-0.8083312	-1.7511846	0.04808126
228966	A_51_P169516	Ppp1r3d	protein phosphatase 1, regula	NM_001085501	1148.1	1251.8	1264.6	1328.4	740.3	636.1	733.9	739.6	1248.225	712.475	-0.8099108	-1.753103	0.0421075
107746	A_55_P2070721	Rapgef1	Rap guanine nucleotide excha	NM_001039087	1158.3	959.2	1130.6	1207.7	596.5	627.3	667.2	643.3	1113.95	633.575	-0.8099217	-1.7531163	0.07774738
27801	A_52_P124173	Zdhhc8	zinc finger, DHHC domain con	NM_172151	1650.6	1578.7	1627.2	1683.8	884.9	880.1	954.6	1014.3	1635.075	933.475	-0.8107654	-1.7541418	0.01600128
26914	A_52_P179238	H2afy	H2A histone family, member	NM_001159514	468.6	507.9	488.5	408.9	267.6	262.8	262.7	271.1	468.475	266.05	-0.8116808	-1.7552552	0.04087639
18131	A_51_P220162	Notch3	Notch gene homolog 3 (Drosc	NM_008716	1536.8	1359.2	1433.5	1458.1	787.8	834.4	839.8	832.3	1446.9	823.575	-0.8120783	-1.7557389	0.00891759
14182	A_55_P2057777	Fgfr1	fibroblast growth factor recep	NM_010206	5011	4843.1	4993	4687.5	2598.9	2836.7	2821.9	2852.7	4883.65	2777.55	-0.8146613	-1.7588852	0.00725886
78653	A_55_P2040367	Bola3	bolA-like 3 (E. coli)	NM_175277	6438.7	7202.2	5951.1	6268.4	3717.5	3474	3669.8	3810.3	6465.1	3667.9	-0.814981	-1.759275	0.03080067
69731	A_55_P2165854	Gemin7	gem (nuclear organelle) assoc	NM_027189	1335.1	1186.6	1281.7	1457.3	708	712.6	791.7	769.2	1315.175	745.375	-0.816924	-1.7616459	0.05059024
29819	A_52_P625624	Stau2	staufen (RNA binding protein	NM_025303	299.8	323.1	372.9	334.3	173.2	197.4	192.8	190.1	332.525	188.375	-0.8171222	-1.761888	0.06215931
67914	A_51_P134551	Coq9	coenzyme Q9 homolog (yeast	NM_026452	2235.7	2225.2	2143.7	1893.2	1279.5	1137.2	1119.9	1279.9	2124.45	1204.125	-0.8187811	-1.763915	0.05929328
13830	A_51_P294807	Stom	stomatin	NM_013515	594.3	599.8	555.4	511.9	319.7	359.1	297	306.8	565.35	320.65	-0.8190491	-1.7642427	0.06983729
12156	A_55_P2041961	Bmp2	bone morphogenetic protein	NM_007553	251.6	276	250.7	254	142.3	149.5	158.6	134.4	258.075	146.2	-0.8213959	-1.767115	0.02301076
67460	A_51_P208555	Decr1	2,4-dienoyl CoA reductase 1,	NM_026172	371.1	368.5	330.7	355.1	222.1	194.7	176.5	214.8	356.35	202.025	-0.8230241	-1.7691105	0.08369321
72333	A_55_P1977653	Palld	palladin, cytoskeletal associat	NM_001081390	1063.2	826.5	898	854.2	507.6	514	510.4	516.3	910.475	512.075	-0.8233367	-1.7694938	0.07108086
442821	A_55_P2326091	9330175M20Rik	RIKEN cDNA 9330175M20 ge	AK034309	223.7	194.2	218	192.2	116.3	117.7	110.8	122.3	207.025	116.775	-0.8236743	-1.7699079	0.02661307
57267	A_55_P1977538	Apba3	amyloid beta (A4) precursor	NM_018758	2684.2	2490.2	2316.8	2502.4	1445.5	1362	1395.2	1436.5	2498.4	1409.8	-0.8239686	-1.770269	0.01069188
210126	A_51_P306067	Lpp	LIM domain containing prefer	NM_178665	2035.3	2164.6	2241.4	2081.5	1143.7	1275.3	1272.3	1125.8	2130.7	1204.275	-0.8246077	-1.7710534	0.01846349
195046	A_55_P1955998	Nlrp1a	NLR family, pyrin domain con	NM_001004142	9023.5	8814.6	8570.2	8200.4	4852.5	5317.8	4566.7	4819.3	8652.175	4889.075	-0.824768	-1.7712502	0.01553385
11532	A_55_P2018482	Adh5	alcohol dehydrogenase 5 (cla	NM_007410	117	140	131.8	140	78.1	67.1	78.9	73.8	132.2	74.475	-0.8270359	-1.7740367	0.06980072
19263	A_55_P2313033	Ptprb	protein tyrosine phosphatase	NM_029928	426	456.8	426.6	462.9	268.7	269.6	251.4	212.9	443.075	250.65	-0.8272558	-1.7743072	0.08926781
170757	A_51_P480328	Eltd1	EGF, latrophilin seven transm	NM_133222	158.1	172.8	165.4	143.7	86.7	83.9	95.6	93.8	160	90	-0.8288427	-1.7762599	0.04268948
105522	A_65_P18433	Ankrd28	ankyrin repeat domain 28	NM_001024604	843.7	907	851.6	956	559.3	466.8	489.7	489.4	889.575	501.3	-0.82892	-1.7763551	0.03736813
100710	A_51_P223946	Pds5b	PDS5, regulator of cohesion n	NM_175310	159.3	195.2	189.3	198.6	100.7	100.2	107.5	108.2	185.6	104.15	-0.829064	-1.7765324	0.06059208
102032	A_52_P95740	AI316807	expressed sequence AI31680	NM_001012667	1087.1	1065.3	1202.8	1128	637.5	545.2	701.1	645.7	1120.8	632.375	-0.8299814	-1.7776624	0.08300879
20364	A_55_P2052924	Sepw1	selenoprotein W, muscle 1	NM_009156	50862.4	42360	46960	42883.4	24239.4	27670.8	26087.9	24694	45766.45	25673.025	-0.8319735	-1.7801188	0.04832283
12577	A_51_P339540	Cdkn1c	cyclin-dependent kinase inhib	NM_009876	1651.3	1736.9	1506.9	1626	831.7	844.2	1015.1	978.6	1630.275	917.4	-0.8332057	-1.7816399	0.0791942
15500	A_55_P2128032	Hsf2	heat shock factor 2	NM_008297	330.9	311.9	347.5	356.9	183.4	192.4	186.8	192.2	336.8	188.7	-0.8342016	-1.7828701	0.00877598
14228	A_51_P185175	Fkbp4	FK506 binding protein 4	NM_010219	834	958.7	1096.1	932.6	532.1	554.8	514	530.7	955.35	532.9	-0.8358407	-1.7848968	0.07547861
230125	A_52_P169901	Mcart1	mitochondrial carrier triple re	NM_001009949	2153.8	2204	2129.2	2190.4	1194.9	1278.2	1272	1115.8	2169.35	1215.225	-0.8380834	-1.7876737	0.00916308
11536	A_51_P436068	Gpr182	G protein-coupled receptor 1	NM_007412	255.6	288.1	263	276.6	141.7	146	165.4	152.2	270.825	151.325	-0.8406464	-1.7908524	0.02055151
233204	A_52_P655084	Tbc1d17	TBC1 domain family, member	NM_001042655	1173.2	1244.9	1319.6	1158.8	591.9	696.8	766.6	686.2	1224.125	685.375	-0.8409306	-1.7912051	0.08992105
56280	A_51_P256304	Mrpl37	mitochondrial ribosomal prot	NM_025500	661.5	607.8	711.1	609.6	372.7	360.6	390.4	322	647.5	361.425	-0.8417063	-1.7921685	0.05807398
29864	A_55_P1970159	Rnf11	ring finger protein 11	NM_013876	4438.4	3639.1	4008.4	3678.8	2294.8	2006.4	2186.7	2256.7	3941.175	2186.15	-0.8474839	-1.79936	0.05232975
74386	A_55_P2118799	Rmi1	RMI1, RecQ mediated genom	NM_001168248	87.9	78.4	85	88.9	50.7	43.7	42.7	52.3	85.05	47.35	-0.8489243	-1.8011574	0.06923932
108097	A_52_P126266	Prkab2	protein kinase, AMP-activated	NM_182997	12658.4	10663	12730.6	12620.5	6761	6652.4	6857.1	6605.1	12168.125	6718.9	-0.8530499	-1.8063156	0.02015024
14159	A_52_P635338	Fes	feline sarcoma oncogene	NM_010194	580.2	560.4	626	555.4	298.1	343.7	354.3	292.3	580.5	322.1	-0.8533324	-1.8066692	0.05391009
18597	A_52_P581435	Pdha1	pyruvate dehydrogenase E1 a	NM_008810	2543.6	2932.1	2597.9	2493.7	1477.5	1495.6	1302.8	1573.3	2641.825	1462.3	-0.853787	-1.8072386	0.04655395
16145	A_51_P112355	Igtp	interferon gamma induced G	NM_018738	884.4	922	922.5	1011.5	509.2	514.7	522.7	517.9	935.1	516.125	-0.8557045	-1.8096423	0.00565513
170718	A_51_P130110	Idh3b	isocitrate dehydrogenase 3 (N	NM_130884	20039.9	18535.3	20012.4	18209.5	10020.8	10911.4	11324.9	10108.2	19199.275	10591.325	-0.8587195	-1.813428	0.01252261
69046	A_52_P304323	Isca1	iron-sulfur cluster assembly 1	NM_026921	2042.9	2151	2016	1980.8	1089.1	1107.6	1110	1205.2	2047.675	1127.975	-0.8606998	-1.815919	0.00537234
100042875	A_55_P1976067	Gm12059	predicted gene 12059	ENSMUST00000128996	143.5	146.9	122.5	135.3	77.6	78.2	78.2	67.7	137.05	75.425	-0.8607478	-1.8159794	0.0426186
66849	A_55_P1960496	Ppp1r2	protein phosphatase 1, regula	NM_025800	541.4	597.7	586	668.4	347.5	318.2	303.6	343.1	598.375	328.1	-0.8649953	-1.8213337	0.0414757
56690	A_51_P222283	Mlycd	malonyl-CoA decarboxylase	NM_019966	15510.5	16733.9	15332.5	16154.9	8157.2	8361.2	8979.7	9513.2	15932.95	8752.825	-0.8659785	-1.8225754	0.01306722
245877	A_55_P1965070	Mtap7d1	microtubule-associated prote	NM_144941	30254.6	28155.3	32477.1	27505.8	14520.3	17862.6	15771	16754.2	29598.2	16227.025	-0.8682274	-1.8254186	0.05558874
16500	A_55_P2320313	Kcnb1	potassium voltage gated char	BC058714	574.7	647.6	701.4	731.8	363.1	357.7	355.8	371.8	663.875	362.1	-0.8687221	-1.8260448	0.04042628
415115	A_51_P418935	Neurl2	neuralized-like 2 (Drosophila)	NM_001082974	7996.3	7196.7	7418.2	7272.2	3962.3	3817.8	4454.2	4128.9	7470.85	4090.8	-0.8700314	-1.8277027	0.01310772
13849	A_55_P2002577	Ephx1	epoxide hydrolase 1, microso	NM_010145	89.7	82.7	84.3	104.4	50.6	50.1	45.2	50.9	90.275	49.2	-0.8711603	-1.8291334	0.06254118
277333	A_52_P12806	Gm5069	glyceraldehyde-3-phosphate	NR_003623	82406.2	71813.8	79556.8	67998.4	38069.3	40850.9	43159.1	42447.8	75443.8	41131.775	-0.8725374	-1.8308802	0.03464538
433594	A_66_P111747	Gm5537	predicted gene 5537	XR_107489	42963.9	40263.6	43293.2	40577.2	22540.1	21903.8	23698.8	22987.6	41774.475	22782.575	-0.8745165	-1.8333935	0.00356253
402752	A_55_P2235970	C130068B02Rik	RIKEN cDNA C130068B02 gen	AK081691	251.7	298.3	281.6	272	150.8	146.2	156	147.2	275.9	150.05	-0.8764549	-1.8358586	0.01016648
18655	A_65_P03442	Pgk1	phosphoglycerate kinase 1	NM_008828	50126.7	46702	50864.3	45888.5	26673.5	24905	28101.4	25701.7	48395.375	26345.4	-0.8773753	-1.8370302	0.0085024
399602	A_55_P2301063	9930024M15Rik	RIKEN cDNA 9930024M15 ge	AK036921	227.8	250.5	285.4	281.1	143.9	143.3	150.1	129.6	261.2	141.725	-0.8781381	-1.8380016	0.0667565
58799	A_52_P32081	Crbn	cereblon	NM_175357	935.5	957.2	980.1	1032.5	465.3	570.3	584	512.3	976.325	532.975	-0.8781794	-1.8380543	0.04523949
228859	A_52_P172441	Fitm2	fat storage-inducing transmer	NM_173397	211.4	165.9	175.9	181.8	105.5	88.9	102	102.4	183.75	99.7	-0.8792784	-1.8394551	0.08192732
73847	A_55_P2118302	Fam110a	family with sequence similarit	NM_028666	933.8	845	816.4	1051.9	449.4	524.4	491.2	506.6	911.775	492.9	-0.8826103	-1.8437082	0.08928942
16796	A_52_P1029978	Lasp1	LIM and SH3 protein 1	NM_010688	2883.5	3107.3	3240	3094	1467.7	1975.1	1651.2	1622.2	3081.2	1679.05	-0.883	-1.8442063	0.09221025
209773	A_51_P155085	Dennd2a	DENN/MADD domain contain	NM_172477	532.4	571.4	552.3	522.8	261.8	343.4	309.1	270.6	544.725	296.225	-0.8865331	-1.8487281	0.08497706
100201	A_52_P10017	Tmem64	transmembrane protein 64	NM_181401	384.8	402.5	378.1	460.4	229	224.5	210.5	211.9	406.45	218.975	-0.8888716	-1.8517272	0.02275088
246293	A_55_P2001589	Klhl8	kelch-like 8 (Drosophila)	NM_178741	2928.8	3042.6	3005.5	3016.5	1717.2	1614.8	1567.2	1575.2	2998.35	1618.6	-0.8902393	-1.8534835	0.00256819
11782	A_66_P105711	Ap4s1	adaptor-related protein comp	NM_021710	556.4	587.3	656	585	329.2	295.8	337.3	321.9	596.175	321.05	-0.8920303	-1.8557859	0.01541908
100040297	A_55_P2019217	Gm2695	predicted gene 2695	XR_106466	388.2	406.7	373.6	377.4	226.7	188.1	202.3	217.1	386.475	208.55	-0.8928034	-1.8567807	0.0155621
100609	A_51_P221495	Nsun5	NOL1/NOP2/Sun domain fam	NM_145414	183.9	194.2	185.3	159.2	92.3	93.4	92.5	110.9	180.65	97.275	-0.8936216	-1.857834	0.06161011
11807	A_55_P2178553	Apoa2	apolipoprotein A-II	NM_013474	493.9	492.8	528.5	474.9	289.6	230.8	273.3	279.7	497.525	268.35	-0.8949195	-1.8595061	0.03523396
56390	A_52_P287052	Sssca1	Sjogrens syndrome/scleroder	NM_020491	962.3	840.3	857.1	800.5	406.6	487.8	526.3	443.2	865.05	465.975	-0.8960032	-1.8609035	0.09646759
77371	A_52_P409711	Sec24a	Sec24 related gene family, me	NM_175255	119.9	107.8	116	108	52.1	60.9	65.9	64.5	112.925	60.85	-0.8964385	-1.861465	0.04866128
17909	A_55_P1993744	Myo10	myosin X	NM_019472	115.5	97.1	88.6	101.3	50.1	57.6	51.5	56.3	100.625	53.875	-0.8971436	-1.862375	0.07266512
68916	A_52_P335259	Cdkal1	CDK5 regulatory subunit asso	NM_144536	2563.8	2095.5	2394	2044.9	1115.4	1228.7	1272.5	1243.5	2274.55	1215.025	-0.9000664	-1.8661519	0.0548864
71436	A_55_P2144556	Flrt3	fibronectin leucine rich transr	NM_001172160	105.5	100.7	82.8	96.9	52.2	52.2	52.8	48.6	96.475	51.45	-0.9019241	-1.8685564	0.03528923
67273	A_51_P272123	Ndufa10	NADH dehydrogenase (ubiqui	NM_024197	5228.7	5519.4	4843.8	4214.8	2601.7	2647.2	2695.5	2596.8	4951.675	2635.3	-0.9028394	-1.8697422	0.04550777
24058	A_51_P145520	Sigirr	single immunoglobulin and to	NM_023059	307.3	253.7	263.4	261.9	126.4	159.6	145.9	149.1	271.575	145.25	-0.9038314	-1.8710283	0.07163121
99939	A_55_P2325648	BB085087	expressed sequence BB08508	AK139301	159.8	186.3	200.7	194.4	99.2	104.1	104.8	87	185.3	98.775	-0.906214	-1.8741208	0.0769671
83815	A_51_P113003	Cenpq	centromere protein Q	NM_031863	267.7	285.4	291.7	277.5	156.1	147	150.7	143.9	280.575	149.425	-0.9088857	-1.8775948	0.00268021
101458	A_55_P2294074	AA536887	expressed sequence AA53688	CB196702	238.9	236.1	246.8	235.3	116.7	122	146	126.7	239.275	127.85	-0.9091445	-1.8779316	0.01977061
66695	A_51_P142813	Aspn	asporin	NM_025711	124.6	131.2	119	131.8	64.2	76.5	65.7	63.7	126.65	67.525	-0.9102191	-1.8793309	0.01907621
23876	A_55_P2088615	Fbln5	fibulin 5	NM_011812	2273.1	2480.5	2349.2	2287.4	1194	1375.3	1156.5	1272.7	2347.55	1249.625	-0.9119909	-1.8816403	0.01104826
67442	A_51_P319070	Retsat	retinol saturase (all trans reti	NM_026159	764.5	881.6	773	736.2	427.3	392	404.3	450.6	788.825	418.55	-0.9129576	-1.8829016	0.01949296
56451	A_51_P491227	Suclg1	succinate-CoA ligase, GDP-for	NM_019879	14095.6	16511	14521.6	13701.3	7320.9	8416.7	7916.2	7537.3	14707.375	7797.775	-0.9136916	-1.8838598	0.02175329
116904	A_51_P211305	Alpk3	alpha-kinase 3	NM_054085	5799.3	4871.2	4783.6	4926.4	2570.5	2565.2	2776.8	2867.6	5095.125	2695.025	-0.9160998	-1.887007	0.02394732
94279	A_55_P2448065	Sfxn2	sideroflexin 2	NM_053196	358.8	434.5	363.9	399.2	203.5	190	217.8	211.7	389.1	205.75	-0.9167841	-1.8879023	0.02556999
229900	A_51_P463846	Gbp7	guanylate binding protein 7	NM_145545	101	105.1	106.6	87.3	57.7	52.6	50	51.2	100	52.875	-0.9170963	-1.8883109	0.029881
70625	A_51_P199567	Med26	mediator complex subunit 26	NM_027485	1015.5	1059.4	968.1	1234.4	594.3	519.5	569.8	572.8	1069.35	564.1	-0.9183464	-1.8899479	0.04230122
226744	A_52_P429774	Cnst	consortin, connexin sorting p	NM_146105	673.2	687.5	650.1	659.2	355.9	383.1	337.9	337.1	667.5	353.5	-0.9187017	-1.8904133	0.00421214
234395	A_55_P2052485	Ushbp1	Usher syndrome 1C binding p	NM_181418	1969	2165.4	2185.9	2381.2	1112.3	1242.3	1156.4	1085.5	2175.375	1149.125	-0.9193633	-1.8912804	0.01679503
269870	A_55_P1954544	Zfp446	zinc finger protein 446	NM_001168562	364	340.6	376.5	318.2	187.5	157.2	200.2	196.3	349.825	185.3	-0.9201517	-1.8923142	0.06930624
102857	A_55_P2000553	Slc6a8	solute carrier family 6 (neurot	NM_133987	12953.9	13895.1	13686.3	13769.8	7205.3	7871.6	6543.8	7115.1	13576.275	7183.95	-0.9207968	-1.8931606	0.00851599
17355	A_52_P381665	Aff1	AF4/FMR2 family, member 1	NM_133919	4356	4504.6	4441.4	4436.5	2332	2461.1	2115.2	2468.9	4434.625	2344.3	-0.9223265	-1.895169	0.00585712
66596	A_51_P307644	Gtf3a	general transcription factor II	NM_025652	2294.4	2145	2186	2029.4	1028.9	1205.7	1190.8	1144	2163.7	1142.35	-0.9228623	-1.895873	0.01088463
102414	A_52_P559498	Clk3	CDC-like kinase 3	NM_007713	932.1	878	864.2	788	440.3	484.4	460.8	435.3	865.575	455.2	-0.9258575	-1.8998131	0.00923022
19056	A_52_P306396	Ppp3cb	protein phosphatase 3, cataly	NM_008914	10535.8	9643.7	11450.2	10616.6	5147.6	5462.6	5870.7	5668.3	10561.575	5537.3	-0.9306073	-1.9060782	0.01102538
84585	A_52_P50478	Rnf123	ring finger protein 123	NM_032543	2175.7	1813.7	1774.1	1578.7	978	963.2	961	924	1835.55	956.55	-0.9309633	-1.9065486	0.06797411
52064	A_51_P125183	Coq5	coenzyme Q5 homolog, meth	NM_026504	557.5	600.5	497	568.1	279.8	282.7	288.9	311.5	555.775	290.725	-0.9327641	-1.9089299	0.0123823
27407	A_52_P445828	Abcf2	ATP-binding cassette, sub-fan	NM_013853	1251.1	1151.4	1315.4	1186.6	680.9	621.6	618	646.6	1226.125	641.775	-0.933181	-1.9094816	0.0054141
17165	A_55_P2049256	Mapkapk5	MAP kinase-activated protein	NM_010765	4274.8	4187.2	4402.3	4421.4	2132.8	2220	2337.2	2365.3	4321.425	2263.825	-0.9336227	-1.9100663	0.00244158
80288	A_51_P340668	Bcl9l	B-cell CLL/lymphoma 9-like	NM_030256	34.4	34.3	31	28.2	15	18.4	17	16.5	31.975	16.725	-0.9339779	-1.9105366	0.04935007
20970	A_52_P282741	Sdc3	syndecan 3	NM_011520	117.3	119.6	110.9	95.1	57.7	62.7	57.9	52.9	110.725	57.8	-0.9347604	-1.9115731	0.04532522
68728	A_55_P1961210	Trp53inp2	transformation related protei	NM_178111	27882	29799.7	25618.8	24905	12853.9	13310.5	14214.1	16215	27051.375	14148.375	-0.9372119	-1.9148241	0.05625266
66396	A_55_P2052181	Ccdc82	coiled-coil domain containing	NM_025534	2969.1	2715.3	2721.6	2594.2	1576.1	1249.8	1327.7	1617.9	2750.05	1442.875	-0.9374435	-1.9151316	0.07500156
104776	A_51_P338485	Aldh6a1	aldehyde dehydrogenase fam	NM_134042	10260.8	11888	11225.1	11698.4	5689.7	5956.3	5647.3	6142.6	11268.075	5858.975	-0.9420554	-1.9212634	0.00571799
13713	A_55_P2018994	Elk3	ELK3, member of ETS oncoge	NM_013508	1535	1563.5	1572.4	1441.4	785.9	880.3	793	727.2	1528.075	796.6	-0.9422888	-1.9215743	0.00917803
67020	A_52_P209484	Tmem88	transmembrane protein 88	NM_025915	1489	1242.4	1375.1	1159	717.8	681.3	666	661.8	1316.375	681.725	-0.9434533	-1.9231261	0.03006571
21957	A_51_P345699	Tnnt3	troponin T3, skeletal, fast	NM_011620	144645.3	131630	128809.4	113038.2	70347.3	73160.4	67427	58240.4	129530.725	67293.775	-0.9444659	-1.9244763	0.08030591
15259	A_55_P2035963	Hipk3	homeodomain interacting pro	NM_010434	272.8	279.6	308.6	288.7	163.2	159.4	137.8	137.5	287.425	149.475	-0.9463042	-1.9269301	0.01941784
80708	A_55_P1968295	Pacsin3	protein kinase C and casein ki	NM_028733	29036.3	30135.6	33755.5	32993.8	15422	17722.4	17725	14537.4	31480.3	16351.7	-0.9476313	-1.9287034	0.03847377
227723	A_52_P686136	Prrc2b	proline-rich coiled-coil 2B	NM_172661	7956.4	6117.2	6724.2	6264.1	3393.9	3520.2	3497.7	3526	6765.475	3484.45	-0.9496042	-1.9313427	0.03313968
399572	A_55_P2277825	E430010N07Rik	RIKEN cDNA E430010N07 gen	AK088305	521.1	428.1	460.9	380.7	218.6	245.1	226.4	231.8	447.7	230.475	-0.9497995	-1.9316042	0.07142529
216848	A_55_P2061386	Chd3	chromodomain helicase DNA	NM_146019	921.4	969.8	886.1	1057	517.5	566.2	484	420.1	958.575	496.95	-0.9530694	-1.9359871	0.08886286
67027	A_51_P150430	Mkrn2	makorin, ring finger protein, 2	NM_023290	2181.3	2042.9	2222.6	1981.2	1108	1110.5	1157	979.9	2107	1088.85	-0.9535418	-1.9366212	0.0090648
67266	A_66_P126485	Fam69a	family with sequence similarit	NM_026062	249	223.5	250	257.2	122.9	124.3	128.1	129.9	244.925	126.3	-0.953814	-1.9369867	0.00339409
19042	A_51_P335306	Ppm1a	protein phosphatase 1A, mag	NM_008910	1803.8	1750.3	2007.2	1874.9	1066.5	989.9	862.8	923	1859.05	960.55	-0.9552251	-1.9388821	0.01982425
214639	A_51_P276479	4930486L24Rik	RIKEN cDNA 4930486L24 gen	NM_178098	97.6	107.2	88.9	92.4	52.1	48.1	51.3	47.3	96.525	49.7	-0.9552678	-1.9389395	0.01065173
76642	A_55_P2219151	1700113A16Rik	RIKEN cDNA 1700113A16 gen	AK008852	27.4	29.3	29.4	28.8	15.7	15.5	13.2	14.9	28.725	14.825	-0.9570196	-1.9412953	0.00726283
68118	A_51_P175758	9430023L20Rik	RIKEN cDNA 9430023L20 gen	NM_026566	4354.8	4245.6	3918.5	3357.1	2181.8	2001.5	1966.5	1993.2	3969	2035.75	-0.9571937	-1.9415296	0.04018246
27425	A_55_P2067682	Atp5l	ATP synthase, H+ transporting	NM_013795	7363.1	7925.1	6908.8	7623	3951.4	3762.1	3603.3	4021.4	7455	3834.55	-0.9586544	-1.9434964	0.00487496
18574	A_55_P1974827	Pde1b	phosphodiesterase 1B, Ca2+-	NM_008800	119.4	138.2	131.8	123.7	60.7	60.8	71.4	70.8	128.275	65.925	-0.9625069	-1.948693	0.02133022
224647	A_51_P397920	D17Wsu92e	DNA segment, Chr 17, Wayne	NM_001033279	4042.6	3857.8	3638.6	3181.7	2004.9	1848.4	1817.9	1853	3680.175	1881.05	-0.963575	-1.9501364	0.02185176
20496	A_55_P2099448	Slc12a2	solute carrier family 12, mem	NM_009194	5916	7273.8	7446.5	8249.8	3842.4	3900.6	3416.9	3568	7221.525	3681.975	-0.9636864	-1.9502869	0.0997809
21349	A_55_P2106690	Tal1	T-cell acute lymphocytic leuke	NM_011527	217.2	212.2	233.3	211.3	118	107.3	119.8	103	218.5	112.025	-0.9655547	-1.9528142	0.00704025
17281	A_52_P667477	Fyco1	FYVE and coiled-coil domain	NM_148925	4613.7	4232.3	3814.8	3970.8	2130.8	2028.3	2305.6	2031.7	4157.9	2124.1	-0.9672268	-1.9550789	0.01381852
268490	A_52_P407871	Lsm12	LSM12 homolog (S. cerevisiae	NM_172947	2468.9	2042.5	2175.4	2146.4	1124.4	1095.6	1271.2	1027.3	2208.3	1129.625	-0.9678698	-1.9559504	0.0288936
71624	A_55_P2360266	4833411C07Rik	RIKEN cDNA 4833411C07 gen	BC052524	104	95.6	97.7	107.8	49.3	46	53.7	58.7	101.275	51.925	-0.9681655	-1.9563514	0.02765549
76167	A_55_P1976689	Snrnp35	small nuclear ribonucleoprote	NM_029532	1989.8	1868.2	1589.4	1862.8	914.2	909	931.6	967.3	1827.55	930.525	-0.9693689	-1.9579839	0.01214892
140481	A_51_P385952	Man2a2	mannosidase 2, alpha 2	ENSMUST00000098346	955	1035.5	972.3	938.7	474	553.8	483.1	483.9	975.375	498.7	-0.9696348	-1.9583448	0.0060244
20181	A_55_P2074331	Rxra	retinoid X receptor alpha	NM_011305	56.6	51.9	53.6	55.4	28.1	27.8	28.9	26.2	54.375	27.75	-0.9705911	-1.9596433	0.00190557
545156	A_51_P400016	Kalrn	kalirin, RhoGEF kinase	ENSMUST00000023522	620.1	604.8	583.6	690.3	320.2	347.4	291.6	314.3	624.7	318.375	-0.9723646	-1.9620538	0.01299682
76454	A_51_P356283	Fbxo31	F-box protein 31	NM_133765	8393.2	8333	8847	7743.5	4118.3	4100.1	4646.7	4104.1	8329.175	4242.3	-0.9738127	-1.9640241	0.00555451
228788	A_55_P2018191	BC020535	cDNA sequence BC020535	NM_145536	762.1	820.7	742.5	770.1	355.7	446	406.8	372.2	773.85	395.175	-0.9740424	-1.9643369	0.01710012
74525	A_55_P1975947	8430419L09Rik	RIKEN cDNA 8430419L09 gen	NM_028982	827.3	748.7	806.8	808.2	383.2	449.1	391.3	399.2	797.75	405.7	-0.9773002	-1.9687776	0.0055637
21898	A_66_P124806	Tlr4	toll-like receptor 4	NM_021297	160.9	157.8	158.2	152.2	69.6	84.8	76.7	89.8	157.275	80.225	-0.9776496	-1.9692545	0.02134013
239126	A_52_P200610	C1qtnf9	C1q and tumor necrosis facto	NM_183175	114.9	114.4	120.6	134.8	63.2	69.7	56.8	56.7	121.175	61.6	-0.9782264	-1.9700421	0.03200171
106877	A_55_P2239317	Afap1l1	actin filament associated prot	NM_178928	1396	1271.6	1532.1	1558.1	759.4	788.1	723.7	648.8	1439.45	730	-0.9786376	-1.9706036	0.0336207
21769	A_55_P2066096	Zfand3	zinc finger, AN1-type domain	NM_148926	13703.1	12518.4	14505.3	15099.3	6582.9	6967.4	7687.3	7061.2	13956.525	7074.7	-0.9788982	-1.9709595	0.01314147

76263	A_55_P2051313	Gstk1	glutathione S-transferase kap	NM_029555	5864	6888.8	6009.5	6215.1	3281.6	2946.1	3199	3224.9	6244.35	3162.9	-0.9797698	-1.9721507	0.00603625
76854	A_51_P185939	Gpr30	G protein-coupled receptor 3	NM_029771	102.2	91.6	88.2	78.6	45.3	47.8	42.9	46.1	90.15	45.525	-0.9804282	-1.9730509	0.02312095
319565	A_55_P1979863	Syne2	synaptic nuclear envelope 2	NM_001005510	2630.7	2684.8	2716.2	2500.7	1361.6	1392.9	1192.5	1395.6	2633.1	1335.65	-0.9814784	-1.9744877	0.0054304
236920	A_51_P251129	Stard8	START domain containing 8	NM_199018	285.4	222.2	219.9	270.5	124	126.3	132.4	119.6	249.5	125.575	-0.9817513	-1.9748612	0.05649968
12876	A_55_P2024704	Cpe	carboxypeptidase E	NM_013494	33190.2	32625.4	34455.8	32088.5	17427	17202.6	16641	15656.1	33089.975	16731.675	-0.9845346	-1.9786749	0.0017389
240725	A_51_P142744	Sulf1	sulfatase 1	NM_172294	777.6	680.6	724.9	766	359.1	407.2	403.8	324.6	737.275	373.675	-0.9846337	-1.9788108	0.02866376
14051	A_55_P2041529	Eya4	eyes absent 4 homolog (Dros	NM_010167	288.6	284.8	272.5	278.1	120.4	157.1	150.7	141.4	281	142.4	-0.9874751	-1.9827119	0.02402286
18187	A_52_P93910	Nrp2	neuropilin 2	NM_001077403	1116.9	1334.4	1160.6	1161.4	589.4	646	597.7	569.8	1193.325	600.725	-0.9883702	-1.9839425	0.00828267
12153	A_55_P2006703	Bmp1	bone morphogenetic protein	NM_009755	1415.2	1455.1	1500	1264.9	707.3	764.7	643.5	719.4	1408.8	708.725	-0.990968	-1.9875181	0.01173246
12457	A_55_P1968723	Ccrn4l	CCR4 carbon catabolite repre	NM_009834	6672.7	7014.3	6583.2	6688.3	3307.4	3594.7	3342.1	3315.2	6739.625	3389.85	-0.9918947	-1.9887951	0.00120029
15412	A_55_P2024993	Hoxb4	homeobox B4	NM_010459	104.6	128.7	111.6	106.8	52.8	54.1	57.2	62.7	112.925	56.7	-0.9923022	-1.989357	0.02406472
100233175	A_52_P464129	AK010878	cDNA sequence AK010878	NM_001142938	956	1184.2	951.8	1048.4	472.9	535.1	506.4	562.4	1035.1	519.2	-0.9926024	-1.989771	0.03074668
52639	A_52_P497534	Wipi1	WD repeat domain, phosphoi	NM_145940	1078.8	1057.4	1023.6	827.9	483.1	537.9	503.8	469.7	996.925	498.625	-0.9936477	-1.9912133	0.04314661
329628	A_52_P675530	Fat4	FAT tumor suppressor homol	NM_183221	50.5	62.5	55.4	59.4	27	28.3	29.3	29.3	56.95	28.475	-0.9962314	-1.9947825	0.00989893
104099	A_51_P382970	Itga9	integrin alpha 9	NM_133721	102.2	105.6	89	81.6	46.7	54.4	45	43.2	94.6	47.325	-0.9970625	-1.995932	0.09038855
269614	A_55_P2146002	Pank4	pantothenate kinase 4	NM_172990	3995.3	4261.1	3961.2	4054	1808.8	2059	2057.6	2236.9	4067.9	2040.575	-0.9988433	-1.9983972	0.00731114
71648	A_66_P119801	Optn	optineurin	NM_181848	277.1	255.3	251	289.9	131.7	150.2	127.5	127.9	268.325	134.325	-0.9990473	-1.9986797	0.01099364
209448	A_51_P375754	Hoxc10	homeobox C10	NM_010462	596	494.5	502.8	526.1	234.9	259.8	272.8	293.3	529.85	265.2	-0.9992339	-1.9989383	0.02803067
11744	A_55_P1977583	Anxa11	annexin A11	NM_013469	6209.5	5980.6	7573.1	5726.5	3188.2	3270.5	3413.1	2818.9	6372.425	3172.675	-1.0012092	-2.0016769	0.06507022
17957	A_52_P660861	Napb	N-ethylmaleimide sensitive fu	NM_019632	505	511.8	549	504	237.7	249.6	275	271.3	517.45	258.4	-1.0035032	-2.0048624	0.00394878
212111	A_55_P2002723	Inpp5a	inositol polyphosphate-5-pho	NM_001127363	9018.5	7730.2	8560.8	7939.7	3999.4	4060.1	4272.4	4225.4	8312.3	4139.325	-1.0036975	-2.0051324	0.0034515
16542	A_51_P316553	Kdr	kinase insert domain protein	NM_010612	405.8	428.1	407.2	465	195	218.8	214	222.2	426.525	212.5	-1.0047821	-2.0066404	0.00508911
66124	A_55_P2055875	Josd2	Josephin domain containing 2	NM_025368	373.3	360.4	419.1	352.5	164.3	198.2	194	194	376.325	187.625	-1.0048624	-2.0067521	0.01832323
66212	A_55_P2045481	Sec61b	Sec61 beta subunit	BC002089	1071.7	1115.7	1023.4	868.4	461.9	552.2	550	466.7	1019.8	507.7	-1.0051665	-2.0071751	0.0625146
238076	A_51_P218975	Kcns3	potassium voltage-gated char	NM_173417	53.8	49.3	55.5	50.7	22.8	30.6	26.9	24.5	52.325	26.2	-1.0051785	-2.0071918	0.04341596
94187	A_55_P2102335	Zfp423	zinc finger protein 423	NM_033327	559.6	461.8	492.6	490.8	221.2	283.2	251.4	242.9	501.2	249.675	-1.0074241	-2.0103185	0.03140553
22273	A_51_P109835	Uqcrc1	ubiquinol-cytochrome c redu	NM_025407	14518.8	12633.7	12035.2	10974.3	6420.6	6325.7	5957	6127	12540.5	6207.575	-1.0076502	-2.0106336	0.02210692
117149	A_52_P676956	Tirap	toll-interleukin 1 receptor (TI	NM_054096	628.2	511.4	616	494.4	251	281.1	292.1	289.5	562.5	278.425	-1.0088722	-2.0123373	0.04925156
54615	A_51_P232708	Npff	neuropeptide FF-amide pepti	NM_018787	389.3	318.3	317.7	405.2	159.8	176.2	174.6	197.4	357.625	177	-1.009728	-2.0135314	0.07916597
76137	A_51_P308681	Ccdc90a	coiled-coil domain containing	NM_001081059	902.1	978.6	915.1	1012.7	412	508.9	497.4	475.5	952.125	473.45	-1.0110482	-2.0153748	0.01312043
360216	A_52_P194680	Zranb1	zinc finger, RAN-binding dom	ENSMUST00000106157	1477	1431	1627.8	1328.3	712.4	764.3	753.6	673	1466.025	725.825	-1.0121696	-2.016942	0.00958386
94186	A_65_P09177	Strn3	striatin, calmodulin binding p	NM_052973	853.3	938.2	923	862.1	446.6	436.8	406.7	484	894.15	443.525	-1.0130516	-2.0181754	0.00471242
72061	A_52_P431859	2010111I01Rik	RIKEN cDNA 2010111I01 gene	ENSMUST00000021911	666.8	724.1	671.4	605.9	319.8	366.7	307.4	328.2	667.05	330.525	-1.0133082	-2.0185344	0.01070532
24004	A_55_P2036007	Rai2	retinoic acid induced 2	NM_198409	2471.7	2557.9	2590.3	3115.8	1409.5	1362	1300.5	1225.3	2683.925	1324.325	-1.0150184	-2.0209287	0.02010557
18018	A_51_P220135	Nfatc1	nuclear factor of activated T-c	NM_016791	268.2	263.7	233.6	249.3	133.3	126.9	130.4	111.6	253.7	125.55	-1.0161201	-2.0224725	0.00881379
18590	A_55_P2007470	Pdgfa	platelet derived growth facto	NM_008808	6655.5	6272	7542	7142.8	3260.6	3349	3746.6	3283.8	6903.075	3410	-1.0162734	-2.0226874	0.00972494
66369	A_55_P2029592	Dus2l	dihydrouridine synthase 2-lik	NM_025518	1605.9	1568.8	1548.1	1599.3	700.9	819	754.6	857.4	1580.525	782.975	-1.0174856	-2.0243877	0.00557774
68241	A_51_P106527	Fam195a	family with sequence similari	NM_026633	6803.5	7297.5	6214.7	5612.8	2939.4	2888	3361.1	3601.2	6482.125	3197.425	-1.0187703	-2.0261912	0.07434001
24136	A_52_P596008	Zeb2	zinc finger E-box binding hom	NM_015753	841.5	902.9	961.5	996.1	466.9	469.8	441.8	442.2	925.5	455.175	-1.0214635	-2.0299772	0.00359479
100182	A_51_P206134	Akna	AT-hook transcription factor	NM_001045514	52.1	52.9	59.4	53.5	29.9	24.8	27.6	25.2	54.475	26.875	-1.0214938	-2.0300198	0.01012998
20292	A_51_P331752	Ccl11	chemokine (C-C motif) ligand	NM_011330	900.1	801.2	786.8	675.4	391.7	393	387.7	377.2	790.875	387.4	-1.0223595	-2.0312383	0.0181389
68545	A_52_P1026777	Ecscr	endothelial cell-specific chem	NM_001033141	448.7	567.3	509	503.9	234.2	295.4	247.9	223.4	507.225	250.225	-1.022717	-2.0317416	0.07097609
56177	A_66_P134501	Olfm1	olfactomedin 1	NM_019498	166.2	207.5	165.8	146.5	92.5	81.8	84.2	76.9	171.5	83.85	-1.0239327	-2.0334545	0.09461681
20928	A_66_P101519	Abcc9	ATP-binding cassette, sub-fan	NM_021041	5147.4	4975.6	4847.4	4638.7	2606.5	2272	2346.8	2418.3	4902.275	2410.9	-1.0247203	-2.0345649	0.00247314
21833	A_51_P475995	Thra	thyroid hormone receptor alp	NM_178060	6286	5763.7	6448.6	5416.2	2765.5	3013.8	3016.4	2932.1	5978.625	2931.95	-1.0253796	-2.0354949	0.00505844
77739	A_55_P2016069	Adamtsl1	ADAMTS-like 1	NM_029967	258.1	311.6	304.4	304.8	139.5	137.6	159.2	142.1	294.725	144.6	-1.025741	-2.0360049	0.01181404
106952	A_52_P195018	Arap3	ArfGAP with RhoGAP domain,	NM_139206	1132.9	1112.9	1048.2	1030.4	516.9	558.4	513.7	533.9	1081.1	530.725	-1.0261239	-2.0365453	0.00139078
53624	A_55_P2158653	Cldn7	claudin 7	NM_016887	19.2	20.7	18.6	18.6	9.9	8.7	10.4	8.9	19.275	9.475	-1.0270735	-2.0378861	0.00738107
21853	A_55_P2081616	Timeless	timeless homolog (Drosophila	NM_001164081	376.8	330.9	443.5	404.4	165.4	194.7	205.6	195.6	388.9	190.325	-1.0274882	-2.038472	0.06941137
329575	A_55_P2115968	Gm14325	predicted gene 14325	NR_036450	1354.6	1392.8	1439.7	1476.9	857.5	663.5	640.3	636.1	1416	699.35	-1.0284183	-2.0397866	0.05142661
17118	A_51_P352968	Marcks	myristoylated alanine rich pro	NM_008538	1205.7	1430.7	1275.6	1254.1	619.7	708	617.3	586.9	1291.525	632.975	-1.0294318	-2.0412201	0.01102127
12494	A_66_P101835	Cd38	CD38 antigen	NM_007646	304.5	323.2	393.3	331.6	166.6	185.1	154.7	154.4	338.15	165.2	-1.0307761	-2.043123	0.03711522
54634	A_55_P2057076	Magix	MAGI family member, X-linke	NM_018832	233.1	212.9	212.1	202.7	102.5	92.1	107.2	120.9	215.2	105.675	-1.0310499	-2.0435108	0.02305761
12862	A_51_P509997	Cox6a2	cytochrome c oxidase, subuni	NM_009943	148935.3	141763.1	141052.4	145856.1	75456	70807.7	65780.8	70866	144401.725	70727.625	-1.0310888	-2.0435659	0.00144797
226830	A_51_P320105	Smyd2	SET and MYND domain conta	NM_026796	31043.2	27721.9	32179.8	33378.5	14887	14883.5	14573.3	16388.6	31080.85	15183.1	-1.0316477	-2.0443578	0.00625134
26901	A_55_P2088715	Deb1	differentially expressed in B1	NM_026794	3478.4	4198.3	3993.3	4852.1	2188.8	1844.2	1846.8	2140.7	4130.525	2005.125	-1.0370436	-2.0520183	0.09114897
72899	A_55_P2179314	Macrod2	MACRO domain containing 2	NM_028387	324.4	372.2	410	435.8	179.5	178.9	205	184.8	385.6	187.05	-1.037104	-2.0521042	0.04214595
20623	A_52_P553316	Snrk	SNF related kinase	NM_133741	2391.8	2555.9	2134.5	2314.3	1351.7	1173.6	1043.1	1028.9	2349.125	1149.325	-1.0371765	-2.0522074	0.04812586
226178	A_55_P2136957	D19Wsu162e	DNA segment, Chr 19, Wayne	NM_001177812	33462.4	28041.7	33552	31296.3	15851.9	15207	15208.6	15116	31588.1	15345.875	-1.0380376	-2.0534326	0.00400041
71901	A_55_P2039125	2310028H24Rik	RIKEN cDNA 2310028H24 gen	NM_001159583	143.8	148.2	131.6	146.6	73.1	71.5	61.6	71.4	142.55	69.4	-1.0401743	-2.056476	0.00571487
74178	A_55_P2090880	Stk40	serine/threonine kinase 40	NM_001145827	14952.1	13654.9	13938.9	14523.5	6734.6	6784.7	7035.3	7187.3	14267.35	6935.475	-1.0402615	-2.0566004	0.00089241
66461	A_55_P1969831	Ptpmt1	protein tyrosine phosphatase	NM_025576	10041.7	10045.3	9399.4	8734.6	4855.4	4519.7	4547	4576.6	9555.25	4624.675	-1.0451706	-2.0636103	0.00220266
226041	A_65_P17602	Pgm5	phosphoglucomutase 5	NM_175013	374.2	301	354.3	330.3	147.1	196.7	160.2	155	339.95	164.75	-1.0493462	-2.0695918	0.06519455
72310	A_55_P2009582	Nkg7	natural killer cell group 7 seq	NM_024253	117.3	96.9	108.2	114.9	51.6	48.4	49.5	62.3	109.325	52.95	-1.0493811	-2.0696418	0.03811706
18028	A_55_P2086692	Nfib	nuclear factor I/B	NM_001113209	2087.6	1911.5	1890.8	2163.5	974	1014	971.9	922.1	2013.35	970.5	-1.051247	-2.0723204	0.0023274
12877	A_55_P2074631	Cpeb1	cytoplasmic polyadenylation	NM_007755	860.4	938.2	1052.5	854.6	439	498.3	409.1	439.7	926.425	446.525	-1.051423	-2.0725732	0.01999893
71921	A_55_P2373852	2310058N22Rik	RIKEN cDNA 2310058N22 gen	AK009987	898.1	897.3	915.8	1082.6	466.9	539.4	421.9	407.2	948.45	458.85	-1.0517049	-2.0729782	0.05786198
68036	A_52_P194805	Zfp706	zinc finger protein 706	NM_026521	3672.3	3843.1	3664.1	3591.2	1610	1785.8	1862.7	1876.1	3692.675	1783.65	-1.052029	-2.0734439	0.00225112
240168	A_52_P198435	Rasgrp3	RAS, guanyl releasing protein	NM_207246	608.5	573.3	590.7	548.1	276.9	282.4	262.1	297.9	580.15	279.825	-1.0523404	-2.0738915	0.00167427
30928	A_55_P1974892	Zfp238	zinc finger protein 238	NM_013915	4953	5158.4	4647.9	4681.7	2775.9	2282	1964.5	2404	4860.25	2356.6	-1.0539961	-2.0762729	0.04885901
68691	A_51_P441387	1110028C15Rik	RIKEN cDNA 1110028C15 gen	NM_177645	395.4	416	416.2	468.3	190.3	207.1	195.6	223.4	423.975	204.1	-1.0546169	-2.0771666	0.00645664
227154	A_52_P145349	Stradb	STE20-related kinase adaptor	NM_172656	1989.4	1855	1741.1	1820.4	930	863.2	888.9	879.4	1851.475	890.375	-1.0550633	-2.0778094	0.00131529
57320	A_55_P1981550	Park7	Parkinson disease (autosomal	NM_020569	40062.6	41109.6	44696	39022.1	20218.2	19994.3	19703.8	19324.3	41222.575	19810.15	-1.0555088	-2.0784511	0.00121269
12345	A_55_P2064995	Capzb	capping protein (actin filamer	NM_001037761	1738.7	1864.8	2027.9	1990.9	948.9	984	868.9	863.6	1905.575	916.35	-1.0559205	-2.0790442	0.0050321
230779	A_55_P1953758	Serinc2	serine incorporator 2	NM_172702	4286.2	3532.1	4221.8	3897	1785.6	1834.1	2041.5	1993	3984.275	1913.55	-1.0560988	-2.0793012	0.00931392
73919	A_55_P2152886	Lyrm1	LYR motif containing 1	NM_029610	170	186	195.6	191.5	84.8	81.1	98.5	93.3	185.775	89.425	-1.0570084	-2.0806126	0.00857654
107239	A_55_P2146520	Carns1	carnosine synthase 1	NM_134148	1322.5	1329.3	1356.3	1352.5	657.1	649.2	574.3	696.7	1340.15	644.325	-1.0599584	-2.0848714	0.0027457
170737	A_52_P17112	Znrf1	zinc and ring finger 1	NM_133206	507.2	479.5	563	542.1	219.1	228.7	281.6	276.3	522.95	251.425	-1.0627127	-2.0888555	0.03937771
11482	A_55_P2011380	Acvrl1	activin A receptor, type II-like	NM_009612	764	796	744.9	895.2	341.8	418.9	366.4	405.5	800.025	383.15	-1.0631795	-2.0895315	0.01597398
100504486	A_55_P2243431	Gdap10	ganglioside-induced different	BC052902	1257.3	1590.7	1378.2	1519.7	816.7	645.7	670.6	620.5	1436.475	688.375	-1.0636802	-2.0902569	0.06452053
218952	A_55_P2012349	Fermt2	fermitin family homolog 2 (Dr	NM_146054	7034.7	7636.7	6946.1	6956.1	3905.3	3496.2	3072.3	3239.5	7143.4	3428.325	-1.0639022	-2.0905785	0.01036265
74048	A_51_P372992	4632428N05Rik	RIKEN cDNA 4632428N05 gen	NM_028732	467.6	482.1	565.8	421.4	218.3	257.7	243.7	204.6	484.225	231.075	-1.0650432	-2.0922325	0.06334198
26374	A_55_P2022104	Rfwd2	ring finger and WD repeat do	NM_011931	791.7	889.6	796.4	1005.3	461.1	400.8	430.4	368.7	870.75	415.25	-1.0662676	-2.0940089	0.03992881
12984	A_51_P146753	Csf2rb2	colony stimulating factor 2 re	NM_007781	165.3	137.8	142.5	135.4	67.1	68.9	73.7	67	145.25	69.175	-1.0667305	-2.094681	0.00597635
83814	A_55_P2030756	Nedd4l	neural precursor cell express	NM_031881	321.7	260	342.9	282.2	138.8	136.9	150.3	146.4	301.7	143.1	-1.0687107	-2.097558	0.02183975
13405	A_55_P2167930	Dmd	dystrophin, muscular dystrop	ENSMUST00000156107	391.9	351.9	347.3	448.2	164.8	196.7	195	174.8	384.825	182.825	-1.0700209	-2.0994638	0.03667418
15983	A_51_P172251	Ifrd2	interferon-related developme	NM_025903	1422.6	1238.2	1430.2	1352.6	593	639.9	676.9	676.4	1360.9	646.55	-1.0734353	-2.1044384	0.00372226
13120	A_55_P2117959	Cyp4b1	cytochrome P450, family 4, su	NM_007823	237.7	241.3	291.2	270.6	110.3	150.5	116.3	119.3	260.2	124.1	-1.0736251	-2.1047154	0.07671034
22240	A_55_P2042487	Dpysl3	dihydropyrimidinase-like 3	NM_009468	817.6	802.7	758.6	842.9	327.5	422.6	450.4	342.4	805.45	385.725	-1.0743199	-2.1057292	0.0627329
56228	A_55_P1990608	Ube2j1	ubiquitin-conjugating enzyme	NM_019586	553.7	469.1	555.5	533.3	234.4	260.5	283.1	226.2	527.9	251.05	-1.0746419	-2.1061992	0.01835336
226646	A_51_P393761	Ndufs2	NADH dehydrogenase (ubiqui	NM_153064	8836	9576.2	9547.7	8861.3	4489.7	4576.2	4050.7	4359.9	9205.3	4369.125	-1.0755707	-2.1075556	0.00144007
17112	A_51_P240614	Tm4sf1	transmembrane 4 superfamil	NM_008536	2057.7	2323.7	1910.1	2182.2	848.7	1201.2	1039.8	948.7	2118.425	1009.6	-1.0771888	-2.1099207	0.07762734
209086	A_55_P2151601	Samd9l	sterile alpha motif domain co	NM_010156	583.6	510.6	571.2	535.9	247.5	281.1	258.6	255.7	550.325	260.725	-1.0773617	-2.1101736	0.00234698
56403	A_52_P80806	Syncrip	synaptotagmin binding, cytop	NM_019796	2836.7	2942.2	2918.7	3055.8	1431	1435.2	1472.6	1239.9	2938.35	1394.675	-1.07778	-2.1107856	0.00258059
105450	A_51_P414396	Mmrn2	multimerin 2	NM_153127	9016.6	8022.7	7197.6	9114.8	3879	3908	3769.1	4175.8	8337.925	3932.975	-1.0785026	-2.111843	0.01182628
12142	A_55_P2027022	Prdm1	PR domain containing 1, with	NM_007548	47	37.3	40.9	38	19.1	20.4	19.2	18.3	40.8	19.25	-1.0787112	-2.1121484	0.00947366
59043	A_55_P1998384	Wsb2	WD repeat and SOCS box-con	NM_021539	629.2	563.4	714.6	730.2	353.4	268.7	286.4	336.8	659.35	311.325	-1.083971	-2.1198629	0.09692783
317677	A_55_P2150179	Gm5077	predicted gene 5077	NM_173864	2006.4	2094.2	2479.8	1903.4	968.7	1079.5	1037.3	904.8	2120.95	997.575	-1.0842055	-2.1202075	0.02440616
211586	A_55_P2073705	Tfdp2	transcription factor Dp 2	NM_178667	1378.2	1192.6	1193.4	1018.9	619.3	490.2	539.1	604.3	1195.775	563.225	-1.0842178	-2.1202256	0.06255033
629557	A_55_P2136832	Gm6981	glyceraldehyde-3-phosphate	NR_023357	48492.3	40532.4	43203.4	38943.7	19193.4	18813.8	22276.6	20278.5	42792.95	20140.575	-1.0853711	-2.1219213	0.01256122
21366	A_52_P339996	Slc6a6	solute carrier family 6 (neuro	NM_009320	3854.1	4178.9	3535.7	4063.6	1882.3	2008.2	1704.5	1768.6	3908.075	1840.9	-1.0859789	-2.1228154	0.00557751
242864	A_55_P2024406	Napepld	N-acyl phosphatidylethanolar	NM_178728	1150	1054.9	1281.7	1335.9	570.4	644.6	559.4	496.9	1205.625	567.825	-1.0862773	-2.1232545	0.03869303
639396	A_52_P352362	Gm7265	predicted gene 7265	XR_105293	970.5	736.4	886.4	927.3	355.6	427.9	419.1	452.5	880.15	413.775	-1.0868676	-2.1241235	0.05221211
208439	A_52_P348250	Klhl29	kelch-like 29 (Drosophila)	NM_001164493	79.8	70.8	74	66.6	31.4	38.2	36.5	31.2	72.8	34.325	-1.0873515	-2.124836	0.01617299
14009	A_66_P135185	Etv1	ets variant gene 1	NM_007960	1264.6	1188.5	934.7	1173.6	530.4	537.1	493.1	571.6	1140.35	533.05	-1.0899735	-2.1287012	0.03098419
66101	A_55_P2004636	Ppih	peptidyl prolyl isomerase H	NM_028677	448.7	485	481.1	447.5	223.3	203.5	223.7	224.2	465.575	218.675	-1.0903992	-2.1293295	0.0010253
330189	A_55_P2019014	Tmem120b	transmembrane protein 120B	NM_001039723	1652.6	1417.8	1542.6	1416.9	784.9	644.3	637.7	767.6	1507.475	708.625	-1.092683	-2.1327029	0.01900738
23945	A_55_P2114863	Mgll	monoglyceride lipase	NM_001166251	1809.5	1649.5	1761.2	1739.6	691.8	957.9	806.7	822.9	1739.95	819.825	-1.0944168	-2.1352675	0.02297391
60322	A_51_P229925	Chst7	carbohydrate (N-acetylglucos	NM_021715	309.1	352.1	347.4	311.6	141.8	160.5	167.4	148.5	330.05	154.55	-1.0950396	-2.1361895	0.00500182
69270	A_51_P337089	Gins1	GINS complex subunit 1 (Psf1	NM_027014	142.1	160.4	138.2	115.5	63.7	67	63.9	63.9	139.05	64.625	-1.0959643	-2.1375591	0.02191888
57259	A_52_P70854	Tob2	transducer of ERBB2, 2	NM_020507	4246.4	4206.4	3521.3	4957.3	2221.9	1777.7	1794.6	2104.3	4232.85	1974.625	-1.0964201	-2.1382346	0.09554694
103844	A_52_P320279	Inca1	inhibitor of CDK, cyclin A1 int	NM_213729	112.8	107.2	107.4	110.4	46.2	53	45.8	60.8	109.45	51.45	-1.0985536	-2.1413989	0.02006586
73429	A_51_P269053	1700109F18Rik	RIKEN cDNA 1700109F18 gen	NR_027899	146.9	145.6	171	144.3	74.4	67.8	70.1	70.8	151.95	70.775	-1.0994683	-2.142757	0.00280151
102103	A_55_P2090798	Mtus1	mitochondrial tumor suppres	NM_001005863	1863.4	1732.2	1803.7	1907.7	892.4	878	819.3	819.6	1826.75	852.325	-1.0999564	-2.1434822	0.00085001
24056	A_55_P2049479	Sh3bp5	SH3-domain binding protein 5	ENSMUST00000100730	1499.8	1424	1505.2	1530.4	710.7	841.8	640.2	607.7	1489.85	700.1	-1.1004239	-2.1441768	0.03037479
57752	A_55_P2004797	Tacc2	transforming, acidic coiled-co	NM_001004468	44496.4	41170.3	48732.7	36700.2	17397.9	23644.1	19791.4	18969.6	42774.9	19950.75	-1.1017536	-2.146154	0.0837204
17850	A_65_P15689	Mut	methylmalonyl-Coenzyme A m	NM_008650	3570.3	2738.2	3056.6	2779.1	1424.8	1266.9	1377.5	1571.2	3036.05	1410.1	-1.1024594	-2.1472041	0.03473653
26556	A_66_P104134	Homer1	homer homolog 1 (Drosophila	NM_147176	446.1	370.1	477.1	426.2	214.3	181.4	194.4	208.4	429.875	199.625	-1.1034787	-2.1487218	0.01581373
67160	A_55_P2085157	Eef1g	eukaryotic translation elonga	NM_026007	8560.4	7707.4	8579.1	7737.7	3624.6	4194.7	3708.2	3639.6	8146.15	3791.775	-1.1039413	-2.1494109	0.00299698
21817	A_52_P220879	Tgm2	transglutaminase 2, C polype	NM_009373	8448.1	7969.4	8648.9	7764	4010.3	4054.7	3951.8	3293.1	8207.6	3827.475	-1.1042883	-2.1499279	0.00673541
16438	A_55_P2008066	Itpr1	inositol 1,4,5-trisphosphate re	NM_010585	2037.5	2332.2	2158.6	2093.7	1079.7	1045.9	862.2	1031.3	2155.5	1004.775	-1.1046771	-2.1505074	0.00884077
76916	A_55_P1975095	4930455C21Rik	RIKEN cDNA 4930455C21 gen	BC002243	259.2	232.3	203	232.7	108	98.6	100.8	123.8	231.8	107.8	-1.104952	-2.1509172	0.02548838
209039	A_51_P395473	Tenc1	tensin like C1 domain-contain	NM_153533	671.6	628.1	621.3	495.1	274.9	326.9	275.7	244.1	604.025	280.4	-1.1058197	-2.1522112	0.08876498
11480	A_52_P664656	Acvr2a	activin receptor IIA	NM_007396	115.9	113.3	136.1	126.6	52	57.2	70.4	50.2	122.975	57.45	-1.1069739	-2.1539338	0.07396412
70052	A_55_P2115003	Prpf4	PRP4 pre-mRNA processing fa	NM_027297	1832.5	1761.4	1768.8	2236.4	895.9	819.4	912.8	883.8	1899.775	877.975	-1.1075683	-2.1548213	0.01111991
20315	A_55_P1966204	Cxcl12	chemokine (C-X-C motif) ligan	NM_021704	544.5	611.3	631	730.1	255.4	335.8	304.8	270.6	629.225	291.65	-1.1095403	-2.1577688	0.06866157
57776	A_55_P1956448	Ttyh1	tweety homolog 1 (Drosophil	NM_021324	118.3	148.9	134.2	116.9	59.9	68.6	62.7	49.3	129.575	60.125	-1.110837	-2.1597091	0.08958741
18451	A_55_P2097808	P4ha1	procollagen-proline, 2-oxoglu	NM_011030	581.8	673	569.5	611.7	299.4	257.5	288.9	281.2	609	281.75	-1.1112091	-2.1602662	0.00378508
21676	A_51_P214423	Tead1	TEA domain family member 1	NM_001166584	11445.2	11971	11071.6	10876.2	5971.1	5357.1	4823.6	4902.6	11341	5263.6	-1.1117327	-2.1610504	0.00542932
224650	A_55_P2064567	Anks1	ankyrin repeat and SAM dom	NM_181413	110.8	121.9	129.1	94.8	49.1	52.1	57.4	51.5	114.15	52.525	-1.1125467	-2.16227	0.03117852
15499	A_55_P2035593	Hsf1	heat shock factor 1	NM_008296	1792	1799.1	1688.6	1875	826.2	768.4	834.7	879.4	1788.675	827.175	-1.1132877	-2.1633809	0.00110922
268977	A_55_P1973033	Ltbp1	latent transforming growth fa	NM_019919	305	349.4	280.3	265.3	132.5	145.5	150.7	124.2	300	138.225	-1.1142323	-2.1647978	0.02940281
66109	A_51_P256246	Tspan13	tetraspanin 13	NM_025359	2818.9	2939.5	2704.9	3343.1	1331.4	1400.3	1397.1	1308.8	2951.6	1359.4	-1.1145262	-2.1652389	0.00362286
16909	A_55_P2083988	Lmo2	LIM domain only 2	NM_008505	509.5	552.5	535.6	539.6	253.7	296.4	239.1	205.5	534.3	248.675	-1.1151704	-2.1662059	0.03709641
52715	A_51_P174720	Ccdc43	coiled-coil domain containing	NM_025918	337.9	363.4	363.2	384.5	147.7	168.6	158.5	194.7	362.25	167.375	-1.1199731	-2.1734292	0.01296018
74136	A_55_P2125778	Sec14l1	SEC14-like 1 (S. cerevisiae)	NM_028777	185.7	186.1	218.7	244.5	99.3	105.7	92.3	85.3	208.75	95.65	-1.1207446	-2.1745918	0.04685044
74143	A_55_P1964842	Opa1	optic atrophy 1 homolog (hur	NM_001199177	1988.9	2437.4	2049	2108.5	1094	963.8	864.2	1023	2145.95	986.25	-1.1224473	-2.1771597	0.01608712
104418	A_55_P2059318	Dgkz	diacylglycerol kinase zeta	NM_001166597	2550.6	2647.4	2779	3323	1264.1	1375.9	1206.6	1322.4	2825	1292.25	-1.1224682	-2.1771913	0.01341286
15980	A_52_P471395	Ifngr2	interferon gamma receptor 2	NM_008338	5220.8	3999.9	5645.7	4769.7	2089.8	2362.4	2299.5	2198.7	4909.025	2237.6	-1.1234242	-2.1786345	0.03816114
12390	A_51_P279552	Cav2	caveolin 2	NM_016900	660.7	710.1	661.5	648.4	287.6	325.1	346.4	274.9	670.175	308.5	-1.1245874	-2.1803918	0.00681524
216150	A_55_P2027312	Cdc34	cell division cycle 34 homolog	NM_177613	70119.1	71245.4	70219.9	65332.6	32453.7	31645.6	31718.1	31076.2	69229.25	31723.4	-1.1251958	-2.1813114	0.00035263
99003	A_51_P338961	Qser1	glutamine and serine rich 1	NM_001123327	2955.1	2547.7	2813.3	2714.7	1238	1139.1	1436.5	1251.6	2757.7	1266.3	-1.1258053	-2.1822333	0.00686958

22145	A_52_P676271	Tuba4a	tubulin, alpha 4A	NM_009447	39896.3	44760.9	43931.5	34175.6	18074.6	17276.4	18956	19970.5	40691.075	18569.375	-1.1258563	-2.1823103	0.01806832
67669	A_51_P251717	l7Rn6	lethal, Chr 7, Rinchik 6	NM_026304	2454.4	2471	2464.4	2470.7	1196.3	1095.8	1158.5	1068.5	2465.125	1129.775	-1.1270532	-2.1841217	0.0004738
207181	A_55_P2341468	Rbms3	RNA binding motif, single stra	NM_001172123	928.1	945.4	818.1	1015.1	377.4	487.8	399.4	432.1	926.675	424.175	-1.1298621	-2.1883783	0.02108315
66387	A_51_P490388	Nudt8	nudix (nucleoside diphosphat	NM_025529	773.8	763.7	720	706.6	335.1	336.1	352.9	329.6	741.025	338.425	-1.1300999	-2.1887389	0.00049171
22341	A_51_P433870	Vegfc	vascular endothelial growth fa	NM_009506	194	256.8	200	214.7	95.8	102.7	90.6	104.5	216.375	98.4	-1.1303511	-2.1891201	0.02014328
211623	A_55_P1966332	Plac9	placenta specific 9	NM_207229	1291.8	1249	1138.5	918.5	486.4	588.6	538	471.7	1149.45	521.175	-1.134362	-2.1952146	0.08499129
103466	A_51_P507023	Nt5dc3	5-nucleotidase domain contai	NM_175331	10366.1	8620.5	10137.4	9963.3	4397	4193.4	4329.1	4861.1	9771.825	4445.15	-1.1349556	-2.196118	0.00427546
228836	A_55_P2074206	Dlgap4	discs, large homolog-associat	NM_146128	3420.9	2704.3	3647.9	2989.2	1346.1	1347.8	1630.8	1464	3190.575	1447.175	-1.1353923	-2.1967829	0.04139403
229613	A_55_P1968544	6330549D23Rik	RIKEN cDNA 6330549D23 gen	NR_003619	53.3	65.5	58.9	72.1	26.1	26.8	27.7	32.8	62.45	28.35	-1.1360082	-2.1977209	0.04772601
214424	A_52_P206925	Parp16	poly (ADP-ribose) polymerase	NM_177460	145.9	154.7	131.4	146.6	74.2	55.9	70.7	63.5	144.65	66.075	-1.1363204	-2.1981966	0.0202998
666317	A_55_P2183208	Prl2c1	Prolactin family 2, subfamily c	NM_001045532	443.2	362.8	347.5	352.1	193.5	174.8	158.8	156.7	376.4	170.95	-1.1367189	-2.1988039	0.02643825
74013	A_51_P245631	Rftn2	raftlin family member 2	NM_028713	205.6	238	193.6	232	85.4	97.3	101.9	110.3	217.3	98.725	-1.1391498	-2.2025118	0.02170898
12362	A_55_P1990944	Casp1	caspase 1	NM_009807	174.7	156.1	161.3	150.5	71.2	76.9	83.3	61.6	160.65	73.25	-1.1396162	-2.203224	0.02007455
22724	A_51_P473229	Zbtb7b	zinc finger and BTB domain co	NM_009565	371.7	343.3	377.8	361.9	173.2	151.2	170.2	166	363.675	165.15	-1.1398778	-2.2036235	0.00105229
23950	A_55_P2013188	Dnajb6	DnaJ (Hsp40) homolog, subfa	NM_001037940	10002.3	10356.9	11183.4	11929.8	4539	4881.3	5168.8	5113.7	10868.1	4925.7	-1.1401821	-2.2040884	0.00311546
99929	A_51_P514961	Tiparp	TCDD-inducible poly(ADP-ribo	NM_178892	2093.5	2284.2	1991	1849.2	920.9	964.3	873.1	961.9	2054.475	930.05	-1.1402881	-2.2042504	0.00334142
52398	A_66_P118513	11-Sep	septin 11	NM_001009818	4552.3	4404.6	4141.3	4504.2	1973.1	2315.8	1774.2	1951.6	4400.6	2003.675	-1.1407901	-2.2050175	0.00721576
75689	A_55_P2111523	Higd1b	HIG1 domain family, member	NM_080846	1138.2	1115.3	1074.9	1047.5	537.8	518.3	492.8	439.4	1093.975	497.075	-1.1414142	-2.2059715	0.00268995
269060	A_52_P127682	Dagla	diacylglycerol lipase, alpha	NM_198114	117.7	103.5	128.5	137.4	49.5	49.4	57.5	64.5	121.775	55.225	-1.1419518	-2.2067937	0.06753968
93765	A_55_P2075769	Ube2n	ubiquitin-conjugating enzyme	NM_080560	2439.2	2467	2333.2	2514.1	1187.9	1089.9	1061.8	1082.5	2438.375	1105.525	-1.1420074	-2.2068788	0.00056712
13132	A_55_P1977473	Dab2	disabled homolog 2 (Drosoph	NM_023118	812.6	928	812.1	831.7	360.3	437	426.6	318.9	846.1	385.7	-1.1428927	-2.2082334	0.03872373
19094	A_52_P168449	Mapk11	mitogen-activated protein kin	NM_011161	62	56.9	58.6	45.9	24.4	27.5	27.3	21.7	55.85	25.225	-1.1442957	-2.210382	0.05577341
72691	A_51_P326994	Calhm2	calcium homeostasis modulat	NM_133746	81.8	68.8	79.3	78.2	30	36.2	40.9	32.9	77.025	35	-1.1444646	-2.2106407	0.02796975
21846	A_51_P177171	Tie1	tyrosine kinase with immunog	NM_011587	205.2	234.8	226.8	228.3	87.9	107	114.5	96.4	223.775	101.45	-1.146704	-2.2140749	0.01137855
15896	A_55_P1982049	Icam2	intercellular adhesion molecu	NM_010494	2514.2	2894.6	3456.5	2924.2	1222.4	1437.1	1257.7	1381.6	2947.375	1324.7	-1.1477032	-2.2156088	0.02539067
11479	A_52_P373893	Acvr1b	activin A receptor, type 1B	ENSMUST00000000544	1782.8	1565.4	1749.7	1499.7	696.5	772.4	679.8	829.1	1649.4	744.45	-1.1485105	-2.216849	0.00905078
286940	A_52_P222350	Flnb	filamin, beta	NM_134080	362.9	320	372.7	299.2	153.1	151.4	154.2	149.2	338.7	151.975	-1.1504698	-2.2198617	0.00381942
29856	A_55_P2065824	Smtn	smoothelin	NM_001159284	7758.4	7753.9	7834.4	7739.3	3388.2	3609.9	3380.1	3620.2	7771.5	3499.6	-1.1517735	-2.2218686	0.00025441
107328	A_55_P1960641	Trpt1	tRNA phosphotransferase 1	NM_153597	2367.3	2670.1	2354.3	2483.7	1107.3	1083.4	1133.6	1113.6	2468.85	1109.475	-1.1522926	-2.2226682	0.00057513
77264	A_55_P2072080	Zfp142	zinc finger protein 142	NM_029888	279.4	349.6	294.9	393.3	160.6	145	128	154.8	329.3	147.1	-1.1544548	-2.2260018	0.08068195
22370	A_51_P109840	Vtn	vitronectin	NM_011707	969	911.6	917.8	925.7	384.8	446.8	442.1	400.8	931.025	418.625	-1.1556572	-2.2278579	0.00115934
213491	A_55_P2116290	D4Ertd22e	DNA segment, Chr 4, ERATO D	NM_001025608	1162.5	1498	1115.2	1195.3	481	646.5	551.9	547.8	1242.75	556.8	-1.1564781	-2.2291259	0.06428887
259097	A_55_P2169039	Olfr558	olfactory receptor 558	NM_147093	171.6	167.3	171.9	190.5	67	93.1	74.6	81.6	175.325	79.075	-1.1574682	-2.2306563	0.02356485
72017	A_51_P438527	Cyb5r1	cytochrome b5 reductase 1	NM_028057	3496	3287.5	3395.9	3232.2	1525.1	1519.4	1614.2	1357.2	3352.9	1503.975	-1.1587871	-2.2326964	0.00124131
71207	A_55_P2097309	Nudt4	nudix (nucleoside diphosphat	NM_027722	3694.7	2981	3344.1	3374.8	1618.8	1560.9	1286.8	1530.6	3348.65	1499.275	-1.1606214	-2.235537	0.01235487
433904	A_55_P2128511	Ociad2	OCIA domain containing 2	NM_026950	1019.1	970.4	1253.8	1179.4	474.9	414.4	594.2	499.5	1105.675	495.75	-1.1614847	-2.2368751	0.09162591
231086	A_55_P2073294	Hadhb	hydroxyacyl-Coenzyme A deh	NM_145558	21160.6	22481.4	19580	24573.3	10354.6	9973.7	9117.2	9699.2	21948.825	9786.175	-1.161878	-2.2374849	0.00437564
60345	A_55_P2161702	Nrip2	nuclear receptor interacting p	NM_021717	80.6	79.9	111.9	94.3	37.6	41.7	44.4	38.9	91.675	40.65	-1.1623153	-2.2381634	0.05426329
100040872	A_55_P1964902	Gm3014	predicted gene 3014	ENSMUST00000110280	250.1	296.5	238.7	348.4	133	134	115.8	119	283.425	125.45	-1.1625561	-2.2385369	0.08204656
13631	A_51_P461504	Eef2k	eukaryotic elongation factor-2	NM_007908	549.6	482.3	608	483.4	255.6	243.4	211.7	235.5	530.825	236.55	-1.1626591	-2.2386967	0.01354432
16443	A_55_P2431118	Itsn1	intersectin 1 (SH3 domain pro	NM_001110275	1862.7	1646.1	1881.6	2236.5	791.9	856.8	864.9	874.8	1906.725	847.1	-1.1628998	-2.2390702	0.01175009
72630	A_51_P130332	Hspa12b	heat shock protein 12B	NM_028306	882.7	1014.1	876.7	957.7	386	428.8	396.9	453.5	932.8	416.3	-1.1642311	-2.2411374	0.00294298
12908	A_55_P1983314	Crat	carnitine acetyltransferase	NM_007760	167.8	128.9	171.6	153.6	68.8	62.9	62.2	83.7	155.475	69.4	-1.1653311	-2.2428468	0.08313562
16777	A_66_P101600	Lamb1	laminin B1	NM_008482	3305.5	3845.8	4483	3176.5	1470.2	1805.4	1754.6	1535.1	3702.7	1641.325	-1.1655623	-2.2432062	0.07599774
14559	A_51_P464300	Gdf1	growth differentiation factor	NM_008107	5717.1	4841.8	6295.6	5379.8	2281.7	2265.4	2381.5	3006.5	5558.575	2483.775	-1.1657232	-2.2434566	0.04975657
16970	A_51_P130079	Lrmp	lymphoid-restricted membran	NM_008511	48.2	48.8	51.7	42.8	21.2	25.6	21.1	17.9	47.875	21.45	-1.1665697	-2.2447732	0.03902027
74319	A_55_P1980966	1110005A03Rik	RIKEN cDNA 1110005A03 gen	NM_028865	3714.6	3856.7	4412.1	4477.5	1720.9	1825.4	1927.4	1838.5	4115.225	1828.05	-1.1670429	-2.2455096	0.00340963
56449	A_55_P1960566	Csda	cold shock domain protein A	NM_139117	85406.5	92210.7	87787.3	92991.1	38473.8	44073.3	38232.7	38919	89598.9	39924.7	-1.1678305	-2.2467358	0.00107426
676974	A_55_P2073789	LOC676974	glucose-6-phosphate isomera	XM_001003154	15070.6	14360.1	13084.2	15703.9	6672.4	6090.4	6440.8	6648.8	14554.7	6463.1	-1.1688468	-2.248319	0.00168305
67834	A_51_P268559	Idh3a	isocitrate dehydrogenase 3 (N	NM_029573	15991.9	19819.7	16160.3	16128.3	7680.9	7840.5	6623.9	8079.8	17025.05	7556.275	-1.1699539	-2.2500451	0.01251747
16452	A_55_P1971458	Jak2	Janus kinase 2	NM_008413	2529.1	2948.3	2839.1	2613.6	1268.7	1226.1	1118.8	1238.8	2732.525	1213.1	-1.1704141	-2.2507629	0.00172642
69908	A_55_P2125311	Rab3b	RAB3B, member RAS oncogen	NM_023537	35.7	33.3	28.3	29.1	12.4	17	14.2	12.7	31.6	14.075	-1.1716683	-2.2527204	0.06243059
12785	A_51_P448203	Cnbp	cellular nucleic acid binding p	NM_013493	15518.4	16442.1	15232.9	15749.9	6976.8	6557.8	7162.6	7181.6	15735.825	6969.7	-1.1752635	-2.2583412	0.00035994
17540	A_52_P409769	Mrvi1	MRV integration site 1	NM_194464	254.1	218.8	281.3	245.1	104.2	118.3	128.5	93	249.825	111	-1.1754032	-2.2585599	0.05106807
78244	A_51_P439857	Dnajc21	DnaJ (Hsp40) homolog, subfa	NM_030046	2346.7	2513.7	2303.5	2416.4	1093.3	1116	999.5	1029.5	2395.075	1059.575	-1.177221	-2.2614076	0.00053926
103710	A_55_P1964787	Slc35e4	solute carrier family 35, mem	NM_153142	4540.5	4384	4840.7	4616	2108.2	2063.2	1885.8	2068.8	4595.3	2031.5	-1.1780229	-2.2626648	0.00055412
414093	A_55_P2217230	A830082N09Rik	RIKEN cDNA A830082N09 gen	AK136944	506.3	630.6	465.5	605	252.1	272.4	228.6	217.6	551.85	242.675	-1.1795518	-2.265064	0.04938913
67095	A_51_P437021	Trak1	trafficking protein, kinesin bin	NM_175114	1163.8	1065.8	1255.9	1043	433.4	503.6	510.8	551.3	1132.125	499.775	-1.1810949	-2.2674879	0.0096249
215280	A_52_P637282	Wipf1	WAS/WASL interacting protei	NM_153138	404.1	384.5	380.5	381.7	154.6	205.1	176.4	152.3	387.7	172.1	-1.1818493	-2.268674	0.01393406
108927	A_51_P505868	Lhfp	lipoma HMGIC fusion partner	NM_175386	271	280.9	266.9	277.8	107.2	153.1	111.8	115.9	274.15	122	-1.1825289	-2.2697429	0.03125488
353169	A_55_P2146555	Slc2a12	solute carrier family 2 (facilita	ENSMUST00000042261	1400.1	1508.1	1417.1	1723	705.9	628.2	636	685.2	1512.075	663.825	-1.1843997	-2.2726881	0.00386569
68758	A_55_P1967504	Abhd11	abhydrolase domain containin	NM_145215	2783.4	2891.2	2715.7	2159.4	1239.7	1108.9	1036.8	1236.7	2637.425	1155.525	-1.1856794	-2.274705	0.02562023
68316	A_55_P2092776	Apoo	apolipoprotein O	NM_001199337	9385.5	10103.4	9340.7	8864.3	4108	3923.6	4283.5	4243.8	9423.475	4139.725	-1.1859948	-2.2752022	0.0005724
21934	A_55_P2325803	Tnfrsf11a	tumor necrosis factor recepto	NM_009399	259.2	279.3	242.9	244.6	108.4	117.2	116.9	107.7	256.5	112.55	-1.1872594	-2.2771975	0.00097615
226251	A_52_P489778	Ablim1	actin-binding LIM protein 1	NM_178688	298	374.3	369	347.3	145.6	183.2	145.6	136	347.15	152.6	-1.1895659	-2.2808411	0.03421271
56222	A_52_P426768	Cited4	Cbp/p300-interacting transac	NM_019563	739.5	543.6	652	492.3	279.2	257.3	260.4	251.7	606.85	262.15	-1.1940801	-2.2879889	0.0662413
378954	A_55_P2091247	3000002C10Rik	glyceraldehyde-3-phosphate d	BC024703	100073.9	85078.6	98601.4	78362.2	37480.5	38155.5	42793.6	39000	90529.025	39357.4	-1.1961639	-2.2912962	0.00872915
100705	A_55_P2104532	Acacb	acetyl-Coenzyme A carboxyla	NM_133904	483.7	587.4	594.6	568.8	253.9	240.5	212.3	266.9	558.625	243.4	-1.1988989	-2.295644	0.01053814
56176	A_55_P2084332	Pigp	phosphatidylinositol glycan an	NM_001159620	77.1	90	96.8	87.3	35.6	40.2	44.1	33.3	87.8	38.3	-1.2005677	-2.298301	0.0223638
18214	A_51_P267796	Ddr2	discoidin domain receptor fam	NM_022563	1134	1159.8	1264	1338.9	521.5	628.4	553.3	439.4	1224.175	535.65	-1.2010266	-2.2990321	0.03233521
56046	A_55_P2180425	Uqcc	ubiquinol-cytochrome c reduc	NM_018888	1319	1287.1	1172.8	1185.2	482.1	535.2	538.1	599.1	1241.025	538.625	-1.2065717	-2.3078856	0.00275924
14862	A_55_P1966432	Gstm1	glutathione S-transferase, mu	NM_010358	2548.5	2088.3	2738.6	2093.2	962.1	1048.7	1143.5	924.1	2367.15	1019.6	-1.209672	-2.3128505	0.03083611
104130	A_55_P2073582	Ndufb11	NADH dehydrogenase (ubiqui	NM_019435	236.2	233.3	259.5	233.9	98	114.5	110.2	94.2	240.725	104.225	-1.2109243	-2.314859	0.00263608
21780	A_52_P351785	Tfam	transcription factor A, mitoch	NM_009360	119.7	143	138.3	145	66.1	57.5	59	53.1	136.5	58.925	-1.2123414	-2.3171339	0.00615632
213389	A_55_P2027052	Prdm9	PR domain containing 9	NM_144809	76.2	90	97.8	91	36.5	40	33.4	42.9	88.75	38.2	-1.2166737	-2.3241025	0.01646503
58916	A_55_P1960192	Myot	myotilin	NM_001033621	34842.5	31642.1	33354.6	34357	12636.8	14846	16538.2	13926	33549.05	14486.75	-1.2174737	-2.3253916	0.00472854
66141	A_51_P128876	Ifitm3	interferon induced transmem	NM_025378	1965.4	1861.3	1917.4	1563	793.7	863	847.8	644.6	1826.775	787.275	-1.2180581	-2.3263338	0.03115902
15415	A_52_P194971	Hoxb7	homeobox B7	NM_010460	156.1	144.2	136.3	141.6	51.3	73.6	68.4	57.4	144.55	62.675	-1.2182873	-2.3267034	0.03630972
241732	A_52_P144297	Tspyl3	TSPY-like 3	NM_198617	79.8	117.2	88	92	34.6	45.3	38.7	42.4	94.25	40.25	-1.2199365	-2.3293646	0.08508767
234797	A_55_P2149363	6430548M08Rik	RIKEN cDNA 6430548M08 gen	NM_172286	593	627.9	539.5	504.3	252.9	222.7	275	222	566.175	243.15	-1.2202031	-2.3297951	0.01139963
67088	A_51_P141071	Cand2	cullin-associated and neddyla	NM_025958	953.6	942.4	1021.5	865.4	394.3	421.8	396.1	406.8	945.725	404.75	-1.2224178	-2.3333743	0.00062494
16773	A_55_P2064328	Lama2	laminin, alpha 2	NM_008481	1644.2	1717.9	1822.9	1488.8	683.6	798.6	740.8	639.1	1668.45	715.525	-1.2225946	-2.3336603	0.00644728
57257	A_52_P613596	Vav3	vav 3 oncogene	NM_020505	40.1	50.2	43.8	42.2	17.4	24.2	18	16.5	44.075	19.025	-1.2237265	-2.3354921	0.07408966
16648	A_52_P680710	Kpna3	karyopherin (importin) alpha	NM_008466	5161.4	5562.7	5649.1	5580.1	2225.4	2456.8	2574	2138.8	5488.325	2348.75	-1.2275503	-2.3416903	0.00146245
16206	A_55_P2109997	Lrig1	leucine-rich repeats and imm	NM_008377	935.9	751.1	978.8	685.2	364.3	346	320.5	388.1	837.75	354.725	-1.2275617	-2.3417088	0.05790137
73296	A_52_P348720	Rhobtb3	Rho-related BTB domain cont	NM_028493	906.5	883.5	1032.7	1036.1	421.4	397.8	410.4	413.6	964.7	410.8	-1.2281193	-2.3426141	0.00105202
26903	A_55_P1964183	Dysf	dysferlin	NM_001077694	4889.7	5375.2	5455.6	4857	2319.4	2190.8	2224.9	2042.3	5144.375	2194.35	-1.2286808	-2.3435259	0.00078357
12391	A_51_P255304	Cav3	caveolin 3	NM_007617	10800.8	10565.5	10581.5	8293.3	4028.7	4488.4	4692.8	3886.9	10060.275	4274.2	-1.2310473	-2.3473734	0.01612293
16523	A_52_P225898	Kcnj8	potassium inwardly-rectifying	NM_008428	340.2	313.1	324.3	376.6	162.5	145.3	145.3	124.8	338.55	144.475	-1.2313104	-2.3478014	0.00772698
67270	A_52_P40367	Mrpl42	mitochondrial ribosomal prot	NM_026065	3999.7	3765.8	3995.8	3287.9	1496.8	1557.5	1787.9	1548.3	3762.3	1597.625	-1.2346086	-2.3531749	0.00429435
13542	A_52_P234958	Dvl1	dishevelled, dsh homolog 1 (D	NM_010091	9104	7690.8	7970.4	7692	3587.7	3058.9	3286.4	3880.3	8114.3	3453.325	-1.2347242	-2.3533635	0.00644211
244886	A_55_P1959833	AI118078	expressed sequence AI118078	NM_172923	176.9	136.9	192.2	153.2	63.5	61.8	74.1	79.9	164.8	69.825	-1.2349403	-2.353716	0.06444139
73162	A_55_P2087923	Otud3	OTU domain containing 3	NM_028453	4557.2	3908	3935.2	3716.7	1784.6	1852.9	1661.3	1533.4	4029.275	1708.05	-1.2376512	-2.358143	0.00422071
26557	A_51_P352303	Homer2	homer homolog 2 (Drosophila	NM_011983	528.6	577.5	434.5	620.9	231.4	243.1	199.4	237	540.375	227.725	-1.2383058	-2.3592132	0.03703824
320878	A_55_P2131677	Mical2	microtubule associated mono	ENSMUST00000106647	31.8	43.7	34.6	32.1	15.8	14	14.9	15.1	35.55	14.95	-1.2386983	-2.3598551	0.01704054
19220	A_52_P153019	Ptgfr	prostaglandin F receptor	NM_008966	110.9	110.5	117.1	116.2	52.5	51.7	48.2	41	113.675	48.35	-1.2395576	-2.3612612	0.00351038
13136	A_55_P2101585	Cd55	CD55 antigen	NM_010016	3660.3	3936.5	4459.4	3608.2	1699.2	1616.1	1661.7	1631	3916.1	1652	-1.2403039	-2.3624829	0.00161917
107227	A_51_P213030	Macrod1	MACRO domain containing 1	NM_134147	17193.2	15227.4	14657.1	12904.1	6747.6	5949.8	6502.6	6070.6	14995.45	6317.65	-1.2413945	-2.3642695	0.00644487
242083	A_55_P1973011	Ppm1l	protein phosphatase 1 (forme	NM_178726	5870.4	5409	5608.7	5351.2	2160.7	2202.4	2420.4	2643.2	5559.825	2356.675	-1.2420608	-2.3653617	0.00179772
14815	A_55_P1967885	Nr3c1	nuclear receptor subfamily 3,	NM_008173	8376.5	8790.6	8455.4	11131	3816.1	3861.5	3737.8	4019.1	9188.375	3858.625	-1.2420928	-2.3654142	0.00805453
15958	A_51_P161021	Ifit2	interferon-induced protein wi	NM_008332	55.9	49	43.7	47.5	16.5	22.8	21.8	22.1	49.025	20.8	-1.2428291	-2.3666217	0.0406451
319801	A_55_P1979402	9630033F20Rik	RIKEN cDNA 9630033F20 gen	NM_177003	2747.3	2657.3	2931.5	2994	1217.9	1279	1189.7	1101.4	2832.525	1197	-1.2430851	-2.3670417	0.00079467
13518	A_51_P300434	Dst	dystonin	NM_134448	1937.2	1672.9	2131.2	1797.1	740.8	830.9	773.3	823.9	1884.6	792.225	-1.2460292	-2.371877	0.00336648
103213	A_51_P211131	Traf3ip2	TRAF3 interacting protein 2	NM_134000	87.1	83.7	74.2	67.3	28.2	38.4	36.8	28.8	78.075	33.05	-1.2468375	-2.3732063	0.06931685
18750	A_66_P105791	Prkca	protein kinase C, alpha	NM_011101	5724.7	5771.2	5488.1	5347.6	2074	2532.7	2435.2	2388.9	5582.9	2357.7	-1.2469477	-2.3733876	0.0012392
71765	A_51_P148122	Klhdc3	kelch domain containing 3	NM_027910	7683.9	6690.4	7508.2	6098	2908.1	2857.8	3048.8	2921.3	6995.125	2934	-1.2477251	-2.3746669	0.00254033
19201	A_55_P1983162	Pstpip2	proline-serine-threonine phos	NM_013831	1214.1	1201.9	1473.1	1287.3	542.3	538.9	548.7	542.2	1294.1	543.025	-1.2480422	-2.3751888	0.0012156
20112	A_55_P1986888	Rps6ka2	ribosomal protein S6 kinase, p	NM_011299	64.2	67.9	61.5	69.2	32.5	29.6	24	25.2	65.7	27.825	-1.2487121	-2.3762919	0.01286564
20474	A_55_P2041095	Six4	sine oculis-related homeobox	NM_011382	326.8	346.8	341.5	344.8	132.6	136.6	152	151.9	339.975	143.275	-1.2489814	-2.3767356	0.00055397
76478	A_55_P2035951	Haus8	4HAUS augmin-like complex,	NM_001163042	661.8	768.8	623.7	926.2	280.6	333.1	338.9	290.6	745.125	310.8	-1.2492037	-2.3771019	0.07095924
52392	A_55_P1954820	D1Ertd622e	DNA segment, Chr 1, ERATO D	NM_133825	1504.5	1440.5	1461.3	1567	662.3	599.8	617.3	631.2	1493.325	627.65	-1.2506971	-2.3795637	0.00024003
30963	A_55_P2103105	Ptpla	protein tyrosine phosphatase	NM_013935	11579.4	12204.9	12746.2	10975.8	4862.8	5249.3	5156.3	4667.3	11876.575	4983.925	-1.2520725	-2.3818334	0.00077844
67680	A_55_P1953980	Sdhb	succinate dehydrogenase com	NM_023374	18876.7	20211.3	15499.7	16401.7	8006.1	7340.1	6753.6	7577.9	17747.35	7419.425	-1.2528031	-2.3830399	0.00887992
19679	A_55_P2004571	Pitpnm2	phosphatidylinositol transfer	NM_011256	941.2	772.2	924.1	959.2	367.1	388.6	401.2	348.8	899.175	376.425	-1.253044	-2.3834378	0.00330958
18023	A_55_P2022277	Nfe2l1	nuclear factor, erythroid deriv	NM_008686	203.1	209.9	210.5	162	88.5	73.9	83.2	82.5	196.375	82.025	-1.2542973	-2.3855094	0.01047754
14710	A_55_P2151986	Gngt2	guanine nucleotide binding pr	NM_001038664	997.2	1107.2	980.6	915.9	331.5	489.9	471.7	398	1000.225	422.775	-1.2558619	-2.3880977	0.05813543
12493	A_55_P2118570	Cd37	CD37 antigen	NM_007645	49.4	59.2	49.5	43	23.2	20.5	19.9	20.2	50.275	20.95	-1.2562502	-2.3887407	0.01138867
19325	A_52_P590392	Rab10	RAB10, member RAS oncogen	NM_016676	9794.8	10298.7	9801.9	9087.5	3478.3	4341.2	4070.8	4487.9	9745.725	4094.55	-1.2563805	-2.3889564	0.00426335
328329	A_51_P168695	Mast4	microtubule associated serine	NM_175171	544.1	431.7	591.6	461.9	208.5	219.9	202.1	212.1	507.325	210.65	-1.2573486	-2.3905601	0.01154742
28000	A_51_P113784	Prpf19	PRP19/PSO4 pre-mRNA proce	NM_134129	418.9	506.3	478.5	419.5	182.7	188.5	196.5	192.3	455.8	190	-1.2579647	-2.3915811	0.00151258
259300	A_51_P343613	Ehd2	EH-domain containing 2	NM_153068	77.6	102.6	90	98.5	39.1	38	40.7	35.6	92.175	38.35	-1.2587475	-2.3928791	0.00677947
20686	A_51_P504065	Spa17	sperm autoantigenic protein 1	NM_011449	65.6	45.4	47.7	57.7	23.1	19.9	22.9	23.5	54.1	22.35	-1.2625698	-2.3992272	0.04309036
53325	A_55_P1990874	Banp	BTG3 associated nuclear prot	NM_016812	545.9	552.2	471.4	509.8	248.8	199.9	231.6	189.1	519.825	217.35	-1.2639153	-2.4014658	0.01000681
64209	A_51_P434101	Herpud1	homocysteine-inducible, endo	NM_022331	7214	8069.6	7518.7	7504.6	2789.7	3180	3320.3	3344.7	7576.725	3158.675	-1.264807	-2.4029505	0.0012018
14595	A_52_P103391	B4galt1	UDP-Gal:betaGlcNAc beta 1,4	NM_022305	3918.1	3953.6	4492.1	2811.9	1489.2	1681.4	1512.9	1541.9	3793.925	1556.35	-1.2665075	-2.4057847	0.0784857
16000	A_55_P2085984	Igf1	insulin-like growth factor 1	NM_010512	123.7	135.9	136.3	106	45.1	53.6	53.4	56.1	125.475	52.05	-1.2669381	-2.4065027	0.01211316
229571	A_55_P2176908	Gm4858	predicted gene 4858	NM_001177694	183.8	148.2	144.3	195.3	76	61.5	65.6	74.6	167.9	69.425	-1.2671751	-2.4068982	0.03655885
17286	A_51_P383001	Meox2	mesenchyme homeobox 2	NM_008584	1509.5	1349.8	1464.4	1245.4	511.1	667.6	550.9	587.9	1392.275	579.375	-1.2678742	-2.4080648	0.00829359
67501	A_52_P399717	Ccdc50	coiled-coil domain containing	NM_026202	435.5	469.6	442.3	549.7	223.9	209.9	156.2	201.4	474.275	197.85	-1.26794	-2.4081746	0.0461753
380928	A_55_P2110513	Lmo7	LIM domain only 7	NM_201529	2374.2	1999.4	1927.7	1815.4	802.7	930.8	842.2	770.6	2029.175	836.575	-1.274603	-2.4193223	0.00749884
330319	A_51_P316951	Wipf3	WAS/WASL interacting protei	NM_001167860	2099.3	1857.3	1546.5	1606.6	767.6	811.1	641.9	707.1	1777.425	731.925	-1.274837	-2.4197147	0.02511312
326618	A_51_P225592	Tpm4	tropomyosin 4	NM_001001491	2406.2	2618.3	2650.5	2732.8	1154.9	1270	941	960.6	2601.95	1081.625	-1.2762902	-2.4221533	0.01282321
546336	A_52_P497188	Prrg1	proline rich Gla (G-carboxyglu	NM_027322	355.8	430.1	440.9	507	180.7	184.7	168.8	176.3	433.45	177.625	-1.276512	-2.4225258	0.01080603
83671	A_51_P290921	Sytl2	synaptotagmin-like 2	NM_001040087	56.2	56.8	65.9	63.8	21.2	24	30.7	24.8	60.675	25.175	-1.2786546	-2.4261262	0.02492056
21961	A_55_P2030578	Tns1	tensin 1	NM_027884	8691.7	8093.9	8251.1	8101.7	3295.1	3357.7	3263.3	3722.5	8284.6	3409.65	-1.2822214	-2.4321317	0.00033524
12013	A_55_P2014337	Bach1	BTB and CNC homology 1	NM_007520	2695.2	3051.2	3263.5	2661.2	1330.5	1084	1214.9	1164.3	2917.775	1198.425	-1.2824081	-2.4324465	0.00469996
20238	A_55_P2045528	Atxn1	ataxin 1	ENSMUST00000099550	129.4	136.1	125.7	160.9	56.8	63.6	48.8	57.6	138.025	56.7	-1.2831246	-2.4336549	0.01239491
218973	A_55_P2440441	Wdhd1	WD repeat and HMG-box DNA	NM_172598	37.4	33.6	34.8	29.8	13.6	17.4	13.4	11.7	33.9	14.025	-1.2836159	-2.4344838	0.0424363
77300	A_55_P2113683	Raph1	Ras association (RalGDS/AF-6	NM_001045513	1027.8	955.8	1086.7	1080.6	398.1	452.4	411.4	442	1037.725	425.975	-1.2846302	-2.4361961	0.00063348
109032	A_55_P2152566	Sp110	Sp110 nuclear body protein	NM_175397	126.6	150.5	118.6	129.2	45.4	59	60	51.5	131.225	53.975	-1.2851303	-2.4370406	0.01744023
73230	A_51_P488196	Bmper	BMP-binding endothelial regu	NM_028472	533.1	600.7	597.6	463.1	196.5	265	252.1	191.2	548.625	226.2	-1.2854886	-2.437646	0.07113556
58861	A_55_P2023818	Cysltr1	cysteinyl leukotriene recepto	NM_021476	164.3	156	127	141.3	58	70.1	66.4	48.2	147.15	60.675	-1.2858743	-2.4382977	0.05987171

108767	A_55_P2102936	Pnrc1	proline-rich nuclear receptor	NM_001033225	3482.5	3358.9	3825.1	3764.6	1506.7	1592.2	1431.4	1380.4	3607.775	1477.675	-1.2877948	-2.4415457	0.00072218
12293	A_55_P1988699	Cacna2d1	calcium channel, voltage-dep	NM_001110843	10857.5	11349.8	12142.4	11613.2	4504.1	4776.4	4880	4653.9	11490.725	4703.6	-1.2881016	-2.442065	0.00020471
12492	A_52_P311245	Scarb2	scavenger receptor class B, m	NM_007644	827.7	894.8	932.6	988.5	389.1	350.3	363.6	385.6	910.9	372.15	-1.2897458	-2.4448498	0.00077326
76551	A_51_P316949	Ccdc6	coiled-coil domain containing	NM_001111121	616.9	586.1	686.6	670.8	254.9	238.5	282.5	270.8	640.1	261.675	-1.2905342	-2.4461862	0.00144536
67383	A_55_P2018480	2410127L17Rik	RIKEN cDNA 2410127L17 gen	NM_026120	10762.3	10005.3	10817.8	10441.1	4024.8	3703.4	4177.3	5450.5	10506.625	4339	-1.2908543	-2.446729	0.02085344
16912	A_51_P369803	Psmb9	proteasome (prosome, macro	NM_013585	217.2	212.6	241.3	193.3	75.6	96.6	84.8	96	216.1	88.25	-1.2947599	-2.4533616	0.00862947
13684	A_55_P1974533	Eif4e	eukaryotic translation initiatio	NM_007917	734.3	706.9	706.8	720.4	290.7	279.5	327.7	272.4	717.1	292.575	-1.2968736	-2.4569586	0.0005702
67956	A_51_P201971	Setd8	SET domain containing (lysine	NM_030241	7156.7	6419.2	7685.9	6494.6	2870.9	2761.2	2571.3	3078.5	6939.1	2820.475	-1.2979047	-2.4587154	0.00208607
407790	A_55_P1971244	Ndufa4l2	NADH dehydrogenase (ubiqui	NM_001098789	896.8	870.9	769.2	855.5	310.8	388.3	333.7	348.2	848.1	345.25	-1.2989485	-2.4604948	0.00216285
15566	A_55_P2100103	Htr7	5-hydroxytryptamine (seroto	NM_008315	118.3	147	153.1	148.9	56.1	59.7	58.9	53.8	141.825	57.125	-1.3057978	-2.472204	0.00362146
237860	A_55_P2403135	Ssh2	slingshot homolog 2 (Drosoph	NM_177710	62.5	61.8	69.1	74	27	26.5	27.1	27.2	66.85	26.95	-1.3067057	-2.4737602	0.00060567
108075	A_55_P2033500	Ltbp4	latent transforming growth fa	NM_175641	1522.7	1274.4	1375.3	1256.4	507.7	666.2	560	472.1	1357.2	551.5	-1.3071884	-2.4745881	0.02049387
17069	A_55_P2031436	Ly6e	lymphocyte antigen 6 comple	NM_001164036	2043	1677.4	1785.6	1401.1	607.1	732.1	786.9	650.3	1726.775	694.1	-1.3090841	-2.4778419	0.04235566
19125	A_51_P215438	Prodh	proline dehydrogenase	NM_011172	1889.6	2128.6	1965.6	1590	754.3	772.4	714	799.3	1893.45	760	-1.3101367	-2.4796504	0.00416437
76142	A_55_P2008407	Ppp1r14c	protein phosphatase 1, regula	NM_133485	732	601.7	699.6	543.8	274.6	242.7	258.6	253.5	644.275	257.35	-1.3153202	-2.4885755	0.00716506
70726	A_51_P259571	Angptl6	angiopoietin-like 6	NM_145154	1600.4	1589.5	1425.8	1839.1	705.7	557.4	706.7	625.4	1613.7	648.8	-1.3154611	-2.4888186	0.00972267
100504104	A_55_P2308283	Gm16062	predicted gene 16062	ENSMUST00000151825	2932.5	3561.4	3486.9	3215.1	1162.4	1096.5	1662.6	1440	3298.975	1340.375	-1.3154655	-2.4888262	0.06811755
17996	A_55_P2116978	Neb	nebulin	NM_010889	29515.1	31532.8	35352.4	32271.5	13734	13152.5	12377.9	12370.6	32167.95	12908.75	-1.3156511	-2.4891464	0.00067456
18053	A_52_P236448	Ngfr	nerve growth factor receptor	NM_033217	23.8	21.7	24.2	21.9	8.8	11.4	7.8	9.1	22.9	9.275	-1.3161252	-2.4899645	0.01618706
56812	A_55_P2023057	Dnajb2	DnaJ (Hsp40) homolog, subfa	NM_178055	155	159.9	182.5	185.2	67.5	64.1	66.2	75.9	170.65	68.425	-1.316997	-2.4914697	0.00211429
73828	A_51_P170641	Dcaf4	DDB1 and CUL4 associated fa	NM_030246	714.6	641.9	633	583.8	278.5	215.2	269.6	269.1	643.325	258.1	-1.3212115	-2.4987585	0.0065711
20720	A_51_P268094	Serpine2	serine (or cysteine) peptidase	NM_009255	220	244.6	201.7	243.5	97.9	94.6	86.4	84.6	227.45	90.875	-1.3217338	-2.4996633	0.00197086
69601	A_55_P1977464	Dab2ip	disabled homolog 2 (Drosoph	NM_001114125	45.8	45.4	48.6	34	18.1	17.4	16.2	17	43.45	17.175	-1.3269813	-2.508772	0.01450863
121021	A_51_P160824	Cspg4	chondroitin sulfate proteogly	NM_139001	201.8	188.1	184.3	161.5	61.4	75	74.9	81.7	183.925	73.25	-1.3313244	-2.5163357	0.00834493
17388	A_51_P220062	Mmp15	matrix metallopeptidase 15	NM_008609	90.6	82.6	104.6	88.1	30.2	32.7	42.3	41.1	91.475	36.575	-1.3319926	-2.5175015	0.0362207
73341	A_55_P1964573	Arhgef6	Rac/Cdc42 guanine nucleotid	NM_152801	6120.8	6736.1	6206.6	6903.5	2459.3	2859.5	2270.7	2749.6	6491.75	2584.775	-1.3325989	-2.5185596	0.00228477
329154	A_52_P29151	Ankrd44	ankyrin repeat domain 44	NM_001081433	425.2	388.6	488.3	371.4	158.9	171.5	170.4	159.7	418.375	165.125	-1.3341379	-2.5212478	0.0029727
22210	A_51_P483557	Ube2b	ubiquitin-conjugating enzyme	NM_009458	4907.3	5982.1	5584	6233.3	2215.1	2210.9	2151.4	2385.9	5676.675	2240.825	-1.3362654	-2.5249685	0.00164903
109652	A_51_P166288	Acy1	aminoacylase 1	NM_025371	73.5	73.9	80.9	78.1	22.7	29.5	39	32.2	76.6	30.85	-1.3377097	-2.5274976	0.09779239
16906	A_51_P120717	Lmnb1	lamin B1	NM_010721	105.7	134	88.9	88.7	42.4	42	41.5	37	104.325	40.725	-1.338023	-2.5280465	0.04868571
233107	A_55_P2162204	Kctd15	potassium channel tetrameris	NM_146188	13785.3	13095.9	14540.2	13008	4971.7	5374.7	5519.3	5667.4	13607.35	5383.275	-1.3380772	-2.5281414	0.00032517
327959	A_55_P1966833	Xaf1	XIAP associated factor 1	NM_001037713	156.8	133.6	134.1	133.1	52.8	55.6	60.1	51.3	139.4	54.95	-1.3421078	-2.5352144	0.0011398
14081	A_51_P463452	Acsl1	acyl-CoA synthetase long-cha	NM_007981	655.8	858.9	662.7	806.7	274.1	336.2	280.2	282.1	746.025	293.15	-1.3423621	-2.5356615	0.01307946
380753	A_55_P2024591	Atxn7l1	ataxin 7-like 1	NM_028139	620.5	485.2	554.3	478.4	181.5	224.7	214.4	220.6	534.6	210.3	-1.3427969	-2.5364258	0.00911601
57278	A_51_P173601	Bcam	basal cell adhesion molecule	NM_020486	263.6	224	292.9	253.3	87.4	111.7	103.2	104.8	258.45	101.775	-1.3436721	-2.5379648	0.0076476
18230	A_55_P2081110	Nxn	nucleoredoxin	ENSMUST00000021204	113.6	91	104.6	115.8	43.4	36	44.1	43.8	106.25	41.825	-1.3436826	-2.5379833	0.00619633
68778	A_55_P2035484	1110038D17Rik	RIKEN cDNA 1110038D17 gen	NM_175133	5531.2	5961.9	6082.5	4662.1	2117.6	2240.3	2109.8	2246.8	5559.425	2178.625	-1.3444773	-2.5393817	0.00260811
56758	A_55_P2005025	Mbnl1	muscleblind-like 1 (Drosophil	NM_020007	8549.4	10418.4	10767	11322.5	3912.8	4207.1	3859.1	4088.3	10264.325	4016.825	-1.3464393	-2.5428375	0.00299211
224273	A_51_P160439	Crybg3	beta-gamma crystallin domai	NM_174848	5390.6	5942.7	5437.6	6655.1	2409.2	2633	2013.7	2166.4	5856.5	2305.575	-1.3471462	-2.5440838	0.00776885
108800	A_65_P05040	Ston2	stonin 2	NM_175367	77.7	52.2	57.6	69.3	24.2	21.7	26	28.3	64.2	25.05	-1.3472182	-2.5442108	0.056364
15483	A_51_P127297	Hsd11b1	hydroxysteroid 11-beta dehy	NM_008288	988.1	879.3	878.2	764.1	332.3	353.6	377.6	312.2	877.425	343.925	-1.3488474	-2.5470855	0.00345243
103554	A_55_P1976007	Psme4	proteasome (prosome, macro	NM_134013	2033.1	1838.8	2418.8	1938	937.3	796.3	762.5	726.4	2057.175	805.625	-1.3514234	-2.5516376	0.01065431
20411	A_55_P2053374	Sorbs1	sorbin and SH3 domain conta	NM_178362	11903.8	12919.5	9571.9	11353.6	4242	5456.3	4103.5	4130	11437.2	4482.95	-1.3532619	-2.5548912	0.0244947
77038	A_52_P285992	Arfgap2	ADP-ribosylation factor GTPa	NM_023854	226.9	220.2	300.2	235.7	93.9	113.3	88.2	88.4	245.75	95.95	-1.3533583	-2.5550619	0.0228321
15451	A_55_P1973583	Hpn	hepsin	NM_001110252	391.4	324.6	342.5	336.6	138.7	121.7	150.6	134.7	348.775	136.425	-1.3546693	-2.5573849	0.00193022
17436	A_55_P2016842	Me1	malic enzyme 1, NADP(+)-dep	NM_001198933	4154.8	3891.8	4516.6	3837.8	1563.2	1580.1	1715.2	1544	4100.25	1600.625	-1.3552914	-2.5584878	0.00048551
54604	A_55_P2071266	Pcnx	pecanex homolog (Drosophila	ENSMUST00000095565	89.7	70.6	75.4	72.5	30.6	26.8	27.9	35.2	77.05	30.125	-1.3564291	-2.5605063	0.0102118
18032	A_55_P2085574	Nfix	nuclear factor I/X	NM_010906	7836.8	6193.5	5987.1	5385.6	2591.8	2371.4	2500.1	2365.4	6350.75	2457.175	-1.3570552	-2.5616177	0.01105578
106529	A_51_P278550	Tecr	trans-2,3-enoyl-CoA reductas	NM_134118	6998.3	5867.6	6224.8	5533.7	2341.3	2361.9	2281.4	2568.7	6156.1	2388.325	-1.3619579	-2.5703376	0.00134779
56715	A_55_P2129975	Rabgef1	RAB guanine nucleotide excha	NM_019983	12080.8	11374.1	14805.7	13802.8	4969.9	5233.4	4678.3	5228.9	13015.85	5027.625	-1.3659593	-2.5774766	0.00294975
21834	A_52_P532559	Thrb	thyroid hormone receptor be	NM_009380	513.9	487.2	600.7	514.7	184.8	215.2	209.1	210.5	529.125	204.9	-1.3666805	-2.5787654	0.00136064
218820	A_51_P126626	Zfp503	zinc finger protein 503	NM_145459	1353.1	1545.3	1159.1	1409.4	517.1	537.8	480.9	577.4	1366.725	528.3	-1.3667832	-2.5789489	0.00446933
70549	A_55_P2071834	Tln2	talin 2	NM_001081242	2193.5	2317.7	2395.2	2745.8	1069	827.8	886.7	963	2413.05	936.625	-1.3668899	-2.5791396	0.00516858
76947	A_52_P150525	2310030N02Rik	RIKEN cDNA 2310030N02 gen	NM_001085493	1547.5	1549.4	1345.5	1375.6	532.1	535.1	550.2	634.9	1454.5	563.075	-1.3698933	-2.5845146	0.00125543
78334	A_51_P158388	Cdk19	cyclin-dependent kinase 19	NM_198164	552.4	577.9	472.1	374.1	173.9	214.6	184	183.5	494.125	189	-1.370914	-2.5863436	0.05683622
246228	A_52_P561650	Vwa1	von Willebrand factor A doma	NM_147776	378.8	400.5	403.8	389.4	138.4	163.6	149.1	157.5	393.125	152.15	-1.3718709	-2.5880597	0.00028341
223697	A_55_P2021119	Sun2	Sad1 and UNC84 domain con	NM_194342	22252.8	19338.5	21208.2	17935.8	7422.3	7997	8003.8	7678.2	20183.825	7775.325	-1.3719652	-2.588229	0.00082424
68394	A_55_P2144636	Ccdc163	coiled-coil domain containing	NM_026714	369.7	379.1	397.3	325.1	120.3	143.7	160	145.4	367.8	142.35	-1.3730625	-2.5901982	0.00513665
56745	A_55_P1998539	C1qtnf1	C1q and tumor necrosis facto	NM_019959	156.5	157.9	199.1	136.8	53.7	72.7	71.7	52.4	162.575	62.625	-1.3800076	-2.6026974	0.09528001
20128	A_51_P275454	Trim30a	tripartite motif-containing 30	NM_009099	166.7	178.3	200	159.1	79.1	64.2	57.7	70.2	176.025	67.8	-1.3807284	-2.6039981	0.01052675
71912	A_55_P2037141	Jsrp1	junctional sarcoplasmic reticu	NM_028001	107565.2	95927.2	103727.8	97800.3	38993	39739.6	39020	37440.4	101255.125	38798.25	-1.3827617	-2.6076708	0.00011737
666794	A_52_P920158	Rbm24	RNA binding motif protein 24	NM_001081425	12149.8	10518.5	12328.6	10841.5	4514.1	4618.1	4164.2	4240.7	11459.6	4384.275	-1.3840169	-2.6099405	0.00052276
216551	A_51_P440047	1110067D22Rik	RIKEN cDNA 1110067D22 gen	NM_173752	6446.8	6111.6	6331.3	5933.6	2477.9	2445.5	2383.7	2206.1	6205.825	2378.3	-1.3843986	-2.6106311	0.00014363
399579	A_55_P2286650	6720462K09Rik	RIKEN cDNA 6720462K09 gen	AK032850	1816.7	1443.8	1918.4	1194.2	555	662.1	630.1	558.6	1593.275	601.45	-1.3844796	-2.6107776	0.09034872
52348	A_52_P88808	Vps37a	vacuolar protein sorting 37A (	NM_033560	446.3	362.4	547.2	417.1	149.2	167.8	173.8	182.5	443.25	168.325	-1.3846859	-2.611151	0.02457234
246221	A_55_P2145531	Mpst	mercaptopyruvate sulfurtrans	NM_138670	4658.7	4478.5	4408.1	3604.5	1819.7	1359.2	1701.5	1688.9	4287.45	1642.325	-1.3858874	-2.6133266	0.01196951
13601	A_66_P104815	Ecm1	extracellular matrix protein 1	NM_007899	48.1	39.6	47.8	42.3	16.6	18.9	19.3	13.6	44.45	17.1	-1.3868572	-2.6150838	0.02073265
107350	A_52_P1020860	AW112010	expressed sequence AW1120	NM_001177351	820.2	916.3	1041.2	827.5	366.1	365.5	376.2	274.9	901.3	345.675	-1.3870536	-2.6154399	0.01954639
14733	A_51_P276943	Gpc1	glypican 1	NM_016696	28154.3	28077	28249.2	24129.2	11072	10028.9	10330.3	9969.5	27152.425	10350.175	-1.3895449	-2.6199603	0.00044584
68888	A_51_P267700	Gkn3	gastrokine 3	NM_026860	72	78.4	108	90.5	37.3	35	27.5	32.6	87.225	33.1	-1.3897234	-2.6202844	0.0587229
330401	A_51_P237834	Tmcc1	transmembrane and coiled co	NM_177412	1444.2	1336.9	1766.8	1184.2	535.4	558	554.8	516	1433.025	541.05	-1.3904262	-2.6215612	0.0119795
22344	A_66_P100440	Vezf1	vascular endothelial zinc finge	NM_016686	9678.8	9629	9911	11638	4059.7	3679.5	3972.2	3810.4	10214.2	3880.45	-1.3928131	-2.6259021	0.00064859
27027	A_55_P2010386	Tspan32	tetraspanin 32	NM_020286	29.6	32.9	28.2	29.6	9.8	11.6	12.2	12.3	30.075	11.475	-1.3936148	-2.6273616	0.00181953
14433	A_55_P2088912	Gapdh	glyceraldehyde-3-phosphate	NM_008084	43638.2	36930.9	47089	38548.5	14172.9	15334.7	18504.2	15264.7	41551.65	15819.125	-1.3936245	-2.6273793	0.00746285
19055	A_55_P1952738	Ppp3ca	protein phosphatase 3, cataly	NM_008913	16957.2	16232.5	19175	19762.9	7289.3	6698.1	6664.2	6678.8	18031.9	6832.6	-1.396241	-2.6321487	0.00076831
216350	A_55_P1978681	Tspan8	tetraspanin 8	NM_146010	3950.2	4316.5	5409	4406.2	1535.1	1471.9	2023.7	1836.8	4520.475	1716.875	-1.3991206	-2.6374076	0.03005146
102626	A_55_P2009762	Mapkapk3	mitogen-activated protein kin	NM_178907	5421.1	6269.7	6342.4	6187.2	2175.3	2387.9	2112.7	2491.2	6055.1	2291.775	-1.402103	-2.6428655	0.00081368
22339	A_52_P638895	Vegfa	vascular endothelial growth f	NM_001025250	2971	3237.9	2677.4	2832.5	1078.3	1062.6	1093.9	1191.7	2929.7	1106.625	-1.4025141	-2.6436187	0.00050261
104215	A_51_P338317	Rhoq	ras homolog gene family, me	NM_145491	13304.6	10450.6	13638.3	14075.2	4868.9	4945.5	4786.8	4730.1	12867.175	4832.825	-1.4033495	-2.64515	0.00299775
117198	A_55_P2124346	Ivns1abp	influenza virus NS1A binding	NM_054102	7459.9	7540.4	8653.7	6856.5	2750.7	3134	2791.8	2818.9	7627.625	2873.85	-1.4051137	-2.6483866	0.00107273
22371	A_51_P103397	Vwf	Von Willebrand factor homol	NM_011708	3363.7	3000.3	4186.8	2637.4	1086.3	1307.1	1368.3	1155	3297.05	1229.175	-1.4085127	-2.6546334	0.05700058
67238	A_55_P1984770	2810453I06Rik	RIKEN cDNA 2810453I06 gene	NM_026050	10049.7	10614.3	11277.4	9844.5	3799.5	4361.3	3645.4	3935.4	10446.475	3935.4	-1.4096358	-2.6567009	0.00053594
71918	A_55_P2002884	Zcchc24	zinc finger, CCHC domain con	NM_001101433	20058.1	19134.8	20365.4	20383.6	7502.3	7952.8	6771.5	7844.4	19985.475	7517.75	-1.4129227	-2.6627605	0.00022682
66838	A_51_P262721	0610009L18Rik	RIKEN cDNA 0610009L18 gen	ENSMUST00000143813	13663.8	14414.6	14418.9	12666.5	5178.1	5316.3	5319.3	4856.8	13790.95	5167.625	-1.4151233	-2.6668252	0.00018946
69181	A_55_P2052939	Dyrk2	dual-specificity tyrosine-(Y)-p	NM_001014390	184.2	150.3	196.6	201.6	64.7	71.3	71.3	65.9	183.175	68.3	-1.4154353	-2.667402	0.00343388
98733	A_51_P479583	Obsl1	obscurin-like 1	NM_178884	1793.4	1759.8	1401.2	1158.2	605.4	553.1	563.2	535.2	1528.15	564.225	-1.4163035	-2.6690078	0.04127024
77072	A_55_P2193424	6720420G18Rik	RIKEN cDNA 6720420G18 gen	AK020112	436.5	423.9	368.5	288.8	148.9	144.5	139.5	128.9	379.425	140.45	-1.4173776	-2.6709956	0.02555752
11787	A_51_P149562	Apbb2	amyloid beta (A4) precursor p	NM_009686	2633.1	1993.4	2399.3	2118.3	762.8	893.3	896.3	855.1	2286.025	851.875	-1.4186755	-2.6733996	0.00381463
16978	A_55_P1959465	Lrrfip1	leucine rich repeat (in FLII) int	NM_008515	9484.1	10255.3	9881.2	12876.9	3684.3	4204.3	4031.8	3869.9	10624.375	3947.575	-1.419558	-2.6750353	0.00414039
108068	A_55_P2171348	Grm2	glutamate receptor, metabot	NM_001160353	120.1	100.7	94.5	113.8	46.6	40.6	34.6	38.8	107.275	40.15	-1.4195652	-2.6750487	0.0079257
74185	A_55_P2129222	Gbe1	glucan (1,4-alpha-), branching	ENSMUST00000099628	240.6	183	237.8	167.3	86.7	84.3	65.7	71.2	207.175	76.975	-1.4197609	-2.6754117	0.06031878
320712	A_55_P2167803	Abi3bp	ABI gene family, member 3 (N	NM_001014423	311.1	363.4	249.4	313.1	100.3	128.2	128.2	104.4	309.25	115.275	-1.4201965	-2.6762196	0.02914629
18541	A_52_P89425	Pcnt	pericentrin (kendrin)	NM_008787	7813.2	7118.6	6636.2	6654.1	2754.6	2608.6	2614.6	2534.2	7055.525	2628	-1.4222172	-2.6799706	0.00027372
50908	A_55_P2042612	C1s	complement component 1, s	NM_144938	2171.6	2309.7	2377.7	1800	791	963.9	827.3	659.4	2164.75	810.4	-1.4224036	-2.6803168	0.02622603
16601	A_65_P19780	Klf9	Kruppel-like factor 9	NM_010638	5857.1	6429.3	5428.2	4894.2	2385.7	2045.9	1963.7	2001	5652.2	2099.075	-1.4262378	-2.6874498	0.00366822
68162	A_55_P2073552	A930003A15Rik	RIKEN cDNA A930003A15 gen	NR_015488	92.8	106.3	79.6	94.4	30.6	31.9	35	41.3	93.275	34.7	-1.4287913	-2.6922106	0.0121373
27883	A_55_P2091494	D16H22S680E	DNA segment, Chr 16, human	NM_138583	4019	4249.5	4276.9	3956	1457	1561	1506.6	1604.6	4125.35	1532.3	-1.428939	-2.6924863	0.0000866
64009	A_51_P314186	Syne1	synaptic nuclear envelope 1	NM_001079686	212.2	215.2	259.2	193.2	77.7	79.5	76.3	92.3	219.95	81.45	-1.4290232	-2.6926434	0.00434831
665113	A_52_P663757	Tnik	TRAF2 and NCK interacting ki	NM_026910	163	184.9	128.8	153	53.4	73.8	51.8	55.2	157.425	58.55	-1.4299782	-2.6944265	0.04906878
192657	A_51_P230507	Ell2	elongation factor RNA polym	NM_138953	694.6	499.2	670.7	592.9	210.1	257	202.8	238.8	614.35	227.175	-1.4301379	-2.6947248	0.01556923
78438	A_55_P1961541	A930028N01Rik	RIKEN cDNA A930028N01 ger	AK020900	142.6	116.5	138	151	47.9	59.5	41.7	55.1	137.025	51.05	-1.4310545	-2.6964374	0.01952049
26457	A_51_P117477	Slc27a1	solute carrier family 27 (fatty	NM_011977	1457.6	1393.4	1294	1515.1	478.5	618.7	435.2	580.3	1415.025	528.175	-1.4337327	-2.7014477	0.01146796
170731	A_55_P1984481	Mfn2	mitofusin 2	NM_133201	2788.6	2486.6	2726.5	3008.9	1158.7	1014.6	895.9	1014.1	2752.65	1020.825	-1.4337435	-2.7014679	0.0019342
17754	A_66_P140452	Mtap1a	microtubule-associated prote	NM_032393	39.3	39.2	32.6	37	16.4	12.2	15.7	11.1	37.025	13.85	-1.4339698	-2.7018915	0.03295182
20391	A_55_P2007384	Sgca	sarcoglycan, alpha (dystrophi	NM_009161	7346.1	6734.2	6676.4	5552	2491.9	2495.8	2435.5	2266.4	6577.175	2422.4	-1.4347985	-2.7034441	0.00156404
70380	A_55_P1958314	Mospd1	motile sperm domain contain	NM_027409	9343	12867.6	11499.4	11217.7	4230.8	4009	4061.3	4202.8	11231.925	4125.975	-1.4358208	-2.7053605	0.00225652
56430	A_51_P288906	Clip1	CAP-GLY domain containing li	NM_019765	4361.7	4635.4	5285	4637.7	1923.8	1716.1	1686.1	1661.8	4729.95	1746.95	-1.435842	-2.7054002	0.00062564
12311	A_52_P469789	Calcr	calcitonin receptor	NM_007588	37.3	46.7	51.4	45.6	15.1	19.8	13.4	19	45.25	16.825	-1.4362797	-2.7062212	0.05923417
18440	A_51_P115346	P2rx6	purinergic receptor P2X, ligan	NM_011028	106	120.7	131.2	102.6	44.3	44.2	40.7	40.1	115.125	42.325	-1.4380042	-2.7094578	0.00153144
240892	A_51_P235088	Dusp27	dual specificity phosphatase 2	NM_001033344	484.2	502.7	528	417.3	159.7	194	162.4	197	483.05	178.275	-1.4394388	-2.7121535	0.0042093
50766	A_55_P2074488	Crim1	cysteine rich transmembrane	NM_015800	351.4	265.8	316.6	324.2	129	119.9	116.4	98.3	314.5	115.9	-1.4398609	-2.712947	0.00691817
14205	A_51_P117739	Figf	c-fos induced growth factor	NM_010216	556.7	611.1	590	474.7	199.1	226.5	238.1	162.9	558.125	206.65	-1.4418703	-2.7167283	0.02569545
18121	A_51_P237040	Nog	noggin	NM_008711	16.9	14.4	13.5	9.7	5.2	5	4.5	5	13.625	4.925	-1.4418819	-2.7167502	0.07869323
621699	A_55_P2010586	Gm6252	predicted gene 6252	XR_001564	1419.9	923.4	1096.2	989.9	452.3	345.9	447.7	372	1107.35	404.475	-1.4427313	-2.7183501	0.05991161
69816	A_51_P452153	2010001M09Rik	RIKEN cDNA 2010001M09 ge	NM_027222	32.5	35	47.8	46.1	14.5	12.6	15.5	16.2	40.35	14.7	-1.4429583	-2.718778	0.04668045
11735	A_65_P13713	Ank3	ankyrin 3, epithelial	NM_146005	380.1	313.6	373.9	248.2	113.7	125.6	116.1	122.1	328.95	119.375	-1.4429901	-2.7188378	0.0261319
78408	A_55_P2031481	Fam131a	family with sequence similarit	NM_133778	14749.7	13904.4	14126.4	13504.9	5450.5	5489.4	4945.1	4817.3	14071.35	5175.575	-1.4446387	-2.7219465	0.00017075
229541	A_55_P2085551	Dennd4b	DENN/MADD domain contain	NM_201407	13578.3	13814	13697.5	15796.7	5720.3	5027.1	4823.8	5312.8	14221.625	5221	-1.4458056	-2.724149	0.00054102
29857	A_52_P252258	Mapk12	mitogen-activated protein kin	NM_013871	7371.2	7306.9	8182.7	7380.7	2489	2818.3	2894.7	2906.9	7560.375	2777.225	-1.4460517	-2.7246137	0.00031662
235599	A_52_P468683	6430571L13Rik	RIKEN cDNA 6430571L13 gen	NM_175486	237.8	246.2	194	191.2	75.4	66.2	82.7	95.4	217.3	79.925	-1.4462897	-2.7250632	0.02534315
12183	A_52_P401640	Bpgm	2,3-bisphosphoglycerate mut	NM_007563	5248.6	4521.5	4092	5120.9	1712.8	1955.3	1673.6	1604.4	4745.75	1736.525	-1.4473006	-2.7269733	0.00299072
238130	A_52_P682745	Dock4	dedicator of cytokinesis 4	NM_172803	491.7	493.8	490.3	485.2	164.5	200.4	204.3	154.8	490.25	181	-1.4479712	-2.7282412	0.00253435
16549	A_51_P281700	Khsrp	KH-type splicing regulatory pr	NM_010613	2563.8	1616.9	2166.7	1758.1	701.8	701.1	728.8	793.4	2026.375	731.275	-1.4486229	-2.7294739	0.03718594
328365	A_65_P16542	Zmiz1	zinc finger, MIZ-type contain	ENSMUST00000100823	2425.2	2000	2100.7	2333.3	795.8	846.2	777.3	815.9	2214.8	808.8	-1.4496974	-2.7315075	0.00040537
14675	A_66_P106611	Gna14	guanine nucleotide binding p	NM_008137	49.3	58.5	53.5	70.5	20	24.9	21.9	17.8	57.95	21.15	-1.4520581	-2.7359809	0.02959968
233199	A_55_P2013665	Mybpc2	myosin binding protein C, fas	NM_146189	103632.8	96901.3	104209.4	98144.3	40752.1	30942.9	47255.4	30740	100721.95	37422.6	-1.4522909	-2.7364223	0.03605977
216739	A_51_P380699	Acsl6	acyl-CoA synthetase long-cha	NM_001033599	689.3	603.8	595.9	737.4	261.4	223.5	223.1	249.7	656.6	239.425	-1.453075	-2.73791	0.00171476
72157	A_55_P1987483	Pgm2	phosphoglucomutase 2	NM_028132	91114.5	84337.8	92257.2	91143.4	33140.9	32753.6	33012.8	32069.5	89713.225	32744.2	-1.4532915	-2.7383209	4.60E-05
192976	A_55_P2090557	BC046404	cDNA sequence BC046404	NM_198861	853.3	880.9	811	929.9	278.1	386.6	302.3	309.7	868.775	319.175	-1.4538778	-2.7394338	0.00396599
63913	A_55_P2083489	Fam129a	family with sequence similarit	NM_022018	181.4	252.7	175.8	201.2	68.4	91.2	72.9	63.3	202.775	73.95	-1.4539309	-2.7395347	0.05016377
56506	A_55_P2120354	Cib2	calcium and integrin binding f	NM_019686	35897.6	34302.3	38238.8	32253.3	12292.3	11929.6	13123.7	13992.5	35173	12834.525	-1.454387	-2.7404009	0.00047797
70127	A_52_P684138	Dpf3	D4, zinc and double PHD finge	NM_058212	341.5	375.7	358.2	294.7	118.2	142	123	116.2	342.525	124.85	-1.4547724	-2.7411332	0.0023739
72937	A_55_P2045876	2900008C10Rik	RIKEN cDNA 2900008C10 gen	AW122206	658.4	719.6	666.8	669.9	261.4	261.7	234.5	233.2	678.675	247.7	-1.4555077	-2.7425305	0.0001601
64297	A_51_P173709	Gprc5b	G protein-coupled receptor, f	NM_022420	2042.1	1572.4	1608.3	2401.5	593.9	827.7	705.6	631.8	1906.075	689.75	-1.45564	-2.7427821	0.08994379
12490	A_51_P204740	Cd34	CD34 antigen	NM_133654	10376.3	11924	11828.5	10602.2	3822	5254.3	4131	3298.2	11182.75	4126.375	-1.4563768	-2.7441832	0.02760147
100043380	A_55_P2013391	Gm4402	predicted gene 4402	AK028917	229.8	166.6	221.2	185.4	82.5	71.7	69.6	66.9	200.75	72.675	-1.4582529	-2.747754	0.00966374
27395	A_55_P2179020	Mrpl15	mitochondrial ribosomal prot	NM_001177658	135	135.9	118.2	123.5	35.6	51.1	52.6	49	128.15	47.075	-1.4589783	-2.7491361	0.01722773
72713	A_51_P357647	Angptl1	angiopoietin-like 1	NM_028333	152.3	177	182.1	171.5	72.6	60.5	65.9	50.9	170.725	62.475	-1.4591171	-2.7494005	0.00760571
18746	A_55_P2060107	Pkm2	pyruvate kinase, muscle	NM_011099	50248.4	34876.5	45502.8	31981	13969.3	14043.9	16195.3	13977	40652.175	14546.375	-1.4609175	-2.7528338	0.04693024
100041585	A_55_P2014506	Amd2	S-adenosylmethionine decarb	NM_007444	59450.6	51772.1	53201.5	41760	17997.1	19579.5	18509.2	18239.4	51546.05	18581.3	-1.4612614	-2.7534901	0.00386536
20472	A_55_P2033308	Six2	sine oculis-related homeobox	NM_011380	2914.5	4059	3864.7	2620.9	1096.2	1106.4	1313	1297.4	3364.775	1203.25	-1.4644793	-2.7596385	0.05850448
381352	A_55_P1994487	Mamdc4	MAM domain containing 4	NM_001081199	167.2	139.5	103.4	152.5	50.5	56.2	46.3	48.2	140.65	50.3	-1.4649247	-2.7604907	0.04378828

18645	A_55_P2128526	Pfn2	profilin 2	NM_019410	19221.6	20980.3	22397.4	25002.7	8625.6	7831.5	7683.5	7462.4	21900.5	7900.75	-1.4663936	-2.7633027	0.00137437
70598	A_55_P2146384	Filip1	filamin A interacting protein 1	NM_001081243	722.2	775.9	853.1	524.6	254	305.4	251	220	718.95	257.6	-1.4678706	-2.7661331	0.08664438
105559	A_51_P189269	Mbnl2	muscleblind-like 2	NM_175341	1582.6	1630.3	1418.5	1572.9	609.3	524.7	513.6	596.4	1551.075	561	-1.4693422	-2.7689561	0.00054942
218215	A_55_P2007878	Rnf144b	ring finger protein 144B	NM_146042	85.9	83.7	81.6	69.4	32.5	31.4	28.5	23.7	80.15	29.025	-1.4710843	-2.7723018	0.0074366
77125	A_55_P1964960	Il33	interleukin 33	NM_001164724	441.1	451.3	413.4	587.5	155.8	168	207.4	150.7	473.325	170.475	-1.471267	-2.7726529	0.02836116
19727	A_52_P484838	Rfxank	regulatory factor X-associated	NM_011266	381.1	413.7	399.3	426.5	109.3	147.8	184.1	152.7	405.15	148.475	-1.471411	-2.7729296	0.03845997
23999	A_55_P2103284	Twf2	twinfilin, actin-binding protei	NM_011876	2016.2	1969.7	2215	1514.3	655.6	817.9	650.1	637.2	1928.8	690.2	-1.4765341	-2.782794	0.02000222
26358	A_51_P383399	Aldh1a7	aldehyde dehydrogenase fam	NM_011921	38.4	43.4	36.1	32.3	11.8	16.2	11.5	14.7	37.55	13.55	-1.4775259	-2.7847077	0.02490516
76375	A_55_P2101751	Det1	de-etiolated homolog 1 (Arab	NM_029585	322.9	300.9	288.1	355.1	112.1	106.1	115.9	119.8	316.75	113.475	-1.4778618	-2.7853561	0.00049637
74205	A_55_P2165324	Acsl3	acyl-CoA synthetase long-cha	NM_028817	264.5	408.5	285.4	286.5	122.5	87.3	115.5	118.7	311.225	111	-1.478269	-2.7861425	0.08111806
14089	A_55_P2115225	Fap	fibroblast activation protein	NM_007986	1936.5	1972.2	2121.3	2034.1	743.4	865.3	682.1	622.9	2016.025	728.425	-1.4784965	-2.7865818	0.00268362
328572	A_52_P411601	Ep300	E1A binding protein p300	NM_177821	147.7	162.6	194.8	163.2	55.4	67	60.7	55.9	167.075	59.75	-1.4804381	-2.7903345	0.00265544
237781	A_52_P232470	Smcr7	Smith-Magenis syndrome chr	NM_001009927	145	173.9	142	129.1	49.4	68	42.7	53.1	147.5	53.3	-1.4808524	-2.7911359	0.04839351
17762	A_55_P2100149	Mapt	microtubule-associated prote	NM_001038609	8501.1	8043.3	8615	9527.9	3413.1	2978.3	3045.6	2978.2	8671.825	3103.8	-1.4819268	-2.7932154	0.00033007
98766	A_55_P2043682	Ubac1	ubiquitin associated domain c	BC021811	19838.6	17248.8	19826.6	17035.4	6947.6	6206.5	6390.2	6834.7	18487.35	6594.75	-1.4848645	-2.7989088	0.00038445
100040462	A_65_P17218	Mndal	myeloid nuclear differentiatio	NM_001170853	248.4	235.5	251.5	239.8	83.7	81.5	107.5	78.3	243.8	87.75	-1.4852975	-2.799749	0.0027038
654493	A_55_P2349752	8030494B02Rik	Riken cDNA 8030494B02 gen	AK136342	726.1	576.5	668.7	601.9	197.9	258.4	255.6	209.2	643.3	230.275	-1.4863059	-2.8017065	0.00704286
68682	A_55_P1984158	Slc44a2	solute carrier family 44, mem	NM_152808	9788.3	8250.2	8984.6	8806.2	3331.2	3000.4	3249.9	3172.4	8957.325	3188.475	-1.4885736	-2.806114	0.00018347
53357	A_55_P2003096	Pla2g6	phospholipase A2, group VI	NM_001199023	798.9	608.5	706.7	627.9	202	289	256	232.2	685.5	244.8	-1.4894921	-2.807901	0.0158697
11551	A_55_P2021505	Adra2a	adrenergic receptor, alpha 2a	NM_007417	110.2	109.4	174	105.6	40.7	42.9	47.5	42.8	124.8	43.475	-1.4909004	-2.8106434	0.0695332
101602	A_52_P458000	AI467606	expressed sequence AI46760	NM_178901	45.6	40.7	48	33.9	16.2	14.8	17.2	11.6	42.05	14.95	-1.4950645	-2.8187675	0.04637868
545366	A_55_P2098995	Cfhr2	complement factor H-related	NM_001025575	359.2	256.6	294.9	274.9	99	104.1	100.2	114.6	296.4	104.475	-1.4951203	-2.8188766	0.0042409
11980	A_55_P2075298	Atp8a1	ATPase, aminophospholipid t	NM_001038999	581.7	546.2	745.5	688.4	236.5	246.1	208.5	212.6	640.45	225.925	-1.4954716	-2.819563	0.00529147
67845	A_55_P2117681	Rnf115	ring finger protein 115	NM_026406	3221.7	3034.7	3740	3330.2	1170	1221.7	1128.7	1181.3	3331.65	1175.425	-1.4993968	-2.8272447	0.00027005
108143	A_55_P2082070	Taf9	TAF9 RNA polymerase II, TATA	NM_027592	1978	2035.8	2176	1763.6	666.9	697.5	747.7	692.8	1988.35	701.225	-1.5007476	-2.8298932	0.00034944
56188	A_55_P2137937	Fxyd1	FXYD domain-containing ion t	NM_052992	51430.6	47571.8	47740.3	50593.9	19213.2	18620.7	16778.6	15346.1	49334.15	17489.65	-1.5008513	-2.8300966	0.00054348
18769	A_55_P2129685	Pkig	protein kinase inhibitor, gam	NM_001164053	273.9	313.8	318.2	380.2	131.3	102	91.5	132	321.525	114.2	-1.5015923	-2.8315506	0.04018302
74762	A_55_P2184339	Mdga1	MAM domain containing glyc	NM_001081160	169.4	131.2	116.1	174.1	54.7	48.9	48.3	53.5	147.7	51.35	-1.5055652	-2.8393588	0.02101101
606735	A_55_P2160043	A330069E16Rik	RIKEN cDNA A330069E16 gen	NR_015464	229.9	267.3	231.5	325	96.8	75.8	91.6	105.6	263.425	92.45	-1.506385	-2.8409728	0.02638635
54403	A_55_P1959228	Slc4a4	solute carrier family 4 (anion	NM_018760	418.7	299.2	447.1	380.6	145.9	102.6	158.4	137.3	386.4	136.05	-1.5082464	-2.8446406	0.08672093
20442	A_51_P301804	St3gal1	ST3 beta-galactoside alpha-2,	NM_009177	450.9	435.5	426.1	470.7	138.9	180	161.4	147.8	445.8	157.025	-1.5112874	-2.8506431	0.00081211
23887	A_55_P2061064	Ggt5	gamma-glutamyltransferase 5	NM_011820	58.9	76.2	57.2	66.6	18.3	25.9	25.8	21.1	64.725	22.775	-1.5125465	-2.8531321	0.0246852
56175	A_55_P2157033	Bace2	beta-site APP-cleaving enzym	NM_019517	429.1	497.4	554.7	544.6	143.4	237.1	181	158.1	506.45	179.9	-1.5125643	-2.8531673	0.06538618
20360	A_55_P2156126	Sema6c	sema domain, transmembran	ENSMUST00000118651	9687.7	8120.5	7853	8588.1	2918.1	3019.1	3089.4	2933.3	8562.325	2989.975	-1.5135766	-2.8551699	0.00027569
97884	A_51_P158120	B3galnt2	UDP-GalNAc:betaGlcNAc beta	NM_178640	3473.6	3080.9	3663.7	3443.1	1212.1	1136	1167.3	1260.4	3415.325	1193.95	-1.5145661	-2.8571288	0.00017529
245827	A_55_P2075080	Fat2	FAT tumor suppressor homol	NM_001029988	62.6	80.5	69.8	76.8	22.2	25.4	31.9	22.5	72.425	25.5	-1.5151538	-2.858293	0.01660842
26372	A_55_P2081214	Clcn6	chloride channel 6	NM_011929	30.3	24.9	29.5	30.2	9.4	9.2	11.4	10.2	28.725	10.05	-1.5156714	-2.8593187	0.00144871
71276	A_51_P114274	Ccdc57	coiled-coil domain containing	NM_027745	153.3	96.2	132	105.1	42.8	35.1	47.3	42.5	121.65	41.925	-1.5205237	-2.8689517	0.06051662
17210	A_52_P93933	Mcl1	myeloid cell leukemia sequen	NM_008562	2607.3	2405.7	2674.2	2210.3	979.7	925.8	779.4	767.6	2474.375	863.125	-1.523579	-2.875034	0.00249487
68632	A_55_P2068125	Myct1	myc target 1	NM_026793	102.8	97.3	106.2	88.9	30.3	37.3	32.5	37.6	98.8	34.425	-1.5238594	-2.8755928	0.00119586
18049	A_55_P2074337	Ngf	nerve growth factor	NM_013609	45.3	40.1	39.2	34.9	13.1	15.8	15.5	11.3	39.875	13.925	-1.5247779	-2.8774242	0.01096141
105352	A_55_P2095213	Dusp22	dual specificity phosphatase 2	NM_134068	870.2	865.9	780.9	909.7	310.9	314.3	277.9	287.2	856.675	297.575	-1.5252154	-2.8782969	0.00018526
109305	A_55_P2147276	Orai1	ORAI calcium release-activate	NM_175423	575	443.1	434.1	451.4	161.9	176.9	149.6	169	475.9	164.35	-1.5268644	-2.8815887	0.00244276
20471	A_51_P268069	Six1	sine oculis-related homeobox	NM_009189	5023.4	4197	4223.4	5585.4	1696.5	1697.4	1561	1601.8	4757.3	1639.175	-1.5275089	-2.8828762	0.00208285
103841	A_51_P379409	Cuedc1	CUE domain containing 1	NM_198013	129.9	126.5	120	103.9	39	39	41.2	47.3	120.075	41.625	-1.5277621	-2.8833823	0.00135046
230861	A_55_P2034355	Eif4g3	eukaryotic translation initiatio	ENSMUST00000105829	38.6	30	35.1	34.8	12	10.6	13	12.3	34.625	11.975	-1.5299633	-2.8877849	0.00134526
14732	A_55_P2050778	Gpam	glycerol-3-phosphate acyltran	NM_008149	118.8	119.5	126.1	158.3	48.1	47	45.4	39.6	130.675	45.025	-1.5308992	-2.889659	0.00368298
320302	A_51_P314652	Glt28d2	glycosyltransferase 28 domai	NM_177130	309	314.6	286.2	231.9	107.6	89	93.7	103.1	285.425	98.35	-1.5309828	-2.8898264	0.00423778
548102	A_55_P2212458	LOC548102	uncharacterized LOC548102	AK046899	478.2	477.4	543.1	491.5	171	192.5	163.6	161.5	497.55	172.15	-1.5326651	-2.893198	0.00030301
110876	A_55_P2126473	Scn2a1	sodium channel, voltage-gate	NM_001099298	86	89.3	96.6	68.2	27.4	33.2	30	26.2	85.025	29.2	-1.5362258	-2.9003476	0.00791904
20851	A_55_P2031043	Stat5b	signal transducer and activato	NM_011489	17485	16663.2	19486.1	17816.4	5848.4	6503.2	5907.9	6360.3	17862.675	6154.95	-1.5363037	-2.9005042	0.00014607
66905	A_51_P223404	Plin3	perilipin 3	NM_025836	7592.1	7426	6363.6	5693.4	2398.7	2012.7	2279.7	2605.9	6768.775	2324.25	-1.5385518	-2.9050275	0.00566216
26381	A_65_P19089	Esrrg	estrogen-related receptor ga	NM_011935	360	409.3	281.9	322.2	124.5	129	106.4	109	343.35	117.225	-1.5417381	-2.9114505	0.00845065
16188	A_55_P2008181	Il3ra	interleukin 3 receptor, alpha	NM_008369	239.4	221.1	223.6	160.6	74	72.7	67.1	73.2	211.175	71.75	-1.5421474	-2.9122766	0.00803631
214642	A_52_P231428	A430107O13Rik	RIKEN cDNA A430107O13 ge	NM_001081351	71.9	77.9	71.7	87.3	23.8	26.4	26.9	28.7	77.2	26.45	-1.5438534	-2.9157224	0.00068513
70025	A_51_P328652	Acot7	acyl-CoA thioesterase 7	NM_133348	2233.8	1990	1506.4	1553	708.9	573.5	545.3	641.2	1820.8	617.225	-1.5482358	-2.924593	0.02878595
217344	A_55_P2028259	Rhbdf2	rhomboid 5 homolog 2 (Dros	NM_172572	1437.6	1463.5	2196.6	1686	551.3	605.9	538.6	589.9	1695.925	571.425	-1.5495181	-2.9271934	0.01490559
70393	A_55_P2420948	2210416O15Rik	RIKEN cDNA 2210416O15 ge	ENSMUST00000131964	215.5	228.8	207.3	186.6	82	70.4	65.2	67.8	209.55	71.35	-1.55595	-2.9402727	0.0010276
231912	A_55_P2279927	Katnal1	katanin p60 subunit A-like 1	ENSMUST00000145042	57	59.8	51.3	62.2	16.9	16	23.5	22.8	57.575	19.8	-1.5575478	-2.9435309	0.0210127
171429	A_55_P2153743	Slc26a6	solute carrier family 26, mem	NM_134420	1914	1892.1	2084.3	1913.2	631.6	709.7	660.3	645.8	1950.9	661.85	-1.5598532	-2.9482383	6.42E-05
12395	A_52_P612137	Runx1t1	runt-related transcription fac	NM_009822	400.9	599.8	460.5	456	133.9	181.5	176.1	152.8	479.3	161.075	-1.5676985	-2.9643144	0.02246469
11732	A_51_P155152	Ank	progressive ankylosis	NM_020332	3848.6	3998.1	3536.8	3391	1291.1	1223.1	1159.9	1303.2	3693.625	1244.325	-1.5681504	-2.9652432	0.00018055
67128	A_51_P273508	Ube2g1	ubiquitin-conjugating enzyme	NM_025985	1567.1	1660.4	1773.6	1438.5	569.1	487.2	528.4	584.4	1609.9	542.275	-1.5692008	-2.967403	0.00059942
216725	A_51_P227222	Adamts2	a disintegrin-like and metallo	NM_175643	3367.5	3572.2	3044.2	3046.5	897.6	1431.3	1192.5	938.1	3257.6	1114.875	-1.5696083	-2.9682411	0.03179086
387314	A_55_P1975645	Tmtc1	transmembrane and tetratric	NM_198967	387.9	465.7	382.4	411	133.8	142.2	131.9	145.4	411.75	138.325	-1.5704588	-2.9699915	0.00025759
14137	A_55_P2033250	Fdft1	farnesyl diphosphate farnesyl	NM_010191	1017.5	795.4	1045	989.6	301.8	334.7	364.7	291.3	961.875	323.125	-1.5713092	-2.9717426	0.00303026
14007	A_51_P182471	Celf2	CUGBP, Elav-like family mem	NM_010160	4387.3	4782.1	4373	5201.3	1603.3	1641.2	1568.6	1480.9	4685.925	1573.5	-1.5716815	-2.9725097	0.00018202
20660	A_66_P123824	Sorl1	sortilin-related receptor, LDL	ENSMUST00000060989	913.9	828.9	863.1	917.1	305.4	312	286	281.1	880.75	296.125	-1.5726241	-2.9744524	6.62E-05
231148	A_55_P2186356	Ablim2	actin-binding LIM protein 2	NM_001177696	79.1	67.5	76.3	75	29.7	21.2	25.9	23.7	74.475	25.125	-1.5761931	-2.9818199	0.00260167
20741	A_51_P489138	Spnb1	spectrin beta 1	NM_013675	2614.3	1982.4	2627.2	2331.2	769.1	817	802.4	795.7	2388.775	796.05	-1.5764826	-2.9824183	0.0010269
216188	A_52_P498193	Aldh1l2	aldehyde dehydrogenase 1 fa	NM_153543	68.2	108.9	73.6	102.3	28.1	34.2	28.6	25.5	88.25	29.1	-1.5795162	-2.9886962	0.07120838
100039631	A_55_P1988388	Gm2347	predicted gene 2347	AK029220	583.5	426.5	467.9	357.2	148.7	152.3	141.3	162.7	458.775	151.25	-1.5799786	-2.9896542	0.01696383
70772	A_51_P158638	Ggnbp1	gametogenetin binding prote	ENSMUST00000142141	3336.3	3274.1	3193.2	2434	1070.4	919.9	1192.7	903	3059.4	1021.5	-1.5807379	-2.991228	0.01077207
69260	A_52_P266459	Ing2	inhibitor of growth family, me	NM_023503	246.4	260.1	349.9	317.2	96.3	88	102.1	102.6	293.4	97.25	-1.5810518	-2.991879	0.00567147
74153	A_55_P2026233	Uba7	ubiquitin-like modifier activat	NM_023738	383.7	407.5	492.5	422.3	128.1	128.2	176	139.7	426.5	143	-1.5828992	-2.9957125	0.00647549
112407	A_52_P387009	Egln3	EGL nine homolog 3 (C. elega	NM_028133	527	640.5	614.9	534.5	172.6	257.2	153.7	201	579.225	196.125	-1.5844769	-2.9989903	0.04076638
70370	A_52_P559817	Fbln7	fibulin 7	NM_024237	319	405.3	408.1	373.6	135.2	148.4	131.7	91.5	376.5	126.7	-1.5873196	-3.0049055	0.03841066
260409	A_51_P267494	Cdc42ep3	CDC42 effector protein (Rho	NM_026514	2257.6	3000.5	2349.5	2538.8	1051.8	834.2	782.3	718.4	2536.6	846.675	-1.5891286	-3.0086758	0.01329438
71699	A_51_P442097	Slc41a3	solute carrier family 41, mem	NM_027868	7433.9	5352.1	5864.4	4644.4	1721.9	1911.5	1720.7	2334.4	5823.7	1922.125	-1.5892365	-3.0089008	0.04102013
68044	A_55_P2065567	Chac2	ChaC, cation transport regula	NM_026527	1143.2	1210.8	1055.4	1133.9	367.6	369.5	444.5	334.5	1135.825	379.025	-1.5894833	-3.0094155	0.00085189
76453	A_52_P679105	Prss23	protease, serine, 23	NM_029614	4670.4	4315.9	4507.2	3664.6	1502.2	1574.3	1251.8	1364.2	4289.525	1423.125	-1.591312	-3.0132326	0.0016367
100038505	A_66_P126984	Gm10523	predicted gene 10523	ENSMUST00000097502	79.3	62.2	54.3	51.5	26.7	18.4	16.8	20.2	61.825	20.525	-1.5925995	-3.0159228	0.09427
207495	A_55_P2066548	Baiap2l2	BAI1-associated protein 2-like	NM_177580	200	161.1	236.2	188.4	65.4	74	58.1	61.4	196.425	64.725	-1.593971	-3.0187913	0.00738164
14600	A_51_P499854	Ghr	growth hormone receptor	NM_010284	11738.3	10618.5	11665.1	13067.6	3614.9	4471.4	3746.8	3769.2	11772.375	3900.575	-1.5947773	-3.0204788	0.00069836
407795	A_66_P126348	BC030870	cDNA sequence BC030870	NR_033217	1497.8	1040.5	1439.2	944.3	344.5	447	429.8	383.9	1230.45	401.3	-1.5953109	-3.0215963	0.05885186
76383	A_55_P1982494	1700012L04Rik	RIKEN cDNA 1700012L04 gen	NM_029588	26.5	16.9	26.9	21.9	6.7	7.2	9.5	6.9	23.05	7.575	-1.5956458	-3.0222977	0.07659102
16184	A_55_P1980796	Il2ra	interleukin 2 receptor, alpha	NM_008367	92.4	94.3	81.4	100.6	23.7	26.6	36.5	37	92.175	30.95	-1.5972507	-3.0256617	0.03694136
235587	A_55_P2055487	Parp3	poly (ADP-ribose) polymerase	NM_145619	1086.7	1081.2	1119.3	1013.8	391.5	327	296.8	417.7	1075.25	358.25	-1.598102	-3.0274477	0.00285305
209268	A_55_P2059864	Igsf1	immunoglobulin superfamily,	NM_177591	269	355.9	279.9	287.4	85.6	119.2	92.8	96.7	298.05	98.575	-1.5985496	-3.0283869	0.0070962
329763	A_55_P2114188	Gm5105	predicted gene 5105	NM_177860	87	104.5	88.1	114.1	29.1	28.2	30.9	42.6	98.425	32.7	-1.6006602	-3.0328207	0.02704445
59027	A_51_P387235	Nampt	nicotinamide phosphoribosyl	NM_021524	3550.2	3702.5	3704.7	3621.2	1177	1373.9	1103.4	1163.2	3644.65	1204.375	-1.6021946	-3.0360479	0.00017802
16950	A_55_P2277019	Loxl3	lysyl oxidase-like 3	NM_013586	46.7	65.8	55.5	58.9	15.2	24.1	17.7	18.2	56.725	18.8	-1.6028683	-3.0374661	0.03380739
11492	A_55_P1983095	Adam19	a disintegrin and metallopept	NM_009616	409.5	482.4	470.2	314.2	118.7	144.8	151.3	131.6	419.075	136.6	-1.6035245	-3.038848	0.0215225
237211	A_52_P208613	Fancb	Fanconi anemia, complement	NM_175027	143.8	169.2	168.2	118.6	46.6	58.4	45.5	45.7	149.95	49.05	-1.6056071	-3.0432378	0.01227803
14735	A_55_P1963434	Gpc4	glypican 4	NM_008150	90.4	85	90.7	71.2	31.1	27.2	25.2	27.1	84.325	27.65	-1.6061319	-3.0443451	0.0012699
20190	A_52_P391110	Ryr1	ryanodine receptor 1, skeleta	NM_009109	44463.9	41271.2	47707.5	44319.3	14263.7	14154.4	16539	13500.4	44440.475	14614.375	-1.606862	-3.0458861	0.00026192
19244	A_52_P585448	Ptp4a2	protein tyrosine phosphatase	NM_008974	6037.7	6138	7173.5	6611.2	1943.7	2262.8	2191.2	2117.4	6490.1	2128.775	-1.6071069	-3.0464031	0.0002254
246728	A_55_P2019719	Oas2	2-5 oligoadenylate synthetase	NM_145227	350.8	335	339.9	358.5	95.7	115.7	145.3	102.6	346.05	114.825	-1.609712	-3.0519092	0.0060385
626578	A_55_P1978521	Gbp10	guanylate-binding protein 10	NM_001039646	30.7	30.5	31.2	35.7	10.5	8.8	10.7	12.1	32.025	10.525	-1.6114839	-3.0556596	0.00164733
17132	A_55_P1962429	Maf	avian musculoaponeurotic fib	ENSMUST00000069009	138.2	122.7	147.3	110.1	38.8	32.9	48.8	50.5	129.575	42.75	-1.6124671	-3.0577429	0.03232398
230721	A_55_P1953093	Pabpc4	poly(A) binding protein, cytop	NM_148917	9383.5	8043	9408.3	8051.7	2734.1	2769.3	2917.4	2954.4	8721.625	2843.8	-1.6132379	-3.059377	0.00017373
75723	A_55_P2244112	Amotl1	angiomotin-like 1	NM_001081395	245.6	176.7	196	183.7	59.1	57.2	69.8	75.4	200.5	65.375	-1.6141414	-3.0612935	0.00894181
246104	A_52_P53019	Rhbdl3	rhomboid, veinlet-like 3 (Dros	NM_139228	353.6	360.4	420.6	394.2	105.3	127.1	124.7	144	382.2	125.275	-1.6145235	-3.0621046	0.00169479
14168	A_55_P2139814	Fgf13	fibroblast growth factor 13	ENSMUST00000131319	113	101.9	85.4	87.4	29.5	29.3	33.9	33.3	96.925	31.5	-1.6151948	-3.0635297	0.00178912
55983	A_55_P2062513	Pdzrn3	PDZ domain containing RING	NM_018884	1088.4	823.9	914.8	742.1	326.6	257.2	289	280.8	892.3	288.4	-1.6201621	-3.0740957	0.00683623
18029	A_51_P477419	Nfic	nuclear factor I/C	NM_008688	11530.2	10696.8	10816	11327.2	3854.8	3698.2	3496.5	3366	11092.55	3603.875	-1.6232104	-3.0805979	5.12E-05
545539	A_55_P2065586	Gm15417	predicted gene 15417	ENSMUST00000126926	1211.7	1173.9	1210.3	1332.3	408.9	356.2	369	473.3	1232.05	401.85	-1.6236317	-3.0814977	0.00095964
15490	A_52_P566605	Hsd17b7	hydroxysteroid (17-beta) deh	NM_010476	223.4	191.1	222.9	209.4	65.6	62.6	76.5	70.1	211.7	68.7	-1.6248987	-3.0842051	0.00033551
67181	A_55_P2042773	Ctdnep1	CTD nuclear envelope phosph	NM_026017	6289.6	6176	6218.2	6616.7	2003.5	2085.8	2031.7	2059.4	6325.125	2045.1	-1.6285538	-3.0920288	1.46E-05
238330	A_55_P2103536	6430527G18Rik	RIKEN cDNA 6430527G18 gen	NM_145836	497.9	502.7	514.6	554.2	152.1	179.5	172.8	164.9	517.35	167.325	-1.6299283	-3.0949762	9.92E-05
106622	A_55_P2221647	AI605517	expressed sequence AI60551	AK032296	69	75.1	62.9	85.8	26.1	23.3	25.2	19.8	73.2	23.6	-1.6315358	-3.0984265	0.00447449
21827	A_55_P2063465	Thbs3	thrombospondin 3	NM_013691	537.9	606.5	605.9	482	155	242.8	189.5	144.8	558.075	183.025	-1.6319156	-3.0992424	0.0472173
268935	A_55_P2167530	Scube3	signal peptide, CUB domain,	ENSMUST00000043503	43.2	31.1	41	49.1	11.6	15.2	14.1	11.7	41.1	13.15	-1.6347233	-3.1052798	0.02572726
52626	A_51_P506312	Cdkn2aipnl	CDKN2A interacting protein N	NM_029976	4703.8	4577.9	5291.6	4936.9	1419.9	1507.2	1794.4	1546.5	4877.55	1567	-1.6414134	-3.1197132	0.00037076
213402	A_55_P2120469	Armc2	armadillo repeat containing 2	NM_001034858	44.7	51.9	50.5	40.8	13.2	21.5	12.6	14	46.975	15.325	-1.6442842	-3.1259272	0.06160723
66397	A_51_P260035	Sar1b	SAR1 gene homolog B (S. cere	NM_025535	16253.2	14351.3	15151.6	14067.9	4519.5	4669.2	5221.9	4720.3	14956	4782.725	-1.6446757	-3.1267756	0.00010755
12834	A_55_P2108768	Col6a2	collagen, type VI, alpha 2	ENSMUST00000105413	70.4	70.5	64.1	79.7	24.4	27.9	20.5	19	71.175	22.95	-1.6448333	-3.1271172	0.00690318
12454	A_55_P1967592	Ccnk	cyclin K	NM_009832	28511.3	21986.2	27581.9	26642.9	8115.6	7620.8	9576.8	8118.9	26180.575	8358.025	-1.6454623	-3.128481	0.00146099
67398	A_52_P134666	Srpr	signal recognition particle rec	NM_026130	1658.2	1407	1334.6	1303.1	388.1	484.3	478.6	470.7	1425.725	455.425	-1.6455876	-3.1287526	0.00138776
19349	A_55_P2080895	Rab7	RAB7, member RAS oncogene	NM_009005	1060.2	1180.7	1118.9	792.2	334.4	348.2	316.2	310.8	1038	327.4	-1.6498485	-3.1380069	0.00492914
72287	A_51_P418725	Plekhf1	pleckstrin homology domain	NM_024413	222.8	278.8	225.8	337.8	87.5	90.3	81.5	75.6	266.3	83.725	-1.6511779	-3.1408998	0.01198667
244058	A_55_P1955382	Rgma	RGM domain family, member	NM_177740	301.6	286	274.5	306.6	72.9	114.5	108.4	82.4	292.175	94.55	-1.651349	-3.1412723	0.016203
208104	A_51_P246727	Mlxip	MLX interacting protein	NM_133917	2028.6	2078.3	2384.9	2212.7	682.8	785.5	604.8	702.8	2176.125	693.975	-1.6521727	-3.1430662	0.00056851
269132	A_51_P331429	Glt25d2	glycosyltransferase 25 domai	NM_177756	109.6	148.7	101.9	114.5	37	39.9	35.8	36.6	118.675	37.325	-1.6547873	-3.1487677	0.00287281
59126	A_55_P1958857	Nek6	NIMA (never in mitosis gene a	NM_001159631	552.9	529.9	607.2	452.9	168.4	173.6	165.1	168.2	535.725	168.825	-1.6582315	-3.1562939	0.0004398
16494	A_52_P130787	Kcna6	potassium voltage-gated cha	NM_013568	373.4	358.4	403.6	416.6	135.8	161.5	107.5	95.9	388	125.175	-1.6592311	-3.1584815	0.02911236
242785	A_51_P477833	Klhl21	kelch-like 21 (Drosophila)	NM_001033352	4948.7	5002.2	5701.3	3901.4	1359.3	1551.8	1633.3	1598.8	4888.4	1535.8	-1.6608273	-3.161978	0.00359653
54153	A_51_P381558	Rasa4	RAS p21 protein activator 4	NM_133914	2013.4	1694.3	2028.2	1882.8	624.2	559.1	624.8	594.2	1904.675	600.575	-1.6629144	-3.1665555	0.00014367
68519	A_55_P2113673	Eml1	echinoderm microtubule asso	NM_001043335	10721.9	10380.4	10883.2	10453.6	3730.2	3429.4	3109.1	3155.9	10609.775	3356.15	-1.66412	-3.1692028	8.6542E-05
319480	A_51_P417720	Itga11	integrin alpha 11	NM_176922	1349	1604.4	1241.1	1364.3	325.3	557.7	509.6	388.4	1389.7	445.25	-1.6683121	-3.1784251	0.05544471
12398	A_51_P380750	Cbfa2t3	core-binding factor, runt dom	NM_009824	818.2	751.2	688.9	967.7	257.2	276.6	227	246	806.5	251.7	-1.6721157	-3.1868159	0.00225394
78541	A_55_P2004096	Asb8	ankyrin repeat and SOCS box-	NM_001170711	794.6	609.5	915.1	686.2	239	234.6	224.7	233.4	751.35	232.925	-1.6730988	-3.1889883	0.00341141
211770	A_55_P2082806	Trib1	tribbles homolog 1 (Drosophi	NM_144549	251.1	342.7	293.3	267.4	86.3	98.2	90.1	85.2	288.625	89.95	-1.6742083	-3.1914416	0.00115042
108682	A_51_P493886	Gpt2	glutamic pyruvate transamina	NM_173866	7812	8475.3	8836.5	7263.6	2484.7	2022.8	2793.8	2914.6	8096.85	2553.975	-1.674541	-3.1921779	0.00432604
11564	A_51_P269320	Adsl	adenylosuccinate lyase	NM_009634	1513.4	1445.6	1613.9	1490	457.8	519.5	465.1	456	1515.725	474.6	-1.6761554	-3.1957519	5.41E-05
68539	A_51_P114049	Tmem109	transmembrane protein 109	NM_134142	54281.1	51843	51379.2	55031	16166.9	16532.5	16443.5	17304.3	53133.575	16611.8	-1.677258	-3.1981953	1.52E-05
241303	A_52_P73475	Fam78a	family with sequence similari	NM_175511	555.3	443.1	471.3	666.5	165.3	172.3	165.2	156.5	534.05	164.825	-1.6784411	-3.2008191	0.00452908
76905	A_51_P346938	Lrg1	leucine-rich alpha-2-glycopro	NM_029796	2078	2016.6	2004.2	1518.3	471.8	651.6	703.8	560.5	1904.275	596.925	-1.6790686	-3.2022115	0.01764423
268857	A_55_P2155546	Nlrc3	NLR family, CARD domain co	NM_001081280	66	63.2	54.3	79.3	18	19.7	18.9	25.3	65.7	20.475	-1.6817369	-3.2081395	0.01205167
16706	A_55_P1973233	Ksr1	kinase suppressor of ras 1	NM_013571	51.7	46.5	51.2	47.9	16.5	13.5	17.1	14.6	49.325	15.425	-1.6820436	-3.2088216	0.00034188
66060	A_55_P2002846	0610010O12Rik	RIKEN cDNA 0610010O12 gen	NM_001081365	3580.3	3641.6	3014.3	3607.8	1164.7	1095.6	1113.5	936.7	3461	1077.625	-1.6837888	-3.2127056	0.00051895
103967	A_52_P164286	Dnm3	dynamin 3	NM_001038619	109.6	114.3	150.1	123.5	37.8	37.6	32.8	46.7	124.375	38.725	-1.6842458	-3.2137236	0.00721411

20289	A_51_P380432	Scx	scleraxis	NM_198885	1683.2	1754.3	1514.4	1799.8	607.9	573.1	523.5	413.6	1687.925	529.525	-1.6843377	-3.2139282	0.00417846
407800	A_55_P2011912	Ecm2	extracellular matrix protein 2,	NM_001012324	542.8	627.5	556.3	837.7	175.7	221.6	198.2	192.6	641.075	197.025	-1.6846741	-3.2146776	0.01319387
225288	A_55_P2088018	Fhod3	formin homology 2 domain co	NM_175276	5517	5356	6585.9	5012.4	1697	1818.3	1619.8	1825.7	5617.825	1740.2	-1.68502	-3.2154485	0.00049621
72948	A_51_P398260	Tppp	tubulin polymerization promo	NM_182839	179.3	204.2	264	191	63.6	65.2	66.4	62.5	209.625	64.425	-1.6863108	-3.2183267	0.00252448
230673	A_55_P1973926	Ipo13	importin 13	NM_146152	15479.6	14653.3	13721.1	13301.5	4468.8	4493.8	4387.6	4376.3	14288.875	4431.625	-1.6865811	-3.2189297	3.6499E-05
20787	A_55_P2002557	Srebf1	sterol regulatory element bin	NM_011480	492.4	491.9	403.4	315.7	101.8	123.7	145	157	425.85	131.875	-1.6873902	-3.2207354	0.0725144
231872	A_55_P1993976	Aimp2	aminoacyl tRNA synthetase co	NM_001172146	43539.4	40030.7	36971.1	32709.8	11671.1	11567.2	12782.3	11281.4	38312.75	11825.5	-1.6896189	-3.2257148	0.0005554
216505	A_51_P463428	Pik3ip1	phosphoinositide-3-kinase int	NM_178149	2180.8	2182.7	2777.1	2261.1	618.4	837.6	884.9	602	2350.425	735.725	-1.689802	-3.2261242	0.01771651
12167	A_52_P586944	Bmpr1b	bone morphogenetic protein	NM_007560	71.2	93.8	87.5	59.2	20.2	26.4	21.7	27.4	77.925	23.925	-1.6923953	-3.2319285	0.03466728
20648	A_55_P2122180	Snta1	syntrophin, acidic 1	NM_009228	16035.8	13866.7	14210.8	13737.9	4528.7	4578	4681	4091.7	14462.8	4469.85	-1.6931127	-3.2335361	9.85E-05
67149	A_55_P2025368	Nkain1	Na+/K+ transporting ATPase i	NM_025998	275.8	256.1	258.7	216.6	69.9	72.6	85.5	82.8	251.8	77.7	-1.6958845	-3.2397546	0.00077918
268903	A_51_P152747	Nrip1	nuclear receptor interacting p	NM_173440	2467.5	2138.3	2536.2	1975.4	667.4	754.9	680.5	696.1	2279.35	699.725	-1.6978283	-3.2441225	0.00047078
17164	A_52_P15008	Mapkapk2	MAP kinase-activated protein	NM_008551	3511.4	3085.4	3410.2	3100.5	1028.9	978.5	1000.5	1021.2	3276.875	1007.275	-1.699782	-3.2485187	3.51E-05
232334	A_52_P205797	Vgll4	vestigial like 4 (Drosophila)	NM_177683	147.4	129.4	149.4	142	36.9	54.2	36.7	49.3	142.05	44.275	-1.7012691	-3.2518688	0.0087514
21885	A_55_P1968362	Tle1	transducin-like enhancer of sp	NM_011599	176.4	132	137	145.3	48.4	35.2	45.9	52.8	147.675	45.575	-1.7026742	-3.2550376	0.01082014
70059	A_51_P122649	Degs2	degenerative spermatocyte h	NM_027299	15	19.9	25.4	14.8	5.2	6.4	6.1	4.9	18.775	5.65	-1.7044236	-3.258987	0.07149217
12905	A_55_P2177386	Cradd	CASP2 and RIPK1 domain con	NM_009950	490.8	467.1	461.8	581.6	152.2	152.7	162	144.8	500.325	152.925	-1.7048596	-3.259972	0.00025014
67468	A_52_P518808	Mmd	monocyte to macrophage diff	ENSMUST00000134929	2131.5	2267.9	2573.2	2142	727.1	758.3	708.6	600.9	2278.65	698.725	-1.7066104	-3.2639307	0.00053495
320183	A_52_P121491	Msrb3	methionine sulfoxide reducta	NM_177092	1218.9	1375.1	1344.9	1550.5	490.7	497	359.5	350.9	1372.35	424.525	-1.7069806	-3.2647682	0.00982821
14469	A_51_P203955	Gbp2	guanylate binding protein 2	NM_010260	311.6	276.5	345	286.8	106.9	86.4	109.8	73.7	304.975	94.2	-1.7084091	-3.2680026	0.00910532
22035	A_55_P2018017	Tnfsf10	tumor necrosis factor (ligand)	NM_009425	253.4	359.7	310.9	218.6	76.3	91	80.6	96.6	285.65	86.125	-1.7100786	-3.2717865	0.0237888
100502767	A_55_P2258832	LOC100502767	uncharacterized LOC1005027	XR_104684	3346	3625.8	3069.5	1992.4	1025.1	892.8	875.9	806	3008.425	899.95	-1.7108461	-3.2735275	0.06608731
18830	A_55_P1993955	Pltp	phospholipid transfer protein	NM_011125	311.3	298.1	279	196.6	95.2	79.9	83	70.1	271.25	82.05	-1.711415	-3.2748186	0.02309509
20148	A_55_P2020128	Dhrs3	dehydrogenase/reductase (SD	NM_011303	7345.3	6386.8	6602.3	7662.4	1876.4	2348.1	2271.3	2058	6999.2	2138.45	-1.7121143	-3.2764064	0.00049387
70028	A_55_P2029203	Dopey2	dopey family member 2	NM_026700	184.3	143.7	156.6	184.7	57.5	50.4	44.7	51.3	167.325	50.975	-1.7122193	-3.2766449	0.00152525
67252	A_51_P116755	Cap2	CAP, adenylate cyclase-associ	NM_026056	3738.7	4753.5	4131.8	4092.4	1333.2	1348.4	1322	1079	4179.1	1270.65	-1.7181714	-3.2901912	0.00079388
209378	A_55_P2077048	Itih5	inter-alpha (globulin) inhibito	NM_172471	873.8	898.3	982.6	957.3	270.4	331.4	307.3	228.3	928	284.35	-1.7189571	-3.2919835	0.00217041
57765	A_51_P501364	Tbx21	T-box 21	NM_019507	102.5	71.8	89.9	67.2	19.4	30	25.3	25.5	82.85	25.05	-1.7219161	-3.2987424	0.040067
76757	A_51_P249608	Trdn	triadin	ENSMUST00000050626	53470.4	49717.5	55605.9	50754.4	15919.5	14836.9	17365.1	15439.7	52387.05	15890.3	-1.7221112	-3.2991886	5.76E-05
11472	A_51_P108266	Actn2	actinin alpha 2	NM_033268	11069.8	10765	7753.4	10958.6	3180.4	4159.4	2592	2477.2	10136.7	3102.25	-1.7243237	-3.3042519	0.07387864
19317	A_55_P2251082	Qk	quaking	AK033279	1863.7	1989.7	1747.5	2081.1	614.7	626.9	506.6	563.6	1920.5	577.95	-1.7343588	-3.3273158	0.00029956
53945	A_51_P389988	Slc40a1	solute carrier family 40 (iron-	NM_016917	1819.6	1792.3	1676	1414.9	477.7	558.8	508.4	464.7	1675.7	502.4	-1.7345419	-3.3277381	0.00061955
68828	A_52_P562467	Sync	syncoilin	NM_023485	1244.6	1244.8	1235.3	1024.1	390	346.5	356.5	327	1187.2	355	-1.7397511	-3.3397754	0.00026306
667572	A_55_P2108690	Gm8709	glyceraldehyde-3-phosphate (	NR_033633	9430.6	8259.6	10247.7	7292.2	2429.1	2508.7	2806.9	2733.8	8807.525	2619.625	-1.7399392	-3.3402108	0.00149408
54357	A_55_P2108790	Epb4.1l4b	erythrocyte protein band 4.1-	ENSMUST00000044022	62.9	53.6	45.6	58	21.2	17.2	11.8	16.6	55.025	16.7	-1.7409842	-3.3426312	0.04994102
78416	A_51_P104608	Rnase6	ribonuclease, RNase A family,	NM_030098	20.2	17.8	19.1	19.1	5.1	8.6	4.8	4.9	19.05	5.85	-1.74761	-3.3580182	0.05498238
68428	A_55_P2096883	Steap3	STEAP family member 3	NM_001085409	360	281.4	323	264	94.1	84.9	103.3	81.4	307.1	90.925	-1.7516618	-3.3674624	0.00211881
75578	A_55_P2190299	Fggy	FGGY carbohydrate kinase do	NM_001113412	551.6	506.5	552	453.9	150.9	155.7	151.7	151.1	516	152.35	-1.7555352	-3.3765157	7.5623E-05
100198	A_55_P1975510	H6pd	hexose-6-phosphate dehydro	NM_173371	2952	2900.2	3106.1	3000.8	834.1	988.9	793.3	916.8	2989.775	883.275	-1.7638726	-3.396085	0.00010567
52468	A_55_P2088325	Ctdsp2	CTD (carboxy-terminal domai	NM_001113470	2026	1824.4	2119.5	2091.2	558.3	627.1	629.7	552.4	2015.275	591.875	-1.7679274	-3.4056434	8.7929E-05
100504346	A_55_P1955821	Gm13304	predicted gene 13304	NM_001193666	2767.1	3107.5	2489.6	2531.3	923.5	783.4	998.1	549.9	2723.875	813.725	-1.7731048	-3.4178873	0.04893456
15414	A_51_P232207	Hoxb6	homeobox B6	NM_008269	99.7	106.7	85.2	110.2	21.1	25.4	37.3	36.1	100.45	29.975	-1.7781854	-3.4299449	0.06930911
18627	A_51_P282760	Per2	period homolog 2 (Drosophila	NM_011066	211.6	303	256.2	325.3	84.9	89.7	73.6	68.4	274.025	79.15	-1.7807091	-3.4359502	0.01082374
114714	A_55_P1955891	Rad51c	RAD51 homolog c (S. cerevisia	ENSMUST00000067692	10999.2	9796.2	13831.4	11235.5	3076	4033.1	3204.6	3020.5	11465.575	3333.55	-1.7808851	-3.4363693	0.00383784
13645	A_52_P38627	Egf	epidermal growth factor	NM_010113	1547	1573.4	1820.5	1572.1	501.3	442.6	471.5	461.2	1628.25	469.15	-1.7934427	-3.466411	5.97E-05
27281	A_51_P325862	Hrasls	HRAS-like suppressor	NM_013751	3521.5	3542.1	3538.6	3868.6	1133.8	1017.7	1011.6	1000	3617.7	1040.775	-1.798167	-3.4777807	2.68E-05
26397	A_51_P272817	Map2k3	mitogen-activated protein kin	NM_008928	352.2	361.3	370.5	317.4	113.6	107	87.1	96	350.35	100.925	-1.8004858	-3.4833751	0.00036635
14664	A_55_P2010788	Slc6a9	solute carrier family 6 (neurot	NM_008135	1332.5	1608.3	1806.8	1956.7	471.5	557.1	442	442.1	1676.075	478.175	-1.8014077	-3.4856016	0.00387528
17260	A_55_P2155620	Mef2c	myocyte enhancer factor 2C	NM_025282	876.7	812.7	885.9	1068.9	279.1	280.9	211.4	274	911.05	261.35	-1.8037537	-3.4912744	0.00196629
30948	A_55_P2073308	Bin1	bridging integrator 1	NM_009668	18618.7	15136	19678.2	15001.4	4909.3	4944.5	5254.5	4366.2	17108.575	4868.625	-1.8057176	-3.4960301	0.00092753
106628	A_55_P2023424	Trip10	thyroid hormone receptor int	NM_134125	19478.3	20848.9	22983.8	24229	6040.7	6621.4	5909.9	6399.2	21885	6242.8	-1.8060066	-3.4967304	0.00012481
77569	A_55_P2023727	Limch1	LIM and calponin homology d	NM_001001980	5483.5	5464.3	5105.5	5805.8	1594.1	1691.6	1519.8	1424.9	5464.775	1557.6	-1.812202	-3.5117789	4.92E-05
72117	A_51_P122845	Naa50	N(alpha)-acetyltransferase 50	NM_028108	3759.4	3539.9	3899.6	3745	1001.7	1092.3	1077	1069.6	3735.975	1060.15	-1.8171484	-3.52384	1.19E-05
14178	A_55_P2035932	Fgf7	fibroblast growth factor 7	NM_008008	339.2	476.5	451.4	666.8	115.6	159.1	143.1	118.8	483.475	134.15	-1.8204098	-3.531815	0.08413182
64074	A_55_P2002903	Smoc2	SPARC related modular calciu	NM_022315	18086.6	17687.4	20062.9	21535.6	5875.1	6759.6	5052.6	4391.8	19343.125	5519.775	-1.8233049	-3.5389096	0.00464789
22682	A_55_P2180071	Zfand5	zinc finger, AN1-type domain	NM_009551	22341.1	24837	25779.9	18609.9	6514.9	6434	6209.6	6484.1	22891.975	6410.65	-1.8253387	-3.543902	0.00052695
208618	A_55_P2102385	Etl4	enhancer trap locus 4	NM_001081006	4345	4317.4	4385.6	4552.4	1186.8	1366.2	1248	1172.7	4400.1	1243.425	-1.8255558	-3.5444352	2.32E-05
117160	A_55_P1985768	Ttyh2	tweety homolog 2 (Drosophila	NM_053273	1011.2	846.7	1247.1	1003	260	342.3	272.9	278.1	1027	288.325	-1.8272133	-3.5485099	0.00349529
68108	A_55_P2034784	9430008C03Rik	RIKEN cDNA 9430008C03 gen	NR_015463	84.9	72.8	89.7	77.7	22.7	29.7	25.5	15.8	81.275	23.425	-1.8272871	-3.5486914	0.0397153
66273	A_55_P1970578	1810020D17Rik	RIKEN cDNA 1810020D17 gen	NM_001177945	6005.8	5710.8	5447.1	4904.9	1507.2	1502.7	1621	1558.5	5517.15	1547.35	-1.8308228	-3.557399	5.29E-05
53601	A_52_P515769	Pcdh12	protocadherin 12	NM_017378	323.5	245.5	416.7	218.7	86.6	82.1	84.4	75.1	301.1	82.05	-1.8318396	-3.559907	0.05078399
15950	A_55_P1988202	Ifi203	interferon activated gene 203	NM_001045481	757.2	816.9	696.1	859.3	191.1	247.2	238	201.7	782.375	219.5	-1.8375278	-3.5739707	0.00066888
16323	A_51_P239750	Inhba	inhibin beta-A	NM_008380	89.6	87.5	88.1	96.6	17.9	28.7	31.7	25	90.45	25.825	-1.8391314	-3.5779455	0.01697645
77630	A_55_P2024525	Prdm8	PR domain containing 8	NM_029947	88.8	98	99.3	75.2	27.2	27.2	23.3	22.6	90.325	25.075	-1.8455004	-3.5937759	0.00083852
100504362	A_55_P2024625	Gm1987	predicted gene 1987	NM_001193667	2173.3	2628.2	2157.4	2336.1	693.5	659.3	818.3	460.6	2323.75	657.925	-1.8460238	-3.5950799	0.01901887
217893	A_55_P2218223	Pacs2	phosphofurin acidic cluster so	NM_001081170	805.4	721.3	680.8	750.9	204.2	193.3	216.8	207.6	739.6	205.475	-1.8462903	-3.5957439	3.47E-05
101563	A_55_P2302577	AI426330	expressed sequence AI42633	AK133434	3289.3	3508.3	4052.1	4005.3	920.4	1086	1014.9	1089.1	3713.75	1027.6	-1.8513254	-3.6083154	0.00022057
231238	A_51_P291078	Sel1l3	sel-1 suppressor of lin-12-like	NM_172710	1194.7	1170.4	1188.3	1283.4	332.3	369.7	318.8	320.7	1209.2	335.375	-1.8518788	-3.6096996	2.73E-05
94089	A_55_P2146663	Trim7	tripartite motif-containing 7	NM_053166	102.8	115.5	91.2	105.4	31.9	31.6	26.8	24.8	103.725	28.775	-1.853093	-3.6127389	0.0006948
219132	A_55_P2015687	D14Ertd668e	DNA segment, Chr 14, ERATO	NM_199015	248.6	296.7	317.2	273.7	63.9	84.6	93.5	74	284.05	79	-1.8548916	-3.6172458	0.00271274
104252	A_52_P155554	Cdc42ep2	CDC42 effector protein (Rho G	NM_026772	1162.4	893.3	824.1	967.6	256.3	300	230.9	268.9	961.85	264.025	-1.8595689	-3.6289921	0.00169804
20348	A_52_P87839	Sema3c	sema domain, immunoglobul	NM_013657	136.2	146	131.7	147.2	34.8	38.3	39.1	42.5	140.275	38.675	-1.8608443	-3.6322017	5.75E-05
105348	A_51_P171200	Golm1	golgi membrane protein 1	NM_027307	2293.6	2157.4	2537.6	1538.5	576.8	648.5	547.9	539.6	2131.775	578.2	-1.8621571	-3.6355083	0.008379
75695	A_55_P2145680	Rilpl1	Rab interacting lysosomal pro	NM_021430	389.7	387	481.9	365.2	124.1	97.4	106.4	117	405.95	111.225	-1.8656536	-3.6443301	0.00076066
15401	A_55_P2219982	Hoxa4	homeobox A4	NM_008265	41.6	24.7	35.6	40.5	9.2	7.5	12.2	9.9	35.6	9.7	-1.868461	-3.6514285	0.06471685
52377	A_55_P2046393	Rcn3	reticulocalbin 3, EF-hand calci	NM_026555	2022.1	2485.4	1843.4	2082.3	476.8	826.3	588.3	462.4	2108.3	588.45	-1.8729621	-3.6628386	0.04248561
66912	A_51_P174681	Bzw2	basic leucine zipper and W2 d	NM_025840	2528.9	2298.5	2626.4	2337.7	652.7	623.3	753.4	643.3	2447.875	668.175	-1.8749593	-3.6679126	7.33E-05
16658	A_52_P495869	Mafb	v-maf musculoaponeurotic fib	NM_010658	876.5	1454	777.8	945.4	300.3	276.7	266.7	233.3	1013.425	269.25	-1.8754756	-3.6692255	0.03913403
208177	A_55_P2021465	Phldb2	pleckstrin homology-like dom	NM_153412	1139.8	1177.3	1115.7	1224.3	311.3	354.9	319.9	284.3	1164.275	317.6	-1.877782	-3.6750962	5.72E-05
107568	A_55_P2003158	Wwp1	WW domain containing E3 ub	NM_177327	1172.1	1062.7	1089.1	1100.5	316	292.2	312.4	282	1106.1	300.65	-1.8799669	-3.6806662	1.51E-05
384071	A_55_P2073248	Slc25a34	solute carrier family 25, mem	NM_001013780	2601.7	3261	1887.1	2897.7	628.5	789.1	623.3	814	2661.875	713.725	-1.881621	-3.6848887	0.02523988
210044	A_51_P337523	Adcy2	adenylate cyclase 2	NM_153534	403.9	482.4	489.3	519.8	126.1	135.8	125.8	124.7	473.85	128.1	-1.8818147	-3.6853834	0.00010993
76508	A_55_P2091889	2210015D19Rik	RIKEN cDNA 2210015D19 gen	NR_015577	51	65.9	70.5	73.1	20.6	14	22.8	14.2	65.125	17.9	-1.8838186	-3.6905059	0.04507529
108079	A_52_P137378	Prkaa2	protein kinase, AMP-activated	NM_178143	6935.1	5549.9	6195.3	5710.8	1588.9	1616.7	1793.7	1590.7	6097.775	1647.5	-1.8843912	-3.6919709	0.00010856
22163	A_55_P2125491	Tnfrsf4	tumor necrosis factor recepto	NM_011659	720.7	679.1	587	980.5	212.2	194.9	221.1	165.4	741.825	198.4	-1.885271	-3.6942231	0.01311698
319603	A_55_P2373987	A730009E18Rik	RIKEN cDNA A730009E18 gen	AK047818	1733.7	1713.8	1955.8	2511.8	602.6	424.3	526	580.7	1978.775	533.4	-1.8865262	-3.6974385	0.00873789
231440	A_51_P114693	Parm1	prostate androgen-regulated	NM_145562	5242.9	4667.8	5755.9	5429.5	1267.8	1427.6	1460.7	1520.8	5274.025	1419.225	-1.8928898	-3.7137838	0.00011613
18670	A_51_P249118	Abcb4	ATP-binding cassette, sub-fam	NM_008830	21371.4	21081.3	22854.3	23346	6590.2	5884	5888	5501.1	22163.25	5965.825	-1.8950953	-3.7194656	3.48E-05
15273	A_51_P443754	Hivep2	human immunodeficiency vir	NM_010437	601	583.3	758.5	598.6	152.7	177.3	190.3	159.6	635.35	169.975	-1.8991789	-3.7300085	0.00057552
11568	A_55_P2035662	Aebp1	AE binding protein 1	NM_009636	40786.3	32728.6	44318.5	40663.8	10418.1	10088.4	11448.5	10202.4	39624.3	10539.35	-1.9036085	-3.7414785	0.00029722
380698	A_52_P642453	Obscn	obscurin, cytoskeletal calmod	NM_199152	5022.6	4513.3	5372.6	4340.3	1287.9	1395	1167.8	1281.1	4812.2	1282.95	-1.9048926	-3.7448101	0.00012985
13685	A_51_P330428	Eif4ebp1	eukaryotic translation initiatio	NM_007918	11190.4	11320.1	14021.1	9666.3	2854.5	3201.4	3114.5	3051	11549.475	3055.35	-1.906818	-3.7498114	0.00061312
20167	A_51_P209930	Rtn2	reticulon 2 (Z-band associated	NM_013648	18528.2	16464.9	17779.3	15185.6	4919	3858.7	5034.8	4340.6	16989.5	4538.275	-1.9083556	-3.7538099	0.00042106
242050	A_51_P155843	Igsf10	immunoglobulin superfamily,	NM_001162884	105.7	151.7	100.3	123.6	25.2	39.5	29.3	33.9	120.325	31.975	-1.9128617	-3.7655529	0.0183084
666945	A_55_P2037702	Gm10638	predicted gene 10638	NR_027829	1628.8	1511.9	1781.5	1414.5	471.8	376.7	442.2	390	1584.175	420.175	-1.9153762	-3.7721215	0.00031859
21939	A_55_P2036693	Cd40	CD40 antigen	NM_011611	26.2	28.4	34.3	25.9	9.1	9	6.4	6.2	28.7	7.675	-1.9170498	-3.7765	0.01004758
76722	A_51_P165293	Ckmt2	creatine kinase, mitochondria	NM_198415	61985.1	66552.4	53702.5	46100.2	15915.5	16450.2	13808.9	13886.5	57085.05	15015.275	-1.9170888	-3.7766022	0.00149231
14962	A_51_P413866	Cfb	complement factor B	NM_008198	362.8	423.4	485.2	300	96.3	143.3	100.5	79.1	392.85	104.8	-1.9177866	-3.7784292	0.06535169
66204	A_55_P2062021	Acyp1	acylphosphatase 1, erythrocy	ENSMUST00000121930	200.5	242.9	311.4	277.5	61.8	55.5	74.2	79.8	258.075	67.825	-1.9237578	-3.7941003	0.01131857
16835	A_55_P2167999	Ldlr	low density lipoprotein recep	NM_010700	730.5	890.8	706	705.8	202.9	231.3	184.3	180.5	758.275	199.75	-1.9245811	-3.796266	0.0005325
76376	A_51_P317542	Slc24a2	solute carrier family 24 (sodiu	NM_172426	60.9	61.4	51.2	53	12.7	19.8	15	12.9	56.625	15.1	-1.9260386	-3.8001033	0.00530115
238871	A_65_P12530	Pde4d	phosphodiesterase 4D, cAMP	NM_011056	1122.8	882.6	1099	906.1	240.4	222.7	260.6	337.3	1002.625	265.25	-1.9280427	-3.8053857	0.00435003
17183	A_55_P2157581	Matn4	matrilin 4	NM_013592	16.8	16.9	19	18.2	4.8	5.4	5.8	3.1	17.725	4.775	-1.9297049	-3.8097728	0.02784154
216011	A_52_P77204	Lrrc20	leucine rich repeat containing	NM_153542	4855.5	4015.6	4701.9	3839	1149.1	978.8	1305.7	1130.4	4353	1141	-1.9319907	-3.8158135	0.00064935
20192	A_55_P1967201	Ryr3	ryanodine receptor 3	NM_177652	50.9	33	44.5	37.2	10.2	9.5	12.6	10.7	41.4	10.75	-1.9334091	-3.8195671	0.00510417
76294	A_51_P170827	Asb5	ankyrin repeat and SOCs box-	NM_029569	10511	9221.2	11747.9	6616.6	2244.4	3226.3	2559.9	1879.3	9524.175	2477.475	-1.9391776	-3.8348698	0.08137324
635504	A_55_P2108845	Gm7160	predicted gene 7160	XM_921685	204.3	198.5	184	228.8	45.6	60.3	44.2	63.8	203.9	53.475	-1.9456347	-3.8520721	0.00284331
218121	A_51_P349495	Mboat1	membrane bound O-acyltrans	NM_153546	120.9	152.5	116	159.3	34.1	51.5	34.8	25.3	137.175	36.425	-1.9459095	-3.8528059	0.07275628
75607	A_55_P2029517	Wnk2	WNK lysine deficient protein	NM_029361	1153.4	879.5	1268.2	1095.3	266.6	264.5	298	303.7	1099.1	283.2	-1.9466414	-3.8547608	0.00076622
74735	A_65_P07361	Trim14	tripartite motif-containing 14	AK172895	23.7	28.8	16.9	21.1	4.3	7.5	6.8	5	22.625	5.9	-1.9485611	-3.8598937	0.0871978
26416	A_55_P2046338	Mapk14	mitogen-activated protein kin	NM_001168514	14621.1	13036.7	14919.3	14816.8	3524.6	3803.7	3598.1	3926.7	14348.475	3713.275	-1.9493353	-3.8619655	1.87E-05
216558	A_51_P475580	Ugp2	UDP-glucose pyrophosphoryla	NM_139297	14070.9	12081.5	15418.9	13261.4	3482.1	3741.7	3434.8	3449.4	13708.175	3527	-1.9537341	-3.8737588	6.4425E-05
73635	A_66_P126563	1700113I22Rik	RIKEN cDNA 1700113I22 gene	NM_026865	5824.8	6012.6	6272.3	4479.1	1376.3	1409.4	1570.5	1433.5	5647.2	1447.425	-1.9539397	-3.874311	0.00053893
23962	A_51_P387123	Oasl2	2-5 oligoadenylate synthetase	NM_011854	176.7	156.1	163.5	117.5	38.2	36.3	49.3	34.1	153.45	39.475	-1.9571337	-3.8828977	0.00713704
13527	A_51_P184300	Dtna	dystrobrevin alpha	NM_010087	274.7	225.2	208.5	171.5	54.1	65.5	49.8	54.9	219.975	56.075	-1.9587392	-3.8872211	0.00465956
270198	A_55_P1992959	Pfkfb4	6-phosphofructo-2-kinase/fru	NM_173019	8394.9	8916.3	10729.9	6413.3	2264.7	2085.3	2270.2	2100.9	8613.6	2180.275	-1.959297	-3.8887245	0.00357022
26390	A_55_P2297806	Mapkbp1	mitogen-activated protein kin	NM_011941	16.9	20	24.4	16.4	5.3	5.4	5	4.1	19.425	4.95	-1.9622022	-3.8965632	0.0040167
66355	A_55_P1992329	Gmpr	guanosine monophosphate re	NM_025508	1189.1	979.4	1210.3	1070	255.8	316.1	268.8	300.9	1112.2	285.4	-1.9623284	-3.8969039	0.00020711
14385	A_51_P385598	Slc37a4	solute carrier family 37 (gluco	NM_008063	5009.1	4353.8	4732	4041.2	1109.5	1128.3	1165.3	1239.1	4534.025	1160.55	-1.9625015	-3.8973716	5.23E-05
75219	A_52_P89064	Dusp18	dual specificity phosphatase 1	NM_173745	85.6	117.4	68.7	59.5	22.2	22.1	18.9	19	82.8	20.55	-1.9662948	-3.9076326	0.04059049
15166	A_55_P2088202	Hcn2	hyperpolarization-activated, c	NM_008226	3830.1	2407.9	3278.4	2545.8	828.3	644	756	818.2	3015.55	761.625	-1.9664818	-3.9081389	0.00820081
12816	A_55_P2062469	Col12a1	collagen, type XII, alpha 1	NM_007730	151.7	240.2	116.8	176.4	34.7	42.8	45.7	47.3	171.275	42.625	-1.9673699	-3.9105456	0.0653834
106522	A_55_P1999790	Pkdcc	protein kinase domain contai	NM_134117	16125.4	15718.8	15632	11887.3	3793.7	4345.2	3607.1	3387	14840.875	3783.25	-1.9673966	-3.9106179	0.00091374
56504	A_51_P375862	Srpk3	serine/arginine-rich protein s	NM_019684	2644.1	2372.9	2536.6	2225.9	618.6	651.1	641.8	582.1	2444.875	623.4	-1.9697871	-3.9171031	2.64E-05
99031	A_55_P1953454	Osbpl6	oxysterol binding protein-like	NM_145525	236.6	232.9	312.6	364.9	93.7	52.5	75.5	71.7	286.75	73.35	-1.9707189	-3.919634	0.05572646
52428	A_55_P1968878	Rhpn2	rhophilin, Rho GTPase binding	NM_027897	506.2	324.4	528.1	398.3	120.4	94.6	106.9	120	439.25	110.475	-1.9712761	-3.9211479	0.00987329
12180	A_51_P468055	Smyd1	SET and MYND domain conta	NM_009762	576.8	742.3	489.8	446.9	150.6	111.4	163.5	141.9	563.95	141.85	-1.9778955	-3.9391805	0.01785175
20300	A_51_P161265	Ccl25	chemokine (C-C motif) ligand	NM_009138	888.4	957.2	981.1	1126.6	226.9	233.5	301.4	244.1	988.325	251.475	-1.9784256	-3.9406282	0.00048291
14571	A_51_P342481	Gpd2	glycerol phosphate dehydrog	NM_010274	596.6	492.4	701.2	501.8	150.6	135.9	134.2	155.7	573	144.1	-1.9792781	-3.9429573	0.00097407
18563	A_55_P2008599	Pcx	pyruvate carboxylase	NM_001162946	18277.1	16340.6	20365.2	16894.3	4137.7	4601.6	4666.5	4765.8	17969.3	4542.9	-1.9807073	-3.9468653	7.53E-05
16562	A_55_P2115732	Kif1c	kinesin family member 1C	NM_153103	468.6	370.3	377.1	425	128.7	93.1	78.2	121.1	410.25	105.275	-1.9842892	-3.9566769	0.0102414
57295	A_55_P2096535	Icmt	isoprenylcysteine carboxyl me	NM_133788	923.3	791.4	753.5	847.9	237.6	181.6	221.6	197.4	829.025	209.55	-1.9875823	-3.9657186	0.00027278
22359	A_55_P2030524	Vldlr	very low density lipoprotein r	NM_013703	14571.3	11880.7	14393.1	9693.7	3067	3306.7	2985.3	3219.8	12634.7	3144.7	-1.9882228	-3.9674796	0.00162724
11931	A_51_P151484	Atp1b1	ATPase, Na+/K+ transporting,	NM_009721	2420.8	2988.7	1541.3	2766.2	549	715.4	526.8	597.8	2429.25	597.25	-1.9905733	-3.9739487	0.0531537
12291	A_51_P466910	Cacna1g	calcium channel, voltage-dep	NM_009783	45.9	69.6	52.6	69.3	14.9	18.8	11.5	14.3	59.35	14.875	-1.9954514	-3.9874085	0.0225068
20266	A_51_P342877	Scn1b	sodium channel, voltage-gate	NM_011322	1162.5	1101.5	1190.6	997.8	290.8	286.8	274.8	262	1113.1	278.6	-1.9962257	-3.9895491	2.45E-05
14369	A_52_P552665	Fzd7	frizzled homolog 7 (Drosophil	NM_008057	499	498.3	606.5	454.4	108.4	170.9	111.1	130.5	514.55	130.225	-1.9987748	-3.9966044	0.00632639
13549	A_55_P2021792	Dyrk1b	dual-specificity tyrosine-(Y)-p	NM_001037957	609.1	505.3	555.5	455.1	141.4	128.3	140.9	118.2	531.25	132.2	-2.0021462	-4.005955	0.00029002
216961	A_55_P2028320	Coro6	coronin 6	NM_139128	116.9	155.9	137.5	138.4	33.2	37.3	27.1	40	137.175	34.4	-2.003308	-4.0091823	0.00212095
81004	A_55_P1987396	Tbl1xr1	transducin (beta)-like 1X-linke	NM_030732	988.5	1146.4	1043.2	961.9	246.1	272.9	264.5	245.8	1035	257.325	-2.0061852	-4.0171857	2.58E-05
70294	A_55_P2071300	Rnf126	ring finger protein 126	NM_144528	7920.8	5904.8	6824	6125.3	1766.2	1503.5	1738	1624.7	6693.725	1658.1	-2.0065894	-4.0183114	0.00027669
18933	A_55_P2131915	Prrx1	paired related homeobox 1	NM_001025570	188.5	194.1	209.5	257.8	52.6	48.6	55	53.4	212.475	52.4	-2.0099973	-4.0278146	0.00027211

13131	A_55_P2112892	Dab1	disabled homolog 1 (Drosoph	NM_010014	24.6	26.5	25	19.4	5.3	5.2	5.8	7.5	23.875	5.95	-2.0107251	-4.029847	0.00286672
330222	A_55_P2144641	Sdk1	sidekick homolog 1 (chicken)	NM_177879	113	152.6	154.5	147.4	31	46.7	37.2	27.6	141.875	35.625	-2.011368	-4.0316432	0.01406662
244867	A_52_P565575	Arhgap20	Rho GTPase activating protei	NM_175535	916.7	765.4	758.5	985.6	216.3	234.4	204	191.9	856.55	211.65	-2.0114712	-4.0319318	0.0003358
235283	A_52_P325116	Gramd1b	GRAM domain containing 1B	ENSMUST00000121357	1750.3	1444.9	1522.3	1796.3	409.4	453.6	355.3	391.1	1628.45	402.35	-2.0165146	-4.0460512	0.00022471
97998	A_51_P445841	Deptor	DEP domain containing MTOI	NM_145470	1198.6	1045.3	984.5	1087.4	258.8	269	260	273.5	1078.95	265.325	-2.0204573	-4.0571238	1.83E-05
104156	A_55_P2037454	Etv5	ets variant gene 5	NM_023794	2811.9	2473.7	2399.5	2494.9	620.8	756.7	581.7	558.2	2545	629.35	-2.0231841	-4.0647994	0.00026816
68817	A_66_P121249	Ddi2	DNA-damage inducible protei	NM_001017966	1096	860.7	1450.6	809	243.6	238.3	279.7	246.2	1054.075	251.95	-2.02835	-4.0793801	0.01394853
100042484	A_52_P119350	4732419C18Rik	RIKEN cDNA 4732419C18 gen	XR_106136	11.6	12	9.4	14.4	2.1	4	3.1	2.6	11.85	2.95	-2.030126	-4.0844051	0.04426204
12176	A_66_P120736	Bnip3	BCL2/adenovirus E1B interact	NM_009760	528	530.7	612.1	490	129.2	131.7	139.9	126.4	540.2	131.8	-2.0314324	-4.0881055	3.44E-05
27389	A_55_P2030647	Dusp13	dual specificity phosphatase 1	NM_001007268	15620.5	13431.1	17236.6	15212.4	3718.9	3436.5	4451.2	3445.5	15375.15	3763.025	-2.0331825	-4.0930675	0.00034009
30938	A_55_P2029051	Fgd3	FYVE, RhoGEF and PH domain	ENSMUST00000110087	151.1	136.8	132.8	113.3	34.8	34.1	30.1	31	133.5	32.5	-2.0334491	-4.0938241	0.00015416
20183	A_51_P513311	Rxrg	retinoid X receptor gamma	NM_009107	13056.7	12308.6	10885.6	14005.6	3203	3144.5	2948.3	2911.6	12564.125	3051.85	-2.036661	-4.1029485	6.09E-05
29811	A_51_P176352	Ndrg2	N-myc downstream regulated	NM_013864	64942.5	59715.1	57627.7	57705.8	14257.6	15467.7	13838	14625.8	59997.775	14547.275	-2.0436492	-4.1228706	9.56E-06
67971	A_51_P246924	Tppp3	tubulin polymerization-prom	NM_026481	377.4	363.7	435.4	290.5	94.1	107	82.4	72.3	366.75	88.95	-2.0442654	-4.124632	0.00466445
20679	A_52_P475356	Sox6	SRY-box containing gene 6	NM_011445	301.4	322.3	357	395	85.5	86.7	72.3	88.2	343.925	83.175	-2.0447105	-4.1259047	0.00023036
16409	A_55_P1977929	Itgam	integrin alpha M	NM_001082960	23.5	28.4	26.1	26.6	8	5.8	6.6	5.2	26.15	6.4	-2.0461774	-4.1301019	0.00145534
13628	A_51_P485862	Eef1a2	eukaryotic translation elonga	NM_007906	3504.5	2530.3	3451.8	2838.2	678.4	743.3	773.7	762.2	3081.2	739.4	-2.0476325	-4.1342696	0.00045709
110253	A_55_P1953356	Triobp	TRIO and F-actin binding prot	NM_001024716	994.6	708	888.8	630.1	214.6	176.4	169.5	209.5	805.375	192.5	-2.0491423	-4.1385986	0.00485028
208076	A_55_P1970954	Pknox2	Pbx/knotted 1 homeobox 2	NM_001029838	1619.8	1506.8	1390.8	1653.7	376.1	373.9	357.8	376.4	1542.775	371.05	-2.0528599	-4.1492769	1.33E-05
70556	A_51_P156438	Slc25a33	solute carrier family 25, mem	NM_027460	2751	3132.1	3327.8	3053.6	883.5	667.1	693.7	710.7	3066.125	738.75	-2.0587982	-4.1663909	0.0002089
231470	A_51_P383270	Fras1	Fraser syndrome 1 homolog (	NM_175473	106	111.4	81.2	111.1	23.1	28.3	23	23.5	102.425	24.475	-2.0589867	-4.1669353	0.00069266
19885	A_55_P2051094	Rorc	RAR-related orphan receptor	NM_011281	3732.9	3288.6	3714.1	4563.7	801.1	889.7	1014.6	947.6	3824.825	913.25	-2.0615702	-4.1744039	0.00043898
20927	A_55_P1979814	Abcc8	ATP-binding cassette, sub-fan	NM_011510	692.6	776.8	771.2	1224.4	230.3	190.9	174.5	217.2	866.25	203.225	-2.0630228	-4.178609	0.01472041
76457	A_55_P2057446	Ccdc134	coiled-coil domain containing	NM_172428	2594	2542.5	3068.3	3823.6	593.5	788.1	753	720.4	3007.1	713.75	-2.0631088	-4.178858	0.00307498
238161	A_55_P2350022	Akap6	A kinase (PRKA) anchor prote	NM_198111	263	289.6	290.9	277.3	64	66.1	76.8	61.8	280.2	67.175	-2.0643431	-4.1824349	3.57E-05
381269	A_55_P2096917	Mreg	melanoregulin	NM_001005423	2626.2	2724.2	2734.1	3280.9	787.5	714.8	623.6	588.3	2841.35	678.55	-2.0699217	-4.1986389	0.00037715
75799	A_55_P1983268	4930444P10Rik	RIKEN cDNA 4930444P10 gen	ENSMUST00000145070	42.2	38.9	44.5	50.5	11.8	13.9	8.4	8.5	44.025	10.65	-2.0748085	-4.212885	0.01077003
13197	A_51_P296608	Gadd45a	growth arrest and DNA-dama	NM_007836	1230.7	1373.8	1481	1101.3	385.5	290.5	294.8	260.8	1296.7	307.9	-2.0807983	-4.2304124	0.00173651
56376	A_55_P2001148	Pdlim5	PDZ and LIM domain 5	NM_019809	7045.3	6914.4	6068.2	5131.8	1422.3	1561.9	1467.1	1439.6	6289.925	1472.725	-2.0842089	-4.2404252	0.00021366
360013	A_52_P135822	Myo18a	myosin XVIIIA	ENSMUST00000092884	28595.1	25773.3	28469.7	23766.3	6188.6	6622.2	6236.5	6025.9	26651.1	6268.3	-2.0847163	-4.2419167	2.21E-05
14936	A_55_P2026315	Gys1	glycogen synthase 1, muscle	NM_030678	2146.9	2041	2434.2	2088.1	498.9	468.5	520.5	558.4	2177.55	511.575	-2.0892213	-4.2551834	3.42E-05
108116	A_55_P1989663	Slco3a1	solute carrier organic anion tr	NM_023908	3427.6	3810.7	2855.8	3757.5	822	895.3	729.7	790.8	3462.9	809.45	-2.0916273	-4.2622858	0.00025662
15482	A_51_P340747	Hspa1l	heat shock protein 1-like	NM_013558	272.2	279.7	274.2	248.8	78.4	61.9	60.7	52.9	268.725	63.475	-2.0951794	-4.2727928	0.00042306
71839	A_51_P189361	Osgin1	oxidative stress induced grow	NM_027950	1509.9	1373.1	1629.8	1255.1	323.1	318.8	342	360.9	1441.975	336.2	-2.0954679	-4.2736474	7.46E-05
80290	A_55_P2027392	Gpr146	G protein-coupled receptor 1	NM_030258	4166.4	3413.2	4077.3	3742.5	967.3	851.7	803.4	982.3	3849.85	901.175	-2.0956661	-4.2742345	9.77E-05
78977	A_52_P486279	Popdc3	popeye domain containing 3	NM_024286	755	734.9	814.3	878.2	211.1	180.3	171.8	181.8	795.6	186.25	-2.0956816	-4.2742805	5.5502E-05
18553	A_55_P1972991	Pcsk6	proprotein convertase subtilis	NM_011048	707.2	872.6	746.9	869.8	164.9	233.6	181.8	170.2	799.125	187.625	-2.0984557	-4.2825072	0.0008327
216616	A_55_P2048767	Efemp1	epidermal growth factor-cont	NM_146015	353	411.4	468.9	281.6	83.1	103.2	94.9	69.6	378.725	87.7	-2.1007838	-4.2894235	0.01144851
21917	A_55_P2137706	Tmpo	thymopoietin	NM_001080129	3673.5	3699.8	4224.9	4059.8	820.4	986.9	961.9	879.6	3914.5	912.2	-2.1026687	-4.2950315	3.48E-05
224796	A_51_P420547	Clic5	chloride intracellular channel	NM_172621	11335.9	11565.6	10484.2	10327.5	2707.9	2665.2	2410.8	2359.8	10928.3	2535.925	-2.1083911	-4.3121014	1.46E-05
235320	A_55_P2024155	Zbtb16	zinc finger and BTB domain co	NM_001033324	14531.7	13855.6	13949	13652.9	3515.9	3328.4	3185.2	2954.6	13997.3	3246.025	-2.1109211	-4.3196701	9.07E-06
56323	A_55_P1982727	Dnajb5	DnaJ (Hsp40) homolog, subfa	NM_019874	12371	11739.2	12718.9	12013.9	2938.7	3101.4	2747.2	2543.8	12210.75	2832.775	-2.1111605	-4.320387	1.65E-05
668212	A_55_P1956418	Efr3b	EFR3 homolog B (S. cerevisiae	NM_001082483	843.5	751.1	591.1	790.4	146.4	257.3	137.7	161.5	744.025	175.725	-2.1162371	-4.3356164	0.03149506
78279	A_55_P2213348	5330421C15Rik	RIKEN cDNA 5330421C15 gen	AK039175	1564.7	1755.2	1969.7	1581.9	376.3	391.6	398.3	410.5	1717.875	394.175	-2.1180916	-4.3411931	3.88E-05
100041488	A_55_P2051039	Gm11937	predicted gene 11937	NM_001099346	231.4	139.5	157.5	209.6	47.6	34.8	35.6	50.5	184.5	42.125	-2.1207869	-4.3493109	0.02094162
70892	A_55_P2075424	Ttll7	tubulin tyrosine ligase-like far	NM_027594	685.9	557.5	582.3	514.2	128.4	151.7	129.7	125.1	584.975	133.725	-2.1252339	-4.3627383	0.00016451
68655	A_51_P153423	Fndc1	fibronectin type III domain co	NM_001081416	2463.8	2695.1	2610.9	2183.8	540.7	658.7	605.5	484.2	2488.4	572.275	-2.1255361	-4.3636521	0.00027565
12450	A_52_P612803	Ccng1	cyclin G1	NM_009831	12557.4	10356.1	12745.3	9582.1	2598.8	2425.8	2537.4	2733.7	11310.225	2573.925	-2.1261495	-4.3655078	0.00016832
20410	A_52_P78373	Sorbs3	sorbin and SH3 domain conta	NM_011366	143.6	125.2	126.8	87.7	34.4	32.2	19.5	24.9	120.825	27.75	-2.1345293	-4.3909383	0.03830536
235584	A_55_P1993836	Dusp7	dual specificity phosphatase 7	NM_153459	549.9	623.6	529.2	519.3	110.2	114.5	141.7	139.8	555.5	126.55	-2.1396239	-4.4064715	0.0001922
21916	A_51_P297069	Tmod1	tropomodulin 1	NM_021883	2241.5	2110.1	2689	2359.1	477.9	552.7	539.2	547.3	2349.925	529.275	-2.1471092	-4.4293936	5.29E-05
329828	A_51_P406557	AI464131	expressed sequence AI46413	NM_001085515	2426.7	2112.6	2549.8	2410.1	580.7	566.3	442.7	559.1	2374.8	537.2	-2.1491024	-4.4355174	0.00015078
14177	A_55_P2073617	Fgf6	fibroblast growth factor 6	ENSMUST00000000187	554	561.6	533.3	517	127.6	127.4	118.3	114.9	541.475	122.05	-2.1501795	-4.4388302	4.65E-06
16531	A_55_P2378486	Kcnma1	potassium large conductance	AK017560	928.3	1186.6	920.3	1005.4	207.2	254.6	204	237.3	1010.15	225.775	-2.1601543	-4.4696265	0.00021017
234686	A_51_P495379	Fhod1	formin homology 2 domain co	NM_177699	4389.4	3512.7	3683.4	3270.5	823.7	786.1	856.3	838.2	3714	826.075	-2.1606558	-4.4711805	6.73E-05
70788	A_51_P205215	Klhl30	kelch-like 30 (Drosophila)	NM_027551	5483.3	4875.5	5291.4	5149.6	1288.8	1197.6	1130.1	1044.7	5199.95	1165.3	-2.1607477	-4.4714653	2.03E-05
18761	A_52_P72587	Prkcq	protein kinase C, theta	NM_008859	2451	2416.1	2389.8	2844.3	586.5	565.7	549.1	546.6	2525.3	561.975	-2.164751	-4.4838903	1.12E-05
14403	A_51_P149623	Gabrd	gamma-aminobutyric acid (G/	NM_008072	31.9	53.3	54.6	65.4	13.4	11.6	10.2	9.3	51.3	11.125	-2.1714135	-4.5046452	0.04296959
18011	A_55_P2023692	Neurl1a	neuralized homolog 1A (Dros	NM_021360	39799.7	34922.4	36645.3	34922.5	8479.9	8038	8035.6	7733.1	36572.475	8071.65	-2.1785178	-4.5268823	5.628E-06
12554	A_51_P114826	Cdh13	cadherin 13	NM_019707	3505.2	3114	3382.1	2703.9	733	688.7	735	639.2	3176.3	698.975	-2.1793097	-4.5293677	6.88E-05
67746	A_55_P2418026	4930577N17Rik	RIKEN cDNA 4930577N17 gen	AK086057	156.4	237.2	218.5	207.4	39.7	41.1	52.2	46.6	204.875	44.9	-2.1816122	-4.5366024	0.00158287
66447	A_51_P215077	Mgst3	microsomal glutathione S-tra	NM_025569	7914.2	7651.3	7243	5575.4	1554.5	1702	1619.3	1326.3	7095.975	1550.525	-2.187338	-4.5546431	0.00062247
19883	A_55_P2078123	Rora	RAR-related orphan receptor	NM_013646	2081.8	2090.6	2285.1	2177	444.9	500	461.8	486.7	2158.625	473.35	-2.1895874	-4.56175	4.556E-06
71355	A_51_P408430	Col24a1	collagen, type XXIV, alpha 1	NM_027770	79.2	103.4	83.9	97.9	12	26.9	22.1	21.4	91.1	20.6	-2.1958367	-4.5815528	0.06173488
67775	A_51_P304170	Rtp4	receptor transporter protein	NM_023386	704.5	564.2	730	547.6	121.5	113.2	183.8	142.6	636.575	140.275	-2.1959711	-4.5819797	0.00506324
140491	A_52_P385489	Ppp1r3a	protein phosphatase 1, regula	NM_080464	6196.1	6829.9	6188.5	6412.1	1311.8	1300	1470.8	1516.6	6406.65	1399.8	-2.1965276	-4.5837476	1.14E-05
11668	A_51_P334942	Aldh1a1	aldehyde dehydrogenase fam	NM_013467	11329	9243.2	7325.2	8589.3	1832	2559.5	1889.8	1684	9121.675	1991.325	-2.1965856	-4.583932	0.00451667
19242	A_55_P2164629	Ptn	pleiotrophin	NM_008973	65.2	98.5	61.6	113.9	14.6	20.1	19.3	17.9	84.8	17.975	-2.1989744	-4.5915282	0.03026953
71795	A_55_P2361437	Pitpnc1	phosphatidylinositol transfer	NM_145823	332.4	261	249.4	274.4	62.9	64.8	56.8	57.5	279.3	60.5	-2.2002294	-4.5955242	9.31E-05
246730	A_55_P1998943	Oas1a	2-5 oligoadenylate synthetase	NM_145211	264.8	225	246	161.9	50.3	34	59.4	52.3	224.425	49	-2.2007337	-4.5971307	0.02374689
226409	A_55_P1990785	Zranb3	zinc finger, RAN-binding dom	NM_027678	1144.2	1437.4	986	1206.8	285.6	255.1	253.1	235.4	1193.6	257.3	-2.2041197	-4.6079328	0.00031804
328087	A_55_P2392370	D930001B02	uncharacterized protein D930	AK147582	115.3	74.1	102	68.9	17.6	23.6	17.9	17.9	90.075	19.25	-2.2043785	-4.6087595	0.00927452
100038730	A_55_P2184449	Gm10387	predicted gene 10387	ENSMUST00000100735	873.5	935	746.6	1493	216.6	199.2	218.1	213.3	1012.025	211.8	-2.2062818	-4.6148438	0.01360616
235302	A_52_P244803	D630033O11Rik	RIKEN cDNA D630033O11 ger	AK052711	107.4	121.9	110.6	93.6	15.5	28.2	21.2	32.1	108.375	24.25	-2.2079338	-4.6201313	0.03371104
246316	A_51_P361830	Lgi2	leucine-rich repeat LGI family	NM_144945	73.4	64.5	80.3	73.4	11.4	15.1	23.2	15.1	72.9	16.2	-2.2135009	-4.6379938	0.0152194
50795	A_55_P2033135	Sh3bgr	SH3-binding domain glutamic	NM_015825	43499.2	36813.7	38840.4	35733.1	8113.9	8926.1	8360.5	7913.7	38721.6	8328.55	-2.214349	-4.6407212	1.62E-05
18104	A_51_P424338	Nqo1	NAD(P)H dehydrogenase, qui	NM_008706	1647.5	1802.1	2142.2	1765.7	412.6	369.1	414.5	376.5	1839.375	393.175	-2.2210565	-4.6623472	4.67E-05
18810	A_55_P2139027	Plec	plectin	NM_001163540	39047.2	32775.5	35157.9	34873.8	7756.5	7433.4	7722.7	7402	35463.6	7578.65	-2.2237733	-4.6711355	5.72E-06
56298	A_66_P134534	Atl2	atlastin GTPase 2	NM_019717	1786.7	2124	2243.7	2531.3	481.3	456.4	394.7	519.3	2171.425	462.925	-2.225748	-4.6775335	0.00042738
20378	A_51_P286748	Frzb	frizzled-related protein	NM_011356	185.4	244.3	153.1	170.1	34.3	41.1	40.4	43.2	188.225	39.75	-2.2262828	-4.6792679	0.0015148
68531	A_66_P107745	1110020A21Rik	RIKEN cDNA 1110020A21 gen	NR_027930	253.9	315	265	275.6	57.1	58.3	53.1	68.7	277.375	59.3	-2.2274711	-4.6831234	8.79E-05
69399	A_51_P328489	1700025G04Rik	RIKEN cDNA 1700025G04 gen	NM_197990	1340.9	1158.5	1149.9	1258.8	275	308.8	237	229.6	1227.025	262.6	-2.2316539	-4.6967209	0.00014089
217012	A_55_P2139396	Unc45b	unc-45 homolog B (C. elegans	NM_178680	1438.2	1519.1	1739.9	1598.6	285.2	353.6	357.7	342.1	1573.95	334.65	-2.2359366	-4.7106842	5.67E-05
381511	A_55_P2162394	Pdp1	pyruvate dehyrogenase phos	NM_001098230	1049.4	960.3	985.8	905.4	203.3	211.8	199.3	210.3	975.225	206.175	-2.2402812	-4.7248916	3.77E-06
20807	A_55_P2149540	Srf	serum response factor	NM_020493	3452.6	2911	3834.8	3187.7	675.5	770.8	688.1	683.8	3346.525	704.55	-2.2425182	-4.7322233	5.37E-05
170786	A_55_P2018061	Cd209a	CD209a antigen	NM_133238	129	135.5	99.9	93.7	20.5	34.2	28.1	16.5	114.525	24.825	-2.2438494	-4.7365918	0.05528872
11937	A_51_P244856	Atp2a1	ATPase, Ca++ transporting, ca	NM_007504	30650.1	22125.2	32040.1	26755.6	6178	5292.5	6169.7	5717.5	27892.75	5839.425	-2.244335	-4.7381867	0.00035458
241431	A_52_P744179	Xirp2	xin actin-binding repeat conta	NM_001024618	4330.6	3996.1	5008.2	5486.5	1081.7	1447.9	891.2	675.6	4705.35	1024.1	-2.2445033	-4.7387393	0.03637339
68515	A_55_P2143139	Myadml2	myeloid-associated differenti	NM_026751	13784.3	13770.9	14741.4	13870.2	3157.9	2766	2725.3	3171.7	14041.7	2955.225	-2.2514463	-4.7615997	8.473E-06
73748	A_55_P2156155	Gadl1	glutamate decarboxylase-like	NM_028638	265.4	215.6	243.8	273.2	48	38.2	88.3	45.7	249.5	55.05	-2.2521697	-4.7639878	0.06146723
21847	A_55_P2022074	Klf10	Kruppel-like factor 10	NM_013692	3862	4350.8	4654.1	4894.7	834	1129.5	973.8	805.6	4440.4	935.725	-2.2541787	-4.7706265	0.00039473
11761	A_51_P333111	Aox1	aldehyde oxidase 1	NM_009676	1952.8	2038.9	2055.8	2432.3	419.9	413.9	484.6	454.4	2119.95	443.2	-2.2557459	-4.7758114	3.28E-05
268527	A_55_P2114776	Greb1	gene regulated by estrogen in	NM_015764	91.5	73.8	72.5	120.5	13.7	26.7	19.4	15.9	89.575	18.925	-2.2575589	-4.7818171	0.05382444
224247	A_51_P279955	E330017A01Rik	RIKEN cDNA E330017A01 gen	NM_175011	133.7	102.6	114.8	105.2	26.3	20.4	32.8	17.9	114.075	24.35	-2.2596781	-4.7888463	0.00964563
225742	A_55_P2174085	St8sia5	ST8 alpha-N-acetyl-neuramini	NM_013666	4646	4031	4586.3	5043.7	841.9	903.5	866.1	1244.5	4576.75	964	-2.2613628	-4.7944415	0.00069795
329251	A_55_P2037328	Ppp1r12b	protein phosphatase 1, regula	NM_001081307	437.4	426.8	424.6	445.5	95.6	90.8	87.2	87.3	433.575	90.225	-2.2654357	-4.8079961	1.76E-06
20878	A_55_P1980636	Aurka	aurora kinase A	NM_011497	713.3	769.6	745.4	749.1	185.4	166.1	130.7	141.5	744.35	155.925	-2.2680091	-4.8165799	0.00014742
237611	A_51_P177261	Stac3	SH3 and cysteine rich domain	NM_177707	37440.8	35094.8	35518.9	34172	7077	7206.1	7483.9	7762.3	35556.625	7382.325	-2.2680879	-4.8168429	2.254E-06
57339	A_55_P2163744	Jph1	junctophilin 1	NM_020604	723.4	673.1	687.3	539	135.8	125.2	143	134.8	655.7	134.7	-2.2760715	-4.8435724	6.81E-05
21823	A_55_P2275249	Th	tyrosine hydroxylase	NM_009377	113.8	94.6	95.3	77.6	16.9	15.3	27.6	20	95.325	19.95	-2.2808946	-4.8597922	0.01075024
104086	A_51_P112817	Cyp27a1	cytochrome P450, family 27, s	NM_024264	228	257.1	306.8	265.6	46.1	62.2	54.4	54.8	264.375	54.375	-2.2815414	-4.8619713	0.00022603
74511	A_51_P301930	Lrrc17	leucine rich repeat containing	NM_028977	175.1	323.2	286.2	287.2	50	69.6	50.8	46.3	267.925	54.175	-2.2876355	-4.8825523	0.01851017
56458	A_52_P453884	Foxo1	forkhead box O1	NM_019739	4228.2	4574	4132.7	2506.5	812.9	722.4	740.9	810.1	3860.35	771.575	-2.2876792	-4.8827	0.00614746
207806	A_55_P2009604	Gm608	predicted gene 608	ENSMUST00000088356	219.5	186.7	179.4	167.7	45.7	42.9	34.8	31.7	188.325	38.775	-2.288744	-4.8863052	0.00070339
99738	A_51_P228706	Kcnc4	potassium voltage gated char	NM_145922	622.9	664	669.2	750	136.8	125.1	140.2	148.8	676.525	137.725	-2.2958752	-4.9105181	1.48E-05
76469	A_51_P493016	Cmya5	cardiomyopathy associated 5	NM_023821	46109.3	34682.8	43805.1	41398.2	8861	7977.9	8566.6	8138.7	41498.85	8386.05	-2.3001644	-4.925139	4.49E-05
217410	A_52_P220810	Trib2	tribbles homolog 2 (Drosophi	NM_144551	380.8	435	516.6	373.1	67.5	113.4	91.2	77.5	426.375	87.4	-2.3012262	-4.9287651	0.00427679
17261	A_55_P1966958	Mef2d	myocyte enhancer factor 2D	NM_133665	214.8	190.8	267	187	40	47	48.1	38.1	214.9	43.3	-2.3035392	-4.9366735	0.0005407
241589	A_51_P519040	D430041D05Rik	RIKEN cDNA D430041D05 ger	NM_001033347	13.2	12.8	10.3	17.5	2.2	2.9	3.2	2.5	13.45	2.7	-2.3052092	-4.9423913	0.00469145
217217	A_55_P2164408	Asb16	ankyrin repeat and SOCS box-	ENSMUST00000036467	5419.8	4197.3	5540.4	5087.2	928.8	1015.8	1146.8	977.9	5061.175	1017.325	-2.3107836	-4.9615248	0.00010282
54725	A_55_P2114118	Cadm1	cell adhesion molecule 1	NM_207675	117.6	109.1	144.4	93.6	19.9	20.3	27.7	25.4	116.175	23.325	-2.313235	-4.9699627	0.00203121
68939	A_51_P293938	Rasl11b	RAS-like, family 11, member E	NM_026878	922	1061.6	870.3	706.6	156.9	277.3	174	129.3	890.125	184.375	-2.3160598	-4.9797033	0.03798464
100126879	A_52_P681016	Gm10759	predicted gene 10759	ENSMUST00000099348	36.6	36	33.6	66.5	10.9	7.2	6.2	9.8	43.175	8.525	-2.3175164	-4.9847334	0.08823742
16956	A_52_P257812	Lpl	lipoprotein lipase	NM_008509	2923.8	4523.2	2732.6	3896.3	667.9	802.8	633.2	669.4	3518.975	693.325	-2.3187693	-4.9890645	0.0031165
399638	A_55_P2257670	A030001D16Rik	RIKEN cDNA A030001D16 ger	AK037146	456.8	385.2	487.8	461	84.2	99.4	65.2	115.7	447.7	91.125	-2.3229211	-5.0034425	0.00365302
12836	A_55_P2064292	Col7a1	collagen, type VII, alpha 1	NM_007738	3249.5	2492.4	3871.7	2843.8	568.4	620.5	587.5	684.9	3114.35	615.325	-2.3238582	-5.0066938	0.00058973
244199	A_55_P2009345	Ovch2	ovochymase 2	NM_172908	47.5	29.3	34.1	37.6	8.9	5.6	8.3	6.7	37.125	7.375	-2.3326351	-5.0372457	0.00704201
329872	A_55_P1999641	Frem1	Fras1 related extracellular ma	NM_177863	22.4	30.1	17.7	19.8	4.1	5.6	3.7	4.3	22.5	4.425	-2.3343279	-5.0431598	0.0064291
21401	A_52_P161297	Tcea3	transcription elongation facto	NM_011542	7863.5	6693.2	7182.2	7532.7	1394.1	1365.2	1615	1395.5	7317.9	1442.45	-2.3436745	-5.0759381	1.17E-05
74165	A_52_P646783	Fbxl22	F-box and leucine-rich repeat	NM_175206	121.1	105.7	135.3	82.1	23.8	25.4	20.1	17.5	111.05	21.7	-2.3462905	-5.0851507	0.00410873
66968	A_55_P2104259	Plin5	perilipin 5	NM_001077348	6923.7	9280.8	5489.7	7724.5	1557.8	1416.8	1260.1	1460.6	7354.675	1423.825	-2.3474289	-5.0891649	0.00145938
79362	A_51_P451176	Bhlhe41	basic helix-loop-helix family, r	NM_024469	63.7	51.9	58.9	65.8	8	12.8	16.8	11.1	60.075	12.175	-2.3475366	-5.0895448	0.01501178
21838	A_55_P2072035	Thy1	thymus cell antigen 1, theta	NM_009382	1142.2	1269.9	1201.3	879.1	172.5	252.3	267.8	195.8	1123.125	222.1	-2.3476662	-5.090002	0.00320713
13808	A_55_P1977533	Eno3	enolase 3, beta muscle	NM_001136062	127419.8	99866.7	111047.9	97847.2	20044.9	20779.9	26338.4	18736.2	109045.4	21474.85	-2.3484355	-5.0927168	0.00033869
11875	A_55_P1957324	Art5	ADP-ribosyltransferase 5	NM_007491	1435.4	1626.7	1559.1	1466.5	313.4	316.2	287.6	271.5	1521.925	297.175	-2.3575864	-5.1251221	7.00E-06
66425	A_55_P1983754	Pcp4l1	Purkinje cell protein 4-like 1	NM_025557	4236.3	6513	4492.4	6830.9	1407.6	1257.9	808.1	838.1	5518.15	1077.925	-2.3659086	-5.1547719	0.03858002
18642	A_51_P117995	Pfkm	phosphofructokinase, muscle	NM_021514	110490.4	100490.9	112015.5	112820.7	20849.1	19651.3	25385.3	18861.3	108954.375	21186.75	-2.370599	-5.1715582	5.11E-05
100502705	A_55_P2371801	LOC100502705	uncharacterized LOC1005027	XR_105398	1921.8	2215.6	1977.6	2711.3	405.4	405.9	403.3	478	2206.575	423.15	-2.3728172	-5.1795158	0.00018796
11790	A_55_P1991851	Speg	SPEG complex locus	NM_001085370	26409.1	25940.3	28774.4	26632.5	5144.2	5189.8	4936.6	5519.4	26939.075	5197.5	-2.3738154	-5.1831005	2.21E-06
269016	A_51_P333518	Sh3rf2	SH3 domain containing ring fi	NM_172966	332.4	329.9	219.8	468	59.6	64.8	62.9	64	337.525	62.825	-2.3757308	-5.1899867	0.00963434
69642	A_51_P427828	2310046A06Rik	RIKEN cDNA 2310046A06 gen	ENSMUST00000093816	584	559	532	521	100.4	119.6	101.6	101.2	549	105.7	-2.37936	-5.2030587	8.399E-06
102093	A_52_P513347	Phkb	phosphorylase kinase beta	NM_199446	2416.4	2582.1	2869.4	2895.9	511.6	499.5	502.9	546.1	2690.95	515.025	-2.3822349	-5.2134375	7.50E-06
12313	A_51_P503937	Calm1	calmodulin 1	NM_009790	6037.1	4747.5	5643	4630.1	886.1	1114.7	982.5	1037.8	5264.425	1005.275	-2.3845687	-5.2218778	0.00010426
319636	A_55_P2100065	Fsd1l	fibronectin type III and SPRY c	NM_176966	1343.2	1098.6	1373.5	1430.2	247.7	203.2	261.3	295.4	1311.375	251.9	-2.3858138	-5.2263865	0.00034078
16401	A_55_P2040026	Itga4	integrin alpha 4	NM_010576	297.7	321.8	370.8	292.7	85.4	39.7	67.9	60.2	320.75	63.3	-2.3878124	-5.2336319	0.01723691
109264	A_55_P1953920	Me3	malic enzyme 3, NADP(+)-dep	NM_181407	5665.7	5087.9	5214.6	4915.3	1102	948.2	992	943.7	5220.875	996.475	-2.3902402	-5.2424464	6.70E-06
68802	A_52_P2706	Mypn	myopalladin	NM_182992	221.9	165.2	227.5	219.8	32.7	35	43	49.1	208.6	39.95	-2.3917971	-5.2481069	0.00138951
21940	A_51_P229664	Cd27	CD27 antigen	NM_001033126	16.8	18.4	14	16.6	2.2	3.1	5.1	2.7	16.45	3.275	-2.3948153	-5.2590976	0.03589587
227721	A_51_P321374	Ppapdc3	phosphatidic acid phosphatas	NM_145521	3958.3	3422.3	3697	3194.2	665	651.9	714.1	674.6	3567.95	676.4	-2.3953015	-5.2608702	8.77E-06
14204	A_55_P2087622	Il4i1	interleukin 4 induced 1	NM_010215	190.7	215.6	253.4	278.7	42	31	59.8	47.2	234.6	45	-2.4064785	-5.3017863	0.01088209
330635	A_55_P2345853	3830612M24	uncharacterized protein 3830	AK028406	427	342.3	357.9	492.8	79.5	102.6	88.9	44.5	405	78.875	-2.4104665	-5.3164622	0.05650028
24052	A_51_P389004	Sgcd	sarcoglycan, delta (dystrophir	NM_011891	128.1	88	100.9	84.2	16.9	18.8	20	18.7	100.3	18.6	-2.4136456	-5.3281903	0.00037927

74490	A_51_P122141	Mamstr	MEF2 activating motif and SA	NM_172418	269.2	212.7	241.9	274.1	42.9	48.9	44.3	50.5	249.475	46.65	-2.4149804	-5.3331224	4.10E-05
12818	A_55_P2124736	Col14a1	collagen, type XIV, alpha 1	NM_181277	486.9	566.5	758.3	508.8	128.1	148.2	100.9	68	580.125	111.3	-2.418555	-5.3463527	0.04723332
93694	A_55_P2115442	Clec2d	C-type lectin domain family 2	NM_053109	212	276.2	238.7	185.3	44.5	26.3	48.4	55.8	228.05	43.75	-2.4196028	-5.3502369	0.02947217
64103	A_51_P108183	Tnmd	tenomodulin	NM_022322	238	341.1	155.7	222.4	32.9	54.8	46.8	40.4	239.3	43.725	-2.4219168	-5.3588253	0.04146569
110880	A_55_P2010454	Scn4a	sodium channel, voltage-gate	NM_133199	298	290.9	282.4	305	51.4	47.7	64.5	57.2	294.075	55.2	-2.4222564	-5.3600868	3.29E-05
243373	A_55_P1952925	AI854703	expressed sequence AI85470	NR_027236	14.7	12.2	18.1	12.5	2.2	2.6	3.3	2.6	14.375	2.675	-2.4228337	-5.3622321	0.00152128
320091	A_55_P2025538	Ano4	anoctamin 4	NM_178773	18.5	9.8	16.4	18.7	2	2.7	3.1	4	15.85	2.95	-2.4243994	-5.368055	0.07262793
57915	A_55_P2113837	Tbc1d1	TBC1 domain family, member	NM_019636	19551.2	20910	21863.1	22704.9	4443.7	4109.8	3849.8	3399.8	21257.3	3950.775	-2.4324003	-5.3979077	2.59E-05
79221	A_55_P1970755	Hdac9	histone deacetylase 9	NM_024124	160.5	120.7	122.9	198.3	34.6	32.9	25.3	19.3	150.6	28.025	-2.4325708	-5.3985455	0.02251354
330812	A_55_P2234361	Rnf150	ring finger protein 150	NM_177378	7864.5	5957.1	7956.7	7549.3	1081	1664.9	1048.5	1751.8	7331.9	1386.55	-2.4333778	-5.4015664	0.00696499
16985	A_55_P1957413	Lsp1	lymphocyte specific 1	NM_019391	6421.7	6208.6	6623.7	5473.5	1030.5	1396.1	1175.8	1000.4	6181.875	1150.7	-2.4345895	-5.4061047	0.00013495
67620	A_52_P428735	Lrp2bp	Lrp2 binding protein	NM_026278	90.7	90.6	98.3	123	20.5	17.8	17.5	18.1	100.65	18.475	-2.4368864	-5.4147188	8.51E-05
11938	A_51_P451075	Atp2a2	ATPase, Ca++ transporting, ca	NM_009722	3076.1	4682.7	2947.6	4409.6	703	668.5	682.5	669.1	3779	680.775	-2.4422102	-5.4347369	0.00118771
229776	A_55_P2017160	Cdc14a	CDC14 cell division cycle 14 h	NM_001173553	1371.8	1721.3	1394.4	1016	233	268.2	247.7	244.3	1375.875	248.3	-2.4472348	-5.4536978	0.00071972
18742	A_51_P477614	Pitx3	paired-like homeodomain tra	NM_008852	300.7	297	343.3	355.2	49.1	90.5	51	54.1	324.05	61.175	-2.4487087	-5.4592726	0.00578271
72472	A_52_P527917	Slc16a10	solute carrier family 16 (mon	NM_028247	139.5	124.4	120.3	138.3	23.9	23.6	23.6	23.7	130.625	23.7	-2.4594826	-5.5001944	2.49E-06
320379	A_55_P2331709	D630028G08Rik	RIKEN cDNA D630028G08 ger	AK085450	191	138.5	197.4	168.6	35.5	28.1	30.1	31.9	173.875	31.4	-2.4610471	-5.5061622	0.0002106
65112	A_55_P1959174	Pmepa1	prostate transmembrane pro	NM_022995	1298.8	1142.6	1284.2	1714.7	190.8	292.9	264	239.7	1360.075	246.85	-2.4629502	-5.5134305	0.0015061
70122	A_55_P2157048	Mllt3	myeloid/lymphoid or mixed-li	NM_027326	942.2	873.3	1156.2	937.8	147.6	191.4	196.2	173.9	977.375	177.275	-2.4635609	-5.5157646	0.00013816
77559	A_55_P2427685	Agl	amylo-1,6-glucosidase, 4-alph	NM_001081326	41908.2	38887	33818.9	28828.8	5194.6	6993.7	7038.9	6635.9	35860.725	6465.775	-2.4677157	-5.5316722	0.00055584
378431	A_51_P315391	Txlnb	taxilin beta	NM_138628	21497.2	22227.7	23583	23353.3	4098.2	3927.7	4552.8	3825.8	22665.3	4101.125	-2.4686007	-5.5350667	4.08E-06
226594	A_51_P371091	Rcsd1	RCSD domain containing 1	NM_178593	9153.5	9371.7	8791.2	9605.6	1850.1	1738.4	1498.7	1594.1	9230.5	1670.325	-2.4701883	-5.5411609	6.74E-06
26399	A_51_P256093	Map2k6	mitogen-activated protein kin	NM_011943	1641.5	1410.1	1399.3	1192.5	243.7	254.7	262.4	250.7	1410.85	252.875	-2.4713961	-5.5458018	2.6647E-05
12335	A_55_P2010066	Capn3	calpain 3	NM_007601	12080.3	12041.4	14594.2	16557.5	2328.7	2505	2765	2289.4	13818.35	2472.025	-2.4736668	-5.5545377	0.000137
11459	A_51_P246854	Acta1	actin, alpha 1, skeletal muscle	NM_009606	184692.8	151794.7	166091.6	175712.5	28247.8	34589.7	39330.4	22285.8	169572.9	31113.425	-2.4749767	-5.559583	0.00196335
12443	A_66_P111562	Ccnd1	cyclin D1	NM_007631	291.5	332.8	300.7	279.9	46.3	72.8	56.5	44.7	301.225	55.075	-2.4764059	-5.5650935	0.00092361
68910	A_55_P2126951	Zfp467	zinc finger protein 467	NM_001085417	2890.3	3218.8	4088.8	2937.3	629.2	512.2	624.5	572.4	3283.8	584.575	-2.4804179	-5.5805909	0.00018467
23796	A_52_P97572	Aplnr	apelin receptor	NM_011784	74.5	90.2	148.2	67.2	14.5	16.6	14.9	19	95.025	16.25	-2.4849387	-5.5981055	0.02504992
170745	A_55_P1985950	Xpnpep2	X-prolyl aminopeptidase (ami	NM_133213	120.5	134.5	107.9	131.2	19.7	23.3	25.7	19.5	123.525	22.05	-2.4905116	-5.6197718	8.92E-05
14245	A_55_P2083474	Lpin1	lipin 1	NM_001130412	148.1	133.8	203	187.1	32.6	23.1	33.6	29.8	168	29.775	-2.4907783	-5.6208108	0.00170897
329554	A_55_P2022231	Gm826	predicted gene 826	NM_001033411	221.9	349.5	136.6	234.9	36.2	46.1	37.4	39.7	235.725	39.85	-2.4929962	-5.6294588	0.04129652
69743	A_66_P102467	Casz1	castor homolog 1, zinc finger	AK048565	490.7	460.2	466.4	505.6	80.4	79	80.9	101.6	480.725	85.475	-2.4985906	-5.6513308	1.8485E-05
381339	A_55_P1961640	Tmem182	transmembrane protein 182	NM_001081198	495.8	687.5	639.6	852.9	148.6	151	75.7	106.6	668.95	120.475	-2.5010273	-5.6608838	0.03763847
15959	A_51_P359570	Ifit3	interferon-induced protein w	NM_010501	327	210.2	414.5	329.9	47	64.4	60.1	49.5	320.4	55.25	-2.5069129	-5.684025	0.00797981
235542	A_55_P2053783	Ppp2r3a	protein phosphatase 2, regula	NM_001161362	102.2	91.5	118.5	102.6	18	19.1	16.9	18.7	103.7	18.175	-2.5078095	-5.6875585	1.28E-05
80891	A_52_P231075	Fcrls	Fc receptor-like S, scavenger	NM_030707	57.2	75.7	70.1	63.1	10.4	9.4	19.9	9.4	66.525	12.275	-2.5081364	-5.6888475	0.02805879
16480	A_65_P13547	Jup	junction plakoglobin	NM_010593	63.3	57.5	63.4	46.9	14.6	9.7	5.8	12.4	57.775	10.625	-2.5133371	-5.7093918	0.06246505
68041	A_55_P2041723	Mid1ip1	Mid1 interacting protein 1 (ga	NM_001166635	4908.5	6051.6	4804.6	4275.7	827.1	964.2	786.2	912.2	5010.1	872.425	-2.5148119	-5.7152312	9.70E-05
18583	A_51_P293269	Pde7a	phosphodiesterase 7A	NM_008802	1236.8	1268.9	1519	996.1	226.7	241.8	202.9	197.8	1255.2	217.3	-2.5189944	-5.7318242	0.00023253
18600	A_55_P2091359	Padi2	peptidyl arginine deiminase, t	NM_008812	4917.8	4764.4	3476.1	5866.3	975.2	881.6	670.5	765.1	4756.15	823.1	-2.5203081	-5.7370461	0.00224684
217830	A_55_P2031999	9030617O03Rik	RIKEN cDNA 9030617O03 ger	NM_145448	1435.5	1755.6	1911	2588.4	334.7	333.4	319.2	317.7	1922.625	326.25	-2.5263425	-5.7610927	0.00106927
74182	A_55_P1976351	Gpcpd1	glycerophosphocholine phosp	NM_001042672	4085.3	3780.1	5225.5	3988.7	691.2	685.3	892.9	690.3	4269.9	739.925	-2.5266264	-5.7622265	0.00020247
58522	A_55_P2305319	Trim54	tripartite motif-containing 54	NM_021447	11774.6	11645.3	13208	9970	2239.2	2070.6	1852.6	1898.7	11649.475	2015.275	-2.528155	-5.7683352	3.32E-05
22042	A_52_P228236	Tfrc	transferrin receptor	NM_011638	926.5	678.3	756	633.9	128.9	152.6	101.8	134.1	748.675	129.35	-2.5328255	-5.7870395	0.00078491
329502	A_52_P203948	Pla2g4e	phospholipase A2, group IVE	NM_177845	544.4	395.1	511.6	424	65.2	94.3	97.4	69.4	468.775	81.575	-2.5331727	-5.7884323	0.00137691
74116	A_55_P1999102	Pi16	peptidase inhibitor 16	NM_023734	7872.2	9162.8	10342.4	5592.9	1419.1	1732.2	1518.9	988.8	8242.575	1414.75	-2.5355729	-5.7980707	0.01625579
170952	A_55_P1962219	Prima1	proline rich membrane ancho	NM_133364	233.3	218.4	201.8	195.3	41	32.7	36.9	35.8	212.2	36.6	-2.5367487	-5.8027979	1.38E-05
215031	A_55_P2042456	Vgll2	vestigial like 2 homolog (Dros	NM_153786	8520.2	10311	6795	9295.7	1324	2250.4	1361.1	1195.7	8730.475	1532.8	-2.5400809	-5.8162162	0.00952556
17929	A_51_P302520	Myom1	myomesin 1	NM_010867	37187.9	30951.6	38339.7	33867.4	6226.3	6298.2	6408.2	5193.3	35086.65	6031.5	-2.5403526	-5.8173118	2.49E-05
208372	A_55_P1969015	Asb18	ankyrin repeat and SOCS box-	NM_139152	16	11.6	13	15.6	2	2.5	2.7	2.4	14.05	2.4	-2.5455112	-5.8381497	0.00022949
66106	A_55_P1956799	Smpx	small muscle protein, X-linked	NM_025357	4748.4	4654.6	4877.9	4077.7	789.6	1013.2	693.3	681.9	4589.65	794.5	-2.5457045	-5.8389318	0.0002326
13143	A_51_P126198	Dapk2	death-associated protein kina	NM_010019	1154.9	1455.2	1053.2	1523.3	233.6	238.5	194.2	214	1296.65	220.075	-2.5463734	-5.8416399	0.00024751
14645	A_55_P2142146	Glul	glutamate-ammonia ligase (gl	NM_008131	13623.4	14004.7	12263.8	8087.4	1875.1	1953.4	2197	1905.9	11994.825	1982.85	-2.5672255	-5.9266855	0.00154714
71416	A_55_P2104884	5430425K12Rik	RIKEN cDNA 5430425K12 gen	AK017339	41.2	50.2	46.5	56.6	8	8.4	7.9	8.3	48.625	8.15	-2.5676809	-5.9285565	2.17E-05
18198	A_55_P2130600	Musk	muscle, skeletal, receptor tyr	NM_001037127	1822.3	1539.9	1657.6	1044.5	221.1	270.6	271	239.4	1516.075	250.525	-2.5724103	-5.9480232	0.00150576
54378	A_55_P2182006	Cacng6	calcium channel, voltage-dep	NM_133183	767.9	573.6	846.6	684.9	148.4	112.5	116.6	104.4	718.25	120.475	-2.5738579	-5.9539947	0.00049873
100042834	A_55_P1972490	Gm4055	predicted gene 4055	BC058988	24172.8	22726.7	23903.5	23317.7	3640.5	4189.7	4113.6	3864.5	23530.175	3952.075	-2.5756164	-5.9612564	1.44E-06
100043232	A_55_P2035311	3110099E03Rik	RIKEN cDNA 3110099E03 gen	NR_030712	93.7	62.2	84.6	85.8	14.6	12.9	12.8	13.8	81.575	13.525	-2.5781119	-5.9715765	0.00014882
51801	A_51_P348665	Ramp1	receptor (calcitonin) activity r	NM_016894	1046.9	1136.9	890	934	175.1	186.3	165.8	138.5	1001.95	166.425	-2.5917941	-6.0284791	6.92E-05
78786	A_55_P2348582	4833439F03Rik	RIKEN cDNA 4833439F03 gen	AK019523	337.4	356.3	424.7	435.2	66.9	59.5	73.9	55.4	388.4	63.925	-2.6032578	-6.0765726	9.73E-05
54613	A_51_P281333	St3gal6	ST3 beta-galactoside alpha-2,	NM_018784	3589.8	3197.4	3909.1	3140.4	555.8	607.4	582.7	522.2	3459.175	567.025	-2.6054328	-6.0857406	1.07E-05
16367	A_52_P175242	Irs1	insulin receptor substrate 1	NM_010570	4587.8	4904.9	5103.3	6808.5	841.7	994.7	789.3	847.1	5351.125	868.2	-2.6119581	-6.1133285	0.00019212
19309	A_55_P1961913	Pygm	muscle glycogen phosphoryla	NM_011224	88900.6	69399.8	89191.8	74054.4	12245	10605.7	18837.5	11819.6	80386.65	13376.95	-2.6152	-6.1270812	0.00221078
234671	A_55_P2124712	Ces2c	carboxylesterase 2C	NM_145603	15.8	18.4	12.8	13.2	1.9	2.5	2.9	2.5	15.05	2.45	-2.619529	-6.145494	0.00074704
56534	A_55_P2039274	Hspb3	heat shock protein 3	NM_019960	2590.4	2519.8	2569.4	2888.6	453.9	448.3	383.6	432.8	2642.05	429.65	-2.6214641	-6.1537424	3.96E-06
68585	A_52_P379337	Rtn4	reticulon 4	NM_194054	8416.8	7878.9	9111.2	8907.7	1359.2	1252.4	1474.7	1488.8	8578.65	1393.775	-2.6229839	-6.1602285	4.87E-06
78739	A_55_P2193809	9530062K07Rik	RIKEN cDNA 9530062K07 gen	AK020619	125.6	146.7	128.1	194.5	15.1	30	27.5	23.8	148.725	24.1	-2.6491385	-6.2729259	0.01343244
18612	A_55_P2078780	Etv4	ets variant gene 4 (E1A enhar	NM_008815	288.7	311.4	222.2	236.5	43.9	39.2	41.1	42.9	264.7	41.775	-2.6511402	-6.2816354	5.50E-05
11686	A_55_P2121682	Alox12b	arachidonate 12-lipoxygenase	NM_009659	19.1	15.4	21	10.1	2	2.5	3.2	2.5	16.4	2.55	-2.651758	-6.2843258	0.01690803
11833	A_55_P2318584	Aqp8	aquaporin 8	NM_007474	13.4	20.8	12.4	15.1	2	2.3	2.9	2.5	15.425	2.425	-2.6529507	-6.2895233	0.00161611
22003	A_55_P2078675	Tpm1	tropomyosin 1, alpha	ENSMUST00000030185	276.9	183.9	323.3	179.2	41.6	33.5	45.3	29.8	240.825	37.55	-2.6537188	-6.2928727	0.01005605
72607	A_51_P104077	Usp13	ubiquitin specific peptidase 1	NM_001013024	3001.6	2854.6	3512.2	2822.5	498.7	491.3	468	465.1	3047.725	480.775	-2.6593138	-6.3173252	4.952E-06
234365	A_51_P181922	Yjefn3	YjeF N-terminal domain conta	ENSMUST00000152456	784.9	800.8	639.6	988.3	102.4	138.8	114.3	153.3	803.4	127.2	-2.6599159	-6.3199619	0.00089746
12487	A_55_P1979491	Cd28	CD28 antigen	NM_007642	290.2	441.8	312.1	411.7	84.3	54.5	36.3	60.2	363.95	58.825	-2.6700583	-6.3645491	0.02595328
74488	A_52_P90805	Lrrc15	leucine rich repeat containing	NM_028973	20.6	12.3	16.6	14.4	1.9	2.6	3.1	2.4	15.975	2.5	-2.6716134	-6.371413	0.00275359
14373	A_52_P681391	G0s2	G0/G1 switch gene 2	NM_008059	575.4	777	280.5	386.8	81.9	78.8	63.1	71.6	504.925	73.85	-2.6750305	-6.3865222	0.06797281
12824	A_55_P2004179	Col2a1	collagen, type II, alpha 1	NM_001113515	46.2	82.5	31.1	50.3	6.6	10.5	8.9	5.8	52.525	7.95	-2.6757077	-6.3895205	0.09478875
17189	A_51_P193185	Mb	myoglobin	NM_013593	88105.2	97573.5	72147.9	84281.7	14562.3	18088.4	10105.5	11758.1	85527.075	13628.575	-2.6764487	-6.3928031	0.00182964
53857	A_66_P119518	Tuba8	tubulin, alpha 8	NM_017379	36860.1	36991.1	37308.3	32401.8	4644.6	5949.5	5519.9	6380.5	35890.325	5623.625	-2.6814717	-6.4150997	2.8138E-05
78749	A_55_P2109594	Filip1l	filamin A interacting protein 1	ENSMUST00000099667	79.3	94.6	54.9	131.7	8.9	13.2	15.9	16.9	90.125	13.725	-2.6866714	-6.4382623	0.06987375
228003	A_52_P647740	Kbtbd10	kelch repeat and BTB (POZ) d	NM_001081087	3453.5	3504.1	4021.5	3549.2	546.7	602.8	640	465.9	3632.075	563.85	-2.6948805	-6.4750015	3.05E-05
14778	A_51_P292008	Gpx3	glutathione peroxidase 3	NM_008161	7444.1	5955.4	6686.1	6060.1	875.8	912.6	1300.7	982.3	6536.425	1017.85	-2.6951377	-6.4761556	0.00017998
11932	A_55_P1968649	Atp1b2	ATPase, Na+/K+ transporting,	NM_013415	5383.9	5022.8	5562.8	4625.5	830.7	665.3	964.4	736.3	5148.75	799.175	-2.6980046	-6.489038	7.34E-05
67399	A_55_P2161865	Pdlim7	PDZ and LIM domain 7	NM_026131	5951	5629.8	7235.8	5321.7	890.8	1082.6	935.6	793.2	6034.575	925.55	-2.7039653	-6.515904	8.89E-05
23936	A_55_P1969497	Lynx1	Ly6/neurotoxin 1	NM_011838	42.6	39.9	48.2	27.5	7.8	6.2	3.8	6.8	39.55	6.15	-2.7040357	-6.5162218	0.0203032
76282	A_51_P426739	Gpt	glutamic pyruvic transaminas	NM_182805	1560.6	1526.7	1303.8	1005.5	195.1	177.9	198.6	248.3	1349.15	204.975	-2.7084088	-6.5360038	0.00061771
208869	A_55_P2155312	Dock3	dedicator of cyto-kinesis 3	NM_153413	928.6	845.4	706.7	429	108.4	91.1	122.1	107.6	727.425	107.3	-2.7102845	-6.5445069	0.01086677
56811	A_51_P241068	Dkk2	dickkopf homolog 2 (Xenopus	NM_020265	212.2	316.8	225.5	285.2	29.8	34.2	58.8	38.8	259.925	40.4	-2.7151573	-6.5666489	0.007811
100039528	A_55_P2414524	1110002E22Rik	RIKEN cDNA 1110002E22 gen	AK003290	12712.5	9873.6	13402.6	11980.1	1829.4	2105.9	1606.6	1730.1	11992.2	1818	-2.7195219	-6.5865448	6.00E-05
74492	A_52_P196632	Kbtbd13	kelch repeat and BTB (POZ) d	NM_028974	168.7	156.1	171.9	191.1	28.3	29.6	16.6	32.3	171.95	26.7	-2.7278559	-6.6247035	0.00325536
67426	A_51_P221651	Adck3	aarF domain containing kinas	NM_023341	8097.9	7287.9	5448.3	7282.6	962.4	1010.3	1158	1075.4	7029.175	1051.525	-2.7293275	-6.6314642	9.0223E-05
11474	A_52_P656699	Actn3	actinin alpha 3	NM_013456	146236.5	122935.6	143424.9	142910.1	25529.9	15476.8	29127.7	16514.9	138876.775	21662.325	-2.7302167	-6.6355531	0.00424249
22061	A_55_P1952056	Trp63	transformation related protei	AK138305	215.8	253.1	186.8	292.6	30.3	44.3	37.4	30.4	237.075	35.6	-2.7334512	-6.6504466	0.00100087
80978	A_51_P284526	Mrgprh	MAS-related GPR, member H	NM_030726	18.2	14.2	18.2	12.2	1.9	2.2	2.8	2.5	15.7	2.35	-2.7343759	-6.6547104	0.00078489
210789	A_55_P2024953	Tbc1d4	TBC1 domain family, member	NM_001081278	3519.1	4983.5	3517.5	4925.4	565.3	754.6	585.7	616.7	4236.375	630.575	-2.7363525	-6.6638342	0.00041033
66497	A_55_P2039444	2610528E23Rik	RIKEN cDNA 2610528E23 gen	NM_025599	5555.7	4845.2	4080.6	4510.6	629.6	724.9	797.3	690.1	4748.025	710.475	-2.7365481	-6.6647376	3.58E-05
18008	A_55_P1953728	Nes	nestin	NM_016701	2073.9	1971.8	1856.4	2170.2	241	414.6	297.2	279.2	2018.075	308	-2.7391053	-6.6765616	0.00044312
12790	A_55_P1991004	Cnga3	cyclic nucleotide gated chann	NM_009918	27.5	24.1	18.6	28.8	4.9	4	3.3	2.7	24.75	3.725	-2.7473353	-6.7147577	0.00386448
14702	A_52_P263518	Gng2	guanine nucleotide binding p	NM_010315	462.9	384.7	277.3	414	68.1	65.5	55.1	40.9	384.725	57.4	-2.7474806	-6.7154337	0.00366245
66993	A_51_P423880	Smarcd3	SWI/SNF related, matrix asso	NM_025891	7803.2	6909.4	7084.5	5767.4	975.1	927.1	1128.8	1028.4	6891.125	1014.85	-2.7589008	-6.7688032	2.21E-05
68841	A_52_P552547	1110054M08Rik	RIKEN cDNA 1110054M08 ger	XR_105768	1881.8	1613.6	1612.9	1393.2	246.1	218.4	257	234.5	1625.375	239	-2.7601486	-6.7746601	1.47E-05
69574	A_51_P272283	Cmbl	carboxymethylenebutenolida	NM_181588	14054.4	13658.2	13775.3	13508.9	2271.8	1781	2050.3	2000.1	13749.2	2025.8	-2.7680163	-6.8117064	2.955E-06
103767	A_55_P2234704	A530047J11Rik	RIKEN cDNA A530047J11 gen	AK040933	2536.2	2425.2	2622.9	2591.4	387.6	412.2	354.6	336.8	2543.925	372.8	-2.7743454	-6.841655	2.40E-06
237928	A_51_P149257	Phospho1	phosphatase, orphan 1	NM_153104	29.4	32.9	36	33.2	7.8	4.4	3	5.1	32.875	5.075	-2.7760897	-6.8499322	0.01924771
18767	A_52_P314129	Pkia	protein kinase inhibitor, alph	NM_008862	4322.9	3990.3	4281.5	4444.2	697.5	574.2	591.8	627.6	4259.725	622.775	-2.7768869	-6.8537182	2.45E-06
433938	A_55_P2174935	Mn1	meningioma 1	NM_001081235	5564.2	5161.6	5619.2	4841.6	836.4	786.9	713.1	730.7	5296.65	766.775	-2.7884492	-6.9088671	2.73E-06
434758	A_55_P1984347	Rhox3h	reproductive homeobox 3H	NM_001114157	16.5	30.5	20.2	17.5	3.7	3	2.9	2.4	21.175	3	-2.7922807	-6.9272402	0.00394205
12322	A_55_P2149209	Camk2a	calcium/calmodulin-depende	NM_009792	234.8	199.3	183.8	185.6	29.4	27.1	28.5	30.5	200.875	28.875	-2.792635	-6.9289414	6.79E-06
20528	A_51_P217498	Slc2a4	solute carrier family 2 (facilita	NM_009204	73544.8	64317.2	71071.6	59309.2	11186.7	10560.9	8220.3	8830.3	67060.7	9699.55	-2.7957606	-6.9439695	4.73E-05
228139	A_51_P116326	P2rx3	purinergic receptor P2X, ligan	NM_145526	13.3	15.8	19.1	25	2.8	2.2	2.9	2.4	18.3	2.575	-2.7981366	-6.9554148	0.00195343
12715	A_51_P380807	Ckm	creatine kinase, muscle	NM_007710	79951.2	66380.1	88513.9	64789.1	9500.8	10025.5	15039.3	9038.7	74908.575	10901.075	-2.7997015	-6.9629636	0.00107581
100503238	A_55_P2262593	Gm19606	predicted gene, 19606	XR_105257	5945.1	6615.7	7037.1	6236.3	907.3	1054.3	979.4	782.1	6458.55	930.775	-2.8004835	-6.9667391	1.65E-05
110326	A_51_P508919	Tas1r1	taste receptor, type 1, memb	NM_031867	36.9	29.4	42.7	26.7	6.1	5.9	3.1	4.7	33.925	4.95	-2.800943	-6.9689582	0.01092317
21425	A_55_P1997898	Tfeb	transcription factor EB	NM_001161722	1151.1	884	1151.6	969.2	140.2	142	141.6	168.9	1038.975	148.175	-2.8049955	-6.9885613	2.55E-05
13190	A_55_P2003053	Dct	dopachrome tautomerase	NM_010024	23.8	29.2	27.9	24.9	4.3	5.4	3.2	2.7	26.45	3.9	-2.8081815	-7.0040115	0.00324953
240595	A_55_P2112504	Kcnv2	potassium channel, subfamily	NM_183179	32	24.7	30.5	15.9	4.8	4.5	2.9	2.5	25.775	3.675	-2.8142977	-7.0337679	0.04093705
93837	A_55_P1956537	Dach2	dachshund 2 (Drosophila)	NM_001142570	26.4	26.5	14.3	18.1	3.7	2.4	3.2	2.6	21.325	2.975	-2.8147761	-7.0361004	0.00746772
18263	A_55_P1995173	Odc1	ornithine decarboxylase, stru	NM_013614	12926	12973	16213	13883.8	1878.8	1972.1	2081.4	1986.5	13998.95	1979.7	-2.8166817	-7.0454003	4.30E-06
100038725	A_66_P115161	Gm9766	predicted gene 9766	ENSMUST00000095691	1282.1	998	1207.8	762.7	174.4	146.2	141.5	132.1	1062.65	148.55	-2.8180316	-7.0519955	0.00068134
14667	A_55_P2282969	Gm2a	GM2 ganglioside activator pr	AK030655	220.3	287.2	244.2	339.7	37.4	45.8	35.6	34.7	272.85	38.375	-2.8190908	-7.0571752	0.00025004
17684	A_55_P2120577	Cited2	Cbp/p300-interacting transac	NM_010828	769.8	848.2	722.6	492.5	101.9	133.5	87.5	78.2	708.275	100.275	-2.821405	-7.0685043	0.00390623
66464	A_55_P2111875	Taf12	TAF12 RNA polymerase II, TA	ENSMUST00000105963	189.3	238.9	244.2	240.3	36.7	28.8	37	27.1	228.175	32.4	-2.8225066	-7.0739039	0.00011037
18679	A_55_P1972192	Phka1	phosphorylase kinase alpha 1	NM_008832	38865	37342.9	47010.6	40844.5	5683.3	5316.9	6056.7	6029.4	41015.75	5771.575	-2.8255713	-7.0889468	4.85E-06
100216343	A_55_P2404658	Gm17501	predicted gene, 17501	XR_106421	144.2	160.8	166.7	186.9	18	34.2	28.8	16	164.65	24.25	-2.8286094	-7.1038909	0.01061914
209224	A_55_P1983988	Enox2	ecto-NOX disulfide-thiol exch	NM_145951	917.4	960.5	928.2	1120.8	131.7	137.5	135.6	139.2	981.725	136	-2.8472565	-7.1963056	1.90E-06
56190	A_51_P262670	Rbm38	RNA binding motif protein 38	NM_019547	209.6	188.9	164.9	143.2	24.5	22.8	26.3	23.7	176.65	24.325	-2.8477078	-7.1985574	4.22E-05
66797	A_52_P168559	Cntnap2	contactin associated protein-	NM_001004357	29.1	18.4	12.6	17.2	2.1	2.4	3.3	2.5	19.325	2.575	-2.8616129	-7.2682746	0.01267966
16515	A_55_P1973362	Kcnj12	potassium inwardly-rectifying	NM_010603	5965.7	5423.9	5787.4	4405.5	607.3	751	758	847.7	5395.625	741	-2.8647454	-7.2840731	7.70E-05
71141	A_52_P5905	4933407L21Rik	RIKEN cDNA 4933407L21 gen	NR_037692	17.1	12.4	17.6	21.3	1.9	2.3	2.8	2.3	17.1	2.325	-2.8659459	-7.290137	0.00083428
74166	A_51_P303725	Tmem38a	transmembrane protein 38A	NM_144534	72271.2	66838.9	71790.9	72532.7	9500.8	9765.1	9660.6	9668.9	70858.425	9648.85	-2.8757763	-7.3399811	2.58E-07
319506	A_51_P231557	7530428D23Rik	RIKEN cDNA 7530428D23 gen	AK033061	88.8	86.4	99.8	75.6	12.8	7.5	22.1	9.3	87.65	12.925	-2.8796404	-7.3596667	0.05501748
16561	A_65_P12993	Kif1b	kinesin family member 1B	NM_008441	5444.7	6042	6173.1	6150.8	818.2	915.4	710.7	799.2	5952.65	810.875	-2.8799268	-7.3611278	4.54E-06
16716	A_55_P2309100	Ky	kyphoscoliosis peptidase	NM_024291	352.5	396.5	463.7	352.3	49.3	48.6	48.9	65.8	391.25	53.15	-2.8830467	-7.3770636	7.86E-05
234214	A_55_P1960857	Sorbs2	sorbin and SH3 domain conta	NM_172752	104.9	131.2	191.2	118.8	18.7	17.5	16	20.1	136.525	18.075	-2.8841129	-7.3825176	0.0008328
240879	A_55_P2165534	Mettl11b	methyltransferase like 11B	NM_001143956	240.5	229.1	270.7	267.4	36.8	30.9	29.5	38.5	251.925	33.925	-2.8981338	-7.4546146	1.60E-05
73598	A_52_P496403	1700001O22Rik	RIKEN cDNA 1700001O22 ger	NM_198000	184.2	178.2	239.9	84	21.1	18.6	23.6	22.6	171.575	21.475	-2.9064305	-7.4976084	0.03739394
72293	A_55_P2143282	Nkd2	naked cuticle 2 homolog (Dro	NM_028186	84.9	74.6	84.5	50.8	7.3	10.1	11.7	9.8	73.7	9.725	-2.9127585	-7.5305673	0.00190036
18578	A_65_P01319	Pde4b	phosphodiesterase 4B, cAMP	NM_019840	434.4	521	582.4	813.7	63.3	75.3	92.1	75.2	587.875	76.475	-2.9164345	-7.5497795	0.00158127
21384	A_52_P232802	Tbx15	T-box 15	NM_009323	6575.1	6679.1	6305.1	5792.9	914.1	902.4	797.3	741.2	6338.05	838.75	-2.9210198	-7.5738132	4.04E-06
18948	A_51_P513153	Pnmt	phenylethanolamine-N-meth	NM_008890	41.8	43.5	53.9	103.6	5.8	5.9	9.9	9	60.7	7.65	-2.9253367	-7.5965095	0.066075
67888	A_52_P368306	Tmem100	transmembrane protein 100	NM_026433	220.1	236.3	223.2	282.4	31.1	37.3	32.7	25.7	240.5	31.7	-2.9288548	-7.6150566	5.8787E-05
11988	A_52_P77764	Slc7a2	solute carrier family 7 (cation	NM_007514	100.7	143.9	136.9	92.3	12.1	18.1	12.7	19.5	118.45	15.6	-2.9302671	-7.6225149	0.00261321

11565	A_55_P2030030	Adssl1	adenylosuccinate synthetase	NM_007421	91122.3	88056.6	87434.4	88866.1	11296.3	11180.5	12898.8	11268.9	88869.85	11661.125	-2.9324127	-7.63386	5.98E-07
215303	A_55_P2020331	Camk1g	calcium/calmodulin-depende	NM_144817	95	124.5	57.6	130.3	13.9	12.1	12.2	12.6	101.85	12.7	-2.9363596	-7.6547732	0.00784194
78286	A_55_P2071970	Nav2	neuron navigator 2	NM_175272	28.6	28.1	42.8	30.7	6.9	4.7	2.9	3.2	32.55	4.425	-2.9441913	-7.6964401	0.02391049
78321	A_55_P2052882	Ankrd23	ankyrin repeat domain 23	NM_153502	2987.9	2938.1	3345.6	3915.5	509.3	482.6	411.2	322.3	3296.775	431.35	-2.9464003	-7.7082336	0.00028647
17869	A_52_P108346	Myc	myelocytomatosis oncogene	NM_010849	520.8	778.2	754.3	320.5	76.7	80.7	80.3	55.2	593.45	73.225	-2.9505455	-7.7304132	0.027884
236428	A_51_P275496	BC026762	cDNA sequence BC026762	BC029971	1800.4	1606.6	1815.9	1745.4	240.2	223.1	227	209.7	1742.075	225	-2.9528343	-7.742687	7.69E-07
21991	A_55_P1988424	Tpi1	triosephosphate isomerase 1	NM_009415	17920.4	17629.9	20114.9	15543.6	2153.9	2451.8	1937.2	2580.6	17802.2	2280.875	-2.9673632	-7.8210548	2.19E-05
76187	A_52_P116264	Adhfe1	alcohol dehydrogenase, iron c	NM_175236	51.7	57.6	76.6	51.3	8.4	8.4	5.2	8.5	59.3	7.625	-2.9683739	-7.8265359	0.00139419
20975	A_55_P2124026	Synj2	synaptojanin 2	NM_001113353	1445	1279.7	1319.3	1132.4	142	216.9	177.6	134.4	1294.1	167.725	-2.9689145	-7.8294694	0.00024941
11818	A_51_P342387	Apoh	apolipoprotein H	NM_013475	18.9	13.7	23.2	19.1	1.9	2.3	2.9	2.4	18.725	2.375	-2.9703128	-7.8370616	0.00069612
75444	A_51_P484559	1700011I03Rik	RIKEN cDNA 1700011I03 gene	NM_029290	16.8	33.7	16.9	16.6	2.1	2.4	3.2	2.6	21	2.575	-2.9717804	-7.8450376	0.00883734
67731	A_51_P109369	Fbxo32	F-box protein 32	NM_026346	22631	27016.5	31402.1	27065	3750	3290.7	3473.5	3161.2	27028.65	3418.85	-2.9762489	-7.8693739	1.28E-05
69537	A_55_P2032128	Dnase1l1	deoxyribonuclease 1-like 1	NM_027109	2234.6	2202	2427.4	2080.7	293.6	269.9	287.4	282.2	2236.175	283.275	-2.9792423	-7.8857191	5.78E-07
11600	A_55_P2158227	Angpt1	angiopoietin 1	NM_009640	629	888.8	630.1	951.7	94.3	113.5	78.2	101.2	774.9	96.8	-2.9876337	-7.9317196	0.00052996
16545	A_51_P123655	Kera	keratocan	NM_008438	990.3	1640	842	2106	129.5	167.4	200.1	167.2	1394.575	166.05	-2.9887989	-7.9381285	0.03057964
20893	A_51_P272553	Bhlhe40	basic helix-loop-helix family, r	NM_011498	1731.5	2159.7	1883.5	1741.2	269.6	245.4	210.5	218.7	1878.975	236.05	-2.9938336	-7.9658793	1.20E-05
621852	A_55_P2016367	Rhox3f	reproductive homeobox 3F	NM_001040089	18.6	21.2	18.1	21.2	2.1	2.3	3.1	2.5	19.775	2.5	-2.9952284	-7.9735845	4.0417E-05
70537	A_55_P2269254	5730419F03Rik	RIKEN cDNA 5730419F03 gen	AK017575	160.8	262.6	108.4	195.1	19.7	14.4	26.9	28.9	181.725	22.475	-2.9958713	-7.9771383	0.04453198
243078	A_51_P123879	Tecrl	trans-2,3-enoyl-CoA reductas	NM_153801	13.7	25.2	12.8	33.2	1.9	2.5	3	2.5	21.225	2.475	-3.0019552	-8.0108495	0.05313975
66270	A_51_P428578	Fam134b	family with sequence similarit	NM_025459	3083.5	2991.3	4047.2	3108.5	406.3	540.1	371.9	344.1	3307.625	415.6	-3.0031705	-8.0176003	0.00022895
14938	A_55_P2094060	Gzma	granzyme A	NM_010370	24.2	19.5	22	14.4	2	2.4	3	2.5	20.025	2.475	-3.0049602	-8.0275526	0.00066069
26360	A_52_P853177	Angptl2	angiopoietin-like 2	NM_011923	33.9	31.1	39.1	53.2	3.5	8.5	4.8	3.6	39.325	5.1	-3.0146645	-8.081732	0.03384258
12292	A_55_P2169923	Cacna1s	calcium channel, voltage-dep	NM_001081023	15872.5	12224.6	13886.8	13138.1	1951.4	1535.1	1774.6	1556.2	13780.5	1704.325	-3.0157841	-8.0880061	1.43E-05
65255	A_52_P594756	Asb4	ankyrin repeat and SOCS box-	NM_023048	1941.9	2213.8	1677.5	1852.2	221.3	276	217	227.4	1921.35	235.425	-3.028415	-8.1591279	1.44E-05
14065	A_55_P2011573	F2rl3	coagulation factor II (thrombi	NM_007975	21.9	15.1	17	23.2	1.9	2.2	2.9	2.4	19.3	2.35	-3.0325653	-8.1826337	0.00046644
14425	A_51_P380005	Galnt3	UDP-N-acetyl-alpha-D-galacto	NM_015736	17	36.2	21.6	16.8	1.9	3.6	3	2.4	22.9	2.725	-3.036684	-8.2060278	0.02277743
408063	A_55_P2340101	BC062258	cDNA sequence BC062258	AK144577	6126.2	6631	6063	7750.1	736.2	816.3	739	947.4	6642.575	809.725	-3.0368582	-8.2070185	1.63E-05
15277	A_51_P204080	Hk2	hexokinase 2	NM_013820	21581.2	24434	24542.3	26417.2	3194.3	3289.4	2577.5	2728.2	24243.675	2947.35	-3.0439699	-8.2475742	8.08E-06
66211	A_51_P243123	Rpl3l	ribosomal protein L3-like	NM_025425	23428	21278	21218.7	18318.5	2418.6	2515.8	3399.1	2019.3	21060.8	2588.2	-3.0449372	-8.2531063	0.000186
69489	A_55_P2288285	2310007J06Rik	RIKEN cDNA 2310007J06 gene	AK009210	4169.2	4785.3	5387.9	4960.9	448.2	673.8	558.4	680.6	4825.825	590.25	-3.045462	-8.2561091	0.00011842
18217	A_52_P266686	Ntsr2	neurotensin receptor 2	NM_008747	137.8	95.2	111.8	177.6	8.8	17.9	13.6	25.5	130.6	16.45	-3.0548087	-8.3097706	0.06324042
244654	A_55_P2056926	Mtss1l	metastasis suppressor 1-like	NM_198625	2048	1747.1	2123.2	2001.1	259.4	205.7	232.7	236.6	1979.85	233.6	-3.0843206	-8.4815066	3.73E-06
106762	A_55_P2361731	AW047481	expressed sequence AW0474	BU848224	20.2	18.5	21.9	19.7	1.9	2.4	2.9	2.3	20.075	2.375	-3.0929997	-8.5326846	3.1801E-05
212448	A_55_P2392485	9330159F19Rik	RIKEN cDNA 9330159F19 gen	NM_001162537	555.8	489.4	574.2	631.3	62.7	70.9	66.1	63.1	562.675	65.7	-3.0941575	-8.539535	2.64E-06
666182	A_55_P1954436	Gm7967	predicted gene 7967	AK140131	740.9	796.5	722.4	842.3	103.8	95.1	84	78.6	775.525	90.375	-3.1069248	-8.6154418	6.24E-06
56012	A_51_P264495	Pgam2	phosphoglycerate mutase 2	NM_018870	105141.9	81741	98119.6	75746.3	10473.6	11140	11292	8765.4	90187.2	10417.75	-3.1083357	-8.6238718	3.6819E-05
23831	A_51_P175424	Car14	carbonic anhydrase 14	NM_011797	6217.6	6614.3	6075.1	3549.1	750.2	708.5	517.8	571.5	5614.025	637	-3.1152071	-8.6650443	0.00199111
628856	A_55_P2003883	Gm9909	predicted gene 9909	ENSMUST00000054120	29.6	15.8	22.5	22.5	2.6	2.3	2.9	2.4	22.6	2.55	-3.1184628	-8.6846206	0.00044387
74249	A_55_P2428967	Lrrc2	leucine rich repeat containing	NM_028838	2463.9	3104.7	3402.5	2696.6	338.2	322	357.5	311.8	2916.925	332.375	-3.1243363	-8.7200493	9.67E-06
75141	A_55_P2107155	Rasd2	RASD family, member 2	NM_029182	5658.6	4030.6	4235.4	4350.4	581.4	419.1	546.1	546.1	4568.75	523.175	-3.1244106	-8.7204987	6.38E-05
328373	A_55_P2312124	A530028O18	uncharacterized protein A530	AK040831	42.4	26.5	22.1	22.9	5.5	2.5	2.9	2.4	28.475	3.325	-3.134179	-8.7797447	0.03094686
68952	A_51_P179697	Fam57b	family with sequence similarit	NM_026884	1364.7	912.8	1028	863.5	120.8	115	130.1	102	1042.25	116.975	-3.1375827	-8.800483	0.0001064
242735	A_51_P446106	Lrrc38	leucine rich repeat containing	NM_001162983	611.3	497.3	577.9	688.9	72.6	54.3	61.5	82.7	593.85	67.775	-3.1398571	-8.8143677	0.00010831
320775	A_55_P1962239	B230319C09Rik	RIKEN cDNA B230319C09 gen	NR_028382	24.4	30.3	31.6	39.7	2.9	2.5	4.8	4.3	31.5	3.625	-3.1494057	-8.8729	0.00359989
77552	A_51_P238523	Shisa4	shisa homolog 4 (Xenopus lae	NM_175259	6552.5	5820.9	7213.6	5931.8	764.3	714.7	743.3	630	6379.7	713.075	-3.159854	-8.9373929	3.48E-06
66733	A_52_P195881	Kcng4	potassium voltage-gated char	NM_025734	21.6	19.7	20.4	23.6	2	2.2	3	2.4	21.325	2.4	-3.1646987	-8.9674558	2.97E-05
14555	A_52_P16419	Gpd1	glycerol-3-phosphate dehydro	NM_010271	66716.3	57737.9	61337.9	55826.8	6810	6598	7030.1	6388.3	60404.725	6706.6	-3.1685865	-8.991654	6.64E-07
68810	A_52_P367520	Nexn	nexilin	NM_199465	17804.3	16560	18171	17544.1	2158	2371.1	1747.3	1602.7	17519.85	1969.775	-3.1698454	-8.9995032	2.53E-05
58200	A_52_P144818	Ppp1r1a	protein phosphatase 1, regula	NM_021391	302	264.6	269.9	317	35	38	26	29.5	288.375	32.125	-3.1776002	-9.0480081	2.98E-05
14061	A_55_P1960683	F2	coagulation factor II	NM_010168	17.2	28	24.3	39.7	1.9	4.7	3.1	2.5	27.3	3.05	-3.1781967	-9.0517495	0.04188244
14431	A_55_P1991505	Gamt	guanidinoacetate methyltrans	NM_010255	1556.6	1480.2	2347.1	1238.7	197.3	188.7	179.3	149.1	1655.65	178.6	-3.1791169	-9.0575254	0.00063679
225115	A_51_P354077	Svil	supervillin	NM_153153	10097.2	7719.6	10324.4	7721.7	1016.2	1086.6	940.1	880.3	8965.725	980.8	-3.1828388	-9.0809224	2.43E-05
74868	A_55_P1979027	Tmem65	transmembrane protein 65	NM_175212	3195.6	3776.8	2621.2	3787.4	335.4	425.3	345.2	351.2	3345.25	364.275	-3.1895775	-9.1234375	4.53E-05
12971	A_51_P264695	Crym	crystallin, mu	NM_016669	921.5	740.4	861.1	608.4	80.6	89.4	94.8	74.2	782.85	84.75	-3.1959604	-9.1638914	5.9067E-05
320949	A_55_P2176663	D830039M14Rik	RIKEN cDNA D830039M14 ge	AK085995	293.1	291.1	285	299.8	37.5	24.6	33	33.8	292.25	32.225	-3.1976361	-9.1745416	2.06E-05
76000	A_51_P286106	5033430I15Rik	RIKEN cDNA 5033430I15 gene	ENSMUST00000038032	530.7	408.5	332.7	485.8	53.9	51.2	40.8	43.5	439.425	47.35	-3.2011289	-9.1967807	0.00014756
216080	A_52_P546459	Ube2d1	ubiquitin-conjugating enzyme	NM_145420	401.7	362.1	460.7	399.8	42.2	43.7	49	41	406.075	43.975	-3.2050108	-9.2215597	2.61E-06
27226	A_66_P119034	Pla2g7	phospholipase A2, group VII (	NM_013737	3226.4	3296.8	3063.1	3554	360.7	373	343.1	344.2	3285.075	355.25	-3.2078222	-9.2395477	3.54E-07
66402	A_52_P413395	Sln	sarcolipin	NM_025540	950.6	1059.3	583.9	1300.5	115.2	105.1	106.2	81.5	973.575	102	-3.2082586	-9.2423428	0.00320571
69443	A_55_P2022429	1700027J07Rik	RIKEN cDNA 1700027J07 gene	AK006428	22.3	30.1	26.2	36.8	5.3	2.4	2.9	2.4	28.85	3.25	-3.2089195	-9.2465778	0.0100635
16828	A_55_P2141878	Ldha	lactate dehydrogenase A	NM_001136069	29868.7	26081.6	30364.1	25309.8	3330.8	3148.4	2941.3	2638.8	27906.05	3014.825	-3.2111546	-9.2609141	3.84E-06
207781	A_52_P330950	C2cd2	C2 calcium-dependent domai	NM_174847	817.6	781.6	1277.6	803.5	91	96.9	108.4	92.1	920.075	97.1	-3.2158358	-9.2910123	0.00015457
11636	A_55_P2082688	Ak1	adenylate kinase 1	NM_001198790	103389.6	89669.4	89495	91356.4	11796.7	10365.8	7899.9	10413	93477.6	10118.85	-3.2198602	-9.316966	1.99E-05
17700	A_51_P384901	Mstn	myostatin	NM_010834	2538	3023.7	3193.3	2692.9	310.8	288.5	312	302.7	2861.975	303.5	-3.2319839	-9.3955911	1.38E-06
245527	A_51_P161323	Eda2r	ectodysplasin A2 receptor	NM_175540	19.2	26.3	27.1	21.3	2	2.3	3.2	2.5	23.475	2.5	-3.2378485	-9.4338619	0.00019682
245683	A_55_P2084177	Klhl34	kelch-like 34 (Drosophila)	NM_001081667	306.9	341.6	231.2	376	30.9	51.6	20.5	35.1	313.925	34.525	-3.2388976	-9.4407243	0.00992957
381835	A_55_P1964282	Gm1078	predicted gene 1078	NM_001200041	133.6	327.7	163	185.5	22.3	16.3	23.2	19.2	202.45	20.25	-3.2492881	-9.5089636	0.00706958
319415	A_66_P132576	Hs3st5	heparan sulfate (glucosamine	NM_001081208	193.3	188.7	191.9	178	25.7	18.5	21.9	14.6	187.975	20.175	-3.2501719	-9.5147904	0.00013108
106393	A_55_P2126391	Srl	sarcalumenin	NM_175347	27448.5	24409.6	28892.7	24118.8	2990.2	2616.1	3105.3	2329.3	26217.4	2760.225	-3.2526157	-9.5309213	7.86E-06
216892	A_55_P2018929	Spns2	spinster homolog 2 (Drosophi	NM_153060	8850.4	7740.2	9887.2	6533.6	843.4	893.3	892	786.6	8252.85	853.825	-3.2578076	-9.5652826	2.21E-05
13384	A_55_P2137867	Mpp3	membrane protein, palmitoyl	NM_007863	192.4	113.2	171.5	198.8	13.8	20.1	19.6	15.9	168.975	17.35	-3.2671193	-9.6272204	0.0007937
77577	A_55_P1960286	Spns3	spinster homolog 3 (Drosophi	NM_029932	49.2	44.3	51.5	95.1	5.7	4.8	7.9	5.5	60.025	5.975	-3.2831036	-9.7344782	0.00513339
399548	A_66_P112495	Scn4b	sodium channel, type IV, beta	NM_001013390	23173.6	19866.8	21997.2	24534.6	2559.4	2086.4	2084.9	2479.4	22393.05	2302.525	-3.2839753	-9.7403612	3.94E-06
68680	A_51_P164630	Fitm1	fat storage-inducing transmer	NM_026808	8026.9	7183.4	7542.4	8101.2	889.6	810.3	740.8	731.4	7713.475	793.025	-3.2847559	-9.7456334	1.05E-06
104027	A_55_P2076787	Synpo	synaptopodin	NM_001109975	26297.3	18987.5	21711.3	22033.5	2370.8	2291.4	2107.2	2274.4	22257.4	2260.95	-3.2908513	-9.7868957	4.00E-06
791403	A_55_P2412214	D830015G02Rik	RIKEN cDNA D830015G02 ger	NR_033497	30.2	25.7	27.8	25.4	1.9	3.9	3.1	2.6	27.275	2.875	-3.2909223	-9.7873773	0.00072348
170768	A_52_P362917	Pfkfb3	6-phosphofructo-2-kinase/fru	NM_133232	179.1	143.3	236.8	92.3	18.9	14.6	16.1	13.7	162.875	15.825	-3.2924992	-9.7980808	0.00691245
268878	A_52_P607195	Atp13a5	ATPase type 13A5	NM_175650	79.2	108.2	88.1	104.5	4.3	11.3	14.4	12	95	10.5	-3.2994669	-9.8455164	0.05975961
109979	A_55_P2096827	Art3	ADP-ribosyltransferase 3	NM_181728	1497.3	1285.5	1459.6	1421.4	126.5	167	136.5	147.1	1415.95	144.275	-3.3001518	-9.8501918	3.046E-06
71887	A_51_P399175	Ppm1j	protein phosphatase 1J	NM_027982	1560.5	1171.4	1368.9	1215.7	118.6	134.8	145.2	138.6	1329.125	134.3	-3.3017164	-9.8608801	6.36E-06
107869	A_55_P1959923	Cth	cystathionase (cystathionine g	NM_145953	136.4	230.8	136.2	153.9	17.5	17.8	15.1	14.7	164.325	16.275	-3.3050806	-9.8839011	0.00022207
229595	A_55_P2006525	Adamtsl4	ADAMTS-like 4	NM_144899	1902.3	2425.4	1629.6	2664.5	227.1	247.8	206.6	176.9	2155.45	214.6	-3.3124461	-9.9344913	0.0002087
69121	A_55_P2021689	Chrdl2	chordin-like 2	NM_133709	407.3	373.5	345.4	213	39.8	38.3	28.3	26.4	334.8	33.2	-3.3156453	-9.9565456	0.00182156
215929	A_51_P436469	AI317395	expressed sequence AI31739	NM_144821	60.1	72.3	76.1	43.2	4.4	5.9	6.3	8.6	62.925	6.3	-3.3275235	-10.038859	0.00260608
17930	A_51_P431785	Myom2	myomesin 2	NM_008664	140242.9	161714.5	125887.1	122563.2	11303.1	14093.1	14140.1	15196	137601.925	13683.075	-3.3298885	-10.05533	1.38E-05
219134	A_51_P408649	Shisa2	shisa homolog 2 (Xenopus lae	NM_145463	2664.8	4003.4	3169.8	3783.8	298	346.8	298.7	400.5	3405.45	336	-3.3343193	-10.086259	0.00007376
229862	A_55_P1963041	Gm4861	predicted gene 4861	NM_177665	19.9	21.7	29.2	27	1.9	2.3	3	2.5	24.45	2.425	-3.3356449	-10.095531	0.00017032
76257	A_51_P139030	Slc38a3	solute carrier family 38, mem	NM_023805	1286.3	1172.8	1060.3	1011	120.1	112.8	90.4	125.7	1132.6	112.25	-3.3396924	-10.123894	1.43E-05
76432	A_55_P2383283	2310001H17Rik	RIKEN cDNA 2310001H17 gen	AK036632	26.8	28.4	39.9	31.5	1.9	2.4	3.1	6.4	31.65	3.45	-3.3420507	-10.140457	0.04883225
109272	A_55_P2008443	Mybpc1	myosin binding protein C, slov	NM_175418	3475.8	4179.9	2752.7	4033.2	341.5	514.1	259.3	317.2	3610.4	358.025	-3.3618372	-10.28049	0.00123105
100040382	A_52_P737521	Gm2745	predicted gene 2745	XM_001474423	27.4	33.4	27.8	17.1	1.9	2.6	3.1	2.5	26.425	2.525	-3.3680276	-10.324697	0.00137858
12409	A_55_P2122604	Cbr2	carbonyl reductase 2	NM_007621	896.8	736.6	990.1	384.5	73.2	79.4	63.4	59.8	752	68.95	-3.3695817	-10.335826	0.00859788
56788	A_55_P2232988	Scube2	signal peptide, CUB domain, E	NM_020052	522.6	602.6	440.5	487.3	38.8	48.5	56.6	54.7	513.25	49.65	-3.375547	-10.378651	4.02E-05
320997	A_51_P385849	Cyp4f39	cytochrome P450, family 4, su	NM_177307	22.1	16.4	42.7	21.9	1.9	2.2	2.9	2.4	25.775	2.35	-3.3770078	-10.389165	0.00803708
93896	A_55_P2073452	Glp2r	glucagon-like peptide 2 recep	NM_175681	43.7	54.2	41	34.6	4.3	4.4	5.9	2.5	43.375	4.275	-3.3888878	-10.475069	0.00385966
11447	A_55_P2110548	Chrnd	cholinergic receptor, nicotinic	NM_021600	457.1	557.7	405.5	626.6	51.3	55.1	41.8	45.2	511.725	48.35	-3.3915303	-10.494273	6.28E-05
17879	A_55_P2147280	Myh1	myosin, heavy polypeptide 1,	NM_030679	66274.5	54996.8	42969.3	50593.5	3760.3	9501.4	4616.8	3944	53708.525	5455.625	-3.3930579	-10.505391	0.01176568
117590	A_51_P406188	Asb10	ankyrin repeat and SOCS box-	NM_080444	3977.4	3180	3850	2613.5	300.6	296.1	337.4	344.4	3405.225	319.625	-3.3967329	-10.532186	3.13E-05
53376	A_55_P1985788	Usp2	ubiquitin specific peptidase 2	NM_198092	17170	14240.2	14838.5	12676	1393.9	1449.9	1391.5	1268.4	14731.175	1375.925	-3.4135714	-10.655832	2.52E-06
228608	A_55_P1998892	Smox	spermine oxidase	NM_001177833	20647	14136.5	17145	8860.9	1286.2	1375.5	1417.6	1365.3	15197.35	1361.15	-3.4151607	-10.667578	0.00171183
17127	A_55_P2101001	Smad3	MAD homolog 3 (Drosophila)	NM_016769	12082.2	10642.2	12090.5	16395.8	1090.6	1256.3	1222.6	1173	12802.675	1185.625	-3.4157834	-10.672183	1.82E-05
70392	A_55_P2100360	Asb12	ankyrin repeat and SOCS box-	NM_080858	199.5	258.7	340.6	280.5	31.6	21.7	24.7	21.8	269.825	24.95	-3.4262504	-10.749893	0.00024363
381792	A_66_P119350	2310040G24Rik	RIKEN cDNA 2310040G24 gen	XR_104992	9728.3	8574.9	9241.4	7903.8	845.4	749.6	924.5	774	8862.1	823.375	-3.428479	-10.766511	1.89E-06
16433	A_51_P155465	Cuzd1	CUB and zona pellucida-like d	NM_008411	35.5	23.2	37.3	24.4	1.9	3.7	3	2.6	30.1	2.8	-3.4346785	-10.812877	0.00191421
11870	A_52_P166393	Art1	ADP-ribosyltransferase 1	NM_009710	11814.6	11059.7	13225.5	11028.1	1026.2	1040	1331.7	883.3	11781.975	1070.3	-3.4724905	-11.100021	1.42E-05
70807	A_55_P1957922	Arrdc2	arrestin domain containing 2	NM_027560	15398.8	16360.2	14549.8	24295.4	1626.1	1726.5	1630.4	1280.7	17651.05	1565.925	-3.4727446	-11.101976	0.00014487
767814	A_55_P2204779	AU019990	expressed sequence AU01999	NR_033469	43	23.5	37	16.8	1.9	2.5	3.2	2.6	30.075	2.55	-3.4890463	-11.228134	0.01169648
12053	A_52_P161495	Bcl6	B-cell leukemia/lymphoma 6	NM_009744	6761.6	5212.6	4514	10632.9	526.1	627.6	607.9	513.3	6780.275	568.725	-3.5007828	-11.319849	0.00227635
68016	A_55_P1954331	Murc	muscle-related coiled-coil pro	NM_026509	12758.3	12082.6	12937.2	13118.8	1177.4	1666.9	1050.9	757.1	12724.225	1163.075	-3.5080718	-11.377186	0.00059543
67902	A_55_P2162835	Sumf2	sulfatase modifying factor 2	NM_026445	24.5	28.2	34.2	24.4	1.9	2.6	2.9	2.4	27.825	2.45	-3.5083671	-11.379515	6.10E-05
17882	A_55_P2106068	Myh2	myosin, heavy polypeptide 2,	NM_001039545	73745.5	59355.6	61708.7	55788	4122.2	9332.9	5804.1	4003.6	62649.45	5815.7	-3.5102425	-11.394317	0.00343293
319455	A_55_P2009841	Pld5	phospholipase D family, mem	NM_176916	28.9	27.4	28.7	32	2.6	2.3	3	2.4	29.25	2.575	-3.5109845	-11.400178	1.79E-06
20913	A_55_P2175195	Stxbp4	syntaxin binding protein 4	NM_011505	62956.6	47019.4	56211.8	52203.9	4821.9	3888.6	6681.3	4015	54597.925	4851.7	-3.5189938	-11.463644	0.00016739
18626	A_55_P2019327	Per1	period homolog 1 (Drosophila	AK081813	41.6	24.9	22.5	30.6	1.9	2.4	3.4	2.6	29.9	2.575	-3.5277045	-11.533069	0.00122081
11448	A_55_P2180470	Chrne	cholinergic receptor, nicotinic	NM_009603	46	24.3	39.8	21.1	1.8	2.2	5.3	2.5	32.8	2.95	-3.5317233	-11.56524	0.05974698
72119	A_51_P369200	Tpx2	TPX2, microtubule-associated	NM_028109	28.4	34.1	26.6	41.2	2.7	2.7	2.9	2.8	32.575	2.775	-3.5325118	-11.571562	1.70E-05
66353	A_51_P183213	Riiad1	regulatory subunit of type II P	NM_025506	100.2	68.4	63.5	79.9	6.9	8	5.6	6.2	78	6.675	-3.536795	-11.605968	8.33E-05
74251	A_52_P276525	Ankrd9	ankyrin repeat domain 9	NM_175207	11090.6	8143.9	9353.5	7339.2	919.1	642.5	668.2	816.1	8981.8	761.475	-3.5582207	-11.779616	6.54E-05
71911	A_52_P468343	Bdh1	3-hydroxybutyrate dehydroge	NM_001122683	147.9	222.6	108.3	160.2	10.1	14.6	16.4	12	159.75	13.275	-3.5661604	-11.844623	0.00119331
21689	A_55_P2132024	Tekt1	tektin 1	NM_011569	395.6	398.1	343.1	564.6	39.3	32.5	36.4	32.9	425.35	35.275	-3.5709372	-11.883906	4.01E-05
11435	A_52_P533707	Chrna1	cholinergic receptor, nicotinic	NM_007389	2228.8	2003.5	1916.8	2564.7	155.7	171.2	202.6	202.7	2178.45	183.05	-3.57289	-11.900003	9.25E-06
30927	A_51_P356186	Snai3	snail homolog 3 (Drosophila)	NM_013914	30.4	37.5	39.1	44.9	4.4	2.2	4.1	2.4	37.975	3.275	-3.5897232	-12.039664	0.00196001
667370	A_55_P1972872	I830012O16Rik	RIKEN cDNA I830012O16 gen	NM_001005858	196.7	115	254.6	230.4	11.1	20.7	15	18	199.175	16.2	-3.5961416	-12.093346	0.00509065
16518	A_52_P503614	Kcnj2	potassium inwardly-rectifying	NM_008425	94.2	107.1	122.3	107.5	11.8	10.3	7.9	6.4	107.775	9.1	-3.5994328	-12.120966	0.00021094
71050	A_55_P2321889	4933404I11Rik	RIKEN cDNA 4933404I11 gene	AK016650	15.2	43.9	32	57.2	2.2	2.6	3.5	2.8	37.075	2.775	-3.6028237	-12.149489	0.052262
244417	A_55_P2090645	Gm501	predicted gene 501	XM_987122	28.2	50.5	30.9	53.1	2.2	4.9	3.5	2.8	40.675	3.35	-3.6082357	-12.19515	0.00789194
434246	A_55_P2026848	Trim72	tripartite motif-containing 72	NM_001079932	2874.3	2486.1	2713.3	2035.3	198.6	195.3	210	212.4	2527.25	204.075	-3.6193417	-12.289392	3.24E-06
114601	A_51_P222475	Ehbp1l1	EH domain binding protein 1-	NM_053252	22894.9	17406.5	22745.4	19509.8	1821.4	1755.2	1487.6	1604.7	20639.15	1667.225	-3.6250413	-12.33804	3.66E-06
58805	A_55_P2119957	Mlxipl	MLX interacting protein-like	NM_021455	12465.4	13987.3	12685	12906.7	1043.8	1116.5	976.6	1060.1	13011.1	1049.25	-3.6325335	-12.402281	1.64E-07
625342	A_55_P2059323	Gm13315	lactate dehydrogenase A pseu	NR_028497	3355.6	2536.1	3005.1	2836.3	262.9	231.2	230.9	215.5	2933.275	235.125	-3.6374266	-12.444416	1.93E-06
16514	A_52_P402705	Kcnj11	potassium inwardly rectifying	NM_010602	453.2	343.2	479.7	347.1	33.5	31.7	29.5	33.9	405.8	32.15	-3.6434374	-12.496372	8.61E-06
194231	A_66_P140974	Cnksr1	connector enhancer of kinase	NM_001081047	398.1	364.8	513.8	383	33.6	32.4	35.1	29.7	414.925	32.7	-3.6550278	-12.59717	4.57E-06
17897	A_55_P2152547	Myl3	myosin, light polypeptide 3	NM_010859	82926.9	112255.9	65065.6	104517.1	5837.4	12319.1	4699.5	7330.7	91191.375	7546.675	-3.6603062	-12.643344	0.00819011
69253	A_52_P222624	Hspb2	heat shock protein 2	NM_024441	21683.3	20843.6	18040.1	19198.5	1647.4	1707.5	1509.1	1381	19941.375	1561.25	-3.676156	-12.783013	9.46E-07
244091	A_52_P505157	Fsd2	fibronectin type III and SPRY d	NM_172904	416.4	380.5	437.1	340.4	36.8	23.2	19.1	52.7	393.6	32.95	-3.6858918	-12.869569	0.00647396
27280	A_51_P329928	Phlda3	pleckstrin homology-like dom	NM_013750	36793.7	37443.7	45775.7	37010.2	2713.3	3470.6	2855.3	3155.7	39255.825	3048.725	-3.6868907	-12.878483	2.39E-06
69982	A_55_P2000027	Spink2	serine peptidase inhibitor, Ka	NM_183284	22.6	44.2	44.9	32.1	1.9	3	3.3	2.7	35.95	2.725	-3.6977457	-12.975747	0.00192214
192188	A_55_P1974028	Stab2	stabilin 2	NM_138673	2948.2	2662	2938.5	3183.5	176.6	226.6	246.8	254.8	2933.05	226.2	-3.7081025	-13.069233	6.37E-06
69585	A_51_P206824	Hfe2	hemochromatosis type 2 (juve	NM_027126	2123.1	2231.5	2336.1	2741.5	218.7	188.8	136.4	182.6	2358.05	181.625	-3.7121559	-13.106003	2.64E-05
74376	A_55_P2106033	Myo18b	myosin XVIIIb	NM_028901	12712.3	12657.4	13881.8	13333	1093.7	1237.4	975.7	749.7	13146.125	1014.125	-3.7191727	-13.169902	2.0144E-05
238021	A_51_P244633	Fscn2	fascin homolog 2, actin-bundl	NM_172802	44.1	34.7	36.4	19.7	1.9	2.5	3	2.5	33.725	2.475	-3.7276857	-13.247844	0.00150747
56471	A_51_P194249	Stmn4	stathmin-like 4	NM_019675	297.5	474.2	321	317.7	21.7	34.9	32.1	19.2	352.6	26.975	-3.7279336	-13.250121	0.00075666

50874	A_55_P1976574	Tmod4	tropomodulin 4	NM_016712	54438.9	52963.8	51339.2	48534.2	4087.3	3860.4	3690.1	3848.3	51819.025	3871.525	-3.7421599	-13.381426	9.72E-08
11811	A_55_P1978351	Apobec2	apolipoprotein B mRNA editir	NM_009694	2003.9	1575.2	2507.7	1904.9	156.1	132.5	155.7	145.2	1997.925	147.375	-3.7442162	-13.400511	1.32E-05
71008	A_55_P2360356	4933401D09Rik	RIKEN cDNA 4933401D09 gen	AK016599	76.1	81.6	77	100.7	6.6	7.9	3.5	8.1	83.85	6.525	-3.7478582	-13.434383	0.00205123
242502	A_52_P1045316	Gm428	predicted gene 428	NM_001081644	43.6	61	40.7	63.8	4.7	6	3	2.5	52.275	4.05	-3.7487303	-13.442507	0.00495436
100041085	A_55_P2153600	G630090E17Rik	RIKEN cDNA G630090E17 gen	NM_001173500	82.4	87.1	94.7	56	3.5	6.8	5.5	8.8	80.05	6.15	-3.752999	-13.48234	0.00425661
22417	A_66_P139703	Wnt4	wingless-related MMTV integ	ENSMUST00000097840	2415	3069.5	2481.7	2635.9	231.3	176.3	172.1	208.8	2650.525	197.125	-3.7535493	-13.487483	5.00E-06
403183	A_66_P107377	4832428D23Rik	RIKEN cDNA 4832428D23 gen	NM_207281	40.4	33.1	38.1	24.1	1.9	2.5	3	2.5	33.925	2.475	-3.7682262	-13.625396	0.0001644
16497	A_55_P2130129	Kcnab1	potassium voltage-gated char	NM_010597	612.6	416.6	605.9	340.5	27.6	35	45.7	34.4	493.9	35.675	-3.7703573	-13.645537	0.00061812
69700	A_55_P2031781	Col22a1	collagen, type XXII, alpha 1	NM_027174	1821.5	2300.4	2120.4	2970.7	119.6	182.7	218.7	153.8	2303.25	168.7	-3.7830402	-13.766026	0.00032957
380780	A_55_P2010191	Serpina11	serine (or cysteine) peptidase	BC024087	491.3	726.1	584.5	850.6	74.6	39.6	53.4	31.1	663.125	49.675	-3.7854346	-13.788892	0.00359538
12839	A_55_P1999532	Col9a1	collagen, type IX, alpha 1	NM_007740	73.6	48.6	83.9	49.8	6.7	7.6	3.1	2.6	63.975	5	-3.7880627	-13.814033	0.03621076
68339	A_55_P2051384	Ccdc88c	coiled-coil domain containing	NM_026681	550.6	323.2	617.8	483.8	35.3	35.2	28.7	39.7	493.85	34.725	-3.7993154	-13.922201	0.0002201
140703	A_55_P1954277	Emid1	EMI domain containing 1	NM_080595	2423.6	2038.1	2459.9	1680.2	147	181.5	160.5	125.1	2150.45	153.525	-3.8044702	-13.972034	2.9923E-05
16502	A_55_P2007243	Kcnc1	potassium voltage gated char	NM_008421	3443	2872.3	2935.5	3679.7	244.4	238.1	228.5	210.2	3232.625	230.3	-3.8055027	-13.982037	1.14E-06
77036	A_51_P176583	1700109H08Rik	RIKEN cDNA 1700109H08 gen	NM_029843	113.3	110.8	123.8	150.8	10.4	11.1	9	5.8	124.675	9.075	-3.8118002	-14.043204	0.00027979
17906	A_55_P1997544	Myl2	myosin, light polypeptide 2, r	ENSMUST00000111750	42.5	49.6	43.9	46.9	3.1	4.2	3.2	2.6	45.725	3.275	-3.8225208	-14.147947	1.26E-05
22229	A_52_P380379	Ucp3	uncoupling protein 3 (mitoch	NM_009464	1208.9	902	1063.7	1008.5	77.9	70.1	92.4	56.9	1045.775	74.325	-3.8285655	-14.20735	2.77E-05
12561	A_55_P2150831	Cdh4	cadherin 4	NM_009867	504.4	391.2	519.8	526	30.2	36.8	34.1	34.6	485.35	33.925	-3.8321021	-14.24222	2.63E-06
108995	A_51_P267314	Tbc1d10c	TBC1 domain family, member	NM_178650	267	258.5	239.5	253.1	23	14	20.7	14.9	254.525	18.15	-3.8406114	-14.326472	3.72E-05
214951	A_52_P256757	Rhbdl1	rhomboid, veinlet-like 1 (Dros	NM_144816	785	569.8	657.5	451.6	44.4	39.8	55.5	30.5	615.975	42.55	-3.859568	-14.515959	0.00037326
69671	A_55_P2089015	Tmem52	transmembrane protein 52	ENSMUST00000023920	2575.7	2654.4	2052.8	2270.2	178.7	143.4	144.2	191.9	2388.275	164.55	-3.8638662	-14.559271	6.24E-06
100041426	A_66_P134109	Gm3331	predicted gene 3331	AK042795	33.2	32.3	39.3	32.1	1.8	2.3	2.9	2.4	34.225	2.35	-3.8797036	-14.719978	1.45E-05
12372	A_51_P199104	Casq1	calsequestrin 1	NM_009813	4932.3	3964.7	4740	4120.7	279.7	333.7	290.7	295.9	4439.425	300	-3.8844721	-14.768712	7.56E-07
13170	A_55_P2032079	Dbp	D site albumin promoter bind	NM_016974	16418.6	17070.7	16957	8873.5	884.1	1304.1	785.5	978.4	14829.95	988.025	-3.8846266	-14.770294	0.00091506
320159	A_55_P2071354	Fam179a	family with sequence similarit	NM_177087	322.8	398.2	237.2	289.7	16.7	21.4	31.6	16.4	311.975	21.525	-3.8853577	-14.77778	0.0007157
211187	A_55_P1954231	Lrtm2	leucine-rich repeats and trans	NM_172492	55.2	41.8	24.8	27.3	1.9	2.3	2.9	2.5	37.275	2.4	-3.8973776	-14.901417	0.00149887
98660	A_52_P227267	Atp1a2	ATPase, Na+/K+ transporting,	NM_178405	7955.8	6349.4	7042.9	8618.8	523.3	520.5	494	439.9	7491.725	494.425	-3.9151933	-15.086574	1.82E-06
75581	A_52_P313102	Yipf7	Yip1 domain family, member	NM_023784	3419.4	3437.5	3436.7	3573	197.9	281.8	267.7	180.8	3466.65	232.05	-3.92663	-15.206645	1.41E-05
59011	A_51_P379750	Myoz1	myozenin 1	NM_021508	91022.4	73992	88304.2	77329.2	5297.8	4964.1	7024.6	4574	82661.95	5465.125	-3.9330002	-15.273938	1.07E-05
30953	A_51_P163252	Schip1	schwannomin interacting pro	NM_013928	779.4	703	864.4	527.9	42.6	52.7	42	46	718.675	45.825	-3.9537213	-15.494897	2.14E-05
668224	A_66_P137890	Gm9054	predicted gene 9054	XR_104793	68.2	62.8	54.2	43.4	4.6	2.5	5.4	2.7	57.15	3.8	-3.968689	-15.65649	0.00180114
21393	A_52_P249733	Tcap	titin-cap	NM_011540	163127.2	144781.4	160211.6	139978	9597.8	14037.2	11241.8	5792.4	152024.55	10167.3	-3.9704069	-15.675145	0.00072187
16495	A_66_P114700	Kcna7	potassium voltage-gated char	NM_010596	9953.9	8707.7	9893.2	10124.5	660.8	576.4	584.1	645.3	9669.825	616.65	-3.9710031	-15.681625	2.03E-07
100040353	A_55_P2010048	2810416G20Rik	RIKEN cDNA 2810416G20 gen	BB667085	1673.7	2023.4	1908.6	1589.7	86.9	115.4	114.6	143.9	1798.85	115.2	-3.9807648	-15.788091	1.95E-05
668940	A_55_P2057321	Myh7b	myosin, heavy chain 7B, cardi	NM_001085378	191.6	348.4	137.2	300.1	19.1	12.5	9.3	19.4	244.325	15.075	-3.9903546	-15.893386	0.01227361
16011	A_52_P281702	Igfbp5	insulin-like growth factor bind	NM_010518	6425.7	6719.9	4467.6	6212.4	317.8	452.3	412.3	315.8	5956.4	374.55	-3.9916379	-15.90753	3.9635E-05
100702	A_55_P2052385	Gbp6	guanylate binding protein 6	NM_194336	101.6	200.6	103.6	151.2	10.4	5.8	8.7	9.3	139.25	8.55	-3.9993296	-15.992566	0.00123275
19245	A_51_P322273	Ptp4a3	protein tyrosine phosphatase	NM_008975	12257.8	11224.8	13070.9	11552.5	738.4	874.9	754.9	639.1	12026.5	751.825	-4.0061326	-16.068157	1.02E-06
83679	A_55_P2058127	Pde4dip	phosphodiesterase 4D interac	NM_177145	2384.6	2733.1	2158.6	3286.1	138.1	180.2	162.9	167.4	2640.6	162.15	-4.0139679	-16.155662	9.755E-06
12723	A_55_P2033020	Clcn1	chloride channel 1	NM_013491	588.5	533	611.8	513.5	29	26	53.3	35.2	561.7	35.875	-4.0220098	-16.245968	0.00019152
545798	A_55_P1953286	Tmem233	transmembrane protein 233	NM_001101546	1373.2	746.7	835.6	850.2	72.5	40.6	56.5	57.4	951.425	56.75	-4.0548908	-16.620488	0.00037883
12295	A_55_P2012563	Cacnb1	calcium channel, voltage-dep	NM_031173	2928.4	2543.1	2496.3	2612	163.1	171.3	162	139.1	2644.95	158.875	-4.0587403	-16.664895	3.22E-07
30052	A_52_P496202	Pcsk1n	proprotein convertase subtilis	NM_013892	1208.3	847.4	1268.8	819.8	48.5	53.2	85.1	61.3	1036.075	62.025	-4.0679675	-16.771821	0.00022022
27528	A_66_P120125	D0H4S114	DNA segment, human D4S114	NM_053078	2498.9	2199.1	2475.1	1562.6	132.7	220	99.7	91.2	2183.925	135.9	-4.0722278	-16.821422	0.00215598
77424	A_55_P1972710	Spinkl	serine protease inhibitor, Kaz	NM_183123	47.1	49.1	36	50.6	2.5	2.6	3.1	2.5	45.7	2.675	-4.0879152	-17.005331	3.61E-06
15464	A_55_P1994229	Hrc	histidine rich calcium binding	NM_010473	87046.2	74424.9	78179.3	72581.2	4979.1	4049.7	4718.1	4389.1	78057.9	4534	-4.1064576	-17.225305	3.60E-07
268859	A_55_P1953400	Rbfox1	RNA binding protein, fox-1 hc	NM_021477	30942.2	31521.8	31887.6	28701.8	1702.8	1682	1818	1923.7	30763.35	1781.625	-4.110863	-17.277984	8.4E-08
17901	A_52_P273120	Myl1	myosin, light polypeptide 1	NM_001113387	57932.5	47646.3	82820.3	49212.8	3283.9	3176.1	4003.2	2944.8	59402.975	3352	-4.1203694	-17.392211	5.79E-05
244071	A_55_P2099615	Agbl1	ATP/GTP binding protein-like	NM_001199224	58.7	52.6	34.8	40.5	1.9	3.7	2.8	2.4	46.65	2.7	-4.1227897	-17.421413	0.00038517
67484	A_51_P317191	Eepd1	endonuclease/exonuclease/p	NM_026189	1189.8	978	1129.5	1000.6	54.2	69.2	59.4	54	1074.475	59.2	-4.1845282	-18.183124	8.79E-07
226922	A_66_P122053	Kcnq5	potassium voltage-gated char	NM_001160139	140.4	160.1	140.8	155.3	9.8	10.4	6	7.3	149.15	8.375	-4.1871235	-18.215863	3.13E-05
791346	A_55_P2012459	Gm10118	predicted gene 10118	ENSMUST00000079279	156.1	102.3	160.2	88.8	10.1	7.6	5.7	4.7	126.85	7.025	-4.1883254	-18.231046	0.00156804
14201	A_55_P2028184	Fhl3	four and a half LIM domains 3	NM_010213	120.5	91.8	104.2	61.5	4.3	3.5	9.9	4.1	94.5	5.45	-4.2060734	-18.456708	0.00749053
68678	A_55_P1993153	Smtnl1	smoothelin-like 1	NM_024230	4975.9	6152.9	4339.2	6136.2	306.9	309.8	274.8	264.9	5401.05	289.1	-4.2114438	-18.525542	3.00E-06
69657	A_55_P2182740	2310047D07Rik	RIKEN cDNA 2310047D07 gen	XR_104959	512.1	529.9	612.7	615.1	22.5	33.1	38.3	29.6	567.45	30.875	-4.2215405	-18.655647	1.61E-05
17306	A_55_P2155103	Sypl2	synaptophysin-like 2	NM_008596	1673.2	1570.2	1872.3	1556.1	82.3	95.7	84.1	92.6	1667.95	88.675	-4.2323	-18.7953	2.21E-07
100504421	A_55_P2279690	2900076A07Rik	RIKEN cDNA 2900076A07 gen	AK085873	1365.1	1258.5	1557.7	1479.1	73.6	74.4	75.3	73.3	1415.1	74.15	-4.2497005	-19.023365	1.16E-07
22004	A_55_P2121408	Tpm2	tropomyosin 2, beta	NM_009416	36022.8	32200.9	35672.4	29016.6	1718.7	2198.3	1690.2	1427.7	33228.175	1758.725	-4.2517044	-19.049806	4.72E-06
71302	A_55_P2170881	Arhgap26	Rho GTPase activating protei	NM_175164	192.8	190.9	265.9	107.3	15.7	8.8	5.3	10.6	189.225	10.1	-4.261425	-19.178593	0.01146615
258505	A_55_P2183955	Olfr97	olfactory receptor 97	NM_146512	103.4	76.8	94	89.2	2.8	4.5	2.9	13.2	90.85	5.85	-4.2687042	-19.275604	0.06082765
50769	A_51_P305628	Atp8a2	ATPase, aminophospholipid t	NM_015803	644.1	584.2	659.4	643.1	35.8	34.5	34.9	26.8	632.7	33	-4.2689101	-19.278356	6.60E-07
18419	A_51_P242687	Otog	otogelin	NM_013624	50	59.7	45.4	49	2	2.7	3.4	2.6	51.025	2.675	-4.2714599	-19.312458	1.55E-05
239790	A_52_P374960	Ostn	osteocrin	NM_198112	722.4	866.6	580.1	890	38.7	35.6	35.7	46.5	764.775	39.125	-4.2771545	-19.388838	1.09E-05
75667	A_51_P102518	Tmem225	transmembrane protein 225	NM_029379	58.8	43.6	44.1	41.2	2	2.3	2.9	2.4	46.925	2.4	-4.2876396	-19.530265	7.36E-06
12922	A_55_P1987156	Crhr2	corticotropin releasing hormc	NM_009953	2958.3	3244.6	3120.9	3758.7	170.3	172.6	156.2	168.3	3270.625	166.85	-4.2881942	-19.537774	2.00E-07
57435	A_51_P495780	Plin4	perilipin 4	NM_020568	59300.3	59310.7	62556.2	53313.6	2478.2	3917.2	2602.4	3160.4	58620.2	3039.55	-4.2911588	-19.577964	6.81E-06
381836	A_55_P2133470	Sbk2	SH3-binding domain kinase fa	NM_001146329	91.6	57.2	94.2	50.7	2.4	3.6	2.8	6.5	73.425	3.825	-4.3199725	-19.972908	0.00539041
100503386	A_55_P2003976	Gm4980	predicted gene 4980	NM_001195529	131.1	100.5	133.7	86.9	6.4	8.3	2.8	6.2	113.05	5.925	-4.3352093	-20.184967	0.00349896
170947	A_55_P2217438	Myoz3	myozenin 3	NM_133363	7329.8	6114.4	6819.8	6634.7	361.8	311.3	360.3	297.2	6724.675	332.65	-4.3398318	-20.249744	2.96E-07
233335	A_55_P2052690	Synm	synemin, intermediate filame	NM_201639	13042.2	12393	15092.2	14722.4	662.3	695.9	729.3	625.6	13812.45	678.275	-4.3454589	-20.328881	2.07E-07
73284	A_52_P311853	Ddit4l	DNA-damage-inducible transc	NM_030143	2876	2210.8	3044.5	5347.8	155.2	164.5	161.6	145.4	3369.775	156.675	-4.3492062	-20.381752	0.00029311
16420	A_51_P161054	Itgb6	integrin beta 6	NM_021359	225.1	220.8	176	203.4	9.3	8.6	10.1	12.4	206.325	10.1	-4.3596268	-20.529503	2.73E-06
76670	A_55_P1981529	Ttc18	tetratricopeptide repeat dom	NM_001163638	73.2	89.7	66.1	109.6	2.6	3	4.7	7.3	84.65	4.4	-4.3598647	-20.532889	0.00354686
381107	A_55_P1974947	Tmem232	transmembrane protein 232	NM_001008973	262.9	171.3	321.4	266.1	15.7	8	16.4	10	255.425	12.525	-4.3781395	-20.794635	0.00093887
20562	A_55_P1958379	Slit1	slit homolog 1 (Drosophila)	NM_015748	120	104.9	141.6	151.4	8.9	7.4	6.9	3.1	129.475	6.575	-4.3868663	-20.920802	0.00234552
59069	A_55_P2090205	Tpm3	tropomyosin 3, gamma	ENSMUST00000121503	4105	8308.5	4754	7616.4	278	317.2	250.4	289.7	6195.975	283.825	-4.3896655	-20.961433	0.00019765
59091	A_51_P218653	Jph2	junctophilin 2	NM_021566	133.2	94.9	111.5	99.8	7.9	6.5	3.1	4.5	109.85	5.5	-4.3957922	-21.05064	0.00091389
207215	A_55_P2016307	Fbxo40	F-box protein 40	NM_001037321	195.1	202.5	204.4	166.3	10	9.6	9.9	6.9	192.075	9.1	-4.4109391	-21.272816	3.30E-06
17878	A_51_P386794	Myf6	myogenic factor 6	NM_008657	10946.9	9839.8	10830.2	8500	481.1	579.7	376.7	437.6	10029.225	468.775	-4.4296427	-21.550399	4.75E-06
11733	A_55_P2063785	Ank1	ankyrin 1, erythroid	NM_001110783	8354.7	8287.2	6764.9	9037.3	386.1	409	314.5	374.5	8111.025	371.025	-4.4490111	-21.841668	1.03E-06
15365	A_55_P2320283	Hmga2-ps1	high mobility group AT-hook 2	AK033703	1840.2	1897	2003.5	2145.2	74.3	102.6	96.9	86	1971.475	89.95	-4.4623718	-22.044882	7.33E-07
228684	A_55_P2047027	Sel1l2	sel-1 suppressor of lin-12-like	NM_001033296	49.8	48.9	44.4	83.8	1.9	2.2	2.9	2.6	56.725	2.4	-4.5332838	-23.155512	0.00010236
432779	A_55_P2052824	Lrrc14b	leucine rich repeat containing	NM_001033042	5477.4	5288.8	6270.7	4912	289.1	218.2	226.6	215.6	5487.225	237.375	-4.5358391	-23.196562	1.03E-06
402767	A_55_P2412319	A830052D11Rik	RIKEN cDNA A830052D11 ger	AK043919	1783.3	2247.8	1886.7	1749.6	94.3	77.8	88	69.6	1916.85	82.425	-4.5419398	-23.294861	1.18E-06
21955	A_55_P2088385	Tnnt1	troponin T1, skeletal, slow	NM_011618	37575.5	59507.2	34311.6	62171.2	1800.3	2675.6	1655.6	2028.6	48391.375	2040.025	-4.5423933	-23.302185	0.00019011
26944	A_51_P283004	Tinag	tubulointerstitial nephritis an	NM_012033	70	54.4	52.9	57.6	1.9	2.4	3.2	2.6	58.725	2.525	-4.5555983	-23.516448	1.03E-05
17907	A_55_P2170381	Mylpf	myosin light chain, phosphory	NM_016754	1983.1	1633.9	2167.7	1797.3	66.4	95	105.3	62.1	1895.5	82.2	-4.5558402	-23.520391	2.78E-05
100040972	A_55_P2012011	Tceal7	transcription elongation facto	NM_001127169	2269	3066.6	2677	3166	93.7	118.4	140.6	118.9	2794.65	117.9	-4.569638	-23.746418	5.08E-06
276829	A_55_P1984655	Smtnl2	smoothelin-like 2	NM_177776	21487.2	19797	23656.3	21598.2	899.9	1031.9	907.6	807.9	21634.675	911.825	-4.5710226	-23.769219	1.98E-07
100042065	A_66_P103780	Gm3646	predicted gene 3646	NM_001177348	165.8	183.6	147.9	175.6	12.2	9.1	3.5	6.3	168.225	7.775	-4.5752418	-23.838834	0.00361275
382571	A_55_P2116536	Kcnf1	potassium voltage-gated char	NM_201531	85.6	105.1	67.2	48.2	2.2	4.2	3.4	2.8	76.525	3.15	-4.5844135	-23.990868	0.00058412
329731	A_52_P57317	Fam19a3	family with sequence similarit	NM_183224	352.9	310.3	364.6	395.1	18.8	14.1	14.2	12.4	355.725	14.875	-4.5916273	-24.111128	2.45E-06
108723	A_51_P316042	Card11	caspase recruitment domain f	NM_175362	137	158.1	150.4	101.2	3.7	6.2	5.5	7.2	136.675	5.65	-4.6173075	-24.544153	0.0001016
100504518	A_55_P2116525	3425401B19Rik	RIKEN cDNA 3425401B19 gen	NM_001195097	1603.5	1090.2	1697.3	1632.7	49	74.6	56.8	59.5	1505.925	59.975	-4.6452513	-25.024187	1.5259E-05
22138	A_55_P2424042	Ttn	titin	NM_028004	2639.6	2501.2	2338.5	2761.2	105.6	147.8	92.3	74.2	2560.125	104.975	-4.6513453	-25.130114	2.98E-05
110902	A_55_P2177513	Chrna2	cholinergic receptor, nicotinic	NM_144803	70.7	110.6	65.2	176	4.2	5.1	2.9	3.4	105.625	3.9	-4.6741508	-25.530517	0.00206597
545641	A_66_P127463	Gm5860	predicted gene 5860	ENSMUST00000161588	680.8	795.5	665.4	473.5	25.7	29.6	20.5	23.1	653.8	24.725	-4.7133773	-26.234208	1.31E-05
68854	A_55_P2122618	Asb11	ankyrin repeat and SOCS box-	ENSMUST00000036858	28113.2	25023.2	28178.1	28702.9	974	1169.5	958.9	926.7	27504.35	1007.275	-4.7751213	-27.381342	1.40E-07
18639	A_55_P2002893	Pfkfb1	6-phosphofructo-2-kinase/fru	NM_008824	7014.1	8087.2	6707.6	4752.8	208.8	333.5	220.8	206.5	6640.425	242.4	-4.7798736	-27.471688	4.20E-05
241113	A_55_P2077681	Prkag3	protein kinase, AMP-activated	NM_153744	396.7	316.8	401.6	381.5	14.8	11.7	14.4	13.3	374.15	13.55	-4.7867937	-27.603775	3.76E-07
58194	A_55_P1970002	Sh3kbp1	SH3-domain kinase binding pr	NM_001135727	483.7	475.8	572.6	345.8	17.5	15.7	13.7	19.6	469.475	16.625	-4.8091242	-28.034359	8.94E-06
435391	A_55_P2140201	Dupd1	dual specificity phosphatase a	NM_001013826	4284.9	3430.6	4190.4	2299.7	122.2	139.6	138.9	94.6	3551.4	123.825	-4.8173666	-28.194984	6.17E-05
71907	A_55_P2092219	Serpina9	serine (or cysteine) peptidase	NM_027997	94.1	75.9	80.3	66.4	1.8	3.8	3.5	2.4	79.175	2.875	-4.8345511	-28.532834	0.0001244
50794	A_52_P281659	Klf13	Kruppel-like factor 13	ENSMUST00000008043	104.4	92.8	93.9	74.7	4.3	2.6	3.2	2.7	91.45	3.2	-4.8560602	-28.961415	1.04E-05
230099	A_55_P2092750	Car9	carbonic anhydrase 9	NM_139305	211.4	167.1	137.2	230.4	9.6	7.8	7.8	2.7	186.525	6.975	-4.8583978	-29.008379	0.00600627
242702	A_55_P2034067	Myom3	myomesin family, member 3	NM_001085509	8160.3	10230.4	5021	10504.5	266.1	402.4	230.8	235.4	8479.05	283.675	-4.8824198	-29.495435	0.00031767
11829	A_55_P2000369	Aqp4	aquaporin 4	NM_009700	898.3	753.6	527.3	857.6	24.4	32.1	27.6	18.3	759.2	25.6	-4.8904178	-29.659406	5.22E-05
100039348	A_66_P101561	Gm2176	glucosamine-6-phosphate dea	NR_028424	44.8	51.5	61.1	181.9	1.8	2.4	3	2.5	84.825	2.425	-4.8985269	-29.826585	0.01072078
77442	A_55_P2303777	9530020I12Rik	RIKEN cDNA 9530020I12 gene	AK020565	130.9	143	133.9	170.6	6.5	5.4	2.7	5.7	144.6	5.075	-4.8985895	-29.82788	0.00022739
53412	A_52_P30451	Ppp1r3c	protein phosphatase 1, regula	NM_016854	34744.7	30165.9	29630.4	26597.7	993.6	1122.1	1190.9	780.9	30284.675	1021.875	-4.9009008	-29.875704	2.32E-06
100038557	A_55_P2003393	Gm10605	predicted gene 10605	ENSMUST00000098265	4398.6	4381.3	4560.8	3355.5	149.6	138.4	119.2	146.8	4174.05	138.5	-4.908685	-30.037338	6.56E-07
19293	A_55_P2114437	Pvalb	parvalbumin	NM_013645	261456.6	205595.9	232260.5	199673.7	5924.2	8955	9580	5983.3	224746.675	7610.625	-4.9112288	-30.090345	1.43E-05
239556	A_55_P2079076	Cacna1i	calcium channel, voltage-dep	NM_001044308	84	112.3	161.2	72.6	3.5	5.4	2.9	2.4	107.525	3.55	-4.9196839	-30.267212	0.00091092
76640	A_51_P155909	1700113H08Rik	RIKEN cDNA 1700113H08 gen	NM_029685	160.7	131.1	126.6	157.9	4.9	5.4	2.8	6.7	144.075	4.95	-4.9236055	-30.349597	0.00014818
77627	A_51_P191726	Efcab6	EF-hand calcium binding dom	NM_029946	81.9	75.9	78.6	79.7	2.3	2.5	3.1	2.5	79.025	2.6	-4.9342566	-30.574492	1.56E-07
26549	A_52_P298088	Itgb1bp2	integrin beta 1 binding protei	NM_013712	3414.1	3663.7	3347.5	2723.2	108.4	106.1	84.8	117.6	3287.125	104.225	-4.9807731	-31.576363	9.14E-07
100043600	A_55_P2071980	Gm4544	predicted gene 4544	XR_105713	418.3	459.8	483.3	525.2	9.4	24.4	15.2	13.6	471.65	15.65	-4.9934377	-31.854775	0.00016881
71037	A_55_P2119613	Prss55	protease, serine, 55	NM_001081063	76	62.8	98	69.5	1.8	2.3	3	2.5	76.575	2.4	-4.9994374	-31.987524	1.25E-05
53318	A_52_P579531	Pdlim3	PDZ and LIM domain 3	NM_016798	35692.4	29411.3	38556.2	35095.1	888.1	1415.2	1094.8	947.8	34688.75	1086.475	-5.0137026	-32.305382	3.40E-06
433294	A_55_P2266679	A530098C11Rik	RIKEN cDNA A530098C11 gen	NM_001013799	3134.7	2513.1	2943.2	2456.5	84.9	79.7	91.4	79.7	2761.875	83.925	-5.035023	-32.78634	1.57E-07
403175	A_55_P2021014	Tigd4	tigger transposable element c	NM_207278	114.7	129.1	92.7	204.5	3.4	8	3.1	2.5	135.25	4.25	-5.0861975	-33.970194	0.00369302
140474	A_55_P2025687	Muc4	mucin 4, ASGP	NM_080457	120.3	69.4	88.7	71.4	1.9	2.5	3.2	2.6	87.45	2.55	-5.08789	-34.010068	3.30E-05
210321	A_55_P2027235	BC048679	cDNA sequence BC048679	NM_001193274	1982.8	2761.8	1263.4	2896.7	106.1	51.9	37.8	69.6	2226.175	66.35	-5.0999334	-34.295168	0.00248795
78910	A_55_P2018676	Asb15	ankyrin repeat and SOCS box-	NM_080847	73.8	97.7	65.4	79	1.7	2.3	2.8	2.4	78.975	2.3	-5.1088013	-34.506621	6.91E-06
15460	A_55_P1958532	Hr	hairless	NM_021877	6732.4	7685.9	6961.6	6953.8	228.2	206.6	206.8	171.5	7083.425	203.275	-5.128671	-34.985157	1.25E-07
21877	A_55_P2056496	Tk1	thymidine kinase 1	NM_009387	431.7	385.2	611.7	441.8	12.3	17.3	9.6	13.8	467.6	13.25	-5.1510905	-35.533071	2.04E-05
80879	A_55_P2067505	Slc16a3	solute carrier family 16 (mon	NM_030696	38769.4	29597.4	37564.2	26915.2	973.1	1088.6	837	794	33211.55	923.175	-5.1630591	-35.82908	2.26E-06
319229	A_66_P111090	Sctr	secretin receptor	NM_001012322	1288.8	1572.3	1601	994.6	27.9	50.8	36.5	36.1	1364.175	37.825	-5.1801256	-36.255441	2.77E-05
17349	A_51_P205106	Mlf1	myeloid leukemia factor 1	NM_010801	20654.3	16411.2	20152.8	16582.3	481.1	618.8	571.8	378.1	18450.15	512.45	-5.1867709	-36.422825	3.88E-06
677289	A_66_P125223	Gm14492	predicted gene 14492	NR_033261	33036.9	29716.6	34226.4	27278.8	812.4	833.3	825.4	870.9	31064.675	835.5	-5.2112588	-37.046332	5.21E-08
24131	A_51_P265348	Ldb3	LIM domain binding 3	NM_001039076	24026.9	19602.4	19673.6	16935.4	588.4	727.3	465.9	380.6	20059.575	540.55	-5.2449412	-37.921424	1.77E-05
71860	A_51_P288558	Wdr16	WD repeat domain 16	NM_027963	134.7	195.2	183.4	194.8	3	3	9.1	5.5	177.025	5.15	-5.247973	-38.001197	0.00154057
74183	A_51_P322473	2310042D19Rik	RIKEN cDNA 2310042D19 gen	NM_172417	5177.1	4718.4	3602.2	3735.4	83.8	121.1	91.8	149.6	4308.275	111.575	-5.2923495	-39.188257	1.75E-05
668257	A_55_P2101830	Dgat2l6	diacylglycerol O-acyltransfera	NM_001114084	113.9	103.9	92.2	214.7	2.7	2.2	6.8	2.4	131.175	3.525	-5.3011292	-39.42747	0.00405456
71886	A_51_P228682	2310002L09Rik	RIKEN cDNA 2310002L09 gen	NM_027981	8422.6	8465.3	7841.6	7762.3	195.4	302.4	192.7	151.6	8122.95	210.525	-5.3154141	-39.819802	9.013E-06
59006	A_51_P248638	Myoz2	myozenin 2	NM_021503	5851.9	7335.8	4163.5	7791.8	148.4	256.3	119.9	120.9	6285.75	161.375	-5.3170887	-39.866048	0.00025597
78102	A_55_P2416494	8430426J06Rik	RIKEN cDNA 8430426J06 gene	XR_105749	770.2	1399.1	796.3	629.5	14.6	31.3	30.3	15.3	898.775	22.875	-5.3204777	-39.959806	0.00097268
382864	A_55_P2043337	Colq	collagen-like tail subunit (sing	NM_009937	981.8	921	952.5	892.8	29.6	22.7	15.8	28.1	937.025	24.05	-5.3244037	-40.068696	8.24E-06
68954	A_55_P2003103	1500012K07Rik	RIKEN cDNA 1500012K07 gen	AK005235	127.9	98.4	54.6	218.5	2	3.2	3.2	2.7	124.85	2.775	-5.3431685	-40.593267	0.00270599
319476	A_51_P326685	Lrtm1	leucine-rich repeats and trans	NM_176920	2706.6	2056.2	1581.4	2252.6	55.1	50.5	43.8	55.1	2149.2	51.125	-5.3733404	-41.451155	2.82E-06
68701	A_51_P189051	Ppp1r27	protein phosphatase 1, regula	NM_026814	26270.8	29291	28883.9	27831.1	591.2	1172.9	760.6	392.7	28069.2	729.35	-5.3775215	-41.571459	0.00025479
13419	A_55_P1985835	Dnase1	deoxyribonuclease I	NM_010061	97.9	168	159.7	86.7	1.9	2.6	3.1	4.7	128.075	3.075	-5.3983237	-42.175221	0.00051257

24053	A_55_P1975045	Sgcg	sarcoglycan, gamma (dystrop	NM_011892	3515.1	3420.9	3746.9	3530.7	135.6	78	82.9	55.3	3553.4	87.95	-5.4114018	-42.559279	4.62E-05
622283	A_55_P2035956	Gm6307	predicted gene 6307	XM_896994	188.7	172.9	205.9	115.1	1.9	15.9	3.1	2.5	170.65	5.85	-5.4137845	-42.629627	0.09281308
414116	A_55_P2334424	D630024D03Rik	RIKEN cDNA D630024D03 ger	AK158188	79.6	86.3	111.1	160.7	2.1	2.1	3.4	2.4	109.425	2.5	-5.4251446	-42.966627	6.45E-05
70100	A_66_P104180	2310015D24Rik	RIKEN cDNA 2310015D24 gen	AK009355	113.6	110	144.6	100.7	2.2	2.5	3.4	2.8	117.225	2.725	-5.4321573	-43.175988	2.12E-06
18682	A_51_P280890	Phkg1	phosphorylase kinase gamma	NM_011079	1403.9	1558.2	1878.5	1281.9	38.3	31.8	36.9	32.6	1530.625	34.9	-5.4444366	-43.545042	4.66E-07
629147	A_51_P115953	Ctxn3	cortexin 3	NM_001134697	1950.9	1369.5	2343.7	1780.4	41.3	42.5	43.7	37.5	1861.125	41.25	-5.4715187	-44.370185	1.64E-06
353287	A_55_P2167537	Clec18a	C-type lectin domain family 1	NM_181549	84.1	109.6	83.9	199.2	1.9	2.6	3.1	2.5	119.2	2.525	-5.4850258	-44.787549	0.0001951
67866	A_51_P194498	Wfdc1	WAP four-disulfide core doma	NM_023395	3689.6	3110.8	3522.9	2816.7	65.3	87.7	75.1	64.8	3285	73.225	-5.4906194	-44.961536	4.41E-07
13400	A_55_P2145833	Dmpk	dystrophia myotonica-protein	NM_032418	14289.9	11294.4	11733.2	9374.7	226.5	301	257	240.2	11673.05	256.175	-5.5020475	-45.319107	8.70E-07
18125	A_55_P2073915	Nos1	nitric oxide synthase 1, neuro	ENSMUST00000111939	189	147.7	214.2	158.7	2.6	2.9	3	9.7	177.4	4.55	-5.5110574	-45.603018	0.00285809
791374	A_66_P122648	Gm9860	predicted gene 9860	ENSMUST00000063311	143.2	98.9	135.5	89.4	1.9	2.4	3.1	2.7	116.75	2.525	-5.5249692	-46.044892	1.06E-05
65973	A_55_P1967414	Asph	aspartate-beta-hydroxylase	NM_001177855	10192.6	9700.3	10386.6	9844.7	199.8	236.2	242.5	195	10031.05	218.375	-5.5277916	-46.135059	4.89E-08
320502	A_51_P427964	Lmod3	leiomodin 3 (fetal)	NM_001081157	16494.5	16735.9	15256.2	14787	394.9	470.9	309.2	238.2	15818.4	353.3	-5.5291148	-46.177392	8.70E-06
118449	A_52_P223127	Synpo2	synaptopodin 2	NM_080451	437.5	449.8	423.7	653.2	12.3	12.7	6.1	12.1	491.05	10.8	-5.542868	-46.619706	7.71E-05
12350	A_51_P431329	Car3	carbonic anhydrase 3	NM_007606	97386.2	88121.4	103445	119824.5	1116.5	4098	1897.1	2289.6	102194.275	2350.3	-5.5879427	-48.099255	0.00076751
140781	A_55_P2093232	Myh7	myosin, heavy polypeptide 7,	NM_080728	44447.6	64873.5	46132.1	59386.3	866.7	1553.1	862.9	1178.7	53709.875	1115.35	-5.6150328	-49.010969	1.70E-05
12299	A_51_P210286	Cacng1	calcium channel, voltage-dep	NM_007582	3540.2	3475.7	4240.2	4217.4	73.3	84.6	93.5	63.1	3868.375	78.625	-5.629992	-49.521806	0.00000057
271424	A_55_P1984695	Ip6k3	inositol hexaphosphate kinase	NM_173027	1553.2	1696.1	1485.5	1488.8	37.9	33.6	20.8	35.3	1555.9	31.9	-5.6427693	-49.962347	4.29E-06
18802	A_55_P2090359	Plcd4	phospholipase C, delta 4	NM_148937	5492.9	5559.1	5961.9	3857.4	94.6	105.9	104.4	106.1	5217.825	102.75	-5.6483429	-50.15574	5.65E-07
69576	A_55_P1956403	2310010M20Rik	RIKEN cDNA 2310010M20 ger	NM_183283	5801.9	5586.3	6352.9	5377	107.7	118.4	105.1	90.6	5779.525	105.45	-5.7800787	-54.951184	5.96E-08
73600	A_55_P2343648	1700120C14Rik	RIKEN cDNA 1700120C14 gen	BX512981	248.4	274.6	251.5	201.9	5	4.9	4.7	3.1	244.1	4.425	-5.8024955	-55.811693	2.22E-06
69563	A_51_P199352	2310015B20Rik	RIKEN cDNA 2310015B20 gen	ENSMUST00000020090	20235.2	26013.4	22253.5	13952.6	318.8	389.9	461	291.4	20613.675	365.275	-5.8056474	-55.93376	1.24E-05
329954	A_55_P1994284	Catsper4	cation channel, sperm associa	NM_177866	526.3	510.7	620.4	594.5	14	9.5	7.7	9.6	562.975	10.2	-5.8163716	-56.35109	2.44E-06
14120	A_51_P499020	Fbp2	fructose bisphosphatase 2	NM_007994	2530.3	2622.5	3242.2	3807	58.8	55.2	55.3	44	3050.5	53.325	-5.8265091	-56.748449	9.49E-07
71146	A_55_P2070045	Golga7b	golgi autoantigen, golgin subf	NM_001141983	201.2	87.7	286.6	229.6	2.9	3.1	3.5	2.9	201.275	3.1	-5.900284	-59.725869	0.00033109
21924	A_51_P461894	Tnnc1	troponin C, cardiac/slow skele	NM_009393	2093.8	4425.7	2040.7	3363.5	34.9	70.6	33.5	31.5	2980.925	42.625	-6.1360183	-70.327563	0.00027875
244923	A_52_P90684	Klhl31	kelch-like 31 (Drosophila)	NM_172925	17400.1	13362	15942.1	12352.5	182.9	195.1	201.2	180.9	14764.175	190.025	-6.2678024	-77.054236	9.71E-08
17927	A_51_P351166	Myod1	myogenic differentiation 1	NM_010866	192.8	246.9	195.2	285.7	3	2.3	3	2.6	230.15	2.725	-6.3889601	-83.804747	4.95E-07
231252	A_51_P381069	Chrna9	cholinergic receptor, nicotinic	NM_001081104	294	216.5	199.1	451.2	5	2.7	3.1	2.5	290.2	3.325	-6.4259461	-85.981007	8.72E-05
69065	A_51_P134812	Chac1	ChaC, cation transport regula	NM_026929	24022.8	29905.4	38869.8	13497.9	275.9	367.8	304.4	177.2	26573.975	281.325	-6.5093015	-91.095094	0.00020496
74184	A_55_P2337033	2310065F04Rik	RIKEN cDNA 2310065F04 gen	ENSMUST00000125538	296.4	231.6	184.1	283.5	2.2	2.5	3.3	2.8	248.9	2.7	-6.5177798	-91.632015	1.40E-06
23956	A_55_P2157770	Neu2	neuraminidase 2	NM_001160165	3007.6	2610.3	3001	3712.9	30.5	33.5	34.2	34.5	3082.95	33.175	-6.52817	-92.29432	5.84E-08
69565	A_66_P123980	2310015K22Rik	RIKEN cDNA 2310015K22 gen	AK009366	305.3	273.3	253.8	224.7	3	3.1	2.8	2.5	264.275	2.85	-6.5308111	-92.463437	6.53E-08
668215	A_55_P2097998	1500017E21Rik	RIKEN cDNA 1500017E21 gen	ENSMUST00000146407	220.7	244.2	151	323.5	2.4	2.1	2.7	2.6	234.85	2.45	-6.5372485	-92.876939	4.84E-06
228785	A_55_P2047043	Mylk2	myosin, light polypeptide kina	NM_001081044	57024.8	39456.8	61100.3	48597.3	513.1	500.1	617.5	454.4	51544.8	521.275	-6.6168713	-98.146935	4.18E-07
380755	A_55_P2109439	Gm889	predicted gene 889	NM_001033437	820	865	793.3	821.8	6.9	7.1	8.2	10.8	825.025	8.25	-6.666851	-101.60665	2.09E-07
117162	A_55_P2364516	AA060545	EST AA060545	AI595487	474.6	422.7	641.8	335.6	4.6	4	3	5.9	468.675	4.375	-6.7458315	-107.32419	1.17E-05
12374	A_55_P1979640	Casr	calcium-sensing receptor	NM_013803	351.7	346.4	319.4	402.1	3.3	3.8	2.9	2.5	354.9	3.125	-6.8396703	-114.53703	1.55E-07
74770	A_51_P285077	Hhatl	hedgehog acyltransferase-like	NM_029095	4361.9	4481	4038.4	3464.4	36.2	36	41.4	23.4	4086.425	34.25	-6.9226164	-121.31519	8.26E-07
229665	A_52_P880457	Ampd1	adenosine monophosphate d	NM_001033303	24143.2	23821.3	28108.9	25294.9	207.2	221.5	241	160.5	25342.075	207.55	-6.9448076	-123.19565	1.02E-07
11464	A_55_P2040951	Actc1	actin, alpha, cardiac muscle 1	NM_009608	34238.2	37471.1	47781.9	20971.5	313.3	300.3	257.1	203.9	35115.675	268.65	-6.9893909	-127.06218	9.96E-06
240328	A_66_P125389	F830016B08Rik	RIKEN cDNA F830016B08 gen	NM_001101475	1728.5	1396.4	1476.6	1403	12.7	8.4	16.7	9.4	1501.125	11.8	-7.0383953	-131.45228	2.31E-06
74843	A_51_P369426	Zmynd17	zinc finger, MYND domain cor	NM_029104	17999.9	17554.8	5940.8	24968.8	125.1	86.7	96.3	140.4	16616.075	112.125	-7.0629496	-133.70871	0.00049925
103988	A_55_P2121956	Gck	glucokinase	NM_010292	695.7	430.5	412.2	279.9	4.2	2.2	2.9	3.8	454.575	3.275	-7.0845535	-135.72602	3.3699E-05
65256	A_51_P115715	Asb2	ankyrin repeat and SOCS box-	NM_023049	6816.4	5826.7	7580.4	7635.1	51.9	44.4	46.3	40.9	6964.65	45.875	-7.2431569	-151.49821	3.66E-08
21952	A_52_P657360	Tnni1	troponin I, skeletal, slow 1	NM_021467	1682.9	3316.8	1617.6	2957.8	19.4	10.3	11.9	17.1	2393.775	14.675	-7.3227217	-160.08804	2.80E-05
238564	A_55_P2026728	Mylk4	myosin light chain kinase fam	NM_001166030	1683.4	1576.8	1627.5	1445	8.6	7.8	10.3	6.2	1583.175	8.225	-7.6101476	-195.38117	1.25E-07
225594	A_55_P2073024	Gm4841	predicted gene 4841	NM_001034859	733.4	931.1	588.3	888.2	5.1	2.2	7.3	2.5	785.25	4.275	-7.6746431	-204.31384	0.00012959
396184	A_55_P2110910	Flrt1	fibronectin leucine rich transr	NM_201411	11998.8	8367.7	11613.7	10662.7	59.5	50.4	40.3	41.5	10660.725	47.925	-7.8017815	-223.13632	1.84E-07
14539	A_55_P1965876	Opn1mw	opsin 1 (cone pigments), med	NM_008106	1799.5	1398.5	1724	1440.3	9.1	13.3	5.3	3.1	1590.575	7.7	-7.8873153	-236.76554	0.00016717
68460	A_55_P1994339	Dhrs7c	dehydrogenase/reductase (SD	NM_001013013	44889.9	37402.1	37071	38535.3	118.1	175.6	177.6	155.3	39474.575	156.65	-7.9913538	-254.47036	7.03E-08
71368	A_66_P111534	5430431A17Rik	RIKEN cDNA 5430431A17 gen	AK017368	6001.3	7627.7	5639.4	7628.5	24.5	27.2	25.2	26.5	6724.225	25.85	-8.0107711	-257.91844	2.41E-08
240131	A_55_P2000574	Lrrc30	leucine rich repeat containing	NM_001033340	2627.2	2596.6	2457.7	2792.6	4.9	10	24.5	8	2618.525	11.85	-8.0456963	-264.23839	0.00019769
268807	A_51_P224064	Klhl38	kelch-like 38 (Drosophila)	NM_177755	1012.4	1163.4	1383.5	1476.9	4.9	5.1	4.5	3	1259.05	4.375	-8.182998	-290.62158	4.33E-07
53311	A_51_P137121	Mybph	myosin binding protein H	NM_016749	10991.2	8743.1	9063.4	11352.6	25.7	40.3	32.1	25.4	10037.575	30.875	-8.361725	-328.95011	1.51E-07
382384	A_66_P110612	Odf3l2	outer dense fiber of sperm ta	NM_001033473	13137.3	10726.1	12401.2	5874.8	25.5	14.7	17.8	19.1	10534.85	19.275	-9.0573149	-532.75001	2.66E-06