Supplementary table S4. Expression changes in the kidney, liver, lung and spleen of 130-week old as compared to 13-week old naturally aging wt mice

code	Gene Symbol	Gene Title	Kidney	p1	Liver	p2	Lung	p3	Spleen	p4	av. FC
1433190_at	4933433N18Rik	RIKEN cDNA 4933433N18 gene	-2.49	0.333	-4.93	0.104	-3.63	0.25	-1.59	0.443	-3.16
1447050_at	---	---	-3.47	0.057	-3.95	0.051	-2.33	0.244	-1.32	0.503	-2.77
1459319_at	Pola1	Polymerase (DNA directed), alpha 1	-4.66	0.176	-3.66	0.003	-2.05	0.241	-1.43	0.584	-2.95
1443451_at	---	---	-5.77	0.099	-2.72	0.183	-1.85	0.247	-3.14	0.002	-3.37
1460418_x_at	H2-T18	histocompatibility 2, T region locus 18	-2.51	0.488	-3.16	0.095	-2.68	0.216	-1.57	0.524	-2.48
1427977_x_at	Oog1	oogenesin 1	-2.26	0.393	-2.97	0.146	-3.15	0.123	-1.2	0.672	-2.39
1458907_at	Slco6b1	Solute carrier organic anion transporter family, member 6b1	-2.78	0.284	-2.54	0.02	-2.8	0.014	-1.56	0.34	-2.42
1420357_s_at	Xlr3a /// Xlr3b /// M(	X-linked lymphocyte-regulated 3A /// X-linked lymphocyte-regulated 3B /// hypothe	-4.4	0.036	-1.81	0.272	-2.99	0.057	-3.56	0.076	-3.19
1459139_at	---	---	-2.88	0.032	-1.78	0.079	-3.62	0.001	-1.19	0.663	-2.37
1419539_at	Irx4	Iroquois related homeobox 4 (Drosophila)	-3.88	0.318	-3.3	0.163	-1.57	0.364	-2.3	0.05	-2.76
1443076_at	D030041N04Rik	RIKEN cDNA D030041N04 gene	-2.24	0.153	-3.33	0.033	-2.07	0.315	-1.6	0.32	-2.31
1416640_at	Kcne1l	potassium voltage-gated channel, Isk-related family, member 1-like	-4.63	0.096	-1.78	0.196	-2.17	0.206	-1.15	0.848	-2.43
1441853_at	Dpp10	Dipeptidylpeptidase 10	-1.83	0.213	-2.9	0.058	-2.87	0.352	-1.37	0.539	-2.24
1443070_at	Auts2	Autism susceptibility candidate 2	-1.31	0.593	-3.74	0.054	-4.67	0.057	-1.36	0.711	-2.77
1427800_at	Krtap16-2	keratin associated protein 16-2	-2.61	0.101	-2.03	0.077	-2.65	0.169	-1.59	0.301	-2.22
1436736_x_at	D0H4S114	DNA segment, human D4S114	-1.36	0.451	-3.85	0.013	-3.89	0.019	-1.19	0.304	-2.57
1443714_at	C530044N13Rik	RIKEN cDNA C530044N13 gene	-2.31	0.154	-3.2	0.048	-1.94	0.089	-1.78	0.381	-2.31
1437954_at	---	---	-2.36	0.224	-2.79	0.331	-2.04	0.02	-1.05	0.936	-2.06
1432440_at	1700111E14Rik	RIKEN cDNA 1700111E14 gene	-2.06	0.302	-3.02	0.076	-2.16	0.34	-1.17	0.208	-2.1
1430938_at	Zfp64	zinc finger protein 64	-3.88	0.004	-1.43	0.556	-2.98	0.331	-1.85	0.241	-2.53
1448964_at	S100g	S100 calcium binding protein G	-2.46	0.048	-2.14	0.029	-2.32	0.093	-1.63	0.511	-2.14
1440001_at	Rian	RNA imprinted and accumulated in nucleus	-2.29	0.146	-3.38	0.111	-1.73	0.106	-1.06	0.689	-2.11
1444919_at	---	---	-2.11	0.142	-3.43	0.053	-1.82	0.422	-1.16	0.828	-2.13
1456139_at	Air	antisense Igf2r RNA	-1.68	0.057	-2.84	0.208	-2.68	0.01	-1.17	0.708	-2.09
1453507_at	Mbd5	methyl-CpG binding domain protein 5	-1.69	0.243	-1.92	0.43	-4.65	0	-1.44	0.401	-2.42
1432627_at	5730507A11Rik	RIKEN cDNA 5730507A11 gene	-2.65	0.182	-2.57	0.029	-1.75	0.212	-1.71	0.407	-2.17
1427686_at	V2r13 /// LOC6326(	vomeronasal 2, receptor, 13 /// similar to vomeronasal 2, receptor, 8	-2.05	0.434	-2.21	0.272	-2.49	0.299	-1.27	0.809	-2
1445745_at	Rbm17 /// LOC5458	RNA binding motif protein 17 /// similar to RNA binding motif protein 17	-2.82	0.182	-1.81	0.237	-2.29	0.026	-2.46	0.043	-2.34
1458225_at	Fkbp14	FK506 binding protein 14	-3.17	0.113	-2.12	0.43	-1.79	0.273	-1.44	0.566	-2.13
1458967_at	---	Transcribed locus	-1.48	0.685	-3.42	0.004	-2.58	0.009	-1.07	0.865	-2.14
1434672_at	Gpr22	G protein-coupled receptor 22	-2.55	0.367	-2.53	0.198	-1.75	0.293	-2.15	0.319	-2.24
1450806_at	Tlx3	T-cell leukemia, homeobox 3	-1.8	0.003	-3.9	0.149	-1.82	0.104	-1.21	0.634	-2.18
1459025_at	1700001J04Rik	RIKEN cDNA 1700001J04 gene	-1.43	0.677	-3.7	0.039	-2.54	0.122	-1.78	0.284	-2.36
1453621_at	Thoc7 /// LOC6708	THO complex 7 homolog (Drosophila) /// similar to Ngg1 interacting factor 3 like 1	-2.45	0.487	-2.42	0.25	-1.84	0.375	-1.68	0.274	-2.1
1437258_at	Sprr2a	small proline-rich protein 2A	-3.62	0.053	-1.99	0.163	-1.69	0.227	-1.38	0.66	-2.17
1433023_at	2310068G24Rik	RIKEN cDNA 2310068G24 gene	-2.52	0.198	-2.26	0.014	-1.88	0.028	-1.42	0.332	-2.02
1432950_at	5330421F21Rik	RIKEN cDNA 5330421F21 gene	-3.67	0.206	-3.31	0.144	-1.25	0.347	-1.42	0.622	-2.41
1433847_at	D330017J20Rik	RIKEN cDNA D330017J20 gene	-2.14	0.144	-3.2	0.194	-1.65	0.058	-1.39	0.178	-2.09
1443270_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-2	0.093	-1.79	0.039	-3.03	0.009	-1.06	0.913	-1.97
1438483_at	Nos1	nitric oxide synthase 1, neuronal	-4.83	0.108	-1.55	0.411	-1.85	0.271	-1.93	0.262	-2.54
1458569_at	Ell2	elongation factor RNA polymerase II 2	-1.71	0.088	-3.05	0.249	-2.09	0.307	-1.39	0.524	-2.06
1446261_at	D1Ertd507e	DNA segment, Chr 1, ERATO Doi 507, expressed	-2.81	0.402	-3.81	0.004	-1.29	0.638	-1.04	0.786	-2.24
1453453_at	1700080O16Rik ///	RIKEN cDNA 1700080O16 gene /// similar to melanoma antigen family A, 5 /// sir	-3.29	0.05	-3.29	0.102	-1.27	0.698	-1.03	0.961	-2.22
1459795_at	Gpr85	G protein-coupled receptor 85	-2.12	0.359	-2.14	0.463	-2.17	0.084	-1.14	0.746	-1.89
1447329_at	---	---	-1.77	0.293	-2.21	0.129	-2.61	0.299	-2.14	0.373	-2.18
1447288_at	---	Transcribed locus	-3.95	0.049	-1.32	0.569	-2.55	0.101	-1.14	0.854	-2.24
1457911_at	A930002I21Rik	RIKEN cDNA A930002I21 gene	-3.61	0.081	-1.51	0.367	-2.12	0.113	-1.18	0.626	-2.1
1417925_at	Ccl22	chemokine (C-C motif) ligand 22	-1.18	0.588	-2.84	0.029	-4.61	0.072	-2.31	0.043	-2.74
1441560_at	Ctnna3	catenin (cadherin associated protein), alpha 3	-2.22	0.054	-2.13	0.226	-2.01	0.138	-1.51	0.425	-1.97
1419740_at	Pde6b	phosphodiesterase 6B, cGMP, rod receptor, beta polypeptide	-4.62	0.037	-1.77	0.336	-1.56	0.306	-1.26	0.252	-2.3
1450825_at	Asah3	N-acylsphingosine amidohydrolase (alkaline ceramidase) 3	-1.44	0.611	-3.76	0.038	-2.17	0.275	-1.52	0.628	-2.22

1422588_at	Krt6b	keratin 6B	-2.16	0.301	-3.29	0.285	-1.52	0.326	-1.04	0.953	-2
1446251_at	4930565A17	hypothetical protein 4930565A17	-2.74	0.126	-2.04	0.238	-1.75	0.066	-1.07	0.906	-1.9
1429424_at	Cst13	cystatin 13	-4.95	0.083	-2.71	0.075	-1.17	0.801	-1.23	0.729	-2.52
1421623_at	Il12rb2	interleukin 12 receptor, beta 2	-1.97	0.293	-2.66	0.022	-1.84	0.029	-1.6	0.07	-2.02
1459037_at	Gm1614	gene model 1614, (NCBI)	-2.4	0.172	-1.31	0.129	-4.01	0.092	-1.56	0.529	-2.32
1438901_at	BC024814	cDNA sequence BC024814	-2.34	0.106	-3.04	0.045	-1.48	0.331	-1.95	0.292	-2.2
1459171_at	Emp1	Epithelial membrane protein 1	-1.79	0.593	-2.74	0.164	-1.97	0.38	-1.08	0.903	-1.89
1443209_at	Hist1h1e	Histone 1, H1e	-2.02	0.385	-2.07	0.285	-2.19	0.193	-1.12	0.829	-1.85
1425290_at	Stx19	syntaxin 19	-3.1	0.232	-2.25	0.061	-1.47	0.143	-1.2	0.772	-2.01
1458702_at	2610316D01Rik	RIKEN cDNA 2610316D01 gene	-1.62	0.474	-2.9	0.037	-2.06	0.21	-2.5	0.299	-2.27
1447183_at	Odz3	Odd Oz/ten-m homolog 3 (Drosophila)	-2.12	0.269	-1.94	0.341	-2.18	0.334	-1.52	0.667	-1.94
1459275_at	Rnf17	ring finger protein 17	-2.41	0.28	-2.01	0.296	-1.87	0.179	-1.18	0.728	-1.87
1415808_at	Tpbpa	trophoblast specific protein alpha	-2.55	0.085	-1.96	0.329	-1.83	0.259	-1.45	0.459	-1.95
1422196_at	Htr5b	5-hydroxytryptamine (serotonin) receptor 5B	-1.41	0.219	-2.46	0.078	-2.96	0.128	-1.71	0.489	-2.14
1439607_at	---	---	-2.25	0.245	-2.71	0.016	-1.55	0.421	-1.06	0.54	-1.89
1420213_x_at	---	---	-2.5	0.095	-1.72	0.504	-2.09	0.083	-3.31	0.252	-2.4
1419019_a_at	Akap4	A kinase (PRKA) anchor protein 4	-2.32	0.28	-2.14	0.331	-1.77	0.392	-1.4	0.039	-1.91
1443618_at	Pdzd2	PDZ domain containing 2	-1.43	0.292	-2.67	0.153	-2.53	0.057	-1.78	0.225	-2.1
1420343_at	Gzmd	granzyme D	-2.16	0.319	-2.57	0.08	-1.61	0.347	-1.08	0.473	-1.86
1444192_at	9630020C08Rik	RIKEN cDNA 9630020C08 gene	-2.9	0.283	-2.67	0.083	-1.33	0.307	-1.95	0.404	-2.21
1445666_at	D15Wsu169e	DNA segment, Chr 15, Wayne State University 169, expressed	-1.54	0.356	-2.97	0.015	-2.06	0.06	-1.01	0.976	-1.89
1457808_at	LOC432842	hypothetical LOC432842	-1.93	0.549	-2.43	0.129	-1.83	0.181	-1.06	0.261	-1.81
1453079_at	5730494M16Rik	RIKEN cDNA 5730494M16 gene	-1.92	0.168	-2.56	0.03	-1.76	0.165	-3.49	0.02	-2.43
1419328_at	Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic dc	-3.99	0.172	-2.92	0.236	-1.13	0.079	-1.45	0.415	-2.37
1453486_a_at	Scube2	signal peptide, CUB domain, EGF-like 2	-2.61	0.159	-1.91	0.152	-1.74	0.171	-1.03	0.881	-1.82
1416905_at	Guca2a	guanylate cyclase activator 2a (guanylin)	-2	0.205	-2.58	0.028	-1.67	0.201	-1.98	0.377	-2.06
1449838_at	Crisp3	cysteine-rich secretory protein 3	-1.4	0.388	-2.34	0.215	-2.9	0.209	-2.89	0.156	-2.38
1454173_at	Sh2d4b	SH2 domain containing 4B	-2.1	0.02	-1.71	0.527	-2.33	0.097	-1.83	0.28	-1.99
1447067_at	---	---	-3.51	0.073	-2.33	0.118	-1.29	0.609	-1.48	0.384	-2.15
1427215_at	Acsm2	acyl-CoA synthetase medium-chain family member 2	-1.31	0.15	-4.37	0.003	-2.01	0.184	-2.39	0.345	-2.52
1429840_at	4933439G12Rik	RIKEN cDNA 4933439G12 gene	-3.08	0.175	-1.3	0.425	-2.49	0.056	-1.47	0.427	-2.09
1457558_at	A330050F15Rik	RIKEN cDNA A330050F15 gene	-2.37	0.077	-1.73	0.312	-2.02	0.166	-1.36	0.62	-1.87
1458593_at	Fbn1	Fibrillin 1	-1.79	0.12	-2.61	0.191	-1.8	0.361	-1.36	0.527	-1.89
1426171_x_at	Klra7	killer cell lectin-like receptor, subfamily A, member 7	-1.73	0.046	-3.8	0.256	-1.52	0.324	-2.6	0.038	-2.41
1455925_at	Prdm8	PR domain containing 8	-3.25	0.016	-2.09	0.116	-1.41	0.229	-2.13	0.018	-2.22
1445054_at	Foxn2	Forkhead box N2	-1.65	0.258	-2.87	0.164	-1.84	0.114	-1.87	0.278	-2.06
1448107_x_at	Klk1	kallikrein 1	-1.34	0.01	-10.89	0.127	-1.51	0.239	-2.45	0.082	-4.05
1443646_at	Igsf10	immunoglobulin superfamily, member 10	-2.18	0.494	-1.97	0.283	-1.87	0.235	-1.48	0.626	-1.87
1450331_s_at	V2r4 /// V2r5 /// LO(	vomeronasal 2, receptor, 4 /// vomeronasal 2, receptor, 5 /// similar to vomeronas	-1.85	0.098	-2.71	0.289	-1.68	0.331	-1.58	0.35	-1.95
1445580_at	Matn2	Matrilin 2	-2.41	0.508	-2.21	0.324	-1.56	0.515	-2.27	0.149	-2.11
1429636_at	1700010D01Rik ///	RIKEN cDNA 1700010D01 gene /// similar to hypothetical protein LOC76386	-2.43	0.476	-1.56	0.126	-2.17	0.299	-1.09	0.784	-1.81
1446128_at	Ebf2	Early B-cell factor 2	-1.7	0.374	-1.76	0.312	-2.79	0.037	-1.64	0.359	-1.98
1439661_at	Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14	-1.98	0.414	-2.63	0.176	-1.59	0.357	-1.76	0.018	-1.99
1444427_at	D930038D03Rik	RIKEN cDNA D930038D03 gene	-2.81	0.432	-1.66	0.238	-1.8	0.21	-1.68	0.339	-1.99
1430842_at	1500002F19Rik	RIKEN cDNA 1500002F19 gene	-3.11	0.018	-1.55	0.442	-1.81	0.071	-1.23	0.325	-1.93
1459988_at	Mbd3l2	methyl-CpG binding domain protein 3-like 2	-2.68	0.03	-3.4	0	-1.18	0.593	-1.12	0.513	-2.1
1456684_at	Tmem74	transmembrane protein 74	-2.26	0.412	-2.43	0.092	-1.5	0.057	-1.12	0.589	-1.83
1447552_s_at	Ctnnd2	Catenin (cadherin associated protein), delta 2	-1.82	0.371	-1.87	0.372	-2.28	0.19	-1.6	0.3	-1.89
1459841_x_at	Laptm5	lysosomal-associated protein transmembrane 5	-2.97	0.104	-2.25	0.044	-1.34	0.467	-1.27	0.554	-1.96
1444492_at	Ptprd	protein tyrosine phosphatase, receptor type, D	-2.17	0.131	-2.5	0.034	-1.51	0.514	-3.16	0.02	-2.33
1429703_at	2900072G11Rik	RIKEN cDNA 2900072G11 gene	-1.41	0.142	-2.39	0.088	-2.52	0.02	-1.2	0.603	-1.88
1420448_at	Rhox2	reproductive homeobox 2	-2.46	0.046	-2.53	0.012	-1.38	0.36	-1.15	0.66	-1.88
1446132_at	---	---	-2.42	0.211	-1.35	0.522	-2.61	0.036	-1.01	0.983	-1.85

1433163_at	6230414M07Rik	RIKEN cDNA 6230414M07 gene	-2.25	0.015	-3.91	0.015	-1.19	0.159	-1.52	0.14	-2.22
1455977_x_at	Klk1 /// Klk1b5	kallikrein 1 /// kallikrein 1-related peptidase b5	-1.42	0.048	-8.54	0.101	-1.4	0.424	-3.26	0.203	-3.65
1458854_at	C78891	expressed sequence C78891	-1.9	0.394	-4.27	0.029	-1.28	0.608	-1.43	0.522	-2.22
1422956_at	D1Pas1	DNA segment, Chr 1, Pasteur Institute 1	-3.32	0.328	-3.59	0.047	-1.04	0.844	-1.31	0.452	-2.31
1454585_at	1110065P19Rik	RIKEN cDNA 1110065P19 gene	-3.72	0.008	-1.9	0.427	-1.34	0.491	-1.02	0.983	-2
1432992_at	4930403L11Rik	RIKEN cDNA 4930403L11 gene	-2.43	0.332	-1.56	0.308	-2.04	0.064	-1.21	0.763	-1.81
1444882_at	---	---	-2.3	0.113	-2.53	0.19	-1.39	0.56	-2.29	0.244	-2.13
1457589_at	Fat3	FAT tumor suppressor homolog 3 (Drosophila)	-2.72	0.039	-2.35	0.147	-1.32	0.045	-1.31	0.613	-1.93
1430732_at	4921525D07Rik	RIKEN cDNA 4921525D07 gene	-1.08	0.91	-3.08	0.006	-3.35	0.113	-1.09	0.917	-2.15
1454821_at	B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-2.08	0.487	-1.29	0.332	-3.37	0.003	-1.33	0.195	-2.02
1443469_at	---	Transcribed locus	-2.13	0.482	-2.63	0.018	-1.42	0.645	-1.18	0.758	-1.84
1442728_at	Nasp	Nuclear autoantigenic sperm protein (histone-binding)	-2.66	0.452	-1.91	0.19	-1.52	0.193	-1.61	0.617	-1.92
1430785_at	Sdro	orphan short chain dehydrogenase/reductase	-3.07	0.069	-1.33	0.232	-2.07	0.082	-1.15	0.717	-1.9
1418218_at	Ceacam9	CEA-related cell adhesion molecule 9	-3.53	0.004	-1.16	0.592	-2.39	0.05	-1.31	0.383	-2.1
1433435_at	AW551984	expressed sequence AW551984	-2.88	0.05	-1.37	0.039	-2.04	0.148	-1.55	0.236	-1.96
1448906_at	Cdh16	cadherin 16	-1.15	0.13	-2.52	0.265	-3.34	0.016	-1.11	0.9	-2.03
1444733_at	---	Transcribed locus	-1.98	0.252	-1.42	0.365	-2.78	0.178	-2.72	0.117	-2.22
1420084_at	---	Transcribed locus	-1.98	0.003	-1.92	0.227	-1.83	0.33	-1.18	0.192	-1.73
1424972_at	---	---	-2.21	0.129	-1.59	0.447	-2.03	0.056	-1.19	0.571	-1.76
1422089_at	Ncr1	natural cytotoxicity triggering receptor 1	-2.45	0.057	-1.63	0.368	-1.82	0.142	-1.44	0.072	-1.83
1430226_at	Xlr4c	X-linked lymphocyte-regulated 4C	-2.27	0.497	-1.96	0.29	-1.61	0.311	-2.9	0.031	-2.18
1439725_at	Ptprt	protein tyrosine phosphatase, receptor type, T	-2.19	0.133	-3.35	0	-1.22	0.358	-1.32	0.617	-2.02
1421080_at	Nr4a3	nuclear receptor subfamily 4, group A, member 3	-2.17	0.299	-2.3	0.033	-1.47	0.182	-1.19	0.413	-1.78
1458525_at	App	Amyloid beta (A4) precursor protein	-1.27	0.525	-3.63	0.141	-1.95	0.024	-1.34	0.076	-2.05
1458068_at	4932417H02Rik	RIKEN cDNA 4932417H02 gene	-1.88	0.515	-2.66	0.075	-1.49	0.624	-1.05	0.894	-1.77
1444081_at	5033428A16Rik	RIKEN cDNA 5033428A16 gene	-2.12	0.11	-3.76	0.139	-1.19	0.827	-1.05	0.933	-2.03
1451062_a_at	Pex2	peroxin 2	-1.67	0.478	-2.43	0.427	-1.75	0.33	-1.8	0.242	-1.91
1434877_at	Nptx1	neuronal pentraxin 1	-1.44	0.591	-4.49	0.034	-1.5	0.339	-1.82	0.351	-2.31
1445929_at	Kcnk2	Potassium channel, subfamily K, member 2	-1.25	0.653	-2.62	0.072	-2.51	0.024	-1.11	0.894	-1.87
1421774_at	Vax1	ventral anterior homeobox containing gene 1	-2.6	0.396	-1.19	0.718	-2.79	0.107	-1.47	0.389	-2.01
1455891_at	4933425K02Rik	RIKEN cDNA 4933425K02 gene	-1.75	0.324	-1.96	0.494	-1.98	0.139	-1.03	0.957	-1.68
1448006_at	Zc3h7b	zinc finger CCCH type containing 7B	-1.43	0.396	-2.21	0.052	-2.29	0.164	-1.62	0.018	-1.89
1459778_at	Rpn1	Ribophorin I	-2.18	0.178	-1.53	0.244	-2.11	0.159	-2.17	0.156	-1.99
1427825_at	---	---	-4.13	0	-1.23	0.667	-1.86	0.382	-1.04	0.943	-2.07
1430405_at	---	---	-2.36	0.024	-1.46	0.386	-2.05	0.014	-1.02	0.977	-1.72
1444253_at	Adamts18	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-2.2	0.202	-2.02	0.466	-1.54	0.445	-1.24	0.69	-1.75
1433036_at	4930564B12Rik	RIKEN cDNA 4930564B12 gene	-1.79	0.303	-2.4	0.044	-1.61	0.378	-1.15	0.828	-1.74
1446903_at	Angpt2	Angiopoietin 2	-2.26	0.243	-1.77	0.061	-1.68	0.315	-3.13	0.087	-2.21
1430714_at	4930451C15Rik	RIKEN cDNA 4930451C15 gene	-2.7	0.316	-2.93	0.004	-1.12	0.685	-1.06	0.906	-1.95
1454435_at	5530400N10Rik	RIKEN cDNA 5530400N10 gene	-3.34	0.396	-3.07	0.225	-1.02	0.899	-1.07	0.666	-2.13
1457918_at	Tnfaip2	Tumor necrosis factor, alpha-induced protein 2	-2.47	0.022	-1.86	0.098	-1.51	0.095	-1.11	0.585	-1.74
1432399_a_at	Epha1	Eph receptor A1	-2.14	0.337	-2.52	0.379	-1.35	0.405	-1.53	0.657	-1.89
1437326_x_at	Ela3 /// LOC638418	elastase 3, pancreatic /// similar to elastase 3B, pancreatic	-2.6	0.409	-2.08	0.222	-1.35	0.346	-2.77	0.157	-2.2
1427545_at	Scml4	sex comb on midleg-like 4 (Drosophila)	-1.74	0.183	-1.97	0.363	-1.91	0.154	-3.18	0.018	-2.2
1447385_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-2.17	0.146	-2.93	0.023	-1.24	0.126	-1.72	0.225	-2.02
1452028_a_at	Cdh23	cadherin 23 (otocadherin)	-1.41	0.161	-3.08	0.215	-1.73	0.255	-1.14	0.858	-1.84
1422282_at	Tacr1	tachykinin receptor 1	-2.11	0.231	-1.46	0.581	-2.21	0.208	-1.39	0.057	-1.79
1457077_at	---	2 days neonate sympathetic ganglion cDNA, RIKEN full-length enriched library, c	-2.69	0.292	-2.12	0.058	-1.3	0.204	-1.21	0.441	-1.83
1450524_at	Cldn9	claudin 9	-1.54	0.592	-2.92	0.004	-1.61	0.117	-1.39	0.008	-1.86
1457604_x_at	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1	-1.45	0.239	-3.21	0.058	-1.63	0.354	-2	0.244	-2.07
1453423_at	4933409L14Rik	RIKEN cDNA 4933409L14 gene	-3.08	0.368	-1.88	0.235	-1.32	0.274	-1.01	0.99	-1.82
1447305_at	Tcba1	T-cell lymphoma breakpoint associated target 1	-2.73	0.021	-2.14	0.112	-1.28	0.357	-1.16	0.687	-1.83
1450532_at	2310002J15Rik	RIKEN cDNA 2310002J15 gene	-3.03	0.169	-1.78	0.254	-1.38	0.216	-1.21	0.171	-1.85

1447081_at	---	---	-2.14	0.451	-3.53	0.01	-1.15	0.535	-2.25	0.064	-2.27
1456185_at	Nalp9a	NACHT, LRR and PYD containing protein 9a	-3.01	0.264	-1.44	0.604	-1.68	0.183	-1.67	0.397	-1.95
1455148_at	Tmem130	transmembrane protein 130	-3.88	0.013	-1.39	0.415	-1.55	0.51	-2.32	0.393	-2.29
1431357_a_at	Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	-1.81	0.202	-2.98	0.034	-1.36	0.31	-1.32	0.714	-1.87
1446841_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.7	0.024	-2.04	0.151	-1.84	0.088	-1.51	0.425	-1.77
1432258_at	9430014N10Rik	RIKEN cDNA 9430014N10 gene	-1.76	0.017	-2.08	0.385	-1.74	0.363	-1.54	0.17	-1.78
1441316_at	LOC677060	similar to wingless related MMTV integration site 8b	-2.53	0.378	-1.91	0.106	-1.42	0.171	-2.52	0.243	-2.1
1445131_at	Fbxl13	F-box and leucine-rich repeat protein 13	-3.25	0.372	-1.3	0.598	-1.83	0.298	-1.34	0.677	-1.93
1430779_at	Ntng1	netrin G1	-1.6	0.346	-3.38	0.001	-1.42	0.031	-1.89	0.128	-2.07
1437970_at	BC053401	CDNA sequence BC053401	-3.22	0.188	-1.19	0.672	-2.11	0.188	-2.33	0.31	-2.21
1459056_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	-3.31	0.062	-1.67	0.477	-1.38	0.064	-1.01	0.979	-1.84
1444529_at	LOC666806	similar to X-linked eukaryotic translation initiation factor 1A	-4.85	0.005	-1.12	0.901	-1.9	0.192	-1.46	0.69	-2.33
1432682_at	5530400K19Rik	RIKEN cDNA 5530400K19 gene	-2.3	0.163	-2.17	0.306	-1.37	0.376	-1.89	0.111	-1.93
1435974_at	Arhgef9	Cdc42 guanine nucleotide exchange factor (GEF) 9	-2.72	0.321	-2.51	0.462	-1.16	0.737	-1.26	0.35	-1.91
1443533_at	Ppp2r5e	Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-1.87	0.018	-1.44	0.042	-2.5	0.053	-1.36	0.087	-1.79
1446607_at	Mtap7	Microtubule-associated protein 7	-2.89	0.466	-1.31	0.59	-1.91	0.071	-2.57	0.434	-2.17
1443802_at	Tnik	TRAF2 and NCK interacting kinase	-1.91	0.04	-2.47	0.082	-1.42	0.323	-1.69	0.076	-1.87
1444652_at	B830004H01Rik	RIKEN cDNA B830004H01 gene	-1.52	0.515	-3.64	0.058	-1.42	0.587	-1.55	0.592	-2.03
1426167_a_at	Camk4	calcium/calmodulin-dependent protein kinase IV	-2.61	0.062	-2.05	0.198	-1.31	0.483	-1.55	0.087	-1.88
1438237_at	Rex2	reduced expression 2	-4	0.349	-1.36	0.197	-1.54	0.387	-1.19	0.439	-2.02
1447988_at	---	---	-1.6	0.117	-1.5	0.573	-2.9	0.001	-1.12	0.681	-1.78
1457619_at	BC015286	cDNA sequence BC015286	-1.99	0.311	-1.75	0.425	-1.77	0.019	-1.61	0.114	-1.78
1433399_at	2900078I11Rik	RIKEN cDNA 2900078I11 gene	-1.25	0.499	-2.4	0.396	-2.36	0.042	-1.16	0.444	-1.79
1460508_at	Mrpl1	mitochondrial ribosomal protein L1	-3.42	0.018	-2.13	0.211	-1.14	0.758	-1.26	0.711	-1.99
1444568_at	Arpc5	Actin related protein 2/3 complex, subunit 5	-2.81	0.005	-1.55	0.437	-1.56	0.171	-2.04	0.452	-1.99
1422396_s_at	Ascl2	achaete-scute complex homolog-like 2 (Drosophila)	-2.52	0.395	-1.14	0.815	-2.72	0.089	-2.93	0.369	-2.33
1443242_at	D5Ertd121e	DNA segment, Chr 5, ERATO Doi 121, expressed	-2.53	0.181	-1.68	0.062	-1.53	0.051	-1.55	0.173	-1.82
1420605_at	Mtag2	metastasis associated gene 2	-2.05	0.397	-1.99	0.228	-1.52	0.286	-1.82	0.115	-1.85
1458166_at	Phf21a	PHD finger protein 21A	-1.81	0.281	-1.64	0.228	-2.05	0.009	-1.23	0.696	-1.68
1460219_at	Mag	myelin-associated glycoprotein	-2.7	0.154	-2.33	0.247	-1.17	0.368	-1.07	0.515	-1.82
1446334_at	---	---	-3.94	0.013	-1.84	0.45	-1.17	0.775	-1.03	0.903	-1.99
1456654_at	Paqr5	progestin and adipoQ receptor family member V	-1.19	0.074	-3.35	0.043	-1.94	0.137	-1.34	0.324	-1.95
1436398_at	Lef1	Lymphoid enhancer binding factor 1	-1.36	0.269	-2.01	0.236	-2.36	0.022	-6.05	0.025	-2.95
1442734_at	---	---	-1.89	0.185	-1.46	0.607	-2.26	0.084	-1.44	0.591	-1.76
1459739_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-2.44	0.208	-1.41	0.587	-1.86	0.216	-1.27	0.667	-1.74
1420230_at	AA414993	expressed sequence AA414993	-2.76	0.043	-2.01	0.028	-1.25	0.502	-1.95	0.039	-1.99
1457654_at	---	Transcribed locus, moderately similar to NP_598437.1 O-sialoglycoprotein endop	-2.07	0.018	-1.29	0.659	-2.5	0.007	-1.25	0.648	-1.78
1443417_at	C87122	expressed sequence C87122	-1.59	0.134	-2.07	0.221	-1.83	0.219	-1.14	0.269	-1.66
1454083_at	4930440C22Rik	RIKEN cDNA 4930440C22 gene	-1.27	0.767	-2.29	0.064	-2.31	0.376	-1.26	0.673	-1.78
1419788_at	---	Transcribed locus	-1.47	0.224	-2.79	0.02	-1.61	0.107	-2.04	0.31	-1.98
1440753_at	---	Transcribed locus	-1.34	0.198	-2.33	0.066	-2.06	0.241	-1.58	0.328	-1.83
1427402_at	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	-2.12	0.094	-2.69	0.283	-1.22	0.105	-1.07	0.704	-1.78
1437501_at	AF529169	cDNA sequence AF529169	-3.7	0.108	-1.51	0.417	-1.37	0.58	-1.02	0.968	-1.9
1459498_at	---	---	-2.95	0.137	-1.6	0.506	-1.43	0.498	-1.34	0.435	-1.83
1444887_at	C79015	expressed sequence C79015	-1.25	0.779	-2.54	0.144	-2.12	0.241	-1.41	0.509	-1.83
1447319_at	---	---	-2.77	0.222	-1.17	0.689	-2.22	0.016	-1.74	0.413	-1.98
1427126_at	Hspa1b	heat shock protein 1B	-1.45	0.279	-1.7	0.141	-2.58	0.198	-1.83	0.537	-1.89
1422523_at	Si	silver	-1.46	0.013	-3.07	0.022	-1.53	0.141	-1.82	0.334	-1.97
1446984_at	Prtg	Protogenin homolog (Gallus gallus)	-1.22	0.811	-4.74	0.179	-1.56	0.387	-1.82	0.454	-2.34
1447236_at	Kif21a	kinesin family member 21A	-3.11	0.053	-2.12	0.271	-1.14	0.769	-2.37	0.284	-2.18
1446746_at	Osbpl3	Oxysterol binding protein-like 3	-1.92	0.292	-2.7	0.191	-1.28	0.504	-2.33	0.4	-2.06
1419514_at	Pitx1	paired-like homeodomain transcription factor 1	-2.95	0.087	-1.39	0.489	-1.64	0.108	-1.06	0.909	-1.76
1432132_at	4933401D09Rik	RIKEN cDNA 4933401D09 gene	-1.29	0.764	-1.76	0.475	-3	0.108	-2.08	0.292	-2.03

1458110_at	D430030G11Rik	RIKEN cDNA D430030G11 gene	-1.87	0.052	-2.05	0.06	-1.53	0.254	-1.16	0.628	-1.65
1442605_at	Bach2	BTB and CNC homology 2	-1.9	0.023	-1.74	0.107	-1.74	0.107	-2.51	0.116	-1.97
1419011_at	Cryba2	crystallin, beta A2	-1.88	0.357	-2.33	0.119	-1.39	0.469	-2.14	0.335	-1.93
1422037_at	Dlx3	distal-less homeobox 3	-1.18	0.57	-2.4	0.137	-2.41	0.022	-2.24	0.107	-2.06
1455277_at	Hhip	Hedgehog-interacting protein	-1.85	0.334	-1.31	0.452	-2.65	0.008	-1.54	0.512	-1.84
1439529_at	A430110N23Rik	RIKEN cDNA A430110N23 gene	-4.17	0.208	-2	0.146	-1.06	0.872	-1.28	0.636	-2.13
1455561_at	Cndp1	carnosine dipeptidase 1 (metallopeptidase M20 family)	-1.28	0.265	-2.23	0.057	-2.22	0.1	-1.18	0.651	-1.73
1443277_at	Ndst3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	-1.42	0.52	-6.15	0.075	-1.22	0.669	-1.47	0.251	-2.57
1457667_x_at	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-2.19	0.236	-2.98	0.293	-1.12	0.776	-1.29	0.48	-1.89
1432022_at	Cdgap	Cdc42 GTPase-activating protein	-1.3	0.048	-2.41	0.053	-2	0.019	-1.07	0.624	-1.69
1448030_at	1700023D09Rik	RIKEN cDNA 1700023D09 gene	-3.97	0.067	-2.19	0.083	-1.02	0.921	-2.92	0.181	-2.53
1432895_at	9030409K20Rik	RIKEN cDNA 9030409K20 gene	-2.43	0.189	-1.91	0.076	-1.33	0.506	-1.43	0.46	-1.77
1432015_a_at	4933428M03Rik	RIKEN cDNA 4933428M03 gene	-2.25	0.002	-1.12	0.876	-2.88	0.015	-1.71	0.306	-1.99
1433061_at	4933423L19Rik	RIKEN cDNA 4933423L19 gene	-2.13	0.326	-1.84	0.328	-1.48	0.061	-2.1	0.301	-1.89
1458231_at	---	PREDICTED: Mus musculus similar to Zinc finger protein 195 (LOC625519), mRI	-1.29	0.406	-2.55	0.185	-1.93	0.348	-1.04	0.931	-1.7
1460071_at	Sap30l	SAP30-like	-1.57	0.629	-1.71	0.085	-2.14	0.048	-4.07	0.022	-2.37
1427952_at	Aipl1	aryl hydrocarbon receptor-interacting protein-like 1	-1.59	0.289	-2.43	0.435	-1.54	0.209	-1.9	0.211	-1.87
1432145_at	2310026I22Rik	RIKEN cDNA 2310026I22 gene	-1.47	0.595	-2.5	0.025	-1.64	0.432	-1.83	0.39	-1.86
1457982_at	1700052M18Rik	RIKEN cDNA 1700052M18 gene	-1.94	0.044	-1.47	0.329	-2.02	0.134	-1.22	0.632	-1.66
1431240_at	Clec2h	C-type lectin domain family 2, member h	-1.13	0.736	-4.18	0.2	-1.76	0.381	-1.09	0.814	-2.04
1442893_at	Ctnna2	Catenin (cadherin associated protein), alpha 2	-1.8	0.263	-1.84	0.187	-1.69	0.311	-1.98	0.366	-1.83
1445279_at	---	Transcribed locus	-1.88	0.303	-3.24	0.033	-1.17	0.566	-2.09	0.345	-2.1
1459640_at	---	---	-1.32	0.559	-2.26	0.227	-2.02	0.12	-1.18	0.736	-1.7
1422391_at	V1rc3	vomeronasal 1 receptor, C3	-1.08	0.721	-3.12	0.344	-2.25	0.162	-2.65	0.139	-2.27
1453291_at	Hmgb2l1	high mobility group box 2-like 1	-1.93	0.01	-2.27	0.138	-1.36	0.102	-1.11	0.524	-1.66
1456370_s_at	0610037L13Rik	RIKEN cDNA 0610037L13 gene	-2.14	0.14	-1.75	0.326	-1.52	0.136	-1.68	0.168	-1.77
1430689_at	2810019C22Rik	RIKEN cDNA 2810019C22 gene	-1.41	0.203	-2.76	0.009	-1.6	0.054	-1.2	0.286	-1.74
1456166_at	---	---	-2.67	0.116	-1.73	0.168	-1.34	0.466	-1.46	0.523	-1.8
1422117_s_at	Khdrbs2	KH domain containing, RNA binding, signal transduction associated 2	-2.28	0.22	-1.22	0.729	-2.26	0.043	-1.27	0.604	-1.76
1444780_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	-5.33	0.004	-1.17	0.602	-1.52	0.031	-1.13	0.635	-2.29
1450989_at	Tdgf1	teratocarcinoma-derived growth factor	-2.15	0.411	-1.21	0.467	-2.47	0.142	-1.2	0.773	-1.76
1434163_at	AU024076	expressed sequence AU024076	-1.82	0.364	-2.81	0.323	-1.26	0.408	-1.68	0.095	-1.89
1460502_at	2010007E15Rik	RIKEN cDNA 2010007E15 gene	-1.57	0.513	-2.86	0.141	-1.4	0.293	-1.49	0.454	-1.83
1459606_at	C79130	expressed sequence C79130	-1.35	0.58	-2.51	0.043	-1.78	0.319	-1.91	0.309	-1.89
1426005_at	Dmp1	dentin matrix protein 1	-2.16	0.331	-1.18	0.807	-2.57	0.214	-1.01	0.992	-1.73
1442955_at	---	---	-1.35	0.579	-2.76	0.126	-1.67	0.291	-1.11	0.848	-1.72
1446487_at	---	---	-3.98	0.289	-1.17	0.819	-1.67	0.276	-1.03	0.936	-1.96
1442563_at	Tmem8	Transmembrane protein 8 (five membrane-spanning domains)	-2.49	0.283	-1.46	0.527	-1.62	0.383	-1.1	0.836	-1.67
1445177_at	---	4 days neonate male adipose cDNA, RIKEN full-length enriched library, clone:B4	-2.33	0.428	-2.6	0.327	-1.12	0.617	-1.18	0.819	-1.81
1445108_at	Lphn3	Latrophilin 3	-2.25	0.453	-1.47	0.417	-1.73	0.198	-1.51	0.218	-1.74
1444823_at	---	---	-1.86	0.169	-2.22	0.076	-1.39	0.194	-2	0.118	-1.87
1456002_at	Xpa	xeroderma pigmentosum, complementation group A	-1.94	0.316	-2.79	0.04	-1.2	0.692	-2.51	0.114	-2.11
1458657_at	Antxr1	Anthrax toxin receptor 1	-1.1	0.045	-4.35	0.032	-1.75	0.189	-1.84	0.128	-2.26
1436927_at	Cypt4 /// Cypt9 /// C	cysteine-rich perinuclear theca 4 /// cysteine-rich perinuclear theca 9 /// cysteine-r	-2.31	0.097	-2.79	0.024	-1.09	0.863	-1.38	0.46	-1.89
1459826_at	Kcnq2	Potassium voltage-gated channel, subfamily Q, member 2	-2.77	0.314	-1.5	0.025	-1.47	0.09	-1.58	0.594	-1.83
1450871_a_at	Bcat1	branched chain aminotransferase 1, cytosolic	-1.69	0.388	-2.83	0.126	-1.31	0.572	-1.19	0.695	-1.75
1422122_at	Fcer2a	Fc receptor, IgE, low affinity II, alpha polypeptide	-3.01	0.138	-1.42	0.678	-1.49	0.31	-3.51	0.07	-2.36
1417923_at	Pak3	p21 (CDKN1A)-activated kinase 3	-1.56	0.35	-2.49	0.019	-1.5	0.037	-1.46	0.038	-1.75
1444436_at	Hsf2 /// 9630030I15	heat shock factor 2 /// RIKEN cDNA 9630030I15 gene	-1.65	0.094	-1.76	0.025	-1.86	0.005	-1.2	0.453	-1.62
1457507_at	Nrg3	Neuregulin 3	-1.34	0.713	-2.5	0.142	-1.77	0.512	-1.78	0.372	-1.85
1441875_at	1700063J08Rik	RIKEN cDNA 1700063J08 gene	-1.77	0.442	-1.86	0.483	-1.65	0.221	-1.48	0.523	-1.69
1434728_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	-1.32	0.255	-2.61	0.037	-1.75	0.074	-1.2	0.338	-1.72
1443927_at	Ube1l2	ubiquitin-activating enzyme E1-like 2	-1.17	0.771	-2.39	0.237	-2.29	0.215	-2.57	0.036	-2.1

1450795_at	Lhb	luteinizing hormone beta	-2.82	0.008	-2.46	0.189	-1.05	0.878	-1.6	0.62	-1.98
1451915_at	Cct3	chaperonin subunit 3 (gamma)	-4.08	0.005	-1.65	0.424	-1.16	0.772	-1.02	0.973	-1.98
1445288_at	---	---	-2.13	0.161	-1.22	0.662	-2.38	0.144	-1.91	0.085	-1.91
1446882_at	---	---	-1.61	0.493	-2.04	0.01	-1.66	0.349	-3.29	0.034	-2.15
1448062_at	Stk11	serine/threonine kinase 11	-3.13	0.024	-1.6	0.498	-1.3	0.5	-1.62	0.424	-1.91
1454054_at	4930459I23Rik	RIKEN cDNA 4930459I23 gene	-1.98	0.469	-2.05	0.282	-1.39	0.475	-1.1	0.873	-1.63
1442924_at	Clstn2	Calsyntenin 2	-1.19	0.317	-1.75	0.175	-3.27	0.03	-1.89	0.295	-2.03
1457244_at	D6Ertd474e	DNA segment, Chr 6, ERATO Doi 474, expressed	-3.26	0.381	-1.54	0.254	-1.31	0.415	-2.59	0.045	-2.18
1453839_a_at	Pi16	peptidase inhibitor 16	-1.91	0.367	-3.41	0.05	-1.11	0.702	-1.38	0.615	-1.95
1456629_at	Ankrd47	ankyrin repeat domain 47	-1.78	0.345	-1.81	0.134	-1.65	0.048	-1.27	0.518	-1.63
1445703_at	AI848149	expressed sequence AI848149	-3.46	0.098	-1.19	0.776	-1.69	0.335	-1.47	0.392	-1.95
1459012_at	A730041O05Rik	RIKEN cDNA A730041O05 gene	-3.36	0.022	-1.6	0.086	-1.25	0.692	-1.81	0.215	-2
1457208_at	Nfxl1	nuclear transcription factor, X-box binding-like 1	-1.64	0.612	-2.15	0.309	-1.54	0.203	-1.01	0.991	-1.58
1442445_at	2610027H17Rik	RIKEN cDNA 2610027H17 gene	-1.17	0.654	-2.15	0.066	-2.46	0.026	-1.13	0.592	-1.73
1441732_at	Tshz1	Teashirt zinc finger family member 1	-1.58	0.076	-1.7	0.159	-1.98	0.081	-1.41	0.227	-1.67
1432077_at	Pot1	protection of telomeres 1	-4.67	0.137	-1.41	0.415	-1.24	0.489	-2.63	0.247	-2.49
1446046_at	BC023818	CDNA sequence BC023818	-2	0.099	-1.38	0.376	-1.99	0.022	-1.77	0.328	-1.79
1457685_at	D330034E10Rik	RIKEN cDNA D330034E10 gene	-1.24	0.801	-1.96	0.085	-2.44	0.003	-1.21	0.727	-1.71
1451308_at	Elovl4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	-2.79	0.009	-1.25	0.707	-1.74	0.093	-2.02	0.263	-1.95
1433474_at	Edil3	EGF-like repeats and discoidin I-like domains 3	-1.11	0.579	-1.82	0.193	-3.61	0.004	-1.37	0.26	-1.98
1433184_at	6720477C19Rik	RIKEN cDNA 6720477C19 gene	-1.29	0.222	-1.47	0.425	-3.66	0.062	-1.13	0.158	-1.88
1446729_at	Disp2	dispatched homolog 2 (Drosophila)	-1.64	0.354	-1.97	0.169	-1.62	0.31	-1.67	0.494	-1.73
1438399_at	Pex2	peroxin 2	-3.56	0.18	-2.21	0.266	-1	0.997	-6.27	0.051	-3.26
1459506_at	---	---	-1.67	0.38	-1.79	0.28	-1.75	0.181	-1.89	0.049	-1.77
1419314_at	Tinag	tubulointerstitial nephritis antigen	-1.18	0.11	-2.9	0.067	-1.85	0.002	-1.3	0.646	-1.81
1458713_at	---	---	-1.82	0.019	-1.47	0.481	-1.98	0.115	-1.31	0.313	-1.65
1453907_at	C030041B07Rik	RIKEN cDNA C030041B07 gene	-1.33	0.712	-2.09	0.233	-1.99	0.302	-1.8	0.536	-1.8
1457187_at	A630071L07Rik	RIKEN cDNA A630071L07 gene	-2.3	0.223	-1.61	0.481	-1.47	0.267	-1.37	0.567	-1.69
1433279_at	5830440H09Rik	RIKEN cDNA 5830440H09 gene	-2.24	0.063	-1.85	0.133	-1.33	0.191	-1.58	0.181	-1.75
1446664_at	D15Ertd154e	DNA segment, Chr 15, ERATO Doi 154, expressed	-2.12	0.264	-1.7	0.32	-1.48	0.487	-1.62	0.448	-1.73
1415837_at	Klk1	kallikrein 1	-1.36	0.036	-10.34	0.111	-1.1	0.643	-1.79	0.121	-3.65
1433404_at	4930423O20Rik	RIKEN cDNA 4930423O20 gene	-1.38	0.677	-1.79	0.248	-2.2	0.018	-1.66	0.049	-1.76
1420135_at	BC021438	CDNA sequence BC021438	-1.38	0.483	-1.8	0.272	-2.19	0.01	-1.18	0.838	-1.64
1444316_at	---	---	-2.91	0.119	-1.41	0.28	-1.46	0.325	-1.06	0.852	-1.71
1445924_at	LOC385211	similar to RIKEN cDNA 1700029I01	-1.57	0.1	-2.44	0.018	-1.44	0.523	-1.76	0.464	-1.8
1445749_at	Rnf4	Ring finger protein 4	-2.16	0.193	-1.94	0.359	-1.31	0.087	-1.64	0.588	-1.76
1423415_at	Gpr83	G protein-coupled receptor 83	-2	0.03	-1.46	0.3	-1.79	0.242	-1.9	0.304	-1.79
1459310_at	5330434G04Rik	RIKEN cDNA 5330434G04 gene	-1.17	0.569	-2.91	0.333	-1.83	0.158	-1.37	0.752	-1.82
1440724_at	AI854703	expressed sequence AI854703	-1.61	0.016	-1.44	0.382	-2.35	0.073	-2.28	0.336	-1.92
1442335_at	---	Transcribed locus	-1.94	0.275	-2.52	0.018	-1.2	0.436	-1.43	0.275	-1.77
1432901_at	BC026657	cDNA sequence BC026657	-2.07	0.038	-1.52	0.104	-1.66	0.011	-1.24	0.579	-1.62
1451711_at	Wnt9b	wingless-type MMTV integration site 9B	-4.76	0.03	-1.87	0.187	-1	0.999	-1.13	0.712	-2.19
1457012_at	Dbx1	developing brain homeobox 1	-2.63	0.269	-2.24	0.053	-1.09	0.836	-1.42	0.387	-1.85
1431910_at	5730460C07Rik	RIKEN cDNA 5730460C07 gene	-1.22	0.558	-2.99	0.006	-1.68	0.185	-1.51	0.537	-1.85
1441373_at	Msi2	Musashi homolog 2 (Drosophila)	-1.56	0.159	-1.6	0.471	-2.1	0.074	-1.5	0.192	-1.69
1444605_at	1700061F12Rik	RIKEN cDNA 1700061F12 gene	-1.27	0.779	-1.98	0.514	-2.19	0.055	-2.4	0.224	-1.96
1422365_at	Olfr17	olfactory receptor 17	-3.21	0.004	-1.03	0.965	-2.17	0.013	-1.18	0.801	-1.9
1439299_at	Spnb2	Spectrin beta 2	-1.58	0.023	-1.54	0.043	-2.15	0.051	-1.22	0.501	-1.62
1447419_at	---	Transcribed locus	-2.49	0.246	-1.59	0.246	-1.39	0.104	-1.19	0.151	-1.67
1425038_at	Slc22a19	solute carrier family 22 (organic anion transporter), member 19	-1.1	0.611	-2.96	0.447	-2.01	0.296	-1.08	0.834	-1.79
1440780_x_at	1500015O10Rik	RIKEN cDNA 1500015O10 gene	-2.07	0.086	-1.86	0.093	-1.37	0.205	-1.57	0.294	-1.72
1456926_at	Rims4	regulating synaptic membrane exocytosis 4	-4.33	0.038	-1.16	0.631	-1.52	0.145	-1.44	0.378	-2.12
1459532_at	Grm7	glutamate receptor, metabotropic 7	-1.2	0.851	-2.37	0.214	-2.02	0.269	-1.99	0.484	-1.9

1449735_at	---	---	-3.71	0.161	-1.64	0.437	-1.15	0.716	-1.45	0.491	-1.99
1429635_at	Ccdc89	coiled-coil domain containing 89	-1.6	0.492	-1.68	0.064	-1.9	0.411	-1.39	0.423	-1.64
1443328_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	-1.92	0.071	-1.81	0.266	-1.48	0.165	-1.64	0.223	-1.71
1421602_at	Shbg	sex hormone binding globulin	-1.89	0.09	-2.33	0.019	-1.26	0.475	-1.46	0.243	-1.73
1451061_at	1700018B24Rik	RIKEN cDNA 1700018B24 gene	-1.29	0.752	-1.44	0.571	-3.5	0.006	-1.44	0.04	-1.92
1430821_at	1700024C24Rik	RIKEN cDNA 1700024C24 gene	-2.19	0.064	-2.48	0.216	-1.12	0.602	-1.35	0.386	-1.79
1440587_at	---	---	-1.41	0.038	-1.77	0.135	-2.08	0.019	-1.96	0.162	-1.8
1447161_at	---	Transcribed locus	-2.22	0.365	-1.33	0.55	-1.8	0.138	-2.75	0.186	-2.03
1445562_at	Zbtb16	Zinc finger and BTB domain containing 16	-1.66	0.394	-1.37	0.322	-2.38	0.154	-1.21	0.59	-1.65
1440304_at	Bach2	BTB and CNC homology 2	-1.46	0.106	-1.59	0.173	-2.27	0.027	-3.23	0.045	-2.14
1433262_at	9430052A13Rik	RIKEN cDNA 9430052A13 gene	-1.95	0.106	-1.54	0.367	-1.68	0.137	-1	0.991	-1.54
1430649_at	Baalc	brain and acute leukemia, cytoplasmic	-2.01	0.21	-2.81	0.043	-1.1	0.797	-1.36	0.675	-1.82
1440678_at	Ltbp1	Latent transforming growth factor beta binding protein 1	-1.77	0.023	-1.81	0.079	-1.56	0.169	-1.1	0.842	-1.56
1455233_at	Mrps11	mitochondrial ribosomal protein S11	-1.28	0.552	-2.06	0.164	-2.01	0.044	-1.04	0.873	-1.6
1455557_at	LOC553095	hypothetical LOC553095	-1.66	0.002	-2.13	0.345	-1.45	0.577	-1.16	0.825	-1.6
1431044_at	Thoc1	THO complex 1	-1.42	0.733	-2.14	0.205	-1.69	0.128	-1.15	0.57	-1.6
1431901_a_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-4.26	0.147	-1.44	0.647	-1.2	0.683	-1.55	0.188	-2.11
1442789_at	---	Transcribed locus	-1.58	0.157	-1.49	0.143	-2.17	0.068	-1.6	0.431	-1.71
1439823_at	Ctbp2	C-terminal binding protein 2	-2.11	0.117	-2.29	0.237	-1.17	0.755	-4.08	0.228	-2.41
1458383_at	Idh2	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	-1.61	0.347	-1.3	0.617	-2.69	0.022	-1.07	0.864	-1.67
1446885_at	---	---	-1.63	0.557	-2.1	0.285	-1.47	0.321	-1.3	0.316	-1.63
1431852_at	Prdm8	PR domain containing 8	-2.5	0.153	-2.19	0.12	-1.1	0.859	-1.32	0.605	-1.78
1459395_at	---	Transcribed locus	-1.21	0.537	-1.88	0.064	-2.43	0.172	-1.3	0.29	-1.7
1420263_at	---	---	-3.24	0.052	-1.08	0.868	-1.87	0.072	-1.1	0.811	-1.82
1443156_at	---	---	-1.29	0.579	-1.57	0.147	-2.8	0.005	-1.72	0.02	-1.84
1445819_at	A830018L16Rik	RIKEN cDNA A830018L16 gene	-3.07	0.013	-1.9	0.023	-1.09	0.561	-1.55	0.098	-1.9
1445664_at	Igf1r	Insulin-like growth factor I receptor	-1.35	0.224	-1.36	0.716	-3.35	0.052	-1.07	0.626	-1.78
1458883_at	---	---	-1.32	0.724	-1.95	0.302	-2	0.202	-1.43	0.381	-1.67
1459721_at	---	CDNA clone IMAGE:6406267	-1.79	0.228	-1.69	0.372	-1.6	0.488	-1.94	0.609	-1.76
1416643_at	Tpt1	tumor protein, translationally-controlled 1	-1.53	0.704	-2.75	0.092	-1.32	0.117	-1.24	0.606	-1.71
1442492_at	DXErtd11e	DNA segment, Chr X, ERATO Doi 11, expressed	-3.23	0.061	-1.16	0.704	-1.66	0.106	-1.14	0.574	-1.8
1422014_at	Foxp2	forkhead box P2	-2	0.255	-1.57	0.22	-1.57	0.32	-1	0.998	-1.54
1459259_at	A030007L22	hypothetical protein A030007L22	-1.76	0.263	-2.66	0.079	-1.21	0.44	-1.58	0.244	-1.8
1445533_at	A630047E20Rik	RIKEN cDNA A630047E20 gene	-2.78	0.061	-1.89	0.303	-1.13	0.76	-3.44	0.025	-2.31
1443112_at	Api5	apoptosis inhibitor 5	-1.41	0.263	-2.47	0.026	-1.51	0.055	-1.31	0.388	-1.67
1445625_at	---	Transcribed locus	-1.5	0.46	-1.72	0.512	-1.89	0.225	-1.33	0.584	-1.61
1437755_at	Slc5a12	solute carrier family 5 (sodium/glucose cotransporter), member 12	-1.02	0.945	-2.46	0.268	-2.57	0.004	-1.22	0.577	-1.82
1420783_at	Trpd52l3	tumor protein D52-like 3	-1.41	0.395	-2.15	0.213	-1.65	0.104	-1.38	0.139	-1.65
1416966_at	Slc22a8	solute carrier family 22 (organic anion transporter), member 8	-1.29	0.253	-2.59	0.126	-1.62	0.293	-1.68	0.194	-1.79
1452318_a_at	Hspa1b	heat shock protein 1B	-1.45	0.164	-1.62	0.192	-2.12	0.188	-2.19	0.534	-1.84
1460264_at	Lats1	large tumor suppressor	-2.01	0.036	-1.35	0.693	-1.84	0.113	-2.6	0.066	-1.95
1454877_at	Sertad4	SERTA domain containing 4	-1.33	0.235	-2.35	0.133	-1.66	0.161	-1.36	0.567	-1.68
1426042_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	-1.53	0.67	-1.9	0.379	-1.67	0.074	-1.16	0.756	-1.56
1436118_at	Vangl2	vang-like 2 (van gogh, Drosophila)	-1.28	0.111	-2.78	0.06	-1.57	0.044	-1.55	0.153	-1.79
1459507_at	---	---	-2.68	0.499	-1.35	0.535	-1.5	0.355	-3.94	0.001	-2.37
1420072_s_at	---	---	-1.22	0.638	-2.13	0.034	-2.02	0.039	-1.63	0.255	-1.75
1454202_a_at	1700061J05Rik	RIKEN cDNA 1700061J05 gene	-1.62	0.449	-1.47	0.528	-2.04	0.096	-1.2	0.543	-1.58
1420627_a_at	Csn1s1	casein alpha s1	-2.24	0.113	-1.5	0.537	-1.48	0.393	-1.08	0.894	-1.58
1447134_at	Setd5	SET domain containing 5	-1.54	0.572	-2.17	0.098	-1.48	0.452	-2.02	0.036	-1.8
1443635_at	Gm128	gene model 128, (NCBI)	-1.23	0.13	-2.29	0.268	-1.86	0.19	-2.48	0.308	-1.97
1433779_at	Casc4	cancer susceptibility candidate 4	-1.12	0.301	-2.24	0.03	-2.24	0.016	-1.23	0.359	-1.71
1420299_at	Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	-1.46	0.652	-2.89	0.003	-1.32	0.608	-1.29	0.392	-1.74
1432643_at	4933411E06Rik	RIKEN cDNA 4933411E06 gene	-1.24	0.593	-2.01	0.183	-2.05	0.108	-1.22	0.721	-1.63

1457446_at	Opcml	opioid binding protein/cell adhesion molecule-like	-1.46	0.173	-1.67	0.527	-1.96	0.094	-2.59	0.338	-1.92
1458004_at	Prrx1	paired related homeobox 1	-1.52	0.021	-2.58	0.269	-1.34	0.528	-1.1	0.476	-1.63
1440276_at	Gm62	gene model 62, (NCBI)	-1.33	0.686	-2.05	0.198	-1.8	0.17	-1.79	0.487	-1.75
1459825_x_at	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	-2.4	0.026	-1.42	0.289	-1.49	0.208	-1.22	0.769	-1.63
1440711_at	C630001G18Rik	RIKEN cDNA C630001G18 gene	-2.12	0.239	-1.74	0.393	-1.34	0.241	-1.69	0.371	-1.72
1440582_at	Itch /// 8030492O04	itchy /// RIKEN cDNA 8030492O04 gene	-1.8	0.176	-1.52	0.023	-1.72	0.062	-1.58	0.078	-1.65
1442040_at	6330530A05Rik	RIKEN cDNA 6330530A05 gene	-1.55	0.311	-1.65	0.189	-1.84	0.121	-1.7	0.064	-1.69
1446762_at	---	Transcribed locus	-1.22	0.131	-2.04	0.143	-2.07	0.002	-1.1	0.596	-1.61
1427127_x_at	Hspa1b	heat shock protein 1B	-1.4	0.308	-1.75	0.075	-1.96	0.242	-2.15	0.51	-1.82
1439480_at	AU015850	Expressed sequence AU015850	-1.91	0.244	-1.34	0.594	-1.89	0.372	-2.45	0.157	-1.9
1458934_at	D5Ertd505e	DNA segment, Chr 5, ERATO Doi 505 , expressed	-1.51	0.584	-1.49	0.156	-2.16	0.031	-1.92	0.146	-1.77
1421405_at	Zim1	zinc finger, imprinted 1	-1.42	0.288	-1.35	0.56	-2.85	0.097	-1.04	0.942	-1.67
1439086_at	A930009L07Rik	RIKEN cDNA A930009L07 gene	-1.16	0.512	-4.37	0.088	-1.42	0.214	-1.53	0.596	-2.12
1432330_at	LOC381294	complement factor H-like	-2.38	0.116	-1.06	0.662	-2.33	0.166	-2.18	0.277	-1.98
1421716_at	V1rd6	vomeronasal 1 receptor, D6	-2.26	0.228	-1.71	0.209	-1.3	0.257	-1.87	0.039	-1.78
1432768_at	6430710M23Rik	RIKEN cDNA 6430710M23 gene	-2.09	0.057	-1.42	0.232	-1.63	0.274	-1.12	0.67	-1.56
1429632_at	Trappc4	trafficking protein particle complex 4	-2.26	0.049	-1.47	0.231	-1.48	0.077	-1.18	0.585	-1.6
1444044_at	Nedd4	Neural precursor cell expressed, developmentally down-regulted gene 4	-2.33	0.02	-1.36	0.581	-1.57	0.167	-1.28	0.725	-1.64
1415832_at	Agtr2	angiotensin II receptor, type 2	-1.67	0.532	-1.24	0.698	-2.51	0.082	-1.17	0.663	-1.65
1455542_at	C630043F03Rik	RIKEN cDNA C630043F03 gene	-1.19	0.705	-2.49	0.024	-1.78	0.117	-1.07	0.896	-1.63
1447380_at	Amdhd1	amidohydrolase domain containing 1	-1.73	0.565	-1.2	0.144	-2.57	0.015	-1.27	0.636	-1.69
1456474_at	---	---	-1.37	0.607	-1.81	0.3	-1.91	0.155	-2.33	0.011	-1.85
1425648_at	Trim60 /// Trim61	tripartite motif-containing 60 /// tripartite motif-containing 61	-2.25	0.126	-1.38	0.44	-1.57	0.183	-1.2	0.826	-1.6
1451774_at	LOC435285	similar to keratin associated protein 4-10; keratin associated protein 4.10	-1.67	0.098	-1.77	0.311	-1.56	0.438	-1.58	0.156	-1.65
1425683_at	---	---	-1.77	0.454	-2.5	0.267	-1.19	0.567	-1.16	0.853	-1.66
1428741_at	Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	-1.27	0.741	-2.25	0.305	-1.73	0.244	-1.11	0.799	-1.59
1437558_at	B130021B11Rik	RIKEN cDNA B130021B11 gene	-1.12	0.084	-2.45	0.029	-1.96	0.027	-1.98	0.028	-1.88
1447458_at	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	-3.4	0.033	-1.18	0.488	-1.49	0.034	-1.22	0.744	-1.82
1439710_at	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	-1.3	0.414	-2.72	0.006	-1.49	0.112	-1.31	0.387	-1.7
1427293_a_at	Auts2	autism susceptibility candidate 2	-1.79	0.048	-1.49	0.592	-1.73	0.294	-1.53	0.608	-1.63
1419779_at	---	---	-1.39	0.436	-1.35	0.442	-2.85	0.006	-1.31	0.618	-1.72
1440910_at	---	CDNA clone IMAGE:5252333	-1.89	0.189	-1.45	0.117	-1.68	0.008	-2.41	0.267	-1.86
1433313_at	6720454L07Rik	RIKEN cDNA 6720454L07 gene	-1.66	0.609	-1.87	0.149	-1.48	0.444	-1.59	0.515	-1.65
1439384_at	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-1.28	0.764	-3.89	0.026	-1.29	0.467	-1.47	0.594	-1.98
1453883_at	4933425B07Rik	RIKEN cDNA 4933425B07 gene	-1.41	0.607	-1.6	0.64	-2.1	0.104	-1.22	0.571	-1.58
1444959_at	D1Ertd83e	DNA segment, Chr 1, ERATO Doi 83, expressed	-2.64	0.353	-1.81	0.435	-1.13	0.54	-1.11	0.83	-1.67
1446497_at	Nav1	Neuron navigator 1	-1.2	0.556	-1.65	0.223	-2.68	0.011	-1.25	0.479	-1.7
1442814_at	Glcci1	Glucocorticoid induced transcript 1	-2.26	0.03	-1.63	0.446	-1.32	0.424	-1.16	0.798	-1.59
1449678_at	---	---	-1.58	0.249	-1.73	0.086	-1.66	0.134	-1.03	0.84	-1.5
1419200_at	Fxyd7	FXYD domain-containing ion transport regulator 7	-1.43	0.39	-1.55	0.243	-2.13	0.209	-1.55	0.233	-1.67
1437826_at	Pfpl	Pore forming protein-like	-1.32	0.489	-2.14	0.163	-1.7	0.338	-1.64	0.417	-1.7
1435307_at	6430502M16Rik	RIKEN cDNA 6430502M16 gene	-1.24	0.225	-1.71	0.389	-2.38	0.223	-1.37	0.506	-1.67
1440069_at	Efnb2	Ephrin B2	-1.46	0.419	-1.69	0.428	-1.86	0.003	-1.57	0.572	-1.64
1439522_at	---	---	-1.6	0.08	-2	0.089	-1.45	0.253	-3.16	0.063	-2.05
1420771_at	Sprr2d	small proline-rich protein 2D	-1.63	0.381	-2.44	0.028	-1.26	0.544	-1.59	0.409	-1.73
1442803_at	Rad51l3	RAD51-like 3 (S. cerevisiae)	-1.73	0.131	-1.51	0.355	-1.73	0.532	-3.47	0.254	-2.11
1436889_at	Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	-3.83	0.015	-1.19	0.745	-1.4	0.202	-1	0.995	-1.85
1427421_at	Tcp10b	t-complex protein 10b	-1.88	0.242	-1.59	0.353	-1.52	0.514	-1.67	0.397	-1.67
1433924_at	Peg3	paternally expressed 3	-1.49	0.464	-1.16	0.708	-3.5	0.008	-2.4	0.151	-2.14
1454176_at	Ercc8	excision repaiross-complementing rodent repair deficiency, complementation grou	-1.18	0.821	-2.3	0.253	-1.88	0.142	-1.32	0.49	-1.67
1431268_at	1700047I17Rik	RIKEN cDNA 1700047I17 gene	-1.16	0.804	-2.71	0.148	-1.69	0.145	-1.9	0.124	-1.87
1460214_at	Pcp4	Purkinje cell protein 4	-1.21	0.304	-2.01	0.353	-2.03	0.1	-2.23	0.194	-1.87
1440644_at	Parp6	poly (ADP-ribose) polymerase family, member 6	-1.44	0.474	-1.77	0.169	-1.79	0.049	-1.87	0.004	-1.72

1442516_at	D2Ertd623e	DNA segment, Chr 2, ERATO Doi 623, expressed	-1.56	0.285	-1.46	0.505	-2.04	0.197	-1.22	0.699	-1.57
1456988_at	AI848258	expressed sequence AI848258	-2.41	0.359	-1.68	0.366	-1.23	0.711	-1.05	0.776	-1.59
1447149_at	---	---	-3.66	0.026	-1.53	0.14	-1.12	0.482	-1.06	0.764	-1.84
1440064_at	BC026657	cDNA sequence BC026657	-4.41	0.102	-1.08	0.846	-1.5	0.254	-1.31	0.087	-2.07
1440258_at	Kcnq2	Potassium voltage-gated channel, subfamily Q, member 2	-2.25	0.052	-1.25	0.678	-1.73	0.152	-1.08	0.931	-1.58
1426077_at	Moxd2	monooxygenase, DBH-like 2	-1.2	0.555	-1.34	0.675	-4.13	0.038	-1.7	0.563	-2.09
1417356_at	Peg3	paternally expressed 3	-1.23	0.769	-1.41	0.608	-3.35	0.166	-1.93	0.23	-1.98
1447791_s_at	Gna14	guanine nucleotide binding protein, alpha 14	-1.54	0.108	-1.65	0.179	-1.77	0.002	-1.06	0.664	-1.5
1431459_at	9430013L14Rik	RIKEN cDNA 9430013L14 gene	-1.13	0.865	-1.62	0.244	-3.14	0.111	-2.06	0.044	-1.99
1426070_a_at	Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	-1.32	0.29	-5.42	0.028	-1.13	0.815	-1.26	0.762	-2.28
1456946_at	4831416G18Rik	RIKEN cDNA 4831416G18 gene	-1.74	0.071	-1.61	0.125	-1.59	0.143	-1.09	0.643	-1.51
1441537_at	Recql5	RecQ protein-like 5	-2.13	0.044	-1.26	0.526	-1.77	0.147	-1.05	0.935	-1.55
1450820_a_at	Ntng2	netrin G2	-1.91	0.287	-2.23	0.219	-1.16	0.543	-1.23	0.439	-1.64
1432078_at	4930453L07Rik	RIKEN cDNA 4930453L07 gene	-1.82	0.48	-1.25	0.524	-2.09	0.123	-1.34	0.363	-1.63
1445169_at	---	---	-2.56	0.031	-1.26	0.677	-1.54	0.041	-1.1	0.616	-1.62
1429856_at	Tspan18	tetraspanin 18	-4.07	0.073	-1.44	0.425	-1.12	0.739	-1.12	0.771	-1.94
1459083_at	A330084C13Rik	RIKEN cDNA A330084C13 gene	-1.87	0.197	-2.34	0.131	-1.15	0.757	-2.38	0.415	-1.94
1458867_at	Edil3	EGF-like repeats and discoidin I-like domains 3	-1.36	0.704	-2.59	0.028	-1.41	0.308	-1.12	0.861	-1.62
1456306_a_at	Umod	uromodulin	-1.18	0.001	-9.02	0.127	-1.14	0.568	-3.46	0.193	-3.7
1459051_at	6530418L21Rik	RIKEN cDNA 6530418L21 gene	-1.69	0.21	-2.71	0.035	-1.15	0.8	-1.24	0.149	-1.7
1425182_x_at	Klk1b22 /// Klk1b9	kallikrein 1-related peptidase b22 /// kallikrein 1-related peptidase b9	-1.66	0.086	-1.68	0.338	-1.57	0.421	-1.56	0.293	-1.62
1433395_at	4921504P13Rik	RIKEN cDNA 4921504P13 gene	-1.85	0.041	-1.22	0.685	-2.13	0.135	-1.22	0.774	-1.6
1425922_a_at	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-1.91	0.223	-2.27	0.154	-1.15	0.707	-1.14	0.804	-1.62
1428077_at	Tmem163	transmembrane protein 163	-3.4	0.007	-1.68	0.261	-1.06	0.823	-1.12	0.623	-1.81
1458805_at	---	---	-1.28	0.094	-1.64	0.166	-2.25	0.041	-1.21	0.539	-1.6
1459550_at	Syn3	Synapsin III	-2.39	0.46	-1.15	0.64	-1.82	0.133	-1.77	0.388	-1.78
1421740_at	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	-2.11	0.302	-2.53	0.109	-1.04	0.706	-1.51	0.339	-1.8
1439693_a_at	Fbxw16	F-box and WD-40 domain protein 16	-1.89	0.191	-1.61	0.211	-1.46	0.443	-1.29	0.238	-1.56
1442695_at	C030007I01Rik	RIKEN cDNA C030007I01 gene	-1.33	0.449	-1.69	0.187	-2.03	0.053	-2.29	0.012	-1.84
1443915_at	Mrpl47	mitochondrial ribosomal protein L47	-1.45	0.15	-2.14	0.085	-1.47	0.275	-1.09	0.853	-1.54
1447098_at	---	---	-1.38	0.616	-1.67	0.284	-1.93	0.179	-2.64	0.184	-1.91
1439261_x_at	Mitd1	MIT, microtubule interacting and transport, domain containing 1	-2.19	0.122	-1.1	0.691	-2.11	0.125	-1.23	0.41	-1.66
1445561_at	Grip1	Glutamate receptor interacting protein 1	-1.57	0.355	-1.32	0.03	-2.25	0	-1.51	0.023	-1.66
1447844_at	---	Transcribed locus	-1.84	0.205	-1.93	0.133	-1.29	0.336	-1.52	0.248	-1.64
1442226_at	6430702L12	hypothetical protein 6430702L12	-1.22	0.539	-2.56	0.272	-1.59	0.013	-3.9	0.148	-2.32
1457482_at	Jarid1b	jumonji, AT rich interactive domain 1B (Rbp2 like)	-1.46	0.153	-2.33	0.123	-1.38	0.369	-2.29	0.047	-1.87
1422839_at	Neurog2	neurogenin 2	-1.26	0.453	-2.15	0.156	-1.72	0.37	-1.73	0.543	-1.72
1458354_x_at	Krt28	keratin 28	-1.2	0.415	-1.48	0.516	-3	0.041	-2.24	0.497	-1.98
1442018_at	AI426953	expressed sequence AI426953	-1.27	0.605	-2.42	0.091	-1.57	0.184	-2.84	0.219	-2.02
1458087_at	Stac3	SH3 and cysteine rich domain 3	-1.46	0.183	-1.82	0.29	-1.65	0.422	-1.71	0.557	-1.66
1429523_a_at	Slc39a5	solute carrier family 39 (metal ion transporter), member 5	-1.02	0.955	-2.25	0.029	-2.38	0.086	-1.22	0.776	-1.72
1455423_at	Ndg1 /// LOC62318	Nur77 downstream gene 1 /// similar to chromosome 6 open reading frame 148	-2.19	0.437	-1.12	0.732	-2.01	0.434	-1.6	0.466	-1.73
1432252_a_at	4933406K04Rik	RIKEN cDNA 4933406K04 gene	-1.91	0.224	-1.78	0.376	-1.32	0.275	-1.36	0.295	-1.59
1457950_at	Lphn3	Latrophilin 3	-2.4	0.223	-1.09	0.815	-1.97	0.277	-1.53	0.516	-1.75
1438918_at	Fdft1 /// LOC62771	farnesyl diphosphate farnesyl transferase 1 /// similar to farnesyl diphosphate farr	-2.33	0.245	-1.04	0.92	-2.2	0.203	-1.4	0.246	-1.74
1435214_at	Gja12	gap junction membrane channel protein alpha 12	-1.6	0.596	-4.52	0.027	-1	0.998	-1.12	0.827	-2.06
1426990_at	Cubn	cubilin (intrinsic factor-cobalamin receptor)	-1.03	0.708	-4.84	0.108	-1.51	0.386	-1.03	0.971	-2.1
1453459_at	1700028I16Rik	RIKEN cDNA 1700028I16 gene	-1.42	0.588	-1.64	0.292	-1.88	0.194	-1.4	0.52	-1.58
1445653_at	BC031361	cDNA sequence BC031361	-1.61	0.484	-2.13	0.17	-1.32	0.131	-1.35	0.284	-1.6
1454049_at	4933426G20Rik	RIKEN cDNA 4933426G20 gene	-1.28	0.237	-1.68	0.312	-2.14	0.4	-2.08	0.179	-1.79
1457543_at	Nsun7	NOL1/NOP2/Sun domain family, member 7	-5.89	0.08	-1.36	0.589	-1.06	0.636	-1.76	0.455	-2.52
1419968_at	C77370	expressed sequence C77370	-2.77	0.267	-1.98	0.148	-1.02	0.941	-1.42	0.582	-1.8
1443510_at	AW822216	expressed sequence AW822216	-1.17	0.509	-2.16	0.322	-1.88	0.377	-3.42	0.23	-2.16

1444567_at	1700066J03Rik	RIKEN cDNA 1700066J03 gene	-1.18	0.711	-1.81	0.377	-2.22	0.004	-1.63	0.353	-1.71
1431650_at	1110054P19Rik	RIKEN cDNA 1110054P19 gene	-3.26	0.291	-1.63	0.129	-1.07	0.875	-1.3	0.574	-1.82
1447620_at	Cno	cappuccino	-1.22	0.381	-2.64	0.232	-1.53	0.185	-1.96	0.389	-1.84
1441441_at	2010007L08Rik	RIKEN cDNA 2010007L08 gene	-1.79	0.002	-1.39	0.494	-1.74	0.012	-1.2	0.493	-1.53
1460265_at	Pa2g4	Proliferation-associated 2G4	-1.39	0.451	-1.85	0.333	-1.69	0.052	-1.86	0.205	-1.7
1421017_at	Nrg3	neuregulin 3	-1.4	0.735	-2.12	0.115	-1.5	0.471	-1.63	0.289	-1.66
1436931_at	Rfx4	regulatory factor X, 4 (influences HLA class II expression)	-2.43	0.038	-1.21	0.487	-1.62	0.436	-2.4	0.153	-1.91
1429037_at	1700019A02Rik	RIKEN cDNA 1700019A02 gene	-2.37	0.317	-1.03	0.962	-2.19	0.043	-1.15	0.753	-1.68
1432065_at	3100003L13Rik	RIKEN cDNA 3100003L13 gene	-1.69	0.072	-2.69	0.028	-1.12	0.745	-1.67	0.121	-1.79
1419629_at	Mesp2	mesoderm posterior 2	-3.45	0.134	-1.19	0.838	-1.38	0.031	-1.66	0.256	-1.92
1450547_x_at	Dub2	deubiquitinating enzyme 2	-2.72	0.227	-1.13	0.86	-1.66	0.321	-1.74	0.273	-1.81
1444023_at	Ank2	ankyrin 2, brain	-1.86	0.149	-1.61	0.178	-1.43	0.188	-1.19	0.759	-1.52
1426338_a_at	Ntng1	netrin G1	-1.15	0.791	-2.7	0.023	-1.62	0.277	-1.24	0.429	-1.68
1422481_at	Krt1	keratin 1	-1.47	0.423	-2.75	0.107	-1.23	0.669	-1.28	0.201	-1.68
1446849_at	Auts2	Autism susceptibility candidate 2	-1.16	0.727	-2.04	0.123	-1.98	0.048	-1.24	0.218	-1.61
1433082_at	4930448K20Rik	RIKEN cDNA 4930448K20 gene	-2.09	0.346	-2.04	0.285	-1.13	0.809	-1.41	0.427	-1.66
1420273_x_at	---	---	-1.39	0.449	-1.56	0.289	-2.01	0.177	-1.26	0.517	-1.55
1449447_at	Cst10	cystatin 10 (chondrocytes)	-1.31	0.515	-2.02	0.26	-1.67	0.358	-1.16	0.577	-1.54
1457344_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	-1.34	0.624	-2.69	0.118	-1.35	0.627	-1.29	0.642	-1.67
1457786_at	Siglech	Sialic acid binding Ig-like lectin H	-1.29	0.581	-1.62	0.263	-2.13	0.06	-1.15	0.695	-1.55
1446892_at	Lrrc16	Leucine rich repeat containing 16	-1.15	0.718	-2.24	0.16	-1.83	0.012	-3.47	0.044	-2.17
1422236_at	4930560E09Rik	RIKEN cDNA 4930560E09 gene	-1.75	0.553	-1.41	0.365	-1.72	0.16	-1.45	0.451	-1.58
1430286_s_at	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	-1.39	0.069	-1.35	0.228	-2.49	0.003	-1.01	0.985	-1.56
1453888_at	Cpne4	copine IV	-1.23	0.693	-1.79	0.164	-2.03	0.223	-1.2	0.764	-1.56
1453698_at	6030451C04Rik	RIKEN cDNA 6030451C04 gene	-1.03	0.943	-1.64	0.229	-3.6	0.004	-1.54	0.002	-1.95
1459774_at	Tspan5	Tetraspanin 5	-1.28	0.256	-1.62	0.479	-2.17	0.057	-2.03	0.173	-1.77
1444754_at	Asxl2	additional sex combs like 2 (Drosophila)	-2.02	0.361	-1.77	0.047	-1.24	0.596	-2.02	0.174	-1.77
1431259_at	---	---	-2.23	0.135	-1.8	0.346	-1.16	0.564	-1.24	0.507	-1.61
1444846_at	D15Ertd529e	DNA segment, Chr 15, ERATO Doi 529, expressed	-2.94	0.162	-1.33	0.731	-1.29	0.459	-1.14	0.786	-1.68
1430478_at	3110043A19Rik	RIKEN cDNA 3110043A19 gene	-1.57	0.148	-2.07	0.143	-1.34	0.367	-1.13	0.836	-1.53
1457844_a_at	8430427H17Rik	RIKEN cDNA 8430427H17 gene	-1.92	0.513	-1.25	0.641	-1.85	0.268	-2.2	0.194	-1.8
1459876_at	Npr1	Natriuretic peptide receptor 1	-1.4	0.08	-1.6	0.145	-1.9	0.063	-1.3	0.145	-1.55
1447428_at	---	---	-1.73	0.557	-2.05	0.154	-1.25	0.481	-2.29	0.227	-1.83
1443134_at	A930005G22Rik	RIKEN cDNA A930005G22 gene	-3.33	0.003	-1.28	0.744	-1.27	0.559	-1.4	0.641	-1.82
1425604_at	Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.85	0.538	-1.24	0.741	-1.92	0.281	-1	0.998	-1.5
1432497_at	Ccdc93	coiled-coil domain containing 93	-1.3	0.723	-2	0.389	-1.67	0.298	-1.09	0.422	-1.52
1440935_at	Grb10	Growth factor receptor bound protein 10	-1.26	0.261	-1.48	0.483	-2.48	0.035	-1.11	0.699	-1.58
1421532_at	Rxfp2	relaxin/insulin-like family peptide receptor 2	-1.22	0.527	-1.99	0.092	-1.82	0.018	-1.6	0.305	-1.66
1431685_at	4930549O18Rik	RIKEN cDNA 4930549O18 gene	-1.75	0.136	-2.13	0.345	-1.21	0.785	-1.3	0.333	-1.6
1459191_at	B130020M22Rik	RIKEN cDNA B130020M22 gene	-1.6	0.506	-2.51	0.254	-1.18	0.765	-1.65	0.224	-1.73
1442576_at	Creb5	CAMP responsive element binding protein 5	-1.92	0.391	-1.57	0.253	-1.4	0.469	-1.62	0.605	-1.63
1456517_at	Tmem44	transmembrane protein 44	-2.03	0.113	-2.16	0.184	-1.09	0.719	-1.02	0.956	-1.58
1456591_x_at	Akap3	A kinase (PRKA) anchor protein 3	-1.49	0.698	-1.92	0.367	-1.47	0.409	-1.21	0.76	-1.52
1443154_at	6030438J01	hypothetical protein 6030438J01	-1.92	0.042	-1.61	0.349	-1.37	0.115	-1.42	0.184	-1.58
1459000_at	---	---	-1.58	0.328	-1.3	0.522	-2.1	0.148	-1.31	0.469	-1.58
1443772_at	---	---	-1.39	0.472	-3.24	0.206	-1.18	0.079	-2.6	0.048	-2.1
1448608_at	Dtprp	decidual/trophoblast prolactin-related protein	-2.6	0.063	-1.15	0.623	-1.61	0.036	-1.02	0.939	-1.59
1442262_at	---	---	-1.94	0.124	-1.72	0.021	-1.28	0.399	-3.65	0.079	-2.15
1439468_at	Bach2	BTB and CNC homology 2	-1.64	0.029	-1.31	0.287	-1.98	0.048	-2.26	0.122	-1.8
1458742_at	Lphn3	latrophilin 3	-1.27	0.777	-2.96	0.051	-1.33	0.297	-1.69	0.405	-1.81
1439044_at	Zfp354c	zinc finger protein 354C	-1.15	0.491	-2.1	0.043	-1.87	0.064	-2.02	0.216	-1.79
1443228_at	---	---	-1.57	0.227	-1.8	0.229	-1.46	0.191	-1.2	0.72	-1.51
1440484_at	Unc5d	unc-5 homolog D (C. elegans)	-1.12	0.693	-2.36	0.016	-1.78	0.182	-1.38	0.637	-1.66

1458804_at	Slco4c1	Solute carrier organic anion transporter family, member 4C1	-4.56	0.025	-1.03	0.962	-1.46	0.493	-1.54	0.489	-2.14
1432854_at	1700018P08Rik	RIKEN cDNA 1700018P08 gene	-1.36	0.281	-1.61	0.154	-1.92	0.378	-1.06	0.819	-1.49
1445318_at	Klhl4	Kelch-like 4 (Drosophila)	-1.22	0.84	-2.05	0.034	-1.75	0.329	-1.57	0.074	-1.65
1433192_at	A430105P17Rik	RIKEN cDNA A430105P17 gene	-1.44	0.296	-3.53	0.043	-1.11	0.704	-1.35	0.557	-1.86
1453218_at	1110014K05Rik	RIKEN cDNA 1110014K05 gene	-1.55	0.091	-2.25	0.233	-1.26	0.35	-1.68	0.026	-1.69
1432878_at	4930544N03Rik	RIKEN cDNA 4930544N03 gene	-1.76	0.216	-2.31	0.232	-1.14	0.494	-3.67	0.033	-2.22
1458238_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	-1.77	0.086	-2.5	0.075	-1.09	0.729	-1.32	0.373	-1.67
1431475_a_at	Hoxa10	homeo box A10	-1.23	0.318	-2.36	0.052	-1.55	0.002	-1.09	0.875	-1.56
1421562_at	Cd209c	CD209c antigen	-3.06	0.023	-1.15	0.68	-1.45	0.208	-4.73	0	-2.6
1457517_at	A730046G19Rik	RIKEN cDNA A730046G19 gene	-1.4	0.312	-1.85	0.239	-1.59	0.154	-1.1	0.633	-1.49
1431195_at	Rnf170	ring finger protein 170	-1.25	0.669	-2	0.285	-1.72	0.077	-1.35	0.157	-1.58
1459654_at	---	---	-1.06	0.535	-1.92	0.069	-2.41	0.152	-1.9	0.062	-1.82
1430460_at	5830410F13Rik	RIKEN cDNA 5830410F13 gene	-1.45	0.201	-1.97	0.034	-1.45	0.003	-1.52	0.151	-1.6
1433416_at	5430432H19Rik	RIKEN cDNA 5430432H19 gene	-1.26	0.711	-2.2	0.148	-1.57	0.415	-1.16	0.79	-1.55
1431376_at	Wdr62	WD repeat domain 62	-1.64	0.609	-1.83	0.246	-1.37	0.422	-1.84	0.288	-1.67
1442541_at	Oaz2	Ornithine decarboxylase antizyme 2	-1.46	0.272	-1.8	0.053	-1.54	0.238	-1.38	0.001	-1.55
1443593_at	---	---	-1.79	0.189	-1.12	0.834	-2.29	0.067	-1.35	0.632	-1.64
1457898_at	Ga17	Dendritic cell protein GA17	-1.13	0.635	-1.41	0.362	-3.45	0.008	-1.89	0.123	-1.97
1456152_at	Paqr5	progestin and adipoQ receptor family member V	-1.02	0.744	-1.82	0.203	-2.81	0.092	-2.13	0.008	-1.94
1442992_at	130004C03	hypothetical LOC403343	-1.3	0.199	-1.58	0.026	-2.05	0.094	-1.68	0.058	-1.65
1421919_a_at	Ccr9	chemokine (C-C motif) receptor 9	-1.69	0.303	-2.48	0.166	-1.12	0.718	-1.63	0.12	-1.73
1437796_at	---	Transcribed locus	-1.58	0.006	-1.21	0.584	-2.33	0.055	-1.74	0.087	-1.71
1459055_at	Foxj3	forkhead box J3	-2.59	0.167	-1.16	0.763	-1.56	0.248	-1.29	0.563	-1.65
1442373_at	2610203C20Rik	RIKEN cDNA 2610203C20 gene	-1.5	0.43	-1.19	0.734	-2.63	0.023	-1.17	0.769	-1.62
1447743_x_at	Ext2	exostoses (multiple) 2	-2.27	0.037	-1.67	0.018	-1.18	0.49	-1.28	0.093	-1.6
1447729_s_at	1700036D21Rik	RIKEN cDNA 1700036D21 gene	-1.84	0.208	-1.75	0.344	-1.29	0.246	-1.56	0.028	-1.61
1454360_at	4930418C01Rik	RIKEN cDNA 4930418C01 gene	-1.09	0.749	-2.15	0.171	-1.95	0.391	-2.06	0.028	-1.81
1443456_at	6330416L07Rik	RIKEN cDNA 6330416L07 gene	-1.45	0.082	-1.62	0.055	-1.72	0.081	-1.08	0.683	-1.46
1458872_at	---	---	-1.24	0.112	-2.23	0.035	-1.57	0.329	-1.17	0.766	-1.55
1423379_at	Nfatc4 /// LOC6720	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4 /// similar	-1.6	0.096	-1.97	0.056	-1.31	0.245	-1.63	0.54	-1.63
1441369_at	C030017B01Rik	RIKEN cDNA C030017B01 gene	-2.47	0.447	-1.08	0.878	-1.78	0.274	-1.07	0.721	-1.6
1442667_at	Cdc40	cell division cycle 40 homolog (yeast)	-1.45	0.696	-1.24	0.559	-2.52	0.032	-1.28	0.544	-1.62
1440624_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	-1.48	0.094	-1.48	0.09	-1.83	0.087	-1.33	0.519	-1.53
1420450_at	Mmp10	matrix metallopeptidase 10	-1.56	0.059	-2.57	0.29	-1.16	0.603	-1.3	0.381	-1.65
1422247_a_at	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	-1.2	0.698	-4.13	0.033	-1.22	0.682	-1.4	0.395	-1.99
1454691_at	Nrxn1	neurexin I	-1.43	0.607	-1.15	0.5	-3.06	0.091	-1.24	0.516	-1.72
1423279_at	Slc34a1	solute carrier family 34 (sodium phosphate), member 1	-1.23	0.16	-4.31	0.153	-1.18	0.622	-1.11	0.764	-1.96
1431407_at	2310024H09Rik	RIKEN cDNA 2310024H09 gene	-1.94	0.424	-1.19	0.696	-1.85	0.222	-1.23	0.709	-1.55
1435460_at	Prkg2	protein kinase, cGMP-dependent, type II	-1.46	0.033	-1.88	0.156	-1.47	0.077	-1.46	0.425	-1.57
1458901_at	Mef2d	Myocyte enhancer factor 2D	-1.46	0.005	-3.15	0.014	-1.12	0.591	-1.21	0.371	-1.73
1441718_at	Edd1	E3 ubiquitin protein ligase, HECT domain containing, 1	-1.37	0.202	-1.42	0.072	-2.15	0.01	-1.22	0.121	-1.54
1418726_a_at	Tnnt2	troponin T2, cardiac	-3.58	0.191	-1.61	0.154	-1	0.991	-1.23	0.077	-1.86
1449967_at	Sim1	single-minded homolog 1 (Drosophila)	-1.09	0.513	-3.21	0.005	-1.5	0.143	-1.62	0.407	-1.86
1454315_at	3300002A11Rik	RIKEN cDNA 3300002A11 gene	-1.93	0.336	-2.31	0.177	-1.06	0.821	-1.09	0.44	-1.59
1441498_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	-1.29	0.312	-1.74	0.069	-1.82	0.052	-1.19	0.593	-1.51
1446967_at	Fbxl7	F-box and leucine-rich repeat protein 7	-1.21	0.093	-1.69	0.027	-2.08	0.007	-1.78	0.038	-1.69
1440549_at	B230334L07Rik	RIKEN cDNA B230334L07 gene	-1.24	0.303	-1.73	0.124	-1.95	0.001	-2.11	0.041	-1.76
1454394_at	4932432N04Rik	RIKEN cDNA 4932432N04 gene	-2.11	0.501	-1.18	0.706	-1.73	0.385	-1.68	0.496	-1.68
1458054_at	Ext1	Exostoses (multiple) 1	-1.35	0.457	-1.68	0.121	-1.76	0.046	-1	0.985	-1.45
1445682_at	2700099C18Rik	RIKEN cDNA 2700099C18 gene	-2.14	0.253	-1.36	0.194	-1.43	0.446	-1.24	0.304	-1.54
1449963_at	2310040M23Rik	RIKEN cDNA 2310040M23 gene	-2.1	0.16	-1.22	0.782	-1.65	0.338	-2.23	0.543	-1.8
1445791_at	---	---	-4.13	0.032	-1.01	0.963	-1.48	0.203	-1.06	0.924	-1.92
1456564_at	C030046I01Rik	RIKEN cDNA C030046I01 gene	-1.36	0.455	-2.27	0.163	-1.38	0.131	-1.07	0.831	-1.52

1423037_at	Agtrl1	angiotensin receptor-like 1	-1.08	0.752	-1.67	0.085	-2.64	0.048	-1.68	0.143	-1.77
1441393_at	---	---	-1.15	0.848	-1.92	0.122	-1.93	0.133	-1.25	0.517	-1.56
1438896_at	Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	-1.29	0.49	-2.72	0	-1.31	0.585	-1.08	0.8	-1.6
1430646_at	5830407P18Rik	RIKEN cDNA 5830407P18 gene	-1.56	0.083	-1.27	0.495	-2.09	0.001	-1.21	0.71	-1.53
1445842_at	---	---	-1.96	0.287	-1.3	0.679	-1.59	0.122	-1.2	0.44	-1.51
1439591_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	-1.18	0.025	-2.08	0.08	-1.73	0.049	-1.32	0.101	-1.58
1459344_at	9630019E01Rik	RIKEN cDNA 9630019E01 gene	-1.47	0.005	-1.33	0.53	-2.1	0.027	-1.56	0.165	-1.62
1443480_at	---	---	-1.15	0.808	-1.8	0.136	-2.07	0.036	-1.29	0.253	-1.58
1444479_at	---	---	-1.04	0.853	-4.31	0.066	-1.39	0.149	-1.09	0.674	-1.96
1445594_at	Hnrpl	Heterogeneous nuclear ribonucleoprotein L	-1.9	0.212	-1.14	0.847	-1.98	0.029	-1.16	0.791	-1.55
1453214_at	Lrrc15	leucine rich repeat containing 15	-1.74	0.504	-1.39	0.48	-1.63	0.436	-1.11	0.849	-1.47
1432485_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	-1.02	0.962	-2.82	0.185	-1.74	0.255	-1.06	0.814	-1.66
1425661_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.32	0.228	-1.14	0.816	-3.65	0.01	-1.42	0.659	-1.88
1443284_at	Satb1	Special AT-rich sequence binding protein 1	-1.17	0.552	-1.44	0.281	-2.77	0.073	-4.26	0.04	-2.41
1439321_at	Arid1b	AT rich interactive domain 1B (Swi1 like)	-1.48	0.199	-1.41	0.146	-1.89	0.062	-1.67	0.161	-1.62
1441446_at	---	---	-1.13	0.837	-2.97	0.128	-1.44	0.197	-1.63	0.276	-1.8
1431590_at	4930521C21Rik	RIKEN cDNA 4930521C21 gene	-1.77	0.117	-1.99	0.269	-1.18	0.068	-1.26	0.26	-1.55
1438697_at	4632425D07Rik	RIKEN cDNA 4632425D07 gene	-1.37	0.471	-1.94	0.116	-1.49	0.02	-1.35	0.113	-1.54
1440309_at	4833430A08Rik	RIKEN cDNA 4833430A08 gene	-1.87	0.135	-1.13	0.727	-2.01	0.006	-1.5	0.051	-1.63
1442107_at	Flnb	filamin, beta	-1.4	0.211	-1.48	0.109	-1.89	0.155	-1.21	0.507	-1.5
1442854_at	---	Transcribed locus	-2.12	0.081	-2.11	0.408	-1.03	0.961	-1	0.995	-1.57
1440097_at	Mirg	miRNA containing gene	-1.75	0.035	-1.29	0.269	-1.76	0.129	-1.01	0.992	-1.45
1431853_at	4933413C19Rik	RIKEN cDNA 4933413C19 gene	-3.02	0.274	-1.26	0.377	-1.27	0.526	-1.56	0.509	-1.78
1457922_at	---	---	-2.31	0.502	-1.03	0.967	-1.96	0.218	-1.12	0.79	-1.6
1429932_at	4930566F21Rik	RIKEN cDNA 4930566F21 gene	-1.34	0.509	-1.76	0.159	-1.65	0.013	-2.07	0.127	-1.71
1460003_at	AI956758	expressed sequence AI956758	-1.17	0.435	-1.9	0.238	-1.87	0.067	-1.03	0.922	-1.49
1422275_at	Gpr44	G protein-coupled receptor 44	-1.78	0.469	-1.35	0.174	-1.63	0.465	-1.76	0.324	-1.63
1423555_a_at	Ifi44	interferon-induced protein 44	-1.57	0.019	-1.07	0.704	-2.88	0.021	-1.18	0.713	-1.67
1432969_at	4933423K11Rik	RIKEN cDNA 4933423K11 gene	-1.67	0.572	-1.24	0.284	-1.94	0.038	-1.38	0.282	-1.56
1432660_at	5830420C07Rik	RIKEN cDNA 5830420C07 gene	-1.17	0.741	-1.61	0.454	-2.25	0.037	-1.45	0.556	-1.62
1432684_at	4921521C08Rik	RIKEN cDNA 4921521C08 gene	-1.37	0.566	-1.2	0.722	-2.84	0.119	-2.21	0.493	-1.9
1422281_at	Sstr4	somatostatin receptor 4	-1.22	0.741	-2.44	0.085	-1.44	0.437	-1.38	0.578	-1.62
1431756_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930516B21 pr	-2.05	0.446	-1.81	0.451	-1.14	0.788	-1.52	0.474	-1.63
1420555_at	Alx3	aristaless 3	-2.67	0.39	-1.09	0.694	-1.59	0.451	-1.44	0.641	-1.7
1443204_at	Rbms3	RNA binding motif, single stranded interacting protein	-1.18	0.604	-1.74	0.068	-2	0.044	-1.1	0.739	-1.51
1442069_at	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	-1.4	0.735	-2.56	0.004	-1.22	0.731	-1.17	0.419	-1.59
1440963_at	AI465270	expressed sequence AI465270	-1.2	0.732	-2.45	0.1	-1.47	0.147	-1.17	0.547	-1.57
1422587_at	Tmem45a	transmembrane protein 45a	-1.03	0.896	-2.14	0.038	-2.05	0.006	-2.6	0.521	-1.96
1446210_at	---	---	-1.8	0.574	-1.42	0.072	-1.51	0.063	-1.2	0.477	-1.48
1440119_at	Sipa1l1	signal-induced proliferation-associated 1 like 1	-1.16	0.602	-3.87	0.099	-1.25	0.38	-1.27	0.415	-1.89
1453785_at	Taz	tafazzin	-1.53	0.454	-1.62	0.32	-1.54	0.056	-2	0.555	-1.67
1459118_at	D230038C21	hypothetical protein D230038C21	-1.5	0.36	-1.91	0.147	-1.36	0.188	-1.1	0.495	-1.47
1425987_a_at	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha men	-1.82	0.062	-2.15	0.299	-1.1	0.578	-1.14	0.447	-1.55
1458431_at	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	-2.01	0.05	-1.54	0.203	-1.29	0.064	-1.14	0.4	-1.49
1446767_at	Bcl9	B-cell CLL/lymphoma 9	-1.36	0.643	-1.93	0.085	-1.5	0.477	-1.91	0.147	-1.67
1441869_x_at	Auts2	Autism susceptibility candidate 2	-1.34	0.07	-1.52	0.106	-1.92	0.08	-1.5	0.286	-1.57
1441744_at	Cacna1c	Calcium channel, voltage-dependent, L type, alpha 1C subunit	-1.71	0.354	-1.22	0.647	-1.92	0.078	-1.45	0.524	-1.57
1438398_at	Rnpc2	RNA-binding region (RNP1, RRM) containing 2	-2.2	0.423	-1.76	0.192	-1.11	0.755	-2.35	0.22	-1.85
1454253_at	2810452K22Rik	RIKEN cDNA 2810452K22 gene	-2.29	0.249	-1.74	0.054	-1.09	0.671	-1.28	0.522	-1.6
1435848_at	D430041D05Rik	RIKEN cDNA D430041D05 gene	-1.48	0.481	-1.41	0.491	-1.86	0.205	-1.66	0.164	-1.6
1457572_at	Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	-2.45	0.222	-1.19	0.089	-1.48	0.234	-1.27	0.741	-1.6
1445706_x_at	---	---	-1.71	0.152	-1.34	0.687	-1.69	0.058	-1.06	0.851	-1.45
1441337_at	---	Transcribed locus	-1.29	0.413	-1.14	0.826	-3.7	0.006	-1.9	0.25	-2.01

1433015_at	6330436F06Rik	RIKEN cDNA 6330436F06 gene	-1.17	0.343	-1.58	0.222	-2.27	0.033	-1.11	0.818	-1.53
1453905_at	5033415L01Rik	RIKEN cDNA 5033415L01 gene	-1.41	0.031	-1.24	0.763	-2.41	0.021	-1.15	0.558	-1.55
1445033_at	Abca16	ATP-binding cassette, sub-family A (ABC1), member 16	-1.25	0.388	-1.84	0.454	-1.71	0.129	-1.02	0.893	-1.46
1457203_at	---	Transcribed locus	-1.39	0.678	-1.79	0.174	-1.54	0.088	-1.27	0.768	-1.5
1446007_at	Bmp1	Bone morphogenetic protein 1	-1.23	0.786	-1.2	0.438	-3.5	0.089	-1.79	0.448	-1.93
1444339_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630003P	-1.27	0.168	-1.49	0.234	-2.13	0.009	-1.06	0.855	-1.49
1452561_at	Lphn3	Latrophilin 3	-1.42	0.338	-1.19	0.791	-2.59	0.042	-1.87	0.156	-1.77
1450289_at	Foxd2	forkhead box D2	-1.81	0.617	-1.21	0.475	-1.82	0.31	-1.62	0.078	-1.61
1430083_at	2610307P16Rik	RIKEN cDNA 2610307P16 gene	-1.77	0.503	-1.44	0.492	-1.49	0.001	-1.18	0.789	-1.47
1430616_at	4930528A17Rik	RIKEN cDNA 4930528A17 gene	-1.49	0.043	-2.55	0.406	-1.16	0.728	-1.06	0.819	-1.57
1459829_x_at	BC031781	CDNA sequence BC031781	-1.74	0.209	-1.49	0.135	-1.46	0.116	-1.19	0.504	-1.47
1431670_at	Ndufc2	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	-2.5	0.171	-1.33	0.624	-1.29	0.625	-2.2	0.316	-1.83
1440537_at	Kcnv2	potassium channel, subfamily V, member 2	-3.01	0.003	-1.27	0.393	-1.24	0.386	-1.55	0.019	-1.77
1452730_at	1110033J19Rik	RIKEN cDNA 1110033J19 gene	-1.19	0.194	-2.65	0.003	-1.41	0.157	-1.83	0.138	-1.77
1447997_s_at	Timm8a2	translocase of inner mitochondrial membrane 8 homolog a2 (yeast)	-2.72	0.133	-1.26	0.73	-1.3	0.555	-1.23	0.762	-1.63
1436646_at	---	Transcribed locus	-1.36	0.224	-3.75	0.103	-1.08	0.803	-1.33	0.067	-1.88
1433303_at	4930483C01Rik	RIKEN cDNA 4930483C01 gene	-1.63	0.634	-3.05	0.253	-1.01	0.975	-1.15	0.643	-1.71
1459595_at	AA516738	Expressed sequence AA516738	-1.31	0.142	-1.5	0.364	-2	0.041	-1.77	0.046	-1.64
1435201_at	0610009B10Rik	RIKEN cDNA 0610009B10 gene	-1.01	0.915	-5.12	0.134	-1.34	0.596	-1.51	0.568	-2.25
1436406_at	A930007I19Rik	RIKEN cDNA A930007I19 gene	-2.11	0.249	-1.3	0.042	-1.46	0.298	-1.37	0.34	-1.56
1457334_at	C130057M05Rik	RIKEN cDNA C130057M05 gene	-1.29	0.044	-1.86	0.114	-1.61	0.047	-1.07	0.804	-1.46
1441242_at	Dpp4	Dipeptidylpeptidase 4	-1.44	0.173	-1.48	0.149	-1.77	0.061	-2.72	0.058	-1.85
1420086_x_at	Fgf4	fibroblast growth factor 4	-2.39	0.302	-1.09	0.822	-1.67	0.232	-1.48	0.294	-1.66
1442752_at	Opcml	Opioid binding protein/cell adhesion molecule-like	-1.56	0.283	-2.09	0.259	-1.23	0.753	-1.06	0.886	-1.49
1458743_at	---	---	-1.02	0.97	-1.67	0.39	-2.86	0.128	-1.48	0.571	-1.75
1446187_at	4831416G18Rik	RIKEN cDNA 4831416G18 gene	-2.92	0.011	-1.29	0.42	-1.22	0.658	-1.31	0.557	-1.69
1440954_at	Pbx1	Pre B-cell leukemia transcription factor 1	-1.43	0.107	-1.26	0.157	-2.26	0.001	-1.12	0.524	-1.52
1459689_at	Gpd2	Glycerol phosphate dehydrogenase 2, mitochondrial	-1.76	0.131	-1.57	0.134	-1.37	0.065	-1.63	0.198	-1.58
1437307_at	Senp8	SUMO/sentrin specific peptidase 8	-1.15	0.205	-2.71	0.396	-1.43	0.161	-1.19	0.305	-1.62
1443151_at	Synj2bp	Synaptojanin 2 binding protein	-1.41	0.027	-1.51	0.075	-1.77	0.027	-1.72	0.122	-1.6
1420195_at	---	---	-1.66	0.316	-1.94	0.138	-1.22	0.541	-1.11	0.556	-1.48
1444185_at	Stim2	Stromal interaction molecule 2	-1.28	0.121	-1.68	0.16	-1.79	0.009	-1.63	0.132	-1.6
1440643_at	---	---	-1.18	0.418	-2.22	0.344	-1.57	0.157	-1.32	0.502	-1.57
1459157_at	Stox2	Storkhead box 2	-1.35	0.358	-1.7	0.11	-1.64	0.494	-1.14	0.601	-1.46
1441325_at	Nkrf	NF-kappaB repressing factor	-1.28	0.055	-1.31	0.532	-2.55	0.113	-1.2	0.55	-1.59
1444939_at	---	---	-1.45	0.291	-1.29	0.694	-2.13	0.044	-2.29	0.258	-1.79
1443129_at	---	---	-1.74	0.431	-1.53	0.251	-1.42	0.188	-1.22	0.595	-1.48
1454115_at	4930572J10Rik	RIKEN cDNA 4930572J10 gene	-1.13	0.816	-1.93	0.319	-1.87	0.081	-1.45	0.321	-1.6
1453143_at	4921509F24Rik	RIKEN cDNA 4921509F24 gene	-3.28	0.158	-1.33	0.689	-1.14	0.607	-1.34	0.478	-1.77
1436035_at	3830431G21Rik	RIKEN cDNA 3830431G21 gene	-1.28	0.047	-1.91	0.268	-1.59	0.02	-1.29	0.637	-1.52
1435775_at	Clock	circadian locomoter output cycles kaput	-1.32	0.123	-1.66	0.031	-1.74	0.151	-1.01	0.975	-1.43
1429977_at	9030425L15Rik	RIKEN cDNA 9030425L15 gene	-1.28	0.124	-1.25	0.363	-2.81	0.007	-1.23	0.492	-1.64
1443302_at	6720403M19Rik	RIKEN cDNA 6720403M19 gene	-1.75	0.043	-1.26	0.293	-1.76	0.109	-1.6	0.041	-1.59
1444684_at	8030475D13Rik	RIKEN cDNA 8030475D13 gene	-1.36	0.498	-1.67	0.16	-1.66	0.461	-1.24	0.603	-1.48
1459809_x_at	1700063D05Rik	RIKEN cDNA 1700063D05 gene	-1.76	0.454	-1.05	0.888	-2.38	0.1	-1.37	0.664	-1.64
1439681_at	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	-1.8	0.462	-1.49	0.427	-1.4	0.484	-3.04	0.067	-1.93
1433247_at	C530007A02Rik	RIKEN cDNA C530007A02 gene	-1.51	0.647	-2.03	0.164	-1.28	0.689	-1.28	0.768	-1.52
1424798_a_at	Adam5	a disintegrin and metallopeptidase domain 5	-1.1	0.832	-1.78	0.075	-2.13	0.034	-1.05	0.912	-1.51
1446545_at	Spnb2	Spectrin beta 2	-1.57	0.331	-1.36	0.213	-1.75	0.181	-1.06	0.92	-1.44
1440023_at	Pcdh12	protocadherin 12	-1.36	0.524	-1.44	0.158	-1.97	0.327	-1.37	0.528	-1.53
1446947_at	---	---	-1.57	0.431	-1.23	0.676	-2.03	0.085	-1.18	0.801	-1.5
1445893_at	Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-2.13	0.018	-1.58	0.314	-1.19	0.455	-1.32	0.541	-1.55
1433317_at	4930477O15Rik	RIKEN cDNA 4930477O15 gene	-3	0.002	-1.35	0.553	-1.16	0.738	-1.07	0.935	-1.64

1439640_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13004	-1.58	0.099	-1.46	0.223	-1.6	0.145	-1.19	0.508	-1.46
1442180_at	Dleu7	deleted in lymphocytic leukemia, 7	-1.32	0.288	-2.04	0.073	-1.44	0.281	-1.46	0.137	-1.57
1432744_at	4930443G03Rik	RIKEN cDNA 4930443G03 gene	-4.41	0.379	-1.38	0.569	-1.01	0.977	-1.94	0.36	-2.18
1420701_at	Klk1b1	kallikrein 1-related peptidase b1	-1.5	0.644	-1.48	0.119	-1.66	0.152	-1.11	0.531	-1.44
1430243_at	1700058C01Rik	RIKEN cDNA 1700058C01 gene	-1.71	0.145	-1.54	0.351	-1.41	0.525	-1.36	0.591	-1.5
1441562_at	A230048O21Rik	RIKEN cDNA A230048O21 gene	-1.23	0.151	-2.3	0.193	-1.44	0.469	-1.26	0.61	-1.56
1429894_a_at	Mtap7	microtubule-associated protein 7	-1.14	0.73	-2.98	0.213	-1.37	0.471	-1.23	0.749	-1.68
1449428_at	Cldn18	claudin 18	-2.65	0.165	-1	0.992	-1.76	0.065	-1.82	0.442	-1.81
1440107_at	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.25	0.099	-1.55	0.018	-2.01	0.009	-1.63	0.032	-1.61
1430380_at	Hemk2	HemK methyltransferase family member 2	-1.15	0.749	-1.58	0.457	-2.27	0.011	-2.1	0.113	-1.77
1447697_at	Ccdc40	Coiled-coil domain containing 40	-1.32	0.373	-1.59	0.516	-1.79	0.066	-1.2	0.713	-1.47
1439354_at	LOC668373 /// LOC	region containing RIKEN cDNA 2310008H09 gene; RIKEN cDNA A230094G09 g	-1.73	0.291	-2.31	0.222	-1.07	0.896	-1.04	0.872	-1.54
1440598_at	Sntg1	syntrophin, gamma 1	-1.1	0.769	-1.73	0.538	-2.19	0.269	-1.63	0.329	-1.66
1442829_at	Rin2	Ras and Rab interactor 2	-1.72	0.202	-1.93	0.305	-1.18	0.216	-1.02	0.857	-1.46
1442863_at	Cacna2d4	calcium channel, voltage-dependent, alpha 2/delta subunit 4	-1.71	0.505	-1.42	0.361	-1.53	0.396	-1.23	0.725	-1.47
1435730_at	D930026N18Rik	RIKEN cDNA D930026N18 gene	-1.94	0.028	-1.19	0.431	-1.7	0.134	-1.41	0.362	-1.56
1446223_at	Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltrans	-1.57	0.231	-1.64	0.283	-1.43	0.299	-1.19	0.215	-1.46
1419776_at	---	---	-1.24	0.216	-2.36	0.214	-1.39	0.536	-1.52	0.573	-1.63
1433245_at	6720475M21Rik	RIKEN cDNA 6720475M21 gene	-1.94	0.12	-1.22	0.311	-1.62	0.167	-1.45	0.028	-1.56
1441051_at	Trim27	tripartite motif protein 27	-2	0.163	-1.6	0.153	-1.22	0.26	-1.32	0.221	-1.53
1433092_at	3110062G12Rik	RIKEN cDNA 3110062G12 gene	-3.11	0.095	-1.17	0.79	-1.29	0.722	-1.39	0.522	-1.74
1457366_at	Cdc40	cell division cycle 40 homolog (yeast)	-1.58	0.204	-1.44	0.07	-1.61	0.005	-1.43	0.139	-1.51
1439943_at	Vps54	vacuolar protein sorting 54 (yeast)	-1.29	0.446	-1.82	0.248	-1.6	0.008	-1.61	0.062	-1.58
1446221_at	Eln	Elastin	-2.36	0.509	-1.06	0.9	-1.72	0.4	-1.15	0.8	-1.57
1439355_at	Plekha5	Pleckstrin homology domain containing, family A member 5	-1.61	0.031	-1.2	0.092	-2.01	0.009	-1.08	0.699	-1.48
1446335_at	BC013481	CDNA sequence BC013481	-1.86	0.089	-1.61	0.207	-1.26	0.081	-1.04	0.558	-1.44
1444810_at	Acaca	Acetyl-Coenzyme A carboxylase alpha	-1.8	0.154	-1.18	0.416	-1.81	0	-1.06	0.527	-1.47
1450838_x_at	Rpl37 /// LOC3834	ribosomal protein L37 /// similar to ribosomal protein L37	-1.49	0.191	-1.98	0.026	-1.29	0.063	-1.07	0.699	-1.46
1440306_at	Nr3c2	Nuclear receptor subfamily 3, group C, member 2	-2.12	0.47	-1.35	0.496	-1.35	0.66	-1.83	0.517	-1.66
1444212_at	Hip2	Huntingtin interacting protein 2	-1.32	0.684	-2.06	0.128	-1.42	0.023	-1.62	0.027	-1.6
1441506_at	Dcn	decorin	-1.83	0.197	-1.26	0.179	-1.64	0.294	-1.08	0.875	-1.45
1447139_at	Bcl7c	B-cell CLL/lymphoma 7C	-1.14	0.501	-1.89	0.128	-1.83	0.063	-1.02	0.965	-1.47
1430357_at	H3f3b	H3 histone, family 3B	-1.89	0.422	-1.13	0.792	-1.87	0.185	-1.38	0.518	-1.57
1432757_at	2900011L18Rik	RIKEN cDNA 2900011L18 gene	-1.13	0.413	-1.61	0.007	-2.26	0.001	-1.3	0.429	-1.57
1457453_at	1700057G04Rik	RIKEN cDNA 1700057G04 gene	-1.64	0.013	-1.59	0.152	-1.41	0.364	-1.45	0.307	-1.52
1446249_at	Antxr2	Anthrax toxin receptor 2	-1.57	0.643	-2.08	0.337	-1.2	0.665	-1.15	0.601	-1.5
1460268_at	---	---	-1.66	0.081	-1.27	0.389	-1.78	0.189	-1.82	0.153	-1.63
1459632_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	-1.14	0.206	-1.69	0.121	-2.07	0.013	-1.28	0.378	-1.54
1454236_a_at	C030004A17Rik	RIKEN cDNA C030004A17 gene	-1.48	0.214	-1.47	0.07	-1.67	0.019	-1.73	0.145	-1.59
1428349_s_at	Ebf3	early B-cell factor 3	-3.66	0.001	-1.3	0.635	-1.1	0.843	-1.85	0.457	-1.98
1417607_at	Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	-1.84	0.044	-2.15	0.075	-1.06	0.811	-1.47	0.078	-1.63
1419304_at	T	brachyury	-2.07	0.306	-1.16	0.745	-1.64	0.313	-1.88	0.259	-1.69
1453233_s_at	Calr3	calreticulin 3	-1.74	0.508	-1.65	0.359	-1.29	0.534	-1.36	0.028	-1.51
1455785_at	---	Transcribed locus	-2.55	0	-1.34	0.479	-1.23	0.538	-1.61	0.276	-1.68
1444135_at	6332401O19Rik	RIKEN cDNA 6332401O19 gene	-1.27	0.261	-1.24	0.53	-2.77	0.135	-1.5	0.361	-1.69
1444313_at	Dym	Dymeclin	-2.7	0.178	-1.43	0.517	-1.13	0.737	-1.57	0.257	-1.71
1423019_at	Gja9	gap junction membrane channel protein alpha 9	-1.47	0.568	-2.4	0.172	-1.16	0.475	-1.28	0.699	-1.58
1418933_at	Slc1a6	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6	-1.11	0.804	-2.23	0.081	-1.64	0.145	-1.19	0.333	-1.54
1459194_at	2210408I21Rik	RIKEN cDNA 2210408I21 gene	-1.42	0.376	-1.77	0.09	-1.45	0.128	-1.09	0.798	-1.43
1437713_x_at	1500010J02Rik	RIKEN cDNA 1500010J02 gene	-1.45	0.592	-2.34	0.117	-1.19	0.676	-1.54	0.364	-1.63
1444869_at	Gphn	Gephyrin	-1.47	0.135	-1.56	0.054	-1.58	0.057	-1.04	0.837	-1.41
1438585_at	Syne2	synaptic nuclear envelope 2	-1.32	0.562	-2.59	0.192	-1.23	0.611	-1.17	0.626	-1.58
1440702_at	AU022297	expressed sequence AU022297	-1.7	0.049	-1.61	0.404	-1.33	0.387	-1.18	0.45	-1.46

1439941_at	---	---	-1.11	0.859	-1.5	0.561	-2.54	0.016	-1.01	0.987	-1.54
1423859_a_at	Ptgds	prostaglandin D2 synthase (brain)	-1.36	0.397	-3.35	0.056	-1.08	0.744	-1.23	0.283	-1.76
1440485_at	---	---	-1.68	0.384	-1.14	0.74	-2.06	0.12	-1.09	0.881	-1.49
1443321_at	Tmtc2	Transmembrane and tetratricopeptide repeat containing 2	-1.38	0.634	-1.71	0.11	-1.55	0.307	-1.79	0.374	-1.6
1433129_at	2900040J22Rik	RIKEN cDNA 2900040J22 gene	-2.05	0.14	-1.09	0.338	-1.8	0.433	-1.26	0.546	-1.55
1459515_at	2610037D02Rik	RIKEN cDNA 2610037D02 gene	-1.94	0.311	-1.48	0.534	-1.31	0.568	-1.41	0.527	-1.53
1447600_at	Tspan5	Tetraspanin 5	-1.27	0.362	-1.59	0.228	-1.85	0.144	-1.35	0.175	-1.51
1440290_at	LOC434089	hypothetical gene supported by AK039686	-1.24	0.66	-1.72	0.472	-1.74	0.369	-1.47	0.607	-1.55
1438114_x_at	Efs	Embryonal Fyn-associated substrate	-1.86	0.314	-1.92	0.29	-1.11	0.263	-1.04	0.844	-1.48
1433845_x_at	Dusp9	dual specificity phosphatase 9	-1.21	0.66	-1.69	0.421	-1.84	0.088	-1.92	0.118	-1.67
1459708_at	Ube4a	Ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	-3.02	0.204	-1.58	0.224	-1	0.957	-1.52	0.453	-1.78
1445080_at	Wwc1	WW, C2 and coiled-coil domain containing 1	-1.32	0.319	-1.78	0.189	-1.56	0.004	-1.95	0.21	-1.65
1458094_at	Zfp407	Zinc finger protein 407	-3.5	0.035	-1.01	0.962	-1.47	0.14	-1.16	0.259	-1.78
1457994_at	4930563J15Rik	RIKEN cDNA 4930563J15 gene	-1.41	0.086	-1.44	0.25	-1.8	0.119	-2.66	0.47	-1.83
1419642_at	Purb	purine rich element binding protein B	-1.6	0.282	-1.42	0.175	-1.59	0.213	-1.45	0.249	-1.51
1457022_at	Dmd	Dystrophin, muscular dystrophy	-2.54	0.412	-1.11	0.793	-1.51	0.105	-1.79	0.246	-1.73
1423608_at	Itm2a	integral membrane protein 2A	-1.69	0.037	-1.1	0.747	-2.17	0.004	-2.99	0.046	-1.99
1447991_at	Pcsk2	proprotein convertase subtilisin/kexin type 2	-2.05	0.508	-1.6	0.31	-1.18	0.811	-3.01	0.471	-1.96
1421524_at	Cfc1	cripto, FRL-1, cryptic family 1	-3.84	0.118	-1.24	0.666	-1.11	0.515	-1.2	0.585	-1.85
1422518_at	Cask	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-1.26	0.506	-1.59	0.046	-1.85	0.01	-1.14	0.598	-1.46
1446184_at	---	---	-3.67	0.121	-1.25	0.711	-1.12	0.802	-1.73	0.393	-1.94
1430625_at	Krtap3-2	keratin associated protein 3-2	-1.39	0.515	-1.59	0.654	-1.62	0.364	-3.28	0.007	-1.97
1440333_at	Mamdc4	MAM domain containing 4	-1.19	0.049	-1.87	0.052	-1.69	0.089	-1.5	0.163	-1.56
1457794_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	-1.5	0.104	-1.39	0.42	-1.73	0.005	-1.12	0.571	-1.44
1442422_at	Tmem55a	Transmembrane protein 55A	-1.27	0.175	-1.62	0.076	-1.8	0.006	-1.57	0.014	-1.56
1443093_at	Ajap1	Adherens junction associated protein 1	-2	0.401	-1.25	0.771	-1.5	0.237	-3.06	0.025	-1.95
1430042_at	A930012M21Rik	RIKEN cDNA A930012M21 gene	-1.18	0.28	-1.71	0.049	-1.87	0.014	-1.08	0.8	-1.46
1446806_at	---	---	-1.48	0.023	-3.4	0.293	-1	0.966	-1.44	0.284	-1.83
1459196_at	Dnmbp	Dynamin binding protein	-1.49	0.498	-1.66	0.124	-1.45	0.398	-2.91	0.095	-1.88
1446156_at	Dmd	Dystrophin, muscular dystrophy	-2.02	0.322	-1.71	0.315	-1.13	0.477	-2.72	0.034	-1.9
1435933_at	Scn2a1	sodium channel, voltage-gated, type II, alpha 1	-1.08	0.929	-1.78	0.36	-2.09	0.021	-1.27	0.671	-1.56
1443027_at	4930523C07Rik	RIKEN cDNA 4930523C07 gene	-1.36	0.49	-1.48	0.034	-1.79	0.019	-2.08	0.028	-1.68
1445395_at	Prkca	Protein kinase C, alpha	-1.22	0.206	-2	0.132	-1.55	0.165	-1.54	0.233	-1.58
1442340_x_at	Cyr61	cysteine rich protein 61	-1.51	0.302	-2.28	0.198	-1.15	0.67	-1.12	0.736	-1.52
1445355_at	Spata6	spermatogenesis associated 6	-2.05	0.061	-1.14	0.766	-1.65	0.279	-2	0.356	-1.71
1453124_at	Tnpo3	transportin 3	-2.14	0.453	-1.62	0.3	-1.14	0.831	-2.7	0.202	-1.9
1458113_at	9530019H20Rik	RIKEN cDNA 9530019H20 gene	-1.23	0.749	-1.73	0.238	-1.74	0.003	-1.35	0.494	-1.51
1458020_at	Reln	Reelin	-1.87	0.271	-1.91	0.087	-1.1	0.732	-2.92	0.221	-1.95
1457105_at	Pkd2l1	polycystic kidney disease 2-like 1	-1.25	0.591	-1.83	0.271	-1.61	0.223	-2.73	0.057	-1.86
1434722_at	Ampd1	adenosine monophosphate deaminase 1 (isoform M)	-1.13	0.786	-5.41	0.028	-1.11	0.771	-2.61	0.355	-2.57
1420070_a_at	Slc9a5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	-2.19	0.207	-1.88	0.28	-1.02	0.956	-1.5	0.545	-1.65
1445792_at	Ppme1	Protein phosphatase methylesterase 1	-1.74	0.59	-1.03	0.958	-2.34	0.114	-1.41	0.633	-1.63
1453798_at	Ccdc93	coiled-coil domain containing 93	-1.06	0.844	-2.81	0.326	-1.49	0.532	-1.62	0.37	-1.74
1420248_at	Tubg2	tubulin, gamma 2	-1.28	0.363	-1.84	0.251	-1.55	0.208	-1.25	0.375	-1.48
1443235_at	Eif2ak4	Eukaryotic translation initiation factor 2 alpha kinase 4	-1.77	0.196	-1.55	0.138	-1.32	0.117	-1.49	0.226	-1.53
1454482_at	5830474E16Rik	RIKEN cDNA 5830474E16 gene	-1.33	0.729	-2.26	0.241	-1.29	0.58	-3.19	0.215	-2.02
1437798_at	6720422M22Rik	RIKEN cDNA 6720422M22 gene	-1.17	0.465	-1.34	0.086	-2.7	0.04	-1.14	0.469	-1.59
1436683_at	1700011M02Rik	RIKEN cDNA 1700011M02 gene	-1.99	0.304	-1.22	0.692	-1.54	0.242	-1.19	0.837	-1.49
1437934_at	Tia1	cytotoxic granule-associated RNA binding protein 1	-1.47	0.04	-1.68	0.075	-1.43	0.014	-1.34	0.261	-1.48
1457505_at	Utrn	Utrophin	-1.38	0.587	-1.22	0.718	-2.32	0.013	-1.22	0.505	-1.54
1444622_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	-1.3	0.224	-2.08	0.021	-1.39	0.121	-4.71	0.023	-2.37
1425836_a_at	Limk1	LIM-domain containing, protein kinase	-1.73	0.603	-1.67	0.173	-1.26	0.646	-3.29	0.254	-1.99
1427470_s_at	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	-1.27	0.287	-1.46	0.514	-1.99	0.017	-1.32	0.306	-1.51

1442785_at	Smyd3	SET and MYND domain containing 3	-1.6	0.259	-1.27	0.19	-1.78	0.245	-2.87	0.025	-1.88
1457823_at	Cyr61	cysteine rich protein 61	-1.68	0.133	-2.17	0.138	-1.09	0.794	-1.18	0.722	-1.53
1447362_at	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	-3.31	0.167	-1.45	0.191	-1.02	0.919	-1.22	0.446	-1.75
1424162_at	Trim29	tripartite motif protein 29	-2.54	0.035	-1.51	0.256	-1.09	0.669	-1.98	0.22	-1.78
1459397_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	-2.01	0.208	-1.14	0.722	-1.66	0.238	-1.36	0.603	-1.54
1439933_at	B430316J06Rik	RIKEN cDNA B430316J06 gene	-1.62	0.208	-1.12	0.515	-2.14	0.011	-1.88	0.223	-1.69
1439311_at	B830012L14Rik	RIKEN cDNA B830012L14 gene	-1.31	0.728	-1.37	0.394	-2.09	0.02	-4.26	0.194	-2.26
1439362_at	---	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:95300	-1.11	0.646	-2.75	0.062	-1.41	0.438	-1.27	0.518	-1.63
1442388_at	2410137F16Rik	RIKEN cDNA 2410137F16 gene	-1.63	0.455	-2.26	0.171	-1.08	0.829	-1.51	0.555	-1.62
1432962_at	2610024D14Rik	RIKEN cDNA 2610024D14 gene	-1.59	0.348	-1.62	0.152	-1.37	0.239	-1.21	0.499	-1.45
1456910_at	---	Transcribed locus	-1.17	0.78	-2.88	0.115	-1.29	0.414	-1.45	0.61	-1.7
1430642_at	2900001G08Rik	RIKEN cDNA 2900001G08 gene	-1.48	0.072	-1.62	0.35	-1.46	0.291	-1.96	0.331	-1.63
1445460_at	---	Transcribed locus	-1.56	0.332	-1.86	0.127	-1.25	0.416	-1.12	0.378	-1.45
1435833_at	---	---	-2.43	0.448	-1.74	0.313	-1.01	0.988	-1.49	0.507	-1.67
1425409_at	Chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	-1.13	0.072	-3.15	0.238	-1.29	0.194	-1.5	0.126	-1.77
1456188_at	Svs2	seminal vesicle protein, secretion 2	-1.08	0.392	-2.69	0.216	-1.47	0.015	-1.37	0.295	-1.65
1435166_at	Cntn2	contactin 2	-1.37	0.18	-1.69	0.119	-1.53	0.304	-1.07	0.79	-1.41
1429342_s_at	2310021H06Rik	RIKEN cDNA 2310021H06 gene	-1.45	0.451	-1.8	0.33	-1.37	0.185	-4.05	0.003	-2.17
1420800_a_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	-2.74	0.073	-1.21	0.584	-1.27	0.563	-1.35	0.182	-1.64
1459588_at	Kit	Kit oncogene	-1.22	0.234	-1.89	0.412	-1.59	0.23	-1.05	0.756	-1.44
1439566_at	C030038J10Rik	RIKEN cDNA C030038J10 gene	-1.02	0.963	-2.18	0.108	-1.86	0.328	-1.23	0.568	-1.57
1457870_at	---	Transcribed locus	-1.1	0.822	-2.76	0.106	-1.41	0.519	-1.23	0.292	-1.63
1459412_at	Mfhas1	Malignant fibrous histiocytoma amplified sequence 1	-1.42	0.134	-1.8	0.061	-1.4	0.049	-1.01	0.97	-1.4
1458546_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	-1.41	0.374	-1.98	0.115	-1.31	0.34	-1.57	0.371	-1.57
1432612_at	9030405F24Rik	RIKEN cDNA 9030405F24 gene	-1.94	0.154	-1.32	0.522	-1.41	0.397	-1.3	0.56	-1.49
1444337_at	Numb	Numb gene homolog (Drosophila)	-1.4	0.227	-1.42	0.092	-1.77	0.015	-1.2	0.334	-1.45
1458588_at	Schip1	Schwannomin interacting protein 1	-1.33	0.067	-1.52	0.429	-1.75	0.039	-1.02	0.949	-1.41
1460117_at	---	---	-1.12	0.317	-1.49	0.175	-2.43	0.008	-1.14	0.356	-1.54
1431894_at	4833424O12Rik	RIKEN cDNA 4833424O12 gene	-1.18	0.423	-1.66	0.163	-1.89	0.085	-1.89	0.086	-1.65
1421766_at	Uchl4	ubiquitin carboxyl-terminal esterase L4	-1.17	0.797	-1.28	0.301	-2.91	0.18	-1.62	0.464	-1.74
1443536_at	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	-1.13	0.88	-3.2	0.021	-1.28	0.489	-1.62	0.208	-1.81
1447193_at	---	---	-1.79	0.286	-1.27	0.584	-1.57	0.033	-1.17	0.453	-1.45
1446946_at	Tgfbr1	Transforming growth factor, beta receptor I	-1.1	0.679	-1.56	0.167	-2.3	0.022	-1.28	0.136	-1.56
1444070_at	---	---	-1.28	0.51	-1.57	0.229	-1.78	0.188	-1.49	0.394	-1.53
1443588_at	---	Transcribed locus	-1.31	0.391	-1.36	0.369	-2.07	0.065	-1.8	0.331	-1.64
1433411_at	---	---	-1.6	0.216	-1.13	0.791	-2.12	0.221	-1.31	0.786	-1.54
1438464_at	Arid4a	AT rich interactive domain 4A (Rbp1 like)	-1.68	0.352	-1.22	0.559	-1.76	0.199	-1.3	0.083	-1.49
1445024_at	Stard7	START domain containing 7	-1.66	0.027	-1.44	0.388	-1.46	0.041	-1.44	0.368	-1.5
1428991_at	Hrasls	HRAS-like suppressor	-1.23	0.392	-2.38	0.05	-1.33	0.296	-1.3	0.523	-1.56
1431981_at	Hif1a	hypoxia inducible factor 1, alpha subunit	-1.53	0.339	-1.78	0.463	-1.3	0.438	-1.05	0.843	-1.41
1443607_at	---	---	-1.76	0.487	-2.13	0.348	-1.06	0.865	-1.06	0.873	-1.5
1446484_at	Mef2c	Myocyte enhancer factor 2C	-1.44	0.176	-1.86	0.205	-1.33	0.399	-2.34	0.085	-1.74
1459947_at	Bmp6	Bone morphogenetic protein 6	-1.38	0.199	-1.4	0.144	-1.83	0.027	-1.01	0.929	-1.41
1459784_x_at	1300002A08Rik	RIKEN cDNA 1300002A08 gene	-1.68	0.042	-2	0.011	-1.12	0.74	-2.11	0.058	-1.73
1421094_at	Zbtb33	zinc finger and BTB domain containing 33	-1.77	0.419	-2.08	0.054	-1.06	0.918	-1.08	0.901	-1.5
1459605_at	Apba1	amyloid beta (A4) precursor protein binding, family A, member 1	-1.19	0.851	-2.27	0.165	-1.42	0.299	-1.03	0.955	-1.48
1456400_at	Terf2ip	telomeric repeat binding factor 2, interacting protein	-2.36	0.473	-1.01	0.982	-1.75	0.402	-4.67	0.209	-2.45
1459442_at	Gnb1	Guanine nucleotide binding protein, beta 1	-1.06	0.658	-1.48	0.41	-2.69	0.005	-1.23	0.374	-1.62
1445171_at	1700067C01Rik ///	RIKEN cDNA 1700067C01 gene /// RIKEN cDNA A230107C01 gene	-1.22	0.615	-1.46	0.501	-2.07	0.127	-1.52	0.31	-1.57
1419215_at	Aox4	aldehyde oxidase 4	-1.28	0.621	-1.68	0.387	-1.63	0.455	-1.1	0.846	-1.42
1453236_at	1700054F22Rik	RIKEN cDNA 1700054F22 gene	-2.06	0.485	-1.47	0.431	-1.22	0.635	-2.58	0.317	-1.83
1457169_at	Ppp1r12b	Protein phosphatase 1, regulatory (inhibitor) subunit 12B	-1.09	0.821	-2.06	0.065	-1.72	0.174	-1.38	0.39	-1.56
1443535_at	Rabgap1	RAB GTPase activating protein 1	-1.27	0.149	-1.46	0.149	-1.94	0.012	-1.32	0.059	-1.5

1439056_at	LOC636791	hypothetical protein LOC636791	-1.61	0.628	-2.42	0.115	-1.05	0.818	-1.09	0.822	-1.54
1458029_at	---	---	-1.19	0.679	-3.59	0.006	-1.15	0.806	-2.08	0.316	-2
1458003_at	Zfp398	zinc finger protein 398	-1.61	0.492	-2.26	0.044	-1.08	0.679	-1.42	0.286	-1.59
1450810_at	Fshr	follicle stimulating hormone receptor	-1.92	0.207	-1.21	0.657	-1.56	0.157	-1.16	0.756	-1.46
1421745_at	Plag1	pleiomorphic adenoma gene 1	-1.1	0.823	-3.94	0.037	-1.21	0.74	-1.11	0.768	-1.84
1458093_at	Mtrr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	-1.35	0.631	-1.54	0.244	-1.68	0.326	-2.23	0.28	-1.7
1450215_at	Rcvrn	recoverin	-1.62	0.421	-1.53	0.625	-1.39	0.276	-1.36	0.519	-1.48
1444693_at	Cacnb2	Calcium channel, voltage-dependent, beta 2 subunit	-1.37	0.276	-1.13	0.762	-2.71	0.004	-1.05	0.82	-1.56
1453626_at	3930402G23Rik	RIKEN cDNA 3930402G23 gene	-4.04	0.001	-1.3	0.233	-1.03	0.871	-1.22	0.478	-1.9
1460060_at	---	---	-1.64	0.288	-1.31	0.657	-1.63	0.326	-1.68	0.378	-1.56
1440848_at	1110028C15Rik	RIKEN cDNA 1110028C15 gene	-1.34	0.519	-1.54	0.298	-1.69	0.031	-1.48	0.038	-1.51
1443961_at	LOC627488 /// LOC	similar to THO complex subunit 4 (Tho4) (RNA and export factor binding protein 1	-1.34	0.462	-1.57	0.2	-1.65	0.145	-1.1	0.798	-1.42
1444381_at	A830005F24Rik	RIKEN cDNA A830005F24 gene	-2.2	0.171	-1.02	0.97	-1.81	0.128	-1.48	0.198	-1.63
1420155_at	AA408954	expressed sequence AA408954	-1.39	0.541	-1.41	0.6	-1.77	0.28	-1.48	0.552	-1.51
1457353_at	Tomm70a	Translocase of outer mitochondrial membrane 70 homolog A (yeast)	-1.63	0.242	-1.48	0.271	-1.42	0.536	-1.69	0.07	-1.56
1447296_at	Fbxo27	F-box protein 27	-1.61	0.217	-1.43	0.207	-1.5	0.502	-1.46	0.162	-1.5
1427744_at	Ccnb3	cyclin B3	-1.08	0.832	-2.3	0.237	-1.58	0.608	-1.01	0.978	-1.49
1457809_at	Pcaf /// LOC330129	p300/CBP-associated factor /// similar to p300/CBP-associated factor	-1.57	0.064	-1.28	0.296	-1.75	0.011	-1.62	0.011	-1.55
1436408_at	Rprml	reprimo-like	-1.67	0.211	-1.41	0.715	-1.46	0.039	-1.07	0.918	-1.4
1456979_at	Zhx3	Zinc fingers and homeoboxes 3	-1.24	0.246	-1.58	0.016	-1.8	0.032	-1.3	0.16	-1.48
1440528_at	---	Transcribed locus	-1.21	0.791	-2.02	0.218	-1.49	0.253	-1.65	0.416	-1.59
1432587_at	5730596P11Rik	RIKEN cDNA 5730596P11 gene	-1.1	0.666	-2.02	0.083	-1.69	0.195	-1.48	0.451	-1.57
1421752_a_at	Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	-1.39	0.741	-2.01	0.29	-1.29	0.343	-1.09	0.751	-1.44
1436267_a_at	Frap1	FK506 binding protein 12-rapamycin associated protein 1	-1.3	0.308	-1.68	0.046	-1.58	0.099	-1.13	0.649	-1.42
1425920_at	Cuedc1	CUE domain containing 1	-1.45	0.254	-2.78	0.063	-1.06	0.732	-1.18	0.373	-1.62
1442447_at	---	---	-1.26	0.135	-1.84	0.119	-1.52	0.19	-1.05	0.302	-1.42
1447705_at	4833432M17Rik	RIKEN cDNA 4833432M17 gene	-2.22	0.056	-1.44	0.015	-1.18	0.666	-1.56	0.158	-1.6
1438470_at	Socs2	suppressor of cytokine signaling 2	-1.07	0.808	-2.39	0.017	-1.54	0.06	-1.44	0.258	-1.61
1458578_at	Rbms1	RNA binding motif, single stranded interacting protein 1	-1.31	0.242	-1.26	0.313	-2.26	0.009	-1.31	0.021	-1.53
1432971_at	4921518B13Rik	RIKEN cDNA 4921518B13 gene	-2.03	0.117	-1.27	0.614	-1.4	0.092	-1.02	0.922	-1.43
1448459_at	Kcnip1	Kv channel-interacting protein 1	-1.57	0.518	-2.67	0.026	-1.01	0.967	-4.31	0.029	-2.39
1432118_at	2410012E07Rik	RIKEN cDNA 2410012E07 gene	-1.13	0.724	-2.98	0.049	-1.29	0.36	-1.11	0.461	-1.63
1431148_at	---	---	-1.85	0.121	-1.47	0.114	-1.28	0.637	-1.15	0.759	-1.44
1435354_at	Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	-1.01	0.925	-2.7	0.132	-1.57	0.017	-1.24	0.711	-1.63
1425945_at	4933426I21Rik	RIKEN cDNA 4933426I21 gene	-3.91	0.371	-1.24	0.682	-1.07	0.881	-2	0.455	-2.05
1441665_at	Iars2	isoleucine-tRNA synthetase 2, mitochondrial	-1.82	0.153	-1.08	0.906	-1.92	0.106	-1.07	0.905	-1.47
1448097_at	Ube3c	Ubiquitin protein ligase E3C	-1	0.988	-2.78	0.089	-1.56	0.449	-2.57	0.404	-1.98
1419982_s_at	---	---	-1.89	0.097	-1.77	0.179	-1.1	0.501	-1.85	0.269	-1.65
1433091_at	6430514K02Rik	RIKEN cDNA 6430514K02 gene	-1.39	0.413	-1.84	0.171	-1.36	0.577	-1.01	0.972	-1.4
1438186_at	Pdlim5	PDZ and LIM domain 5	-1.16	0.762	-1.66	0.19	-1.87	0.309	-1.67	0.328	-1.59
1421776_at	Olfr74	olfactory receptor 74	-1.29	0.606	-1.46	0.405	-1.86	0.356	-1.17	0.782	-1.44
1440599_at	Olfr658	olfactory receptor 658	-1.09	0.922	-1.5	0.471	-2.43	0.201	-2.74	0.095	-1.94
1437785_at	Adamts9	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.38	0.287	-1.53	0.034	-1.61	0.022	-1.38	0.247	-1.47
1448421_s_at	Aspn	asporin	-1.71	0.441	-1.39	0.661	-1.44	0.188	-1.04	0.914	-1.39
1432530_s_at	Boll	bol, boule-like (Drosophila)	-1.75	0.211	-1.1	0.886	-1.92	0.04	-1.14	0.777	-1.48
1447765_at	Wdr48	WD repeat domain 48	-1.99	0.274	-1.34	0.627	-1.33	0.246	-1.78	0.495	-1.61
1445934_at	Arih2 /// LOC43256	ariadne homolog 2 (Drosophila) /// similar to ariadne homolog 2	-1.57	0.115	-1.35	0.183	-1.6	0.112	-1.05	0.824	-1.39
1447706_at	---	---	-1.41	0.441	-1.55	0.03	-1.54	0.313	-1.59	0.32	-1.52
1445773_at	Meis1	Myeloid ecotropic viral integration site 1	-1.12	0.836	-1.5	0.123	-2.26	0.01	-1.19	0.17	-1.52
1444500_at	Ahsa1	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)	-1.66	0.018	-1.73	0.033	-1.22	0.188	-1.12	0.582	-1.43
1445807_at	Prkg1	Protein kinase, cGMP-dependent, type I	-1.58	0.514	-1.38	0.42	-1.55	0.056	-1.06	0.871	-1.39
1454111_at	4930404A10Rik	RIKEN cDNA 4930404A10 gene	-1.75	0.524	-1.24	0.625	-1.6	0.184	-1.62	0.393	-1.55
1447103_at	Cdk5rap2	CDK5 regulatory subunit associated protein 2	-1.04	0.959	-3.79	0.149	-1.28	0.676	-1.1	0.892	-1.8

1458346_x_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	-1.58	0.242	-1.23	0.357	-1.8	0.177	-2.45	0.09	-1.76
1436474_at	Mrcl	mannose receptor-like precursor	-1.48	0.146	-1.43	0.204	-1.58	0.404	-1.38	0.442	-1.47
1427871_at	Ptafr	platelet-activating factor receptor	-1.79	0.444	-1.59	0.568	-1.22	0.766	-1.56	0.483	-1.54
1440126_at	BC037704	cDNA sequence BC037704	-1.72	0.378	-1.54	0.379	-1.28	0.551	-1.56	0.327	-1.53
1417355_at	Peg3	paternally expressed 3	-1.25	0.558	-1.22	0.512	-2.58	0.006	-2.35	0.126	-1.85
1459644_at	AU020772	expressed sequence AU020772	-1.23	0.294	-1.86	0.148	-1.53	0.363	-1.03	0.848	-1.41
1437531_at	Trpm1	transient receptor potential cation channel, subfamily M, member 1	-1.07	0.823	-1.88	0.127	-1.84	0.26	-1.8	0.296	-1.65
1436613_at	Coro6	Coronin, actin binding protein 6	-2.78	0.028	-1.19	0.768	-1.24	0.608	-2.17	0.528	-1.84
1437599_at	Chchd3	Coiled-coil-helix-coiled-coil-helix domain containing 3	-1.41	0.056	-1.38	0.127	-1.74	0.012	-1.13	0.421	-1.41
1450559_at	5730559C18Rik	RIKEN cDNA 5730559C18 gene	-1.72	0.107	-1.46	0.432	-1.35	0.405	-3.22	0.105	-1.94
1421319_at	Ptgfrn	prostaglandin F2 receptor negative regulator	-2.28	0.108	-1.72	0.108	-1.01	0.958	-1.72	0.147	-1.68
1442399_at	Xrn1	5'-3' exoribonuclease 1	-1.13	0.443	-1.58	0.162	-2.03	0.08	-1.03	0.857	-1.44
1445433_at	Glt8d2	glycosyltransferase 8 domain containing 2	-3.48	0.085	-1.06	0.919	-1.29	0.268	-1.07	0.925	-1.72
1439310_at	A630012P03Rik	RIKEN cDNA A630012P03 gene	-1.77	0.451	-1.23	0.601	-1.58	0.35	-1.53	0.569	-1.53
1431855_at	4930570E03Rik	RIKEN cDNA 4930570E03 gene	-1.14	0.825	-1.91	0.125	-1.63	0.273	-1.14	0.646	-1.46
1453012_at	Tsc22d2	TSC22 domain family 2	-1.43	0.403	-1.47	0.284	-1.59	0.049	-1.14	0.414	-1.41
1421190_at	Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	-1.32	0.487	-1.26	0.602	-2.19	0.203	-1.46	0.316	-1.56
1435592_at	Eif5b	eukaryotic translation initiation factor 5B	-1.48	0.127	-1.29	0.44	-1.79	0.068	-1.17	0.516	-1.43
1442491_at	Dpp10	Dipeptidylpeptidase 10	-1.66	0.232	-1.74	0.166	-1.2	0.681	-2.59	0.074	-1.8
1432293_at	4930579G18Rik	RIKEN cDNA 4930579G18 gene	-1.77	0.305	-1.5	0.329	-1.28	0.637	-1.03	0.954	-1.4
1433121_at	5830490A04Rik	RIKEN cDNA 5830490A04 gene	-1.16	0.745	-1.71	0.462	-1.76	0.258	-1.33	0.691	-1.49
1451801_at	Trdn	triadin	-1.65	0.028	-2.05	0.438	-1.09	0.8	-1.44	0.745	-1.56
1440201_at	Mapk10	mitogen activated protein kinase 10	-1.22	0.019	-2.41	0.014	-1.29	0.4	-1.38	0.367	-1.57
1448606_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-1.36	0.257	-1.64	0.013	-1.5	0.109	-1.47	0.174	-1.49
1454370_at	4930557B21Rik	RIKEN cDNA 4930557B21 gene	-1.6	0.553	-1.72	0.404	-1.24	0.681	-2.52	0.15	-1.77
1436309_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	-2.06	0.356	-1.41	0.52	-1.22	0.446	-1.33	0.479	-1.51
1446174_at	LOC245440	similar to melanoma antigen family A, 10	-1.61	0.324	-2.33	0.13	-1.04	0.947	-1.17	0.837	-1.54
1458000_at	Dsg1a	desmoglein 1 alpha	-1.85	0.364	-1.63	0.356	-1.16	0.717	-1.95	0.318	-1.65
1445850_at	9530009M10Rik	RIKEN cDNA 9530009M10 gene	-1.31	0.481	-1.23	0.559	-2.27	0.015	-1.33	0.292	-1.54
1436138_at	---	---	-1.48	0.182	-1.47	0.233	-1.52	0.117	-1.22	0.557	-1.42
1440116_at	D630045J12Rik	RIKEN cDNA D630045J12 gene	-1.13	0.203	-2.62	0.221	-1.34	0.338	-1.2	0.685	-1.57
1445966_at	Igf2r	Insulin-like growth factor 2 receptor	-1.29	0.105	-1.26	0.417	-2.25	0	-1.07	0.638	-1.47
1444857_at	C87312	expressed sequence C87312	-1.03	0.751	-1.45	0.549	-2.87	0.133	-1.54	0.374	-1.72
1425476_at	Col4a5	procollagen, type IV, alpha 5	-1.37	0.163	-1.96	0.044	-1.29	0.353	-1.18	0.479	-1.45
1446025_at	AI462493	Expressed sequence AI462493	-2.3	0.197	-1.12	0.758	-1.45	0.277	-1.04	0.91	-1.48
1432938_at	5430439C14Rik	RIKEN cDNA 5430439C14 gene	-2.35	0.479	-1.03	0.966	-1.61	0.299	-4.79	0.153	-2.45
1457410_at	Arhgap5	Rho GTPase activating protein 5	-1.41	0.005	-1.32	0.429	-1.83	0.016	-1.74	0.007	-1.57
1441874_x_at	Prlpe	prolactin-like protein E	-5.5	0.004	-1.12	0.78	-1.06	0.895	-1.8	0.453	-2.37
1432582_at	3110054G05Rik	RIKEN cDNA 3110054G05 gene	-1.15	0.759	-1.36	0.669	-2.4	0.037	-1.11	0.86	-1.51
1441798_at	---	---	-1.26	0.782	-2.94	0.184	-1.13	0.661	-3.1	0.224	-2.11
1446581_at	Pcdh11x	Protocadherin 11 X-linked	-1.91	0.378	-1.15	0.254	-1.6	0.525	-3.08	0.324	-1.94
1423400_at	Kl	klotho	-1.57	0.091	-1.3	0.387	-1.62	0.147	-1.21	0.763	-1.43
1421691_at	Krtap16-7	keratin associated protein 16-7	-1.48	0.408	-1.3	0.673	-1.73	0.241	-2.47	0.201	-1.75
1454496_at	5031415H12Rik	RIKEN cDNA 5031415H12 gene	-2.26	0.017	-1.25	0.289	-1.29	0.598	-1.2	0.758	-1.5
1422305_at	Ifnb1	interferon beta 1, fibroblast	-1.5	0.143	-1.93	0.444	-1.19	0.705	-1.11	0.681	-1.44
1439250_at	Slitrk3	SLIT and NTRK-like family, member 3	-1.75	0.029	-1.07	0.762	-1.94	0.463	-1.61	0.474	-1.59
1424633_at	Camk1g	calcium/calmodulin-dependent protein kinase I gamma	-1.49	0.438	-1.64	0.071	-1.35	0.505	-1.44	0.573	-1.48
1460064_at	BC028789	cDNA sequence BC028789	-3.01	0.082	-1.19	0.454	-1.18	0.798	-1.18	0.678	-1.64
1429836_at	Ugcgl2	UDP-glucose ceramide glucosyltransferase-like 2	-1.26	0.345	-1.51	0.189	-1.76	0.053	-1.97	0.147	-1.63
1436459_at	Gpr161	G protein-coupled receptor 161	-1.11	0.831	-1.95	0.202	-1.63	0.338	-2.03	0.503	-1.68
1447712_x_at	Ep400	E1A binding protein p400	-1.58	0.224	-1.47	0.48	-1.4	0.09	-1.26	0.439	-1.43
1422378_at	V1rb7	vomeronasal 1 receptor, B7	-1.14	0.853	-2.7	0.034	-1.29	0.662	-1.36	0.684	-1.62
1443430_at	Cradd	CASP2 and RIPK1 domain containing adaptor with death domain	-1.34	0.021	-1.42	0.025	-1.73	0.031	-1.21	0.512	-1.43

1441748_at	Zzz3	Zinc finger, ZZ domain containing 3	-1.57	0.234	-1.45	0.283	-1.43	0.23	-1.19	0.07	-1.41
1430267_at	4833422M21Rik	RIKEN cDNA 4833422M21 gene	-2.19	0.224	-1.08	0.825	-1.55	0.481	-3.38	0.013	-2.05
1416039_x_at	Cyr61	cysteine rich protein 61	-1.29	0.492	-1.57	0.085	-1.63	0.281	-1.42	0.329	-1.48
1450490_at	Kcna7	potassium voltage-gated channel, shaker-related subfamily, member 7	-1.39	0.674	-2.42	0.148	-1.12	0.787	-2.45	0.046	-1.85
1441634_at	Ntng1	netrin G1	-1.55	0.173	-2	0.248	-1.14	0.809	-1.02	0.976	-1.43
1453938_at	9330198N18Rik	RIKEN cDNA 9330198N18 gene	-1.48	0.135	-1.44	0.621	-1.52	0.3	-1.04	0.781	-1.37
1446118_at	D17Ertd165e	DNA segment, Chr 17, ERATO Doi 165, expressed	-1.04	0.675	-1.44	0.058	-2.69	0.01	-1.17	0.652	-1.59
1430673_a_at	2210009G21Rik	RIKEN cDNA 2210009G21 gene	-1.68	0.478	-1.85	0.196	-1.12	0.748	-1	0.997	-1.41
1429646_at	1700112C13Rik	RIKEN cDNA 1700112C13 gene	-2.07	0.317	-1.16	0.81	-1.46	0.239	-1.45	0.565	-1.54
1431613_a_at	1700024D23Rik	RIKEN cDNA 1700024D23 gene	-1.7	0.008	-2.24	0.369	-1.01	0.984	-2.15	0.19	-1.78
1450758_at	Cntnap2	contactin associated protein-like 2	-1.43	0.604	-1.95	0.439	-1.23	0.21	-1.18	0.719	-1.45
1445151_at	---	---	-1.59	0.029	-1.76	0.19	-1.2	0.391	-1.46	0.14	-1.5
1423802_at	Camkv	CaM kinase-like vesicle-associated	-2.33	0.438	-1.03	0.869	-1.59	0.049	-1.83	0.519	-1.7
1453221_at	Gopc	golgi associated PDZ and coiled-coil motif containing	-1.55	0.1	-1.54	0.007	-1.36	0.106	-2.14	0.076	-1.65
1427618_at	Cdh9	cadherin 9	-1.25	0.799	-1.79	0.068	-1.49	0.475	-1.73	0.293	-1.57
1446723_at	---	---	-2.03	0.444	-1.24	0.338	-1.37	0.569	-2.31	0.363	-1.74
1420144_x_at	Mnab	membrane associated DNA binding protein	-1.04	0.972	-3.04	0.01	-1.35	0.557	-1.13	0.873	-1.64
1447523_at	Zfp294	Zinc finger protein 294	-1.5	0.311	-2.04	0.042	-1.15	0.651	-1.24	0.246	-1.48
1430471_at	9230110K08Rik	RIKEN cDNA 9230110K08 gene	-1.9	0.182	-1.76	0.327	-1.07	0.788	-1.02	0.945	-1.44
1443949_at	Ppp2r5e	Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-1.2	0.347	-1.4	0.089	-2.07	0.004	-1.19	0.478	-1.46
1439536_at	AI846133	Expressed sequence AI846133	-1.22	0.102	-1.99	0.296	-1.41	0.103	-1.51	0.342	-1.53
1456644_at	5730528L13Rik	RIKEN cDNA 5730528L13 gene	-1.89	0.128	-1.37	0.662	-1.3	0.428	-1.17	0.805	-1.43
1457332_at	Prmt3	protein arginine N-methyltransferase 3	-1.74	0.208	-1.92	0.416	-1.07	0.587	-1.2	0.443	-1.48
1444826_at	---	---	-2.92	0.018	-1.12	0.543	-1.26	0.397	-1.16	0.562	-1.61
1427133_s_at	Lrp2	low density lipoprotein receptor-related protein 2	-1.12	0.196	-3.89	0.125	-1.13	0.534	-1.46	0.457	-1.9
1421800_at	Phxr1	per-hexamer repeat gene 1	-1.3	0.485	-1.82	0.063	-1.4	0.16	-1.19	0.009	-1.43
1440401_at	---	---	-1.99	0.592	-1.24	0.735	-1.38	0.527	-1.04	0.914	-1.41
1421598_at	---	---	-1.13	0.529	-2.34	0.058	-1.39	0.233	-2.2	0.089	-1.77
1451582_at	Tulp1	tubby like protein 1	-1.54	0.055	-1.23	0.172	-1.76	0.227	-1.77	0.509	-1.57
1441684_at	Ttc3	tetratricopeptide repeat domain 3	-1.08	0.845	-1.79	0.304	-1.83	0.053	-1.77	0.189	-1.62
1433344_at	4930448K20Rik	RIKEN cDNA 4930448K20 gene	-1.34	0.502	-1.5	0.274	-1.61	0.235	-1.08	0.864	-1.38
1457991_at	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	-1.23	0.673	-1.77	0.111	-1.52	0.152	-1.95	0.406	-1.62
1459768_x_at	Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	-1.09	0.776	-1.85	0.12	-1.75	0.158	-1.04	0.909	-1.43
1430754_at	4930511H11Rik	RIKEN cDNA 4930511H11 gene	-1.82	0.111	-1.68	0.337	-1.13	0.794	-1.28	0.104	-1.48
1447142_at	Cts7	cathepsin 7	-1.21	0.436	-1.54	0.52	-1.79	0.494	-1.05	0.807	-1.4
1450625_at	Col5a2	procollagen, type V, alpha 2	-1.41	0.132	-1.32	0.652	-1.76	0.02	-1.26	0.389	-1.44
1455235_x_at	Ldhb	lactate dehydrogenase B	-1.26	0.154	-2.13	0.107	-1.29	0.132	-1.49	0.281	-1.54
1432067_at	4930473O22Rik	RIKEN cDNA 4930473O22 gene	-2.36	0.015	-1.19	0.77	-1.3	0.586	-1.24	0.772	-1.52
1446201_at	9030420J04Rik	RIKEN cDNA 9030420J04 gene	-1.16	0.479	-1.58	0.147	-1.86	0.114	-1.24	0.771	-1.46
1450760_a_at	Ing3	inhibitor of growth family, member 3	-1.86	0.373	-1.3	0.397	-1.37	0.294	-2.07	0.161	-1.65
1438279_at	Dpp4	Dipeptidylpeptidase 4	-1.31	0.135	-1.38	0.233	-1.82	0.081	-2.15	0.113	-1.67
1428948_at	5730414M22Rik	RIKEN cDNA 5730414M22 gene	-1.24	0.045	-3.46	0.048	-1.06	0.855	-1.09	0.885	-1.71
1443817_x_at	Nkx2-6	NK2 transcription factor related, locus 6 (Drosophila)	-1.26	0.799	-2.49	0.052	-1.19	0.557	-1.49	0.325	-1.61
1433213_at	2700008E08Rik	RIKEN cDNA 2700008E08 gene	-1.51	0.34	-1.27	0.481	-1.69	0.101	-1.31	0.569	-1.45
1440111_at	Fmnl2	Formin-like 2	-1.52	0.173	-1.25	0.435	-1.74	0.086	-1.82	0.005	-1.58
1454762_at	Xkrx	X Kell blood group precursor related X linked	-1.83	0.356	-1.68	0.61	-1.11	0.61	-2.3	0.128	-1.73
1445083_at	---	Transcribed locus	-2.6	0.141	-1.15	0.653	-1.28	0.619	-1.21	0.61	-1.56
1442592_at	Ppapdc3	Phosphatidic acid phosphatase type 2 domain containing 3	-1.33	0.62	-1.48	0.153	-1.63	0.388	-1.53	0.39	-1.49
1437676_at	Spag9	sperm associated antigen 9	-1.49	0.024	-1.19	0.285	-1.89	0.02	-1.52	0.232	-1.52
1444677_at	C77673	expressed sequence C77673	-1.54	0.145	-1.28	0.182	-1.64	0.098	-1.2	0.141	-1.42
1447741_x_at	Acad10	acyl-Coenzyme A dehydrogenase family, member 10	-1.95	0.29	-1.44	0.563	-1.2	0.724	-1.52	0.601	-1.53
1459434_at	Pdhx	Pyruvate dehydrogenase complex, component X	-1.2	0.555	-1.64	0.139	-1.68	0.217	-1.31	0.439	-1.46
1452270_s_at	Cubn	cubilin (intrinsic factor-cobalamin receptor)	-1.1	0.085	-3.97	0.174	-1.13	0.859	-1.1	0.857	-1.83

1422134_at	Fosb	FBJ osteosarcoma oncogene B	-2.33	0.241	-1.54	0.231	-1.04	0.927	-1.43	0.12	-1.58
1441479_at	Ppm1b	Protein phosphatase 1B, magnesium dependent, beta isoform	-1.35	0.399	-1.36	0.298	-1.77	0.022	-1.18	0.29	-1.41
1439679_at	Cct3	chaperonin subunit 3 (gamma)	-1.58	0.113	-1.38	0.615	-1.46	0.385	-1.35	0.685	-1.44
1457712_at	Chd8	chromodomain helicase DNA binding protein 8	-1.16	0.125	-1.58	0.022	-1.84	0.002	-1.43	0.098	-1.5
1445895_at	Tcrb-V8.2	T-cell receptor beta, variable 8.2	-2.22	0.279	-1.18	0.723	-1.34	0.259	-1.43	0.029	-1.54
1435298_at	Cog5	component of oligomeric golgi complex 5	-1.33	0.556	-1.63	0.027	-1.48	0.017	-1.9	0.2	-1.58
1435673_at	AI448005	expressed sequence AI448005	-1.48	0.036	-1.39	0.402	-1.54	0.145	-1.11	0.636	-1.38
1441167_at	---	Transcribed locus	-1.45	0.48	-1.53	0.249	-1.43	0.441	-1.5	0.165	-1.48
1438109_at	Clca5	chloride channel calcium activated 5	-1.3	0.671	-1.58	0.486	-1.55	0.356	-1.15	0.783	-1.4
1447313_at	---	---	-1.36	0.169	-1.45	0.172	-1.61	0.087	-1.01	0.976	-1.36
1443299_at	Pdlim3	PDZ and LIM domain 3	-1.63	0.029	-1.47	0.202	-1.33	0.287	-1.69	0.153	-1.53
1440638_at	A230107N01Rik	RIKEN cDNA A230107N01 gene	-1	0.996	-1.75	0.119	-2.1	0.084	-2.17	0.401	-1.75
1428030_at	Adam34	a disintegrin and metallopeptidase domain 34	-2.24	0.038	-1.06	0.903	-1.53	0.494	-1.78	0.075	-1.65
1453494_at	4921513H07Rik	RIKEN cDNA 4921513H07 gene	-1.48	0.591	-1.32	0.662	-1.64	0.026	-1.02	0.97	-1.36
1438674_a_at	Sfrs8	splicing factor, arginine/serine-rich 8	-1.48	0.074	-1.31	0.037	-1.64	0.207	-1.36	0.129	-1.45
1427648_at	Rgs3	Regulator of G-protein signaling 3	-1.34	0.516	-1.71	0.253	-1.39	0.685	-1.67	0.53	-1.53
1445914_at	Nrf1	Nuclear respiratory factor 1	-1.34	0.119	-1.32	0.327	-1.85	0.04	-1.01	0.88	-1.38
1419439_at	Stk22s1 /// LOC672	serine/threonine kinase 22 substrate 1 /// similar to serine/threonine kinase 22 sul	-1.71	0.205	-1.23	0.171	-1.56	0.155	-1.84	0.055	-1.58
1458240_at	Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.22	0.229	-1.4	0.191	-1.97	0.033	-1.56	0.224	-1.54
1436629_at	A830041P22Rik	RIKEN cDNA A830041P22 gene	-1.23	0.325	-2.27	0.106	-1.26	0.644	-4.88	0.022	-2.41
1443416_at	C79741	expressed sequence C79741	-1.48	0.266	-1.42	0.113	-1.5	0.002	-1.06	0.673	-1.36
1427791_a_at	Adam1a	a disintegrin and metallopeptidase domain 1a	-1.1	0.616	-1.43	0.422	-2.29	0.013	-1.8	0.067	-1.65
1441342_at	Dpp4	Dipeptidylpeptidase 4	-1.15	0.185	-1.46	0.015	-2.02	0.01	-2.74	0.066	-1.84
1421437_x_at	Pcdhb14	protocadherin beta 14	-1.48	0.6	-1.19	0.471	-1.87	0.196	-2.39	0.229	-1.73
1458326_at	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	-1.55	0.322	-1.43	0.539	-1.43	0.456	-1.29	0.155	-1.42
1440675_at	Grlf1	Glucocorticoid receptor DNA binding factor 1	-1.34	0.039	-1.43	0.02	-1.67	0.143	-1.53	0.395	-1.49
1448831_at	Angpt2	angiopoietin 2	-1.19	0.2	-1.35	0.386	-2.13	0.018	-1.76	0.073	-1.61
1442067_at	Ror1	Receptor tyrosine kinase-like orphan receptor 1	-1.15	0.4	-1.32	0.219	-2.39	0.033	-1.55	0.166	-1.6
1457544_at	Ube2w	ubiquitin-conjugating enzyme E2W (putative)	-1.12	0.888	-3.04	0.024	-1.2	0.583	-1.24	0.749	-1.65
1446943_at	Dst	Dystonin	-1.05	0.873	-1.47	0.497	-2.39	0.015	-1.13	0.864	-1.51
1437919_at	Bdp1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	-1.16	0.593	-1.38	0.318	-2.14	0.001	-1.29	0.365	-1.5
1459512_at	Meis1	Myeloid ecotropic viral integration site 1	-1.03	0.889	-1.68	0.215	-2.05	0.057	-1.13	0.629	-1.47
1437493_at	5230400M03Rik	RIKEN cDNA 5230400M03 gene	-1.21	0.704	-1.41	0.218	-1.93	0.031	-2.03	0.013	-1.65
1441362_at	Ptprg	Protein tyrosine phosphatase, receptor type, G	-1.55	0.29	-1.45	0.126	-1.4	0.013	-1.29	0.404	-1.42
1430185_at	5830460E08Rik	RIKEN cDNA 5830460E08 gene	-1.43	0.087	-1.28	0.177	-1.76	0.009	-1.22	0.555	-1.42
1456723_at	Prr14	Proline rich 14	-1.27	0.693	-1.93	0.127	-1.34	0.3	-1.08	0.769	-1.41
1446400_at	Olfr558	olfactory receptor 558	-1.18	0.274	-1.43	0.1	-1.97	0.24	-2.92	0.341	-1.88
1445710_x_at	1110051B16Rik	RIKEN cDNA 1110051B16 gene	-1.29	0.754	-1.42	0.337	-1.75	0.032	-1.17	0.752	-1.41
1444378_at	Csnk1d	Casein kinase 1, delta	-1.55	0.161	-1.58	0.014	-1.29	0.366	-1.11	0.033	-1.38
1444591_at	Pik3r1	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	-1.15	0.61	-1.47	0.069	-1.99	0.038	-2.14	0.035	-1.69
1440432_at	Lztfl1	Leucine zipper transcription factor-like 1	-1.19	0.733	-2.39	0.081	-1.26	0.437	-2.6	0.054	-1.86
1423014_at	Pcdhb6	protocadherin beta 6	-1.41	0.68	-1.67	0.226	-1.34	0.171	-1.03	0.937	-1.36
1456692_at	Brd1	Bromodomain containing 1	-1.35	0.411	-1.12	0.352	-2.39	0.374	-1.21	0.569	-1.52
1457742_at	D9Wsu74e	DNA segment, Chr 9, Wayne State University 74, expressed	-1.04	0.581	-2.52	0.219	-1.43	0.123	-1.06	0.913	-1.51
1458426_at	Kif1b	Kinesin family member 1B	-1.33	0.123	-1.32	0.285	-1.85	0.012	-1.38	0.021	-1.47
1420281_at	---	---	-1.07	0.937	-1.75	0.323	-1.83	0.255	-1.35	0.655	-1.5
1441657_at	Bach2	BTB and CNC homology 2	-2.05	0.012	-1.48	0.35	-1.12	0.703	-1.89	0.142	-1.64
1438538_at	D630021H01Rik	RIKEN cDNA D630021H01 gene	-1.31	0.291	-1.32	0.081	-1.88	0.05	-1.17	0.562	-1.42
1446818_at	Mib1	Mindbomb homolog 1 (Drosophila)	-1.27	0.439	-2.06	0.062	-1.28	0.203	-1.3	0.476	-1.48
1454413_at	4933424H11Rik	RIKEN cDNA 4933424H11 gene	-1.09	0.495	-2.02	0.334	-1.55	0.346	-1.33	0.651	-1.5
1434760_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	-1.19	0.758	-1.72	0.332	-1.59	0.36	-1.97	0.09	-1.62
1439348_at	S100a10	S100 calcium binding protein A10 (calpactin)	-1.3	0.553	-1.48	0.077	-1.65	0.157	-1.5	0.214	-1.48
1429903_at	Gja10 /// Dpf2	gap junction membrane channel protein alpha 10 /// D4, zinc and double PHD fin	-1.53	0.194	-1.31	0.246	-1.58	0.09	-1.24	0.181	-1.41

1446110_at	D3Ertd711e	DNA segment, Chr 3, ERATO Doi 711, expressed	-2.06	0.32	-1.25	0.329	-1.31	0.548	-1.23	0.477	-1.46
1426129_at	Brms1	breast cancer metastasis-suppressor 1	-1.82	0.197	-1.15	0.574	-1.57	0.057	-1.19	0.492	-1.43
1447010_at	Zfp609	Zinc finger protein 609	-1.06	0.692	-1.36	0.242	-2.62	0.028	-1.48	0.176	-1.63
1441452_at	Lsm1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.07	0.235	-2.17	0.121	-1.51	0.095	-1.43	0.061	-1.55
1431880_at	3100003M19Rik	RIKEN cDNA 3100003M19 gene	-1.14	0.805	-1.48	0.318	-1.99	0.103	-1.06	0.886	-1.42
1441357_at	Kirrel3	kin of IRRE like 3 (Drosophila)	-1.22	0.395	-3.16	0.169	-1.09	0.696	-1.06	0.876	-1.63
1460152_at	---	---	-1.7	0.194	-1.54	0.556	-1.22	0.675	-1.64	0.417	-1.53
1456067_at	Gli3	GLI-Kruppel family member GLI3	-1.09	0.737	-2.44	0.236	-1.37	0.121	-1.23	0.475	-1.53
1453672_at	2810038L03Rik	RIKEN cDNA 2810038L03 gene	-2.14	0.239	-1	0.995	-1.68	0.224	-1.05	0.933	-1.47
1441135_at	Zfp672	Zinc finger protein 672	-1.5	0.227	-1.24	0.539	-1.7	0.224	-1.13	0.585	-1.39
1432285_at	1700128F08Rik	RIKEN cDNA 1700128F08 gene	-1.49	0.63	-1.12	0.748	-2.02	0.036	-2.1	0.554	-1.68
1434862_at	Fut2	fucosyltransferase 2	-1.44	0.563	-1.56	0.614	-1.38	0.476	-1.43	0.382	-1.45
1442740_at	---	---	-1.62	0.407	-1.04	0.868	-2.09	0.081	-1.16	0.321	-1.48
1453881_x_at	Cetn1	centrin 1	-1.51	0.184	-1.79	0.482	-1.2	0.605	-1.1	0.792	-1.4
1441614_at	---	---	-1.66	0.352	-1.08	0.903	-1.89	0.103	-1.69	0.206	-1.58
1440615_at	Dusp16	dual specificity phosphatase 16	-1.13	0.489	-1.32	0.465	-2.38	0.105	-2.56	0.021	-1.85
1430774_at	A430106A12Rik	RIKEN cDNA A430106A12 gene	-1.27	0.56	-1.56	0.04	-1.58	0.164	-1.41	0.231	-1.46
1453387_at	4833432E10Rik	RIKEN cDNA 4833432E10 gene	-1.36	0.716	-1.29	0.605	-1.82	0.103	-1.01	0.988	-1.37
1416687_at	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	-1.15	0.656	-1.44	0.442	-2.01	0.008	-1.16	0.095	-1.44
1458826_at	C78809	expressed sequence C78809	-1.11	0.866	-2.08	0.325	-1.47	0.335	-1.75	0.223	-1.6
1442017_at	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	-1.32	0.442	-1.6	0.072	-1.48	0.031	-1.37	0.03	-1.44
1445958_at	---	Transcribed locus	-2.27	0.142	-1.57	0.273	-1.02	0.966	-1.47	0.472	-1.58
1442653_at	---	---	-1.62	0.451	-1.49	0.284	-1.29	0.284	-1.25	0.544	-1.41
1442916_at	4931420C21Rik	RIKEN cDNA 4931420C21 gene	-1.37	0.414	-1.39	0.074	-1.63	0.02	-2.62	0.064	-1.75
1437294_at	Exosc10	exosome component 10	-1.06	0.051	-2.03	0.027	-1.6	0.136	-1.42	0.037	-1.53
1440989_at	---	---	-1.78	0.198	-1.41	0.045	-1.27	0.386	-1.2	0.441	-1.41
1443424_at	2210018M11Rik	RIKEN cDNA 2210018M11 gene	-1.78	0.245	-1.82	0.007	-1.06	0.871	-1.14	0.514	-1.45
1438133_a_at	Cyr61	cysteine rich protein 61	-1.38	0.362	-1.81	0.103	-1.28	0.646	-1.27	0.425	-1.43
1460593_at	Susd4	sushi domain containing 4	-1.12	0.582	-2.32	0.015	-1.36	0.094	-2.11	0.191	-1.73
1432306_at	A930023M06Rik	RIKEN cDNA A930023M06 gene	-1.29	0.084	-1.84	0.282	-1.35	0.385	-1.48	0.136	-1.49
1430818_at	Tmc1	transmembrane channel-like gene family 1	-1.47	0.136	-1.4	0.335	-1.5	0.245	-1.7	0.08	-1.52
1440012_at	---	---	-1.17	0.385	-1.66	0.028	-1.65	0.088	-1.19	0.599	-1.42
1432509_at	5033430I15Rik	RIKEN cDNA 5033430I15 gene	-1.27	0.357	-1.78	0.112	-1.4	0.188	-1.59	0.293	-1.51
1457282_x_at	Tubgcp5	Tubulin, gamma complex associated protein 5	-1.59	0.275	-1.26	0.556	-1.57	0.068	-1.16	0.391	-1.39
1459049_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	-2.43	0.093	-1.44	0.331	-1.04	0.924	-1.84	0.107	-1.69
1445996_at	Plac9	Placenta specific 9	-1.17	0.63	-1.54	0.095	-1.78	0.084	-1.11	0.817	-1.4
1430121_at	1700006E09Rik	RIKEN cDNA 1700006E09 gene	-1.27	0.556	-1.62	0.353	-1.53	0.417	-1.21	0.541	-1.4
1458337_at	Tcf12	Transcription factor 12	-1.74	0.256	-1.2	0.774	-1.52	0.467	-1.29	0.572	-1.44
1446850_at	Ppap2b	Phosphatidic acid phosphatase type 2B	-1.36	0.04	-1.23	0.323	-1.94	0.03	-1.32	0.478	-1.46
1430685_at	6330503C03Rik	RIKEN cDNA 6330503C03 gene	-2.05	0.295	-1.14	0.748	-1.43	0.405	-1.59	0.156	-1.55
1442755_at	---	Transcribed locus	-1.12	0.693	-2	0.051	-1.49	0.26	-1.26	0.235	-1.47
1420747_at	Ppnr	per-pentamer repeat gene	-1.52	0.332	-1.13	0.689	-1.94	0.135	-1.05	0.859	-1.41
1433197_at	4930445B03Rik	RIKEN cDNA 4930445B03 gene	-1.4	0.296	-1.56	0.298	-1.42	0.35	-1.13	0.471	-1.37
1455419_at	D630045J12Rik	RIKEN cDNA D630045J12 gene	-1.44	0.084	-2.07	0.313	-1.12	0.327	-1.14	0.823	-1.44
1438879_at	Ddah1	Dimethylarginine dimethylaminohydrolase 1	-1.32	0.083	-2.08	0.072	-1.21	0.521	-2.39	0.251	-1.75
1456708_at	2610028E06Rik	RIKEN cDNA 2610028E06 gene	-2.45	0.129	-1.42	0.255	-1.05	0.586	-1.06	0.87	-1.49
1442214_at	Nfib	Nuclear factor I/B	-1.17	0.346	-1.4	0.132	-2.01	0.005	-1.03	0.746	-1.4
1446477_at	Zfp622	zinc finger protein 622	-1.61	0.484	-1.94	0.102	-1.07	0.786	-1.59	0.108	-1.55
1425688_a_at	Dpys	dihydropyrimidinase	-1.33	0.496	-1.28	0.035	-1.88	0.2	-1.88	0.221	-1.59
1432888_at	4930455M05Rik	RIKEN cDNA 4930455M05 gene	-1.35	0.112	-1.86	0	-1.27	0.312	-1.4	0.339	-1.47
1439131_at	4932441K18Rik	RIKEN cDNA 4932441K18 gene	-1.88	0.208	-1.47	0.255	-1.17	0.382	-1.22	0.199	-1.44
1429597_at	Dppa4	developmental pluripotency associated 4	-1.79	0.027	-1.32	0.499	-1.33	0.448	-1.16	0.309	-1.4
1442405_at	Csrp2bp	Cysteine and glycine-rich protein 2 binding protein	-1.29	0.619	-1.6	0.039	-1.5	0.232	-1.53	0.063	-1.48

1440794_x_at	1700029M03Rik	RIKEN cDNA 1700029M03 gene	-1.39	0.583	-2.28	0.247	-1.1	0.818	-1.3	0.556	-1.52
1427790_at	Mapkapk5 /// Adam	MAP kinase-activated protein kinase 5 /// a disintegrin and metallopeptidase dom	-1.75	0.136	-1.56	0.188	-1.16	0.676	-1.29	0.385	-1.44
1441596_at	5730601F06Rik	RIKEN cDNA 5730601F06 gene	-1.13	0.777	-1.39	0.387	-2.15	0.271	-1.76	0.145	-1.61
1441620_at	Grb10	Growth factor receptor bound protein 10	-1.44	0.282	-1.31	0.494	-1.63	0.082	-1.28	0.686	-1.42
1442184_at	Slc24a3	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	-1.87	0.43	-1.69	0.269	-1.06	0.893	-1.56	0.528	-1.55
1458648_at	AU042950	expressed sequence AU042950	-1.3	0.2	-1.21	0.638	-2.1	0.002	-1.21	0.569	-1.46
1425124_at	Rnf183	ring finger protein 183	-1.33	0.33	-1.45	0.273	-1.59	0.168	-1.38	0.694	-1.44
1441148_at	Fcmd	Fukuyama type congenital muscular dystrophy homolog (human)	-1.32	0.047	-1.73	0.113	-1.37	0.241	-1.22	0.543	-1.41
1431399_at	Adamts9	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.34	0.353	-1.4	0.375	-1.63	0.237	-1.59	0.312	-1.49
1445225_at	2410001C21Rik	RIKEN cDNA 2410001C21 gene	-1.32	0.437	-2.33	0.053	-1.13	0.352	-1.2	0.09	-1.5
1429813_at	Pank1	pantothenate kinase 1	-1.17	0.662	-1.48	0.261	-1.85	0.327	-1.05	0.934	-1.39
1446220_at	Gm484	gene model 484, (NCBI)	-1.36	0.499	-1.64	0.368	-1.38	0.626	-1.08	0.899	-1.37
1428662_a_at	Hod	homeobox only domain	-1.49	0.024	-1.39	0.157	-1.47	0.005	-1.15	0.754	-1.37
1430846_at	1700061G19Rik	RIKEN cDNA 1700061G19 gene	-1.35	0.436	-1.76	0.234	-1.31	0.415	-1.39	0.079	-1.45
1460421_at	Zfp133	zinc finger protein 133	-1.29	0.363	-2.58	0.062	-1.1	0.792	-1.03	0.532	-1.5
1445610_at	BC039093	CDNA sequence BC039093	-1.92	0.39	-1.1	0.859	-1.56	0.293	-1.32	0.392	-1.48
1429068_at	2810488G03Rik	RIKEN cDNA 2810488G03 gene	-1.12	0.675	-2.19	0.111	-1.39	0.142	-1.2	0.558	-1.48
1457245_at	Dirc2	disrupted in renal carcinoma 2 (human)	-1.08	0.66	-2.13	0.132	-1.48	0.151	-1.17	0.143	-1.46
1437884_at	Arl5b	ADP-ribosylation factor-like 5B	-1.21	0.048	-1.3	0.136	-2.09	0.011	-1.09	0.791	-1.42
1458502_at	Ktn1	Kinectin 1	-1.32	0.153	-3.16	0.129	-1	0.994	-2.16	0.039	-1.91
1441038_at	Utrn	Utrophin	-1.12	0.501	-1.19	0.194	-2.97	0.028	-1.71	0.135	-1.75
1459033_at	Plxna2	Plexin A2	-1.33	0.305	-1.11	0.877	-2.42	0.123	-1.09	0.865	-1.48
1430103_at	9030607L20Rik	RIKEN cDNA 9030607L20 gene	-1.36	0.075	-1.67	0.265	-1.36	0.011	-1.14	0.588	-1.38
1435603_at	Sned1	sushi, nidogen and EGF-like domains 1	-1.14	0.034	-2.11	0.061	-1.38	0.278	-1.3	0.609	-1.48
1435411_at	---	Transcribed locus	-1.35	0.59	-1.36	0.098	-1.68	0.26	-2.14	0.181	-1.63
1447409_at	---	---	-1.75	0.028	-1.41	0.1	-1.27	0.169	-1.64	0.101	-1.52
1444208_at	Dnahc1	Dynein, axonemal, heavy chain 1	-1.45	0.498	-1.29	0.382	-1.65	0.109	-1.04	0.931	-1.36
1442901_at	Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	-1.46	0.314	-1.89	0.192	-1.17	0.6	-1.03	0.896	-1.38
1456101_at	LOC640072 /// LOC	hypothetical protein LOC640072 /// hypothetical protein LOC677194	-1.34	0.647	-1.53	0.334	-1.48	0.507	-1.61	0.305	-1.49
1446386_at	Tcf4	Transcription factor 4	-1.2	0.622	-1.64	0.006	-1.58	0.002	-1.58	0.245	-1.5
1444917_at	Ube2w	Ubiquitin-conjugating enzyme E2W (putative)	-2.16	0.012	-1.19	0.823	-1.3	0.072	-1.86	0.163	-1.63
1420149_at	Pcnt	Pericentrin (kendrin)	-1.58	0.242	-1.15	0.755	-1.75	0.431	-1.7	0.478	-1.55
1459142_at	Spag17	sperm associated antigen 17	-1.79	0.477	-1.86	0.473	-1.02	0.653	-1.99	0.441	-1.67
1441763_at	Zdhhc6	zinc finger, DHHC domain containing 6	-1.24	0.681	-1.59	0.189	-1.56	0.106	-1.43	0.181	-1.46
1430175_at	4930588G05Rik	RIKEN cDNA 4930588G05 gene	-1.1	0.891	-1.85	0.017	-1.59	0.134	-1.54	0.154	-1.52
1453847_at	A930037O16Rik	RIKEN cDNA A930037O16 gene	-1.12	0.866	-2.76	0.219	-1.22	0.477	-1.07	0.935	-1.54
1445720_at	Sltm	SAFB-like, transcription modulator	-1.73	0.025	-1.67	0.1	-1.11	0.422	-1.52	0.274	-1.51
1421084_at	Rs1h	retinoschisis 1 homolog (human)	-1.14	0.771	-1.69	0.287	-1.65	0.093	-1.46	0.204	-1.49
1425709_at	Rnf17	ring finger protein 17	-1.53	0.638	-1.53	0.575	-1.3	0.583	-3.87	0.122	-2.06
1443661_at	---	---	-1.51	0.269	-2.01	0.264	-1.1	0.821	-1.07	0.908	-1.42
1418188_a_at	Malat1	Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	-1.18	0.656	-1.54	0.123	-1.73	0.02	-1.69	0.34	-1.54
1443376_at	---	Transcribed locus	-1.61	0.317	-1.32	0.595	-1.44	0.401	-1.06	0.876	-1.36
1445834_at	---	Transcribed locus	-2.31	0.397	-1.08	0.669	-1.4	0.464	-1.25	0.391	-1.51
1444318_at	Chchd7	Coiled-coil-helix-coiled-coil-helix domain containing 7	-1.11	0.314	-2.41	0.021	-1.31	0.251	-1.81	0	-1.66
1441449_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	-1.05	0.949	-1.44	0.25	-2.33	0.01	-1.02	0.92	-1.46
1440155_at	Fstl4	follistatin-like 4	-1.71	0.298	-1.85	0.336	-1.05	0.858	-2.51	0.116	-1.78
1418660_at	Clock /// LOC62072	circadian locomoter output cycles kaput /// hypothetical protein LOC620729	-1.38	0.022	-1.24	0.159	-1.83	0.014	-1.39	0.292	-1.46
1433226_at	6330403N20Rik	RIKEN cDNA 6330403N20 gene	-1.54	0.566	-1.49	0.598	-1.32	0.302	-1.28	0.25	-1.41
1429302_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	-1.29	0.193	-1.38	0.079	-1.73	0.086	-1.16	0.045	-1.39
1440271_at	---	Transcribed locus	-1.51	0.446	-1.55	0.17	-1.3	0.052	-1.52	0.147	-1.47
1459078_at	Rbpms	RNA binding protein gene with multiple splicing	-1.36	0.357	-1.25	0.43	-1.83	0.013	-1.68	0.462	-1.53
1447038_x_at	Phip	pleckstrin homology domain interacting protein	-1.37	0.283	-1.89	0.202	-1.22	0.222	-1.67	0.308	-1.54
1447542_at	AY702102	cDNA sequence AY702102	-1.36	0.456	-2.22	0.448	-1.12	0.447	-1.99	0.211	-1.67

1431940_at	LOC74457	hypothetical protein LOC74457	-1.3	0.29	-1.55	0.305	-1.51	0.121	-1.22	0.048	-1.39
1419065_at	5730521E12Rik	RIKEN cDNA 5730521E12 gene	-1.27	0.353	-1.03	0.847	-3.15	0.05	-1.44	0.515	-1.72
1445135_at	---	---	-1.02	0.988	-2.9	0.153	-1.34	0.428	-1.5	0.635	-1.69
1457386_at	9530010C24Rik	RIKEN cDNA 9530010C24 gene	-1.12	0.607	-1.23	0.305	-2.69	0.014	-3.37	0.13	-2.1
1451529_at	Sgtb	small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	-1.67	0.094	-1.39	0.311	-1.31	0.026	-3.08	0.243	-1.86
1438900_at	Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	-1.27	0.553	-1.37	0.197	-1.77	0.016	-1.09	0.781	-1.38
1433152_at	2900022B07Rik	RIKEN cDNA 2900022B07 gene	-1.77	0.472	-1.24	0.634	-1.42	0.701	-1.42	0.59	-1.46
1454649_at	Srd5a1	steroid 5 alpha-reductase 1	-1.18	0.438	-2.27	0.008	-1.26	0.53	-1.63	0.21	-1.59
1441787_at	Zc3h12c	Zinc finger CCCH-type containing 12C	-1.19	0.56	-2.55	0.114	-1.18	0.591	-1.3	0.56	-1.56
1441267_at	Rsrc1	Arginine/serine-rich coiled-coil 1	-1.74	0.33	-1.19	0.192	-1.51	0.4	-2.74	0.102	-1.79
1456132_x_at	Tsc22d1	TSC22 domain family, member 1	-1.28	0.741	-1.37	0.258	-1.75	0.278	-1.01	0.987	-1.35
1458836_at	Calb1	calbindin-28K	-1.5	0.227	-1.47	0.622	-1.36	0.264	-1.26	0.698	-1.4
1440947_at	Bat2d	BAT2 domain containing 1	-1.38	0.307	-1.56	0.294	-1.4	0.128	-1.52	0.141	-1.46
1449599_at	---	---	-1.77	0.544	-1.1	0.844	-1.64	0.115	-1.81	0.362	-1.58
1436413_at	Frk	fyn-related kinase	-1.29	0.093	-1.53	0.124	-1.54	0.171	-1.03	0.948	-1.35
1432182_at	4922502B01Rik	RIKEN cDNA 4922502B01 gene	-1.25	0.781	-1.47	0.156	-1.67	0.546	-1.14	0.768	-1.38
1456341_a_at	Klf9	Kruppel-like factor 9	-1.42	0.479	-1.65	0.102	-1.3	0.302	-1.12	0.788	-1.37
1432686_at	4833406M21Rik	RIKEN cDNA 4833406M21 gene	-1.43	0.097	-1.1	0.806	-2.11	0.016	-1.2	0.232	-1.46
1447328_at	Itpr2	Inositol 1,4,5-triphosphate receptor 2	-1.12	0.692	-1.74	0.164	-1.63	0.184	-1.35	0.436	-1.46
1458691_at	Synpo2l	Synaptopodin 2-like	-1.41	0.488	-1.73	0.378	-1.26	0.623	-1.83	0.068	-1.56
1430955_at	2810403A07Rik	RIKEN cDNA 2810403A07 gene	-1.58	0.146	-1.55	0.012	-1.24	0.375	-1.35	0.335	-1.43
1451725_a_at	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	-1.38	0.153	-2.27	0.103	-1.09	0.864	-1.07	0.761	-1.45
1435269_at	2510005D08Rik	RIKEN cDNA 2510005D08 gene	-1.05	0.871	-2.19	0.223	-1.47	0.593	-1.16	0.829	-1.47
1447595_x_at	1810012K16Rik	RIKEN cDNA 1810012K16 gene	-1.68	0.262	-1.18	0.719	-1.57	0.429	-1.61	0.508	-1.51
1420212_at	---	---	-1.16	0.796	-1.55	0.372	-1.73	0.28	-3.22	0.15	-1.92
1456973_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	-1.21	0.202	-1.34	0.219	-1.94	0.001	-1.79	0.114	-1.57
1446127_at	Zfhx1a	Zinc finger homeobox 1a	-1.1	0.576	-1.51	0.199	-1.97	0.047	-1.37	0.444	-1.49
1453331_at	1700013H16Rik	RIKEN cDNA 1700013H16 gene	-1.44	0.515	-1.44	0.397	-1.44	0.461	-1.38	0.663	-1.42
1437652_at	Sema6c	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-2.78	0.004	-1.03	0.942	-1.32	0.497	-3.05	0.1	-2.05
1440250_at	Col4a4	procollagen, type IV, alpha 4	-1.24	0.256	-1.6	0.326	-1.52	0.063	-2.71	0.031	-1.77
1427806_at	---	---	-1.42	0.141	-1.65	0.031	-1.29	0.526	-2.48	0.021	-1.71
1444763_at	Ptprk	protein tyrosine phosphatase, receptor type, K	-1.11	0.773	-1.81	0.079	-1.58	0.01	-1.17	0.656	-1.42
1448024_at	Npr3	natriuretic peptide receptor 3	-1.25	0.497	-2.38	0.007	-1.16	0.462	-2.08	0.166	-1.72
1442778_at	AA511254	expressed sequence AA511254	-1.79	0.005	-1.43	0.098	-1.21	0.422	-1.11	0.84	-1.38
1454560_at	4930519N06Rik	RIKEN cDNA 4930519N06 gene	-1.02	0.958	-2.69	0.175	-1.35	0.441	-1.28	0.722	-1.59
1422048_at	Trpc5	transient receptor potential cation channel, subfamily C, member 5	-1.8	0.212	-1.43	0.303	-1.21	0.471	-1.13	0.694	-1.39
1441799_at	6030422H21Rik	RIKEN cDNA 6030422H21 gene	-1.16	0.844	-1.56	0.477	-1.7	0.375	-1.38	0.395	-1.45
1442607_a_at	---	---	-1.36	0.196	-1.19	0.424	-1.95	0.075	-1.54	0.392	-1.51
1442821_at	Tm9sf3	Transmembrane 9 superfamily member 3	-1.3	0.372	-1.48	0.027	-1.56	0.143	-1.49	0.27	-1.46
1445802_at	AU017455	Expressed sequence AU017455	-1.95	0.229	-1.38	0.381	-1.18	0.482	-1.07	0.664	-1.39
1435184_at	Npr3	natriuretic peptide receptor 3	-1.28	0.408	-1.5	0.262	-1.57	0.253	-1.59	0.278	-1.48
1446006_at	Immp1l	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	-1.3	0.155	-1.45	0.043	-1.59	0.027	-1.34	0.349	-1.42
1431819_at	---	---	-1.34	0.527	-1.59	0.305	-1.4	0.015	-1.56	0.495	-1.47
1438338_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	-1.23	0.305	-1.84	0.022	-1.36	0.047	-1.72	0.147	-1.54
1430415_at	Phf6	PHD finger protein 6	-1.22	0.591	-1.62	0.051	-1.53	0.009	-1.5	0.154	-1.47
1437071_at	Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	-1.18	0.62	-1.44	0.286	-1.83	0.024	-1.08	0.777	-1.38
1430792_at	---	---	-1.16	0.617	-1.47	0.313	-1.84	0.028	-1.32	0.626	-1.45
1438152_at	Gpaa1	GPI anchor attachment protein 1	-3.13	0.021	-1.12	0.557	-1.15	0.491	-1.14	0.806	-1.63
1447268_at	Nol12	nucleolar protein 12	-1.8	0.123	-1.35	0.515	-1.26	0.396	-1.45	0.551	-1.47
1436650_at	Filip1	filamin A interacting protein 1	-1.23	0.633	-2.38	0.395	-1.17	0.399	-1.15	0.664	-1.48
1434788_at	D930050A07Rik	RIKEN cDNA D930050A07 gene	-1.32	0.013	-1.53	0.513	-1.48	0.017	-1.13	0.544	-1.36
1441738_at	---	---	-2.03	0.062	-1.46	0.237	-1.1	0.737	-1.01	0.946	-1.4
1445598_at	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransfe	-1.06	0.658	-2.01	0.123	-1.55	0.457	-1.35	0.489	-1.49

1446672_at	---	---	-1.33	0.798	-1.39	0.505	-1.62	0.303	-1.34	0.588	-1.42
1450784_at	Reck	reversion-inducing-cysteine-rich protein with kazal motifs	-1.11	0.384	-1.81	0.054	-1.58	0.015	-1	0.993	-1.37
1452989_at	2900009J20Rik	RIKEN cDNA 2900009J20 gene	-1.23	0.151	-1.28	0.355	-2.02	0.016	-1.69	0.167	-1.56
1447062_at	Vps24	Vacuolar protein sorting 24 (yeast)	-1.15	0.302	-1.42	0.024	-1.93	0.131	-1.12	0.484	-1.4
1458134_at	Gstz1	Glutathione transferase zeta 1 (maleylacetoacetate isomerase)	-1.47	0.237	-1.63	0.157	-1.26	0.024	-1.27	0.412	-1.41
1446069_at	Ablim3	Actin binding LIM protein family, member 3	-1.06	0.855	-2.55	0.002	-1.33	0.109	-1.06	0.591	-1.5
1446464_at	Psme4	Proteasome (prosome, macropain) activator subunit 4	-1.09	0.617	-1.3	0.182	-2.46	0.033	-1.14	0.438	-1.5
1446609_at	---	---	-1.07	0.832	-1.51	0.124	-2.01	0.049	-1.37	0.421	-1.49
1441287_at	---	---	-1.03	0.897	-3.71	0.019	-1.17	0.599	-1.15	0.136	-1.77
1443094_at	BB031773	expressed sequence BB031773	-1.21	0.109	-2.58	0.253	-1.14	0.238	-2.28	0.471	-1.8
1430008_x_at	Speer5-ps1	spermatogenesis associated glutamate (E)-rich protein 5, pseudogene 1	-1.01	0.99	-2.81	0.104	-1.34	0.542	-1.31	0.671	-1.62
1437971_at	Skiv2l2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	-2.7	0.347	-1.09	0.767	-1.25	0.388	-1.14	0.799	-1.54
1438831_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	-1.15	0.138	-1.47	0.105	-1.83	0.013	-1.23	0.178	-1.42
1442613_at	---	---	-1.3	0.15	-1.99	0.183	-1.22	0.304	-1.38	0.128	-1.47
1421538_at	Kcnd1	potassium voltage-gated channel, Shal-related family, member 1	-1.25	0.629	-1.46	0.427	-1.64	0.244	-1.39	0.086	-1.43
1442168_at	A230071A22Rik	RIKEN cDNA A230071A22 gene	-1.45	0.46	-1.22	0.473	-1.71	0.031	-1.45	0.149	-1.46
1441633_at	Nudt9	Nudix (nucleoside diphosphate linked moiety X)-type motif 9	-1.07	0.869	-1.44	0.512	-2.13	0.018	-1.43	0.464	-1.52
1433431_at	Pnlip	pancreatic lipase	-1.35	0.585	-1.95	0.237	-1.19	0.694	-2.39	0.152	-1.72
1421393_at	Grin2d	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	-1.98	0.3	-1.05	0.83	-1.56	0.236	-1.48	0.52	-1.52
1431492_at	2210418G03Rik	RIKEN cDNA 2210418G03 gene	-2.03	0.101	-1.16	0.63	-1.35	0.513	-1.05	0.905	-1.4
1418745_at	Omd	osteomodulin	-1.58	0.532	-1.33	0.634	-1.41	0.237	-2.22	0.303	-1.63
1432105_at	Sirt5	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	-1.61	0.514	-1.93	0.357	-1.04	0.953	-1.3	0.175	-1.47
1459338_at	Auts2	Autism susceptibility candidate 2	-1.18	0.613	-1.56	0.187	-1.65	0.113	-1.73	0.112	-1.53
1459170_at	Foxo1	Forkhead box O1	-1.2	0.659	-1.31	0.387	-1.99	0.018	-2.39	0.093	-1.72
1450349_at	Stx1b1	syntaxin 1B1	-1.36	0.434	-1.27	0.402	-1.74	0.446	-1.29	0.577	-1.41
1453217_at	LOC625508 /// LOC	similar to Xlr-related, meiosis regulated /// similar to Xlr-related, meiosis regulated	-2.13	0.179	-1.58	0.479	-1.01	0.991	-2.11	0.169	-1.71
1431960_at	Wwox	WW domain-containing oxidoreductase	-1.18	0.117	-1.45	0.056	-1.79	0.022	-1.04	0.791	-1.36
1458386_at	C030009J22Rik	RIKEN cDNA C030009J22 gene	-1.5	0.446	-1.68	0.106	-1.2	0.057	-1.3	0.657	-1.42
1445820_at	---	---	-1.37	0.238	-1.51	0.039	-1.41	0.528	-1.77	0.023	-1.52
1458065_at	---	---	-1.38	0.147	-1.25	0.512	-1.75	0.145	-1.68	0.1	-1.51
1446105_at	Exoc1	exocyst complex component 1	-1.69	0.539	-1.37	0.01	-1.29	0.588	-1.88	0.345	-1.56
1421599_at	Hs6st3	heparan sulfate 6-O-sulfotransferase 3	-1.69	0.457	-1.48	0.018	-1.2	0.448	-1.01	0.934	-1.35
1449109_at	Socs2	suppressor of cytokine signaling 2	-1.03	0.955	-2.56	0.182	-1.35	0.007	-1.28	0.197	-1.56
1442991_at	B3gat2	beta-1,3-glucuronyltransferase 2 (glucuronosyltransferase S)	-1.04	0.929	-1.69	0.498	-1.84	0.308	-1.13	0.732	-1.42
1426215_at	Ddc	dopa decarboxylase	-1.11	0.624	-1.26	0.374	-2.45	0	-1.53	0.216	-1.59
1430890_at	2210010C17Rik	RIKEN cDNA 2210010C17 gene	-2.01	0.322	-1.52	0.089	-1.06	0.781	-3.77	0.014	-2.09
1442090_at	8030463A06Rik	RIKEN cDNA 8030463A06 gene	-1.97	0.502	-1.23	0.623	-1.28	0.617	-1.14	0.625	-1.4
1437880_at	Lbxcor1	ladybird homeobox 1 homolog (Drosophila) corepressor 1	-1.18	0.821	-1.48	0.52	-1.73	0.2	-1.02	0.942	-1.35
1446348_at	Map4k5	Mitogen-activated protein kinase kinase kinase kinase 5	-1.21	0.329	-2.08	0.08	-1.26	0.433	-1.35	0.113	-1.48
1441217_at	Rabgap1	RAB GTPase activating protein 1	-1.31	0.13	-1.28	0.597	-1.79	0.022	-1.06	0.772	-1.36
1447051_at	Rnf43	Ring finger protein 43	-1.17	0.836	-1.53	0.199	-1.68	0.462	-1.03	0.954	-1.35
1440513_at	C80258	expressed sequence C80258	-1.29	0.033	-1.28	0.166	-1.83	0.047	-1.29	0.057	-1.42
1454884_at	Btbd4	BTB (POZ) domain containing 4	-1.91	0.038	-1.24	0.277	-1.29	0.335	-1.5	0.038	-1.49
1444453_at	Trp53rk	Trp53 regulating kinase	-1.08	0.724	-1.68	0.049	-1.71	0.323	-3.09	0.069	-1.89
1459314_at	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	-1.64	0.248	-1.12	0.694	-1.67	0.143	-1.11	0.841	-1.38
1457360_at	Cfdp1	Craniofacial development protein 1	-1.04	0.689	-1.58	0.051	-1.98	0.02	-1.12	0.763	-1.43
1417595_at	Meox1	mesenchyme homeobox 1	-1.38	0.16	-1.12	0.861	-2.07	0.029	-1.25	0.743	-1.45
1423004_at	Vipr1	vasoactive intestinal peptide receptor 1	-1.08	0.449	-2.61	0.358	-1.26	0.579	-1.96	0.528	-1.73
1459572_at	C86371	expressed sequence C86371	-1.32	0.735	-1.11	0.766	-2.25	0.195	-1.34	0.562	-1.5
1457230_at	Gnpda2	glucosamine-6-phosphate deaminase 2	-1.34	0.135	-1.82	0.319	-1.23	0.457	-1.29	0.248	-1.42
1454069_at	9030409C19Rik	RIKEN cDNA 9030409C19 gene	-2.07	0.053	-1.03	0.933	-1.54	0.189	-1.27	0.606	-1.48
1416710_at	Tmem35	transmembrane protein 35	-1.35	0.013	-1.77	0.358	-1.25	0.634	-1.14	0.62	-1.38
1432687_at	4833406M21Rik	RIKEN cDNA 4833406M21 gene	-1.49	0.532	-1.37	0.354	-1.42	0.244	-1.51	0.148	-1.45

1456451_at	Ceacam15	CEA-related cell adhesion molecule 15	-1.43	0.253	-1.37	0.502	-1.48	0.426	-1.14	0.482	-1.35
1453606_at	4931403G20Rik	RIKEN cDNA 4931403G20 gene	-1.19	0.069	-1.31	0.253	-1.99	0.359	-1.48	0.193	-1.49
1455635_at	---	Transcribed locus	-1.2	0.626	-1.96	0.071	-1.31	0.268	-1.27	0.639	-1.44
1443231_at	Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.19	0.464	-1.27	0.017	-2.09	0.015	-1.23	0.203	-1.45
1457752_at	AU014876	expressed sequence AU014876	-1.15	0.663	-2.03	0.247	-1.35	0.018	-2.17	0.352	-1.67
1457548_at	Adamts6	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin typ	-1.76	0.152	-1.41	0.542	-1.2	0.497	-1.63	0.207	-1.5
1441231_at	---	PREDICTED: Mus musculus hypothetical protein LOC626097 (LOC626097), mR	-1.24	0.069	-1.28	0.519	-1.93	0.074	-1.53	0.226	-1.49
1424211_at	5730438N18Rik	RIKEN cDNA 5730438N18 gene	-1.75	0.424	-1.44	0.283	-1.19	0.454	-1.21	0.065	-1.4
1419698_at	Cxcl11	chemokine (C-X-C motif) ligand 11	-1.83	0.273	-1.51	0.11	-1.11	0.546	-1.19	0.468	-1.41
1445022_at	---	Transcribed locus	-1.19	0.653	-1.85	0.311	-1.38	0.591	-1.02	0.954	-1.36
1458814_at	AU022855	expressed sequence AU022855	-1.1	0.475	-2.01	0.037	-1.42	0.103	-1.24	0.483	-1.44
1439596_at	---	---	-1.28	0.399	-1.63	0.113	-1.4	0.026	-1.91	0.175	-1.55
1458124_at	Iqgap1	IQ motif containing GTPase activating protein 1	-1.39	0.215	-1.29	0.544	-1.64	0.25	-1.44	0.032	-1.44
1427029_at	Htra3	HtrA serine peptidase 3	-2.4	0.217	-1.1	0.847	-1.28	0.468	-1.49	0.083	-1.57
1435832_at	Lrrc4	leucine rich repeat containing 4	-1.34	0.588	-1.86	0.141	-1.21	0.528	-1.31	0.661	-1.43
1425077_at	Dnajc18	DnaJ (Hsp40) homolog, subfamily C, member 18	-1.32	0.088	-1.46	0.138	-1.5	0.13	-1.02	0.949	-1.33
1420218_at	---	---	-1.13	0.597	-1.39	0.371	-1.99	0.015	-2.13	0.218	-1.66
1430306_a_at	Atp6v1c2	ATPase, H+ transporting, lysosomal V1 subunit C2	-1.42	0.078	-1.49	0.555	-1.36	0.135	-1.91	0.086	-1.55
1443595_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	-1.08	0.773	-1.79	0.02	-1.6	0.215	-1.12	0.856	-1.4
1446290_at	2410129H14Rik	RIKEN cDNA 2410129H14 gene	-1.19	0.588	-1.38	0.431	-1.85	0.115	-1.18	0.317	-1.4
1452875_at	Hddc3	HD domain containing 3	-1.26	0.607	-2.33	0.145	-1.13	0.639	-1.49	0.123	-1.55
1430923_at	2610300M13Rik	RIKEN cDNA 2610300M13 gene	-1.14	0.71	-2.13	0.237	-1.31	0.569	-1.13	0.837	-1.43
1458748_at	Rbm27	RNA binding motif protein 27	-1.05	0.745	-2.1	0.006	-1.47	0.101	-1.17	0.449	-1.45
1445370_at	Vapb	Vesicle-associated membrane protein, associated protein B and C	-1.24	0.196	-1.41	0.572	-1.68	0.057	-2	0.078	-1.58
1445770_at	---	---	-2.1	0.2	-1.18	0.735	-1.26	0.214	-1.75	0.392	-1.57
1432107_at	2310010M20Rik	RIKEN cDNA 2310010M20 gene	-1.83	0.169	-1.42	0.635	-1.16	0.596	-1.33	0.589	-1.44
1454212_x_at	Gsdmdc2 /// 49334	gasdermin domain containing 2 /// RIKEN cDNA 4933426G20 gene /// RIKEN cDI	-1.4	0.674	-1.74	0.517	-1.21	0.151	-1.9	0.155	-1.56
1419391_at	Myog	myogenin	-1.44	0.441	-1.8	0.52	-1.16	0.778	-1.36	0.414	-1.44
1442845_at	C130075A20Rik	RIKEN cDNA C130075A20 gene	-1.21	0.117	-1.03	0.82	-3.16	0.009	-1.4	0.077	-1.7
1420067_at	Cd160	CD160 antigen	-1.91	0.41	-1.04	0.89	-1.59	0.038	-1.46	0.51	-1.5
1456124_x_at	Svs5	seminal vesicle secretion 5	-3.17	0.001	-1.17	0.762	-1.06	0.894	-1.38	0.609	-1.7
1458050_at	---	---	-1.12	0.844	-2.88	0.01	-1.14	0.475	-1.41	0.165	-1.64
1436392_s_at	Tcfap2c	transcription factor AP-2, gamma	-1.48	0.281	-1.46	0.167	-1.33	0.308	-1.34	0.596	-1.4
1440540_at	Gle1l	GLE1 RNA export mediator-like (yeast	-1.21	0.589	-1.47	0.342	-1.65	0.052	-1.22	0.387	-1.39
1456816_at	Rai17	Retinoic acid induced 17	-1.49	0.28	-1.43	0.241	-1.35	0.287	-1.5	0.232	-1.44
1425935_at	2900042B11Rik	RIKEN cDNA 2900042B11 gene	-1.14	0.714	-3.01	0.114	-1.1	0.531	-1.27	0.284	-1.63
1430277_at	9430034F23Rik	RIKEN cDNA 9430034F23 gene	-1.17	0.493	-1.6	0.405	-1.58	0.093	-1.21	0.479	-1.39
1456050_at	C80998	expressed sequence C80998	-1.22	0.427	-1.27	0.385	-1.99	0.058	-1.06	0.523	-1.38
1435656_at	Gmps	guanine monphosphate synthetase	-1.25	0.425	-1.38	0.019	-1.7	0.12	-1.17	0.113	-1.37
1416505_at	Nr4a1	nuclear receptor subfamily 4, group A, member 1	-1.92	0.057	-1.17	0.409	-1.36	0.506	-1.93	0.154	-1.59
1453841_at	2310050P20Rik	RIKEN cDNA 2310050P20 gene	-1.34	0.688	-1.1	0.782	-2.17	0.095	-2.01	0.11	-1.66
1432375_a_at	Spata3	spermatogenesis associated 3	-1.05	0.961	-1.12	0.601	-3.74	0.119	-1.6	0.153	-1.88
1440693_at	Palld	palladin, cytoskeletal associated protein	-1.01	0.963	-1.65	0.254	-1.92	0.083	-1.05	0.923	-1.41
1447464_at	Anks1b	ankyrin repeat and sterile alpha motif domain containing 1B	-1.19	0.697	-2.71	0.01	-1.1	0.805	-1.07	0.721	-1.52
1443770_x_at	Auts2	Autism susceptibility candidate 2	-1.3	0.243	-1.21	0.789	-1.92	0.177	-1.07	0.617	-1.38
1453598_at	3110082D06Rik	RIKEN cDNA 3110082D06 gene	-2.13	0.438	-1.22	0.449	-1.21	0.731	-1.08	0.595	-1.41
1454348_at	4933407C09Rik	RIKEN cDNA 4933407C09 gene	-2.16	0.117	-1.24	0.058	-1.18	0.714	-1.3	0.756	-1.47
1433035_at	5430430K15Rik	RIKEN cDNA 5430430K15 gene	-1.29	0.564	-1.74	0.181	-1.3	0.677	-1.59	0.236	-1.48
1433410_at	C030014O09Rik	RIKEN cDNA C030014O09 gene	-1.57	0.412	-1.14	0.841	-1.66	0.209	-1.67	0.418	-1.51
1441082_at	Dscam	Down syndrome cell adhesion molecule	-1.36	0.116	-1.86	0.086	-1.18	0.674	-1.91	0.39	-1.58
1447202_at	1200009F10Rik	RIKEN cDNA 1200009F10 gene	-1.6	0.359	-1.4	0.438	-1.28	0.162	-1.19	0.462	-1.37
1447167_at	AL033314	Expressed sequence AL033314	-1.33	0.327	-1.2	0.363	-1.87	0.031	-1.36	0.237	-1.44
1447820_x_at	Cpt2	carnitine palmitoyltransferase 2	-1.59	0.156	-1.24	0.52	-1.46	0.118	-1.08	0.661	-1.34

1437957_at	7030407O06Rik	RIKEN cDNA 7030407O06 gene	-1.29	0.053	-1.5	0.24	-1.48	0.178	-1.1	0.645	-1.34
1430828_at	Trmu	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	-1.26	0.478	-1.79	0.483	-1.31	0.526	-1.67	0.155	-1.51
1456782_at	Tada1l	transcriptional adaptor 1 (HFI1 homolog, yeast) like	-1.32	0.146	-2.07	0.018	-1.14	0.426	-1	0.989	-1.38
1455610_at	Dmn	desmuslin	-1.09	0.765	-1.87	0.139	-1.51	0.087	-1.22	0.105	-1.42
1452477_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	-1.52	0.14	-1.19	0.682	-1.61	0.192	-1	0.998	-1.33
1460108_at	Trit1	TRNA isopentenyltransferase 1	-1.3	0.597	-1.35	0.357	-1.64	0.191	-1.04	0.931	-1.33
1438590_at	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	-1.24	0.258	-1.63	0.139	-1.42	0.325	-1.34	0.289	-1.41
1440802_at	Clasp2	CLIP associating protein 2	-1.29	0.503	-1.31	0.327	-1.71	0.019	-1.39	0.24	-1.43
1457567_at	Nagk	N-acetylglucosamine kinase	-1.5	0.041	-1.53	0.008	-1.25	0.26	-1.03	0.887	-1.33
1437744_at	Slitrk4	SLIT and NTRK-like family, member 4	-1.99	0.203	-1.54	0.2	-1.03	0.921	-1.25	0.754	-1.45
1445637_at	Dnmt1	DNA methyltransferase (cytosine-5) 1	-2.73	0.357	-1.23	0.772	-1.06	0.931	-1.28	0.733	-1.57
1431697_at	Synj2	synaptojanin 2	-2.64	0.03	-1.2	0.516	-1.1	0.698	-1.03	0.891	-1.49
1443020_at	Hmbox1	Homeobox containing 1	-1.37	0.012	-1.15	0.585	-1.91	0.052	-1.15	0.362	-1.4
1455281_at	Wdr33	WD repeat domain 33	-1.2	0.338	-1.51	0.153	-1.59	0.025	-1.29	0.352	-1.4
1454257_at	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	-1.33	0.413	-1.25	0.512	-1.77	0.083	-1.11	0.31	-1.36
1453456_at	2900084O13Rik	RIKEN cDNA 2900084O13 gene	-1.18	0.759	-1.23	0.606	-2.16	0.01	-2.38	0.167	-1.74
1459074_at	---	---	-1.67	0.352	-1	0.99	-1.9	0.316	-2.6	0.094	-1.79
1444377_at	Psmb2	Proteasome (prosome, macropain) subunit, beta type 2	-1.41	0.258	-1.42	0.103	-1.42	0.405	-1.51	0.124	-1.44
1456783_at	9330107J05Rik	RIKEN cDNA 9330107J05 gene	-1.22	0.044	-1.28	0.119	-1.93	0.06	-3.19	0.085	-1.9
1459444_at	Zfp91	zinc finger protein 91	-1.52	0.029	-1.14	0.785	-1.71	0.017	-1.6	0.012	-1.49
1439833_at	3-Sep	septin 3	-1.51	0.336	-1.01	0.977	-2.11	0.013	-1.02	0.884	-1.41
1457247_at	AI465495	expressed sequence AI465495	-1.74	0.147	-1.32	0.568	-1.26	0.119	-1.18	0.687	-1.38
1436067_at	Zbtb10 /// LOC669(	zinc finger and BTB domain containing 10 /// similar to zinc finger and BTB domai	-1.2	0.173	-1.66	0.065	-1.46	0.078	-1.99	0.079	-1.57
1447736_at	Fkbp5	FK506 binding protein 5	-1.04	0.82	-1.59	0.526	-1.88	0.298	-1.22	0.838	-1.43
1441771_at	Atrx	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-1.2	0.53	-1.38	0.171	-1.77	0.065	-1.11	0.727	-1.36
1441608_at	Cacna2d1	Calcium channel, voltage-dependent, alpha2/delta subunit 1	-1.11	0.903	-2.24	0.129	-1.28	0.383	-1.09	0.804	-1.43
1454138_a_at	Stk31	serine threonine kinase 31	-1.14	0.757	-2.9	0.04	-1.11	0.471	-2.04	0.416	-1.8
1418189_s_at	Malat1	Metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	-1.17	0.582	-1.63	0.15	-1.51	0.057	-1.41	0.248	-1.43
1417803_at	1110032A04Rik	RIKEN cDNA 1110032A04 gene	-1.52	0.066	-1.26	0.639	-1.48	0.151	-2.24	0.099	-1.63
1457199_at	---	---	-1.12	0.554	-1.68	0.102	-1.57	0.014	-1.19	0.285	-1.39
1446485_at	4930553C11Rik	RIKEN cDNA 4930553C11 gene	-1.12	0.821	-1.83	0.18	-1.46	0.513	-1.22	0.51	-1.41
1458497_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	-1.2	0.023	-1.31	0.24	-1.89	0.014	-1.36	0.058	-1.44
1442401_at	Sorbs1	Sorbin and SH3 domain containing 1	-1.62	0.464	-1.29	0.454	-1.37	0.517	-1.73	0.199	-1.5
1445347_at	---	---	-1.03	0.93	-1.65	0.411	-1.82	0.28	-4.26	0.212	-2.19
1455846_at	Aqp11	aquaporin 11	-3.32	0.08	-1.09	0.756	-1.1	0.741	-1.27	0.672	-1.7
1443622_at	Dscr3	Down syndrome critical region gene 3	-1.93	0.575	-1.15	0.76	-1.35	0.173	-1.19	0.678	-1.41
1447426_at	Dip3b	Dip3 beta	-1.21	0.422	-1.24	0.418	-2.03	0.054	-1.25	0.343	-1.43
1427142_s_at	Jarid1b	jumonji, AT rich interactive domain 1B (Rbp2 like)	-1.39	0.155	-1.44	0.02	-1.41	0.051	-1.07	0.524	-1.33
1454377_at	2700080J24Rik	RIKEN cDNA 2700080J24 gene	-1.92	0.031	-1.18	0.485	-1.31	0.024	-1.06	0.801	-1.37
1427403_at	Slco1a5	solute carrier organic anion transporter family, member 1a5	-1.19	0.775	-2.03	0.455	-1.26	0.63	-1.28	0.69	-1.44
1439801_at	Sunc1	Sad1 and UNC84 domain containing 1	-1.16	0.674	-1.81	0.189	-1.41	0.5	-1.73	0.361	-1.52
1429333_at	Kif2b	kinesin family member 2B	-4.06	0.084	-1.08	0.798	-1.05	0.883	-1.16	0.872	-1.84
1419881_x_at	---	---	-1.18	0.57	-1.19	0.825	-2.25	0.134	-1.27	0.761	-1.47
1440683_at	A930004D18Rik	RIKEN cDNA A930004D18 gene	-1.27	0.689	-1.54	0.279	-1.44	0.368	-1.05	0.838	-1.33
1430341_at	Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	-1.3	0.073	-1.75	0.006	-1.27	0.275	-1.11	0.395	-1.36
1455361_at	Dgkb	diacylglycerol kinase, beta	-1.25	0.247	-1.3	0.36	-1.78	0.039	-1.85	0.385	-1.55
1446703_at	Rfwd2	Ring finger and WD repeat domain 2	-1.53	0.531	-1.26	0.637	-1.47	0.406	-1.05	0.935	-1.33
1456413_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	-1.32	0.277	-1.35	0.152	-1.58	0.163	-1.72	0.117	-1.49
1447116_at	Parl	Presenilin associated, rhomboid-like	-1.42	0.439	-1.95	0.076	-1.09	0.758	-3.27	0.029	-1.94
1436373_at	Map3k10	mitogen activated protein kinase kinase kinase 10	-1.6	0.591	-1.4	0.441	-1.26	0.475	-2.08	0.113	-1.59
1458096_at	Nhs	Nance-Horan syndrome (human)	-1.02	0.885	-1.59	0.003	-1.91	0.009	-1.12	0.621	-1.41
1457588_at	C76213	expressed sequence C76213	-1.18	0.176	-1.41	0.036	-1.75	0.02	-1.21	0.28	-1.39
1454105_at	---	---	-1.43	0.586	-2.03	0.264	-1.07	0.911	-1.85	0.594	-1.59

1421647_at	Cd1d2	CD1d2 antigen	-1.03	0.98	-2.8	0.022	-1.25	0.575	-1.24	0.628	-1.58
1419498_at	Tmigd1	transmembrane and immunoglobulin domain containing 1	-1.09	0.32	-2.05	0.092	-1.38	0.334	-1.15	0.566	-1.42
1445337_at	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.2	0.136	-1.32	0.041	-1.84	0.02	-1.35	0.386	-1.43
1442698_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.44	0.494	-2.18	0.356	-1.03	0.892	-2.88	0.356	-1.88
1442364_at	Mapk14	Mitogen activated protein kinase 14	-1.08	0.909	-1.83	0.175	-1.53	0.29	-2.69	0.026	-1.78
1457928_at	4930435E12Rik	RIKEN cDNA 4930435E12 gene	-1.42	0.443	-1.84	0.336	-1.13	0.527	-1.07	0.911	-1.37
1439928_at	Spnb2	Spectrin beta 2	-1.2	0.1	-1.15	0.624	-2.35	0.014	-1.59	0.222	-1.57
1459540_at	Cdc26	Cell division cycle 26	-1.11	0.623	-1.65	0.165	-1.61	0.293	-1.34	0.424	-1.43
1442012_at	AU015791	expressed sequence AU015791	-2.56	0.518	-1.18	0.195	-1.12	0.655	-1.44	0.425	-1.57
1419567_at	Fank1	fibronectin type 3 and ankyrin repeat domains 1	-1.68	0.056	-1.61	0.208	-1.09	0.784	-1.59	0.542	-1.49
1430503_at	6330522J23Rik	RIKEN cDNA 6330522J23 gene	-1.65	0.236	-1.3	0.497	-1.33	0.436	-1.49	0.67	-1.44
1439828_at	Mapkapk5	MAP kinase-activated protein kinase 5	-1.7	0.033	-1.32	0.293	-1.27	0.486	-1.61	0.083	-1.48
1432196_a_at	Dscaml1	Down syndrome cell adhesion molecule-like 1	-1.26	0.754	-1.51	0.448	-1.48	0.117	-1.7	0.385	-1.49
1444933_at	---	Transcribed locus, moderately similar to XP_231006.3 PREDICTED: similar to fo	-1.14	0.685	-1.26	0.623	-2.16	0.184	-2.08	0.297	-1.66
1444538_at	AL033314	Expressed sequence AL033314	-1.22	0.445	-1.43	0.111	-1.63	0.011	-1.34	0.154	-1.41
1422279_at	Fv1	Friend virus susceptibility 1	-2.02	0.267	-1.37	0.507	-1.1	0.743	-2.13	0.557	-1.65
1452388_at	Hspa1a	heat shock protein 1A	-1.51	0.014	-1.45	0.14	-1.28	0.639	-1.79	0.418	-1.51
1430433_at	4933406J08Rik /// l	RIKEN cDNA 4933406J08 gene /// hypothetical protein LOC640572	-3.65	0.134	-1.06	0.865	-1.09	0.428	-1.06	0.895	-1.72
1420446_at	Odf3	outer dense fiber of sperm tails 3	-1.63	0.044	-1.33	0.138	-1.3	0.095	-1.39	0.312	-1.41
1457223_at	Elmod1	ELMO domain containing 1	-1.1	0.487	-1.02	0.951	-4.12	0.005	-1.03	0.847	-1.82
1430749_at	2810040C05Rik	RIKEN cDNA 2810040C05 gene	-1.27	0.338	-1.26	0.392	-1.81	0.1	-1.46	0.385	-1.45
1431732_at	Spag16	sperm associated antigen 16	-1.68	0.109	-1.09	0.901	-1.62	0.241	-2.69	0.24	-1.77
1458694_at	AI789011	expressed sequence AI789011	-2.43	0.113	-1.14	0.796	-1.18	0.263	-1.03	0.813	-1.45
1458191_at	Foxp2	forkhead box P2	-1.27	0.454	-1.54	0.023	-1.43	0.088	-1.08	0.821	-1.33
1416129_at	Errfi1	ERBB receptor feedback inhibitor 1	-1.47	0.162	-1.19	0.229	-1.63	0.004	-2.22	0.215	-1.63
1450432_s_at	Mus81	MUS81 endonuclease homolog (yeast)	-1.45	0.133	-2	0.011	-1.06	0.819	-1.34	0.271	-1.46
1437190_at	Styk1	serine/threonine/tyrosine kinase 1	-1.23	0.584	-2.12	0.389	-1.18	0.5	-1.05	0.923	-1.39
1449392_at	Hsd17b1	hydroxysteroid (17-beta) dehydrogenase 1	-1.11	0.89	-2.89	0.054	-1.13	0.857	-1.14	0.539	-1.57
1439800_at	Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	-1.15	0.101	-1.32	0.251	-1.96	0.04	-1.33	0.298	-1.44
1458763_at	C78024	expressed sequence C78024	-1	0.999	-1.2	0.746	-3.26	0.002	-1.13	0.748	-1.65
1437367_at	H2-K1	Histocompatibility 2, K1, K region	-1.04	#DIV/0!	-2.72	0.099	-1.24	0.413	-1.35	0.268	-1.59
1441493_at	Erc1	ELKS/RAB6-interacting/CAST family member 1	-1.18	0.452	-1.63	0.042	-1.47	0.006	-1.07	0.74	-1.34
1456659_at	LOC552902	hypothetical LOC552902	-1.39	0.238	-1.04	0.588	-2.2	0.023	-2.2	0.053	-1.71
1450936_a_at	Dnase1l2	deoxyribonuclease 1-like 2	-1.19	0.417	-2.79	0.12	-1.06	0.9	-1.29	0.222	-1.58
1440143_at	Pigz	phosphatidylinositol glycan anchor biosynthesis, class Z	-1.14	0.533	-1.75	0.259	-1.45	0.022	-1.09	0.38	-1.36
1442772_at	Ehbp1	EH domain binding protein 1	-1.05	0.91	-2.23	0.009	-1.36	0.095	-1.81	0.443	-1.61
1458542_at	Msi2	Musashi homolog 2 (Drosophila)	-1.08	0.912	-1.71	0.319	-1.59	0.155	-1.42	0.475	-1.45
1443257_at	9630050E16Rik	RIKEN cDNA 9630050E16 gene	-1.12	0.414	-1.19	0.174	-2.47	0.014	-1.47	0.064	-1.56
1425107_a_at	Lifr	leukemia inhibitory factor receptor	-1.03	0.778	-2.68	0.005	-1.26	0.11	-1.92	0.025	-1.72
1440977_at	Akap13	A kinase (PRKA) anchor protein 13	-1.35	0.182	-1.33	0.23	-1.55	0.023	-1.11	0.436	-1.33
1433164_at	4930570E01Rik	RIKEN cDNA 4930570E01 gene	-1.37	0.612	-1.95	0.103	-1.12	0.776	-1.1	0.693	-1.39
1444130_at	1700081L11Rik	RIKEN cDNA 1700081L11 gene	-1.27	0.076	-1.34	0.017	-1.65	0.042	-1.79	0.069	-1.51
1454338_at	Bat2d	BAT2 domain containing 1	-1.35	0.313	-1.32	0.672	-1.55	0.22	-1.26	0.578	-1.37
1458467_at	1110032D16Rik	RIKEN cDNA 1110032D16 gene	-2.19	0.224	-1.18	0.741	-1.2	0.694	-1.14	0.547	-1.43
1446182_at	Zmynd11	Zinc finger, MYND domain containing 11	-1.21	0.262	-1.51	0.036	-1.53	0.142	-1.92	0.009	-1.54
1442052_at	C330019G07Rik	RIKEN cDNA C330019G07 gene	-1.47	0.037	-1.32	0.082	-1.43	0.178	-1.27	0.45	-1.37
1432887_at	3110048L19Rik	RIKEN cDNA 3110048L19 gene	-1.19	0.386	-1.41	0.14	-1.69	0.112	-1.47	0.537	-1.44
1449673_s_at	---	---	-1.14	0.731	-1.35	0.492	-1.9	0.353	-1.46	0.621	-1.46
1459026_at	Snw1	SNW domain containing 1	-1.05	0.909	-1.52	0.201	-1.89	0.065	-1.67	0.027	-1.53
1431919_at	Rttn	rotatin	-1.27	0.744	-1.82	0.176	-1.24	0.649	-1.03	0.905	-1.34
1438682_at	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	-1.69	0.406	-1.71	0.092	-1.04	0.915	-1.54	0.352	-1.49
1458482_at	Tnni3k	TNNI3 interacting kinase	-1.01	0.973	-2.52	0.123	-1.32	0.646	-1.26	0.661	-1.53
1444961_at	---	---	-1.14	0.485	-2.62	0.099	-1.13	0.605	-1.07	0.918	-1.49

1437587_at	---	Transcribed locus	-1.76	0.075	-1.41	0.255	-1.15	0.382	-1.13	0.523	-1.37
1421804_at	Fabp9	fatty acid binding protein 9, testis	-1.87	0.415	-1.45	0.44	-1.09	0.503	-1	0.986	-1.35
1459427_at	Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	-1.32	0.703	-1.73	0.148	-1.24	0.648	-1.62	0.604	-1.48
1457417_at	---	---	-1.12	0.643	-1.8	0.02	-1.44	0.179	-2.17	0.095	-1.63
1457738_at	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	-1.71	0.609	-1.01	0.924	-1.75	0.432	-1.86	0.41	-1.58
1444514_at	B930096F20Rik	RIKEN cDNA B930096F20 gene	-1.23	0.668	-1.29	0.695	-1.81	0.079	-1.17	0.39	-1.37
1438064_at	Ybx1	Y box protein 1	-1.43	0.165	-1.24	0.621	-1.57	0.126	-1.28	0.225	-1.38
1458159_at	Gnaq	Guanine nucleotide binding protein, alpha q polypeptide	-1.16	0.629	-1.29	0.033	-1.98	0.048	-1.71	0.009	-1.53
1457636_x_at	---	---	-1.36	0.503	-1.41	0.043	-1.44	0.068	-1.94	0.162	-1.53
1430488_at	1700066B19Rik	RIKEN cDNA 1700066B19 gene	-1.44	0.1	-1.86	0.14	-1.09	0.463	-1.35	0.243	-1.44
1431121_at	Amotl1	angiomotin-like 1	-1.61	0.223	-1.22	0.774	-1.42	0.415	-1.15	0.763	-1.35
1457524_at	Tcf12	Transcription factor 12	-1.07	0.834	-2.59	0.085	-1.21	0.314	-1.6	0.259	-1.62
1441015_at	Fut8	Fucosyltransferase 8	-1.61	0.219	-1.55	0.604	-1.14	0.363	-2.34	0.183	-1.66
1420062_at	---	Transcribed locus	-1.69	0.185	-1.33	0.093	-1.25	0.428	-1.14	0.429	-1.35
1447120_at	Btrc	Beta-transducin repeat containing protein	-1.47	0.095	-1.19	0.25	-1.62	0.087	-1.17	0.413	-1.36
1421342_at	Kcns2	K+ voltage-gated channel, subfamily S, 2	-1.85	0.018	-1.03	0.88	-1.58	0.319	-1.2	0.452	-1.41
1427819_at	---	---	-1.52	0.113	-1.68	0.355	-1.12	0.834	-1.29	0.526	-1.4
1447740_at	1700034J05Rik /// l	RIKEN cDNA 1700034J05 gene /// hypothetical protein LOC635035	-1.97	0.371	-1.31	0.671	-1.14	0.633	-1.07	0.935	-1.37
1443653_at	---	---	-1.69	0.059	-1.18	0.776	-1.42	0.134	-1.79	0.065	-1.52
1444364_at	Rcor3	REST corepressor 3	-1.29	0.549	-1.34	0.103	-1.61	0.139	-1.19	0.514	-1.36
1434201_at	Chrdl1	Chordin-like 1	-1.24	0.694	-1.52	0.037	-1.46	0.319	-1.18	0.683	-1.35
1440892_at	BC017647	CDNA sequence BC017647	-1.19	0.291	-1.42	0.007	-1.67	0.104	-1.26	0.346	-1.38
1437833_at	Ltbp3	latent transforming growth factor beta binding protein 3	-2.8	0.238	-1.08	0.792	-1.15	0.738	-1.02	0.972	-1.51
1447209_at	Foxp1	Forkhead box P1	-1.37	0.183	-1.22	0.263	-1.67	0.147	-2.59	0.114	-1.71
1430363_at	4933407O12Rik	RIKEN cDNA 4933407O12 gene	-3.51	0.145	-1.1	0.795	-1.05	0.851	-1.07	0.628	-1.68
1441552_at	A430107P09Rik	RIKEN cDNA A430107P09 gene	-1.13	0.876	-1.38	0.528	-1.87	0.058	-1.92	0.176	-1.57
1439328_at	Nfat5	nuclear factor of activated T-cells 5	-1.23	0.464	-1.64	0.016	-1.39	0.086	-1.41	0.159	-1.42
1451432_x_at	Alkbh4	alkB, alkylation repair homolog 4 (E. coli)	-1.42	0.061	-1.53	0.33	-1.26	0.279	-1.22	0.258	-1.36
1456843_at	Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-1.24	0.49	-1.5	0.128	-1.48	0.161	-1.1	0.858	-1.33
1447571_at	Elk4	ELK4, member of ETS oncogene family	-1.54	0.017	-1.37	0.005	-1.31	0.414	-1.05	0.815	-1.32
1430345_at	5530402H23Rik	RIKEN cDNA 5530402H23 gene	-1.25	0.11	-1.48	0.086	-1.5	0.022	-1.78	0.158	-1.5
1445686_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.2	0.588	-1.22	0.583	-2.04	0.17	-2.53	0.285	-1.75
1445689_at	---	Transcribed locus	-1.14	0.628	-1.26	0.484	-2.11	0.075	-1.08	0.818	-1.4
1444045_at	---	Transcribed locus	-1.15	0.66	-1.11	0.585	-2.64	0.035	-1.09	0.851	-1.5
1439243_x_at	Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	-1.12	0.818	-1.46	0.61	-1.75	0.077	-1.88	0.013	-1.55
1452547_s_at	H2-T18 /// LOC633	histocompatibility 2, T region locus 18 /// similar to histocompatibility 2, T region lo	-1.52	0.657	-1.23	0.681	-1.48	0.426	-1.02	0.962	-1.31
1439673_at	E230008O15Rik	RIKEN cDNA E230008O15 gene	-1.54	0.162	-1.23	0.35	-1.46	0.086	-1.02	0.906	-1.31
1455063_at	4921513D11Rik ///	RIKEN cDNA 4921513D11 gene /// expressed sequence AW061290	-1.46	0.329	-1.42	0.179	-1.32	0.095	-1.47	0.226	-1.42
1445535_at	AA407107	expressed sequence AA407107	-1.23	0.077	-1.37	0.282	-1.66	0.205	-2.84	0.045	-1.77
1446636_at	Tns3	tensin 3	-1.3	0.065	-1.21	0.326	-1.81	0.005	-1.09	0.215	-1.35
1427303_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-1.64	0.154	-1.03	0.921	-1.77	0.024	-2.67	0.013	-1.77
1458821_at	Sec24d	SEC24 related gene family, member D (S. cerevisiae)	-2.22	0.231	-1.24	0.777	-1.12	0.816	-1.34	0.279	-1.48
1433248_at	2310075M01Rik	RIKEN cDNA 2310075M01 gene	-1.13	0.816	-2.73	0.046	-1.11	0.719	-1.41	0.385	-1.6
1430093_at	4933406P04Rik	RIKEN cDNA 4933406P04 gene	-1.25	0.612	-1.46	0.326	-1.51	0.156	-1.15	0.419	-1.34
1421053_at	Kif1a	kinesin family member 1A	-2.13	0.395	-1.3	0.314	-1.1	0.696	-1.08	0.777	-1.4
1437822_at	Yme1l1	YME1-like 1 (S. cerevisiae)	-1.34	0.176	-1.22	0.637	-1.71	0.172	-1	0.993	-1.32
1439233_at	Tloc1	Translocation protein 1	-1.23	0.6	-1.16	0.389	-2.12	0.047	-1.03	0.662	-1.39
1420994_at	B3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	-1.09	0.783	-2.86	0.098	-1.13	0.587	-2.39	0.127	-1.87
1422335_at	Adra2c	adrenergic receptor, alpha 2c	-1.52	0.544	-1.64	0.339	-1.13	0.861	-1.03	0.968	-1.33
1439752_at	---	PREDICTED: Mus musculus similar to O-acyltransferase (membrane bound) don	-1.01	0.981	-1.22	0.602	-2.95	0.047	-1.65	0.454	-1.71
1440937_at	Rbm41	RNA binding motif protein 41	-1.23	0.473	-1.59	0.415	-1.41	0.527	-1.06	0.901	-1.32
1432100_a_at	4930478P22Rik	RIKEN cDNA 4930478P22 gene	-1.42	0.266	-1.39	0.361	-1.38	0.106	-1.13	0.472	-1.33
1434671_at	B230337E12Rik	RIKEN cDNA B230337E12 gene	-1.15	0.32	-1.46	0.025	-1.68	0.003	-1.31	0.275	-1.4

1432834_at	Cpb2	carboxypeptidase B2 (plasma)	-1.39	0.329	-1.69	0.307	-1.19	0.693	-1.46	0.664	-1.43
1451705_a_at	Oprm1	opioid receptor, mu 1	-2.18	0.219	-1.01	0.955	-1.41	0.302	-1.77	0.413	-1.6
1433731_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	-1.59	0.005	-1.38	0.095	-1.25	0.431	-1.08	0.603	-1.33
1439216_at	2900075B16Rik	RIKEN cDNA 2900075B16 gene	-1.24	0.563	-1.95	0.01	-1.2	0.413	-1.5	0.128	-1.47
1447168_at	---	Transcribed locus	-1.73	0.106	-1.08	0.868	-1.54	0.319	-2.07	0.194	-1.61
1430263_at	1700109F18Rik	RIKEN cDNA 1700109F18 gene	-1.04	0.957	-2.72	0.089	-1.22	0.482	-1.48	0.56	-1.61
1444019_at	Lrrc19	leucine rich repeat containing 19	-1.04	0.387	-1.51	0.144	-1.89	0.211	-1.17	0.591	-1.4
1440121_at	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	-1.33	0.191	-1.08	0.891	-2.1	0.007	-1.48	0.257	-1.5
1416288_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-1.2	0.106	-1.58	0.014	-1.46	0.026	-1.6	0.292	-1.46
1442424_at	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	-1.4	0.201	-1.26	0.501	-1.56	0.011	-1.1	0.346	-1.33
1428978_at	2900009J20Rik	RIKEN cDNA 2900009J20 gene	-1.24	0.577	-1.45	0.186	-1.52	0.212	-1.21	0.055	-1.36
1446433_at	Acbd5	acyl-Coenzyme A binding domain containing 5	-1.66	0.034	-1.38	0.105	-1.21	0.548	-1.32	0.168	-1.39
1451406_a_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	-1.21	0.374	-1.59	0.035	-1.44	0.299	-1.53	0.485	-1.44
1440041_at	Tgfbr3	Transforming growth factor, beta receptor III	-1.15	0.216	-1.28	0.645	-2	0.074	-1.49	0.057	-1.48
1431854_a_at	4930452B06Rik	RIKEN cDNA 4930452B06 gene	-2.31	0.087	-1.16	0.813	-1.17	0.344	-1.22	0.699	-1.46
1455932_at	Mtdh	Metadherin	-2.99	0.332	-1.03	0.952	-1.18	0.662	-1.03	0.952	-1.56
1441352_at	9430034N14Rik	RIKEN cDNA 9430034N14 gene	-1.07	0.405	-1.98	0.026	-1.41	0.12	-1.69	0.184	-1.54
1446437_at	9630028H03Rik	RIKEN cDNA 9630028H03 gene	-2.41	0.268	-1.04	0.956	-1.28	0.6	-2.19	0.257	-1.73
1440854_at	2810403A07Rik	RIKEN cDNA 2810403A07 gene	-1.06	0.826	-1.49	0.05	-1.85	0.033	-1.49	0.193	-1.47
1460139_at	C79256	expressed sequence C79256	-1.08	0.207	-2.86	0.303	-1.14	0.734	-1.71	0.195	-1.7
1441750_x_at	4930447F24Rik	RIKEN cDNA 4930447F24 gene	-2.31	0.378	-1.27	0.729	-1.07	0.891	-1.61	0.368	-1.57
1430146_at	4933402N03Rik	RIKEN cDNA 4933402N03 gene	-1.62	0.223	-1.66	0.369	-1.07	0.89	-1.6	0.486	-1.49
1454551_at	9530034D02Rik	RIKEN cDNA 9530034D02 gene	-1.18	0.664	-1.58	0.031	-1.49	0.058	-1.13	0.829	-1.34
1442981_at	---	---	-1.51	0.192	-1.97	0.123	-1.01	0.917	-1.13	0.731	-1.41
1430330_at	Wiz	widely-interspaced zinc finger motifs	-1.33	0.314	-1.77	0.194	-1.19	0.642	-1.07	0.809	-1.34
1418690_at	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	-2.22	0.159	-1.11	0.835	-1.24	0.554	-1	1	-1.39
1436049_at	5730589K01Rik	RIKEN cDNA 5730589K01 gene	-1.25	0.491	-1.48	0.029	-1.48	0.017	-1.32	0.461	-1.38
1438105_at	LOC632687	hypothetical protein LOC632686	-1.38	0.35	-1.58	0.066	-1.25	0.601	-1.34	0.495	-1.39
1424928_at	2210018M11Rik	RIKEN cDNA 2210018M11 gene	-1.13	0.324	-1.71	0.036	-1.46	0.006	-1.07	0.633	-1.34
1455280_at	Frem1	Fras1 related extracellular matrix protein 1	-1.38	0.044	-1.08	0.91	-1.96	0.008	-1.25	0.394	-1.42
1430479_at	2010007H06Rik	RIKEN cDNA 2010007H06 gene	-2.01	0.215	-1.2	0.794	-1.22	0.333	-1.37	0.519	-1.45
1455260_at	Lcorl	ligand dependent nuclear receptor corepressor-like	-1.52	0.131	-1.4	0.18	-1.27	0.059	-1.33	0.268	-1.38
1433131_at	5033425B01Rik	RIKEN cDNA 5033425B01 gene	-1.18	0.458	-1.6	0.266	-1.46	0.313	-1.46	0.587	-1.42
1445038_at	---	---	-1.26	0.768	-1.24	0.555	-1.78	0.312	-1.42	0.313	-1.43
1459242_at	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	-1.62	0.136	-1.12	0.864	-1.55	0.093	-1.21	0.411	-1.38
1460101_at	Nrxn3	Neurexin III	-1.27	0.598	-2.21	0.219	-1.09	0.88	-2.52	0.021	-1.77
1420278_at	BC048599	cDNA sequence BC048599	-1.83	0.462	-1.04	0.909	-1.54	0.516	-1.1	0.76	-1.38
1424886_at	Ptprd	protein tyrosine phosphatase, receptor type, D	-1.02	0.754	-1.45	0.11	-2.04	0.035	-1.03	0.921	-1.39
1432997_at	5830462P14Rik	RIKEN cDNA 5830462P14 gene	-1.36	0.164	-1.33	0.335	-1.49	0.098	-2.14	0.07	-1.58
1441939_x_at	2410003I16Rik	RIKEN cDNA 2410003I16 gene	-1.08	0.924	-1.35	0.534	-2.04	0.116	-1.32	0.663	-1.45
1437570_at	AI503301	expressed sequence AI503301	-1.36	0.324	-1.48	0.362	-1.34	0.353	-1.01	0.919	-1.3
1429902_at	5830443J22Rik	RIKEN cDNA 5830443J22 gene	-1.42	0.022	-1.19	0.161	-1.63	0.002	-1.55	0.038	-1.45
1458618_at	Ireb2	Iron responsive element binding protein 2	-1.46	0.407	-1.07	0.635	-1.87	0.034	-1.76	0.014	-1.54
1442775_at	St13	Suppression of tumorigenicity 13	-1.28	0.481	-1.63	0.022	-1.31	0.329	-1.71	0.238	-1.48
1440680_at	---	Transcribed locus	-1.37	0.168	-1.54	0.429	-1.29	0.219	-1.01	0.993	-1.3
1439717_at	B230362M20Rik	RIKEN cDNA B230362M20 gene	-1.46	0.464	-1.4	0.161	-1.32	0.051	-1.04	0.804	-1.3
1460073_at	Prkar1b	Protein kinase, cAMP dependent regulatory, type I beta	-1.29	0.453	-1.5	0.509	-1.39	0.029	-1.21	0.651	-1.35
1429526_at	Brd8	bromodomain containing 8	-1.05	0.324	-1.89	0.056	-1.48	0.061	-1.01	0.978	-1.36
1443384_at	Ptk2	PTK2 protein tyrosine kinase 2	-1.39	0.405	-1.12	0.74	-1.82	0.006	-1.86	0.008	-1.55
1447592_at	Dbh	dopamine beta hydroxylase	-1.67	0.396	-1.06	0.773	-1.62	0.476	-2.99	0.23	-1.84
1430039_at	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	-1.23	0.507	-1.36	0.237	-1.62	0.028	-1.45	0.011	-1.42
1456906_at	4833432P19Rik	RIKEN cDNA 4833432P19 gene	-1.32	0.187	-1.22	0.376	-1.72	0.125	-1.06	0.787	-1.33
1447201_at	---	---	-1.25	0.724	-1.57	0.229	-1.38	0.441	-2.85	0.117	-1.76

1431902_at	4930401A09Rik	RIKEN cDNA 4930401A09 gene	-1.09	0.812	-1.36	0.595	-1.96	0.36	-1.54	0.026	-1.49
1456209_x_at	---	---	-1.4	0.547	-1.17	0.563	-1.69	0.025	-1.46	0.009	-1.43
1458019_at	---	---	-2.35	0.338	-1.08	0.897	-1.23	0.689	-1.15	0.864	-1.45
1433450_at	Cdk5r1	cyclin-dependent kinase 5, regulatory subunit (p35) 1	-1.33	0.51	-2.39	0.024	-1.01	0.97	-1.58	0.044	-1.58
1444682_at	BC037032	cDNA Sequence BC037032	-1.09	0.404	-1.91	0.233	-1.38	0.052	-1.07	0.878	-1.37
1427480_at	Leap2	liver-expressed antimicrobial peptide 2	-1.51	0.375	-1.04	0.839	-1.87	0.281	-1.66	0.249	-1.52
1449682_s_at	Tubb2b	tubulin, beta 2b	-1.16	0.842	-1.38	0.646	-1.76	0.244	-1.46	0.506	-1.44
1445055_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.34	0.6	-1.26	0.703	-1.61	0.223	-2.67	0.237	-1.72
1430418_at	Tmem57	transmembrane protein 57	-1.35	0.089	-1.46	0.107	-1.36	0.132	-1.24	0.504	-1.35
1459956_at	---	---	-1.1	0.314	-2.83	0.078	-1.11	0.21	-2.49	0.058	-1.88
1430350_at	2610035F20Rik	RIKEN cDNA 2610035F20 gene	-1.72	0.531	-1.06	0.721	-1.58	0.414	-1.02	0.974	-1.34
1455092_at	Zfp207	zinc finger protein 207	-1.32	0.63	-1.57	0.053	-1.31	0.266	-1.08	0.869	-1.32
1417836_at	Gpx7	glutathione peroxidase 7	-1.09	0.711	-1.59	0.007	-1.62	0.007	-1.02	0.811	-1.33
1425282_at	Ibrdc2	IBR domain containing 2	-2.17	0.085	-1.15	0.674	-1.2	0.491	-1.01	0.948	-1.38
1432935_at	5330433J24Rik	RIKEN cDNA 5330433J24 gene	-1.8	0.24	-1.04	0.935	-1.55	0.457	-1.51	0.141	-1.48
1419633_at	Uncx4.1	Unc4.1 homeobox (C. elegans)	-1.09	0.846	-1.48	0.623	-1.77	0.003	-1.02	0.967	-1.34
1419469_at	Gnb4	guanine nucleotide binding protein, beta 4	-1.58	0.177	-1.37	0.193	-1.25	0.009	-1.2	0.315	-1.35
1436154_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430066P	-1.31	0.693	-1.85	0.248	-1.16	0.74	-1.2	0.767	-1.38
1442812_at	LOC433844	similar to Anapc5 protein	-1.66	0.44	-1.29	0.515	-1.28	0.036	-1.51	0.185	-1.43
1457021_x_at	Amhr2	anti-Mullerian hormone type 2 receptor	-1.15	0.79	-2.51	0.33	-1.12	0.297	-1.08	0.897	-1.46
1440642_at	D630042P16Rik	RIKEN cDNA D630042P16 gene	-1.36	0.205	-1.52	0.084	-1.3	0.247	-1.14	0.813	-1.33
1437504_at	Sla2	Src-like-adaptor 2	-2	0.554	-1.14	0.709	-1.28	0.214	-1.39	0.078	-1.45
1443592_at	AA617406	expressed sequence AA617406	-1.31	0.261	-1.19	0.671	-1.79	0.155	-1.71	0.212	-1.5
1446694_at	Dnm3	Dynamin 3	-1.19	0.506	-1.81	0.433	-1.3	0.552	-1.06	0.512	-1.34
1442296_at	Wdr75	WD repeat domain 75	-1.49	0.043	-1.36	0.156	-1.32	0.03	-1.7	0.043	-1.47
1457813_at	Mrps18a	Mitochondrial ribosomal protein S18A	-1.38	0.437	-1.41	0.317	-1.37	0.312	-1.46	0.195	-1.41
1427193_at	Brd8	bromodomain containing 8	-1.66	0.053	-1.13	0.724	-1.48	0.05	-1.05	0.879	-1.33
1453967_at	1700093J21Rik	RIKEN cDNA 1700093J21 gene	-1.32	0.385	-1.21	0.812	-1.72	0.06	-3.53	0.002	-1.95
1433058_at	4933411O13Rik	RIKEN cDNA 4933411O13 gene	-1.29	0.741	-1.18	0.789	-1.85	0.117	-1.76	0.439	-1.52
1437617_x_at	1110034G24Rik	RIKEN cDNA 1110034G24 gene	-1.37	0.274	-1.16	0.491	-1.76	0.034	-1.01	0.735	-1.32
1442470_at	---	---	-1.08	0.568	-1.41	0.11	-1.88	0.058	-1.12	0.157	-1.37
1420077_at	AI452102	expressed sequence AI452102	-1.08	0.619	-1.62	0.46	-1.61	0.213	-1.17	0.797	-1.37
1420092_at	Morc3	microrchidia 3	-1.54	0.415	-1.09	0.776	-1.67	0.039	-1.27	0.012	-1.39
1451585_x_at	Spsb2	splA/ryanodine receptor domain and SOCS box containing 2	-1.44	0.114	-1.69	0.003	-1.14	0.318	-1.05	0.694	-1.33
1459451_at	---	---	-2.62	0.329	-1.14	0.769	-1.1	0.789	-1.44	0.122	-1.58
1421377_at	Traf6	Tnf receptor-associated factor 6	-1.65	0.043	-1.25	0.73	-1.32	0.652	-1.54	0.571	-1.44
1446700_at	---	---	-1.2	0.646	-1.39	0.589	-1.63	0.119	-1.64	0.533	-1.46
1422144_at	Inhbe	inhibin beta E	-1.15	0.549	-1.36	0.327	-1.79	0.021	-1.69	0.209	-1.5
1432875_at	4632409D06Rik	RIKEN cDNA 4632409D06 gene	-1.94	0.128	-1.53	0.451	-1	0.998	-2.31	0.221	-1.7
1440227_at	BF642829	expressed sequence BF642829	-1	0.968	-1.8	0.107	-1.63	0.033	-1	0.993	-1.36
1423377_at	Igfbpl1	insulin-like growth factor binding protein-like 1	-1.55	0.061	-1.55	0.288	-1.14	0.454	-1.24	0.481	-1.37
1457146_at	Dock4	dedicator of cytokinesis 4	-1.2	0.077	-1.1	0.247	-2.35	0.012	-1.17	0.333	-1.45
1455526_at	Diras1	DIRAS family, GTP-binding RAS-like 1	-1.22	0.378	-1.79	0.149	-1.27	0.111	-1.54	0.034	-1.46
1424387_at	Prlpc3	prolactin-like protein C 3	-1	0.992	-1.52	0.493	-1.95	0.246	-1.32	0.57	-1.45
1442620_at	4931420C21Rik	RIKEN cDNA 4931420C21 gene	-1.21	0.252	-1.22	0.259	-1.93	0	-2.25	0.088	-1.65
1451642_at	Kif1b	kinesin family member 1B	-1.09	0.261	-1.76	0	-1.46	0.115	-1.33	0.227	-1.41
1459206_at	---	---	-1.02	0.934	-1.44	0.132	-2.05	0.146	-4.61	0	-2.28
1421479_at	Zfp318	zinc finger protein 318	-1.58	0.389	-1.48	0.004	-1.16	0.367	-3.12	0.087	-1.84
1439546_at	4933417O08Rik	RIKEN cDNA 4933417O08 gene	-1.27	0.426	-1.22	0.213	-1.79	0.437	-1.47	0.316	-1.44
1444106_at	D330012F22Rik	RIKEN cDNA D330012F22 gene	-1.38	0.242	-1.51	0.168	-1.28	0.149	-1.07	0.76	-1.31
1440158_x_at	Chchd7	Coiled-coil-helix-coiled-coil-helix domain containing 7	-1.1	0.554	-3.25	0.014	-1.05	0.9	-1.11	0.81	-1.63
1424529_s_at	Cgref1	cell growth regulator with EF hand domain 1	-1.01	0.775	-1.82	0.168	-1.59	0.015	-1.04	0.886	-1.36
1447711_x_at	4933412E12Rik	RIKEN cDNA 4933412E12 gene	-1.52	0.412	-1.8	0.127	-1.05	0.73	-1.36	0.455	-1.43

1446871_at	D7Ertd481e	DNA segment, Chr 7, ERATO Doi 481, expressed	-1.01	0.987	-2.35	0.141	-1.33	0.361	-1.4	0.192	-1.52
1431147_at	Rint1	RAD50 interactor 1	-2.08	0.244	-1.14	0.681	-1.23	0.2	-1.01	0.952	-1.37
1422177_at	Il13ra2	interleukin 13 receptor, alpha 2	-1.24	0.642	-1.69	0.198	-1.3	0.145	-1.36	0.322	-1.4
1457821_at	2610511M17Rik	RIKEN cDNA 2610511M17 gene	-1.08	0.319	-1.56	0.127	-1.66	0.071	-2.79	0.27	-1.77
1430512_a_at	Igbp1b	immunoglobulin (CD79A) binding protein 1b	-1.76	0.037	-1.52	0.442	-1.06	0.674	-1.16	0.642	-1.38
1434499_a_at	Ldhb	lactate dehydrogenase B	-1.07	0.361	-2.23	0.172	-1.27	0.188	-1.91	0.032	-1.62
1443025_at	---	10 days neonate medulla oblongata cDNA, RIKEN full-length enriched library, clo	-2.43	0.083	-1.03	0.85	-1.26	0.711	-2	0.383	-1.68
1432811_at	---	---	-1.3	0.27	-1.35	0.572	-1.5	0.115	-1.5	0.333	-1.42
1459885_s_at	Cox7c	cytochrome c oxidase, subunit VIIc	-1.4	0.215	-1.4	0.123	-1.35	0.122	-1.16	0.41	-1.33
1448040_at	Tfpt	TCF3 (E2A) fusion partner	-1.55	0.114	-1.64	0.405	-1.09	0.751	-1.29	0.177	-1.39
1438999_a_at	Nfat5	nuclear factor of activated T-cells 5	-1.23	0.158	-1.52	0.001	-1.43	0.143	-1.46	0.356	-1.41
1421416_at	Map2k7	mitogen activated protein kinase kinase 7	-1.63	0.026	-1.11	0.839	-1.51	0.377	-1.15	0.358	-1.35
1454318_at	2810403D21Rik	RIKEN cDNA 2810403D21 gene	-1.37	0.267	-1.51	0.172	-1.28	0.553	-1.47	0.279	-1.41
1427657_at	2310042L06Rik	RIKEN cDNA 2310042L06 gene	-2.5	0.098	-1.01	0.951	-1.27	0.317	-1.19	0.191	-1.49
1432002_at	2810471M01Rik	RIKEN cDNA 2810471M01 gene	-1.68	0.572	-1.62	0.364	-1.04	0.917	-1.54	0.313	-1.47
1435926_at	E030003F13Rik	RIKEN cDNA E030003F13 gene	-1.2	0.165	-1.29	0.182	-1.77	0.005	-1.39	0.132	-1.41
1457748_at	Pogz	pogo transposable element with ZNF domain	-2.15	0.118	-1.25	0.638	-1.1	0.762	-1.51	0.194	-1.5
1432715_at	Lrrn1	leucine rich repeat protein 1, neuronal	-1.77	0.483	-1.18	0.732	-1.32	0.43	-1.07	0.896	-1.34
1445552_at	A830039H10Rik	RIKEN cDNA A830039H10 gene	-1.48	0.244	-1.42	0.365	-1.26	0.126	-1.5	0.048	-1.42
1459959_at	Gldc	Glycine decarboxylase	-1.04	0.925	-1.86	0.238	-1.48	0.307	-1.05	0.95	-1.36
1440430_at	A130004G07Rik	RIKEN cDNA A130004G07 gene	-1.18	0.418	-1.27	0.158	-1.86	0.049	-1.37	0.065	-1.42
1457182_at	Map2k7	mitogen activated protein kinase kinase 7	-1.91	0.172	-1.1	0.839	-1.35	0.281	-2.01	0.434	-1.59
1441292_at	RP23-14F5.7	Hypothetical gene Rp23-14f5.7	-1.55	0.086	-1.12	0.874	-1.57	0.462	-5.35	0.129	-2.4
1448340_at	Tmem30a	transmembrane protein 30A	-1.18	0.088	-1.55	0.059	-1.47	0.043	-1.21	0.268	-1.35
1454401_at	5730488B01Rik	RIKEN cDNA 5730488B01 gene	-2.46	0.253	-1.22	0.691	-1.06	0.845	-1.76	0.155	-1.62
1453540_at	5430404G13Rik	RIKEN cDNA 5430404G13 gene	-1.3	0.245	-1.03	0.877	-2.33	0.021	-1.43	0.243	-1.52
1443300_at	Notch3	Notch gene homolog 3 (Drosophila)	-1.18	0.566	-1.36	0.732	-1.69	0.015	-2.3	0.349	-1.63
1419974_at	Scp2	sterol carrier protein 2, liver	-1.8	0.082	-1.46	0.111	-1.07	0.776	-1.1	0.523	-1.36
1446098_at	Zfp407	Zinc finger protein 407	-1.47	0.001	-1.02	0.951	-1.97	0.005	-1.33	0.2	-1.45
1457653_at	A630042L21Rik	RIKEN cDNA A630042L21 gene	-1.12	0.811	-1.72	0.158	-1.43	0.053	-1.55	0.172	-1.45
1459709_at	---	---	-1.15	0.486	-1.07	0.895	-2.74	0.098	-1.71	0.502	-1.67
1416552_at	Dppa5	developmental pluripotency associated 5	-1.5	0.092	-1.44	0.303	-1.23	0.251	-1.14	0.51	-1.33
1447982_at	1110008P14Rik	RIKEN cDNA 1110008P14 gene	-1.69	0.003	-1.22	0.369	-1.31	0.282	-1.04	0.938	-1.32
1433401_at	5033405D04Rik	RIKEN cDNA 5033405D04 gene	-1.1	0.674	-1.35	0.24	-1.92	0.379	-1.26	0.696	-1.41
1430404_at	4833416J08Rik	RIKEN cDNA 4833416J08 gene	-1.02	0.931	-1.63	0.108	-1.73	0.009	-1.13	0.325	-1.38
1446403_at	AU022899	expressed sequence AU022899	-1.38	0.5	-1.63	0.534	-1.2	0.643	-1.03	0.964	-1.31
1420758_at	5830411J07Rik	RIKEN cDNA 5830411J07 gene	-1.28	0.442	-1.11	0.83	-2.03	0.155	-1.35	0.7	-1.44
1447147_at	Atg7	Autophagy-related 7 (yeast)	-1.59	0.165	-1.1	0.769	-1.57	0.176	-1.55	0.236	-1.45
1427743_at	Gm672	Gene model 672, (NCBI)	-1.41	0.298	-1.31	0.18	-1.42	0.126	-1.12	0.564	-1.32
1437958_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	-1.48	0.015	-1.37	0.45	-1.3	0.048	-1.06	0.749	-1.3
1439493_at	D630040G17Rik ///	RIKEN cDNA D630040G17 gene /// similar to zinc finger protein 64 (predicted)	-1.36	0.075	-1.42	0.456	-1.36	0.161	-1.91	0.044	-1.51
1442684_x_at	Hmg20a	high mobility group 20A	-1.61	0.064	-1.11	0.657	-1.52	0.106	-1.75	0.298	-1.5
1437793_at	Tnks2	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.06	0.436	-1.5	0.309	-1.76	0.008	-1.34	0.159	-1.42
1440398_at	---	---	-1.53	0.072	-1.51	0.08	-1.16	0.586	-1.22	0.015	-1.36
1440976_at	1110035M17Rik	RIKEN cDNA 1110035M17 gene	-1.58	0.171	-1.53	0.146	-1.12	0.141	-1.01	0.928	-1.31
1439475_at	AI929863	expressed sequence AI929863	-1.58	0.072	-1.69	0.055	-1.05	0.75	-2.13	0.016	-1.61
1434943_at	BC023055	cDNA sequence BC023055	-1.21	0.438	-2.34	0.132	-1.08	0.683	-1.62	0.432	-1.56
1439275_s_at	9530010C24Rik	RIKEN cDNA 9530010C24 gene	-1.23	0.061	-1.13	0.816	-2.07	0.025	-2.54	0.175	-1.75
1441840_x_at	Stno	Strawberry notch homolog (Drosophila)	-1.66	0.466	-1.05	0.791	-1.59	0.002	-1.47	0.206	-1.44
1428298_at	1700029G01Rik	RIKEN cDNA 1700029G01 gene	-1.64	0.026	-1.07	0.88	-1.58	0.015	-1	0.998	-1.32
1450174_at	Ptprt	protein tyrosine phosphatase, receptor type, T	-2.43	0.239	-1.24	0.305	-1.04	0.876	-1.27	0.595	-1.5
1458182_at	Rbm18	RNA binding motif protein 18	-1.45	0.015	-1.29	0.012	-1.41	0.217	-1.21	0.373	-1.34
1443128_at	Ints6	integrator complex subunit 6	-1.45	0.033	-1.71	0.031	-1.1	0.593	-1.03	0.897	-1.32

1444522_at	---	Transcribed locus	-1.29	0.481	-1.93	0.182	-1.13	0.801	-1.32	0.607	-1.42
1433266_at	2810416A17Rik	RIKEN cDNA 2810416A17 gene	-1.15	0.463	-1.36	0.177	-1.74	0.009	-1.69	0.015	-1.49
1439316_at	Rbm39	RNA binding motif protein 39	-1.21	0.268	-1.25	0.144	-1.8	0.056	-1.32	0.104	-1.4
1440010_at	C230066K19Rik	RIKEN cDNA C230066K19 gene	-1.57	0.243	-1.36	0.289	-1.24	0.172	-1.62	0	-1.45
1455492_at	B330016D10Rik	RIKEN cDNA B330016D10 gene	-1.19	0.043	-1.96	0.016	-1.2	0.245	-1.41	0.149	-1.44
1459559_at	---	---	-1.01	0.967	-1.73	0.454	-1.63	0.06	-1.52	0.621	-1.47
1446200_at	Dcc	Deleted in colorectal carcinoma	-1.98	0.233	-1.05	0.942	-1.38	0.477	-1.12	0.86	-1.38
1440066_at	Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subf	-1.41	0.068	-1.26	0.142	-1.46	0.058	-1.03	0.867	-1.29
1450591_at	Olfr154	olfactory receptor 154	-1.05	0.823	-1.86	0.534	-1.44	0.129	-1.58	0.092	-1.48
1439046_at	Ccdc55	coiled-coil domain containing 55	-1.08	0.545	-1.66	0.031	-1.53	0.123	-1.25	0.366	-1.38
1444400_at	Rb1	retinoblastoma 1	-1	0.999	-2.96	0.243	-1.19	0.779	-1.8	0.449	-1.74
1422096_at	4933434I20Rik	RIKEN cDNA 4933434I20 gene	-1.4	0.035	-1.78	0.363	-1.1	0.702	-3.04	0.203	-1.83
1435119_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	-1.71	0.487	-1.1	0.729	-1.45	0.107	-1.42	0.494	-1.42
1457449_at	Lass6	Longevity assurance homolog 6 (S. cerevisiae)	-2.18	0.002	-1.04	0.891	-1.32	0.449	-1.07	0.852	-1.4
1421467_at	Runx3	runt related transcription factor 3	-1.04	0.971	-3.42	0.181	-1.08	0.907	-1.36	0.694	-1.73
1443399_at	AU021001	expressed sequence AU021001	-1.31	0.249	-1.45	0.47	-1.38	0.297	-1.57	0.006	-1.43
1421270_at	Sh3rf1	SH3 domain containing ring finger 1	-1.58	0.286	-1.25	0.754	-1.34	0.444	-2.6	0.315	-1.69
1444188_at	---	---	-1.16	0.357	-1.34	0.435	-1.74	0.006	-2.17	0.026	-1.6
1452572_at	Camk4	calcium/calmodulin-dependent protein kinase IV	-1.39	0.236	-1.27	0.532	-1.47	0.169	-1.09	0.849	-1.31
1434294_at	---	Transcribed locus	-1.24	0.572	-1.21	0.349	-1.83	0.019	-1.5	0.187	-1.44
1449727_x_at	---	---	-1.33	0.62	-1.56	0.279	-1.27	0.628	-1.03	0.942	-1.3
1457399_at	Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	-1.37	0.1	-1.17	0.488	-1.68	0.135	-1.06	0.715	-1.32
1438871_at	Son	Son cell proliferation protein	-1.09	0.663	-1.49	0.085	-1.69	0.078	-1.5	0.19	-1.44
1441463_at	---	---	-1.48	0.46	-1.19	0.414	-1.49	0.076	-1.21	0.378	-1.34
1433325_at	9330154F10Rik	RIKEN cDNA 9330154F10 gene	-1.31	0.297	-1.98	0.338	-1.09	0.858	-1.61	0.433	-1.5
1445814_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930402N10 pr	-1.95	0.365	-1.39	0.631	-1.05	0.898	-1.37	0.653	-1.44
1426104_at	Mapk14	mitogen activated protein kinase 14	-1.15	0.817	-2.77	0.021	-1.05	0.909	-1.02	0.96	-1.5
1425883_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.71	0.248	-1.66	0.237	-1	0.991	-1.34	0.465	-1.43
1440959_s_at	Mynn	myoneurin	-1.25	0.519	-1.26	0.163	-1.69	0.013	-1.15	0.455	-1.34
1439639_at	Phc2	Polyhomeotic-like 2 (Drosophila)	-1.21	0.642	-1.32	0.687	-1.65	0.177	-1.48	0.328	-1.42
1442375_at	Ubap2	Ubiquitin-associated protein 2	-1.2	0.219	-1.2	0.64	-1.91	0.003	-1.02	0.958	-1.33
1457608_at	Gimap8	GTPase, IMAP family member 8	-1.42	0.411	-1.18	0.667	-1.58	0.142	-1.92	0.346	-1.52
1429542_at	1700007B14Rik	RIKEN cDNA 1700007B14 gene	-1.04	0.95	-1.94	0.042	-1.4	0.51	-1.3	0.584	-1.42
1455421_x_at	6330503C03Rik	RIKEN cDNA 6330503C03 gene	-1.21	0.786	-2.06	0.031	-1.15	0.718	-1.94	0.334	-1.59
1433221_at	2610311E24Rik	RIKEN cDNA 2610311E24 gene	-1.82	0.036	-1.32	0.632	-1.13	0.456	-1.13	0.565	-1.35
1456812_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	-1.16	0.462	-1.71	0.194	-1.35	0.336	-1.06	0.897	-1.32
1427789_s_at	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	-1.55	0.088	-1.46	0.44	-1.17	0.734	-2.09	0.115	-1.57
1441844_at	Eps15l1	Epidermal growth factor receptor pathway substrate 15-like 1	-1.42	0.19	-1.29	0.219	-1.41	0.223	-1.19	0.64	-1.33
1420059_at	2410166I05Rik	RIKEN cDNA 2410166I05 gene	-1.26	0.016	-1.37	0.134	-1.51	0.27	-1.05	0.833	-1.3
1439810_s_at	Pramel7	preferentially expressed antigen in melanoma like 7	-1.1	0.504	-1.09	0.87	-2.78	0.293	-3.11	0.015	-2.02
1436223_at	Itgb8	integrin beta 8	-1.05	0.639	-2.38	0.079	-1.23	0.134	-1.17	0.691	-1.46
1447506_at	---	---	-1.35	0.246	-1.37	0.156	-1.39	0.254	-1.04	0.908	-1.29
1454951_at	Zfp606	zinc finger protein 606	-1.24	0.168	-1.45	0.139	-1.44	0.022	-1.52	0.162	-1.41
1446066_at	Zcchc17	zinc finger, CCHC domain containing 17	-1.47	0.204	-1.09	0.746	-1.69	0.118	-1.3	0.42	-1.39
1419245_at	Rab14	RAB14, member RAS oncogene family	-1.3	0.251	-1.64	0.051	-1.23	0.376	-1.1	0.763	-1.32
1449500_at	Serpinb7	serine (or cysteine) peptidase inhibitor, clade B, member 7	-1.32	0.666	-1.79	0.269	-1.14	0.814	-1.43	0.384	-1.42
1436818_a_at	Msi2	Musashi homolog 2 (Drosophila)	-1.31	0.18	-1.16	0.406	-1.75	0.045	-2.03	0.002	-1.56
1439818_at	AI931714	expressed sequence AI931714	-1.44	0.186	-1.14	0.668	-1.61	0.157	-1.36	0.194	-1.39
1432106_at	6530403M18Rik	RIKEN cDNA 6530403M18 gene	-1.31	0.624	-1.42	0.598	-1.38	0.51	-1.34	0.39	-1.36
1445794_at	Spag16	Sperm associated antigen 16	-1.11	0.816	-1.34	0.617	-1.83	0.194	-2.46	0.16	-1.68
1450836_at	Neurog1	neurogenin 1	-1.65	0.061	-1.2	0.765	-1.33	0.655	-1.27	0.695	-1.36
1440092_at	Ext1	Exostoses (multiple) 1	-1.16	0.346	-1.16	0.494	-2.17	0.006	-1.01	0.939	-1.37
1455203_at	A930003A15Rik	RIKEN cDNA A930003A15 gene	-2.05	0.323	-1.19	0.793	-1.16	0.764	-1.27	0.438	-1.42

1443649_at	Huwe1	HECT, UBA and WWE domain containing 1	-1.3	0.19	-1.34	0.23	-1.48	0.107	-1.3	0.371	-1.35
1441588_at	Kcnq1ot1	KCNQ1 overlapping transcript 1	-2.13	0.141	-1.09	0.903	-1.25	0.484	-1.29	0.649	-1.44
1445432_at	---	---	-1.18	0.684	-1.06	0.796	-2.51	0.209	-1.53	0.158	-1.57
1441859_x_at	Ccdc64	Coiled-coil domain containing 64	-1.25	0.707	-1.46	0.349	-1.41	0.384	-3.48	0.007	-1.9
1450079_at	Nrk	Nik related kinase	-1.82	0.253	-1.11	0.63	-1.35	0.53	-1.47	0.507	-1.44
1443011_at	Prmt7	protein arginine N-methyltransferase 7	-3.14	0.14	-1.06	0.853	-1.07	0.857	-1.41	0.397	-1.67
1419950_s_at	Tnpo3	transportin 3	-2.09	0.342	-1.25	0.535	-1.09	0.827	-1.84	0.292	-1.57
1430043_at	Ttc19	tetratricopeptide repeat domain 19	-1.3	0.483	-1.23	0.178	-1.65	0.015	-1.19	0.516	-1.34
1444936_at	D5Ertd566e	DNA segment, Chr 5, ERATO Doi 566, expressed	-2.37	0.125	-1.26	0.365	-1.02	0.923	-1.03	0.92	-1.42
1452958_at	Asphd2	aspartate beta-hydroxylase domain containing 2	-1.28	0.703	-1.82	0.166	-1.16	0.468	-1.26	0.476	-1.38
1438802_at	Foxp1	Forkhead box P1	-1.37	0.366	-1.23	0.384	-1.54	0.166	-2.58	0.091	-1.68
1432387_at	Pgcp	plasma glutamate carboxypeptidase	-2.63	0.044	-1.17	0.456	-1.04	0.943	-1.91	0.342	-1.69
1445178_at	Sh3rf1	SH3 domain containing ring finger 1	-1.01	0.969	-1.3	0.33	-2.27	0.061	-1.82	0.144	-1.6
1458879_at	C76798	expressed sequence C76798	-1.42	0.105	-1.66	0.202	-1.12	0.56	-1.43	0.161	-1.41
1445838_at	Galnt5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.08	0.237	-2.52	0.076	-1.15	0.689	-1.9	0.379	-1.66
1434494_at	Zar1	zygote arrest 1	-1.26	0.416	-1.48	0.089	-1.37	0.348	-1.4	0.623	-1.38
1458716_at	Dusp27	dual specificity phosphatase 27 (putative)	-1.4	0.635	-1.38	0.352	-1.33	0.23	-2.25	0.108	-1.59
1431528_at	5830427D02Rik	RIKEN cDNA 5830427D02 gene	-1.31	0.355	-1.25	0.066	-1.59	0.032	-1.61	0.123	-1.44
1455648_at	LOC278757 /// LOC	similar to reduced expression 2 /// similar to reduced expression 2	-1.47	0.268	-1.19	0.466	-1.49	0.049	-1.45	0.233	-1.4
1441243_at	Zfp532	Zinc finger protein 532	-1.28	0.429	-1.6	0.046	-1.27	0.263	-1.14	0.511	-1.32
1455680_at	9630025H16Rik	RIKEN cDNA 9630025H16 gene	-1.19	0.136	-1.48	0.057	-1.48	0.073	-1.51	0.013	-1.41
1447838_x_at	Eml4	echinoderm microtubule associated protein like 4	-1.77	0.116	-1.22	0.665	-1.23	0.332	-1.36	0.274	-1.4
1460616_at	Slco4c1	solute carrier organic anion transporter family, member 4C1	-1.09	0.858	-1.57	0.204	-1.57	0.203	-1.16	0.889	-1.35
1453676_at	A930041D05Rik	RIKEN cDNA A930041D05 gene	-1.31	0.157	-1.27	0.481	-1.56	0.2	-1.26	0.347	-1.35
1437170_x_at	Pdlim1 /// LOC5457	PDZ and LIM domain 1 (elfin) /// similar to PDZ and LIM domain protein 1 (Elfin) (	-1.25	0.623	-1.59	0.381	-1.3	0.653	-2.93	0.014	-1.77
1453844_at	Chit1	chitinase 1 (chitotriosidase)	-2.13	0.45	-1.3	0.426	-1.04	0.891	-2.75	0.009	-1.81
1420514_at	Tmem47	Transmembrane protein 47	-1.26	0.551	-1.05	0.324	-2.21	0.001	-2.18	0.129	-1.67
1451855_at	Bcl7a	B-cell CLL/lymphoma 7A	-1.38	0.581	-1.97	0.258	-1.04	0.958	-1.53	0.474	-1.48
1436876_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	-1.6	0.047	-1.4	0.058	-1.17	0.126	-1.78	0.179	-1.49
1458221_at	G630014P10Rik	RIKEN cDNA G630014P10 gene	-1.35	0.234	-1.52	0.068	-1.25	0.04	-1.38	0.244	-1.38
1457592_x_at	2210018M03Rik	RIKEN cDNA 2210018M03 gene	-1.39	0.287	-2.08	0.002	-1.01	0.978	-1.21	0.299	-1.42
1456638_at	Wdr59	WD repeat domain 59	-1.52	0.046	-1.27	0.063	-1.32	0.238	-1.15	0.398	-1.32
1422226_at	---	---	-1.06	0.838	-1.7	0.444	-1.5	0.097	-1.16	0.798	-1.35
1440219_at	Cspp1	Centrosome and spindle pole associated protein 1	-1.32	0.214	-1.15	0.371	-1.75	0.022	-1.22	0.068	-1.36
1455877_a_at	Nanos1	nanos homolog 1 (Drosophila)	-1.5	0.662	-1.16	0.71	-1.49	0.155	-1.04	0.844	-1.3
1440651_at	Dusp16	Dual specificity phosphatase 16	-1.02	0.888	-1.67	0.03	-1.61	0.132	-1.69	0.038	-1.5
1430910_at	4930544L04Rik	RIKEN cDNA 4930544L04 gene	-2.14	0.512	-1.22	0.667	-1.1	0.512	-1.93	0.378	-1.6
1422646_at	Mga	MAX gene associated	-1.69	0.221	-1.23	0.404	-1.26	0.212	-1	0.987	-1.3
1441155_at	2810446P07Rik	RIKEN cDNA 2810446P07 gene	-1.37	0.054	-1.14	0.46	-1.69	0.043	-1.23	0.325	-1.36
1444551_at	Itpr2	Inositol 1,4,5-triphosphate receptor 2	-1.32	0.193	-1.16	0.601	-1.72	0.376	-1.47	0.263	-1.42
1449796_at	Prph1	Peripherin 1	-1.2	0.69	-1.71	0.339	-1.29	0.724	-1.09	0.847	-1.32
1421703_at	Zfp59	zinc finger protein 59	-1.15	0.477	-2.18	0.075	-1.15	0.581	-1.05	0.865	-1.38
1451933_a_at	Cts7	cathepsin 7	-1.37	0.412	-1.93	0.34	-1.05	0.786	-1.02	0.931	-1.34
1447555_at	Utrn	Utrophin	-1.08	0.862	-1.15	0.564	-2.47	0.003	-1.51	0.135	-1.55
1454456_at	6530413G14Rik	RIKEN cDNA 6530413G14 gene	-1.48	0.415	-1.28	0.165	-1.35	0.425	-1.25	0.547	-1.34
1432352_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	-1.16	0.055	-1.12	0.203	-2.24	0.008	-1.59	0.151	-1.53
1421420_at	Ccr10	chemokine (C-C motif) receptor 10	-1.54	0.254	-1.06	0.932	-1.65	0.452	-1.77	0.212	-1.51
1437420_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	-1.37	0.275	-1.1	0.863	-1.79	0.156	-1.12	0.879	-1.34
1454919_at	AU044698	Expressed sequence AU044698	-1.19	0.152	-1.46	0.079	-1.48	0.007	-1.06	0.695	-1.3
1435639_at	2610528A11Rik	RIKEN cDNA 2610528A11 gene	-1.01	0.965	-3.14	0.037	-1.12	0.131	-1.53	0.48	-1.7
1427724_at	Top2a	topoisomerase (DNA) II alpha	-1.33	0.477	-1.56	0.017	-1.23	0.315	-1.13	0.229	-1.32
1457591_at	Nol10	Nucleolar protein 10	-1.15	0.537	-1.75	0.042	-1.31	0.379	-1.51	0.131	-1.43
1422091_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-1.56	0.298	-1.64	0.395	-1.05	0.871	-1.64	0.275	-1.47

1446014_at	---	---	-1.17	0.216	-1.49	0.056	-1.48	0.024	-1.12	0.596	-1.32
1426073_at	Twsg1	twisted gastrulation homolog 1 (Drosophila)	-1.19	0.321	-1.89	0.223	-1.2	0.352	-1.07	0.837	-1.34
1458564_at	---	---	-1.4	0.485	-1.04	0.874	-1.9	0.033	-1.6	0.505	-1.49
1419313_at	Ccnt1	cyclin T1	-1.19	0.017	-1.25	0.333	-1.79	0.05	-1.06	0.837	-1.32
1447505_at	1700020G03Rik	RIKEN cDNA 1700020G03 gene	-1.71	0.221	-1.11	0.731	-1.39	0.175	-1.45	0.408	-1.42
1440563_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	-1.09	0.831	-1.3	0.468	-1.94	0.028	-1.21	0.362	-1.39
1433140_a_at	Btbd14b	BTB (POZ) domain containing 14B	-1.76	0.291	-1.02	0.96	-1.52	0.571	-1	0.982	-1.33
1458220_at	Dlc1	deleted in liver cancer 1	-1.16	0.59	-1.07	0.847	-2.48	0.063	-1.18	0.555	-1.47
1422357_at	Magea6	melanoma antigen, family A, 6	-1.06	0.948	-2.09	0.29	-1.28	0.631	-1.66	0.527	-1.52
1429898_at	2310008M10Rik	RIKEN cDNA 2310008M10 gene	-1.19	0.616	-1.51	0.087	-1.44	0.139	-1.12	0.246	-1.31
1443468_at	---	---	-1.38	0.165	-1.15	0.559	-1.66	0.113	-1.5	0.184	-1.42
1438814_at	---	---	-1.43	0.111	-1.28	0.178	-1.38	0.453	-1.37	0.292	-1.37
1456924_at	AW492981	expressed sequence AW492981	-1.28	0.498	-1.89	0.285	-1.12	0.557	-1.21	0.59	-1.37
1456550_at	---	---	-1.23	0.209	-1.4	0.481	-1.49	0.195	-1.01	0.986	-1.28
1448329_at	Adam3	a disintegrin and metallopeptidase domain 3 (cyritestin)	-1.26	0.528	-1.33	0.35	-1.52	0.291	-1.08	0.826	-1.3
1459343_at	2700008B19Rik	RIKEN cDNA 2700008B19 gene	-2.12	0.197	-1.3	0.445	-1.04	0.887	-1.17	0.713	-1.41
1435392_at	Wdr17	WD repeat domain 17	-1.26	0.691	-1.99	0.253	-1.1	0.876	-3.07	0.375	-1.86
1437916_at	---	---	-1.49	0.414	-1.14	0.458	-1.53	0.067	-1.42	0.018	-1.39
1421079_at	Nr4a3	nuclear receptor subfamily 4, group A, member 3	-1.33	0.568	-1.32	0.684	-1.44	0.478	-1.81	0.24	-1.48
1447653_x_at	Rpl24 /// LOC6249	ribosomal protein L24 /// similar to ribosomal protein L24 /// similar to ribosomal p	-1.17	0.514	-1.53	0.005	-1.45	0.234	-1.24	0.169	-1.34
1422354_at	Olfr544	olfactory receptor 544	-1.48	0.38	-1.78	0.153	-1.03	0.918	-2.01	0.09	-1.58
1458704_at	---	Transcribed locus, moderately similar to NP_663461.2 membrane-associated rin	-1.23	0.269	-1.23	0.628	-1.73	0.206	-2.23	0.172	-1.6
1457228_x_at	Gle1l	GLE1 RNA export mediator-like (yeast	-1.3	0.165	-1.16	0.493	-1.75	0.081	-1.79	0.151	-1.5
1427522_at	Arhgap20	Rho GTPase activating protein 20	-1.46	0.65	-1.05	0.94	-1.75	0.002	-1.47	0.508	-1.43
1445204_at	Ccdc85a	Coiled-coil domain containing 85A	-1.12	0.452	-1.27	0.57	-1.89	0.149	-1.55	0.263	-1.46
1457781_at	Kcnq1ot1	KCNQ1 overlapping transcript 1	-1.28	0.15	-1.08	0.57	-2.02	0.014	-1.46	0.004	-1.46
1430902_at	Ankrd24	ankyrin repeat domain 24	-1.02	0.929	-1.23	0.631	-2.43	0.041	-1.83	0.051	-1.63
1447951_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	-1.07	0.88	-1.38	0.318	-1.84	0.087	-1.43	0.264	-1.43
1422960_at	Srd5a2	steroid 5 alpha-reductase 2	-1.22	0.032	-1	0.988	-2.59	0.066	-1.18	0.782	-1.5
1445026_at	Acvr2a	Activin receptor IIA	-1.92	0.125	-1.06	0.902	-1.34	0.6	-1.14	0.729	-1.37
1447339_at	---	Transcribed locus	-1.16	0.625	-1.68	0.447	-1.34	0.227	-1.7	0.263	-1.47
1421021_at	---	---	-1.01	0.926	-1.58	0.184	-1.7	0.052	-1.72	0.177	-1.51
1437426_at	Wac	WW domain containing adaptor with coiled-coil	-1.25	0.129	-1.25	0.127	-1.66	0.009	-1.08	0.137	-1.31
1448125_at	Rit2	Ras-like without CAAX 2	-1.3	0.787	-1.72	0.046	-1.17	0.75	-1.96	0.221	-1.54
1432010_at	4933408N05Rik	RIKEN cDNA 4933408N05 gene	-1.3	0.762	-1.69	0.146	-1.19	0.337	-1.72	0.305	-1.47
1422402_a_at	Asz1	ankyrin repeat, SAM and basic leucine zipper domain containing 1	-1.49	0.29	-1.47	0.395	-1.17	0.57	-1.22	0.67	-1.34
1418091_at	Tcfcp2l1	transcription factor CP2-like 1	-1.31	0.143	-1.16	0.66	-1.72	0.061	-1.27	0.615	-1.37
1446815_at	Zcsl3	Zinc finger, CSL-type containing 3	-1.21	0.658	-1.3	0.21	-1.62	0.048	-1.65	0.254	-1.45
1441618_at	Arhgap29	Rho GTPase activating protein 29	-1.39	0.247	-1.03	0.911	-1.94	0.005	-1.1	0.748	-1.36
1446840_at	Thrap1	Thyroid hormone receptor associated protein 1	-1.27	0.142	-1.32	0.484	-1.51	0.071	-1.29	0.289	-1.35
1450824_at	Ptch1	patched homolog 1	-1.28	0.742	-1.6	0.018	-1.25	0.579	-1.94	0.249	-1.52
1440162_x_at	A630043P06	hypothetical protein A630043P06	-1.46	0.147	-1.45	0.407	-1.21	0.654	-3.38	0.04	-1.87
1453917_at	Ifitm7	interferon induced transmembrane protein 7	-1.39	0.328	-1.37	0.589	-1.32	0.074	-1.3	0.461	-1.34
1456661_at	Jarid2	Jumonji, AT rich interactive domain 2	-1.47	0.042	-1.17	0.333	-1.49	0.068	-1.69	0.044	-1.46
1443263_at	Bach2	BTB and CNC homology 2	-1.08	0.669	-1.4	0.369	-1.77	0.062	-3.87	0.039	-2.03
1422682_s_at	Prss3 /// Prss1 /// L	protease, serine, 3 /// protease, serine, 1 (trypsin 1) /// trypsinogen 12	-1.16	0.728	-1.66	0.562	-1.36	0.585	-3.1	0.422	-1.82
1456787_at	---	---	-1.15	0.423	-1.18	0.495	-2.05	0.053	-1.92	0.199	-1.57
1454426_at	4930519E07Rik	RIKEN cDNA 4930519E07 gene	-1.03	0.973	-1.89	0.358	-1.42	0.527	-1.18	0.549	-1.38
1457489_at	Eif4e	Eukaryotic translation initiation factor 4E	-1.4	0.33	-1.14	0.689	-1.63	0.028	-1.31	0.033	-1.37
1416117_at	Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	-1.09	0.837	-1.88	0.045	-1.31	0.184	-1.46	0.139	-1.44
1422644_at	Sh3bgr	SH3-binding domain glutamic acid-rich protein	-1.07	0.864	-1.66	0.281	-1.5	0.296	-1.06	0.753	-1.32
1449590_a_at	Mras	muscle and microspikes RAS	-1.01	0.951	-1.95	0.129	-1.42	0.015	-1.75	0.043	-1.53
1446365_at	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	-1.36	0.127	-1.23	0.182	-1.51	0.002	-1.15	0.391	-1.31

1430200_at	4930579D07Rik	RIKEN cDNA 4930579D07 gene	-1.97	0.543	-1.21	0.698	-1.14	0.717	-1.25	0.744	-1.39
1440137_at	Bcl11b	B-cell leukemia/lymphoma 11B	-1.97	0.553	-1.13	0.24	-1.23	0.333	-2.11	0.235	-1.61
1441839_s_at	BC024814	cDNA sequence BC024814	-1.87	0.12	-1.34	0.405	-1.08	0.664	-1.45	0.165	-1.43
1440685_at	Calcrl	Calcitonin receptor-like	-1.36	0.182	-1.32	0.431	-1.4	0.478	-1.32	0.091	-1.35
1419166_at	Slc5a2	solute carrier family 5 (sodium/glucose cotransporter), member 2	-1.21	0.053	-2.05	0.269	-1.12	0.278	-1.89	0.496	-1.57
1453397_at	9130016M20Rik	RIKEN cDNA 9130016M20 gene	-1.31	0.021	-1.1	0.498	-1.87	0.122	-1.36	0.541	-1.41
1430827_a_at	Ptk2	PTK2 protein tyrosine kinase 2	-1.37	0.612	-1.6	0.065	-1.17	0.783	-1.1	0.831	-1.31
1423380_s_at	Nfatc4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	-1.21	0.138	-1.58	0.057	-1.33	0.253	-1.43	0.099	-1.39
1445835_at	---	Transcribed locus	-1.95	0.052	-1.18	0.737	-1.18	0.684	-1.01	0.984	-1.33
1438595_at	Gm546	gene model 546, (NCBI)	-1.85	0.008	-1.43	0.236	-1.03	0.842	-1.34	0.342	-1.41
1423253_at	Mpz	myelin protein zero	-1.93	0.361	-1.15	0.687	-1.22	0.603	-1.95	0.532	-1.56
1450374_at	Tifp39	tuberoinfundibular peptide of 39 residues (TIP39) preprohormone	-2.46	0.026	-1.01	0.991	-1.23	0.614	-3.81	0.255	-2.13
1444343_at	A130064L14Rik	RIKEN cDNA A130064L14 gene	-1.24	0.221	-1.07	0.794	-2.13	0.001	-1.94	0.06	-1.59
1426357_at	Taok1	TAO kinase 1	-1.37	0.022	-1.31	0.061	-1.39	0.059	-1.06	0.779	-1.28
1459624_at	---	---	-1.14	0.543	-1.4	0.702	-1.62	0.508	-1.17	0.735	-1.33
1447213_at	Sp100	Nuclear antigen Sp100	-1.15	0.401	-1.63	0.06	-1.37	0.283	-1.9	0.08	-1.51
1427317_at	Kin	antigenic determinant of rec-A protein	-1.7	0.141	-1.22	0.305	-1.24	0.034	-1.01	0.955	-1.29
1456832_at	Atrx	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-1.49	0.049	-1.11	0.749	-1.56	0.024	-1.31	0.211	-1.37
1453611_at	Rbbp6	retinoblastoma binding protein 6	-1.73	0.14	-1.5	0.222	-1.04	0.899	-2.41	0.278	-1.67
1458928_at	---	---	-1.32	0.056	-1.16	0.739	-1.7	0.324	-1.63	0.427	-1.45
1460622_x_at	Wdr18	WD repeat domain 18	-1.79	0.053	-1.37	0.314	-1.09	0.76	-1.34	0.129	-1.4
1432370_at	4933411E02Rik	RIKEN cDNA 4933411E02 gene	-1.22	0.639	-1.83	0.277	-1.19	0.609	-2.47	0.239	-1.68
1436918_at	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-1.37	0.037	-1.31	0.109	-1.39	0.056	-1.72	0.108	-1.45
1431040_at	6530401N04Rik ///	RIKEN cDNA 6530401N04 gene /// hypothetical protein LOC638977	-1.27	0.645	-1.14	0.797	-1.84	0.307	-1.03	0.917	-1.32
1442706_at	Nelf	nasal embryonic LHRH factor	-1.6	0.156	-1.02	0.972	-1.64	0.395	-2.31	0.373	-1.64
1438336_at	Fbxw11	F-box and WD-40 domain protein 11	-1.35	0.361	-1.38	0.411	-1.34	0.229	-1.23	0.134	-1.32
1416515_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	-1.95	0.315	-1.01	0.992	-1.41	0.4	-1.27	0.359	-1.41
1420702_at	1700093K21Rik	RIKEN cDNA 1700093K21 gene	-1.22	0.858	-1.07	0.911	-2.2	0.132	-1.28	0.318	-1.44
1457056_at	Ftcd	Formiminotransferase cyclodeaminase	-1.07	0.767	-1.47	0.534	-1.67	0.066	-1.67	0.499	-1.47
1421706_at	Mmp20	matrix metallopeptidase 20 (enamelysin)	-1.59	0.073	-1.5	0.064	-1.09	0.832	-1.09	0.863	-1.32
1451779_at	BC027061	cDNA sequence BC027061	-1.47	0.381	-1.02	0.832	-1.81	0.061	-2.22	0.151	-1.63
1457605_at	Atxn1	Ataxin 1	-1.13	0.691	-1.37	0.257	-1.67	0.018	-1.51	0.144	-1.42
1449652_at	Nudcd1	NudC domain containing 1	-1.29	0.539	-1.48	0.187	-1.3	0.443	-1.2	0.749	-1.32
1452321_at	Brwd1	bromodomain and WD repeat domain containing 1	-1.05	0.801	-1.28	0.057	-2.07	0.011	-2.5	0.058	-1.73
1434368_at	1700008K24Rik	RIKEN cDNA 1700008K24 gene	-2.47	0.214	-1.23	0.489	-1.01	0.982	-1.18	0.775	-1.47
1446697_at	---	---	-1.07	0.84	-1.47	0.493	-1.67	0.154	-1.08	0.84	-1.32
1460326_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	-1.22	0.01	-1.26	0.144	-1.66	0.05	-1.21	0.296	-1.34
1425905_at	---	---	-1.16	0.868	-1.29	0.684	-1.72	0.274	-1.99	0.144	-1.54
1439687_at	Rab14	RAB14, member RAS oncogene family	-1.22	0.302	-1.3	0	-1.6	0.112	-1.38	0.234	-1.37
1439949_at	Gsk3b	Glycogen synthase kinase 3 beta	-1.11	0.702	-1.29	0.438	-1.85	0.005	-1.04	0.273	-1.32
1455032_at	9630037P07Rik	RIKEN cDNA 9630037P07 gene	-1.14	0.148	-1.51	0.074	-1.47	0.031	-1.11	0.383	-1.31
1423104_at	Irs1	insulin receptor substrate 1	-1.16	0.153	-1.34	0.228	-1.64	0.156	-1.71	0.142	-1.46
1425673_at	Lpp	LIM domain containing preferred translocation partner in lipoma	-1.11	0.435	-1.18	0.261	-2.15	0.015	-1.69	0.184	-1.53
1445965_at	---	---	-1.18	0.339	-1.07	0.797	-2.3	0.116	-1.09	0.796	-1.41
1430683_at	Dock6 /// LOC6700	dedicator of cytokinesis 6 /// similar to Dedicator of cytokinesis protein 6	-1.23	0.289	-1.28	0.387	-1.61	0.097	-1.5	0.266	-1.4
1443736_at	Ttll10	Tubulin tyrosine ligase-like family, member 10	-1.27	0.362	-1.13	0.878	-1.84	0.153	-1.72	0.519	-1.49
1436084_at	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	-1.52	0.151	-1.45	0.299	-1.15	0.797	-1.57	0.474	-1.42
1458116_at	9530079D04Rik	RIKEN cDNA 9530079D04 gene	-1.19	0.825	-1.8	0.275	-1.21	0.474	-2.09	0.065	-1.57
1458335_x_at	2900073H19Rik	RIKEN cDNA 2900073H19 gene	-1.26	0.254	-1.57	0.301	-1.28	0.586	-2.01	0.161	-1.53
1430665_at	5730480H06Rik	RIKEN cDNA 5730480H06 gene	-1.47	0.008	-1.43	0.104	-1.2	0.191	-1.43	0.183	-1.38
1455258_at	Kcnc2	potassium voltage gated channel, Shaw-related subfamily, member 2	-1.12	0.513	-1.13	0.824	-2.24	0.34	-1.71	0.297	-1.55
1450510_a_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.06	0.569	-2.44	0.099	-1.16	0.485	-1.22	0.253	-1.47
1457776_at	D9Ertd720e	DNA segment, Chr 9, ERATO Doi 720, expressed	-1.48	0.463	-1.15	0.623	-1.48	0.038	-1.35	0.329	-1.37

1456667_at	Hdh	Huntington disease gene homolog	-1.5	0.048	-1.51	0.087	-1.12	0.378	-1.09	0.293	-1.31
1447371_at	---	---	-1.67	0.161	-1.42	0.191	-1.1	0.784	-1.23	0.617	-1.35
1434122_at	Fbxo27	F-box protein 27	-1.39	0.51	-1.69	0.048	-1.1	0.493	-1.53	0.046	-1.43
1435670_at	Tcfap2b	transcription factor AP-2 beta	-1.2	0.044	-1.12	0.802	-2.04	0.078	-1.15	0.64	-1.38
1459567_at	C77905	expressed sequence C77905	-1.25	0.622	-1.6	0.303	-1.25	0.583	-1.49	0.387	-1.4
1428815_at	4930583C14Rik	RIKEN cDNA 4930583C14 gene	-1.03	0.962	-1.83	0.343	-1.42	0.117	-1.74	0.386	-1.51
1444033_at	Anapc10	Anaphase promoting complex subunit 10	-1.14	0.113	-1.24	0.557	-1.85	0.023	-1.56	0.261	-1.45
1433801_at	9930012K11Rik	RIKEN cDNA 9930012K11 gene	-1.1	0.733	-1.83	0.052	-1.3	0.307	-1.71	0.111	-1.49
1457722_at	Klrb1f	killer cell lectin-like receptor subfamily B member 1F	-1.72	0.337	-1.27	0.336	-1.17	0.72	-1.43	0.145	-1.4
1432906_at	1700126A01Rik	RIKEN cDNA 1700126A01 gene	-1.29	0.707	-1.56	0.421	-1.24	0.47	-2.39	0.204	-1.62
1459409_at	D130073L02Rik	RIKEN cDNA D130073L02 gene	-1.14	0.036	-1.52	0.222	-1.46	0.062	-1.22	0.558	-1.34
1450687_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	-1.21	0.634	-1	0.996	-2.53	0.236	-1.25	0.452	-1.5
1419255_at	Spnb2	spectrin beta 2	-1.13	0.013	-1.24	0.383	-1.89	0.065	-1.47	0.078	-1.43
1459756_at	Cnot10	CCR4-NOT transcription complex, subunit 10	-1.6	0.05	-1.27	0.109	-1.24	0.233	-1.25	0.102	-1.34
1457806_at	Dock1	dedicator of cyto-kinesis 1	-1.14	0.476	-1.16	0.372	-2.08	0.071	-1.1	0.713	-1.37
1441739_at	Ebf4	Early B-cell factor 4	-1.65	0.282	-1.23	0.61	-1.25	0.745	-1.65	0.27	-1.44
1446100_at	Trp53bp1	Transformation related protein 53 binding protein 1	-2	0.033	-1.26	0.382	-1.08	0.871	-1.12	0.155	-1.36
1458400_at	9630050P21Rik	RIKEN cDNA 9630050P21 gene	-1.03	0.714	-1.63	0.052	-1.57	0.033	-1.46	0.224	-1.42
1452320_at	Lrp2	low density lipoprotein receptor-related protein 2	-1	0.992	-4.28	0.243	-1.01	0.955	-1.18	0.263	-1.87
1455126_x_at	2310028O11Rik	RIKEN cDNA 2310028O11 gene	-1.2	0.065	-1.3	0.091	-1.6	0.027	-1.44	0.305	-1.39
1440225_at	Gpr116	G protein-coupled receptor 116	-1.32	0.431	-1.49	0.088	-1.26	0.371	-1.67	0.076	-1.43
1418881_at	Efcbp2	EF hand calcium binding protein 2	-1.78	0.138	-1.07	0.721	-1.38	0.107	-1.18	0.616	-1.35
1435880_at	Ankrd50	ankrin repeat domain 50	-1.26	0.481	-1.26	0.003	-1.57	0.029	-1.19	0.395	-1.32
1423327_at	4930517K11Rik	RIKEN cDNA 4930517K11 gene	-1.19	0.807	-1.84	0.162	-1.19	0.65	-2.16	0.341	-1.6
1444872_at	D3Ertd740e	DNA segment, Chr 3, ERATO Doi 740, expressed	-1.09	0.791	-1.51	0.137	-1.55	0.037	-1.11	0.625	-1.32
1430069_at	4921517L17Rik	RIKEN cDNA 4921517L17 gene	-1.58	0.325	-1.15	0.671	-1.38	0.254	-1.24	0.569	-1.34
1421305_x_at	Rabep1	rabaptin, RAB GTPase binding effector protein 1	-1.27	0.217	-1.46	0.001	-1.33	0.18	-1.5	0.078	-1.39
1458615_at	Depdc5	DEP domain containing 5	-1.47	0.2	-1.49	0.07	-1.15	0.769	-1.24	0.564	-1.34
1454536_at	4933401B01Rik	RIKEN cDNA 4933401B01 gene	-1.29	0.05	-1.53	0.498	-1.26	0.144	-1.52	0.032	-1.4
1432828_at	---	---	-1.62	0.187	-1.45	0.148	-1.09	0.864	-1.35	0.512	-1.38
1421658_x_at	Psg18	pregnancy specific glycoprotein 18	-1.65	0.233	-1.07	0.886	-1.47	0.455	-1.82	0.321	-1.5
1431393_at	Six6os1	Six6 opposite strand transcript 1	-1.66	0.198	-1.01	0.992	-1.59	0.441	-1.29	0.554	-1.39
1453858_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	-1.06	0.778	-1.51	0.224	-1.62	0.082	-1.01	0.954	-1.3
1444475_at	---	---	-1.71	0.085	-1.03	0.781	-1.5	0.525	-1.35	0.638	-1.4
1447902_at	1810013A23Rik	RIKEN cDNA 1810013A23 gene	-1.16	0.686	-1.66	0.292	-1.31	0.274	-1	0.993	-1.28
1458441_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	-1.17	0.648	-1.98	0.164	-1.16	0.712	-2.28	0.06	-1.65
1456938_at	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.28	0.568	-1.03	0.912	-2.09	0.197	-1.4	0.554	-1.45
1441233_at	Srp54	Signal recognition particle 54	-1.03	0.796	-1.38	0.241	-1.91	0.002	-1.46	0.094	-1.44
1430728_at	Krtap5-5	keratin associated protein 5-5	-1.12	0.765	-1.12	0.838	-2.29	0.061	-1.61	0.263	-1.54
1443426_at	Sltm	SAFB-like, transcription modulator	-1.11	0.309	-1.54	0.069	-1.48	0.012	-1.5	0.173	-1.41
1442525_at	---	Transcribed locus	-1.13	0.683	-1.56	0.088	-1.43	0.272	-1.33	0.374	-1.36
1448081_at	Colq	Collagen-like tail subunit (single strand of homotrimer) of asymmetric acetylcholin	-1.16	0.368	-1.94	0.184	-1.18	0.659	-1.67	0.183	-1.49
1453806_at	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	-1.24	0.707	-1.59	0.273	-1.26	0.588	-1.05	0.646	-1.29
1450252_at	Onecut1	one cut domain, family member 1	-1.07	0.742	-2.14	0.265	-1.21	0.065	-1.25	0.426	-1.42
1454493_at	5033425B01Rik	RIKEN cDNA 5033425B01 gene	-1.22	0.345	-1.31	0.534	-1.54	0.479	-1.45	0.394	-1.38
1455638_at	Zfp319	zinc finger protein 319	-1	0.999	-1.76	0.476	-1.52	0.046	-2.4	0.027	-1.67
1453580_at	5630401D24Rik	RIKEN cDNA 5630401D24 gene	-1.29	0.662	-1.53	0.225	-1.25	0.175	-1.05	0.846	-1.28
1444653_at	---	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732412F1	-1.22	0.731	-1.4	0.058	-1.44	0.627	-2.26	0.09	-1.58
1447314_at	Tgfbr3	Transforming growth factor, beta receptor III	-1.24	0.384	-1.1	0.752	-1.95	0.071	-1.35	0.247	-1.41
1453237_at	Qars	glutaminyl-tRNA synthetase	-1.18	0.653	-1.83	0.052	-1.21	0.53	-2.33	0.006	-1.64
1455327_at	Senp2	SUMO/sentrin specific peptidase 2	-1.31	0.402	-1.32	0.281	-1.42	0	-1.02	0.929	-1.27
1437665_at	Il22ra2	Interleukin 22 receptor, alpha 2	-1.94	0.178	-1.04	0.932	-1.34	0.487	-1.84	0.249	-1.54
1446079_at	Zmat2	zinc finger, matrin type 2	-1.14	0.335	-1.71	0.158	-1.32	0.091	-1.22	0.323	-1.35

1443355_at	---	---	-1.03	0.925	-1.25	0.346	-2.21	0.006	-1.28	0.444	-1.44
1432781_at	Pdzd6	PDZ domain containing 6	-1.01	0.984	-1.31	0.413	-2.11	0.34	-1.24	0.443	-1.42
1431569_a_at	Lypd1	Ly6/Plaur domain containing 1	-1.25	0.61	-1.35	0.651	-1.46	0.584	-1.33	0.71	-1.35
1440394_at	---	---	-1.64	0.229	-1.32	0.166	-1.17	0.494	-1.31	0.458	-1.36
1440467_at	BC028799 /// 4922	cDNA sequence BC028799 /// RIKEN cDNA 4922501C03 gene	-1.39	0.546	-1.58	0.411	-1.14	0.509	-1.11	0.663	-1.3
1419095_a_at	Apom	apolipoprotein M	-1.15	0.455	-1.21	0.096	-1.9	0.356	-1.25	0.448	-1.38
1428512_at	Bhlhb9	basic helix-loop-helix domain containing, class B9	-1.12	0.196	-1.71	0.086	-1.34	0.035	-1.36	0.189	-1.38
1457908_at	Zfp407	Zinc finger protein 407	-1.02	0.956	-1.4	0.18	-1.89	0.043	-1.32	0.147	-1.41
1456683_at	Sltm	SAFB-like, transcription modulator	-1.33	0.093	-1.24	0.14	-1.48	0.001	-1.43	0.22	-1.37
1431865_a_at	4933405K07Rik	RIKEN cDNA 4933405K07 gene	-1.07	0.829	-1.42	0.211	-1.7	0.408	-1.89	0.199	-1.52
1442983_at	Slc23a2	Solute carrier family 23 (nucleobase transporters), member 2	-1.24	0.356	-1.1	0.64	-1.92	0.027	-1.19	0.144	-1.37
1450514_at	Zscan2	zinc finger and SCAN domain containing 2	-1.13	0.16	-1.38	0.656	-1.62	0.44	-1.25	0.715	-1.34
1424491_at	---	---	-1.02	0.943	-1.61	0.338	-1.6	0.208	-1.19	0.391	-1.35
1444621_at	Iqsec2	IQ motif and Sec7 domain 2	-1.55	0.44	-1.08	0.852	-1.51	0.557	-1.85	0.485	-1.5
1437775_at	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate comple	-1.22	0.209	-1.34	0.214	-1.51	0.086	-1.1	0.549	-1.29
1441378_at	---	---	-1.1	0.163	-1.49	0.179	-1.54	0.2	-1.22	0.649	-1.34
1442111_at	D430033H22Rik	RIKEN cDNA D430033H22 gene	-1.06	0.527	-1.37	0.004	-1.79	0.032	-1.24	0.335	-1.36
1446353_at	Tubb6	Tubulin, beta 6	-1.14	0.652	-1.4	0.477	-1.56	0.063	-1.42	0.153	-1.38
1432676_at	---	---	-1.29	0.394	-1.84	0.073	-1.1	0.648	-1.71	0.018	-1.48
1451590_at	Cplx4	complexin 4	-1.99	0.073	-1.19	0.735	-1.13	0.783	-1.6	0.532	-1.48
1420275_at	---	---	-2.21	0.048	-1.24	0.572	-1.03	0.93	-1.19	0.522	-1.42
1419167_at	Prap1	proline-rich acidic protein 1	-1.22	0.595	-1.79	0.15	-1.17	0.5	-1.23	0.199	-1.35
1435904_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	-1.31	0.015	-1.3	0.037	-1.44	0.187	-1.17	0.564	-1.3
1430068_at	C030011L09Rik	RIKEN cDNA C030011L09 gene	-1.4	0.411	-1.4	0.555	-1.25	0.4	-2.08	0.33	-1.53
1453083_at	6430701C03Rik	RIKEN cDNA 6430701C03 gene	-1.48	0.071	-1.24	0.292	-1.33	0.175	-1.17	0.34	-1.31
1452108_at	Igf1r	insulin-like growth factor I receptor	-1.74	0.01	-1.5	0.344	-1.01	0.934	-1.02	0.979	-1.32
1419363_a_at	Mrpl35	mitochondrial ribosomal protein L35	-1.3	0.024	-1.43	0.013	-1.3	0.039	-1.07	0.712	-1.28
1449921_s_at	Cpne6	copine VI	-1.45	0.128	-1.21	0.448	-1.4	0.468	-1.12	0.488	-1.29
1442181_at	Grlf1	Glucocorticoid receptor DNA binding factor 1	-1.17	0.505	-1.21	0.242	-1.79	0.059	-1.52	0.013	-1.43
1443538_at	---	---	-1.09	0.806	-1.19	0.75	-2.08	0.174	-1.06	0.8	-1.36
1432897_at	4930435N07Rik	RIKEN cDNA 4930435N07 gene	-1.05	0.716	-2.32	0.047	-1.17	0.407	-1.79	0.37	-1.58
1420662_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	-1.28	0.073	-1.5	0.59	-1.27	0.492	-1.19	0.442	-1.31
1418207_at	Fxyd4	FXYD domain-containing ion transport regulator 4	-1.2	0.359	-1.63	0.169	-1.27	0.214	-1.31	0.568	-1.35
1432656_at	3222402N08Rik	RIKEN cDNA 3222402N08 gene	-2.16	0.391	-1.27	0.548	-1.02	0.711	-1.02	0.971	-1.37
1439283_at	Osbpl9	Oxysterol binding protein-like 9	-1.34	0.351	-1.05	0.579	-1.86	0.038	-1.57	0.153	-1.46
1454215_at	2410007B07Rik	RIKEN cDNA 2410007B07 gene	-1.2	0.283	-1.62	0.223	-1.28	0.069	-1.63	0.622	-1.43
1442206_at	Mamdc1	MAM domain containing 1	-1.83	0.343	-1.11	0.639	-1.27	0.024	-1.43	0.066	-1.41
1440353_at	Ntf5	neurotrophin 5	-1.47	0.308	-1.38	0.206	-1.21	0.222	-1.33	0.663	-1.35
1431302_a_at	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-1.15	0.282	-1.92	0.103	-1.18	0.138	-1.18	0.438	-1.36
1456712_at	Lcorl	ligand dependent nuclear receptor corepressor-like	-1.31	0.056	-1.41	0.017	-1.31	0.115	-1.16	0.527	-1.3
1459322_at	Syne2	Synaptic nuclear envelope 2	-1.21	0.405	-1.32	0.432	-1.55	0.119	-1.05	0.741	-1.28
1425662_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.09	0.689	-1.68	0.123	-1.38	0.096	-1.42	0.427	-1.39
1433337_at	6720460K10Rik	RIKEN cDNA 6720460K10 gene	-1.63	0.411	-1.05	0.812	-1.5	0.288	-1.22	0.73	-1.35
1439163_at	Zbtb16	zinc finger and BTB domain containing 16	-1.48	0.758	-1.46	0.45	-1.15	0.785	-1.98	0.381	-1.52
1440274_at	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	-1.61	0.022	-1	0.989	-1.62	0.1	-2.88	0.13	-1.78
1445001_at	---	---	-1.1	0.536	-1.29	0.185	-1.81	0.03	-1.15	0.547	-1.34
1455789_x_at	LOC621284	similar to heat shock protein 8	-1.35	0.114	-1.31	0.266	-1.36	0.056	-1.17	0.139	-1.3
1458226_at	Flnb	filamin, beta	-1.16	0.459	-2.43	0.281	-1.04	0.877	-1.18	0.813	-1.45
1446790_at	C78948	expressed sequence C78948	-1.55	0.469	-1.13	0.737	-1.42	0.125	-4.34	0.063	-2.11
1438273_at	---	---	-1.11	0.752	-1.03	0.951	-2.71	0.027	-1.36	0.287	-1.55
1425083_at	Otor	otoraplin	-1.5	0.494	-1.29	0.609	-1.26	0.572	-1.73	0.405	-1.45
1430196_at	8430408J09Rik	RIKEN cDNA 8430408J09 gene	-1.37	0.118	-1.14	0.626	-1.59	0.061	-1.75	0.096	-1.46
1437963_at	C530045E16Rik	RIKEN cDNA C530045E16 gene	-1.35	0.497	-1.98	0.255	-1.01	0.973	-1.67	0.146	-1.5

1458185_at	Thap4	THAP domain containing 4	-1.38	0.111	-1.3	0.338	-1.35	0.121	-1.25	0.082	-1.32
1456121_at	Lrriq2	leucine-rich repeats and IQ motif containing 2	-1.49	0.276	-1.12	0.785	-1.49	0.068	-1.31	0.371	-1.35
1452549_at	Gm1549	gene model 1549, (NCBI)	-3.51	0.039	-1.05	0.939	-1	0.994	-1.8	0.007	-1.84
1458186_at	---	Transcribed locus	-1.42	0.036	-1.09	0.729	-1.63	0.064	-1.29	0.513	-1.36
1458977_at	A530021J07	hypothetical protein A530021J07	-1.6	0.3	-1.06	0.923	-1.49	0.431	-2.33	0.151	-1.62
1426320_at	4933437K13Rik	RIKEN cDNA 4933437K13 gene	-1.22	0.368	-1.6	0.139	-1.26	0.266	-2.15	0.033	-1.56
1420577_at	Aicda	activation-induced cytidine deaminase	-1.97	0.099	-1.02	0.946	-1.33	0.422	-1.69	0.331	-1.5
1422800_at	Bat2	HLA-B associated transcript 2	-1.74	0.255	-1.5	0.37	-1	0.993	-1.54	0.252	-1.45
1442485_at	---	---	-1.71	0.183	-1.13	0.616	-1.31	0.519	-1.26	0.523	-1.35
1439945_at	Zfp449	zinc finger protein 449	-1.27	0.358	-1.35	0.299	-1.42	0.134	-1.29	0.353	-1.33
1451614_a_at	Amelx	amelogenin X chromosome	-1.63	0.259	-1.57	0.019	-1.01	0.955	-1.68	0.543	-1.47
1449793_at	---	---	-1.2	0.525	-1.31	0.581	-1.55	0.101	-1.94	0.155	-1.5
1435559_at	Myo6	myosin VI	-1.23	0.288	-1.38	0.07	-1.43	0.024	-1.26	0.682	-1.32
1460081_at	Syt7	Synaptotagmin VII	-1.84	0.051	-1.14	0.321	-1.22	0.337	-1.83	0.253	-1.51
1460103_at	---	---	-2.11	0.116	-1.11	0.685	-1.15	0.742	-1.22	0.512	-1.4
1431403_a_at	2900002G04Rik	RIKEN cDNA 2900002G04 gene	-1.19	0.2	-1.58	0.254	-1.31	0.417	-1.07	0.897	-1.29
1446138_at	Kifap3	Kinesin-associated protein 3	-1.02	0.939	-1.52	0.484	-1.67	0.111	-1.64	0.135	-1.46
1438285_at	2210015D19Rik	RIKEN cDNA 2210015D19 gene	-1.26	0.16	-1.38	0.155	-1.39	0.152	-1.29	0.219	-1.33
1458881_at	9530001P21Rik	RIKEN cDNA 9530001P21 gene	-2.43	0.116	-1.18	0.655	-1.02	0.941	-1.36	0.484	-1.5
1438127_at	LOC552906	hypothetical LOC552906	-1.1	0.698	-1.34	0.184	-1.71	0.114	-1.18	0.33	-1.33
1427944_at	C1qdc1	C1q domain containing 1	-1.38	0.036	-1.19	0.551	-1.49	0.065	-1.2	0.271	-1.31
1441046_at	---	---	-1.26	0.429	-1.3	0.243	-1.49	0.144	-1.27	0.244	-1.33
1438457_at	---	Transcribed locus, strongly similar to XP_574375.1 PREDICTED: similar to MGC	-1.82	0.178	-1.38	0.386	-1.04	0.83	-1.03	0.965	-1.31
1433800_a_at	Pomc1	pro-opiomelanocortin-alpha	-1.42	0.019	-1.36	0.545	-1.25	0.395	-1.73	0.021	-1.44
1459481_at	Pcdh11x	Protocadherin 11 X-linked	-2.1	0.028	-1.12	0.871	-1.14	0.762	-1.79	0.345	-1.54
1434490_at	Scarf1	scavenger receptor class F, member 1	-1.28	0.398	-1.49	0.303	-1.27	0.42	-1.1	0.715	-1.28
1459276_at	A530088E08Rik	RIKEN cDNA A530088E08 gene	-2.44	0.441	-1.04	0.943	-1.15	0.767	-1.38	0.395	-1.5
1455425_at	BB001228	expressed sequence BB001228	-1.29	0.087	-1.24	0.717	-1.52	0.083	-2.25	0.032	-1.58
1441779_at	9530006C21Rik	RIKEN cDNA 9530006C21 gene	-1.29	0.191	-1.09	0.694	-1.84	0.055	-1.92	0.124	-1.53
1459398_at	---	---	-1.26	0.449	-1.45	0.502	-1.32	0.273	-1.97	0.192	-1.5
1445543_at	9830124H08Rik	RIKEN cDNA 9830124H08 gene	-1.09	0.268	-1.44	0.16	-1.6	0.027	-1.31	0.442	-1.36
1439484_at	4930431H11Rik	RIKEN cDNA 4930431H11 gene	-1.1	0.745	-1.91	0.101	-1.24	0.197	-1.62	0.22	-1.46
1423595_at	Mina	myc induced nuclear antigen	-1.32	0.087	-1.47	0.05	-1.25	0.084	-1.22	0.118	-1.31
1443086_at	Alcam	activated leukocyte cell adhesion molecule	-1.17	0.411	-1.18	0.158	-1.85	0.001	-1.37	0.313	-1.39
1433863_at	Btf3 /// LOC640665	basic transcription factor 3 /// similar to basic transcription factor 3 /// similar to ba	-1.32	0.115	-1.18	0.493	-1.58	0.07	-1.18	0.502	-1.31
1440247_at	Phf14	PHD finger protein 14	-1.58	0.196	-1.09	0.757	-1.46	0.35	-2.15	0.033	-1.57
1435480_at	Braf	Braf transforming gene	-1.15	0.279	-1.29	0.001	-1.67	0.03	-1.17	0.07	-1.32
1443862_at	---	---	-1.02	0.892	-1.39	0.049	-1.84	0.025	-1.58	0.169	-1.46
1416602_a_at	Rad52	RAD52 homolog (S. cerevisiae)	-1.56	0.004	-1.33	0.002	-1.18	0.65	-1.35	0.118	-1.35
1432222_at	A930015G24Rik	RIKEN cDNA A930015G24 gene	-1.4	0.066	-1.11	0.864	-1.6	0.205	-1.14	0.78	-1.31
1456257_at	C130065N10Rik	RIKEN cDNA C130065N10 gene	-1.09	0.628	-1.45	0.346	-1.58	0.047	-1.24	0.38	-1.34
1456321_at	Npal1	NIPA-like domain containing 1	-1.73	0.673	-1.04	0.933	-1.43	0.247	-1.98	0.019	-1.54
1442749_at	Braf	Braf transforming gene	-1.01	0.958	-1.49	0.281	-1.71	0.032	-1.49	0.333	-1.43
1444909_at	---	Transcribed locus	-2.56	0.187	-1.15	0.522	-1.02	0.94	-1.18	0.785	-1.48
1445231_at	B230112C05Rik	RIKEN cDNA B230112C05 gene	-1.58	0.114	-1.07	0.642	-1.48	0.42	-1.71	0.229	-1.46
1425223_at	Birc3	baculoviral IAP repeat-containing 3	-1.28	0.602	-1.23	0.361	-1.54	0.244	-2.17	0.174	-1.55
1444345_at	---	Transcribed locus	-1.02	0.938	-1.55	0.443	-1.62	0.313	-2.05	0.239	-1.56
1440365_at	Actb	Actin, beta, cytoplasmic	-1.24	0.292	-1.19	0.557	-1.68	0.016	-1.14	0.347	-1.31
1447983_at	Zfml	Zinc finger, matrin-like	-1.84	0.28	-1.13	0.853	-1.23	0.55	-1.46	0.354	-1.41
1460546_at	Lgi3	leucine-rich repeat LGI family, member 3	-1.14	0.672	-1.91	0.007	-1.19	0.209	-2.19	0.214	-1.61
1447387_at	---	---	-1.23	0.464	-1.26	0.573	-1.58	0.261	-1.41	0.674	-1.37
1436093_at	Epha10	Eph receptor A10	-1.12	0.598	-1.23	0.453	-1.85	0.202	-1.22	0.175	-1.36
1446504_at	---	---	-1.01	0.933	-1.49	0.043	-1.71	0.056	-1.3	0.268	-1.38

1451980_at	Casd1	CAS1 domain containing 1	-1.3	0.351	-1.24	0.105	-1.5	0.002	-1.47	0.09	-1.38
1432813_at	2900064F13Rik	RIKEN cDNA 2900064F13 gene	-1.33	0.621	-1.64	0.402	-1.13	0.574	-1.38	0.275	-1.37
1434311_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	-1.22	0.176	-1.26	0.289	-1.59	0.049	-1.28	0.289	-1.34
1457398_at	Gdi2	Guanosine diphosphate (GDP) dissociation inhibitor 2	-1.18	0.071	-1.3	0.13	-1.59	0.008	-1.81	0.12	-1.47
1438842_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	-1.19	0.399	-1.59	0.348	-1.3	0.431	-1.34	0.415	-1.35
1441100_at	Mbtd1	mbt domain containing 1	-1.15	0.195	-1.38	0.04	-1.54	0.049	-1.75	0.054	-1.45
1446940_at	Traf6	Tnf receptor-associated factor 6	-2.01	0.343	-1.02	0.982	-1.31	0.435	-1.09	0.902	-1.36
1452646_at	Trp53inp2	tumor protein p53 inducible nuclear protein 2	-1.25	0.021	-1.58	0.213	-1.23	0.458	-1.29	0.279	-1.34
1429721_s_at	4930579C15Rik	RIKEN cDNA 4930579C15 gene	-1.19	0.484	-1.06	0.794	-2.15	0.164	-1.77	0.291	-1.54
1439689_at	9030224M15Rik	RIKEN cDNA 9030224M15 gene	-1.29	0.255	-1.12	0.839	-1.74	0.042	-1.29	0.464	-1.36
1429820_at	Rutbc2	RUN and TBC1 domain containing 2	-1.05	0.935	-2.27	0.008	-1.18	0.781	-2.5	0.097	-1.75
1438036_x_at	AW061290	expressed sequence AW061290	-1.32	0.27	-1.44	0.029	-1.26	0.226	-1.09	0.707	-1.28
1432915_at	5730407I07Rik	RIKEN cDNA 5730407I07 gene	-1.31	0.742	-1.25	0.591	-1.47	0.4	-1.89	0.317	-1.48
1434467_at	Atcay	ataxia, cerebellar, Cayman type homolog (human)	-1.16	0.563	-1.71	0.17	-1.26	0.619	-1.52	0.468	-1.41
1440698_at	Unc5c	Unc-5 homolog C (C. elegans)	-1.27	0.109	-1.35	0.621	-1.39	0.309	-1.01	0.988	-1.25
1444647_at	Plaa	phospholipase A2, activating protein	-1.05	0.248	-1.34	0.327	-1.83	0.046	-1.18	0.296	-1.35
1441925_at	Slc15a4	solute carrier family 15, member 4	-1.77	0.518	-1.25	0.091	-1.13	0.631	-2.13	0.401	-1.57
1445589_at	Slc23a2	Solute carrier family 23 (nucleobase transporters), member 2	-1.01	0.979	-1.23	0.221	-2.29	0.002	-1.44	0.152	-1.49
1440653_at	Phip	Pleckstrin homology domain interacting protein	-1	0.992	-2.61	0.064	-1.15	0.707	-1.17	0.317	-1.49
1445733_at	2610206G21Rik	RIKEN cDNA 2610206G21 gene	-1.29	0.115	-1.1	0.82	-1.77	0.269	-1.22	0.697	-1.35
1457775_at	Sacs	sacsin	-2.05	0.168	-1.03	0.954	-1.28	0.56	-1.7	0.473	-1.51
1447948_at	A430107O13Rik	RIKEN cDNA A430107O13 gene	-1.19	0.192	-1.36	0.097	-1.48	0.217	-1.22	0.142	-1.31
1437431_at	---	---	-1.44	0.328	-1.03	0.903	-1.73	0.096	-1.51	0.181	-1.43
1458790_at	---	---	-1.45	0.484	-1.22	0.691	-1.35	0.642	-2.33	0.36	-1.59
1442535_at	Zfp609	Zinc finger protein 609	-1.18	0.04	-1.18	0.52	-1.8	0.008	-1.26	0.443	-1.36
1440223_at	Rbm6	RNA binding motif protein 6	-1.07	0.499	-1.29	0.001	-1.85	0.006	-1.34	0.085	-1.39
1418559_at	Tesp1	testicular serine protease 1	-1.3	0.728	-1.61	0.445	-1.17	0.756	-1.31	0.701	-1.35
1440649_at	Tes	Testis derived transcript	-1.21	0.492	-1.83	0.202	-1.14	0.765	-1.75	0.081	-1.48
1456771_at	Zyg11bl	zyg-11 homolog B (C. elegans)-like	-1.13	0.322	-2.2	0.026	-1.1	0.656	-1.73	0.261	-1.54
1456453_at	Evl	Ena-vasodilator stimulated phosphoprotein	-2.03	0.166	-1.13	0.504	-1.15	0.456	-2.58	0.03	-1.72
1444496_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	-1.48	0.117	-1.52	0.16	-1.09	0.754	-1.69	0.197	-1.45
1425292_at	Dtna	dystrobrevin alpha	-1.17	0.048	-1.21	0.643	-1.75	0.043	-1.47	0.6	-1.4
1437073_x_at	AV025504	expressed sequence AV025504	-1.02	0.707	-2.78	0.004	-1.1	0.43	-1.08	0.367	-1.49
1447016_at	Tbc1d1	TBC1 domain family, member 1	-1.48	0.073	-1.51	0.289	-1.1	0.745	-2.69	0.076	-1.69
1460119_at	---	16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430415C1	-1.12	0.547	-1.26	0.357	-1.78	0.079	-1.3	0.111	-1.36
1449068_at	Zfp148	zinc finger protein 148	-1.16	0.212	-1.32	0.022	-1.59	0.054	-1.36	0.114	-1.36
1417757_at	Unc13b	unc-13 homolog B (C. elegans)	-1.63	0.285	-1.04	0.91	-1.49	0.132	-1.16	0.711	-1.33
1424272_at	Stat3	signal transducer and activator of transcription 3	-1.57	0.302	-1.52	0.36	-1.05	0.757	-1.32	0.54	-1.36
1449542_at	Pbx1	pre B-cell leukemia transcription factor 1	-1.13	0.589	-1.4	0.315	-1.53	0.083	-1.99	0.015	-1.52
1440931_at	Scrt2	scratch homolog 2, zinc finger protein (Drosophila)	-1.48	0.595	-1.06	0.632	-1.58	0.467	-1.09	0.708	-1.3
1441490_at	Tmem39a	transmembrane protein 39a	-1.93	0.008	-1.05	0.736	-1.28	0.109	-1.26	0.317	-1.38
1454229_a_at	Exod1	exonuclease domain containing 1	-1.52	0.117	-1.21	0.66	-1.31	0.578	-1.06	0.922	-1.28
1439958_at	LOC546257 /// LOC	similar to transcription elongation factor B polypeptide 3 binding protein 1 isoform	-1.69	0.464	-1.08	0.828	-1.37	0.285	-1.26	0.609	-1.35
1443169_at	Cnot4	CCR4-NOT transcription complex, subunit 4	-1.81	0.121	-1.41	0.587	-1.01	0.977	-1.22	0.289	-1.36
1429131_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	-1.45	0.089	-1.13	0.517	-1.49	0.112	-1.1	0.253	-1.29
1448700_at	G0s2	G0/G1 switch gene 2	-1.18	0.462	-1.33	0.56	-1.53	0.244	-1.46	0.016	-1.38
1449125_at	Tnfaip8l1	tumor necrosis factor, alpha-induced protein 8-like 1	-1.71	0.394	-1.44	0.091	-1.03	0.81	-1.3	0.089	-1.37
1442750_at	---	Transcribed locus	-1.29	0.673	-1.02	0.923	-2	0.068	-1.03	0.905	-1.34
1442392_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430024M	-1.32	0.216	-1.64	0.523	-1.13	0.699	-1.08	0.6	-1.29
1459906_at	Dgkh	Diacylglycerol kinase, eta	-1.3	0.422	-1.52	0.119	-1.21	0.248	-1.42	0	-1.36
1456656_at	Lin7a	lin-7 homolog A (C. elegans)	-1.35	0.517	-1.4	0.112	-1.25	0.591	-1.05	0.924	-1.26
1460128_at	Tmed2	Transmembrane emp24 domain trafficking protein 2	-1.74	0.165	-1.04	0.938	-1.4	0.15	-1.39	0.645	-1.39
1441964_at	1110003F05Rik	RIKEN cDNA 1110003F05 gene	-1.24	0.265	-1.29	0.116	-1.5	0.103	-1.17	0.771	-1.3

1441002_at	Pop1	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae)	-1.48	0.423	-1.04	0.926	-1.62	0.101	-1.61	0.068	-1.44
1442907_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	-1.4	0.429	-1.73	0.112	-1.04	0.871	-1.09	0.696	-1.32
1422148_at	Matn3	matrilin 3	-1.81	0.532	-1.02	0.974	-1.39	0.398	-1.77	0.389	-1.5
1428940_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	-1.29	0.022	-1.51	0.142	-1.23	0.078	-1.08	0.821	-1.28
1447719_at	Apoh	Apolipoprotein H	-2.01	0.185	-1.14	0.486	-1.14	0.733	-1.33	0.471	-1.4
1454839_a_at	Ccdc84	coiled-coil domain containing 84	-1.31	0.287	-1.41	0.029	-1.29	0.02	-1.44	0.087	-1.36
1444902_at	Fbxl10	F-box and leucine-rich repeat protein 10	-1.36	0.037	-1.23	0.243	-1.42	0.179	-1.25	0.245	-1.32
1421652_at	Htr3b	5-hydroxytryptamine (serotonin) receptor 3B	-1.65	0.334	-1.21	0.799	-1.22	0.708	-2.5	0.164	-1.65
1438034_at	2410005O16Rik	RIKEN cDNA 2410005O16 gene	-1.29	0.316	-1.23	0.028	-1.52	0.13	-1.19	0.351	-1.31
1431024_a_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-1.41	0.298	-1.36	0.109	-1.24	0.345	-1.18	0.543	-1.3
1431660_at	4930564D02Rik	RIKEN cDNA 4930564D02 gene	-1.08	0.819	-1.41	0.278	-1.62	0.483	-1.57	0.333	-1.42
1430397_at	Got2 /// LOC64084	glutamate oxaloacetate transaminase 2, mitochondrial /// similar to Aspartate ami	-1.03	0.741	-1.93	0.166	-1.31	0.456	-1.52	0.166	-1.45
1437037_x_at	AL033314	expressed sequence AL033314	-1.46	0.341	-1.37	0.406	-1.19	0.711	-1.51	0.163	-1.38
1418863_at	Gata4	GATA binding protein 4	-1.51	0.304	-1.27	0.361	-1.25	0.662	-4.28	0	-2.08
1454367_at	4930413G21Rik	RIKEN cDNA 4930413G21 gene	-1.09	0.868	-1.46	0.202	-1.53	0.191	-1.1	0.678	-1.3
1422419_s_at	Tnp2	transition protein 2	-1.38	0.004	-1.12	0.825	-1.58	0.141	-1.23	0.165	-1.33
1458507_at	2810055G22Rik	RIKEN cDNA 2810055G22 gene	-1.94	0.315	-1.06	0.91	-1.25	0.275	-1.34	0.425	-1.4
1449995_at	4933421I07Rik	RIKEN cDNA 4933421I07 gene	-1.36	0.162	-1.5	0.273	-1.17	0.723	-1.47	0.547	-1.38
1430014_at	5430419D17Rik	RIKEN cDNA 5430419D17 gene	-1.5	0.506	-1.12	0.715	-1.44	0.216	-1.63	0.236	-1.42
1455687_at	Ick	intestinal cell kinase	-1.22	0.591	-1.42	0.175	-1.36	0.213	-1.4	0.448	-1.35
1454984_at	AW061234	expressed sequence AW061234	-1.12	0.656	-1.63	0.093	-1.34	0.163	-1.49	0.126	-1.4
1442497_at	Smchd1	SMC hinge domain containing 1	-1.32	0.562	-1.84	0.043	-1.05	0.853	-1.21	0.306	-1.35
1454233_at	2310006M14Rik	RIKEN cDNA 2310006M14 gene	-1.45	0.381	-1.39	0.273	-1.18	0.548	-2.69	0.06	-1.68
1433212_at	2700008E08Rik	RIKEN cDNA 2700008E08 gene	-1.17	0.738	-1.47	0.217	-1.39	0.152	-1.12	0.74	-1.29
1438035_at	AW061290	expressed sequence AW061290	-1.32	0.237	-1.43	0.019	-1.26	0.289	-1.18	0.235	-1.3
1440028_at	Atg7	Autophagy-related 7 (yeast)	-1.19	0.294	-1.16	0.669	-1.83	0.135	-1.77	0.08	-1.48
1442079_at	Tmem23	transmembrane protein 23	-1.12	0.037	-1.22	0.616	-1.83	0.024	-1.24	0.517	-1.35
1423934_at	---	---	-1.39	0.163	-1.38	0.422	-1.23	0.518	-1.92	0.22	-1.48
1443286_at	AU019754	expressed sequence AU019754	-1.24	0.564	-1.23	0.648	-1.57	0.163	-1.06	0.893	-1.28
1459680_at	Tomm40	Translocase of outer mitochondrial membrane 40 homolog (yeast)	-1.2	0.326	-1.57	0.228	-1.27	0.586	-1.1	0.619	-1.28
1417319_at	Pvrl3	poliovirus receptor-related 3	-1.22	0.056	-1.07	0.582	-1.98	0.009	-1.55	0.172	-1.46
1427714_at	Smyd1	SET and MYND domain containing 1	-1.56	0.542	-1.17	0.31	-1.32	0.588	-1.11	0.725	-1.29
1429811_at	4933424B01Rik	RIKEN cDNA 4933424B01 gene	-1.48	0.178	-1.42	0.114	-1.14	0.665	-1.37	0.099	-1.35
1455878_at	2700023E23Rik	RIKEN cDNA 2700023E23 gene	-1.27	0.164	-1.44	0.141	-1.29	0.191	-1.24	0.528	-1.31
1453390_at	4930428F12Rik	RIKEN cDNA 4930428F12 gene	-1.22	0.542	-1.49	0.225	-1.3	0.386	-2.34	0.301	-1.59
1431911_at	4931423N10Rik	RIKEN cDNA 4931423N10 gene	-1.27	0.479	-1.61	0.561	-1.18	0.334	-1	0.997	-1.27
1430075_at	Sf3b3	splicing factor 3b, subunit 3	-1.25	0.254	-1.16	0.563	-1.67	0.022	-1.38	0.2	-1.37
1450523_at	Cntn2	contactin 2	-1.39	0.412	-1.26	0.202	-1.35	0.255	-1.45	0.718	-1.36
1458643_at	Dtx1	deltex 1 homolog (Drosophila)	-1.92	0.424	-1.33	0.513	-1.02	0.847	-1.25	0.698	-1.38
1457896_at	Esrrg	estrogen-related receptor gamma	-1.31	0.058	-1.57	0.333	-1.17	0.208	-1.99	0.196	-1.51
1458464_at	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2	-1.07	0.91	-1.23	0.538	-1.95	0.073	-1.84	0.082	-1.52
1418721_at	Cops7b	COP9 (constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana	-1.09	0.476	-1.49	0.036	-1.5	0.01	-1.3	0.04	-1.34
1452602_a_at	1700001C19Rik	RIKEN cDNA 1700001C19 gene	-2.1	0.248	-1.01	0.964	-1.26	0.517	-1.24	0.691	-1.4
1439192_at	Nova2	neuro-oncological ventral antigen 2	-1.44	0.247	-1.22	0.178	-1.34	0.391	-1.23	0.338	-1.31
1458632_at	Dpysl2	Dihydropyrimidinase-like 2	-1.55	0.335	-1.2	0.776	-1.28	0.328	-1.38	0.029	-1.35
1423633_at	6530403A03Rik	RIKEN cDNA 6530403A03 gene	-1.01	0.975	-1.48	0.101	-1.67	0.152	-1.2	0.08	-1.34
1459821_x_at	A630082K20Rik	RIKEN cDNA A630082K20 gene	-1.31	0.257	-1.58	0.605	-1.16	0.643	-1.63	0.496	-1.42
1458144_at	BC031353	CDNA sequence BC031353	-1	0.997	-1.81	0.105	-1.42	0.341	-1.31	0.57	-1.38
1459923_at	Bex6	brain expressed gene 6	-1	0.998	-1.7	0.077	-1.49	0.316	-2.24	0.021	-1.61
1459743_at	---	Transcribed locus	-1.68	0.342	-1.11	0.607	-1.31	0.343	-1.41	0.475	-1.38
1451375_at	Ehf	ets homologous factor	-1.27	0.38	-1.36	0.55	-1.36	0.037	-1.48	0.22	-1.37
1456955_at	---	---	-1.21	0.383	-1.43	0.026	-1.36	0.227	-1.25	0.553	-1.31
1432752_at	4930403O18Rik	RIKEN cDNA 4930403O18 gene	-1.63	0.429	-1.27	0.711	-1.17	0.844	-1.02	0.976	-1.27

1438828_at	Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	-1.23	0.39	-1.5	0.314	-1.28	0.121	-2.05	0.053	-1.51
1441880_x_at	MGC30332	hypothetical protein MGC30332	-1.3	0.42	-1.24	0.288	-1.46	0.069	-1.65	0.104	-1.41
1420974_at	Setdb1	SET domain, bifurcated 1	-1.2	0.5	-1.36	0.087	-1.45	0.096	-1.05	0.84	-1.26
1432852_at	Phactr1	phosphatase and actin regulator 1	-1.28	0.621	-1.22	0.189	-1.51	0.162	-3.66	0.13	-1.92
1456868_at	2900073G15Rik	RIKEN cDNA 2900073G15 gene	-1.13	0.613	-1.13	0.792	-2.04	0.028	-1.28	0.333	-1.4
1420220_x_at	4930461P20Rik	RIKEN cDNA 4930461P20 gene	-1.28	0.531	-1.19	0.681	-1.56	0.162	-1.1	0.877	-1.28
1420147_at	AA407331	expressed sequence AA407331	-2.18	0.42	-1.12	0.805	-1.1	0.851	-1.79	0.386	-1.55
1432465_at	4933414I06Rik	RIKEN cDNA 4933414I06 gene	-1.86	0.066	-1.22	0.396	-1.1	0.566	-1.09	0.737	-1.32
1450083_at	Cnot4	CCR4-NOT transcription complex, subunit 4	-1.18	0.396	-1.39	0.214	-1.45	0.312	-1.02	0.939	-1.26
1455751_at	Cand1	cullin associated and neddylation disassociated 1	-1.28	0.736	-1.84	0.298	-1.07	0.662	-1.08	0.78	-1.32
1457388_at	A830080L01Rik	RIKEN cDNA A830080L01 gene	-1.15	0.829	-2.26	0.252	-1.05	0.914	-1.19	0.656	-1.41
1459009_at	Utrn	Utrophin	-1.13	0.611	-1.09	0.76	-2.18	0.027	-1.88	0.118	-1.57
1437440_at	---	Transcribed locus	-1.3	0.691	-1.2	0.738	-1.52	0.357	-1.11	0.589	-1.28
1430114_at	5430420C16Rik	RIKEN cDNA 5430420C16 gene	-1.04	0.952	-1.6	0.563	-1.47	0.493	-1.54	0.355	-1.41
1428923_at	Ppp1r3g	protein phosphatase 1, regulatory (inhibitor) subunit 3G	-1.5	0.494	-1.14	0.847	-1.39	0.183	-1.57	0.196	-1.4
1420724_at	1700067P10Rik	RIKEN cDNA 1700067P10 gene	-1.19	0.688	-1.18	0.434	-1.73	0.482	-2.78	0.212	-1.72
1424464_s_at	2210010L05Rik	RIKEN cDNA 2210010L05 gene	-1.27	0.243	-1.1	0.777	-1.76	0.058	-1.11	0.687	-1.31
1438721_a_at	Irf3	interferon regulatory factor 3	-1.59	0.24	-1.14	0.723	-1.32	0.044	-1.55	0.281	-1.4
1442456_at	Spata5	spermatogenesis associated 5	-1.56	0.022	-1.12	0.69	-1.37	0.424	-1.42	0.564	-1.37
1442151_at	D230040A04Rik	RIKEN cDNA D230040A04 gene	-1.04	0.643	-1.17	0.358	-2.27	0.026	-1.42	0.034	-1.47
1438197_at	Vezt	vezatin, adherens junctions transmembrane protein	-1.24	0.215	-1.23	0.032	-1.55	0.013	-1.02	0.936	-1.26
1429114_at	Sestd1	SEC14 and spectrin domains 1	-1.26	0.098	-1.34	0.312	-1.38	0.135	-1.36	0.122	-1.34
1425817_a_at	Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	-1.33	0.208	-1.34	0.269	-1.31	0.109	-1.12	0.812	-1.27
1427549_s_at	Krtap16-10 /// Krtap	keratin associated protein 16-10 /// keratin associated protein 16-3 /// keratin assc	-1.33	0.488	-1.48	0.354	-1.2	0.706	-1.5	0.668	-1.38
1445975_at	---	---	-1.17	0.186	-1.39	0.163	-1.45	0.074	-1.2	0.239	-1.3
1447344_at	---	Transcribed locus	-1.02	0.646	-1.59	0.036	-1.53	0.034	-1.13	0.499	-1.32
1456821_at	4932439K10Rik	RIKEN cDNA 4932439K10 gene	-1.27	0.619	-1.33	0.351	-1.38	0.163	-1.6	0.099	-1.4
1444248_at	Rcn2	reticulocalbin 2	-1.23	0.468	-1.33	0.511	-1.43	0.263	-1.76	0.237	-1.44
1459862_at	---	Transcribed locus	-1.18	0.604	-1.15	0.789	-1.82	0.012	-1.06	0.897	-1.3
1430195_at	2810043O03Rik	RIKEN cDNA 2810043O03 gene	-1.16	0.466	-1.28	0.152	-1.61	0.011	-1.45	0.295	-1.37
1446584_at	Txndc4	Thioredoxin domain containing 4 (endoplasmic reticulum)	-1.25	0.25	-1.25	0.658	-1.51	0.465	-2.1	0.12	-1.53
1424860_at	D930016D06Rik	RIKEN cDNA D930016D06 gene	-1.33	0.273	-1.15	0.279	-1.55	0.004	-1.13	0.634	-1.29
1459408_at	Sec22a	SEC22 vesicle trafficking protein-like A (S. cerevisiae)	-2.4	0.215	-1.1	0.771	-1.06	0.946	-1.11	0.788	-1.42
1445259_at	Scn2a1	sodium channel, voltage-gated, type II, alpha 1	-1.4	0.582	-1.18	0.698	-1.41	0.297	-1.47	0.374	-1.37
1430737_at	2810409K11Rik	RIKEN cDNA 2810409K11 gene	-1.12	0.861	-1.2	0.797	-1.83	0.053	-1.86	0.324	-1.5
1444079_at	Defb8	defensin beta 8	-1.59	0.371	-1.33	0.259	-1.13	0.677	-1.86	0.011	-1.48
1453356_at	5730453I16Rik	RIKEN cDNA 5730453I16 gene	-1.01	0.967	-1.29	0.435	-1.99	0.069	-1.64	0.213	-1.48
1425903_at	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.07	0.904	-1.55	0.573	-1.45	0.361	-1.22	0.676	-1.32
1436925_at	Ches1	checkpoint suppressor 1	-1.38	0.071	-1.25	0.002	-1.34	0.223	-1.6	0.117	-1.39
1455166_at	AW146430	expressed sequence AW146430	-1.18	0.156	-1.27	0.036	-1.58	0.009	-1.38	0.019	-1.35
1428010_at	Timm9	translocase of inner mitochondrial membrane 9 homolog (yeast)	-1.11	0.489	-1.51	0.142	-1.41	0.238	-1.59	0.023	-1.41
1435466_at	A830091I15Rik	RIKEN cDNA A830091I15 gene	-1.39	0.071	-1.63	0.457	-1.07	0.89	-1.63	0.347	-1.43
1443192_at	---	---	-2.14	0.098	-1.12	0.794	-1.1	0.506	-2.37	0.054	-1.68
1420606_at	Npff	neuropeptide FF-amide peptide precursor	-1.48	0.529	-1.03	0.954	-1.61	0.093	-1.39	0.292	-1.38
1440961_at	9130604C24Rik	RIKEN cDNA 9130604C24 gene	-1.58	0.373	-1.55	0.276	-1.01	0.973	-1.43	0.095	-1.39
1458660_at	AI414330	expressed sequence AI414330	-1.28	0.559	-1.75	0.207	-1.09	0.725	-1.12	0.723	-1.31
1439846_at	Klf12	Kruppel-like factor 12	-1.22	0.43	-1.35	0.281	-1.41	0.216	-1.16	0.614	-1.29
1443891_at	Rad51l3	RAD51-like 3 (S. cerevisiae)	-1.18	0.654	-1.54	0.078	-1.29	0.489	-1.21	0.406	-1.3
1425355_at	BC018371 /// LOC4	cDNA sequence BC018371 /// hypothetical LOC433604	-1.33	0.553	-1.22	0.498	-1.43	0.414	-1.12	0.86	-1.28
1441185_at	Msi2	Musashi homolog 2 (Drosophila)	-1.25	0.181	-1.08	0.84	-1.83	0.075	-1.43	0.111	-1.4
1456991_at	Cobll1	Cobl-like 1	-1.14	0.603	-1.18	0.218	-1.83	0.009	-1.97	0.119	-1.53
1439887_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130025B	-1.41	0.1	-1.22	0.521	-1.35	0.36	-1.03	0.932	-1.25
1432880_at	6820402A03Rik	RIKEN cDNA 6820402A03 gene	-1.09	0.678	-1.65	0.007	-1.34	0.228	-2.45	0.002	-1.63

1429057_at	Narg1l	NMDA receptor regulated 1-like	-1.2	0.347	-1.3	0.046	-1.5	0.057	-1.01	0.984	-1.25
1435194_at	---	---	-1.41	0.119	-1.34	0.543	-1.23	0.509	-1.03	0.879	-1.25
1448096_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	-1.39	0.045	-1.21	0.124	-1.38	0.162	-1.34	0.167	-1.33
1444742_at	Asb14	Ankyrin repeat and SOCS box-containing protein 14	-1.67	0.328	-1.1	0.872	-1.31	0.53	-1.98	0.19	-1.51
1447408_at	Nipbl	Nipped-B homolog (Drosophila)	-1.1	0.313	-1.37	0.001	-1.57	0.035	-1.41	0.045	-1.36
1430555_s_at	Lrig3	leucine-rich repeats and immunoglobulin-like domains 3	-1.2	0.283	-1.44	0.088	-1.34	0.303	-1.11	0.889	-1.27
1423249_at	Nktr	natural killer tumor recognition sequence	-1.51	0.298	-1.36	0.216	-1.14	0.565	-1.53	0.127	-1.38
1440377_at	Tigd5	tigger transposable element derived 5	-1.18	0.851	-1.66	0.513	-1.21	0.678	-1.2	0.699	-1.31
1438771_at	Brd1	bromodomain containing 1	-1.11	0.674	-1.63	0.007	-1.32	0.21	-1.36	0.231	-1.35
1443253_at	Glis3	GLIS family zinc finger 3	-1	0.993	-1.14	0.567	-2.49	0.008	-1.4	0.272	-1.51
1460082_at	Ing3	inhibitor of growth family, member 3	-1.33	0.563	-1.56	0.101	-1.14	0.316	-1.55	0.267	-1.39
1447023_at	---	---	-1.12	0.619	-1.94	0.009	-1.16	0.261	-1.09	0.485	-1.33
1418777_at	Ccl25	chemokine (C-C motif) ligand 25	-1.33	0.097	-1.56	0.21	-1.14	0.551	-1.02	0.954	-1.26
1447400_at	Ryk	receptor-like tyrosine kinase	-1.08	0.855	-2.29	0.191	-1.09	0.765	-1.61	0.542	-1.52
1434511_at	Phkb	phosphorylase kinase beta	-1.18	0.546	-1.48	0.011	-1.33	0.186	-1.22	0.365	-1.3
1460147_at	A730009E18Rik	RIKEN cDNA A730009E18 gene	-1.08	0.827	-1.16	0.67	-2.05	0.032	-1.13	0.856	-1.35
1438363_at	LOC434128	similar to KIAA1183 protein	-1.5	0.431	-1.47	0.396	-1.08	0.707	-2.27	0.14	-1.58
1459570_at	Gpr143	G protein-coupled receptor 143	-1.38	0.567	-1.49	0.596	-1.14	0.823	-1.05	0.886	-1.27
1460200_s_at	Lztfl1	leucine zipper transcription factor-like 1	-1.37	0.151	-1.21	0.112	-1.39	0.29	-1.29	0.368	-1.32
1437387_at	Susd5	sushi domain containing 5	-1.2	0.712	-1.54	0.238	-1.27	0.584	-1.68	0.384	-1.42
1456526_at	C130034I24Rik	RIKEN cDNA C130034I24 gene	-1.07	0.349	-1.24	0.385	-1.86	0.007	-1.43	0.124	-1.4
1441550_at	9330184L24Rik	RIKEN cDNA 9330184L24 gene	-2.41	0.465	-1	1	-1.16	0.832	-1.84	0.322	-1.6
1451160_s_at	Pvr	poliovirus receptor	-1.55	0.095	-1.17	0.586	-1.29	0.346	-1.19	0.317	-1.3
1456916_at	Nsd1	Nuclear receptor-binding SET-domain protein 1	-1.22	0.418	-1.15	0.243	-1.69	0.03	-1.44	0.208	-1.38
1454617_at	Arrdc3	arrestin domain containing 3	-1.25	0.234	-1.22	0.507	-1.54	0.039	-1.06	0.831	-1.27
1446598_at	Prkca	Protein kinase C, alpha	-1.38	0.488	-1.11	0.712	-1.53	0.16	-1.33	0.313	-1.34
1430220_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	-1.23	0.446	-1.21	0.474	-1.56	0.143	-1.36	0.126	-1.34
1445182_at	Zfp672	Zinc finger protein 672	-1.08	0.768	-1.11	0.698	-2.2	0.211	-2.38	0.004	-1.69
1445941_at	Atbf1	AT motif binding factor 1	-1.18	0.489	-1.3	0.257	-1.51	0.103	-1.3	0.456	-1.32
1442710_at	Pdlim5	PDZ and LIM domain 5	-1.22	0.447	-1.19	0.226	-1.62	0.076	-1.4	0.23	-1.36
1445758_at	BC049816	CDNA sequence BC049816	-1.34	0.063	-1.06	0.209	-1.7	0.019	-1.44	0.065	-1.39
1443126_at	Slc12a1	Solute carrier family 12, member 1	-1.25	0.027	-1.08	0.838	-1.83	0.249	-1.64	0.444	-1.45
1422216_at	Mid2	midline 2	-1.14	0.489	-1.62	0.06	-1.28	0.364	-1.05	0.67	-1.27
1459682_at	LOC434249	hypothetical LOC434249	-1.12	0.637	-1.6	0.12	-1.32	0.428	-1.64	0.218	-1.42
1448673_at	Pvrl3	poliovirus receptor-related 3	-1.23	0.179	-1.14	0.01	-1.7	0.007	-1.41	0.108	-1.37
1458048_at	6720406K03	hypothetical protein 6720406K03	-1.26	0.536	-1.2	0.664	-1.53	0.247	-1.61	0.633	-1.4
1457346_at	---	Transcribed locus	-1.02	0.984	-1.85	0.307	-1.33	0.533	-2.32	0.383	-1.63
1455987_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	-1.11	0.632	-1.5	0.044	-1.4	0.177	-1.47	0.049	-1.37
1442738_at	Crebl2	CAMP responsive element binding protein-like 2	-1.15	0.438	-1.1	0.871	-1.99	0.286	-1.95	0.062	-1.55
1446293_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	-1.39	0.077	-1.52	0.274	-1.11	0.667	-1.25	0.404	-1.32
1438310_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-1.1	0.812	-1.45	0.493	-1.48	0.152	-1.45	0.043	-1.37
1445421_at	---	Transcribed locus	-1.14	0.487	-1.17	0.734	-1.83	0.098	-1.03	0.871	-1.29
1427818_at	Bcl2	B-cell leukemia/lymphoma 2	-1.71	0.411	-1.13	0.764	-1.24	0.577	-1.14	0.589	-1.3
1457381_at	Angpt1	Angiopoietin 1	-1.08	0.856	-1.92	0.001	-1.21	0.405	-4.76	0.05	-2.24
1428536_at	Kcng4	potassium voltage-gated channel, subfamily G, member 4	-2.03	0.143	-1.17	0.8	-1.07	0.806	-1.1	0.269	-1.34
1430247_at	Daam2	dishevelled associated activator of morphogenesis 2	-1.27	0.154	-1.91	0.127	-1.03	0.942	-1.47	0.649	-1.42
1455549_at	Sestd1	SEC14 and spectrin domains 1	-1.21	0.17	-1.19	0.198	-1.64	0.022	-1.49	0.158	-1.38
1445737_at	1700057H21Rik	RIKEN cDNA 1700057H21 gene	-1.41	0.617	-1.35	0.107	-1.2	0.359	-1.12	0.793	-1.27
1458266_at	Mad1l1	Mitotic arrest deficient 1-like 1	-1.18	0.701	-2.01	0.314	-1.07	0.866	-2.26	0.352	-1.63
1441956_s_at	---	---	-1.3	0.447	-1.12	0.634	-1.62	0.126	-1.68	0.086	-1.43
1436273_at	Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	-1.54	0.043	-1.54	0.184	-1.02	0.941	-1.04	0.863	-1.28
1449241_at	Klhl1	kelch-like 1 (Drosophila)	-1.08	0.366	-1.64	0.178	-1.34	0.356	-1.3	0.229	-1.34
1431205_at	Slc9a8	Solute carrier family 9 (sodium/hydrogen exchanger), member 8	-1.4	0.58	-1.04	0.957	-1.65	0.08	-2.77	0.056	-1.71

1442198_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	-1.1	0.757	-1.77	0.144	-1.24	0.413	-1.23	0.426	-1.33
1442241_at	Srpk2	Serine/arginine-rich protein specific kinase 2	-1.28	0.487	-1.11	0.612	-1.68	0.032	-1.4	0.156	-1.37
1447203_at	---	---	-1.35	0.541	-1.44	0.069	-1.18	0.363	-1.05	0.931	-1.25
1429054_at	Mrpl47	mitochondrial ribosomal protein L47	-1.19	0.203	-1.4	0.02	-1.38	0.028	-1.13	0.489	-1.27
1419457_at	Rgnef	Rho-guanine nucleotide exchange factor	-1.1	0.202	-2.44	0.001	-1.04	0.813	-3.45	0.054	-2.01
1429933_at	Agtpbp1	ATP/GTP binding protein 1	-1.13	0.836	-1.27	0.557	-1.64	0.029	-1.38	0.308	-1.35
1440046_at	BC031748	cDNA sequence BC031748	-1.03	0.969	-2.9	0.211	-1.03	0.939	-1.13	0.75	-1.52
1448359_a_at	Higd1a	HIG1 domain family, member 1A	-1.31	0.059	-1.28	0.136	-1.35	0.172	-1.23	0.616	-1.29
1432688_at	4631422I05Rik	RIKEN cDNA 4631422I05 gene	-1.05	0.918	-2.18	0.103	-1.15	0.803	-1.44	0.601	-1.45
1425162_at	Rorb	RAR-related orphan receptor beta	-1.28	0.805	-1.98	0.093	-1	1	-1.15	0.773	-1.35
1445105_at	Pcaf	P300/CBP-associated factor	-1.05	0.899	-1.44	0.299	-1.58	0.082	-1.41	0.351	-1.37
1443730_at	9130404D14Rik	RIKEN cDNA 9130404D14 gene	-1.1	0.885	-1.26	0.631	-1.72	0.383	-1.34	0.575	-1.35
1459224_at	Ppp1r13b	Protein phosphatase 1, regulatory (inhibitor) subunit 13B	-1.66	0.417	-1.08	0.774	-1.32	0.095	-1.33	0.363	-1.35
1417740_at	Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	-1.41	0.263	-1.3	0.006	-1.24	0.136	-1.07	0.481	-1.26
1418659_at	Clock	circadian locomoter output cycles kaput	-1.07	0.716	-1.45	0.081	-1.52	0.01	-1.25	0.409	-1.32
1416183_a_at	Ldhb	lactate dehydrogenase B	-1.32	0.121	-1.45	0.21	-1.2	0.327	-1.14	0.319	-1.27
1457468_at	Tnks2	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.4	0.173	-1.05	0.896	-1.62	0.129	-2.03	0.087	-1.53
1433062_at	Wdr66	WD repeat domain 66	-1.44	0.17	-1.22	0.465	-1.3	0.075	-1.31	0.414	-1.32
1442416_at	D930001B02	hypothetical protein D930001B02	-1.14	0.38	-1.24	0.024	-1.65	0.089	-1.41	0.286	-1.36
1444876_at	2700049A03Rik	RIKEN cDNA 2700049A03 gene	-1.21	0.389	-1.36	0.078	-1.38	0.169	-1.07	0.672	-1.26
1418835_at	Phlda1	pleckstrin homology-like domain, family A, member 1	-1.15	0.457	-1.7	0.138	-1.21	0.328	-1.04	0.86	-1.27
1432861_at	2900046F13Rik	RIKEN cDNA 2900046F13 gene	-1.56	0.472	-1.31	0.451	-1.14	0.548	-1.08	0.764	-1.27
1431181_a_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	-1.49	0.038	-1.5	0.095	-1.06	0.735	-1.3	0.003	-1.34
1440331_at	9430079B08Rik	RIKEN cDNA 9430079B08 gene	-1.12	0.522	-1.38	0.309	-1.49	0.141	-1.12	0.402	-1.28
1457587_at	Ga17	Dendritic cell protein GA17	-1.02	0.745	-1.22	0.699	-2.07	0.013	-1.51	0.207	-1.45
1446875_at	Il1rapl2	Interleukin 1 receptor accessory protein-like 2	-1.52	0.264	-1.22	0.514	-1.24	0.143	-1.77	0.173	-1.44
1441685_at	Prosc	proline synthetase co-transcribed	-1.24	0.03	-1.54	0.309	-1.21	0.607	-1.09	0.844	-1.27
1417485_at	Ibsp	integrin binding sialoprotein	-1.04	0.92	-1.16	0.13	-2.15	0.046	-1.16	0.095	-1.38
1434449_at	Aqp4	aquaporin 4	-1.11	0.506	-1.54	0.373	-1.36	0.164	-1.8	0.121	-1.45
1440679_at	---	Transcribed locus	-1.26	0.182	-1.42	0.156	-1.27	0.164	-1.37	0.226	-1.33
1440717_at	AA407881	expressed sequence AA407881	-1.21	0.379	-1.21	0.014	-1.58	0.087	-1.41	0.238	-1.35
1442732_at	---	---	-1.43	0.17	-1.16	0.52	-1.38	0.435	-1.5	0.038	-1.37
1458148_at	D230007K08Rik	RIKEN cDNA D230007K08 gene	-1.33	0.015	-1.77	0.217	-1.03	0.922	-2.47	0.048	-1.65
1439569_at	Gpr83	G protein-coupled receptor 83	-1.02	0.955	-1.73	0.289	-1.38	0.593	-4.41	0.006	-2.13
1437667_a_at	Bach2	BTB and CNC homology 2	-1.29	0.322	-1.51	0.186	-1.18	0.588	-2.6	0.19	-1.64
1430776_s_at	Ankrd24	ankyrin repeat domain 24	-1.36	0.32	-1.39	0.247	-1.21	0.034	-1.17	0.538	-1.28
1459237_at	Atf2	Activating transcription factor 2	-1.26	0.497	-1.22	0.424	-1.47	0.037	-1.15	0.715	-1.28
1440896_at	Sod1	Superoxide dismutase 1, soluble	-1.55	0.157	-1.1	0.688	-1.36	0.319	-1.34	0.317	-1.34
1418042_a_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.17	0.496	-1.95	0.099	-1.08	0.254	-1.13	0.669	-1.33
1421715_at	V2rx	pheromone receptor V2Rx	-1.13	0.237	-1.95	0.285	-1.12	0.741	-1.38	0.568	-1.4
1441157_at	C230006B20	hypothetical LOC403344	-1.36	0.061	-1.78	0.099	-1.01	0.965	-1.19	0.416	-1.33
1435629_at	---	Transcribed locus	-1.17	0.62	-1.37	0.382	-1.43	0.006	-1.07	0.908	-1.26
1436096_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.36	0.127	-1.09	0.844	-1.57	0.148	-1.15	0.703	-1.29
1422207_at	Htr5a	5-hydroxytryptamine (serotonin) receptor 5A	-1.08	0.89	-2.11	0.135	-1.13	0.842	-2.57	0.222	-1.72
1419413_at	Ccl17	chemokine (C-C motif) ligand 17	-1.08	0.705	-1.07	0.843	-2.35	0.116	-2.46	0.063	-1.74
1459734_at	Psmd14	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-1.23	0.071	-1.3	0.27	-1.42	0.271	-1.04	0.84	-1.25
1459710_at	---	Transcribed locus	-1.16	0.588	-1.89	0.006	-1.11	0.652	-1.1	0.272	-1.32
1458541_at	Dctn4	dynactin 4	-1.88	0.096	-1.11	0.613	-1.17	0.207	-1.03	0.859	-1.3
1460035_at	Phb2	prohibitin 2	-1.04	0.832	-1.37	0.2	-1.67	0.109	-1.21	0.013	-1.32
1427643_at	1200009O22Rik	RIKEN cDNA 1200009O22 gene	-1.56	0.044	-1.14	0.752	-1.29	0.414	-1.2	0.66	-1.3
1451834_at	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	-1.18	0.644	-1.07	0.791	-1.96	0.011	-1.16	0.841	-1.34
1427702_at	Zfp1	zinc finger protein 1	-1.22	0.564	-1.78	0.31	-1.1	0.475	-1.68	0.248	-1.45
1455472_at	A630071D13Rik	RIKEN cDNA A630071D13 gene	-1.28	0.173	-1.31	0.286	-1.34	0.31	-1.22	0.139	-1.29

1430928_at	2900002J02Rik	RIKEN cDNA 2900002J02 gene	-1.15	0.758	-1.24	0.68	-1.64	0.317	-1.62	0.498	-1.41
1439683_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420434E0	-1.25	0.784	-1.67	0.456	-1.12	0.883	-1.19	0.774	-1.31
1432076_at	4933430H16Rik	RIKEN cDNA 4933430H16 gene	-1.11	0.882	-2.34	0.245	-1.04	0.87	-1.12	0.826	-1.4
1458547_at	---	Transcribed locus	-1.46	0.608	-1.28	0.486	-1.22	0.594	-1.57	0.209	-1.38
1420040_at	5730472N09Rik	RIKEN cDNA 5730472N09 gene	-1.07	0.918	-1.63	0.227	-1.34	0.26	-1.46	0.421	-1.38
1453268_at	5730409G07Rik	RIKEN cDNA 5730409G07 gene	-1.19	0.616	-1.94	0.115	-1.07	0.468	-1.16	0.458	-1.34
1418916_a_at	Spp2	secreted phosphoprotein 2	-1.22	0.165	-1.38	0.047	-1.34	0.557	-1.14	0.835	-1.27
1438488_at	Esd	esterase D/formylglutathione hydrolase	-1.65	0.191	-1.36	0.594	-1.05	0.883	-2.14	0.046	-1.55
1418590_at	Kpna6	karyopherin (importin) alpha 6	-1.38	0.144	-1.4	0.107	-1.17	0.57	-1.27	0.425	-1.31
1418452_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	-1.33	0.671	-1.82	0.506	-1.01	0.985	-1.4	0.306	-1.39
1438231_at	Foxp2	forkhead box P2	-1.06	0.802	-1.22	0.341	-1.89	0.022	-1.38	0.382	-1.39
1441022_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	-1.15	0.74	-1.43	0.349	-1.39	0.081	-1.18	0.629	-1.29
1429846_at	9030411K21Rik	RIKEN cDNA 9030411K21 gene	-1.58	0.047	-1.04	0.906	-1.44	0.136	-1.47	0.286	-1.38
1457832_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.2	0.485	-1.64	0.064	-1.17	0.137	-1.1	0.697	-1.28
1441522_at	AW495713	expressed sequence AW495713	-1.27	0.472	-1.71	0.004	-1.08	0.532	-1.1	0.506	-1.29
1443943_at	Plag1	pleiomorphic adenoma gene 1	-1.11	0.857	-2.07	0.172	-1.1	0.889	-2.23	0.298	-1.63
1460667_at	U90926	cDNA sequence U90926	-1.06	0.882	-2.49	0.32	-1.06	0.232	-1.17	0.327	-1.44
1431783_at	1700010L04Rik	RIKEN cDNA 1700010L04 gene	-1.58	0.276	-1.28	0.697	-1.14	0.58	-2.02	0.313	-1.5
1446326_at	Col1a2	procollagen, type I, alpha 2	-1.04	0.901	-1.11	0.844	-2.35	0.005	-1.6	0.072	-1.52
1421152_a_at	Gnao1	guanine nucleotide binding protein, alpha o	-1.3	0.257	-1.12	0.445	-1.6	0.206	-1.21	0.454	-1.3
1445933_at	Slc12a5	solute carrier family 12, member 5	-1.12	0.252	-1.22	0.364	-1.74	0.016	-1.19	0.581	-1.31
1457488_at	B230339M05Rik	RIKEN cDNA B230339M05 gene	-1.11	0.89	-1.67	0.111	-1.26	0.305	-3.03	0.09	-1.77
1445255_at	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	-1.03	0.842	-1.73	0.344	-1.34	0.623	-1.05	0.94	-1.29
1441997_at	Zfp184	zinc finger protein 184 (Kruppel-like)	-1.14	0.794	-1.92	0.342	-1.12	0.611	-1.47	0.487	-1.41
1458719_at	---	Transcribed locus	-1.3	0.038	-1.33	0.374	-1.28	0.335	-1.08	0.296	-1.25
1430145_at	Lrrc28	leucine rich repeat containing 28	-1.59	0.024	-1.22	0.592	-1.18	0.59	-1.08	0.799	-1.27
1420801_at	Npas1	neuronal PAS domain protein 1	-1.18	0.012	-1.52	0.473	-1.27	0.16	-1.58	0.011	-1.39
1431281_at	Dysfip1	dysferlin interacting protein 1	-1.49	0.29	-1.51	0.427	-1.04	0.911	-2.62	0.114	-1.67
1444246_at	Chd2	Chromodomain helicase DNA binding protein 2	-1.53	0.177	-1.23	0.416	-1.21	0.561	-1.52	0.188	-1.37
1445280_at	Ap3d1	adaptor-related protein complex 3, delta 1 subunit	-1.05	0.923	-1.45	0.322	-1.54	0.009	-1.02	0.899	-1.26
1420492_s_at	Smr1 /// Smr3	submaxillary gland androgen regulated protein 1 /// submaxillary gland androgen	-1.35	0.004	-1.13	0.832	-1.49	0.257	-2.49	0.492	-1.62
1444018_at	B930098A02Rik	RIKEN cDNA B930098A02 gene	-1.16	0.628	-1.37	0.165	-1.42	0.02	-1.18	0.51	-1.28
1447249_at	---	Transcribed locus	-1.8	0.076	-1.03	0.864	-1.29	0.515	-1.51	0.105	-1.41
1454380_at	Phactr4	phosphatase and actin regulator 4	-1.32	0.655	-1.54	0.093	-1.12	0.615	-1.31	0.74	-1.32
1447589_at	Ppp4r1	Protein phosphatase 4, regulatory subunit 1	-1.44	0.488	-1.34	0.655	-1.17	0.171	-1.16	0.446	-1.28
1421012_at	Srprb	signal recognition particle receptor, B subunit	-1.32	0.392	-1.67	0.016	-1.07	0.708	-1.16	0.509	-1.3
1440616_at	AU042410	expressed sequence AU042410	-1.2	0.611	-1.33	0.485	-1.4	0.596	-1.04	0.924	-1.24
1446835_at	Ftl1	Ferritin light chain 1	-1.18	0.143	-1.22	0.128	-1.58	0.165	-1.95	0.091	-1.48
1430320_at	Dmd	dystrophin, muscular dystrophy	-1.06	0.656	-1.41	0.004	-1.54	0.354	-1.6	0.373	-1.41
1441426_at	BC002230	CDNA sequence BC002230	-1.54	0.426	-1.18	0.341	-1.25	0.287	-1.05	0.909	-1.25
1419640_at	Purb	purine rich element binding protein B	-1.27	0.32	-1.18	0.485	-1.51	0.096	-1.14	0.188	-1.28
1460109_at	Tcf25	Transcription factor 25 (basic helix-loop-helix)	-1.29	0.576	-1.61	0.002	-1.12	0.366	-1.1	0.283	-1.28
1430152_at	Eps15	epidermal growth factor receptor pathway substrate 15	-1.19	0.38	-1.21	0.428	-1.59	0.003	-1.07	0.809	-1.26
1445566_at	Centb2	Centaurin, beta 2	-1.14	0.652	-1.66	0.353	-1.22	0.581	-1.15	0.544	-1.29
1441769_at	Arl15	ADP-ribosylation factor-like 15	-1.16	0.25	-1.04	0.817	-2.11	0.053	-1.28	0.35	-1.4
1419218_at	Vangl2	vang-like 2 (van gogh, Drosophila)	-1.89	0.033	-1.13	0.322	-1.13	0.698	-1.39	0.031	-1.38
1435543_at	Apc	adenomatosis polyposis coli	-1.24	0.069	-1.13	0.353	-1.64	0.011	-1.35	0.288	-1.34
1417623_at	Slc12a2	solute carrier family 12, member 2	-1.1	0.731	-1.16	0.799	-1.9	0.041	-1.08	0.854	-1.31
1419224_at	Cecr6	cat eye syndrome chromosome region, candidate 6 homolog (human)	-1.35	0.615	-1.15	0.764	-1.45	0.299	-1.13	0.865	-1.27
1446058_at	---	PREDICTED: Mus musculus hypothetical protein LOC628925 (LOC628925), mR	-1.18	0.448	-1.41	0.46	-1.36	0.222	-1.12	0.566	-1.26
1453193_s_at	Kif12	kinesin family member 12	-1.08	0.816	-1.56	0.355	-1.37	0.446	-1.5	0.51	-1.38
1455329_at	---	---	-1.5	0.359	-1.27	0.131	-1.18	0.314	-1.4	0.137	-1.34
1438735_at	Rsf1	remodeling and spacing factor 1	-1.62	0.034	-1.05	0.737	-1.37	0.122	-1.17	0.137	-1.3

1432622_a_at	4930507D05Rik	RIKEN cDNA 4930507D05 gene	-1.07	0.94	-1.29	0.341	-1.71	0.213	-1.21	0.306	-1.32
1419115_at	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	-1.14	0.489	-1.37	0.036	-1.44	0.059	-1.06	0.87	-1.25
1429634_at	Zfp580	zinc finger protein 580	-1.19	0.392	-1.53	0.006	-1.24	0.177	-1.02	0.965	-1.24
1450176_at	Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	-1.16	0.529	-1.64	0.075	-1.2	0.65	-1.31	0.626	-1.33
1439169_at	Eif4enif1	Eukaryotic translation initiation factor 4E nuclear import factor 1	-1.16	0.519	-1.11	0.23	-1.86	0.047	-1.17	0.308	-1.32
1437705_at	Zfp551	zinc fingr protein 551	-1.09	0.723	-1.39	0.562	-1.5	0.043	-1.06	0.9	-1.26
1445492_at	Mapre2	Microtubule-associated protein, RP/EB family, member 2	-1.12	0.413	-1.13	0.739	-1.93	0.04	-1.24	0.501	-1.35
1438221_at	C130065N10Rik	RIKEN cDNA C130065N10 gene	-1.24	0.459	-1.33	0.253	-1.35	0.116	-1.36	0.033	-1.32
1446705_at	---	---	-1.11	0.713	-1.39	0.617	-1.46	0.23	-1.57	0.354	-1.38
1442616_at	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	-1.17	0.585	-1.59	0.186	-1.23	0.213	-1.05	0.485	-1.26
1443233_at	Gtf2f2	General transcription factor IIF, polypeptide 2	-1.14	0.205	-1.36	0.107	-1.45	0.04	-1.04	0.731	-1.25
1434212_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	-1.14	0.551	-1.5	0.135	-1.32	0.348	-1.07	0.813	-1.26
1446876_at	Wdr22	WD repeat domain 22	-1.06	0.877	-1.23	0.509	-1.82	0.183	-1.86	0.162	-1.49
1423499_at	Sncaip	synuclein, alpha interacting protein (synphilin)	-1.77	0.018	-1.06	0.843	-1.25	0.197	-1.73	0.307	-1.45
1421189_at	Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	-1.4	0.067	-1.28	0.107	-1.24	0.559	-1.16	0.815	-1.27
1419722_at	Klk8	kallikrein 8	-1.16	0.282	-1.22	0.708	-1.61	0.033	-2.76	0.236	-1.69
1427794_at	AJ242955	hypothetical protein, P4(21)n gene	-1.16	0.623	-1.73	0.274	-1.16	0.703	-2.18	0.207	-1.56
1435574_at	Chordc1	Cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	-1.09	0.766	-1.41	0.145	-1.48	0.034	-1.53	0.116	-1.38
1456216_at	Csnk1a1	Casein kinase 1, alpha 1	-1.24	0.328	-1.09	0.513	-1.72	0.014	-1.12	0.031	-1.29
1453635_at	4932416N17Rik	RIKEN cDNA 4932416N17 gene	-1.41	0.398	-1.43	0.261	-1.11	0.393	-1.02	0.843	-1.25
1425229_a_at	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	-1.09	0.76	-1.41	0.212	-1.47	0.082	-1.34	0.145	-1.33
1459324_at	---	---	-1.07	0.55	-1.13	0.42	-2.06	0.013	-1.84	0.317	-1.53
1440163_at	6030490B17Rik	RIKEN cDNA 6030490B17 gene	-1.36	0.274	-1.08	0.619	-1.57	0.044	-1.12	0.709	-1.28
1444506_at	Tram1	Translocating chain-associating membrane protein 1	-1.15	0.193	-1.23	0.447	-1.62	0.122	-1.26	0.236	-1.31
1440552_at	Ubr1	Ubiquitin protein ligase E3 component n-recognin 1	-2.95	0.02	-1.03	0.939	-1	0.979	-2.13	0.369	-1.78
1421368_at	Scrt1	scratch homolog 1, zinc finger protein (Drosophila)	-1.37	0.56	-1.4	0.488	-1.17	0.659	-1.43	0.335	-1.34
1426302_at	Tmprss4	transmembrane protease, serine 4	-1.21	0.415	-1.31	0.624	-1.39	0.019	-1.35	0.57	-1.32
1459312_at	---	Transcribed locus	-1.12	0.668	-1.09	0.849	-2.01	0.241	-1.48	0.654	-1.43
1451004_at	Acvr2a	activin receptor IIA	-1.05	0.897	-1.61	0.103	-1.37	0.073	-1.09	0.883	-1.28
1429435_x_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	-1.26	0.248	-1.18	0.363	-1.5	0.065	-1.09	0.469	-1.26
1430319_at	4833411C07Rik	RIKEN cDNA 4833411C07 gene	-1.51	0.335	-1.16	0.589	-1.28	0.018	-1.11	0.773	-1.27
1459109_at	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmeml	-1.65	0.65	-1.29	0.635	-1.08	0.841	-1.46	0.464	-1.37
1436045_at	Tsga10	testis specific 10	-1.22	0.583	-1.22	0.525	-1.5	0.168	-1.1	0.669	-1.26
1456302_at	Pex6	peroxisomal biogenesis factor 6	-1.33	0.125	-1.56	0.033	-1.1	0.811	-1.42	0.3	-1.35
1420074_at	D8Ertd738e	DNA segment, Chr 8, ERATO Doi 738, expressed	-1.28	0.315	-1.06	0.686	-1.72	0.142	-1.18	0.771	-1.31
1441327_a_at	Ssr1	signal sequence receptor, alpha	-1.14	0.169	-1.2	0.116	-1.67	0.06	-1.02	0.951	-1.26
1440950_at	Akt1	Thymoma viral proto-oncogene 1	-1.39	0.328	-1.25	0.311	-1.27	0.569	-1.25	0.135	-1.29
1429413_at	Cpm	carboxypeptidase M	-1.25	0.091	-1.53	0.123	-1.18	0.461	-3	0.066	-1.74
1455659_at	---	---	-1.41	0.222	-1.19	0.315	-1.33	0.072	-1.01	0.982	-1.23
1455134_at	A630051L19Rik	RIKEN cDNA A630051L19 gene	-1.12	0.095	-1.38	0.126	-1.45	0.117	-1.67	0.215	-1.4
1436679_at	2210010N04Rik	RIKEN cDNA 2210010N04 gene	-1.18	0.59	-1.19	0.704	-1.61	0.488	-2.15	0.21	-1.53
1433107_at	---	---	-1.46	0.169	-1.03	0.944	-1.53	0.023	-1.11	0.804	-1.28
1459746_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	-1.27	0.369	-1.28	0.34	-1.36	0.017	-1.08	0.825	-1.25
1444817_at	Plekhh2	Pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	-1.05	0.77	-1.34	0.662	-1.65	0.217	-1.07	0.837	-1.28
1436261_at	Dysf	Dysferlin	-1.46	0.565	-1.05	0.898	-1.5	0.476	-1.35	0.675	-1.34
1425339_at	Plcb4	phospholipase C, beta 4	-1.41	0.497	-1.43	0.356	-1.11	0.562	-2.25	0.314	-1.55
1423312_at	Tpbg	trophoblast glycoprotein	-1.05	0.595	-1.52	0.551	-1.43	0.353	-2.76	0.169	-1.69
1445138_at	A530083I20Rik	RIKEN cDNA A530083I20 gene	-1.09	0.84	-1.75	0.217	-1.21	0.406	-2.32	0.066	-1.6
1440511_at	Psme4	Proteasome (prosome, macropain) activator subunit 4	-1.19	0.546	-1.41	0.074	-1.31	0.28	-1.13	0.588	-1.26
1435484_at	BF642829	expressed sequence BF642829	-1.14	0.694	-1.82	0.133	-1.14	0.477	-1.6	0.026	-1.42
1433729_x_at	Pmpcb	peptidase (mitochondrial processing) beta	-1.43	0.166	-1.44	0.024	-1.1	0.314	-1.16	0.195	-1.28
1429345_at	D2Ertd435e	DNA segment, Chr 2, ERATO Doi 435, expressed	-1.33	0.266	-1.2	0.114	-1.39	0.151	-1.3	0.063	-1.3
1442240_at	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.16	0.579	-1.49	0	-1.29	0.384	-1.35	0.144	-1.32

1447560_at	---	---	-1.39	0.696	-1.31	0.166	-1.21	0.306	-1.15	0.649	-1.27
1432843_at	5730405O12Rik	RIKEN cDNA 5730405O12 gene	-1.11	0.608	-1.52	0.313	-1.33	0.143	-1.28	0.274	-1.31
1447516_at	---	Transcribed locus	-1.37	0.445	-1.3	0.621	-1.24	0.396	-1.31	0.068	-1.3
1446101_at	---	---	-1.19	0.724	-1.11	0.702	-1.78	0.065	-1.6	0.077	-1.42
1441354_at	AU018740	expressed sequence AU018740	-1.14	0.673	-1.23	0.462	-1.62	0.208	-1.41	0.394	-1.35
1430261_at	---	---	-1.5	0.265	-1	0.997	-1.55	0.008	-1.32	0.701	-1.34
1456221_at	Cdh8	Cadherin 8	-2.04	0.44	-1.05	0.876	-1.16	0.747	-1.07	0.885	-1.33
1443795_at	Tcf19	transcription factor 19	-1.01	0.992	-1.66	0.473	-1.41	0.579	-1.4	0.437	-1.37
1457154_at	6-Mar	Membrane-associated ring finger (C3HC4) 6	-1.02	0.942	-1.49	0.146	-1.53	0.24	-1.17	0.595	-1.3
1460179_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-1.15	0.193	-1.31	0.053	-1.48	0.014	-1.43	0.274	-1.34
1459696_at	Fry	Furry homolog (Drosophila)	-1.78	0.134	-1.14	0.574	-1.15	0.807	-1.93	0.218	-1.5
1445148_at	Plcl1	Phospholipase C-like 1	-1.04	0.885	-1.03	0.919	-2.66	0.056	-1.44	0.247	-1.54
1454210_at	4933428M09Rik	RIKEN cDNA 4933428M09 gene	-1.94	0.307	-1.25	0.603	-1.01	0.978	-1.66	0.319	-1.46
1460063_at	D5Ertd798e	DNA segment, Chr 5, ERATO Doi 798, expressed	-1.07	0.675	-1.33	0.073	-1.59	0.015	-1.32	0.357	-1.33
1429715_at	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	-1.02	0.856	-1.27	0.438	-1.83	0.005	-1	0.987	-1.28
1458033_at	Ubr1	Ubiquitin protein ligase E3 component n-recognin 1	-1.03	0.898	-1.39	0.074	-1.61	0.001	-1.16	0.53	-1.3
1453565_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-1.29	0.112	-1.33	0.525	-1.27	0.159	-1.22	0.299	-1.28
1430386_at	E030024N20Rik	RIKEN cDNA E030024N20 gene	-1.14	0.313	-1.13	0.414	-1.83	0.03	-1.07	0.623	-1.29
1423561_at	Nell2	NEL-like 2 (chicken)	-1.11	0.873	-1.84	0.48	-1.15	0.757	-4.24	0.348	-2.09
1444195_at	Rmnd5a	Required for meiotic nuclear division 5 homolog A (S. cerevisiae)	-1.04	0.76	-1.13	0.368	-2.17	0.079	-1.1	0.667	-1.36
1445345_at	Plekha5	Pleckstrin homology domain containing, family A member 5	-1.51	0.024	-1.08	0.648	-1.39	0.058	-1.38	0.639	-1.34
1420728_at	Krt32	keratin 32	-1.28	0.17	-1.48	0.332	-1.17	0.472	-1.01	0.964	-1.23
1427157_at	Ccdc85a	coiled-coil domain containing 85A	-1.26	0.397	-1.33	0.669	-1.3	0.229	-1.31	0.573	-1.3
1439408_a_at	Pparbp	peroxisome proliferator activated receptor binding protein	-1.42	0.362	-1.37	0.147	-1.14	0.689	-1.09	0.784	-1.25
1430115_at	4833413E03Rik	RIKEN cDNA 4833413E03 gene	-1.32	0.441	-1	0.992	-1.79	0.143	-1.07	0.72	-1.29
1420175_at	Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	-1.18	0.773	-1.45	0.293	-1.29	0.289	-1.03	0.89	-1.24
1453451_at	6820402I19Rik	RIKEN cDNA 6820402I19 gene	-1.24	0.251	-1.09	0.494	-1.7	0.027	-1.16	0.374	-1.3
1449425_at	Wnt2	wingless-related MMTV integration site 2	-1.6	0.572	-1.39	0.027	-1.03	0.92	-1.94	0.106	-1.49
1459873_x_at	Maged2	Melanoma antigen, family D, 2	-1.02	0.944	-1.74	0.165	-1.31	0.357	-2.03	0.238	-1.53
1449571_at	Trhr	thyrotropin releasing hormone receptor	-2.02	0.291	-1.08	0.727	-1.12	0.702	-2.59	0.001	-1.7
1416718_at	Bcan	brevican	-1.46	0.707	-1.34	0.591	-1.13	0.602	-1.07	0.906	-1.25
1427656_at	Tcrb-V13	T-cell receptor beta, variable 13	-1.52	0.635	-1.06	0.892	-1.41	0.367	-3.71	0.148	-1.92
1440295_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	-1.61	0.147	-1.21	0.336	-1.16	0.522	-1.09	0.74	-1.27
1457356_at	Igf2r	Insulin-like growth factor 2 receptor	-1.11	0.68	-1.06	0.86	-2.14	0.038	-1.27	0.41	-1.39
1422597_at	Mmp15	matrix metallopeptidase 15	-1.24	0.593	-1.51	0.12	-1.19	0.235	-1.52	0.366	-1.36
1447824_x_at	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)	-1.61	0.121	-1.27	0.172	-1.1	0.545	-1.07	0.319	-1.26
1425489_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	-1.39	0.093	-1.28	0.394	-1.23	0.12	-1.08	0.882	-1.25
1416679_at	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	-1.14	0.458	-1.52	0.064	-1.29	0.047	-1.06	0.788	-1.25
1422574_at	Mxd4	Max dimerization protein 4	-1.02	0.489	-1.46	0.057	-1.54	0.079	-1.36	0.14	-1.35
1417261_at	Mbtd1	mbt domain containing 1	-1.24	0.211	-1.38	0.088	-1.28	0.142	-1.11	0.647	-1.25
1455519_at	Dsg1b	desmoglein 1 beta	-1.29	0.7	-1.5	0.548	-1.15	0.501	-2.79	0.289	-1.68
1425771_at	Akr1d1	aldo-keto reductase family 1, member D1	-1.6	0.047	-1.31	0.042	-1.08	0.856	-1.16	0.718	-1.29
1453863_at	3300002P09Rik	RIKEN cDNA 3300002P09 gene	-1.25	0.745	-1.63	0.43	-1.11	0.394	-1.04	0.907	-1.26
1421330_at	Ptpn4	protein tyrosine phosphatase, non-receptor type 4	-1.17	0.841	-1.54	0.041	-1.23	0.411	-1.27	0.291	-1.3
1439537_at	---	---	-1.15	0.439	-1.23	0.12	-1.58	0.182	-1.64	0.26	-1.4
1442306_at	---	Transcribed locus	-1.36	0.635	-1.23	0.55	-1.31	0.473	-2.55	0.331	-1.61
1445128_at	---	CDNA clone IMAGE:30463708	-1.4	0.33	-1.12	0.855	-1.4	0.041	-1.17	0.458	-1.27
1432310_at	6530401F13Rik	RIKEN cDNA 6530401F13 gene	-1.45	0.579	-1.24	0.68	-1.22	0.723	-1.82	0.428	-1.43
1454232_at	9430027B09Rik	RIKEN cDNA 9430027B09 gene	-1.01	0.963	-1.86	0.28	-1.26	0.562	-1.79	0.023	-1.48
1437619_x_at	Ddr1	discoidin domain receptor family, member 1	-1.65	0.041	-1.22	0.274	-1.12	0.434	-1.57	0.045	-1.39
1418446_at	Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	-1.32	0.15	-1.21	0.357	-1.37	0.069	-1.51	0.243	-1.35
1436427_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-1.22	0.14	-1.15	0.492	-1.59	0.074	-1.16	0.662	-1.28
1436857_at	Defcr21 /// Defcr22	defensin related cryptdin 21 /// defensin related cryptdin 22	-1.1	0.254	-1.53	0.532	-1.33	0.336	-1.1	0.568	-1.26

1459270_at	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	-1.07	0.71	-1.46	0.139	-1.43	0.185	-1.07	0.791	-1.26
1430659_at	4930548H24Rik	RIKEN cDNA 4930548H24 gene	-1.28	0.142	-1.06	0.867	-1.69	0.162	-1.22	0.271	-1.31
1436318_at	Tardbp	TAR DNA binding protein	-1.26	0.355	-1.38	0.076	-1.25	0.158	-1.18	0.493	-1.27
1442022_at	E430004N04Rik	RIKEN cDNA E430004N04 gene	-1.38	0.772	-1.68	0.431	-1	0.996	-2.07	0.331	-1.53
1446299_at	6720456B07Rik	RIKEN cDNA 6720456B07 gene	-1.03	0.881	-1.42	0	-1.56	0.118	-1.2	0.518	-1.3
1428540_at	3321401G04Rik	RIKEN cDNA 3321401G04 gene	-1.44	0.302	-1.21	0.468	-1.25	0.26	-1.47	0.019	-1.34
1419176_at	Vps37a	vacuolar protein sorting 37A (yeast)	-1.12	0.022	-1.43	0.039	-1.38	0.069	-1.11	0.564	-1.26
1445952_at	Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.28	0.612	-1.11	0.742	-1.56	0.072	-2.36	0.015	-1.58
1457649_x_at	AI848149	expressed sequence AI848149	-1.46	0.345	-1.16	0.684	-1.29	0.397	-1.86	0.047	-1.44
1421274_at	Socs4	suppressor of cytokine signaling 4	-1.39	0.464	-1.08	0.79	-1.48	0.416	-1.07	0.784	-1.26
1424921_at	Brd4 /// Bst2	bromodomain containing 4 /// bone marrow stromal cell antigen 2	-1.54	0.116	-1.1	0.17	-1.32	0.035	-2.27	0.086	-1.56
1457062_at	1700081L11Rik	RIKEN cDNA 1700081L11 gene	-1.15	0.129	-1.18	0	-1.66	0.018	-1.29	0.165	-1.32
1430272_at	Gtpbp5	GTP binding protein 5	-1.45	0.029	-1.4	0.281	-1.09	0.632	-1.19	0.248	-1.28
1441225_at	Gsn	Gelsolin	-1.08	0.619	-1.21	0.504	-1.78	0.361	-1.1	0.827	-1.29
1431165_at	A030009A09Rik	RIKEN cDNA A030009A09 gene	-1.6	0.207	-1.15	0.539	-1.22	0.096	-1.2	0.748	-1.29
1429741_at	Kcnv1	potassium channel, subfamily V, member 1	-1	0.99	-1.49	0.47	-1.53	0.294	-1.35	0.613	-1.34
1447693_s_at	Neo1	neogenin	-1.22	0.032	-1.21	0.066	-1.49	0.036	-1.18	0.495	-1.27
1440764_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	-1.04	0.701	-1.22	0.046	-1.86	0.016	-1.44	0.36	-1.39
1423752_at	Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	-1.43	0.118	-1.24	0.005	-1.23	0.007	-1.1	0.413	-1.25
1433010_at	5530400N10Rik	RIKEN cDNA 5530400N10 gene	-1.77	0.058	-1.13	0.503	-1.15	0.595	-1.06	0.64	-1.28
1438121_at	Sec24a	SEC24 related gene family, member A (S. cerevisiae)	-1.17	0.524	-1.26	0.101	-1.49	0.339	-1	0.998	-1.23
1459265_at	Myohd1	myosin head domain containing 1	-1.17	0.586	-1.59	0.43	-1.19	0.561	-1.07	0.827	-1.26
1446298_at	C630016I17Rik	RIKEN cDNA C630016I17 gene	-1.07	0.484	-1.3	0.096	-1.63	0.028	-1.81	0.184	-1.45
1418291_at	Zfp87	zinc finger protein 87	-1.25	0.143	-1.12	0.662	-1.59	0.007	-1.77	0.057	-1.43
1453897_at	C030014A21Rik	RIKEN cDNA C030014A21 gene	-1.04	0.915	-2	0.036	-1.16	0.622	-1.02	0.963	-1.31
1442568_at	C330002I19Rik	RIKEN cDNA C330002I19 gene	-1.46	0.02	-1.16	0.398	-1.28	0.186	-1.6	0.04	-1.38
1435917_at	---	Transcribed locus	-1.36	0.093	-1	0.969	-1.69	0.033	-1.05	0.872	-1.28
1430958_at	4933430N04Rik	RIKEN cDNA 4933430N04 gene	-1.64	0.527	-1.11	0.862	-1.24	0.669	-1.35	0.716	-1.33
1429983_at	2010002M09Rik	RIKEN cDNA 2010002M09 gene	-1.31	0.477	-1.2	0.121	-1.37	0.071	-1.42	0.313	-1.33
1424462_at	Ergic2	ERGIC and golgi 2	-1.09	0.369	-1.38	0.011	-1.46	0.021	-1.07	0.431	-1.25
1446276_at	2310008H04Rik	RIKEN cDNA 2310008H04 gene	-1.08	0.722	-1.33	0.107	-1.55	0.051	-1.18	0.46	-1.28
1455144_s_at	AU040829	expressed sequence AU040829	-1.01	0.936	-1.96	0.035	-1.22	0.075	-1.17	0.56	-1.34
1451271_a_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	-1.23	0.116	-1.48	0.157	-1.2	0.191	-1.09	0.113	-1.25
1434951_at	Armc8	armadillo repeat containing 8	-1.36	0.047	-1.44	0.065	-1.12	0.247	-1.41	0.133	-1.33
1424671_at	Plekhf1	pleckstrin homology domain containing, family F (with FYVE domain) member 1	-1.11	0.443	-1.63	0.215	-1.24	0.178	-1.21	0.244	-1.3
1442939_at	Rif1 /// LOC671598	Rap1 interacting factor 1 homolog (yeast) /// similar to Telomere-associated prote	-1.37	0.669	-1.57	0.157	-1.05	0.745	-1.09	0.763	-1.27
1436632_at	D130059P03Rik	RIKEN cDNA D130059P03 gene	-1.19	0.11	-1.35	0.214	-1.35	0.15	-1.07	0.78	-1.24
1417549_at	Zfp68	zinc finger protein 68	-1.17	0.091	-1.2	0.581	-1.56	0.102	-1.22	0.311	-1.29
1445455_at	D3Ertd270e	DNA segment, Chr 3, ERATO Doi 270, expressed	-1.1	0.89	-1.96	0.08	-1.1	0.847	-1.02	0.93	-1.3
1458084_at	Zdhhc17	Zinc finger, DHHC domain containing 17	-1.31	0.02	-1.25	0.07	-1.31	0.277	-1.26	0.288	-1.28
1428254_at	Purb	Purine rich element binding protein B	-1.15	0.64	-1.19	0.143	-1.61	0.025	-1.08	0.397	-1.26
1437872_at	AB112350	cDNA sequence AB112350	-1.18	0.446	-1.76	0.374	-1.1	0.776	-1.21	0.555	-1.31
1457138_x_at	Optc	Opticin	-1.28	0.193	-1.31	0.51	-1.28	0.4	-1.59	0.474	-1.36
1456156_at	Lepr	leptin receptor	-1.03	0.704	-1.53	0.359	-1.42	0.199	-1.14	0.682	-1.28
1435899_at	9430079B08Rik	RIKEN cDNA 9430079B08 gene	-1.17	0.356	-1.44	0.332	-1.29	0.411	-1.21	0.273	-1.28
1435691_at	C630028N24Rik	RIKEN cDNA C630028N24 gene	-1.12	0.36	-1.34	0.366	-1.47	0.005	-1.23	0.5	-1.29
1458921_at	LOC434348	hypothetical gene supported by AK043371	-1.18	0.571	-1.33	0.483	-1.38	0.047	-1.03	0.946	-1.23
1430270_at	4933411K05Rik	RIKEN cDNA 4933411K05 gene	-1.11	0.691	-1.41	0.139	-1.39	0.294	-1.22	0.325	-1.28
1439676_at	Aatf	apoptosis antagonizing transcription factor	-1.21	0.55	-1.21	0.653	-1.48	0.031	-1.34	0.455	-1.31
1419888_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	-1.19	0.168	-1.28	0.549	-1.41	0.128	-1.59	0.27	-1.37
1440356_at	Ciapin1	cytokine induced apoptosis inhibitor 1	-1.51	0.493	-1	0.995	-1.49	0.218	-1.47	0.327	-1.37
1442956_at	Ppp1r13b	Protein phosphatase 1, regulatory (inhibitor) subunit 13B	-1.17	0.787	-1.67	0.271	-1.14	0.399	-1.54	0.127	-1.38
1436487_x_at	Fbxw2	F-box and WD-40 domain protein 2	-1.11	0.644	-1.65	0.246	-1.21	0.519	-1.57	0.041	-1.39

1431316_at	Itch	itchy	-1.08	0.587	-1.18	0.273	-1.81	0.005	-1.33	0.482	-1.35
1447204_at	Map4k5	Mitogen-activated protein kinase kinase kinase kinase 5	-1.04	0.889	-2.46	0.067	-1.04	0.911	-1.58	0.007	-1.53
1443755_at	---	---	-1.12	0.865	-1.16	0.759	-1.74	0.098	-1.96	0.122	-1.49
1448008_at	Ankhd1	ankyrin repeat and KH domain containing 1	-1.2	0.409	-1.41	0.023	-1.27	0.339	-1.28	0.456	-1.29
1441140_at	---	---	-1.09	0.511	-1.34	0.057	-1.51	0.048	-1.37	0.188	-1.33
1442307_at	---	Transcribed locus	-1.13	0.676	-1.68	0.176	-1.18	0.504	-1.01	0.978	-1.25
1439775_at	Brwd3	bromodomain and WD repeat domain containing 3	-1.4	0.237	-1.11	0.449	-1.39	0.008	-1.1	0.25	-1.25
1441385_at	Rhoh	ras homolog gene family, member H	-1.34	0.265	-1.42	0.304	-1.14	0.667	-5.48	0.002	-2.34
1422218_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	-1.04	0.877	-1.61	0.247	-1.34	0.289	-1.46	0.057	-1.36
1437819_s_at	9530020G05Rik	RIKEN cDNA 9530020G05 gene	-1.19	0.675	-1.63	0.072	-1.15	0.272	-1.21	0.323	-1.29
1457107_at	Nmt2	N-myristoyltransferase 2	-1.39	0.017	-1.19	0.624	-1.31	0.306	-1.09	0.699	-1.24
1444444_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	-1.36	0.42	-1.2	0.332	-1.31	0.554	-1.75	0.25	-1.41
1432331_a_at	Prrx2	paired related homeobox 2	-1.39	0.492	-1.3	0.626	-1.19	0.313	-1.42	0.023	-1.32
1420098_s_at	D13Ertd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	-1.14	0.418	-1.18	0.404	-1.65	0.022	-1.76	0.139	-1.43
1445107_at	A530064N14Rik	RIKEN cDNA A530064N14 gene	-1.64	0.031	-1.11	0.767	-1.22	0.575	-1.2	0.384	-1.29
1443495_at	Zfp99	Zinc finger protein 99	-1.4	0.158	-1.45	0.111	-1.08	0.777	-1.33	0.225	-1.31
1422850_at	Pabpn1	poly(A) binding protein, nuclear 1	-1.3	0.135	-1.27	0.049	-1.3	0.292	-1.16	0.511	-1.26
1421350_a_at	Grip1	glutamate receptor interacting protein 1	-1.47	0.33	-1.34	0.441	-1.1	0.69	-1.05	0.951	-1.24
1457593_at	2610202C22Rik	RIKEN cDNA 2610202C22 gene	-1.11	0.799	-1.15	0.289	-1.79	0.065	-1.18	0.583	-1.31
1442385_at	Msra	Methionine sulfoxide reductase A	-1.28	0.813	-1.77	0.076	-1.01	0.965	-1.27	0.51	-1.33
1443023_at	---	Transcribed locus	-1.24	0.677	-1.53	0.162	-1.14	0.714	-1.34	0.123	-1.32
1427177_at	Fyco1	FYVE and coiled-coil domain containing 1	-1.03	0.917	-1.36	0.103	-1.61	0.017	-1.28	0.431	-1.32
1420939_at	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	-1.12	0.696	-1.96	0.277	-1.07	0.912	-1.23	0.722	-1.35
1459323_at	1700106N22Rik	RIKEN cDNA 1700106N22 gene	-1.55	0.183	-1.27	0.183	-1.11	0.676	-1.07	0.848	-1.25
1455927_x_at	---	---	-1.16	0.112	-1.29	0.059	-1.44	0.036	-1.13	0.58	-1.26
1438960_at	---	---	-1.41	0.632	-1.15	0.836	-1.32	0.561	-4.11	0.024	-2
1456272_at	Setd5	SET domain containing 5	-1.04	0.887	-1.22	0.321	-1.81	0.001	-1.11	0.709	-1.3
1425993_a_at	Hsp110	heat shock protein 110	-1.11	0.628	-1.54	0.106	-1.28	0.285	-1.09	0.824	-1.25
1441644_at	Ptprk	Protein tyrosine phosphatase, receptor type, K	-1.05	0.862	-1.31	0.535	-1.63	0.428	-3.82	0.095	-1.95
1419915_at	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	-1.36	0.36	-1.26	0.267	-1.24	0.116	-1.22	0.525	-1.27
1433016_s_at	4933412F11Rik ///	RIKEN cDNA 4933412F11 gene /// RIKEN cDNA 4930529H12 gene /// hypothetic	-1.51	0.013	-1.24	0.38	-1.16	0.483	-1.02	0.864	-1.23
1429434_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	-1.11	0.57	-1.25	0.437	-1.57	0.101	-1.14	0.488	-1.27
1425848_a_at	Dusp26	dual specificity phosphatase 26 (putative)	-1.15	0.706	-1.67	0.36	-1.16	0.587	-1.17	0.635	-1.29
1440647_at	Sipa1l1	signal-induced proliferation-associated 1 like 1	-1.1	0.812	-1.38	0.369	-1.43	0.039	-1.3	0.235	-1.3
1459552_at	---	Transcribed locus	-1.45	0.592	-1.07	0.829	-1.4	0.157	-1.19	0.755	-1.28
1447021_at	---	CDNA clone IMAGE:5686051	-1.08	0.877	-1.31	0.679	-1.54	0.379	-1.2	0.833	-1.28
1434843_at	A430041B07Rik	RIKEN cDNA A430041B07 gene	-1.3	0.173	-1.19	0.033	-1.38	0.073	-1.34	0.064	-1.3
1433764_at	Clec2l /// LOC6651	C-type lectin domain family, member l /// similar to CD69 antigen (p60, early T-ce	-1.33	0.246	-1.41	0.053	-1.14	0.036	-1.12	0.269	-1.25
1435779_at	Cep110	centrosomal protein 110	-1.19	0.29	-1.71	0.001	-1.1	0.363	-1.57	0.017	-1.39
1417568_at	Ncald	neurocalcin delta	-1.15	0.219	-1.21	0.3	-1.57	0.028	-1.21	0.569	-1.28
1453434_at	1110019D14Rik	RIKEN cDNA 1110019D14 gene	-1.25	0.105	-1.19	0.104	-1.43	0.092	-1.1	0.515	-1.25
1424665_at	5430405G24Rik	RIKEN cDNA 5430405G24 gene	-1.34	0.177	-1.12	0.57	-1.44	0.057	-1.01	0.897	-1.23
1432601_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5	-1.22	0.395	-1.64	0.071	-1.11	0.716	-1.5	0.223	-1.37
1460527_at	4933407C09Rik	RIKEN cDNA 4933407C09 gene	-1.05	0.767	-1.33	0.658	-1.6	0.129	-1.14	0.423	-1.28
1447034_at	Tnpo1	Transportin 1	-1.05	0.748	-1.13	0.492	-2.02	0.052	-1.53	0.036	-1.43
1443425_at	Adamts6	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin typ	-1.3	0.209	-1.73	0.068	-1.01	0.979	-1.4	0.127	-1.36
1437788_at	Sp6	trans-acting transcription factor 6	-1.54	0.647	-1.08	0.784	-1.32	0.372	-1.39	0.001	-1.33
1430917_at	9130401L11Rik	RIKEN cDNA 9130401L11 gene	-1.03	0.929	-1.48	0.468	-1.45	0.477	-1.52	0.413	-1.37
1456899_at	1500004F05Rik	RIKEN cDNA 1500004F05 gene	-1.23	0.078	-1.65	0.609	-1.09	0.744	-1.5	0.302	-1.37
1441597_at	Ankhd1	Ankyrin repeat and KH domain containing 1	-1.12	0.511	-1.14	0.591	-1.77	0.01	-1.12	0.288	-1.29
1445570_at	Nsun4	NOL1/NOP2/Sun domain family, member 4	-1.36	0.277	-1.1	0.74	-1.43	0.001	-1.62	0.113	-1.38
1438245_at	---	---	-1.03	0.893	-1.07	0.724	-2.32	0.036	-1.17	0.6	-1.4
1444387_at	Nmt2	N-myristoyltransferase 2	-1.14	0.333	-1.16	0.513	-1.66	0.076	-1.41	0.013	-1.34

1438708_x_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	-1.25	0.303	-1.05	0.774	-1.7	0.108	-1.71	0.099	-1.43
1436493_at	LOC626281	similar to Cortexin-1	-1.35	0.084	-1.36	0.399	-1.16	0.561	-1.79	0.222	-1.42
1453591_at	5730437N04Rik	RIKEN cDNA 5730437N04 gene	-1.74	0.107	-1.14	0.48	-1.13	0.059	-1.09	0.607	-1.28
1423314_s_at	Pde7a	phosphodiesterase 7A	-1.12	0.136	-1.45	0.255	-1.32	0.059	-1.75	0.137	-1.41
1429937_at	D530033C11Rik	RIKEN cDNA D530033C11 gene	-2.14	0.063	-1.06	0.833	-1.08	0.675	-1.04	0.883	-1.33
1455459_at	Prdm15	PR domain containing 15	-1.17	0.564	-1.35	0.158	-1.34	0.075	-1.36	0.121	-1.31
1449306_at	Hsf2	heat shock factor 2	-1.16	0.835	-1.37	0.297	-1.34	0.585	-1.18	0.799	-1.26
1457358_at	---	---	-1.23	0.156	-1.2	0.566	-1.43	0.264	-1.04	0.809	-1.23
1439992_at	2610206G21Rik	RIKEN cDNA 2610206G21 gene	-1.15	0.81	-1.63	0.154	-1.17	0.62	-2.14	0.512	-1.52
1419582_at	Cyp2c55	cytochrome P450, family 2, subfamily c, polypeptide 55	-1.21	0.405	-1.24	0.706	-1.42	0.489	-1.1	0.899	-1.24
1451859_at	Krtap6-1	keratin associated protein 6-1	-1.16	0.799	-1.46	0.393	-1.27	0.451	-1.66	0.302	-1.38
1417221_at	---	---	-1.08	0.733	-1.44	0.298	-1.38	0.207	-1.78	0.467	-1.42
1440429_at	Arpp21	cyclic AMP-regulated phosphoprotein, 21	-1.38	0.692	-1.03	0.962	-1.56	0.309	-2.17	0.122	-1.53
1421093_at	Slc7a10	solute carrier family 7 (cationic amino acid transporter, y+ system), member 10	-1.49	0.171	-1.18	0.709	-1.22	0.498	-1.2	0.253	-1.27
1437129_at	E330018D03Rik	RIKEN cDNA E330018D03 gene	-1.31	0.11	-1.1	0.68	-1.49	0.111	-1.54	0.375	-1.36
1457174_at	AU015680	expressed sequence AU015680	-1.16	0.685	-1.11	0.81	-1.74	0.046	-3.57	0.093	-1.89
1450896_at	Arhgap5	Rho GTPase activating protein 5	-1.41	0.416	-1.07	0.763	-1.45	0.076	-1.51	0.223	-1.36
1447086_at	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	-1.29	0.56	-1.04	0.895	-1.65	0.051	-1.13	0.798	-1.28
1427564_at	Diap2	diaphanous homolog 2 (Drosophila)	-1.08	0.708	-1.31	0.037	-1.53	0.04	-1.3	0.583	-1.31
1444229_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	-1.15	0.391	-1.57	0.174	-1.2	0.507	-1.1	0.806	-1.26
1447537_at	1500032P08Rik	RIKEN cDNA 1500032P08 gene	-1.02	0.838	-1.63	0.058	-1.34	0.268	-1.21	0.525	-1.3
1422289_a_at	Ctsq	cathepsin Q	-1.4	0.142	-1.22	0.107	-1.25	0.235	-1.05	0.85	-1.23
1431568_at	4933427E13Rik	RIKEN cDNA 4933427E13 gene	-1.03	0.734	-2.37	0.377	-1.05	0.825	-1.22	0.507	-1.42
1459864_at	Gpr146	G protein-coupled receptor 146	-1.24	0.529	-1.6	0.2	-1.1	0.793	-1.13	0.659	-1.27
1439167_at	Pecr	peroxisomal trans-2-enoyl-CoA reductase	-1.65	0.036	-1.28	0.319	-1.05	0.838	-1.06	0.897	-1.26
1458097_at	Cobll1	Cobl-like 1	-1.17	0.061	-1.18	0.185	-1.56	0.021	-1.68	0.104	-1.4
1432822_at	4930557B21Rik	RIKEN cDNA 4930557B21 gene	-1.85	0.43	-1	0.987	-1.24	0.356	-1.35	0.582	-1.36
1439980_at	D14Ertd725e	DNA segment, Chr 14, ERATO Doi 725, expressed	-1.31	0.219	-1.03	0.762	-1.64	0.089	-1.28	0.226	-1.31
1453534_at	2810004I08Rik	RIKEN cDNA 2810004I08 gene	-1.37	0.396	-1.01	0.969	-1.6	0.06	-1.11	0.693	-1.27
1417179_at	Tspan5	tetraspanin 5	-1.01	0.984	-1.51	0.159	-1.46	0.156	-1.14	0.408	-1.28
1458284_at	Ptbp1	polypyrimidine tract binding protein 1	-1.49	0.006	-1.33	0.221	-1.09	0.693	-1.08	0.788	-1.25
1429358_at	4921533L14Rik	RIKEN cDNA 4921533L14 gene	-1.16	0.822	-1.46	0.381	-1.26	0.637	-3.55	0.025	-1.86
1448156_at	Tff1	trefoil factor 1	-1.29	0.568	-1.51	0.235	-1.11	0.676	-1.01	0.951	-1.23
1418008_at	1810007M14Rik	RIKEN cDNA 1810007M14 gene	-1.25	0.143	-1.43	0.084	-1.19	0.386	-1.22	0.564	-1.27
1444890_at	AA536749	Expressed sequence AA536749	-1.17	0.453	-1.11	0.711	-1.7	0.069	-1.3	0.319	-1.32
1453353_at	1700047I16Rik	RIKEN cDNA 1700047I16 gene	-2.24	0.478	-1.03	0.901	-1.08	0.877	-1.08	0.585	-1.36
1436540_at	6720427I07Rik	RIKEN cDNA 6720427I07 gene	-1.39	0.334	-1.17	0.56	-1.29	0.254	-1.35	0.219	-1.3
1437388_at	Fut10	fucosyltransferase 10	-1.12	0.619	-1.62	0.359	-1.19	0.494	-1.5	0.143	-1.36
1441462_at	Dock4	dedicator of cytokinesis 4	-1.12	0.429	-1.1	0.083	-1.84	0.031	-1.12	0.558	-1.29
1437942_x_at	Tube1	epsilon-tubulin 1	-1.27	0.439	-1.43	0.38	-1.17	0.347	-1.07	0.799	-1.23
1442759_at	Akt1	thymoma viral proto-oncogene 1	-1.2	0.52	-1.12	0.839	-1.62	0.151	-1.02	0.905	-1.24
1457639_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	-1.18	0.402	-1	0.99	-2	0.039	-1.99	0.186	-1.54
1421101_a_at	Ldb2	LIM domain binding 2	-1.34	0.11	-1.21	0.407	-1.3	0.263	-1.62	0.071	-1.37
1420187_at	C76628	expressed sequence C76628	-1.95	0.056	-1.19	0.815	-1.01	0.979	-1.26	0.665	-1.35
1429784_at	C130032J12Rik	RIKEN cDNA C130032J12 gene	-1.15	0.392	-1.22	0.16	-1.53	0.006	-1.23	0.245	-1.28
1442671_at	Hip2	Huntingtin interacting protein 2	-1.41	0.214	-1.05	0.795	-1.46	0.075	-1.02	0.872	-1.24
1450666_s_at	Atxn10	ataxin 10	-1.5	0.066	-1.09	0.679	-1.31	0.362	-1.28	0.277	-1.3
1425644_at	Lepr	leptin receptor	-1.21	0.359	-1.44	0.599	-1.22	0.35	-1.28	0.251	-1.28
1443362_at	Zfp277	zinc finger protein 277	-1.23	0.261	-1.28	0.183	-1.33	0.012	-1.67	0.281	-1.38
1440068_at	Rfxdc2	Regulatory factor X domain containing 2 homolog (human)	-1.38	0.183	-1.47	0.092	-1.07	0.607	-2.08	0.13	-1.5
1422223_at	Grin2b	glutamate receptor, ionotropic, NMDA2B (epsilon 2)	-1.43	0.476	-1.06	0.906	-1.42	0.572	-2.74	0.2	-1.66
1421364_at	Lrfn1	leucine rich repeat and fibronectin type III domain containing 1	-1.6	0.055	-1.25	0.279	-1.09	0.663	-1.22	0.259	-1.29
1447859_at	Adck2	aarF domain containing kinase 2	-1.06	0.861	-1.28	0.71	-1.6	0.277	-1.28	0.167	-1.31

1459086_at	A430107P09Rik	RIKEN cDNA A430107P09 gene	-1.09	0.867	-2.06	0.373	-1.06	0.882	-1.35	0.474	-1.39
1434172_at	Cnr1	cannabinoid receptor 1 (brain)	-1.15	0.844	-1.08	0.915	-1.82	0.067	-2.46	0.046	-1.63
1456514_at	---	---	-1.11	0.109	-1.34	0.057	-1.42	0.116	-1.28	0.245	-1.29
1419261_at	Acad8	acyl-Coenzyme A dehydrogenase family, member 8	-1.14	0.765	-1.62	0.037	-1.18	0.273	-1.02	0.932	-1.24
1459722_at	Zswim6	Zinc finger, SWIM domain containing 6	-1.13	0.316	-1.12	0.27	-1.77	0.041	-1.74	0.077	-1.44
1456822_at	Rad23b	RAD23b homolog (S. cerevisiae)	-1.37	0.485	-1.17	0.069	-1.32	0.182	-1.52	0.339	-1.34
1442703_at	AK220484	cDNA sequence AK220484	-1.59	0.312	-1.31	0.552	-1.05	0.913	-1.23	0.594	-1.29
1421312_a_at	Kifc2	kinesin family member C2	-1.31	0.647	-1.4	0.237	-1.15	0.723	-1.91	0.361	-1.44
1442494_at	Ubr2	Ubiquitin protein ligase E3 component n-recognin 2	-1.38	0.161	-1.09	0.553	-1.42	0.016	-1.37	0.036	-1.31
1437994_x_at	Mier2	mesoderm induction early response 1, family member 2	-1.41	0.026	-1.23	0.245	-1.21	0.055	-1.81	0.024	-1.42
1450242_at	Tlr5	toll-like receptor 5	-1.22	0.684	-1.83	0.162	-1.02	0.91	-1.17	0.435	-1.31
1420378_at	Sftpd	surfactant associated protein D	-1.34	0.418	-1.09	0.884	-1.46	0.003	-1.08	0.801	-1.24
1459573_at	Bxdc5	brix domain containing 5	-1.19	0.394	-1.21	0.1	-1.48	0.023	-1.31	0.252	-1.29
1457197_at	Prkacb	protein kinase, cAMP dependent, catalytic, beta	-1.09	0.933	-1.14	0.733	-1.81	0.064	-1.02	0.945	-1.27
1432504_at	1700106N22Rik	RIKEN cDNA 1700106N22 gene	-1.32	0.505	-1.45	0.204	-1.11	0.788	-2.05	0.038	-1.48
1426061_x_at	---	---	-1.79	0.373	-1.21	0.473	-1.04	0.831	-1.59	0.182	-1.41
1424690_at	5930434B04Rik	RIKEN cDNA 5930434B04 gene	-1.04	0.918	-1.45	0.091	-1.43	0.254	-1.72	0.073	-1.41
1419581_at	Dlgh4	discs, large homolog 4 (Drosophila)	-1.11	0.787	-1.81	0.213	-1.12	0.697	-1.43	0.516	-1.37
1436873_at	4732454E20Rik	RIKEN cDNA 4732454E20 gene	-1.15	0.691	-1.6	0.284	-1.18	0.731	-1.46	0.514	-1.35
1426082_a_at	Slc16a4	solute carrier family 16 (monocarboxylic acid transporters), member 4	-1.06	0.265	-1.95	0.093	-1.12	0.079	-1.02	0.934	-1.29
1452227_at	2310045A20Rik	RIKEN cDNA 2310045A20 gene	-1.28	0.231	-1.68	0.171	-1.03	0.858	-1.27	0.394	-1.31
1440872_at	BC010304	CDNA sequence BC010304	-1.68	0.165	-1.31	0.511	-1.01	0.964	-1.27	0.487	-1.32
1446244_at	2810482G21Rik	RIKEN cDNA 2810482G21 gene	-1.33	0.303	-1.25	0.078	-1.25	0.29	-1.88	0.122	-1.43
1444406_at	Map4k3	Mitogen-activated protein kinase kinase kinase kinase 3	-1.02	0.893	-1.15	0.479	-2.01	0.014	-1.2	0.107	-1.34
1428412_at	Tm9sf3	transmembrane 9 superfamily member 3	-1.14	0.385	-1.26	0.055	-1.48	0.033	-1.26	0.162	-1.28
1452728_at	Kirrel3	kin of IRRE like 3 (Drosophila)	-1.24	0.627	-1.42	0.174	-1.19	0.416	-1.49	0.581	-1.34
1440374_at	Pde1c	Phosphodiesterase 1C	-1.31	0.428	-1.05	0.891	-1.57	0.089	-1	0.996	-1.23
1436052_at	1700020O03Rik	RIKEN cDNA 1700020O03 gene	-1.18	0.634	-1.15	0.457	-1.59	0.01	-1.42	0.11	-1.33
1456171_at	Rnf190	ring finger protein 190	-1.4	0.266	-1.37	0.444	-1.1	0.489	-1.1	0.822	-1.24
1429900_at	5330406M23Rik	RIKEN cDNA 5330406M23 gene	-1.12	0.576	-1.16	0.39	-1.68	0.073	-1.51	0.184	-1.37
1437045_at	Mapk8	mitogen activated protein kinase 8	-1.18	0.126	-1.21	0.298	-1.47	0.057	-1.33	0.292	-1.3
1430017_at	1600016N20Rik	RIKEN cDNA 1600016N20 gene	-1.38	0.015	-1.6	0.43	-1	0.997	-1.3	0.152	-1.32
1446521_at	Psmd14	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-1.17	0.534	-1.46	0.013	-1.23	0.195	-1.24	0.103	-1.28
1437339_s_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	-1.1	0.393	-1.13	0.68	-1.8	0.012	-1.58	0.333	-1.4
1456879_at	C130022K22Rik	RIKEN cDNA C130022K22 gene	-1.15	0.62	-1.51	0.208	-1.22	0.166	-1.09	0.407	-1.24
1446773_at	E230025N22	Hypothetical protein E230025N22	-1.12	0.897	-1.07	0.874	-1.93	0.045	-1.29	0.449	-1.35
1442026_at	---	---	-1.2	0.846	-1.18	0.645	-1.5	0.476	-1.46	0.15	-1.33
1417406_at	Sertad1	SERTA domain containing 1	-1.1	0.575	-1.3	0.004	-1.48	0.106	-1.16	0.338	-1.26
1444302_at	BC049816	cDNA sequence BC049816	-1.66	0.427	-1.17	0.743	-1.12	0.761	-2.15	0.151	-1.52
1440022_at	Poldip3	polymerase (DNA-directed), delta interacting protein 3	-1.06	0.852	-1.48	0.323	-1.37	0.14	-1.35	0.244	-1.31
1443260_at	Meis1	myeloid ecotropic viral integration site 1	-1.09	0.5	-1.17	0.692	-1.74	0.116	-1.17	0.575	-1.29
1458510_at	AU019823	expressed sequence AU019823	-1.42	0.187	-1.07	0.808	-1.39	0.069	-1.51	0.301	-1.35
1442979_at	---	PREDICTED: Mus musculus similar to zinc finger protein 709 (LOC629191), mRN	-1.17	0.864	-1.95	0.408	-1.02	0.889	-1.19	0.679	-1.33
1459942_at	ORF34	Open reading frame 34	-1.17	0.544	-1.14	0.738	-1.61	0.163	-1	0.997	-1.23
1447450_at	Pparbp	Peroxisome proliferator activated receptor binding protein	-1.25	0.603	-1.26	0.068	-1.33	0.088	-1.3	0.328	-1.28
1427200_at	Zranb1	zinc finger, RAN-binding domain containing 1	-1.11	0.492	-1.34	0.019	-1.41	0.031	-1.01	0.943	-1.22
1428583_at	Nufip2	nuclear fragile X mental retardation protein interacting protein 2	-1.06	0.734	-1.42	0.088	-1.42	0.093	-1.09	0.67	-1.25
1441408_at	AU044856	expressed sequence AU044856	-1.11	0.782	-1.34	0.58	-1.41	0.31	-1.16	0.778	-1.26
1429963_at	Mapk6	mitogen-activated protein kinase 6	-1.24	0.722	-1.2	0.74	-1.41	0.03	-1.23	0.319	-1.27
1426361_at	Zc3h11a	zinc finger CCCH type containing 11A	-1.14	0.433	-1.32	0.121	-1.4	0.025	-1.23	0.348	-1.27
1444473_at	Pcaf	P300/CBP-associated factor	-1.2	0.418	-1.19	0.087	-1.47	0.099	-1.26	0.185	-1.28
1446889_at	D2Ertd105e	DNA segment, Chr 2, ERATO Doi 105, expressed	-1.12	0.911	-1.32	0.468	-1.43	0.418	-1.4	0.442	-1.32
1441169_at	B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	-1.38	0.268	-1.19	0.797	-1.27	0.449	-1.01	0.977	-1.21

1434081_at	Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	-1.16	0.567	-1.3	0.143	-1.39	0.061	-1.31	0.399	-1.29
1443993_at	Zc3h12a	zinc finger CCCH type containing 12A	-1.56	0.468	-1.11	0.743	-1.23	0.507	-1.29	0.266	-1.3
1438033_at	Tef	thyrotroph embryonic factor	-1.54	0.405	-1.28	0.498	-1.08	0.769	-1.2	0.23	-1.27
1427512_a_at	Lama3 /// LOC669	laminin, alpha 3 /// similar to Laminin alpha-3 chain precursor (Nicein alpha subur	-1.41	0.062	-1.24	0.799	-1.19	0.636	-1.59	0.334	-1.36
1457218_at	6430510M02Rik	RIKEN cDNA 6430510M02 gene	-1.02	0.837	-1.47	0.162	-1.44	0.233	-2.02	0.193	-1.49
1436854_at	Trpc2	transient receptor potential cation channel, subfamily C, member 2	-1.26	0.301	-1.44	0.186	-1.16	0.518	-1.41	0.151	-1.32
1459173_at	Ptprd	protein tyrosine phosphatase, receptor type, D	-2.17	0.018	-1.06	0.865	-1.05	0.924	-1.8	0.015	-1.52
1454230_a_at	Slc25a27	solute carrier family 25, member 27	-1.04	0.921	-1.59	0.392	-1.3	0.44	-1.66	0.389	-1.4
1442351_a_at	BC029214	cDNA sequence BC029214	-1.03	0.934	-2.05	0.097	-1.12	0.554	-2.52	0.081	-1.68
1446571_at	A830039H10Rik	RIKEN cDNA A830039H10 gene	-1.03	0.724	-1.28	0.118	-1.64	0.007	-1.16	0.237	-1.28
1420721_at	4921536K21Rik	RIKEN cDNA 4921536K21 gene	-1.14	0.696	-1.18	0.696	-1.59	0.256	-1.7	0.232	-1.4
1431560_at	Dcakd	dephospho-CoA kinase domain containing	-1.21	0.507	-1.58	0.231	-1.11	0.696	-1.4	0.036	-1.33
1417425_at	Prkrip1	Prkr interacting protein 1 (IL11 inducible)	-1.02	0.932	-1.41	0.027	-1.49	0.015	-1.15	0.667	-1.27
1418416_x_at	Psg23	pregnancy-specific glycoprotein 23	-1.8	0.144	-1.21	0.533	-1.03	0.913	-1.66	0.33	-1.42
1446722_at	Gna13	Guanine nucleotide binding protein, alpha 13	-1.06	0.715	-1.2	0.35	-1.73	0.072	-1.33	0.181	-1.33
1450935_at	Ercc5	excision repair cross-complementing rodent repair deficiency, complementation g	-1.21	0.43	-1.36	0.002	-1.26	0.256	-1.39	0.069	-1.31
1457478_at	Strbp	Spermatid perinuclear RNA binding protein	-1.17	0.68	-1.35	0.561	-1.32	0.119	-1.98	0.253	-1.45
1442683_at	Hmg20a	high mobility group 20A	-1.33	0.45	-1.07	0.867	-1.5	0.107	-2.26	0.107	-1.54
1440873_at	---	---	-1.71	0.033	-1.08	0.582	-1.18	0.359	-1.04	0.942	-1.25
1438987_at	---	---	-1.63	0.042	-1.24	0.618	-1.06	0.802	-1.15	0.675	-1.27
1440579_at	---	---	-1.16	0.189	-1.13	0.333	-1.65	0.007	-1.13	0.633	-1.27
1457642_at	5730507N06Rik	RIKEN cDNA 5730507N06 gene	-1.26	0.225	-1.17	0.258	-1.41	0.321	-1.08	0.881	-1.23
1426899_at	Tbc1d23	TBC1 domain family, member 23	-1.53	0.123	-1.23	0.191	-1.12	0.35	-1.24	0.633	-1.28
1428288_at	Klf9	Kruppel-like factor 9	-1.2	0.651	-1.25	0.229	-1.38	0.166	-1.05	0.883	-1.22
1423473_at	2-Sep	septin 2	-1.27	0.525	-1.15	0.672	-1.42	0.299	-1	0.995	-1.21
1457454_at	Usp47	ubiquitin specific peptidase 47	-1.01	0.966	-1.35	0.313	-1.59	0.043	-1.3	0.234	-1.31
1451568_at	A630054L15Rik	RIKEN cDNA A630054L15 gene	-1.11	0.506	-1.3	0.426	-1.45	0.13	-1.04	0.887	-1.23
1428651_at	Klhl24	kelch-like 24 (Drosophila)	-1.16	0.313	-1.29	0.232	-1.39	0.37	-1.86	0.155	-1.42
1453874_at	4933401B06Rik	RIKEN cDNA 4933401B06 gene	-1.26	0.531	-1	0.994	-1.75	0.052	-1.33	0.303	-1.34
1459332_at	Itch	itchy	-1.16	0.227	-1.18	0.328	-1.54	0.091	-1.46	0.045	-1.34
1429538_a_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	-1.26	0.016	-1.15	0.377	-1.44	0.14	-1.29	0.371	-1.28
1448112_at	Cox7c	cytochrome c oxidase, subunit VIIc	-1.18	0.027	-1.33	0.013	-1.31	0.019	-1.12	0.16	-1.24
1429914_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	-1.08	0.313	-1.62	0.134	-1.22	0.098	-1.13	0.66	-1.26
1433063_at	Wdr66	WD repeat domain 66	-1.24	0.712	-1.36	0.528	-1.22	0.392	-1.55	0.041	-1.34
1428637_at	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-1.04	0.803	-1.25	0.062	-1.67	0.024	-1.72	0.122	-1.42
1419730_at	4631427C17Rik	RIKEN cDNA 4631427C17 gene	-1.26	0.206	-1.15	0.437	-1.44	0.04	-1.09	0.527	-1.23
1441364_at	Gata4	GATA binding protein 4	-1.02	0.97	-1.14	0.409	-1.99	0.166	-1.48	0.594	-1.41
1431391_at	Ralgps1	Ral GEF with PH domain and SH3 binding motif 1	-1.37	0.262	-1.06	0.855	-1.46	0.012	-1.03	0.851	-1.23
1460487_at	1110014L15Rik	RIKEN cDNA 1110014L15 gene	-1.44	0.599	-1.13	0.871	-1.28	0.164	-1.16	0.538	-1.25
1440734_at	Ttbk2	tau tubulin kinase 2	-1.13	0.69	-1.4	0.208	-1.32	0.477	-1.3	0.73	-1.29
1459008_at	---	---	-1.12	0.32	-1.13	0.177	-1.72	0.021	-1.11	0.098	-1.27
1443279_at	Nlk	Nemo like kinase	-1.3	0.36	-1.04	0.903	-1.59	0.059	-1.33	0.289	-1.32
1445605_s_at	4921533L14Rik	RIKEN cDNA 4921533L14 gene	-1.39	0.213	-1.14	0.789	-1.32	0.435	-2.44	0.238	-1.57
1421829_at	Ak3l1	adenylate kinase 3 alpha-like 1	-1.04	0.848	-2.26	0.042	-1.04	0.945	-1.1	0.654	-1.36
1446802_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	-1.09	0.205	-1.1	0.639	-1.86	0.021	-1.08	0.717	-1.28
1443312_at	Rfx4	Regulatory factor X, 4 (influences HLA class II expression)	-1.18	0.534	-1.41	0.288	-1.25	0.784	-1.06	0.903	-1.22
1426192_at	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.39	0.029	-1.16	0.564	-1.28	0.268	-1.32	0.298	-1.29
1429565_s_at	Lce5a	late cornified envelope 5A	-1.18	0.872	-1.69	0.253	-1.09	0.807	-2.19	0.019	-1.54
1421951_at	Lhx1	LIM homeobox protein 1	-1.15	0.134	-1.56	0.141	-1.18	0.822	-2.89	0.054	-1.69
1444396_at	Trp53inp2	Tumor protein p53 inducible nuclear protein 2	-1.22	0.251	-1.59	0.112	-1.1	0.748	-1.39	0.471	-1.32
1428467_at	Tardbp	TAR DNA binding protein	-1.21	0.057	-1.31	0.135	-1.29	0.249	-1.31	0.4	-1.28
1457895_at	Kif18a	kinesin family member 18A	-1.34	0.545	-1.57	0.629	-1.02	0.95	-1.17	0.809	-1.27
1449329_at	Zfp235	zinc finger protein 235	-1.14	0.769	-1.7	0.079	-1.12	0.723	-2	0.268	-1.49

1444184_at	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	-1.4	0.04	-1.13	0.433	-1.3	0.303	-1.01	0.818	-1.21
1434770_at	Iqcb1	IQ calmodulin-binding motif containing 1	-1.25	0.321	-1.39	0.105	-1.19	0.092	-1.13	0.601	-1.24
1455170_at	2810001G20Rik	RIKEN cDNA 2810001G20 gene	-1.07	0.522	-1.58	0.003	-1.25	0.418	-1.28	0.524	-1.3
1438429_at	2610319H10Rik	RIKEN cDNA 2610319H10 gene	-1.1	0.523	-1.25	0.295	-1.51	0.208	-1.55	0.16	-1.36
1454770_at	Cckbr	cholecystokinin B receptor	-1.67	0.599	-1	0.993	-1.3	0.167	-1.08	0.606	-1.26
1431135_at	---	---	-1.21	0.405	-1.45	0.18	-1.18	0.546	-1.14	0.841	-1.24
1444934_at	Zfp276	zinc finger protein (C2H2 type) 276	-1.15	0.414	-1.38	0.103	-1.3	0.192	-1.25	0.063	-1.27
1432716_at	Lrrn1	leucine rich repeat protein 1, neuronal	-1.23	0.772	-1.07	0.829	-1.63	0.212	-1.44	0.567	-1.34
1418066_at	Cfl2	cofilin 2, muscle	-1.28	0.082	-1.18	0.335	-1.36	0.062	-1.21	0.529	-1.26
1455449_at	Gm468	gene model 468, (NCBI)	-1.07	0.662	-1.17	0.684	-1.72	0.343	-1.4	0.358	-1.34
1445759_at	Smpd3	Sphingomyelin phosphodiesterase 3, neutral	-1.21	0.336	-1.18	0.705	-1.44	0.044	-1.48	0.024	-1.33
1439089_at	Zbtb41	zinc finger and BTB domain containing 41 homolog	-1.16	0.21	-1.48	0.009	-1.21	0.037	-1.01	0.914	-1.22
1447690_at	Lsr	lipolysis stimulated lipoprotein receptor	-2.36	0.415	-1.05	0.863	-1.01	0.971	-2.27	0.181	-1.67
1437205_at	Tcf25	transcription factor 25 (basic helix-loop-helix)	-1.18	0.182	-1.28	0.005	-1.35	0.108	-1.24	0.311	-1.26
1447442_at	Helz	Helicase with zinc finger domain	-1.31	0.221	-1.18	0.194	-1.33	0.179	-1.52	0.204	-1.34
1442766_at	---	Transcribed locus	-1.63	0.309	-1.03	0.904	-1.27	0.453	-1.51	0.047	-1.36
1426568_at	Slc2a9	solute carrier family 2 (facilitated glucose transporter), member 9	-1.44	0.349	-1.44	0.247	-1.02	0.895	-1.77	0.268	-1.42
1420056_s_at	Ptdsr	phosphatidylserine receptor	-1.06	0.714	-1.55	0.031	-1.29	0.132	-1.12	0.067	-1.25
1456575_at	Ndn	Necdin	-2.23	0.166	-1.07	0.909	-1.02	0.961	-1.07	0.923	-1.35
1429284_at	8430436F23Rik	RIKEN cDNA 8430436F23 gene	-1.13	0.006	-1.22	0.297	-1.51	0.104	-1.55	0.13	-1.35
1455366_at	Mrpl52	mitochondrial ribosomal protein L52	-1.59	0.348	-1.29	0.177	-1.04	0.88	-1.25	0.478	-1.29
1442864_at	Esrra	estrogen related receptor, alpha	-1.33	0.316	-1.18	0.682	-1.3	0.353	-1.51	0.32	-1.33
1454970_at	---	---	-1.35	0.364	-1.59	0.207	-1.01	0.981	-1.02	0.879	-1.24
1445021_at	6030465E24Rik	RIKEN cDNA 6030465E24 gene	-1.18	0.688	-1.41	0.547	-1.24	0.647	-2.13	0.011	-1.49
1427666_a_at	Tcrb-J	T-cell receptor beta, joining region	-1.19	0.544	-1.28	0.374	-1.35	0.092	-3.86	0.06	-1.92
1448975_s_at	Ren1 /// Ren2	renin 1 structural /// renin 2 tandem duplication of Ren1	-1.69	0.307	-1.09	0.777	-1.16	0.239	-1.42	0.502	-1.34
1434420_x_at	Tomm22	translocase of outer mitochondrial membrane 22 homolog (yeast)	-1.17	0.234	-1.21	0.244	-1.46	0.039	-1.14	0.547	-1.25
1453384_at	4632404N19Rik	RIKEN cDNA 4632404N19 gene	-1.05	0.87	-1.47	0.021	-1.37	0.081	-1.7	0.2	-1.4
1454604_s_at	Tspan12	tetraspanin 12	-1.31	0.315	-1.09	0.516	-1.47	0.101	-1.08	0.599	-1.24
1458156_at	E230012J19Rik	RIKEN cDNA E230012J19 gene	-1.21	0.059	-1.23	0.289	-1.38	0.237	-1.22	0.421	-1.26
1453710_at	Tmem116	transmembrane protein 116	-1.04	0.507	-1.31	0.658	-1.56	0.229	-2.27	0.145	-1.54
1434656_at	B230339M05Rik	RIKEN cDNA B230339M05 gene	-1.14	0.231	-1.39	0.043	-1.3	0.089	-1.2	0.12	-1.26
1447913_x_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	-1.18	0.144	-1.6	0.165	-1.12	0.714	-1.42	0.333	-1.33
1441253_at	Rfx3	Regulatory factor X, 3 (influences HLA class II expression)	-1.13	0.698	-1.31	0.092	-1.39	0.197	-1.43	0.047	-1.32
1442692_at	Mapkap1	Mitogen-activated protein kinase associated protein 1	-1.15	0.662	-1.28	0.357	-1.4	0.271	-1.26	0.338	-1.27
1434283_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	-1.14	0.315	-1.57	0.166	-1.18	0.254	-1.28	0.293	-1.29
1439317_at	Krit1	KRIT1, ankyrin repeat containing	-1.18	0.603	-1.3	0.24	-1.33	0.164	-1.62	0.024	-1.36
1439209_at	Tcf12	Transcription factor 12	-1.29	0.416	-1.04	0.91	-1.58	0.004	-1.38	0.084	-1.32
1434642_at	Dhrs8	dehydrogenase/reductase (SDR family) member 8	-1.05	0.531	-1.78	0.032	-1.17	0.21	-1.31	0.459	-1.33
1421433_at	Zfhx4	zinc finger homeodomain 4	-1.69	0.368	-1.09	0.626	-1.16	0.789	-1.97	0.268	-1.48
1442358_at	AA409587	expressed sequence AA409587	-1.23	0.001	-1.11	0.239	-1.53	0.032	-1.23	0.267	-1.27
1454284_at	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	-1.02	0.966	-1.38	0.556	-1.51	0.314	-1.08	0.88	-1.25
1445866_at	Mast4	microtubule associated serine/threonine kinase family member 4	-1.15	0.371	-1.12	0.514	-1.63	0.076	-1.6	0.021	-1.38
1436673_at	2610020H08Rik	RIKEN cDNA 2610020H08 gene	-1.18	0.509	-1.14	0.653	-1.55	0.016	-1.64	0.035	-1.38
1454819_at	---	---	-1.04	0.814	-1.49	0.101	-1.36	0.041	-1.03	0.875	-1.23
1458919_at	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	-1.14	0.194	-1.08	0.503	-1.77	0.024	-1.03	0.862	-1.26
1434692_at	1110034B05Rik	RIKEN cDNA 1110034B05 gene	-1.21	0.045	-1.39	0.025	-1.22	0.146	-1.37	0.258	-1.3
1444877_at	---	---	-1.8	0.261	-1.01	0.979	-1.22	0.576	-2.56	0.048	-1.65
1431222_at	Tiam2	T-cell lymphoma invasion and metastasis 2	-1.17	0.494	-1.31	0.099	-1.33	0.241	-1.04	0.819	-1.21
1415769_at	Itch	itchy	-1.28	0.249	-1.23	0.23	-1.29	0.049	-1.57	0.012	-1.34
1432160_at	Git2	G protein-coupled receptor kinase-interactor 2	-1.18	0.676	-1.53	0.47	-1.15	0.568	-1.92	0.118	-1.44
1454635_at	Fbxl3	F-box and leucine-rich repeat protein 3	-1.33	0.103	-1.06	0.334	-1.47	0.113	-1.41	0.162	-1.32
1440622_at	Sec15l2	SEC15-like 2 (S. cerevisiae)	-1.2	0.654	-1.03	0.885	-1.77	0.04	-1.52	0.503	-1.38

1453321_at	Fndc1	fibronectin type III domain containing 1	-1.18	0.372	-1.36	0.205	-1.27	0.478	-1.03	0.838	-1.21
1430681_at	Cryl1	crystallin, lamda 1	-1.34	0.057	-1.27	0.428	-1.2	0.278	-1.46	0.378	-1.32
1432351_at	9030625G05Rik	RIKEN cDNA 9030625G05 gene	-1.11	0.856	-1.5	0.136	-1.25	0.76	-2.07	0.314	-1.48
1431961_at	Dock8	dedicator of cytokinesis 8	-1.09	0.486	-1.25	0.193	-1.54	0.223	-2.24	0.06	-1.53
1429650_at	Stk40	serine/threonine kinase 40	-1.28	0.166	-1.3	0.02	-1.22	0.431	-1.06	0.767	-1.21
1447153_x_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	-1.03	0.926	-1.44	0.158	-1.42	0.235	-1.49	0.248	-1.35
1430856_at	Pex11c	peroxisomal biogenesis factor 11c	-1.46	0.282	-1.37	0.006	-1.04	0.857	-1.7	0.183	-1.39
1415731_at	Angel2	angel homolog 2 (Drosophila)	-1.35	0.194	-1.2	0.494	-1.25	0.133	-1.24	0.179	-1.26
1459143_at	Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	-1.07	0.777	-1.64	0.038	-1.21	0.579	-1.59	0.169	-1.38
1459150_at	Lrch1	Leucine-rich repeats and calponin homology (CH) domain containing 1	-1.29	0.008	-1.11	0.612	-1.43	0.12	-1.73	0.074	-1.39
1423533_a_at	Rhot1	ras homolog gene family, member T1	-1.17	0.192	-1.38	0.03	-1.26	0.105	-1.08	0.478	-1.22
1456439_x_at	Mical1	microtubule associated monoxygenase, calponin and LIM domain containing 1	-1.12	0.688	-1.68	0.36	-1.13	0.355	-2.13	0.07	-1.51
1418563_at	Serbp1	Serpine1 mRNA binding protein 1	-1.15	0.099	-1.26	0.032	-1.4	0.02	-1.06	0.38	-1.22
1449647_at	---	Transcribed locus	-1.65	0.226	-1.28	0.626	-1.02	0.978	-1.03	0.86	-1.25
1456997_at	Ncoa5	Nuclear receptor coactivator 5	-1.08	0.702	-1.17	0.548	-1.7	0.027	-1.16	0.273	-1.28
1443068_at	D130084N16Rik	RIKEN cDNA D130084N16 gene	-1.18	0.273	-1.33	0.295	-1.29	0.207	-1.42	0.522	-1.31
1446269_at	Hbp1	high mobility group box transcription factor 1	-1.33	0.284	-1.34	0.512	-1.14	0.686	-1.41	0.208	-1.31
1437839_x_at	Mrpl11	mitochondrial ribosomal protein L11	-1.34	0.141	-1.03	0.888	-1.52	0.003	-1.35	0.296	-1.31
1433252_at	4932703K07Rik	RIKEN cDNA 4932703K07 gene	-1.77	0.417	-1.04	0.935	-1.19	0.633	-1.34	0.381	-1.33
1418374_at	Fxyd3	FXYD domain-containing ion transport regulator 3	-1.12	0.783	-1.06	0.734	-1.85	0.018	-1.28	0.459	-1.33
1454177_at	4930597G03Rik	RIKEN cDNA 4930597G03 gene	-1.4	0.599	-1.4	0.408	-1.06	0.8	-1.07	0.676	-1.23
1428996_at	4833426J09Rik	RIKEN cDNA 4833426J09 gene	-1.09	0.78	-1.64	0.217	-1.19	0.542	-1.07	0.746	-1.25
1447504_at	Ghitm	Growth hormone inducible transmembrane protein	-1.17	0.438	-1.13	0.555	-1.58	0.169	-1.11	0.577	-1.25
1430833_at	Itk	IL2-inducible T-cell kinase	-1.04	0.926	-1.31	0.683	-1.54	0.207	-1.72	0.342	-1.4
1422980_a_at	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like	-1.24	0.265	-1.22	0.029	-1.35	0.058	-1.45	0.016	-1.31
1447821_at	1700051K22Rik	RIKEN cDNA 1700051K22 gene	-1.61	0.072	-1.27	0.065	-1.04	0.824	-1.5	0.051	-1.35
1441823_at	Rai17	retinoic acid induced 17	-1.18	0.475	-1.16	0.464	-1.5	0.101	-1.62	0.088	-1.37
1436316_at	9430029L20Rik	RIKEN cDNA 9430029L20 gene	-1.33	0.642	-1.19	0.573	-1.28	0.393	-1.28	0.498	-1.27
1435350_at	Traf6	Tnf receptor-associated factor 6	-1.17	0.339	-1.38	0.41	-1.27	0.116	-1.36	0.323	-1.29
1422575_at	Mxd4 /// LOC63515	Max dimerization protein 4 /// similar to Max dimerization protein 4	-1.54	0.05	-1.27	0.176	-1.07	0.848	-1.17	0.731	-1.26
1429356_s_at	Ggps1	geranylgeranyl diphosphate synthase 1	-1.11	0.408	-1.99	0.038	-1.04	0.746	-1.07	0.629	-1.3
1417866_at	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-1.23	0.2	-1.13	0.514	-1.47	0.04	-1.38	0.064	-1.3
1444726_at	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	-1.19	0.315	-1.49	0.101	-1.16	0.534	-1.4	0.209	-1.31
1432719_at	4833412K13Rik	RIKEN cDNA 4833412K13 gene	-1.19	0.019	-1.2	0.031	-1.43	0.124	-1.17	0.594	-1.25
1436798_at	Rpl9 /// LOC43276	ribosomal protein L9 /// similar to ribosomal protein L9 /// similar to ribosomal prot	-1.25	0.018	-1.34	0.066	-1.2	0.233	-1.36	0.141	-1.29
1457455_at	Suhw4	suppressor of hairy wing homolog 4 (Drosophila)	-1.13	0.403	-1.17	0.135	-1.58	0.133	-1	0.972	-1.22
1455086_at	Uchl5	Ubiquitin carboxyl-terminal esterase L5	-1.12	0.724	-1.36	0.437	-1.34	0.338	-1.83	0.174	-1.41
1417622_at	Slc12a2	solute carrier family 12, member 2	-1.16	0.498	-1.08	0.29	-1.7	0.026	-1.02	0.963	-1.24
1441716_at	---	12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D23002	-1.49	0.295	-1.15	0.659	-1.2	0.103	-1.12	0.16	-1.24
1431566_at	---	---	-1.24	0.519	-1.37	0.029	-1.19	0.284	-1.14	0.635	-1.24
1429463_at	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit	-1	0.998	-1.42	0.302	-1.49	0.193	-1.21	0.745	-1.28
1449775_x_at	Slc35a4 /// LOC545	solute carrier family 35, member A4 /// similar to solute carrier family 35, member	-1.56	0.536	-1.28	0.686	-1.05	0.918	-1.02	0.952	-1.23
1428364_at	Scnm1	sodium channel modifier 1	-1.23	0.172	-1.36	0.103	-1.21	0.156	-1.13	0.55	-1.23
1437557_at	D3Ertd254e	DNA segment, Chr 3, ERATO Doi 254, expressed	-1.26	0.101	-1.28	0.154	-1.24	0.078	-1.47	0.068	-1.31
1425289_a_at	Cr2	complement receptor 2	-1.18	0.527	-1.5	0.63	-1.16	0.586	-4.2	0.027	-2.01
1449581_at	Emid1	EMI domain containing 1	-1.05	0.779	-1.21	0.679	-1.68	0.162	-2.73	0.059	-1.67
1443350_at	Mta3	metastasis associated 3	-1.31	0.328	-1.25	0.484	-1.23	0.202	-1.47	0.169	-1.32
1439262_x_at	2310001A20Rik	RIKEN cDNA 2310001A20 gene	-1.21	0.584	-1.31	0.232	-1.27	0.066	-1.43	0.204	-1.31
1442704_at	Baz2b	Bromodomain adjacent to zinc finger domain, 2B	-1.04	0.702	-1.23	0.097	-1.66	0.057	-1.76	0.063	-1.42
1417525_at	Hand1	heart and neural crest derivatives expressed transcript 1	-2.01	0.227	-1.1	0.793	-1.03	0.921	-1.35	0.537	-1.37
1446470_at	---	---	-1.5	0.088	-1.21	0.543	-1.13	0.613	-1.21	0.496	-1.26
1432174_a_at	4933425K02Rik	RIKEN cDNA 4933425K02 gene	-1.26	0.64	-1.36	0.553	-1.18	0.628	-1.28	0.679	-1.27
1431552_at	1810006J02Rik	RIKEN cDNA 1810006J02 gene	-1.51	0.2	-1.1	0.883	-1.25	0.58	-1.43	0.483	-1.32

1459995_at	1700015G11Rik	RIKEN cDNA 1700015G11 gene	-1.21	0.831	-1.01	0.925	-1.79	0.154	-1.61	0.507	-1.4
1456001_at	LOC545548	similar to late cornified envelope protein	-1.27	0.362	-1.38	0.409	-1.16	0.471	-1.51	0.496	-1.33
1418720_at	Cops7b	COP9 (constitutive photomorphogenic) homolog, subunit 7b (Arabidopsis thaliana	-1.34	0.086	-1.57	0.01	-1	0.979	-1.07	0.722	-1.25
1449187_at	Pdgfa	platelet derived growth factor, alpha	-1	0.96	-1.54	0.088	-1.37	0.163	-1.19	0.396	-1.28
1445695_at	Atxn1	Ataxin 1	-1.1	0.723	-1.13	0.344	-1.71	0.017	-1.25	0.364	-1.3
1460085_at	Zfp281	Zinc finger protein 281	-1.73	0.049	-1.14	0.418	-1.08	0.462	-1.3	0.224	-1.31
1440051_at	Ppp3ca	Protein phosphatase 3, catalytic subunit, alpha isoform	-1.1	0.783	-1.06	0.791	-1.91	0.004	-1.87	0.186	-1.49
1457598_at	Txnl2	Thioredoxin-like 2	-1.09	0.665	-1.75	0.099	-1.13	0.678	-1.16	0.317	-1.28
1440853_at	Rhot1	ras homolog gene family, member T1	-1.12	0.829	-1.61	0.046	-1.16	0.239	-1.06	0.82	-1.24
1435074_at	Tmem106b	transmembrane protein 106B	-1.23	0.294	-1.24	0.106	-1.31	0.231	-1.6	0.238	-1.35
1446304_at	---	---	-1.25	0.294	-1.18	0.409	-1.37	0.273	-1.17	0.588	-1.24
1443719_x_at	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	-1.06	0.68	-1.22	0.302	-1.63	0.038	-1.2	0.169	-1.28
1434584_a_at	Pramel5 /// LOC384	preferentially expressed antigen in melanoma like 5 /// Unknown (protein for IMAG	-1.34	0.685	-1.4	0.397	-1.1	0.73	-2.5	0.094	-1.58
1455322_at	Ttc21b	tetratricopeptide repeat domain 21B	-1.34	0.187	-1.27	0.14	-1.19	0.226	-1.2	0.326	-1.25
1433766_at	C330023M02Rik	RIKEN cDNA C330023M02 gene	-1.22	0.242	-1.26	0.017	-1.31	0.009	-1.15	0.011	-1.24
1451058_at	Mcts2	malignant T cell amplified sequence 2	-1.16	0.104	-1.17	0.112	-1.52	0.023	-1.34	0.062	-1.3
1447002_at	---	---	-1.75	0.618	-1.23	0.666	-1.01	0.991	-1.12	0.79	-1.28
1452899_at	Rian	RNA imprinted and accumulated in nucleus	-1.26	0.398	-1.02	0.925	-1.65	0.329	-1.11	0.882	-1.26
1435218_at	Rasgef1a	RasGEF domain family, member 1A	-1.39	0.513	-1.05	0.776	-1.42	0.125	-1.53	0.192	-1.35
1418623_at	Rab2	RAB2, member RAS oncogene family	-1.44	0.194	-1.38	0.457	-1.04	0.837	-1.64	0.221	-1.38
1458994_at	Csnk1g3	Casein kinase 1, gamma 3	-1.16	0.101	-1.13	0.487	-1.58	0.016	-1.98	0.089	-1.46
1423278_at	Ptprk	protein tyrosine phosphatase, receptor type, K	-1.16	0.27	-1.09	0.226	-1.66	0.016	-1.27	0.153	-1.3
1429996_at	6330417A16Rik	RIKEN cDNA 6330417A16 gene	-1.14	0.405	-1.27	0.184	-1.4	0.179	-1.26	0.299	-1.27
1453270_a_at	Phf14	PHD finger protein 14	-1.08	0.881	-1.35	0.413	-1.4	0.22	-1.37	0.271	-1.3
1442823_at	---	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130001F	-1.04	0.588	-1.8	0.203	-1.16	0.515	-1.29	0.711	-1.32
1437264_at	BC051142	cDNA sequence BC051142	-1.81	0.44	-1.06	0.893	-1.13	0.468	-1.12	0.721	-1.28
1457064_at	D030002E05Rik	RIKEN cDNA D030002E05 gene	-1.08	0.867	-1.36	0.315	-1.39	0.126	-1.59	0.061	-1.36
1429518_at	Faim2	Fas apoptotic inhibitory molecule 2	-1.43	0.226	-1.37	0.117	-1.05	0.861	-1.02	0.955	-1.22
1435300_at	---	---	-1.45	0.021	-1.36	0.142	-1.05	0.78	-1.78	0.009	-1.41
1456913_at	Tmod3	Tropomodulin 3	-1.09	0.776	-1.18	0.373	-1.63	0.02	-1.59	0.132	-1.37
1437227_at	2900073H19Rik	RIKEN cDNA 2900073H19 gene	-1.12	0.749	-1.73	0.01	-1.1	0.797	-1.9	0.222	-1.46
1446608_at	Cbl	Casitas B-lineage lymphoma	-1.46	0.063	-1.28	0.506	-1.09	0.765	-1.12	0.714	-1.24
1421569_at	Grid1	glutamate receptor, ionotropic, delta 1	-1.32	0.586	-1.23	0.734	-1.24	0.618	-1.25	0.198	-1.26
1424664_at	BC017647	cDNA sequence BC017647	-1.6	0.179	-1.27	0.415	-1.03	0.899	-1.19	0.784	-1.27
1443338_at	Ap2m1	Adaptor protein complex AP-2, mu1	-1.06	0.826	-1.27	0.118	-1.54	0.027	-1.19	0.029	-1.26
1424377_at	LOC670726	similar to ribosomal protein L24-like	-1.14	0.17	-1.39	0.061	-1.28	0.128	-1.01	0.885	-1.2
1440167_s_at	Lpp	LIM domain containing preferred translocation partner in lipoma	-1.05	0.558	-1.18	0.396	-1.72	0.03	-1.33	0.37	-1.32
1435788_at	2900086B20Rik	RIKEN cDNA 2900086B20 gene	-1.13	0.035	-1.33	0.135	-1.34	0.129	-1.13	0.394	-1.23
1444371_at	A630007B06Rik	RIKEN cDNA A630007B06 gene	-1.11	0.564	-1.22	0.558	-1.51	0.07	-1.54	0.017	-1.35
1457051_at	Trim27	tripartite motif protein 27	-1.43	0.539	-1.25	0.268	-1.13	0.68	-1.17	0.476	-1.25
1456952_at	Arid1b	AT rich interactive domain 1B (Swi1 like)	-1.2	0.38	-1.14	0.255	-1.49	0.071	-1.79	0.042	-1.4
1432665_at	2210416J07Rik	RIKEN cDNA 2210416J07 gene	-1.28	0.34	-1.26	0.748	-1.24	0.3	-1.04	0.779	-1.21
1423637_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.32	0.267	-1.14	0.766	-1.35	0.253	-1.7	0.024	-1.37
1452041_at	Klhl26	kelch-like 26 (Drosophila)	-1.44	0.201	-1.25	0.058	-1.13	0.58	-1.45	0.01	-1.32
1455617_at	Lmbrd1	LMBR1 domain containing 1	-1.13	0.143	-1.33	0.254	-1.34	0.204	-1.41	0.02	-1.3
1453790_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	-1.03	0.899	-1.86	0.012	-1.15	0.541	-1.32	0.441	-1.34
1439769_at	Zfp644	Zinc finger protein 644	-1.02	0.925	-1.69	0.162	-1.23	0.139	-1.09	0.565	-1.26
1432536_at	1700055M20Rik	RIKEN cDNA 1700055M20 gene	-1.43	0.682	-1.04	0.947	-1.39	0.292	-1.06	0.75	-1.23
1453106_a_at	Rnmt	RNA (guanine-7-) methyltransferase	-1.26	0.091	-1.16	0.149	-1.36	0.025	-1.01	0.954	-1.2
1425895_a_at	Id1	inhibitor of DNA binding 1	-1.87	0.317	-1.11	0.837	-1.06	0.777	-1.51	0.082	-1.39
1455115_a_at	Crb3	crumbs homolog 3 (Drosophila)	-1.22	0.51	-1.16	0.736	-1.41	0.149	-1.88	0.414	-1.42
1439221_s_at	Cd40	CD40 antigen	-1.27	0.628	-1.03	0.948	-1.6	0.006	-2.76	0.147	-1.66
1448773_at	Rpl11 /// LOC1941	ribosomal protein L11 /// similar to 60S ribosomal protein L11 /// similar to 60S rib	-1.39	0.325	-1.14	0.314	-1.26	0.334	-1.22	0.201	-1.25

1418749_at	Psd3	pleckstrin and Sec7 domain containing 3	-1.08	0.48	-1.2	0.12	-1.6	0.016	-1.08	0.659	-1.24
1439583_x_at	D130029J02Rik	RIKEN cDNA D130029J02 gene	-1.55	0.32	-1.02	0.863	-1.32	0.045	-1.78	0.011	-1.42
1443148_at	Hip2	huntingtin interacting protein 2	-1.2	0.518	-1.09	0.505	-1.58	0.061	-1.55	0.031	-1.36
1450809_at	Sval2	seminal vesicle antigen-like 2	-1.64	0.413	-1.11	0.839	-1.14	0.844	-1.05	0.953	-1.24
1440013_at	Trim44	Tripartite motif-containing 44	-1.06	0.437	-1.09	0.522	-1.91	0.004	-1.27	0.256	-1.33
1439010_at	D330037H05Rik ///	RIKEN cDNA D330037H05 gene /// similar to La-related protein 4 (La ribonucleop	-1.18	0.06	-1.17	0.156	-1.46	0.07	-1.04	0.659	-1.21
1453286_at	Plxna2	plexin A2	-1.09	0.75	-1.27	0.3	-1.49	0.161	-1.03	0.879	-1.22
1458556_at	Tnrc6c	Trinucleotide repeat containing 6C	-1.01	0.938	-1.31	0.477	-1.6	0.17	-2.11	0.297	-1.51
1458023_at	DXErtd697e	DNA segment, Chr X, ERATO Doi 697, expressed	-1.19	0.121	-1.15	0.627	-1.47	0.035	-1.53	0.033	-1.34
1423342_at	Barx1	BarH-like homeobox 1	-1.59	0.064	-1.23	0.371	-1.06	0.796	-2.6	0.002	-1.62
1418116_at	Ifrg15	interferon alpha responsive gene	-1.14	0.502	-1.34	0.103	-1.32	0.03	-1.08	0.533	-1.22
1442415_at	5830454E08Rik	RIKEN cDNA 5830454E08 gene	-1.01	0.973	-1.91	0.019	-1.16	0.408	-1.38	0.269	-1.36
1434954_at	---	---	-1.17	0.717	-1.14	0.365	-1.53	0.134	-1.18	0.312	-1.26
1456430_at	Ccdc39	coiled-coil domain containing 39	-1.15	0.266	-1.08	0.699	-1.7	0.125	-1.37	0.152	-1.33
1416483_at	Ttc3	tetratricopeptide repeat domain 3	-1.17	0.252	-1.09	0.4	-1.64	0.098	-1.6	0.101	-1.37
1445199_at	---	Transcribed locus	-1.68	0.439	-1.13	0.814	-1.11	0.598	-1.03	0.902	-1.24
1436145_at	Igf2bp3	Insulin-like growth factor 2, binding protein 3	-1.11	0.55	-1.2	0.308	-1.54	0.055	-1.23	0.493	-1.27
1435321_at	3732412D22Rik	RIKEN cDNA 3732412D22 gene	-1.14	0.199	-1.31	0.463	-1.34	0.153	-1.67	0.065	-1.37
1460151_at	---	---	-1.04	0.912	-1.2	0.331	-1.68	0.066	-1.21	0.081	-1.29
1422692_at	Sub1	SUB1 homolog (S. cerevisia	-1.12	0.136	-1.4	0.003	-1.29	0.114	-1.16	0.609	-1.24
1451552_at	MGC28431	Similar to lipoyltransferase	-1.28	0.071	-1.3	0.048	-1.2	0.295	-1.18	0.32	-1.24
1419977_s_at	Rbm35b	RNA binding motif protein 35b	-1.45	0.107	-1.01	0.959	-1.42	0.12	-1.17	0.217	-1.26
1455014_at	AV009015	expressed sequence AV009015	-1.21	0.157	-1.12	0.067	-1.5	0.013	-1.28	0.103	-1.28
1442660_at	Ypel1	Yippee-like 1 (Drosophila)	-1.12	0.61	-1.39	0.065	-1.29	0.359	-1.29	0.306	-1.27
1441324_at	Zfp395	Zinc finger protein 395	-1.24	0.642	-1.28	0.408	-1.25	0.436	-1.4	0.287	-1.29
1450657_at	Ppie	peptidylprolyl isomerase E (cyclophilin E)	-1.25	0.404	-1	0.969	-1.7	0.156	-1.19	0.163	-1.28
1439467_at	Mtap4	Microtubule-associated protein 4	-1.11	0.651	-1.09	0.117	-1.77	0.022	-1.49	0.133	-1.36
1430064_at	4933424A20Rik	RIKEN cDNA 4933424A20 gene	-1.23	0.328	-1.73	0.294	-1	0.988	-1.2	0.201	-1.29
1439276_at	---	---	-1.47	0.061	-1.3	0.241	-1.07	0.84	-1.5	0.092	-1.33
1427849_a_at	Tcrb-V13	T-cell receptor beta, variable 13	-1.07	0.923	-1.23	0.604	-1.58	0.41	-2.15	0.041	-1.5
1439447_x_at	Rpl37a /// LOC629	ribosomal protein L37a /// similar to 60S ribosomal protein L37a /// similar to 60S	-1.53	0.126	-1.04	0.778	-1.3	0.315	-1.47	0.131	-1.33
1423873_at	Lsm1	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.12	0.085	-1.05	0.716	-1.86	0.024	-1.49	0.072	-1.38
1429215_at	2310058N22Rik	RIKEN cDNA 2310058N22 gene	-1.15	0.649	-1.15	0.489	-1.54	0.018	-1.12	0.664	-1.24
1440650_at	Slit2	Slit homolog 2 (Drosophila)	-1.33	0.119	-1.01	0.964	-1.56	0.17	-1.46	0.653	-1.34
1419177_at	Vps37a	vacuolar protein sorting 37A (yeast)	-1.06	0.669	-1.23	0.2	-1.58	0.045	-1.27	0.442	-1.29
1446209_at	Usp40	ubiquitin specific peptidase 40	-1.26	0.047	-1.02	0.727	-1.63	0.008	-1.53	0.149	-1.36
1420295_x_at	Clcn5	chloride channel 5	-1.12	0.359	-1.4	0.216	-1.27	0.43	-1.24	0.694	-1.26
1444224_at	Tnfaip8	Tumor necrosis factor, alpha-induced protein 8	-1.4	0.557	-1.41	0.349	-1.04	0.941	-1.4	0.36	-1.31
1437238_x_at	Nmd3	NMD3 homolog (S. cerevisiae)	-1.11	0.402	-1.41	0.079	-1.29	0.129	-1.45	0.031	-1.31
1428658_at	Pin4 /// LOC628161	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) /// simil	-1.1	0.423	-1.16	0.154	-1.63	0.006	-1.04	0.808	-1.23
1455146_at	C230082I21Rik	RIKEN cDNA C230082I21 gene	-1.3	0.17	-1.11	0.725	-1.39	0.107	-1.93	0.281	-1.43
1442258_at	---	---	-1.1	0.621	-1.65	0	-1.15	0.468	-1.49	0.111	-1.34
1459063_at	---	Transcribed locus	-1.11	0.786	-1.66	0.052	-1.13	0.796	-1	0.998	-1.23
1429611_at	1700034E13Rik	RIKEN cDNA 1700034E13 gene	-1.86	0.344	-1.01	0.972	-1.16	0.629	-1.17	0.879	-1.3
1453023_at	Ankhd1	ankyrin repeat and KH domain containing 1	-1.22	0.518	-1.26	0.589	-1.28	0.064	-1.2	0.222	-1.24
1444818_at	---	---	-1.37	0.631	-1.21	0.491	-1.2	0.72	-1.1	0.666	-1.22
1454439_at	4833419G08Rik	RIKEN cDNA 4833419G08 gene	-1.14	0.615	-1.58	0.181	-1.13	0.745	-1.48	0.035	-1.34
1445985_at	Traf3ip2	Traf3 interacting protein 2	-1.02	0.981	-1.28	0.716	-1.59	0.158	-2.06	0.236	-1.49
1440906_at	Bcl7c	B-cell CLL/lymphoma 7C	-1.17	0.635	-1.3	0.36	-1.3	0.439	-1.54	0.583	-1.33
1432933_at	4930429N05Rik	RIKEN cDNA 4930429N05 gene	-1.08	0.502	-2.14	0.158	-1.01	0.993	-1.69	0.43	-1.48
1447860_x_at	Cog8	component of oligomeric golgi complex 8	-1.06	0.696	-1.25	0.169	-1.55	0.146	-1.91	0.173	-1.44
1460548_a_at	Eral1	Era (G-protein)-like 1 (E. coli)	-1.08	0.661	-1.26	0.186	-1.49	0.014	-1.69	0.052	-1.38
1454678_s_at	A130022J15Rik	RIKEN cDNA A130022J15 gene	-1.15	0.099	-1.34	0.047	-1.29	0.118	-1.15	0.571	-1.23

1417984_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	-1.34	0.326	-1.34	0.109	-1.11	0.319	-1	0.982	-1.2
1425087_at	2310003F16Rik	RIKEN cDNA 2310003F16 gene	-1.22	0.58	-1.71	0.164	-1.01	0.962	-1.32	0.267	-1.32
1436515_at	E030004N02Rik	RIKEN cDNA E030004N02 gene	-1.21	0.017	-1.33	0.485	-1.23	0.428	-2.55	0.085	-1.58
1437647_at	Dido1	death inducer-obliterator 1	-1.4	0.081	-1.43	0.008	-1.02	0.928	-1.12	0.622	-1.24
1445513_at	Vezt	Vezatin, adherens junctions transmembrane protein	-1.21	0.519	-1.62	0.027	-1.05	0.671	-1.15	0.802	-1.26
1430216_at	Zfp292	zinc finger protein 292	-1.42	0.374	-1.26	0.561	-1.12	0.628	-1.53	0.387	-1.33
1453109_at	Arsk	arylsulfatase K	-1.33	0.105	-1.12	0.187	-1.34	0.122	-1.15	0.412	-1.24
1423592_at	Rock2	Rho-associated coiled-coil containing protein kinase 2	-1.12	0.465	-1.13	0.565	-1.63	0.105	-1.3	0.352	-1.3
1429264_at	C030044B11Rik	RIKEN cDNA C030044B11 gene	-1.04	0.182	-1.36	0.109	-1.44	0.088	-1.12	0.383	-1.24
1445211_at	---	PREDICTED: Mus musculus hypothetical protein LOC626411 (LOC626411), mR	-1.19	0.438	-1.38	0.08	-1.2	0.401	-1.52	0.026	-1.32
1422074_at	Cdx2	caudal type homeo box 2	-1.03	0.957	-1.25	0.326	-1.61	0.015	-1.17	0.522	-1.27
1423666_s_at	Rpl5 /// LOC38274(	ribosomal protein L5 /// similar to 60S ribosomal protein L5 /// similar to 60S ribos	-1.03	0.783	-1.17	0.216	-1.75	0.015	-1.15	0.322	-1.28
1446615_at	---	---	-1.25	0.208	-1.17	0.704	-1.36	0.141	-1.51	0.153	-1.32
1445585_at	Zfp313	zinc finger protein 313	-1.19	0.259	-1.23	0.609	-1.35	0.721	-1.2	0.765	-1.24
1440658_at	E230022H04Rik	RIKEN cDNA E230022H04 gene	-1.02	0.96	-1.25	0.454	-1.62	0.131	-1.28	0.45	-1.29
1444432_at	D330040H18Rik	RIKEN cDNA D330040H18 gene	-1.16	0.654	-1.03	0.872	-1.77	0.005	-1.44	0.363	-1.35
1439097_at	D10Wsu52e	DNA segment, Chr 10, Wayne State University 52, expressed	-1.23	0.219	-1.31	0.152	-1.23	0.435	-1.8	0.064	-1.39
1460272_at	Ubl4b	ubiquitin-like 4B	-1.71	0.134	-1.17	0.142	-1.05	0.827	-1.14	0.541	-1.27
1428373_at	Ihpk2	inositol hexaphosphate kinase 2	-1.42	0.199	-1.14	0.554	-1.23	0.281	-1.69	0.186	-1.37
1444021_at	---	---	-1.23	0.513	-1.33	0.617	-1.2	0.115	-1.35	0.285	-1.28
1434029_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	-1.08	0.459	-1.51	0.083	-1.24	0.423	-1.01	0.959	-1.21
1429874_at	Spata17	spermatogenesis associated 17	-1.18	0.777	-1.7	0.149	-1.05	0.583	-1.93	0.1	-1.46
1424813_at	AA536717	expressed sequence AA536717	-1.24	0.208	-1.24	0.02	-1.28	0.138	-1.16	0.273	-1.23
1446955_at	Nr2c2	Nuclear receptor subfamily 2, group C, member 2	-1.1	0.652	-1.3	0.024	-1.39	0.244	-1.04	0.86	-1.21
1424861_at	D930016D06Rik	RIKEN cDNA D930016D06 gene	-1.11	0.622	-1.14	0.153	-1.62	0.002	-1.45	0.028	-1.33
1439398_x_at	Nelf	nasal embryonic LHRH factor	-1.4	0.329	-1.23	0.088	-1.15	0.385	-1.31	0.163	-1.27
1427057_at	C630002B14Rik	RIKEN cDNA C630002B14 gene	-1.57	0.301	-1.25	0.014	-1.05	0.611	-1.1	0.629	-1.24
1438065_at	---	---	-1.43	0.251	-1.21	0.438	-1.15	0.535	-1.17	0.455	-1.24
1435109_at	0710007G10Rik ///	RIKEN cDNA 0710007G10 gene /// RIKEN cDNA 3010001K23 gene	-1.14	0.411	-1.25	0.317	-1.39	0.122	-1.27	0.154	-1.26
1436263_at	Mobp	myelin-associated oligodendrocytic basic protein	-1.85	0.009	-1.09	0.68	-1.07	0.817	-1.62	0.045	-1.41
1460408_at	Gabrg1	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	-1.37	0.627	-1.26	0.739	-1.15	0.739	-1	0.995	-1.2
1433409_at	C030014O09Rik	RIKEN cDNA C030014O09 gene	-1.15	0.415	-1.35	0.184	-1.27	0.01	-1.34	0.512	-1.28
1451195_a_at	Txndc1	thioredoxin domain containing 1	-1.94	0.368	-1.1	0.831	-1.03	0.937	-1.13	0.76	-1.3
1446033_at	C87882	expressed sequence C87882	-1.21	0.754	-1.09	0.847	-1.52	0.202	-1.56	0.227	-1.35
1451360_at	Ergic2	ERGIC and golgi 2	-1.21	0.091	-1.09	0.404	-1.53	0.007	-1.14	0.447	-1.24
1440994_at	Shprh	SNF2 histone linker PHD RING helicase	-1.35	0.184	-1.26	0.254	-1.16	0.303	-1.19	0.388	-1.24
1450232_at	Birc4	baculoviral IAP repeat-containing 4	-1.07	0.854	-1.28	0.067	-1.47	0.091	-1.11	0.687	-1.23
1432011_at	2900052L18Rik	RIKEN cDNA 2900052L18 gene	-1.16	0.257	-1.34	0.103	-1.26	0.332	-1.82	0.023	-1.4
1431823_at	Moap1	modulator of apoptosis 1	-1.17	0.099	-1.39	0.153	-1.21	0.067	-1.33	0.053	-1.28
1458490_at	9230116N13Rik	RIKEN cDNA 9230116N13 gene	-1.09	0.798	-1.38	0.175	-1.33	0.177	-1.42	0.243	-1.31
1447322_at	---	---	-1.11	0.561	-1.13	0.58	-1.64	0.019	-1.39	0.132	-1.32
1436217_at	Zfp148	zinc finger protein 148	-1.15	0.041	-1.08	0.547	-1.67	0.079	-1.32	0.08	-1.3
1444271_at	Anapc1	anaphase promoting complex subunit 1	-1.02	0.929	-1.21	0.575	-1.68	0.068	-1.28	0.297	-1.3
1431158_at	8430406H22Rik	RIKEN cDNA 8430406H22 gene	-1.04	0.94	-1.31	0.213	-1.49	0.018	-1	0.991	-1.21
1443039_at	---	---	-1.14	0.812	-1.05	0.924	-1.77	0.337	-4.09	0.03	-2.01
1430077_at	Sfrs11	splicing factor, arginine/serine-rich 11	-1.24	0.343	-1.17	0.09	-1.36	0.115	-1.18	0.555	-1.24
1443798_at	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	-1.61	0.095	-1.03	0.794	-1.24	0.358	-1.02	0.902	-1.23
1426359_at	Zc3h11a	zinc finger CCCH type containing 11A	-1.06	0.552	-1.33	0.132	-1.41	0.067	-1.31	0.071	-1.28
1440062_at	2510009E07Rik	RIKEN cDNA 2510009E07 gene	-1.53	0.568	-1.07	0.902	-1.23	0.584	-1.4	0.248	-1.31
1455605_at	Rufy3	RUN and FYVE domain containing 3	-1.2	0.04	-1.15	0.209	-1.44	0.007	-1.7	0.031	-1.37
1453951_a_at	D19Ertd652e /// LO	DNA segment, Chr 19, ERATO Doi 652, expressed /// similar to DNA segment, C	-1.02	0.972	-1.68	0.031	-1.21	0.537	-1.3	0.322	-1.31
1457161_at	9530029O12Rik	RIKEN cDNA 9530029O12 gene	-1.02	0.904	-1.22	0.143	-1.69	0.005	-1.16	0.373	-1.27
1447486_at	Ppp1r9b	protein phosphatase 1, regulatory subunit 9B	-1.48	0.131	-1.03	0.931	-1.33	0.161	-1.05	0.875	-1.22

1452042_a_at	Tmem144	transmembrane protein 144	-1.25	0.324	-1.32	0.373	-1.19	0.243	-1.17	0.776	-1.23
1457480_at	Pcgf3	Polycomb group ring finger 3	-1.03	0.911	-1.32	0.083	-1.49	0.041	-1.22	0.336	-1.27
1444465_at	Ube4b	Ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	-1.11	0.828	-1.45	0.531	-1.24	0.491	-1.63	0.163	-1.36
1437392_at	LOC433485	hypothetical LOC433485	-1.95	0.332	-1.07	0.892	-1.05	0.944	-1.09	0.742	-1.29
1419672_at	Spock1	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1	-1.1	0.742	-1.19	0.599	-1.53	0.38	-1.74	0.271	-1.39
1446242_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	-1.33	0.051	-1.25	0.516	-1.18	0.589	-1.13	0.68	-1.22
1443856_at	---	---	-1.12	0.123	-1.22	0.059	-1.46	0.191	-1.3	0.306	-1.27
1418684_at	2310012P17Rik	RIKEN cDNA 2310012P17 gene	-1.34	0.23	-1.15	0.497	-1.27	0.329	-1.09	0.672	-1.21
1439392_x_at	Psmc1 /// LOC3860	protease (prosome, macropain) 26S subunit, ATPase 1 /// hypothetical gene supp	-1.51	0.336	-1.02	0.917	-1.33	0.668	-2.29	0.055	-1.54
1455728_at	Pten	phosphatase and tensin homolog	-1.25	0.069	-1.14	0.143	-1.39	0.135	-1.56	0.122	-1.33
1459483_at	Tmem28	Transmembrane protein 28	-1.39	0.426	-1.01	0.985	-1.46	0.072	-1	0.928	-1.21
1421897_at	Elk1	ELK1, member of ETS oncogene family	-2.09	0.134	-1.02	0.956	-1.06	0.85	-1.17	0.528	-1.34
1457956_at	2310058O09Rik	RIKEN cDNA 2310058O09 gene	-1.67	0.148	-1.23	0.663	-1.01	0.98	-1.42	0.257	-1.33
1430219_at	Fts	fused toes	-1.78	0.33	-1.16	0.864	-1.03	0.961	-1.32	0.743	-1.32
1459362_at	---	Transcribed locus	-1.67	0.316	-1.03	0.957	-1.2	0.608	-2.09	0.088	-1.5
1451776_s_at	Hod	homeobox only domain	-1.2	0.385	-1.29	0.306	-1.27	0.186	-1.15	0.687	-1.22
1445909_at	---	---	-1.03	0.885	-1.8	0.133	-1.14	0.323	-1.03	0.965	-1.25
1459098_at	Dst	Dystonin	-1.21	0.601	-1.2	0.439	-1.35	0.227	-1	0.994	-1.19
1445290_at	Hunk	Hormonally upregulated Neu-associated kinase	-1.54	0.554	-1.1	0.88	-1.18	0.63	-1.62	0.296	-1.36
1448049_at	Jmjd1c	jumonji domain containing 1C	-1.15	0.377	-1.2	0.233	-1.43	0.08	-1.7	0.07	-1.37
1440590_at	---	---	-1.07	0.736	-1.16	0.678	-1.66	0.033	-1.07	0.723	-1.24
1427322_at	Brwd1	bromodomain and WD repeat domain containing 1	-1.24	0.502	-1.27	0.306	-1.23	0.299	-2.12	0.194	-1.47
1444096_at	Zfr	Zinc finger RNA binding protein	-1.12	0.653	-1.2	0.181	-1.48	0.065	-1.09	0.729	-1.22
1443095_at	---	---	-1.12	0.16	-1.13	0.425	-1.61	0.034	-1.17	0.417	-1.26
1441794_at	4933437K13Rik	RIKEN cDNA 4933437K13 gene	-1.34	0.264	-1.21	0.566	-1.21	0.574	-2.89	0.067	-1.66
1445242_at	Gyk	glycerol kinase	-1.09	0.17	-1.29	0.017	-1.42	0.27	-1.53	0.332	-1.33
1460605_at	Crxos1	Crx opposite strand transcript 1	-1.3	0.704	-1.25	0.586	-1.2	0.813	-1.22	0.738	-1.24
1419475_a_at	Ehf	ets homologous factor	-1.03	0.882	-2.17	0.251	-1.03	0.9	-1.07	0.824	-1.33
1447908_x_at	Ttc3	tetratricopeptide repeat domain 3	-1.57	0.106	-1.07	0.354	-1.21	0.323	-1.11	0.442	-1.24
1424867_a_at	Glyat	glycine-N-acyltransferase	-1.37	0.097	-1.13	0.291	-1.27	0.55	-1.13	0.852	-1.23
1456576_x_at	Cnot2	CCR4-NOT transcription complex, subunit 2	-1.14	0.477	-1.18	0.226	-1.47	0.09	-1.54	0.123	-1.33
1447092_at	Pecam1	Platelet/endothelial cell adhesion molecule 1	-1.19	0.51	-1.03	0.878	-1.7	0.128	-1.64	0.231	-1.39
1433988_s_at	C230098O21Rik	RIKEN cDNA C230098O21 gene	-1.29	0.032	-1.32	0.147	-1.15	0.424	-1.62	0.023	-1.34
1450190_at	Zfp106	zinc finger protein 106	-1.24	0.635	-1.11	0.841	-1.44	0.552	-1.13	0.805	-1.23
1442679_at	Map2k4	Mitogen activated protein kinase kinase 4	-1.33	0.378	-1.1	0.724	-1.36	0.477	-1.35	0.2	-1.28
1456880_at	Sfrs8	Splicing factor, arginine/serine-rich 8	-1.14	0.567	-1.35	0.001	-1.27	0.379	-1.25	0.08	-1.25
1419506_at	Ggps1	geranylgeranyl diphosphate synthase 1	-1.02	0.88	-1.38	0.029	-1.44	0.02	-1.29	0.212	-1.28
1446709_at	---	---	-1.3	0.712	-1.13	0.614	-1.34	0.469	-1.14	0.828	-1.23
1453036_at	5430439M09Rik	RIKEN cDNA 5430439M09 gene	-1.31	0.268	-1.2	0.426	-1.24	0.077	-1.12	0.526	-1.22
1455035_s_at	Nol5a	nucleolar protein 5A	-1.08	0.723	-1.53	0.001	-1.21	0.422	-1.31	0.118	-1.28
1434471_at	BC003331	cDNA sequence BC003331	-1.09	0.616	-1.15	0.398	-1.63	0.062	-1.12	0.588	-1.25
1456734_at	Txn1	thioredoxin 1	-1.09	0.791	-1.63	0.243	-1.14	0.701	-1.19	0.758	-1.26
1432216_s_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-1.2	0.543	-1.12	0.675	-1.47	0.019	-1.45	0.098	-1.31
1448094_at	LOC546100	hypothetical LOC546100	-1.39	0.728	-1.45	0.474	-1	0.992	-1.26	0.563	-1.28
1428654_at	1200016B10Rik	RIKEN cDNA 1200016B10 gene	-1.05	0.766	-1.22	0.13	-1.6	0.034	-1	0.991	-1.22
1436756_x_at	Hadhsc	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-1.85	0.05	-1.05	0.847	-1.09	0.531	-2.34	0.153	-1.58
1457188_at	Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11	-1.24	0.188	-1.02	0.958	-1.62	0.07	-1.67	0.279	-1.39
1437498_at	---	---	-1.1	0.629	-1.27	0.265	-1.4	0.168	-1.35	0.513	-1.28
1459005_at	D030051N19Rik	RIKEN cDNA D030051N19 gene	-1.23	0.317	-1.01	0.972	-1.66	0.006	-1.59	0.028	-1.37
1455442_at	Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19	-1.17	0.395	-1.59	0.305	-1.08	0.736	-2.23	0.052	-1.52
1424034_at	Rora	RAR-related orphan receptor alpha	-1.1	0.683	-1.25	0.041	-1.44	0.146	-1.61	0.128	-1.35
1420543_at	ORF28	open reading frame 28	-1.23	0.217	-1.13	0.506	-1.4	0.138	-1.05	0.701	-1.21
1453311_at	2310008B10Rik	RIKEN cDNA 2310008B10 gene	-1.21	0.246	-1.22	0.524	-1.31	0.311	-1.64	0.177	-1.35

1424811_at	Cml5	camello-like 5	-1.03	0.975	-1.8	0.059	-1.14	0.845	-3.03	0.182	-1.75
1442186_at	Atxn7	ataxin 7	-1.17	0.486	-1.08	0.779	-1.62	0.131	-1.26	0.258	-1.28
1438072_at	Nfib	Nuclear factor I/B	-1.03	0.85	-1.08	0.549	-1.94	0.016	-1.22	0.561	-1.32
1423560_at	Nell2	NEL-like 2 (chicken)	-1.07	0.597	-1.74	0.014	-1.12	0.385	-1.56	0.093	-1.37
1430328_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	-1.09	0.339	-1.42	0.239	-1.28	0.22	-1.13	0.707	-1.23
1460645_at	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	-1.06	0.742	-1.32	0.176	-1.41	0.012	-1.29	0.279	-1.27
1442569_at	Cct4	Chaperonin subunit 4 (delta)	-1.18	0.549	-1.19	0.412	-1.4	0.104	-1.49	0.425	-1.31
1417814_at	Pla2g5	phospholipase A2, group V	-1.14	0.566	-1.31	0.701	-1.31	0.549	-2.2	0.088	-1.49
1452984_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	-1.16	0.202	-1.34	0.096	-1.26	0.334	-1.15	0.38	-1.23
1442387_at	Hars	Histidyl-tRNA synthetase	-1.36	0.578	-1.33	0.522	-1.08	0.737	-1.08	0.726	-1.22
1444557_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	-1.17	0.119	-1.06	0.763	-1.64	0.027	-1.36	0.032	-1.31
1429041_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	-1.5	0.016	-1.18	0.302	-1.12	0.453	-1.23	0.272	-1.26
1457193_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	-1.12	0.434	-1.13	0.53	-1.59	0.106	-1.15	0.321	-1.25
1432053_at	Rfx4	regulatory factor X, 4 (influences HLA class II expression)	-1.54	0.262	-1.08	0.8	-1.21	0.449	-1	0.971	-1.21
1445786_at	Braf	Braf transforming gene	-1.03	0.83	-1.26	0.364	-1.54	0.004	-1.03	0.898	-1.22
1426455_at	Sdccag10	serologically defined colon cancer antigen 10	-1.15	0.338	-1.48	0.189	-1.17	0.427	-1.35	0.188	-1.29
1419473_a_at	Cck	cholecystokinin	-1.12	0.356	-1.66	0.37	-1.09	0.501	-2.74	0.078	-1.65
1421426_at	Hhip	Hedgehog-interacting protein	-1.11	0.893	-1.83	0.355	-1.04	0.905	-1.01	0.973	-1.25
1445907_at	---	---	-1.05	0.941	-1.65	0.228	-1.17	0.611	-1.26	0.254	-1.29
1437990_x_at	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	-1.03	0.937	-1.31	0.687	-1.49	0.376	-1.53	0.526	-1.34
1416480_a_at	Higd1a	HIG1 domain family, member 1A	-1.06	0.608	-1.46	0.005	-1.29	0.02	-1.06	0.742	-1.22
1431189_a_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	-1.12	0.267	-1.7	0.032	-1.08	0.402	-1.7	0.156	-1.4
1429328_at	Nsfl1c	NSFL1 (p97) cofactor (p47)	-1.25	0.593	-1.58	0.064	-1.03	0.859	-1.01	0.973	-1.22
1459067_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	-1.1	0.603	-1.3	0.45	-1.37	0.691	-2.76	0.02	-1.63
1451693_a_at	Fgf12	fibroblast growth factor 12	-1.62	0.349	-1.08	0.783	-1.16	0.326	-1.75	0.448	-1.4
1445034_at	Coro2a	Coronin, actin binding protein 2A	-1.38	0.041	-1	0.998	-1.46	0.246	-1.66	0.136	-1.37
1458126_at	D030041H20Rik	RIKEN cDNA D030041H20 gene	-1.02	0.927	-1.14	0.585	-1.82	0.124	-1.29	0.415	-1.32
1441296_at	---	---	-1.33	0.471	-1.33	0.172	-1.1	0.85	-1.19	0.433	-1.24
1434394_at	B3bp	Bcl3 binding protein	-1.2	0.547	-1.47	0.009	-1.12	0.467	-1.45	0.196	-1.31
1429735_at	1110003F05Rik	RIKEN cDNA 1110003F05 gene	-1.06	0.236	-1.1	0.013	-1.8	0.003	-1.06	0.131	-1.25
1434002_at	Ches1	checkpoint suppressor 1	-1.14	0.228	-1.2	0.136	-1.44	0.052	-1.51	0.129	-1.32
1426224_x_at	Cmtm2a	CKLF-like MARVEL transmembrane domain containing 2A	-1.51	0.41	-1.29	0.592	-1.03	0.96	-1.02	0.975	-1.21
1441905_x_at	Snrpn	Small nuclear ribonucleoprotein N	-1.34	0.312	-1.46	0.571	-1.02	0.967	-1.96	0.229	-1.45
1420490_at	Klk1b16	kallikrein 1-related peptidase b16	-1.14	0.789	-1.71	0.304	-1.05	0.938	-1.49	0.338	-1.35
1427370_at	Amdhd1	amidohydrolase domain containing 1	-1.31	0.526	-1.15	0.202	-1.29	0.541	-1.6	0.548	-1.34
1450395_at	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	-1.16	0.511	-1.44	0.319	-1.18	0.486	-1.18	0.584	-1.24
1420614_at	Dynlt3	dynein light chain Tctex-type 3	-1.3	0.053	-1.13	0.211	-1.33	0.191	-1.07	0.833	-1.21
1450873_at	Gtpbp4	GTP binding protein 4	-1.39	0.249	-1.18	0.106	-1.19	0.144	-1.19	0.263	-1.24
1442150_at	---	---	-1.02	0.813	-1.21	0.492	-1.67	0.042	-1.23	0.372	-1.28
1447032_at	Clybl	Citrate lyase beta like	-1.1	0.36	-1.04	0.91	-1.83	0.03	-1.48	0.606	-1.37
1444589_at	LOC240038	similar to reduced expression 2	-1.34	0.112	-1.07	0.748	-1.37	0.029	-1.42	0.192	-1.3
1450356_at	Trhr2	thyrotropin releasing hormone receptor 2	-1.26	0.333	-1.05	0.95	-1.51	0.068	-1.01	0.986	-1.21
1440267_at	Pex1	peroxisome biogenesis factor 1	-1.1	0.686	-1.24	0.275	-1.45	0.102	-1.44	0.405	-1.31
1449923_at	1700018F24Rik	RIKEN cDNA 1700018F24 gene	-1.5	0.131	-1.12	0.683	-1.17	0.102	-1.15	0.125	-1.24
1459575_at	D1Ertd704e	DNA segment, Chr 1, ERATO Doi 704, expressed	-1.5	0.388	-1.23	0.612	-1.07	0.875	-1.81	0.39	-1.4
1434901_at	Gm1103	gene model 1103, (NCBI)	-1.21	0.268	-1.46	0.013	-1.11	0.146	-1.22	0.011	-1.25
1455091_at	3222402P14Rik	RIKEN cDNA 3222402P14 gene	-1.11	0.394	-1.27	0.125	-1.38	0.131	-1.43	0.178	-1.3
1437543_at	Fubp1	far upstream element (FUSE) binding protein 1	-1.13	0.218	-1.26	0.275	-1.37	0.088	-1.17	0.372	-1.23
1447491_at	Lrrc8d	Leucine rich repeat containing 8D	-1.39	0.016	-1.28	0.191	-1.1	0.722	-1.26	0.39	-1.26
1434807_s_at	Mtx3	metaxin 3	-1.28	0.092	-1.08	0.724	-1.42	0.058	-1.19	0.578	-1.24
1426850_a_at	Map2k6	mitogen activated protein kinase kinase 6	-1.17	0.17	-1.44	0.396	-1.16	0.519	-1.36	0.127	-1.28
1442361_at	Itga2b	Integrin alpha 2b	-1.14	0.618	-1.65	0.38	-1.07	0.903	-1.02	0.964	-1.22
1448095_at	---	Transcribed locus	-1.15	0.232	-1.46	0.447	-1.16	0.37	-1.42	0.281	-1.3

1436581_at	Ccdc39	coiled-coil domain containing 39	-1.16	0.238	-1.55	0.119	-1.11	0.671	-1.18	0.309	-1.25
1435982_at	Stx12	syntaxin 12	-1.12	0.463	-1.08	0.612	-1.68	0.064	-1.05	0.523	-1.23
1429819_at	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	-1.09	0.57	-1.33	0.246	-1.35	0.166	-2.21	0.037	-1.49
1439837_at	Tnrc15	trinucleotide repeat containing 15	-1.26	0.232	-1.23	0.42	-1.24	0.016	-1.46	0.034	-1.3
1428214_at	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	-1.14	0.264	-1.27	0.182	-1.34	0.18	-1.22	0.229	-1.24
1457112_at	A230106N23	hypothetical protein A230106N23	-1.1	0.805	-1.45	0.162	-1.23	0.226	-1.18	0.366	-1.24
1419205_x_at	Gpatc4	G patch domain containing 4	-1.02	0.704	-1.27	0.332	-1.55	0.11	-1.19	0.234	-1.26
1454402_at	3110048L19Rik	RIKEN cDNA 3110048L19 gene	-1.32	0.162	-1.03	0.867	-1.45	0.009	-1.71	0.065	-1.38
1421762_at	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	-1.14	0.71	-1.24	0.079	-1.36	0.246	-1.38	0.541	-1.28
1456825_at	Wdr33	WD repeat domain 33	-1.1	0.574	-1.14	0.807	-1.59	0.15	-1.58	0.026	-1.35
1447522_s_at	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.19	0.027	-1.1	0.541	-1.51	0	-1.29	0.123	-1.27
1430713_s_at	Ndufa13	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13	-1.29	0.222	-1.31	0.12	-1.14	0.318	-1.29	0.176	-1.26
1456142_x_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// RIKEN cD	-1.2	0.133	-1.26	0.047	-1.27	0.042	-1.2	0.019	-1.23
1430476_at	Srp54	signal recognition particle 54	-1.03	0.972	-2.11	0.065	-1.03	0.931	-1.27	0.271	-1.36
1434062_at	Rabgap1l	RAB GTPase activating protein 1-like	-1.24	0.098	-1.16	0.336	-1.35	0.011	-1.39	0.374	-1.28
1425358_at	Riok1	RIO kinase 1 (yeast)	-1.12	0.665	-1.36	0.081	-1.27	0.315	-1.21	0.507	-1.24
1455630_at	1700010H15Rik	RIKEN cDNA 1700010H15 gene	-1.23	0.216	-1.26	0.601	-1.23	0.092	-1.41	0.256	-1.29
1437359_at	Rnps1	Ribonucleic acid binding protein S1	-1.53	0.239	-1.22	0.19	-1.07	0.799	-1.07	0.517	-1.22
1456928_at	---	---	-1.06	0.887	-1.44	0.066	-1.29	0.119	-1.08	0.846	-1.22
1458414_at	D2Ertd93e	DNA segment, Chr 2, ERATO Doi 93, expressed	-1.06	0.756	-1.32	0.409	-1.41	0.108	-1.11	0.402	-1.22
1430180_at	Map2k5	mitogen activated protein kinase kinase 5	-1.16	0.644	-1.32	0.29	-1.26	0.223	-1.73	0.039	-1.37
1457111_at	AA415038	expressed sequence AA415038	-1.04	0.753	-1.09	0.552	-1.84	0.102	-1.31	0.501	-1.32
1441063_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	-1.11	0.541	-1.1	0.552	-1.67	0.087	-1.14	0.318	-1.25
1450640_x_at	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	-1.25	0.012	-1.35	0.029	-1.14	0.09	-1.04	0.488	-1.2
1434343_at	5730403M16Rik	RIKEN cDNA 5730403M16 gene	-1.18	0.601	-1.1	0.659	-1.51	0.018	-1.5	0.148	-1.32
1457510_at	Phf14	PHD finger protein 14	-1	0.998	-1.19	0.325	-1.74	0.081	-1.56	0.195	-1.37
1437721_at	Coro1c	coronin, actin binding protein 1C	-1.15	0.896	-1.25	0.631	-1.34	0.479	-1.1	0.64	-1.21
1429283_at	1500009M05Rik	RIKEN cDNA 1500009M05 gene	-1.09	0.785	-1.15	0.228	-1.6	0.13	-1.36	0.297	-1.3
1429940_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	-1.12	0.687	-1.23	0.232	-1.41	0.052	-1.27	0.239	-1.26
1439931_at	Gsk3b	glycogen synthase kinase 3 beta	-1.15	0.006	-1.05	0.837	-1.69	0.022	-1.22	0.03	-1.28
1420982_at	Rbm39	RNA binding motif protein 39	-1.04	0.887	-1.5	0.194	-1.28	0.064	-1.13	0.214	-1.23
1442510_at	LOC665792 /// LOC	hypothetical protein LOC665792 /// hypothetical protein LOC669957 /// hypothetic	-1.07	0.757	-1.32	0.278	-1.38	0.562	-1.47	0.196	-1.31
1421867_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	-1.25	0.104	-1.1	0.122	-1.41	0.202	-1.55	0.109	-1.33
1454810_s_at	AI315068	expressed sequence AI315068	-1.45	0.13	-1.16	0.278	-1.16	0.351	-1.13	0.208	-1.22
1419365_at	Pex11a	peroxisomal biogenesis factor 11a	-1.15	0.656	-1.56	0.309	-1.11	0.656	-1.21	0.586	-1.26
1419886_at	DXErtd223e	DNA segment, Chr X, ERATO Doi 223, expressed	-1.1	0.721	-1.27	0.158	-1.4	0.148	-1.01	0.973	-1.19
1428844_a_at	Bclaf1	BCL2-associated transcription factor 1	-1.16	0.642	-1.26	0.129	-1.32	0.062	-1.4	0.058	-1.28
1425319_s_at	6530403A03Rik	RIKEN cDNA 6530403A03 gene	-1.05	0.833	-1.28	0.32	-1.45	0.042	-1.65	0.029	-1.36
1444408_at	B130040O20Rik	RIKEN cDNA B130040O20 gene	-1.27	0.208	-1.19	0.408	-1.27	0.102	-1.77	0.143	-1.38
1428951_at	Nol8	nucleolar protein 8	-1.07	0.8	-1.3	0.115	-1.4	0.042	-1.09	0.57	-1.22
1425728_at	RP23-14F5.7	hypothetical gene Rp23-14f5.7	-1.17	0.715	-1.01	0.971	-1.73	0.024	-2.12	0.002	-1.51
1438675_at	Sfrs8	splicing factor, arginine/serine-rich 8	-1.04	0.867	-1.21	0.135	-1.6	0.306	-1.52	0.066	-1.34
1445884_at	1110007A13Rik	RIKEN cDNA 1110007A13 gene	-1.35	0.014	-1.08	0.828	-1.33	0.094	-1.38	0.097	-1.29
1440260_at	A930007B11Rik	RIKEN cDNA A930007B11 gene	-1.1	0.628	-1.09	0.447	-1.69	0.031	-1.71	0.081	-1.4
1445091_at	Atr	ataxia telangiectasia and Rad3 related	-1.22	0.315	-1.32	0.407	-1.19	0.196	-1.64	0.089	-1.34
1424423_at	Lenep /// Flad1	lens epithelial protein /// RFad1, flavin adenine dinucleotide synthetase, homolog	-1.08	0.883	-1.27	0.224	-1.41	0.142	-1.11	0.474	-1.22
1424276_at	Snx16	sorting nexin 16	-1.11	0.55	-1.35	0.127	-1.29	0.018	-1.26	0.315	-1.25
1441901_x_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	-1.44	0.019	-1.14	0.177	-1.18	0.473	-1.26	0.192	-1.25
1445484_at	Cycs	cytochrome c, somatic	-1.05	0.826	-1.63	0.491	-1.18	0.536	-1.13	0.839	-1.25
1439582_at	Macf1	Microtubule-actin crosslinking factor 1	-1.06	0.636	-1.05	0.698	-1.93	0.024	-1.81	0.243	-1.46
1437699_at	E430014B02Rik	RIKEN cDNA E430014B02 gene	-1.06	0.882	-1.04	0.919	-1.96	0.031	-3.88	0.055	-1.98
1452491_at	2900060N18Rik	RIKEN cDNA 2900060N18 gene	-1.04	0.073	-1.27	0.647	-1.49	0.343	-1.03	0.965	-1.21
1448047_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	-1.33	0.045	-1.42	0.203	-1.04	0.843	-1.08	0.699	-1.22

1452642_at	Tmem16f	Transmembrane protein 16F	-1.2	0.381	-1.44	0.319	-1.12	0.328	-1.31	0.299	-1.27
1420623_x_at	Hspa8 /// LOC6212	heat shock protein 8 /// similar to heat shock protein 8 /// heat shock protein 8 pse	-1.25	0.265	-1.3	0.088	-1.18	0.018	-1.25	0.042	-1.24
1433941_at	Pib5pa	phosphatidylinositol (4,5) bisphosphate 5-phosphatase, A	-1.17	0.539	-1.27	0.044	-1.29	0.554	-1.03	0.865	-1.19
1450340_a_at	Clcnkb	chloride channel Kb	-1.03	0.781	-1.03	0.961	-2.11	0.08	-1.61	0.565	-1.44
1425043_s_at	0610037D15Rik	RIKEN cDNA 0610037D15 gene	-1.66	0.004	-1.02	0.977	-1.2	0.456	-1.7	0.042	-1.39
1420068_at	---	---	-1.12	0.848	-1.14	0.705	-1.53	0.178	-1.47	0.577	-1.32
1437224_at	Rtn4	reticulon 4	-1.21	0.331	-1.05	0.818	-1.55	0.011	-1.07	0.691	-1.22
1450966_at	Crot	carnitine O-octanoyltransferase	-1.18	0.201	-1.72	0.006	-1.01	0.98	-1.33	0.216	-1.31
1444728_at	Exoc4	Exocyst complex component 4	-1.02	0.947	-1.21	0.132	-1.63	0.061	-1.17	0.389	-1.26
1445556_at	---	Transcribed locus	-1.36	0.442	-1.13	0.773	-1.25	0.7	-1.67	0.408	-1.35
1446205_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430057L	-1.05	0.729	-1.51	0.335	-1.25	0.41	-1.34	0.196	-1.28
1440690_at	Nipbl	Nipped-B homolog (Drosophila)	-1.06	0.68	-1.16	0.175	-1.63	0.011	-1.29	0.377	-1.28
1433574_at	Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	-1.11	0.591	-1.11	0.146	-1.63	0.006	-1.41	0.061	-1.31
1441624_at	Sorbs2	sorbin and SH3 domain containing 2	-1.25	0.444	-1.34	0.279	-1.14	0.221	-1.34	0.224	-1.27
1417980_a_at	Insig2	insulin induced gene 2	-1.03	0.861	-1.46	0.071	-1.32	0.016	-1.46	0.054	-1.31
1437290_at	Impad1	inositol monophosphatase domain containing 1	-1.31	0.296	-1.1	0.331	-1.34	0.059	-1.23	0.543	-1.25
1420932_at	Mapk8	mitogen activated protein kinase 8	-1.41	0.027	-1.08	0.084	-1.27	0	-1.3	0.146	-1.27
1428175_at	Tmem161b	transmembrane protein 161B	-1.19	0.342	-1.18	0.434	-1.36	0.049	-1	0.989	-1.18
1432995_at	2900057E15Rik	RIKEN cDNA 2900057E15 gene	-1.21	0.389	-1.26	0.42	-1.25	0.225	-1.08	0.767	-1.2
1447150_at	Phr1	pam, highwire, rpm 1	-1.23	0.173	-1.41	0.125	-1.11	0.462	-1.85	0.075	-1.4
1420586_at	2900054J07Rik	RIKEN cDNA 2900054J07 gene	-1.43	0.313	-1.24	0.65	-1.1	0.559	-1.07	0.848	-1.21
1416977_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	-1.73	0.082	-1.05	0.888	-1.12	0.477	-1.57	0.012	-1.37
1459305_at	Rai17	Retinoic acid induced 17	-1.21	0.188	-1.34	0.271	-1.18	0.279	-1.01	0.965	-1.19
1457679_at	Dclre1c	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)	-1	0.995	-1.41	0.454	-1.4	0.03	-1.4	0.409	-1.3
1454703_x_at	Snord22	small nucleolar RNA, C/D box 22	-1.41	0.394	-1.33	0.177	-1.04	0.874	-1.06	0.84	-1.21
1434166_at	9330151L19Rik	RIKEN cDNA 9330151L19 gene	-1.2	0.389	-1.41	0.186	-1.13	0.535	-1.09	0.704	-1.21
1429595_at	2700049A03Rik	RIKEN cDNA 2700049A03 gene	-1.38	0.03	-1.23	0.513	-1.13	0.549	-1.04	0.835	-1.2
1441753_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	-1.11	0.481	-1.09	0.805	-1.65	0.127	-1.35	0.154	-1.3
1428755_at	Creb1	cAMP responsive element binding protein 1	-1.34	0.022	-1.13	0.254	-1.26	0.007	-1.39	0.13	-1.28
1459928_at	Lcor	ligand dependent nuclear receptor corepressor	-1.37	0.574	-1.2	0.718	-1.16	0.269	-1.01	0.967	-1.19
1435565_at	1500011H22Rik	RIKEN cDNA 1500011H22 gene	-1.2	0.323	-1.09	0.559	-1.49	0.052	-1.41	0.015	-1.3
1456806_at	A130010C12Rik	RIKEN cDNA A130010C12 gene	-1.55	0.283	-1.14	0.77	-1.11	0.671	-1.22	0.183	-1.26
1419608_a_at	Mia1	melanoma inhibitory activity 1	-1.18	0.148	-1.16	0.79	-1.41	0.251	-1.46	0.475	-1.3
1458508_at	Matr3	matrin 3	-1.01	0.942	-1.18	0.379	-1.69	0.004	-1.56	0.076	-1.36
1437384_at	1700015E13Rik	RIKEN cDNA 1700015E13 gene	-1.47	0.147	-1.25	0.378	-1.06	0.848	-1.77	0.086	-1.39
1435274_at	4921517N04Rik	RIKEN cDNA 4921517N04 gene	-1.14	0.142	-1.17	0.097	-1.44	0.036	-1.16	0.478	-1.23
1442213_at	LOC552908	hypothetical LOC552908	-1.01	0.974	-1.14	0.769	-1.79	0.035	-1.07	0.879	-1.25
1430680_a_at	5830417I10Rik /// L	RIKEN cDNA 5830417I10 gene /// similar to Dingo protein isoform 2 /// similar to I	-1.19	0.111	-1.69	0.08	-1.01	0.914	-1.35	0.291	-1.31
1440861_a_at	---	---	-1.16	0.261	-1.03	0.863	-1.68	0.004	-1.29	0.06	-1.29
1427208_at	Zfp451	zinc finger protein 451	-1.27	0.282	-1.4	0.033	-1.09	0.662	-1.15	0.621	-1.23
1454640_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	-1.07	0.462	-1.54	0.003	-1.2	0.093	-1.05	0.622	-1.21
1443579_s_at	Depdc6	DEP domain containing 6	-1.04	0.581	-1.35	0.053	-1.39	0.329	-1.02	0.965	-1.2
1452322_a_at	Brwd1	bromodomain and WD repeat domain containing 1	-1.39	0.028	-1.12	0.677	-1.23	0.208	-1.73	0.029	-1.37
1428920_at	---	---	-1.25	0.345	-1.37	0.198	-1.11	0.482	-1.38	0.265	-1.28
1459011_at	Uchl5	Ubiquitin carboxyl-terminal esterase L5	-1.25	0.045	-1.09	0.636	-1.41	0.008	-1.36	0.419	-1.28
1435980_x_at	Wnt6	wingless-related MMTV integration site 6	-1.2	0.453	-1.47	0.309	-1.1	0.544	-1.08	0.785	-1.21
1418211_at	p	pink-eyed dilution	-1.49	0.284	-1.3	0.102	-1.01	0.946	-1.05	0.85	-1.21
1458369_at	2310050B05Rik	RIKEN cDNA 2310050B05 gene	-1.22	0.249	-1.27	0.536	-1.22	0.323	-1.01	0.944	-1.18
1420107_at	Bbs4	Bardet-Biedl syndrome 4 homolog (human)	-1.01	0.971	-1.55	0.416	-1.26	0.089	-1.19	0.348	-1.25
1443088_at	9930031P18Rik	RIKEN cDNA 9930031P18 gene	-1.01	0.972	-1.08	0.602	-1.98	0.034	-1.54	0.156	-1.4
1424252_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	-1.31	0.194	-1.21	0.104	-1.2	0.213	-1.34	0.225	-1.26
1445870_at	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	-1.12	0.426	-1.34	0.395	-1.26	0.473	-1.29	0.388	-1.26
1451464_at	Mfap3	microfibrillar-associated protein 3	-1.16	0.716	-1.42	0.386	-1.17	0.444	-1.11	0.507	-1.21

1432099_a_at	Prodh2	proline dehydrogenase (oxidase) 2	-1.27	0.125	-1.2	0.128	-1.24	0.203	-1.24	0.178	-1.24
1428084_at	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	-1.14	0.052	-1.2	0.025	-1.39	0.034	-1.11	0.333	-1.21
1426232_at	BC024479	cDNA sequence BC024479	-1.19	0.535	-1.07	0.793	-1.53	0.113	-1.42	0.062	-1.3
1425788_a_at	Echdc2	enoyl Coenzyme A hydratase domain containing 2	-1.05	0.781	-1.1	0.07	-1.79	0.032	-2.25	0.081	-1.55
1454969_at	Lypd6	LY6/PLAUR domain containing 6	-1.13	0.017	-1.39	0.1	-1.22	0.287	-1.85	0.222	-1.4
1454921_at	Gm561	gene model 561, (NCBI)	-1.05	0.321	-1.4	0.046	-1.32	0.121	-1.25	0.18	-1.25
1437461_s_at	Rnpc3	RNA-binding region (RNP1, RRM) containing 3	-1.3	0.458	-1.16	0.425	-1.26	0.164	-1.05	0.707	-1.19
1429128_x_at	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	-1.09	0.558	-1.35	0.714	-1.3	0.199	-1.78	0.213	-1.38
1431239_at	Nono	non-POU-domain-containing, octamer binding protein	-1.13	0.512	-1.29	0.157	-1.3	0.155	-1.12	0.551	-1.21
1437022_at	D130059P03Rik	RIKEN cDNA D130059P03 gene	-1.05	0.114	-1.16	0.394	-1.63	0.018	-1.18	0.263	-1.25
1444753_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	-1	0.981	-1.18	0.549	-1.72	0.042	-1.38	0.431	-1.32
1438497_at	2810423E13Rik	RIKEN cDNA 2810423E13 gene	-1.1	0.44	-1.44	0.161	-1.21	0.337	-1.32	0.218	-1.27
1432073_at	1700113I22Rik	RIKEN cDNA 1700113I22 gene	-1.65	0.049	-1.2	0.402	-1.01	0.927	-1.3	0.429	-1.29
1440254_at	---	Transcribed locus, weakly similar to XP_417295.1 PREDICTED: similar to TAF3	-1.08	0.685	-1.22	0.013	-1.45	0.196	-1.21	0.249	-1.24
1426013_s_at	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specif	-1.18	0.258	-1.12	0.767	-1.44	0.104	-1.17	0.576	-1.23
1435041_at	Myl6	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	-1.77	0.276	-1.11	0.489	-1.04	0.868	-1.68	0.161	-1.4
1433756_at	S100pbp	S100P binding protein	-1.2	0.573	-1.21	0.226	-1.3	0.297	-1.46	0.357	-1.29
1437717_x_at	2610005L07Rik /// A	RIKEN cDNA 2610005L07 gene /// RIKEN cDNA A430108E01 gene /// similar to	-1.17	0.669	-1.13	0.669	-1.45	0.3	-1.31	0.593	-1.27
1460564_at	Suhw2	suppressor of hairy wing homolog 2 (Drosophila)	-1.19	0.641	-1.32	0.126	-1.21	0.231	-1.11	0.302	-1.21
1458419_at	E130215H24Rik	RIKEN cDNA E130215H24 gene	-1.06	0.736	-1.93	0.153	-1.03	0.855	-1.2	0.571	-1.31
1455406_at	---	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833431M13	-1.04	0.744	-1.48	0.062	-1.26	0.129	-1.18	0.688	-1.24
1458677_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	-1.2	0.426	-1.17	0.73	-1.36	0.154	-1.63	0.065	-1.34
1429760_at	Rps6ka6	ribosomal protein S6 kinase polypeptide 6	-1.27	0.497	-1.53	0.461	-1.01	0.957	-2.39	0.058	-1.55
1459736_at	Stk10	Serine/threonine kinase 10	-1.65	0.594	-1.04	0.928	-1.16	0.684	-1.69	0.087	-1.39
1448959_at	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	-1.19	0.061	-1.34	0.028	-1.18	0.118	-1.3	0.154	-1.25
1440886_at	Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	-1.29	0.463	-1.17	0.578	-1.25	0.248	-1.97	0.054	-1.42
1438597_x_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// similar to	-1.34	0.122	-1.09	0.779	-1.31	0.01	-1.16	0.076	-1.22
1421372_at	Klk1b4	kallikrein 1-related pepidase b4	-1.05	0.869	-1.74	0.031	-1.1	0.665	-1.36	0.509	-1.31
1436455_at	Asph	aspartate-beta-hydroxylase	-1.02	0.937	-1.72	0.475	-1.14	0.757	-1.51	0.359	-1.35
1440636_at	Mrpl3	Mitochondrial ribosomal protein L3	-1.38	0.115	-1.09	0.759	-1.27	0.036	-1.4	0.385	-1.28
1420177_at	Igll1	immunoglobulin lambda-like polypeptide 1	-1.06	0.842	-1.32	0.367	-1.37	0.516	-1.42	0.641	-1.29
1439642_at	5930403N24Rik	RIKEN cDNA 5930403N24 gene	-1.12	0.857	-1.08	0.837	-1.63	0.259	-1.07	0.922	-1.22
1454375_at	5730458M16Rik	RIKEN cDNA 5730458M16 gene	-1.41	0.084	-1.08	0.137	-1.25	0.021	-1.31	0.365	-1.26
1452613_at	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	-1.3	0.284	-1.18	0.557	-1.22	0.748	-1.08	0.536	-1.2
1438888_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	-1.31	0.482	-1.01	0.979	-1.47	0.074	-1.53	0.156	-1.33
1430444_at	0610006L08Rik	RIKEN cDNA 0610006L08 gene	-1.34	0.064	-1.35	0.506	-1.06	0.903	-1.43	0.458	-1.29
1432084_at	4921515G04Rik	RIKEN cDNA 4921515G04 gene	-1.06	0.923	-1.66	0.36	-1.13	0.763	-2.98	0.091	-1.71
1447956_at	C76614	expressed sequence C76614	-1.05	0.937	-1.21	0.421	-1.53	0.321	-1.69	0.323	-1.37
1457205_at	Nsf	N-ethylmaleimide sensitive fusion protein	-1.11	0.769	-1.16	0.161	-1.49	0.179	-1.49	0.087	-1.31
1426420_at	Rbm26	RNA binding motif protein 26	-1.34	0.125	-1.1	0.763	-1.3	0.148	-1.15	0.459	-1.22
1425001_at	Rnf146	ring finger protein 146	-1.22	0.494	-1.23	0.183	-1.25	0.176	-1.01	0.931	-1.18
1430375_a_at	Ccl27	chemokine (C-C motif) ligand 27	-1.17	0.094	-1.15	0.478	-1.41	0.222	-1.15	0.642	-1.22
1422537_a_at	Id2	inhibitor of DNA binding 2	-1.33	0.57	-1.09	0.728	-1.31	0.051	-1.16	0.614	-1.22
1459791_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	-1.03	0.942	-1.53	0.244	-1.24	0.373	-1.99	0.193	-1.45
1451347_at	Ccdc95	coiled-coil domain containing 95	-1.37	0.109	-1.4	0.351	-1.01	0.958	-1.07	0.515	-1.21
1438762_at	Tcf12	Transcription factor 12	-1.02	0.917	-1.11	0.318	-1.84	0.005	-1.73	0.105	-1.42
1424658_at	Taok1	TAO kinase 1	-1.02	0.931	-1.29	0.05	-1.47	0.128	-1.1	0.655	-1.22
1438898_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.26	0.669	-1.45	0.392	-1.05	0.936	-3.56	0.016	-1.83
1419772_at	Mllt10	Myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosop	-1.3	0.441	-1.23	0.406	-1.18	0.621	-1.28	0.635	-1.25
1419815_at	Mett11d1	methyltransferase 11 domain containing 1	-1.49	0.084	-1.26	0.201	-1.03	0.717	-2.09	0.102	-1.47
1446693_at	---	---	-1.13	0.52	-1.02	0.938	-1.76	0.274	-1.56	0.438	-1.37
1427352_at	BC031593	cDNA sequence BC031593	-1.24	0.284	-1.31	0.456	-1.15	0.545	-2.65	0.105	-1.59
1439466_s_at	Bud31	BUD31 homolog (yeast)	-1.14	0.358	-1.15	0.016	-1.46	0.018	-1.08	0.268	-1.21

1460728_s_at	Ing4	inhibitor of growth family, member 4	-1.3	0.186	-1.11	0.525	-1.31	0.343	-1.17	0.286	-1.22
1449535_at	Znrf4	zinc and ring finger 4	-1.02	0.945	-1.14	0.742	-1.73	0.086	-1.64	0.087	-1.38
1450226_at	Prlr	prolactin receptor	-1.46	0.266	-1.03	0.881	-1.29	0.434	-2.02	0.506	-1.45
1444351_at	Cyfip2	Cytoplasmic FMR1 interacting protein 2	-1.23	0.451	-1.57	0.414	-1.02	0.959	-1.42	0.235	-1.31
1416817_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	-1.18	0.239	-1.15	0.377	-1.39	0.063	-1.61	0.052	-1.33
1443654_at	Ankfy1	Ankyrin repeat and FYVE domain containing 1	-1.19	0.285	-1.28	0.351	-1.23	0.16	-1.54	0.382	-1.31
1446489_at	Sufu	Suppressor of fused homolog (Drosophila)	-1.29	0.232	-1.22	0.359	-1.19	0.454	-1.76	0.06	-1.36
1446097_at	Rbbp8	Retinoblastoma binding protein 8	-1.24	0.505	-1.13	0.735	-1.34	0.37	-1	0.995	-1.18
1438532_at	Hmcn1	hemicentin 1	-1.19	0.323	-1.11	0.697	-1.45	0.24	-1	0.992	-1.19
1457690_at	Kalrn	kalirin, RhoGEF kinase	-1.05	0.942	-1.22	0.139	-1.51	0.182	-1.46	0.616	-1.31
1434307_at	Tmem64	transmembrane protein 64	-1.49	0.075	-1.18	0.091	-1.09	0.599	-1.03	0.842	-1.2
1430585_at	5930436O19Rik	RIKEN cDNA 5930436O19 gene	-1.21	0.278	-1.1	0.64	-1.41	0.165	-1.68	0.117	-1.35
1445651_at	Atp11b	ATPase, Class VI, type 11B	-1.36	0.654	-1.15	0.182	-1.21	0.459	-1.07	0.629	-1.2
1436602_x_at	Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	-1.57	0.467	-1.24	0.719	-1	0.993	-2.06	0.183	-1.47
1443386_at	C86727	expressed sequence C86727	-1.01	0.983	-1.6	0.596	-1.22	0.695	-1.74	0.33	-1.39
1456583_x_at	Tmem144	transmembrane protein 144	-1.34	0.392	-1.08	0.809	-1.31	0.6	-1.02	0.959	-1.19
1455530_at	Igh-1a	Immunoglobulin heavy chain 1a (serum IgG2a)	-1.29	0.719	-1.12	0.675	-1.3	0.483	-2.91	0.106	-1.66
1438326_at	3300001M20Rik	RIKEN cDNA 3300001M20 gene	-1.23	0.189	-1.26	0.334	-1.2	0.315	-1.08	0.567	-1.19
1416665_at	Coq7	demethyl-Q 7	-1.22	0.044	-1.23	0.045	-1.24	0.028	-1.1	0.587	-1.2
1449985_at	1700072E05Rik	RIKEN cDNA 1700072E05 gene	-1.32	0.777	-1.15	0.777	-1.23	0.635	-1.78	0.539	-1.37
1438887_a_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	-1.37	0.189	-1.28	0.402	-1.08	0.742	-1.85	0.133	-1.39
1429108_at	Msl2l1	male-specific lethal 2-like 1 (Drosophila)	-1.05	0.697	-1.4	0.019	-1.3	0.045	-1.12	0.437	-1.22
1460506_s_at	Ndufc2 /// LOC675	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 /// similar to NAD	-1.21	0.067	-1.14	0.12	-1.36	0.038	-1.12	0.167	-1.21
1445534_at	Flnb	Filamin, beta	-1.08	0.762	-1.3	0.245	-1.36	0.321	-1.42	0.318	-1.29
1438046_at	AU019823	expressed sequence AU019823	-1.15	0.495	-1.26	0.329	-1.29	0.166	-1.16	0.364	-1.21
1434942_at	2610101J03Rik	RIKEN cDNA 2610101J03 gene	-1.18	0.144	-1.11	0.311	-1.45	0.003	-1.12	0.577	-1.22
1457552_at	Zfp295	zinc finger protein 295	-1.17	0.4	-1.24	0.232	-1.28	0.154	-1.45	0.142	-1.29
1438247_at	Klhl15	kelch-like 15 (Drosophila)	-1.24	0.381	-1.21	0.293	-1.24	0.438	-1.22	0.42	-1.23
1459465_at	9630020C08Rik	RIKEN cDNA 9630020C08 gene	-1.18	0.756	-1.33	0.681	-1.19	0.709	-1.31	0.432	-1.25
1439341_at	AK220484	cDNA sequence AK220484	-1.21	0.646	-1.55	0.105	-1.03	0.707	-1.72	0.15	-1.38
1457904_at	Car8	carbonic anhydrase 8	-1	0.982	-1.23	0.297	-1.58	0.019	-1.09	0.841	-1.23
1423063_at	Dnmt3a	DNA methyltransferase 3A	-1.44	0.067	-1.14	0.286	-1.15	0.595	-1.22	0.567	-1.24
1451466_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	-1.43	0.059	-1.08	0.382	-1.23	0.092	-1.43	0.078	-1.29
1457309_at	AU015228	expressed sequence AU015228	-1.09	0.885	-1.13	0.804	-1.58	0.369	-1	0.997	-1.2
1458032_at	Tpd52l2	Tumor protein D52-like 2	-1.2	0.779	-1.31	0.687	-1.19	0.737	-1.11	0.775	-1.2
1453303_at	4833417J20Rik	RIKEN cDNA 4833417J20 gene	-1.11	0.663	-1.41	0.379	-1.21	0.516	-1.26	0.45	-1.25
1448519_at	Tead2	TEA domain family member 2	-1.11	0.92	-1.35	0.714	-1.25	0.185	-1.18	0.693	-1.22
1444955_at	D6Ertd469e	DNA segment, Chr 6, ERATO Doi 469, expressed	-1.05	0.931	-1.23	0.556	-1.48	0.213	-1.18	0.698	-1.24
1440640_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	-1.08	0.579	-1.14	0.482	-1.58	0.052	-1.52	0.365	-1.33
1428280_at	Fip1l1	FIP1 like 1 (S. cerevisiae)	-1.03	0.909	-1.39	0.112	-1.34	0.025	-1.29	0.101	-1.26
1447818_x_at	Rhebl1	Ras homolog enriched in brain like 1	-1.3	0.22	-1.11	0.69	-1.31	0.388	-1.54	0.221	-1.31
1416791_a_at	Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	-1.04	0.737	-1.28	0.034	-1.44	0.072	-1.39	0.175	-1.29
1455783_at	---	---	-1.15	0.066	-1.23	0.763	-1.32	0.556	-1.67	0.242	-1.34
1443516_at	Atxn2	Ataxin 2	-1.03	0.933	-1.08	0.67	-1.85	0.032	-1.01	0.984	-1.24
1434395_at	Man1a2	mannosidase, alpha, class 1A, member 2	-1.17	0.488	-1.08	0.635	-1.51	0.119	-1.15	0.552	-1.23
1452988_at	2610306M01Rik	RIKEN cDNA 2610306M01 gene	-1.15	0.486	-1.29	0.351	-1.26	0.383	-1.23	0.265	-1.23
1436484_at	C030019I05Rik	RIKEN cDNA C030019I05 gene	-1.03	0.972	-1.07	0.801	-1.89	0.382	-2.59	0.174	-1.65
1440303_at	Slc7a6os	Solute carrier family 7, member 6 opposite strand	-1.55	0.261	-1.14	0.745	-1.09	0.216	-1.39	0.39	-1.29
1423246_at	Txndc4	thioredoxin domain containing 4 (endoplasmic reticulum)	-1.25	0.022	-1.23	0.172	-1.2	0.332	-1.18	0.174	-1.22
1455997_a_at	Uqcrb	ubiquinol-cytochrome c reductase binding protein	-1.21	0.018	-1.22	0.457	-1.26	0.008	-1.05	0.107	-1.19
1444232_at	Prkg1	protein kinase, cGMP-dependent, type I	-1.15	0.225	-1.02	0.931	-1.69	0.028	-1	0.996	-1.22
1455696_a_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-1.15	0.602	-1.14	0.506	-1.45	0.071	-1.31	0.399	-1.26
1437274_at	Copa	coatomer protein complex subunit alpha	-1.05	0.817	-1.04	0.85	-1.9	0	-2.02	0.065	-1.5

1434613_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	-1.08	0.662	-1.14	0.136	-1.58	0.034	-1.42	0.047	-1.3
1454532_at	C030043A13Rik	RIKEN cDNA C030043A13 gene	-1	0.999	-1.47	0.01	-1.32	0.163	-1.25	0.182	-1.26
1454149_a_at	Ccnl2	cyclin L2	-1.32	0.452	-1.18	0.399	-1.19	0.222	-1.3	0.142	-1.25
1456148_a_at	1110014K08Rik	RIKEN cDNA 1110014K08 gene	-1.22	0.55	-1.19	0.231	-1.28	0.368	-2.22	0.167	-1.48
1447679_s_at	Bms1l	BMS1-like, ribosome assembly protein (yeast)	-1.02	0.832	-1.29	0.03	-1.46	0.094	-1.75	0.249	-1.38
1427935_at	2610208E05Rik	RIKEN cDNA 2610208E05 gene	-1.03	0.837	-1.32	0.044	-1.4	0.188	-1.3	0.508	-1.26
1440144_x_at	C330046E03	hypothetical protein C330046E03	-1.81	0.181	-1.03	0.919	-1.09	0.663	-1.36	0.018	-1.32
1455165_at	Rora	RAR-related orphan receptor alpha	-1.05	0.9	-1.13	0.308	-1.67	0.12	-1.64	0.103	-1.37
1442078_at	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	-1.33	0.409	-1.12	0.589	-1.26	0.294	-1.26	0.207	-1.24
1428213_at	2410003A14Rik	RIKEN cDNA 2410003A14 gene	-1.24	0.019	-1.38	0.018	-1.1	0.354	-1.07	0.501	-1.2
1432806_at	9430099H24Rik	RIKEN cDNA 9430099H24 gene	-1.46	0.08	-1.09	0.643	-1.19	0.484	-1.47	0.14	-1.3
1434633_at	Crebbp	CREB binding protein	-1.07	0.395	-1.26	0.073	-1.39	0.098	-1.31	0.141	-1.26
1460113_at	B930093H17Rik	RIKEN cDNA B930093H17 gene	-1.09	0.789	-1.23	0.464	-1.4	0.065	-1.32	0.454	-1.26
1441262_at	Slk	STE20-like kinase (yeast)	-1.02	0.89	-1.03	0.914	-2.04	0.007	-1.4	0.1	-1.37
1435499_at	D030041N04Rik	RIKEN cDNA D030041N04 gene	-1.42	0.118	-1.18	0.628	-1.12	0.582	-1.51	0.057	-1.31
1437338_x_at	Elp3	Elongation protein 3 homolog (S. cerevisiae)	-1.18	0.15	-1.26	0.152	-1.25	0.136	-1.47	0.075	-1.29
1447970_at	---	---	-1.33	0.37	-1.28	0.355	-1.1	0.685	-1.11	0.661	-1.21
1460430_at	Rap2c	RAP2C, member of RAS oncogene family	-1.18	0.301	-1.41	0.067	-1.13	0.515	-1.15	0.508	-1.22
1439123_at	Phf21a	PHD finger protein 21A	-1.18	0.232	-1.02	0.844	-1.63	0.015	-2.01	0.077	-1.46
1457214_at	Ncoa3	Nuclear receptor coactivator 3	-1.31	0.547	-1.17	0.57	-1.21	0.526	-1.77	0.223	-1.37
1439080_at	Erbb2ip	Erbb2 interacting protein	-1.14	0.36	-1.15	0.588	-1.42	0.142	-1.55	0.203	-1.32
1441285_at	4833426J09Rik	RIKEN cDNA 4833426J09 gene	-1.06	0.872	-1.73	0.019	-1.09	0.701	-1.89	0.025	-1.44
1458974_at	Tox	Thymocyte selection-associated HMG box gene	-1.06	0.793	-1.64	0.058	-1.12	0.276	-1.81	0.142	-1.41
1428546_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	-1.13	0.528	-1.22	0.03	-1.35	0	-1.03	0.876	-1.18
1437111_at	Zc3h12c	zinc finger CCCH type containing 12C	-1.06	0.52	-1.21	0.247	-1.49	0.058	-1.03	0.768	-1.2
1438198_at	Bri3bp	Bri3 binding protein	-1.08	0.663	-1.45	0.008	-1.21	0.108	-1.08	0.721	-1.2
1430603_at	4930579K19Rik	RIKEN cDNA 4930579K19 gene	-1.05	0.717	-1.65	0.295	-1.13	0.706	-1.27	0.213	-1.27
1424834_s_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	-1.39	0.052	-1.29	0.095	-1.05	0.791	-1.59	0.31	-1.33
1423336_at	Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	-1.12	0.545	-1.23	0.134	-1.36	0.024	-1.23	0.055	-1.24
1435995_at	Mrpl22	mitochondrial ribosomal protein L22	-1.12	0.237	-1.21	0.071	-1.38	0.049	-1.12	0.214	-1.21
1455644_at	Vps53	vacuolar protein sorting 53 (yeast)	-1.25	0.032	-1.24	0.197	-1.19	0.251	-1.28	0.117	-1.24
1430694_at	---	---	-1.36	0.377	-1.15	0.482	-1.2	0.564	-1.32	0.265	-1.26
1434931_at	Neo1	neogenin	-1.24	0.056	-1.4	0.06	-1.08	0.709	-1.63	0.52	-1.34
1449939_s_at	Dlk1	delta-like 1 homolog (Drosophila)	-1.48	0.229	-1.01	0.978	-1.29	0.664	-1.04	0.759	-1.2
1453198_at	Zfp422-rs1	zinc finger protein 422, related sequence 1	-1.19	0.591	-1.23	0.277	-1.26	0.314	-1.24	0.298	-1.23
1434842_s_at	Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	-1.1	0.226	-1.35	0.098	-1.26	0.145	-1.09	0.633	-1.2
1439329_a_at	Brsk2	BR serine/threonine kinase 2	-1.37	0.563	-1.18	0.787	-1.15	0.82	-1.62	0.313	-1.33
1455103_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	-1.32	0.121	-1.21	0.249	-1.17	0.235	-1.29	0.137	-1.24
1448974_at	Dcx	doublecortin	-1.04	0.95	-1.51	0.099	-1.22	0.297	-2.84	0.174	-1.65
1453306_at	6330531I01Rik	RIKEN cDNA 6330531I01 gene	-1.17	0.12	-1.23	0.574	-1.29	0.246	-1.54	0.158	-1.31
1441006_at	Dus4l	dihydrouridine synthase 4-like (S. cerevisiae)	-1.01	0.972	-1.19	0.549	-1.64	0.11	-1.14	0.459	-1.24
1429016_at	D1Ertd161e /// Glb1	DNA segment, Chr 1, ERATO Doi 161, expressed /// galactosidase, beta 1-like	-1	0.997	-1.64	0.194	-1.2	0.505	-1.02	0.926	-1.21
1436660_at	Rrbp1	ribosome binding protein 1	-1.1	0.371	-1.18	0.474	-1.45	0.289	-1.39	0.277	-1.28
1455441_at	---	---	-1.09	0.395	-1.26	0.127	-1.36	0.05	-1.02	0.891	-1.18
1455986_at	Zdhhc17	zinc finger, DHHC domain containing 17	-1.05	0.556	-1.39	0.535	-1.29	0.482	-1.53	0.242	-1.32
1428273_at	Abhd13	abhydrolase domain containing 13	-1.17	0.198	-1.24	0.328	-1.28	0.124	-1.22	0.391	-1.23
1419222_at	Tbxa2r	thromboxane A2 receptor	-1.34	0.398	-1.32	0.135	-1.06	0.767	-1.58	0	-1.32
1439170_at	---	---	-1.05	0.776	-1.26	0.408	-1.43	0.05	-1	0.97	-1.19
1451997_at	Zfp426	zinc finger protein 426	-1.07	0.677	-1.15	0.156	-1.54	0.038	-1.34	0.045	-1.28
1443037_at	Nptn	Neuroplastin	-1.02	0.923	-1.15	0.479	-1.69	0.031	-1.16	0.189	-1.25
1436429_at	Zfp606	zinc finger protein 606	-1.17	0.571	-1.42	0.451	-1.13	0.499	-2.18	0.029	-1.47
1434629_at	Zbtb26	zinc finger and BTB domain containing 26	-1.14	0.719	-1.19	0.42	-1.38	0.057	-1.3	0.364	-1.25
1454406_at	4930453J04Rik	RIKEN cDNA 4930453J04 gene	-1.17	0.757	-1.36	0.617	-1.17	0.515	-2.48	0.079	-1.54

1421023_at	Pik3c2a	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide	-1.12	0.191	-1.19	0.012	-1.41	0.1	-1.6	0.144	-1.33
1434451_at	---	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library,	-1.26	0.125	-1.26	0.128	-1.16	0.331	-1.21	0.46	-1.22
1449750_at	AA407331	expressed sequence AA407331	-1.1	0.727	-1.08	0.213	-1.64	0.005	-1.26	0.448	-1.27
1446804_at	Nxn	nucleoredoxin	-1.11	0.759	-1.21	0.54	-1.39	0.31	-1.71	0.01	-1.36
1425082_s_at	9030416H16Rik	RIKEN cDNA 9030416H16 gene	-1.13	0.514	-1.1	0.333	-1.52	0.014	-1.12	0.396	-1.22
1457005_at	Mtfmt	mitochondrial methionyl-tRNA formyltransferase	-1.13	0.203	-1.38	0.231	-1.19	0.357	-1.28	0.493	-1.25
1452762_at	8430436O14Rik	RIKEN cDNA 8430436O14 gene	-1.07	0.705	-1.12	0.59	-1.61	0.076	-1.41	0.224	-1.3
1452977_at	Zhx3	zinc fingers and homeoboxes 3	-1.16	0.53	-1.27	0.109	-1.26	0.259	-1.62	0.086	-1.33
1437719_x_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	-1.07	0.606	-1.16	0.287	-1.53	0.003	-1.98	0.192	-1.44
1455653_at	Ccnj	cyclin J	-1.13	0.637	-1.27	0.427	-1.29	0.252	-1.65	0.098	-1.33
1438580_at	Zcchc7	zinc finger, CCHC domain containing 7	-1.2	0.531	-1.1	0.424	-1.42	0.026	-1.79	0.111	-1.38
1431126_a_at	0610011F06Rik	RIKEN cDNA 0610011F06 gene	-1.1	0.149	-1.46	0.021	-1.18	0.402	-1.06	0.813	-1.2
1455589_at	1700100M05Rik	RIKEN cDNA 1700100M05 gene	-1.32	0.098	-1.18	0.213	-1.19	0.349	-1.43	0.096	-1.28
1457020_at	Gpbp1l1	GC-rich promoter binding protein 1-like 1	-1.06	0.781	-1.18	0.366	-1.53	0.159	-1.16	0.465	-1.23
1430366_at	5430405H02Rik	RIKEN cDNA 5430405H02 gene	-1.21	0.342	-1.08	0.864	-1.45	0.249	-1.01	0.984	-1.18
1455314_at	Lpp	LIM domain containing preferred translocation partner in lipoma	-1.1	0.578	-1.07	0.504	-1.65	0.016	-1.58	0.088	-1.35
1431161_at	Rgnef	Rho-guanine nucleotide exchange factor	-1.03	0.866	-1.93	0.376	-1.04	0.911	-2.59	0.428	-1.65
1434390_at	Hnrpu	Heterogeneous nuclear ribonucleoprotein U	-1.2	0.535	-1.28	0.349	-1.2	0.455	-1.13	0.702	-1.2
1448391_at	Rab9	RAB9, member RAS oncogene family	-1.12	0.151	-1.16	0.016	-1.44	0.006	-1.02	0.772	-1.19
1440533_at	Bfar	Bifunctional apoptosis regulator	-1.03	0.895	-1.13	0.482	-1.69	0.088	-1.28	0.457	-1.28
1439705_at	Ptpn12	Protein tyrosine phosphatase, non-receptor type 12	-1.14	0.469	-1.02	0.911	-1.69	0.007	-1.08	0.355	-1.23
1425820_x_at	Gpatc4	G patch domain containing 4	-1.44	0.216	-1.12	0.702	-1.16	0.287	-1.26	0.282	-1.25
1450328_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:1700129L04 prc	-1.01	0.983	-1.85	0.39	-1.09	0.455	-2.92	0.215	-1.72
1419793_at	D5Ertd615e	DNA segment, Chr 5, ERATO Doi 615, expressed	-1.47	0.073	-1.06	0.875	-1.21	0.384	-1.23	0.714	-1.24
1446302_at	Ccbl1	Cysteine conjugate-beta lyase 1	-1.15	0.54	-1.15	0.625	-1.41	0.214	-1.55	0.523	-1.31
1458712_at	---	---	-1.02	0.957	-1.42	0.345	-1.31	0.38	-2.55	0.129	-1.57
1442465_s_at	Strbp	spermatid perinuclear RNA binding protein	-1.04	0.438	-1.32	0.104	-1.37	0.124	-1.79	0.055	-1.38
1453934_at	4930535C22Rik	RIKEN cDNA 4930535C22 gene	-1.86	0.247	-1.06	0.799	-1.03	0.827	-1.51	0.256	-1.37
1446245_at	Fmnl2	Formin-like 2	-1.04	0.904	-1.06	0.826	-1.83	0.014	-1.4	0.098	-1.33
1453024_at	Wdr37	WD repeat domain 37	-1.47	0.187	-1.05	0.808	-1.23	0.296	-1.37	0.426	-1.28
1424590_at	Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	-1.36	0.059	-1.32	0.147	-1.04	0.875	-1.52	0.136	-1.31
1455776_x_at	Bola2	bolA-like 2 (E. coli)	-1.39	0.059	-1.13	0.409	-1.18	0.179	-1.03	0.843	-1.18
1439820_at	Ebf1	Early B-cell factor 1	-1.11	0.64	-1.48	0.403	-1.14	0.568	-2.18	0.124	-1.48
1439293_at	C130047D21Rik	RIKEN cDNA C130047D21 gene	-1.21	0.7	-1.49	0.108	-1.05	0.884	-1.82	0.224	-1.39
1456320_at	BC049806	cDNA sequence BC049806	-1.04	0.824	-1.5	0.022	-1.21	0.349	-1.12	0.537	-1.22
1437635_at	Dcbld2	discoidin, CUB and LCCL domain containing 2	-1.09	0.571	-1.23	0.073	-1.39	0.02	-1.03	0.87	-1.18
1415826_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	-1.27	0.173	-1.15	0.264	-1.25	0.054	-1.22	0.36	-1.23
1421318_at	Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	-1.01	0.929	-1.2	0.792	-1.6	0.269	-1.71	0.293	-1.38
1448237_x_at	Ldhb	lactate dehydrogenase B	-1.2	0.108	-1.43	0.169	-1.09	0.575	-1.42	0.088	-1.28
1416141_a_at	Rps6 /// LOC66657	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	-1.06	0.526	-1.37	0.118	-1.29	0.012	-1.18	0.004	-1.22
1441549_at	---	---	-1.32	0.111	-1.19	0.283	-1.18	0.377	-1.36	0.367	-1.26
1434478_at	Heca	headcase homolog (Drosophila)	-1.17	0.383	-1.3	0.098	-1.2	0.358	-1.6	0.236	-1.32
1429080_at	Mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	-1.35	0.224	-1.11	0.461	-1.22	0.141	-1.01	0.956	-1.18
1457033_at	Gm397 /// XM_486	gene model 397, (NCBI) /// Mus musculus sequence XM_486399 /// similar to zin	-1.14	0.55	-1.54	0.475	-1.08	0.839	-1.14	0.491	-1.22
1456715_at	Phr1	Pam, highwire, rpm 1	-1.52	0.488	-1.23	0.378	-1.02	0.965	-2.25	0.155	-1.51
1448018_at	---	---	-1.1	0.704	-1.11	0.593	-1.56	0.142	-1.3	0.571	-1.27
1438781_at	E130014J05Rik	RIKEN cDNA E130014J05 gene	-1.21	0.12	-1.07	0.669	-1.44	0.08	-1.38	0.239	-1.27
1460155_at	2410005O16Rik	RIKEN cDNA 2410005O16 gene	-1.3	0.332	-1.36	0.12	-1.05	0.847	-1.6	0.237	-1.33
1423930_at	Anapc4	anaphase promoting complex subunit 4	-1.2	0.171	-1.06	0.498	-1.48	0.154	-1.1	0.598	-1.21
1453254_at	1700034O15Rik	RIKEN cDNA 1700034O15 gene	-1.13	0.72	-1.62	0.377	-1.05	0.81	-2.79	0.238	-1.65
1426148_at	Gbgt1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	-1.39	0.479	-1.2	0.27	-1.11	0.797	-1.29	0.212	-1.25
1442178_at	Gmds	GDP-mannose 4, 6-dehydratase	-1.21	0.476	-1.11	0.705	-1.37	0.226	-1.39	0.01	-1.27
1428914_at	2310014D11Rik	RIKEN cDNA 2310014D11 gene	-1.05	0.759	-1.32	0.059	-1.34	0.191	-1.72	0.085	-1.36

1444558_at	Wdr33	WD repeat domain 33	-1.26	0.502	-1.46	0.343	-1.02	0.938	-1.3	0.396	-1.26
1417886_at	1810009A15Rik	RIKEN cDNA 1810009A15 gene	-1.14	0.023	-1.23	0.011	-1.3	0.213	-1.15	0.234	-1.21
1436133_at	0610011N22Rik	RIKEN cDNA 0610011N22 gene	-1.32	0.317	-1.33	0.532	-1.05	0.787	-1.2	0.613	-1.23
1428231_at	Cpsf6	cleavage and polyadenylation specific factor 6	-1.09	0.5	-1.33	0.171	-1.27	0.075	-1.43	0.132	-1.28
1446412_at	Wwox	WW domain-containing oxidoreductase	-1	0.999	-1.59	0.34	-1.21	0.34	-1.97	0.047	-1.44
1432800_at	C030011G24Rik	RIKEN cDNA C030011G24 gene	-1.21	0.606	-1.35	0.16	-1.12	0.317	-1.45	0.172	-1.28
1441843_s_at	5230400M03Rik	RIKEN cDNA 5230400M03 gene	-1.05	0.197	-1.1	0.521	-1.69	0.058	-1.2	0.438	-1.26
1429640_at	1700025F22Rik	RIKEN cDNA 1700025F22 gene	-1.44	0.705	-1.2	0.429	-1.08	0.698	-1.03	0.822	-1.18
1450366_at	Hrk	harakiri, BCL2 interacting protein (contains only BH3 domain)	-1.44	0.589	-1.02	0.918	-1.27	0.205	-1.53	0.553	-1.32
1442663_at	---	---	-1.12	0.098	-1.27	0.388	-1.29	0.334	-1.27	0.27	-1.24
1423903_at	Pvr	poliovirus receptor	-1.32	0.006	-1.42	0.003	-1	0.985	-1.16	0.265	-1.23
1457717_at	AI987986	expressed sequence AI987986	-1.27	0.09	-1.04	0.802	-1.41	0.067	-1.63	0.26	-1.34
1441346_at	2810421E14Rik	RIKEN cDNA 2810421E14 gene	-1.15	0.688	-1.46	0.387	-1.1	0.574	-1.57	0.031	-1.32
1423470_at	Ptbp2	polypyrimidine tract binding protein 2	-1.13	0.644	-1.37	0.009	-1.18	0.338	-1.39	0.336	-1.27
1458136_at	Msi2	Musashi homolog 2 (Drosophila)	-1.5	0.11	-1.1	0.723	-1.13	0.537	-1.09	0.692	-1.21
1454980_at	4930402E16Rik	RIKEN cDNA 4930402E16 gene	-1.16	0.184	-1.32	0.144	-1.19	0.24	-1.37	0.235	-1.26
1441402_at	LOC674229	similar to cysteine and glycine-rich protein 2 binding protein	-1.21	0.489	-1.48	0.081	-1.04	0.916	-1.25	0.187	-1.25
1455564_at	Bcr	breakpoint cluster region homolog	-1.29	0.071	-1.1	0.303	-1.29	0.312	-1.12	0.064	-1.2
1423432_at	Phip	pleckstrin homology domain interacting protein	-1.17	0.398	-1.14	0.407	-1.38	0.148	-1.42	0.174	-1.28
1460579_at	Dnpep	aspartyl aminopeptidase	-1.32	0.586	-1.1	0.397	-1.26	0.422	-1.31	0.125	-1.25
1451732_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-1.12	0.47	-1.44	0.049	-1.14	0.3	-1.26	0.363	-1.24
1460425_at	1700001C19Rik	RIKEN cDNA 1700001C19 gene	-1.66	0.003	-1.12	0.062	-1.04	0.871	-1.22	0.152	-1.26
1443052_at	C330019L16Rik	RIKEN cDNA C330019L16 gene	-1.58	0.15	-1.12	0.73	-1.07	0.697	-1.35	0.472	-1.28
1416320_at	Sec22a	SEC22 vesicle trafficking protein-like A (S. cerevisiae)	-1.19	0.001	-1.11	0.464	-1.39	0.031	-1.16	0.257	-1.21
1438895_at	A430102J17Rik	RIKEN cDNA A430102J17 gene	-1.18	0.217	-1.19	0.193	-1.3	0.212	-1.15	0.068	-1.2
1435595_at	1810011O10Rik	RIKEN cDNA 1810011O10 gene	-1.26	0.425	-1.19	0.43	-1.21	0.165	-1.58	0.205	-1.31
1436001_at	2310028O11Rik	RIKEN cDNA 2310028O11 gene	-1.35	0.11	-1.07	0.774	-1.27	0.043	-1.34	0.119	-1.26
1428593_at	1700029F09Rik	RIKEN cDNA 1700029F09 gene	-1.22	0.126	-1.26	0.018	-1.18	0.166	-1	0.986	-1.17
1457464_at	C130015C19	hypothetical LOC403342	-1.05	0.855	-1.36	0.01	-1.3	0.299	-1.71	0.041	-1.35
1434632_at	---	Transcribed locus	-1.19	0.325	-1.18	0.524	-1.29	0.364	-1.43	0.233	-1.27
1418582_at	Cbfa2t3h	core-binding factor, runt domain, alpha subunit 2, translocated to, 3 homolog (hur	-1.23	0.106	-1.4	0.121	-1.07	0.784	-1.15	0.275	-1.21
1453171_s_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	-1.03	0.566	-1.22	0.064	-1.49	0.034	-1.04	0.476	-1.2
1441077_at	AW124847	expressed sequence AW124847	-1.5	0.179	-1.14	0.455	-1.09	0.855	-1.47	0.097	-1.3
1454166_at	1700040N02Rik	RIKEN cDNA 1700040N02 gene	-1.23	0.335	-1.24	0.071	-1.19	0.464	-1.61	0.415	-1.32
1441318_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	-1.46	0.037	-1.04	0.924	-1.22	0.253	-1.25	0.377	-1.25
1456663_x_at	Tm2d2	TM2 domain containing 2	-1	0.97	-1.34	0.126	-1.39	0.021	-1.36	0.091	-1.27
1457528_at	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	-1.15	0.705	-1.18	0.217	-1.35	0.148	-2.49	0.129	-1.54
1431594_at	Dpp3	dipeptidylpeptidase 3	-1.02	0.969	-1.38	0.652	-1.32	0.566	-1.7	0.004	-1.36
1422109_at	Rfx1	regulatory factor X, 1 (influences HLA class II expression)	-1.36	0.125	-1.25	0.56	-1.08	0.735	-1.73	0.087	-1.35
1435695_a_at	A030007L17Rik	RIKEN cDNA A030007L17 gene	-1.37	0.13	-1.21	0.3	-1.11	0.103	-2.23	0.064	-1.48
1453596_at	Id2	inhibitor of DNA binding 2	-1.23	0.597	-1.45	0.371	-1.04	0.747	-1.22	0.338	-1.24
1418801_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	-1.15	0.184	-1.21	0.146	-1.3	0.208	-1.06	0.76	-1.18
1443339_at	2310056P07Rik	RIKEN cDNA 2310056P07 gene	-1.04	0.917	-1.76	0.037	-1.07	0.882	-1.63	0.262	-1.38
1459731_at	---	---	-1.19	0.826	-1.21	0.608	-1.26	0.463	-1.58	0.539	-1.31
1422322_at	Chml	choroideremia-like	-1.38	0.548	-1.13	0.705	-1.17	0.655	-1.6	0.192	-1.32
1441371_at	Plxna4	plexin A4	-1.08	0.769	-1.33	0.01	-1.28	0.09	-1.07	0.566	-1.19
1438405_at	Fgf7	fibroblast growth factor 7	-1.12	0.505	-1.37	0.538	-1.19	0.014	-1.07	0.686	-1.19
1449472_at	Gpr12	G-protein coupled receptor 12	-1.08	0.881	-1.81	0.236	-1.02	0.867	-1.26	0.181	-1.29
1448521_at	Brd7 /// LOC63432	bromodomain containing 7 /// similar to bromodomain containing 7	-1.13	0.496	-1.32	0.087	-1.23	0.18	-1.36	0.069	-1.26
1432224_at	4831407H17Rik	RIKEN cDNA 4831407H17 gene	-1.06	0.852	-1.4	0.045	-1.24	0.29	-1.21	0.517	-1.23
1452759_s_at	Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	-1.05	0.36	-1.16	0.251	-1.55	0.03	-1.6	0.056	-1.34
1446511_at	Msh3	mutS homolog 3 (E. coli)	-1.24	0.426	-1.06	0.631	-1.41	0.194	-1.37	0.379	-1.27
1455113_at	Armc8	armadillo repeat containing 8	-1.21	0.149	-1.18	0.12	-1.26	0.175	-1.06	0.514	-1.18

1420209_at	Dus4l	Dihydrouridine synthase 4-like (S. cerevisiae)	-1.34	0.423	-1.28	0.404	-1.07	0.728	-2.21	0.487	-1.47
1448203_at	Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	-1.24	0.02	-1.23	0.043	-1.18	0.013	-1.14	0.352	-1.2
1459835_s_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-1.24	0.294	-1.13	0.302	-1.29	0.001	-1.68	0.327	-1.34
1419765_at	Cul2	cullin 2	-1.01	0.924	-1.24	0.515	-1.51	0.302	-1.59	0.125	-1.34
1435608_at	Znrf3 /// LOC63180	zinc and ring finger 3 /// similar to Goliath homolog precursor (Ring finger protein	-1.12	0.351	-1.4	0.204	-1.17	0.492	-1.02	0.609	-1.18
1424333_at	Rg9mtd1	RNA (guanine-9-) methyltransferase domain containing 1	-1.13	0.455	-1.3	0.112	-1.24	0.026	-1.22	0.356	-1.22
1456234_at	Limk1	LIM-domain containing, protein kinase	-1.22	0.153	-1.34	0.237	-1.12	0.543	-1.29	0.268	-1.24
1442164_at	Blzf1	basic leucine zipper nuclear factor 1	-1.06	0.772	-1.07	0.87	-1.7	0.032	-1.29	0.238	-1.28
1441946_at	Itih5	inter-alpha (globulin) inhibitor H5	-1.23	0.118	-1.44	0.298	-1.05	0.808	-3.69	0.057	-1.85
1426259_at	Pank3	pantothenate kinase 3	-1.01	0.937	-1.15	0.389	-1.66	0.044	-1.05	0.827	-1.22
1455831_at	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	-1.47	0.497	-1.08	0.815	-1.17	0.178	-1.35	0.136	-1.27
1449075_at	Exdl2	exonuclease 3''-5'' domain-like 2	-1.16	0.303	-1.33	0.089	-1.18	0.396	-1	0.987	-1.17
1438678_at	1500011K16Rik	RIKEN cDNA 1500011K16 gene	-1.3	0.142	-1.17	0.187	-1.19	0.053	-1.36	0.245	-1.25
1458281_at	Arsb	Arylsulfatase B	-1.22	0.277	-1.28	0.579	-1.16	0.121	-1.96	0.043	-1.4
1452596_at	Polr2k	polymerase (RNA) II (DNA directed) polypeptide K	-1.08	0.733	-1.25	0.342	-1.36	0.001	-1.25	0.314	-1.24
1441099_at	Plekhg3	Pleckstrin homology domain containing, family G (with RhoGef domain) member	-1.22	0.761	-1.2	0.232	-1.23	0.308	-1.03	0.922	-1.17
1428474_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	-1.12	0.777	-1.24	0.202	-1.31	0.014	-1.14	0.251	-1.2
1434834_at	Socs7	suppressor of cytokine signaling 7	-1.23	0.166	-1.53	0.05	-1	0.989	-1.26	0.11	-1.25
1419204_at	Dll1	delta-like 1 (Drosophila)	-1.47	0.171	-1.25	0.334	-1.01	0.97	-1.48	0.155	-1.3
1453583_at	Zzef1	zinc finger, ZZ-type with EF hand domain 1	-1.27	0.26	-1.03	0.794	-1.4	0.089	-1.32	0.184	-1.26
1454132_at	7630402F16Rik	RIKEN cDNA 7630402F16 gene	-1.11	0.873	-1.06	0.802	-1.6	0.433	-1.24	0.776	-1.25
1434194_at	Mtap2	microtubule-associated protein 2	-1.44	0.007	-1.08	0.911	-1.19	0.418	-1.97	0.036	-1.42
1456282_at	---	CDNA clone IMAGE:30014192	-1.02	0.88	-1.44	0.256	-1.26	0.408	-1.42	0.113	-1.29
1435239_at	Gria1	glutamate receptor, ionotropic, AMPA1 (alpha 1)	-1.13	0.803	-1.64	0.458	-1.03	0.861	-1.04	0.834	-1.21
1440719_at	Gle1l	GLE1 RNA export mediator-like (yeast	-1.07	0.803	-1.2	0.444	-1.43	0.249	-1.79	0.036	-1.37
1454554_at	9330159N22Rik	RIKEN cDNA 9330159N22 gene	-1.32	0.62	-1.29	0.603	-1.07	0.733	-1.22	0.768	-1.22
1439817_at	2900064A13Rik	RIKEN cDNA 2900064A13 gene	-1.21	0.034	-1.1	0.381	-1.37	0.143	-1.34	0.388	-1.25
1429624_at	Sltm	SAFB-like, transcription modulator	-1.23	0.288	-1.14	0.506	-1.29	0.093	-1.34	0.291	-1.25
1437182_at	Dido1	death inducer-obliterator 1	-1.13	0.375	-1.19	0.358	-1.34	0.098	-1.58	0.101	-1.31
1436157_at	Ccar1	cell division cycle and apoptosis regulator 1	-1.19	0.487	-1.1	0.188	-1.39	0.043	-1.02	0.909	-1.17
1419575_s_at	Zfp292	zinc finger protein 292	-1.21	0.201	-1.01	0.939	-1.53	0.101	-1.39	0.205	-1.29
1434105_at	Epm2aip1	EPM2A (laforin) interacting protein 1	-1.1	0.228	-1.2	0.116	-1.37	0.172	-1.19	0.469	-1.22
1442656_at	---	---	-1.13	0.771	-1.24	0.231	-1.29	0.588	-1.01	0.959	-1.17
1424546_at	BC003965	cDNA sequence BC003965	-1.14	0.631	-1.49	0.14	-1.09	0.275	-1.02	0.9	-1.18
1418664_at	Mpdz	multiple PDZ domain protein	-1.2	0.595	-1.26	0.106	-1.19	0.524	-1.61	0.032	-1.31
1416630_at	Id3	inhibitor of DNA binding 3	-1.46	0.132	-1.06	0.806	-1.19	0.436	-2.42	0.047	-1.53
1445862_at	4921513D23Rik	RIKEN cDNA 4921513D23 gene	-1.15	0.119	-1.02	0.755	-1.6	0.072	-1.32	0.237	-1.28
1459517_at	Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-1.32	0.56	-1.02	0.961	-1.37	0.137	-1.13	0.678	-1.21
1452799_at	2310009E04Rik	RIKEN cDNA 2310009E04 gene	-1.2	0.138	-1.15	0.015	-1.3	0.042	-1.17	0.668	-1.2
1428257_s_at	Dynlrb1	dynein light chain roadblock-type 1	-1.14	0.194	-1.2	0.003	-1.31	0.044	-1.39	0.15	-1.26
1457303_at	Anks3	Ankyrin repeat and sterile alpha motif domain containing 3	-1.24	0.274	-1.17	0.592	-1.24	0.128	-1.5	0.299	-1.29
1456855_at	---	---	-1.32	0.485	-1.06	0.226	-1.3	0.235	-1.2	0.422	-1.22
1437490_x_at	Uap1 /// LOC64050	UDP-N-acetylglucosamine pyrophosphorylase 1 /// similar to UDP-N-acetylhexos	-1.17	0.492	-1.21	0.124	-1.27	0.042	-1.21	0.349	-1.21
1435283_s_at	Gm967	gene model 967, (NCBI)	-1.03	0.854	-1.45	0.158	-1.24	0.198	-1.09	0.637	-1.2
1456662_at	LOC546058	Hypothetical protein LOC546058	-1.15	0.55	-1.04	0.865	-1.56	0.039	-1.61	0.083	-1.34
1444237_at	C330019G07Rik	RIKEN cDNA C330019G07 gene	-1.19	0.542	-1.11	0.382	-1.37	0.011	-1.15	0.357	-1.2
1449108_at	Fdx1	ferredoxin 1	-1.07	0.429	-1.2	0.208	-1.43	0.065	-1.43	0.144	-1.28
1457785_at	Zswim3	Zinc finger, SWIM domain containing 3	-1.31	0.619	-1.12	0.832	-1.23	0.549	-1.29	0.685	-1.24
1446166_at	---	---	-1.03	0.755	-1.86	0.193	-1.04	0.812	-1.14	0.851	-1.27
1457129_at	Zfp458	Zinc finger protein 458	-1.45	0.348	-1.02	0.926	-1.25	0.019	-1.19	0.61	-1.23
1443115_at	Tgfbr2	Transforming growth factor, beta receptor II	-1.12	0.737	-1.13	0.798	-1.46	0.252	-1.88	0.146	-1.39
1443464_at	Sntb1	Syntrophin, basic 1	-1.11	0.742	-1.18	0.693	-1.38	0.258	-1.67	0.374	-1.34
1443099_at	BC087945	CDNA sequence BC087945	-1.22	0.666	-1.36	0.367	-1.09	0.644	-1.11	0.462	-1.2

1455196_s_at	AA987161	expressed sequence AA987161	-1.3	0.445	-1.11	0.599	-1.25	0.205	-1.41	0.2	-1.27
1417254_at	Spata5	spermatogenesis associated 5	-1.35	0.073	-1.21	0.287	-1.11	0.407	-1.5	0.186	-1.29
1438110_at	Zbtb1	Zinc finger and BTB domain containing 1	-1.05	0.893	-1.39	0.352	-1.25	0.364	-1.23	0.355	-1.23
1453134_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	-1.04	0.915	-1.1	0.585	-1.66	0.007	-1.67	0.039	-1.37
1439940_at	2900019G14Rik	RIKEN cDNA 2900019G14 gene	-1.63	0.468	-1.16	0.522	-1.01	0.985	-1.2	0.706	-1.25
1427158_at	Mrps30	mitochondrial ribosomal protein S30	-1.3	0.059	-1.27	0.009	-1.09	0.527	-1.11	0.382	-1.19
1445959_at	---	---	-1.05	0.782	-1.27	0.274	-1.36	0.668	-1.75	0.616	-1.36
1443643_at	---	---	-1.45	0.467	-1.09	0.838	-1.16	0.459	-1.13	0.802	-1.21
1452854_at	---	---	-1.08	0.224	-1.2	0.029	-1.41	0.128	-1.65	0.259	-1.33
1440736_at	AI131651	expressed sequence AI131651	-1.22	0.021	-1.03	0.884	-1.47	0.057	-1.61	0.112	-1.33
1459154_at	---	Transcribed locus	-1.21	0.568	-1.06	0.852	-1.43	0.35	-1.47	0.153	-1.29
1420593_a_at	Tead3	TEA domain family member 3	-1.39	0.172	-1.07	0.762	-1.23	0.458	-1.06	0.841	-1.19
1429625_at	2900054C01Rik	RIKEN cDNA 2900054C01 gene	-1.1	0.28	-1.04	0.77	-1.65	0.011	-1.28	0.389	-1.27
1452774_at	Hnrpa3	heterogeneous nuclear ribonucleoprotein A3	-1.07	0.741	-1.31	0.084	-1.29	0.19	-1.39	0.136	-1.26
1445529_at	---	---	-1.03	0.857	-1.51	0.373	-1.19	0.689	-1.26	0.667	-1.25
1434207_at	2900057K09Rik	RIKEN cDNA 2900057K09 gene	-1.19	0.579	-1.15	0.447	-1.31	0.223	-1.55	0.097	-1.3
1440607_at	Ches1	Checkpoint suppressor 1	-1.06	0.63	-1.3	0.169	-1.31	0.511	-1.72	0.162	-1.35
1453302_at	Tmem81	transmembrane protein 81	-1.01	0.965	-1.99	0.16	-1.02	0.928	-1.34	0.12	-1.34
1446195_at	LOC632689	similar to WD repeat and SOCS box containing protein 2 (WSB-2) (SOCS box-co	-1.45	0.636	-1.02	0.954	-1.25	0.693	-1.06	0.234	-1.19
1418301_at	Irf6	interferon regulatory factor 6	-1.15	0.317	-1.18	0.299	-1.31	0.19	-1.76	0.216	-1.35
1460017_at	LOC434179	hypothetical LOC434179	-1.29	0.246	-1.02	0.919	-1.39	0.207	-1.54	0.164	-1.31
1448136_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.24	0.229	-1.13	0.22	-1.28	0.237	-1.51	0.425	-1.29
1432974_at	4933421H12Rik	RIKEN cDNA 4933421H12 gene	-1.09	0.706	-1.21	0.77	-1.37	0.579	-1.7	0.393	-1.34
1438961_s_at	Blmh	bleomycin hydrolase	-1.19	0.322	-1.19	0.047	-1.27	0.044	-1.49	0.034	-1.28
1439090_at	D030022P07Rik	RIKEN cDNA D030022P07 gene	-1.15	0.003	-1.11	0.436	-1.42	0.149	-1.63	0.082	-1.33
1458228_at	Opcml	Opioid binding protein/cell adhesion molecule-like	-1.48	0.295	-1.14	0.25	-1.08	0.82	-1.58	0.508	-1.32
1452158_at	Eprs /// LOC633677	glutamyl-prolyl-tRNA synthetase /// similar to Bifunctional aminoacyl-tRNA synthe	-1.28	0.161	-1.03	0.802	-1.39	0.08	-1.05	0.853	-1.18
1452107_s_at	Npnt	Nephronectin	-1.09	0.535	-1.13	0.85	-1.48	0.253	-2.1	0.157	-1.45
1454449_at	Rabepk	Rab9 effector protein with kelch motifs	-1.11	0.592	-1.19	0.699	-1.37	0.029	-1.07	0.839	-1.18
1416766_at	Mosc2	MOCO sulphurase C-terminal domain containing 2	-1.04	0.702	-1.36	0.126	-1.28	0.059	-1.17	0.228	-1.21
1446284_at	Mtss1	metastasis suppressor 1	-1.09	0.804	-1.09	0.777	-1.55	0.39	-2.17	0.132	-1.48
1445490_at	C77805	expressed sequence C77805	-1.19	0.59	-1.03	0.915	-1.5	0.154	-1.77	0.053	-1.37
1446621_at	Chd7	Chromodomain helicase DNA binding protein 7	-1.03	0.941	-1.36	0.441	-1.31	0.077	-1.88	0.097	-1.39
1435614_s_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	-1.56	0.479	-1.02	0.895	-1.17	0.474	-1	0.993	-1.19
1439388_s_at	Bcar1	breast cancer anti-estrogen resistance 1	-1.09	0.42	-1.22	0.23	-1.35	0.121	-1.35	0.379	-1.25
1457522_at	1110034C04Rik	RIKEN cDNA 1110034C04 gene	-1.09	0.286	-1.25	0.271	-1.33	0.36	-1.33	0.223	-1.25
1456856_at	Ppfia2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	-1.2	0.685	-1.34	0.353	-1.12	0.751	-1.22	0.535	-1.22
1457503_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	-1.26	0.124	-1.15	0.542	-1.22	0.17	-1.68	0.057	-1.33
1441010_at	---	Adult male vesicular gland cDNA, RIKEN full-length enriched library, clone:G630(	-1.3	0.039	-1.02	0.966	-1.37	0.328	-1.1	0.76	-1.2
1430335_a_at	Pax3	paired box gene 3	-1.09	0.867	-1.68	0.378	-1.04	0.946	-1.02	0.946	-1.21
1432312_a_at	4931440B09Rik	RIKEN cDNA 4931440B09 gene	-1.26	0.051	-1.18	0.75	-1.2	0.705	-1.29	0.215	-1.23
1433951_at	Arl5a	ADP-ribosylation factor-like 5A	-1.06	0.474	-1.2	0.004	-1.42	0.042	-1.47	0.148	-1.29
1456516_x_at	Uap1 /// LOC64050	UDP-N-acetylglucosamine pyrophosphorylase 1 /// similar to UDP-N-acetylhexos	-1.25	0.468	-1.15	0.167	-1.24	0.007	-1.34	0.186	-1.24
1426147_s_at	Cldn10	claudin 10	-1.25	0.112	-1.32	0.693	-1.09	0.748	-1.47	0.005	-1.28
1431023_at	C030046E11Rik	RIKEN cDNA C030046E11 gene	-1.06	0.861	-1.36	0.634	-1.25	0.447	-1.72	0.302	-1.35
1444806_at	6720456B07Rik	RIKEN cDNA 6720456B07 gene	-1.22	0.563	-1.07	0.785	-1.39	0.1	-1.42	0.13	-1.27
1426807_at	Lta4h	Leukotriene A4 hydrolase	-1.12	0.129	-1.16	0.519	-1.39	0.131	-1.11	0.694	-1.19
1429480_at	1700011N24Rik	RIKEN cDNA 1700011N24 gene	-1.09	0.845	-1.5	0.071	-1.12	0.435	-2.22	0.301	-1.48
1457938_at	Ncor1	Nuclear receptor co-repressor 1	-1.44	0.39	-1.02	0.92	-1.25	0.356	-1.47	0.211	-1.29
1431913_a_at	Pde3a	phosphodiesterase 3A, cGMP inhibited	-1.02	0.971	-1.64	0.456	-1.13	0.801	-1.26	0.027	-1.26
1435157_at	5830454D03Rik	RIKEN cDNA 5830454D03 gene	-1.29	0.183	-1.16	0.211	-1.19	0.293	-1.06	0.85	-1.17
1420996_at	Plxna3	plexin A3	-1.61	0.048	-1.07	0.725	-1.08	0.339	-1.15	0.048	-1.23
1424632_a_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	-1.22	0.393	-1.15	0.189	-1.27	0.023	-1.18	0.228	-1.21

1440317_at	C130068B02Rik	RIKEN cDNA C130068B02 gene	-1.15	0.355	-1.01	0.941	-1.63	0.113	-1.34	0.157	-1.28
1430808_at	Tbc1d5	TBC1 domain family, member 5	-1.02	0.943	-1.45	0.013	-1.24	0.266	-1.53	0.248	-1.31
1436775_a_at	Ankrd17	ankyrin repeat domain 17	-1.16	0.412	-1.16	0.097	-1.33	0.092	-1.45	0.028	-1.27
1455676_x_at	Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	-1.36	0.081	-1.08	0.588	-1.22	0.367	-1.01	0.921	-1.17
1458292_at	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	-1.08	0.759	-1.47	0.183	-1.15	0.123	-1.16	0.271	-1.21
1459981_s_at	Rsbn1	rosbin, round spermatid basic protein 1	-1.24	0.451	-1.14	0.504	-1.26	0.126	-1.28	0.058	-1.23
1415785_a_at	Cct8	chaperonin subunit 8 (theta)	-1.27	0.167	-1.14	0.086	-1.23	0.053	-1.11	0.324	-1.19
1445042_at	Aass	Aminoadipate-semialdehyde synthase	-1.09	0.008	-1.59	0.386	-1.07	0.853	-1.22	0.668	-1.24
1428729_at	Krit1	KRIT1, ankyrin repeat containing	-1.21	0.004	-1.15	0.275	-1.27	0.333	-1.23	0.347	-1.22
1434966_at	Sfrs8	splicing factor, arginine/serine-rich 8	-1.16	0.431	-1.46	0.063	-1.08	0.221	-1.31	0.256	-1.25
1440856_at	Mapk8	mitogen activated protein kinase 8	-1.16	0.087	-1.12	0.289	-1.38	0.058	-1.32	0.256	-1.25
1433937_at	Trp53bp2	transformation related protein 53 binding protein 2	-1.38	0.352	-1.26	0.247	-1.04	0.597	-1.4	0.229	-1.27
1428210_s_at	Chuk	conserved helix-loop-helix ubiquitous kinase	-1.3	0.069	-1.15	0.308	-1.18	0.313	-1.63	0.06	-1.32
1442585_at	B230220N19Rik	RIKEN cDNA B230220N19 gene	-1.42	0.326	-1.12	0.843	-1.14	0.61	-1	0.989	-1.17
1419972_at	Slc35a5	Solute carrier family 35, member A5	-1.02	0.914	-1.31	0.55	-1.35	0.213	-1.58	0.399	-1.32
1416547_at	Ndufb3	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	-1.14	0.257	-1.22	0.065	-1.28	0.042	-1.23	0.072	-1.22
1428226_at	Ngdn	neuroguidin, EIF4E binding protein	-1.07	0.14	-1.35	0.065	-1.24	0.071	-1.38	0.017	-1.26
1419778_at	---	---	-1.06	0.935	-1.22	0.586	-1.4	0.139	-2.89	0.165	-1.64
1429779_at	Eif2c4	eukaryotic translation initiation factor 2C, 4	-1.32	0.453	-1.11	0.258	-1.22	0.349	-1.37	0.385	-1.25
1423248_at	Nktr	natural killer tumor recognition sequence	-1.18	0.366	-1.1	0.368	-1.38	0.216	-1.25	0.446	-1.23
1444273_at	AW555355	expressed sequence AW555355	-1.03	0.901	-1.33	0.006	-1.32	0.428	-1.73	0.175	-1.35
1443065_at	Rhbdd1	Rhomboid domain containing 1	-1.49	0.624	-1.15	0.603	-1.06	0.726	-1.04	0.839	-1.19
1448803_at	Golga4	golgi autoantigen, golgin subfamily a, 4	-1.02	0.823	-1.34	0.063	-1.32	0.191	-1.25	0.562	-1.23
1441705_at	AU015680	expressed sequence AU015680	-1.17	0.693	-1.25	0.619	-1.21	0.596	-1.91	0.116	-1.39
1435632_at	Nufip2	nuclear fragile X mental retardation protein interacting protein 2	-1.11	0.31	-1.15	0.224	-1.39	0.043	-1.2	0.379	-1.21
1428616_at	Zfp131	zinc finger protein 131	-1.03	0.833	-1.21	0.072	-1.45	0.004	-1.12	0.104	-1.2
1425346_at	Zfp318	zinc finger protein 318	-1.02	0.806	-1.21	0.025	-1.48	0.005	-2.12	0.123	-1.46
1451234_at	BC021381	cDNA sequence BC021381	-1.09	0.416	-1.18	0.275	-1.38	0.159	-1.29	0.457	-1.24
1418982_at	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	-1.4	0.29	-1.09	0.747	-1.18	0.424	-1.21	0.427	-1.22
1441208_at	Hdhd2	Haloacid dehalogenase-like hydrolase domain containing 2	-1.13	0.491	-1.26	0.255	-1.25	0.228	-1.28	0.249	-1.23
1451953_at	Smr2	submaxillary gland androgen regulated protein 2	-1.4	0.294	-1.06	0.93	-1.22	0.736	-1.13	0.772	-1.2
1428831_at	6230429P13Rik	RIKEN cDNA 6230429P13 gene	-1.03	0.84	-1.32	0.04	-1.33	0.058	-1.12	0.472	-1.2
1434999_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.11	0.536	-1.15	0.38	-1.41	0.036	-1.49	0.086	-1.29
1433640_at	Fubp1	Far upstream element (FUSE) binding protein 1	-1.37	0.312	-1.2	0.563	-1.09	0.6	-1.26	0.37	-1.23
1417488_at	Fosl1	fos-like antigen 1	-1.15	0.728	-1.4	0.167	-1.11	0.674	-1.67	0.365	-1.33
1433888_at	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	-1.46	0.305	-1.18	0.711	-1.06	0.805	-1	0.931	-1.17
1442089_at	---	---	-1.37	0.584	-1.1	0.855	-1.19	0.759	-2.39	0.064	-1.51
1454826_at	Zbtb11	zinc finger and BTB domain containing 11	-1.27	0.28	-1.21	0.152	-1.15	0.14	-1.32	0.07	-1.24
1443450_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.29	0.621	-1.22	0.668	-1.12	0.761	-1.2	0.498	-1.21
1437763_at	Dcun1d3	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	-1.2	0.44	-1.24	0.432	-1.18	0.281	-1.02	0.882	-1.16
1419114_at	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	-1.08	0.511	-1.31	0.014	-1.25	0.104	-1.04	0.723	-1.17
1430317_at	Ube2j2	ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	-1.09	0.818	-1.17	0.392	-1.4	0.208	-1.46	0.054	-1.28
1441604_at	Esd	Esterase D/formylglutathione hydrolase	-1.09	0.602	-1.2	0.403	-1.36	0.083	-1.28	0.214	-1.23
1460625_at	Gm1568	gene model 1568, (NCBI)	-1.24	0.799	-1.27	0.607	-1.12	0.78	-1.42	0.251	-1.26
1451391_at	2700050L05Rik	RIKEN cDNA 2700050L05 gene	-1.17	0.389	-1.14	0.475	-1.33	0.192	-1.08	0.648	-1.18
1439826_at	Hspa14	heat shock protein 14	-1.07	0.708	-1.73	0.012	-1.02	0.929	-1.36	0.304	-1.3
1444560_at	---	Transcribed locus	-1.13	0.497	-1.39	0.154	-1.14	0.287	-1.27	0.372	-1.23
1416694_at	Gk2	glycerol kinase 2	-1.64	0.216	-1.12	0.679	-1.02	0.974	-1.45	0.405	-1.31
1434749_at	BC067068	cDNA sequence BC067068	-1.5	0.002	-1.03	0.875	-1.18	0.206	-1.21	0.441	-1.23
1445831_at	---	---	-1.12	0.429	-1.04	0.73	-1.58	0.008	-1.1	0.685	-1.21
1427044_a_at	Amph	amphiphysin	-1.36	0.293	-1.15	0.762	-1.13	0.48	-2.17	0.115	-1.45
1436085_at	Zbtb34	zinc finger and BTB domain containing 34	-1.57	0.209	-1.18	0.458	-1	0.997	-1.23	0.522	-1.24
1422366_at	V1ra9	vomeronasal 1 receptor, A9	-1.23	0.119	-1.21	0.611	-1.18	0.588	-1.28	0.628	-1.23

1459966_at	Osbpl7	Oxysterol binding protein-like 7	-1.17	0.677	-1.05	0.905	-1.48	0.018	-1.54	0.314	-1.31
1434284_at	Bdp1	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	-1.13	0.632	-1.32	0.022	-1.19	0.091	-1.07	0.642	-1.18
1449217_at	Casp8ap2	caspase 8 associated protein 2	-1.17	0.371	-1.04	0.762	-1.48	0.011	-1.07	0.734	-1.19
1433417_at	8030497O21Rik	RIKEN cDNA 8030497O21 gene	-1.23	0.24	-1.23	0.312	-1.16	0.713	-1.51	0.405	-1.28
1436980_x_at	Cnot2	CCR4-NOT transcription complex, subunit 2	-1.03	0.734	-1.16	0.363	-1.53	0.042	-1.4	0.085	-1.28
1450486_a_at	Oprl1	opioid receptor-like 1	-1.29	0.583	-1.25	0.498	-1.1	0.874	-2.75	0.085	-1.6
1437643_at	Cenpj	centromere protein J	-1.29	0.149	-1.11	0.608	-1.23	0.433	-1.07	0.752	-1.18
1433740_at	2610301K12Rik	RIKEN cDNA 2610301K12 gene	-1.38	0.115	-1.07	0.588	-1.2	0.141	-1.27	0.263	-1.23
AFFX-MURINE_B2_	---	---	-1.11	0.039	-1.2	0.457	-1.33	0.001	-1.2	0.046	-1.21
1436032_at	---	Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I8300	-1.19	0.509	-1.28	0.26	-1.15	0.359	-2.01	0.099	-1.41
1446235_at	BC002199	cDNA sequence BC002199	-1.16	0.066	-1.1	0.536	-1.39	0.031	-1.22	0.52	-1.22
1442381_at	Mkln1	Muskelin 1, intracellular mediator containing kelch motifs	-1.12	0.271	-1.08	0.605	-1.51	0.024	-1.16	0.544	-1.21
1416275_at	Slc26a6	solute carrier family 26, member 6	-1.56	0.02	-1.02	0.929	-1.15	0.373	-1.53	0.094	-1.32
1446183_at	Als2	Amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	-1.31	0.183	-1.03	0.961	-1.32	0.386	-1.21	0.054	-1.22
1416006_at	Mdk	midkine	-1.15	0.281	-1.05	0.814	-1.51	0.001	-1.43	0.311	-1.28
1454521_at	2810421E14Rik	RIKEN cDNA 2810421E14 gene	-1.05	0.87	-1.34	0.409	-1.27	0.384	-1.35	0.48	-1.25
1453421_at	Srr	serine racemase	-1.05	0.78	-1.23	0.347	-1.38	0.138	-1.2	0.575	-1.22
1447406_at	---	PREDICTED: Mus musculus similar to Hemoglobin alpha subunit (Hemoglobin al	-1.45	0.331	-1.22	0.696	-1.02	0.955	-1.14	0.625	-1.21
1447947_at	Zfyve16	zinc finger, FYVE domain containing 16	-1.19	0.393	-1.13	0.67	-1.32	0.241	-1.18	0.585	-1.2
1440604_at	8030494B02Rik	Riken cDNA 8030494B02 gene	-1.01	0.916	-1.1	0.41	-1.68	0.224	-1.27	0.25	-1.27
1419555_at	Elf5	E74-like factor 5	-1.07	0.771	-1.24	0.103	-1.33	0.194	-1.12	0.826	-1.19
1439059_at	BC031748	CDNA sequence BC031748	-1.06	0.735	-1.12	0.505	-1.52	0.065	-1.56	0.111	-1.32
1446830_at	AU015892	expressed sequence AU015892	-1.22	0.739	-1.25	0.478	-1.15	0.783	-1.43	0.208	-1.26
1440369_at	Ptger3	Prostaglandin E receptor 3 (subtype EP3)	-1.21	0.637	-1.06	0.857	-1.4	0.018	-1.36	0.131	-1.26
1440551_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	-1.1	0.199	-1.07	0.442	-1.54	0.003	-1.3	0.095	-1.25
1429823_at	5430420E18Rik	RIKEN cDNA 5430420E18 gene	-1.08	0.876	-1.33	0.685	-1.23	0.605	-2.39	0.128	-1.51
1439771_s_at	D13Ertd608e	DNA segment, Chr 13, ERATO Doi 608, expressed	-1.33	0.462	-1.21	0.481	-1.1	0.692	-2.62	0.025	-1.56
1459238_at	---	---	-1.19	0.017	-1.11	0.416	-1.33	0.039	-1.3	0.309	-1.23
1433961_at	BC023814	cDNA sequence BC023814	-1.54	0.028	-1.01	0.93	-1.17	0.143	-1.44	0.012	-1.29
1453824_at	A930028L21Rik	RIKEN cDNA A930028L21 gene	-1.27	0.095	-1.26	0.252	-1.1	0.648	-1.36	0.373	-1.25
1429226_at	2310014F06Rik	RIKEN cDNA 2310014F06 gene	-1.19	0.489	-1.29	0.099	-1.15	0.301	-1.07	0.808	-1.17
1457677_at	BC057593	CDNA sequence BC057593	-1.2	0.135	-1.18	0.153	-1.24	0.435	-1.41	0.065	-1.26
1417154_at	Slc25a14	solute carrier family 25 (mitochondrial carrier, brain), member 14	-1.41	0.419	-1.09	0.84	-1.15	0.606	-1.29	0.318	-1.24
1426088_at	---	---	-1.04	0.746	-1.24	0.364	-1.37	0.144	-1.21	0.487	-1.22
1433757_a_at	Nisch	nischarin	-1.25	0.473	-1.01	0.933	-1.43	0.125	-1.65	0.143	-1.33
1428409_at	Nat13	N-acetyltransferase 13	-1.16	0.408	-1.12	0.057	-1.36	0.1	-1.29	0.193	-1.23
1416375_at	Ap3m1	adaptor-related protein complex 3, mu 1 subunit	-1.02	0.906	-1.41	0.066	-1.25	0.125	-1.38	0.002	-1.26
1420861_at	Dctn4	dynactin 4	-1.07	0.638	-1.04	0.741	-1.68	0.036	-1.05	0.536	-1.21
1451847_s_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-1.31	0.706	-1.11	0.734	-1.2	0.335	-1.79	0.215	-1.36
1439161_at	Saps3	SAPS domain family, member 3	-1.13	0.356	-1.06	0.337	-1.51	0.029	-1.31	0.056	-1.25
1449374_at	Pipox	pipecolic acid oxidase	-1.06	0.726	-1.17	0.108	-1.44	0.161	-1.9	0.378	-1.39
1434631_at	D3Ertd751e	DNA segment, Chr 3, ERATO Doi 751, expressed	-1.2	0.554	-1.45	0.008	-1.03	0.854	-1.42	0.205	-1.28
1426719_at	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	-1.13	0.065	-1.2	0.111	-1.3	0.33	-1.33	0.058	-1.24
1453381_at	C030033M12Rik	RIKEN cDNA C030033M12 gene	-1.04	0.845	-1.26	0.067	-1.35	0.229	-1.34	0.277	-1.25
1432792_at	4930401B11Rik	RIKEN cDNA 4930401B11 gene	-1.16	0.871	-1.3	0.631	-1.16	0.792	-1.15	0.826	-1.19
1458747_at	Fbxo45	F-box protein 45	-1.37	0.696	-1.05	0.946	-1.23	0.641	-1.11	0.638	-1.19
1433992_at	Shroom2 /// LOC67	shroom family member 2 /// similar to Apical-like protein (APXL protein)	-1.04	0.682	-1.33	0.027	-1.29	0.226	-1.19	0.665	-1.21
1451757_at	BC003883	cDNA sequence BC003883	-1.42	0.072	-1.12	0.748	-1.12	0.681	-1.92	0.019	-1.39
1434708_at	Vhlh	von Hippel-Lindau syndrome homolog	-1.24	0.097	-1.24	0.235	-1.14	0.422	-1.32	0.054	-1.23
1432548_at	Parp14	poly (ADP-ribose) polymerase family, member 14	-1.05	0.115	-1.16	0.757	-1.47	0.181	-1.7	0.117	-1.35
1451211_a_at	Lgtn	ligatin	-1.14	0.407	-1.21	0.028	-1.27	0.179	-1.11	0.347	-1.18
1446062_at	B830028B13Rik	RIKEN cDNA B830028B13 gene	-1.13	0.851	-1.2	0.65	-1.29	0.201	-1.46	0.389	-1.27
1417943_at	Gng4	guanine nucleotide binding protein (G protein), gamma 4 subunit	-1.92	0.283	-1.03	0.962	-1	0.998	-1.78	0.41	-1.43

1422435_at	2210010C04Rik	RIKEN cDNA 2210010C04 gene	-1.06	0.823	-1.02	0.946	-1.75	0.26	-1.58	0.4	-1.35
1419445_s_at	Sap18	Sin3-associated polypeptide 18	-1.14	0.144	-1.41	0.015	-1.1	0.572	-1.26	0.504	-1.23
1427055_at	Them4	thioesterase superfamily member 4	-1.05	0.803	-1.33	0.136	-1.27	0.179	-1.9	0.222	-1.39
1458311_at	Usp36	ubiquitin specific peptidase 36	-1.2	0.499	-1.06	0.8	-1.4	0.105	-1.08	0.838	-1.19
1428219_at	Rybp /// LOC62874	RING1 and YY1 binding protein /// similar to RING1 and YY1 binding protein	-1.12	0.234	-1.22	0.093	-1.28	0.04	-1.11	0.069	-1.18
1445827_at	Prkcbp1	Protein kinase C binding protein 1	-1.22	0.306	-1.17	0.279	-1.22	0.374	-1.05	0.788	-1.17
1455121_at	Lcor	ligand dependent nuclear receptor corepressor	-1.2	0.039	-1.13	0.193	-1.29	0.009	-1.01	0.956	-1.16
1439005_x_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	-1.25	0.511	-1.22	0.485	-1.14	0.29	-1.08	0.456	-1.17
1423551_at	Cdh13	cadherin 13	-1.22	0.06	-1.11	0.644	-1.28	0.495	-1.72	0.309	-1.33
1434957_at	Cdon	cell adhesion molecule-related/down-regulated by oncogenes	-1.3	0.046	-1.17	0.605	-1.16	0.713	-1.97	0.078	-1.4
1455668_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	-1.16	0.252	-1.33	0.073	-1.14	0.248	-1.15	0.201	-1.19
1430376_at	Lrrc9	leucine rich repeat containing 9	-1.04	0.95	-1.45	0.524	-1.19	0.772	-1.33	0.556	-1.25
1426695_at	9030624J02Rik	RIKEN cDNA 9030624J02 gene	-1.39	0.159	-1.06	0.845	-1.2	0.371	-1.28	0.351	-1.23
1443526_at	---	---	-1.12	0.414	-1.05	0.593	-1.53	0.101	-1.76	0.117	-1.37
1428507_at	Hdhd2	haloacid dehalogenase-like hydrolase domain containing 2	-1.24	0.014	-1.25	0.003	-1.12	0.425	-1.07	0.674	-1.17
1454697_at	Tloc1	translocation protein 1	-1.05	0.731	-1.14	0.111	-1.5	0.03	-1.05	0.595	-1.19
1434890_at	Opa1	optic atrophy 1 homolog (human)	-1.19	0.192	-1.15	0.066	-1.28	0.03	-1.32	0.121	-1.23
1420451_at	Accn5	amiloride-sensitive cation channel 5, intestinal	-1.22	0.693	-1.36	0.249	-1.06	0.909	-1.28	0.755	-1.23
1429675_at	1700023A16Rik	RIKEN cDNA 1700023A16 gene	-1.2	0.747	-1.29	0.641	-1.13	0.862	-2.11	0.449	-1.43
1428453_at	Nat12	N-acetyltransferase 12	-1.12	0.353	-1.15	0.033	-1.36	0.005	-1.21	0.152	-1.21
1450901_a_at	AW011752	expressed sequence AW011752	-1.16	0.31	-1.33	0.043	-1.14	0.26	-1.24	0.227	-1.21
1445374_at	Vti1a	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	-1.14	0.08	-1.13	0.59	-1.35	0.141	-1.2	0.329	-1.21
1446219_at	D930015E06Rik	RIKEN cDNA D930015E06 gene	-1.41	0.096	-1.15	0.736	-1.09	0.72	-1.06	0.607	-1.18
1454612_at	Rkhd2	ring finger and KH domain containing 2	-1.21	0.268	-1.03	0.82	-1.43	0.13	-1.13	0.444	-1.2
1424693_at	4933407N01Rik	RIKEN cDNA 4933407N01 gene	-1.19	0.038	-1.17	0.179	-1.24	0.388	-1.1	0.53	-1.18
1449630_s_at	Mark1	MAP/microtubule affinity-regulating kinase 1	-1.1	0.028	-1.47	0.219	-1.11	0.534	-1.31	0.117	-1.25
1420188_at	Syt6	synaptotagmin VI	-1.31	0.736	-1.34	0.52	-1.01	0.978	-1.1	0.728	-1.19
1440364_a_at	A230062G08Rik	RIKEN cDNA A230062G08 gene	-1.04	0.943	-1.59	0.035	-1.11	0.632	-1.73	0.029	-1.37
1422621_at	Ranbp2	RAN binding protein 2	-1.19	0.537	-1.21	0.109	-1.21	0.209	-1.04	0.839	-1.16
1454195_at	4933433G19Rik	RIKEN cDNA 4933433G19 gene	-1.12	0.674	-1.51	0.328	-1.06	0.819	-1.02	0.899	-1.18
1429060_at	---	---	-1.26	0.325	-1.34	0.061	-1.04	0.724	-1.29	0.372	-1.23
1423286_at	Cbln1	cerebellin 1 precursor protein	-1.63	0.089	-1.11	0.754	-1.02	0.942	-1.22	0.611	-1.24
1416947_s_at	Acaa1a /// Acaa1b	acetyl-Coenzyme A acyltransferase 1A /// acetyl-Coenzyme A acyltransferase 1B	-1.05	0.867	-1.73	0.235	-1.03	0.739	-1.38	0.241	-1.3
1443610_at	---	Transcribed locus	-1.73	0.015	-1.05	0.881	-1.04	0.876	-1.61	0.012	-1.36
1421664_a_at	Styx	phosphoserine/threonine/tyrosine interaction protein	-1.14	0.145	-1.1	0.619	-1.4	0.007	-1.21	0.041	-1.21
1425217_a_at	Synj2	synaptojanin 2	-1.38	0.751	-1.14	0.841	-1.12	0.811	-1.55	0.515	-1.3
1435198_at	LOC545228	hypothetical protein LOC545228	-1.27	0.128	-1.29	0.314	-1.07	0.712	-1.25	0.328	-1.22
1419637_s_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	-1.12	0.57	-1.41	0.069	-1.12	0.516	-1.37	0.204	-1.25
1419845_at	Dlx1as	distal-less homeobox 1, antisense	-1.55	0.136	-1.02	0.952	-1.15	0.792	-1.03	0.937	-1.19
1438783_at	LOC637870	similar to Nedd4 WW binding protein 4	-1.1	0.859	-1.3	0.527	-1.23	0.64	-1.93	0.184	-1.39
1437869_at	3222402P14Rik	RIKEN cDNA 3222402P14 gene	-1.04	0.84	-1.4	0.279	-1.22	0.438	-1.22	0.545	-1.22
1433331_at	C030046M01Rik	RIKEN cDNA C030046M01 gene	-1.15	0.821	-1.45	0.547	-1.07	0.937	-1.5	0.456	-1.29
1430131_at	Crry	complement receptor related protein	-1.07	0.777	-1.17	0.551	-1.41	0.222	-1.7	0.003	-1.34
1434787_at	Arf3	ADP-ribosylation factor 3	-1.11	0.555	-1.26	0.055	-1.25	0.375	-1.38	0.13	-1.25
1443758_at	Wdr18	WD repeat domain 18	-1.29	0.776	-1.25	0.623	-1.09	0.865	-1.58	0.331	-1.3
1416143_at	Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	-1.13	0.177	-1.23	0.097	-1.25	0.028	-1.03	0.809	-1.16
1443444_at	Mgat5	Mannoside acetylglucosaminyltransferase 5	-1.1	0.829	-1.19	0.683	-1.33	0.39	-1.48	0.127	-1.28
1452122_at	AI314180	expressed sequence AI314180	-1.14	0	-1.33	0.036	-1.15	0.583	-1.18	0.44	-1.2
1425287_at	Zfp189	zinc finger protein 189	-1.37	0.213	-1.15	0.334	-1.11	0.526	-1.4	0.11	-1.26
1459704_at	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	-1.25	0.128	-1.32	0.414	-1.06	0.859	-1.18	0.226	-1.2
1431381_at	3110005L24Rik	RIKEN cDNA 3110005L24 gene	-1.01	0.857	-1.45	0.115	-1.21	0.422	-1.51	0.011	-1.3
1460311_at	Srst	simple repeat sequence-containing transcript	-1.52	0.176	-1.12	0.855	-1.05	0.893	-2.78	0.111	-1.62
1444662_at	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)	-1.37	0.158	-1.16	0.257	-1.1	0.69	-1.14	0.402	-1.19

1434010_at	Als2cr13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (hum	-1.1	0.599	-1.22	0.095	-1.29	0.292	-1.21	0.28	-1.21
1439847_s_at	Klf12	Kruppel-like factor 12	-1.05	0.861	-1.01	0.967	-1.8	0.036	-1.63	0.292	-1.37
1421075_s_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	-1.13	0.496	-1.54	0.075	-1.03	0.705	-1.43	0.158	-1.29
1434389_at	AI449023	expressed sequence AI449023	-1.18	0.299	-1.15	0.303	-1.28	0.31	-1.19	0.176	-1.2
1451383_a_at	Chuk	conserved helix-loop-helix ubiquitous kinase	-1.15	0.057	-1.24	0.001	-1.21	0.03	-1.44	0.021	-1.26
1453191_at	Col27a1	procollagen, type XXVII, alpha 1	-1.19	0.195	-1.04	0.828	-1.44	0.035	-1.25	0.182	-1.23
1434100_x_at	Ppargc1a	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	-1.19	0.536	-1.25	0.514	-1.17	0.37	-1.13	0.856	-1.18
1428374_at	Glce	glucuronyl C5-epimerase	-1.03	0.85	-1.17	0.269	-1.49	0.046	-1.16	0.382	-1.21
1434933_at	5730557L09Rik	RIKEN cDNA 5730557L09 gene	-1.13	0.105	-1.06	0.394	-1.49	0.048	-1.12	0.338	-1.2
1440952_at	Smad7	MAD homolog 7 (Drosophila)	-1.41	0.236	-1.07	0.867	-1.17	0.658	-2.13	0.037	-1.45
1418322_at	Crem	cAMP responsive element modulator	-1.1	0.654	-1.21	0.305	-1.31	0.08	-1.17	0.409	-1.2
1436757_a_at	Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	-1.12	0.213	-1.24	0.258	-1.25	0	-1.01	0.857	-1.15
1444995_at	Cdyl2	Chromodomain protein, Y chromosome-like 2	-1.05	0.959	-1.66	0.311	-1.06	0.838	-1.12	0.603	-1.22
1453108_at	Arsk	arylsulfatase K	-1.19	0.114	-1.13	0.244	-1.3	0.164	-1.17	0.011	-1.19
1435333_at	1110007M04Rik	RIKEN cDNA 1110007M04 gene	-1.25	0.425	-1.09	0.597	-1.28	0.165	-1.04	0.884	-1.16
1444284_at	A130050O07Rik	RIKEN cDNA A130050O07 gene	-1.03	0.967	-1.85	0.316	-1.01	0.955	-3.92	0.327	-1.95
1446516_at	Bcl7c	B-cell CLL/lymphoma 7C	-1.42	0.413	-1.25	0.766	-1	0.98	-1.04	0.891	-1.18
1439121_at	H2-T22	histocompatibility 2, T region locus 22	-1.51	0.419	-1.05	0.925	-1.12	0.737	-1.93	0.097	-1.4
1459625_at	Frap1	FK506 binding protein 12-rapamycin associated protein 1	-1.01	0.955	-1.29	0.211	-1.36	0.224	-1.12	0.156	-1.19
1424361_at	BC019943	cDNA sequence BC019943	-1.24	0.245	-1.17	0.248	-1.19	0.319	-1.25	0.568	-1.21
1445844_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930547H19 pr	-1.24	0.683	-1.19	0.658	-1.16	0.636	-1.05	0.908	-1.16
1423869_s_at	Txnrd3	thioredoxin reductase 3	-1.12	0.579	-1.32	0.329	-1.18	0.458	-1.18	0.501	-1.2
1433342_at	5730416F02Rik	RIKEN cDNA 5730416F02 gene	-1.17	0.795	-1.48	0.394	-1.03	0.833	-1.82	0.23	-1.37
1417194_at	Sod2	superoxide dismutase 2, mitochondrial	-1.1	0.741	-1.04	0.846	-1.58	0.056	-1.75	0.017	-1.37
1440042_at	Ank2	ankyrin 2, brain	-1.12	0.492	-1.3	0.691	-1.19	0.14	-1.28	0.273	-1.22
1434723_at	AI426748	expressed sequence AI426748	-1.1	0.696	-1.45	0.378	-1.11	0.262	-1.34	0.074	-1.25
1416201_at	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	-1.21	0.314	-1.21	0.151	-1.18	0.068	-1.09	0.693	-1.17
1446324_at	Cacna2d1	Calcium channel, voltage-dependent, alpha2/delta subunit 1	-1.04	0.715	-1.11	0.785	-1.57	0.029	-1.28	0.282	-1.25
1421765_at	Pax5	paired box gene 5	-1.35	0.328	-1.23	0.598	-1.05	0.909	-5.14	0.051	-2.19
1449867_at	Hoxc9	homeo box C9	-1.07	0.504	-1.35	0.161	-1.21	0.384	-2.47	0.415	-1.53
1459875_x_at	5730494M16Rik	RIKEN cDNA 5730494M16 gene	-1.36	0.129	-1.17	0.373	-1.1	0.369	-1.21	0.398	-1.21
1448830_at	Dusp1	dual specificity phosphatase 1	-1.18	0.674	-1.32	0.28	-1.11	0.631	-1.13	0.726	-1.18
1459460_at	---	---	-1.05	0.905	-1.19	0.519	-1.41	0.418	-1.16	0.72	-1.2
1427224_at	Acsm2	Acyl-CoA synthetase medium-chain family member 2	-1.12	0.863	-1.25	0.741	-1.23	0.611	-1.89	0.056	-1.37
1441970_at	E430010N07Rik	RIKEN cDNA E430010N07 gene	-1.05	0.746	-1.02	0.93	-1.78	0.035	-1.13	0.606	-1.24
1446188_at	Lrriq2	leucine-rich repeats and IQ motif containing 2	-1.54	0.381	-1.12	0.467	-1.04	0.853	-1.3	0.299	-1.25
1457715_at	1010001B22Rik	RIKEN cDNA 1010001B22 gene	-1.25	0.778	-1.21	0.432	-1.14	0.49	-1.16	0.756	-1.19
1435461_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	-1.07	0.271	-1.08	0.301	-1.57	0.08	-1.37	0.216	-1.27
1424372_at	Mrpl32	mitochondrial ribosomal protein L32	-1.21	0.017	-1.09	0.137	-1.32	0.128	-1.11	0.639	-1.18
1427043_s_at	Cova1	cytosolic ovarian carcinoma antigen 1	-1.2	0.019	-1.1	0.514	-1.32	0.014	-1.25	0.426	-1.22
1456397_at	Cdh4	cadherin 4	-1.27	0.09	-1.09	0.716	-1.25	0.243	-1.62	0.004	-1.31
1419183_at	Papd4	PAP associated domain containing 4	-1.28	0.263	-1.11	0.323	-1.22	0.061	-1.03	0.828	-1.16
1439721_at	C85627	expressed sequence C85627	-1.18	0.641	-1.19	0.702	-1.23	0.542	-1	0.999	-1.15
1456274_at	C230071H18Rik	RIKEN cDNA C230071H18 gene	-1.58	0.319	-1.11	0.684	-1.03	0.888	-2.53	0.053	-1.56
1442195_at	BB283564	expressed sequence BB283564	-1.05	0.93	-1.2	0.474	-1.39	0.049	-1.27	0.263	-1.23
1454369_a_at	Nfatc4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	-1.25	0.34	-1.26	0.695	-1.1	0.667	-1.08	0.763	-1.17
1442053_at	Phkb	Phosphorylase kinase beta	-1.15	0.713	-1.3	0.206	-1.15	0.527	-1.56	0.365	-1.29
1455160_at	2610203C20Rik	RIKEN cDNA 2610203C20 gene	-1.28	0.32	-1.13	0.472	-1.19	0.479	-1.08	0.793	-1.17
1422442_at	Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	-1.18	0.014	-1.21	0.003	-1.2	0.033	-1.2	0.213	-1.2
1428563_at	Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	-1.01	0.907	-1.68	0.044	-1.09	0.716	-1.38	0.207	-1.29
1433749_at	Gna13	guanine nucleotide binding protein, alpha 13	-1.08	0.597	-1.26	0.084	-1.27	0.101	-1.1	0.598	-1.18
1420952_at	Son	Son cell proliferation protein	-1.06	0.578	-1.18	0.221	-1.41	0.09	-1.29	0.198	-1.23
1439292_at	2210408F21Rik	RIKEN cDNA 2210408F21 gene	-1.04	0.865	-1.17	0.556	-1.45	0.139	-1.41	0.21	-1.27

1438805_at	9230106B05Rik	RIKEN cDNA 9230106B05 gene	-1	0.991	-1.76	0.262	-1.06	0.865	-2.32	0.273	-1.54
1425309_at	Catsper2	cation channel, sperm associated 2	-1.29	0.096	-1.28	0.088	-1.05	0.833	-1.09	0.437	-1.18
1455637_x_at	LOC245305	Similar to hypothetical protein FLJ38281	-1.05	0.867	-1.23	0.165	-1.34	0.22	-1.37	0.222	-1.25
1455070_at	Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)	-1.19	0.023	-1.14	0.061	-1.26	0.129	-1.28	0.056	-1.22
1457298_at	---	---	-1.03	0.944	-1.27	0.646	-1.34	0.127	-1.39	0.385	-1.26
1442281_at	D4Ertd796e	DNA segment, Chr 4, ERATO Doi 796, expressed	-1.14	0.084	-1.49	0.404	-1.04	0.858	-1.94	0.127	-1.4
1443187_at	---	---	-1.89	0.383	-1.02	0.971	-1.01	0.987	-1.97	0.094	-1.47
1434609_at	B930007L02Rik	RIKEN cDNA B930007L02 gene	-1.23	0.156	-1.25	0.004	-1.11	0.447	-1.04	0.349	-1.16
1446720_at	Alcam	Activated leukocyte cell adhesion molecule	-1.07	0.87	-1.12	0.576	-1.47	0.144	-1.32	0.144	-1.25
1435251_at	Snx13	sorting nexin 13	-1.21	0.142	-1.14	0.048	-1.25	0.179	-1.35	0.258	-1.24
1455702_at	---	---	-1.03	0.925	-1.38	0.257	-1.23	0.543	-1.29	0.317	-1.23
1452502_at	Serf1	small EDRK-rich factor 1	-1.27	0.438	-1.07	0.454	-1.28	0.341	-1.11	0.774	-1.18
1419180_at	Bcl9l	B-cell CLL/lymphoma 9-like	-1.15	0.202	-1.2	0.251	-1.25	0.304	-1.17	0.557	-1.19
1435511_at	Syn2	synapsin II	-1.2	0.111	-1.16	0.702	-1.23	0.501	-1.53	0.097	-1.28
1459119_at	Cenpo	centromere protein O	-1.21	0.566	-1	0.998	-1.47	0.148	-1.17	0.547	-1.21
1455681_at	Zfp369	zinc finger protein 369	-1.22	0.066	-1.14	0.294	-1.23	0.293	-1.27	0.455	-1.22
1429004_at	Phip	pleckstrin homology domain interacting protein	-1.16	0.245	-1.1	0.367	-1.36	0.063	-1.38	0.104	-1.25
1456162_x_at	Add3	adducin 3 (gamma)	-1.26	0.394	-1.07	0.527	-1.29	0.281	-1.7	0.234	-1.33
1442643_at	Jmjd3	jumonji domain containing 3	-1.29	0.692	-1.36	0.038	-1	0.99	-1.77	0.231	-1.36
1429137_at	2810422O20Rik	RIKEN cDNA 2810422O20 gene	-1.13	0.696	-1.22	0.036	-1.25	0.22	-1.76	0.049	-1.34
1429868_at	---	---	-1.11	0.605	-1.34	0.235	-1.16	0.29	-1.4	0.545	-1.25
1416642_a_at	Tpt1	tumor protein, translationally-controlled 1	-1.13	0.015	-1.16	0.481	-1.31	0.01	-1.2	0.013	-1.2
1444149_at	Zfp96	zinc finger protein 96	-1.02	0.925	-1.07	0.869	-1.69	0.073	-1.15	0.39	-1.23
1439486_at	Kcnt1	potassium channel, subfamily T, member 1	-1.18	0.451	-1.18	0.698	-1.22	0.369	-1.57	0.352	-1.29
1456116_at	Ctnnd2	catenin (cadherin associated protein), delta 2	-1.02	0.924	-1.14	0.751	-1.52	0.08	-1.28	0.476	-1.24
1447575_at	---	---	-1.01	0.808	-1.12	0.738	-1.59	0.268	-1.13	0.383	-1.21
1443779_s_at	Lcor	ligand dependent nuclear receptor corepressor	-1.02	0.826	-1.17	0.038	-1.49	0.012	-1.26	0.003	-1.23
1455158_at	Itga3	integrin alpha 3	-1.25	0.052	-1.17	0.124	-1.17	0.421	-1.07	0.819	-1.16
1449410_a_at	Gas5	growth arrest specific 5	-1.14	0.102	-1.14	0.337	-1.33	0.179	-1.46	0.004	-1.27
1419916_at	Rnf20	Ring finger protein 20	-1.43	0.496	-1.05	0.897	-1.16	0.412	-1.08	0.668	-1.18
1431425_a_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	-1.18	0.245	-1.27	0.697	-1.13	0.44	-1.18	0.537	-1.19
1443899_at	BC028799 /// 4922	cDNA sequence BC028799 /// RIKEN cDNA 4922501C03 gene	-1.15	0.327	-1.08	0.628	-1.4	0.069	-1.15	0.409	-1.19
1444772_at	Smyd3	SET and MYND domain containing 3	-1.33	0.31	-1.13	0.522	-1.15	0.328	-1.4	0.119	-1.25
1441359_at	9230115F04Rik	RIKEN cDNA 9230115F04 gene	-1.1	0.641	-1.28	0.503	-1.22	0.102	-2.71	0.062	-1.58
1429806_at	Eral1	Era (G-protein)-like 1 (E. coli)	-1.01	0.968	-1.27	0.292	-1.37	0.363	-1.24	0.36	-1.22
1421742_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	-1.16	0.194	-1.12	0.725	-1.33	0.513	-1.89	0.099	-1.37
1416064_a_at	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)	-1.12	0.591	-1.09	0.647	-1.43	0.088	-1.28	0.063	-1.23
1436344_at	---	---	-1.2	0.324	-1.3	0.084	-1.1	0.646	-1.29	0.063	-1.22
1460317_s_at	Gna13	guanine nucleotide binding protein, alpha 13	-1.33	0.221	-1.12	0.362	-1.16	0.592	-1.22	0.15	-1.21
1447700_x_at	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	-1.15	0.323	-1.18	0.775	-1.26	0.247	-1.51	0.269	-1.27
1417747_at	Cplx1	complexin 1	-1.16	0.39	-1.39	0.101	-1.07	0.679	-1.57	0.011	-1.3
1438876_at	A130014A01Rik	RIKEN cDNA A130014A01 gene	-1.43	0.081	-1.12	0.686	-1.09	0.725	-1.24	0.584	-1.22
1437706_x_at	Rps14 /// LOC6728	ribosomal protein S14 /// similar to ribosomal protein S14	-1.13	0.057	-1.17	0.186	-1.3	0.007	-1.19	0.039	-1.2
1433732_x_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	-1.09	0.655	-1.29	0.216	-1.22	0.336	-1.23	0.352	-1.21
1417388_at	Bex2	brain expressed X-linked 2	-1.01	0.968	-1.11	0.806	-1.61	0.163	-1.14	0.709	-1.22
1447432_s_at	Zfp263	zinc finger protein 263	-1.16	0.37	-1.07	0.651	-1.39	0.057	-1.71	0.117	-1.33
1452061_s_at	Strbp	spermatid perinuclear RNA binding protein	-1.28	0.123	-1.22	0.104	-1.1	0.39	-1.94	0.152	-1.38
1443843_x_at	LOC433546	similar to ribosomal protein L9	-1.15	0.061	-1.14	0.536	-1.31	0.001	-1.25	0.004	-1.21
1418433_at	Cab39	calcium binding protein 39	-1.14	0.388	-1.19	0.112	-1.26	0.116	-1.07	0.688	-1.16
1452141_a_at	Sepp1	selenoprotein P, plasma, 1	-1.07	0.045	-1.17	0.435	-1.38	0.001	-1.13	0.338	-1.19
1429503_at	2900024C23Rik	RIKEN cDNA 2900024C23 gene	-1.36	0.111	-1.15	0.347	-1.1	0.505	-1.68	0.134	-1.32
1458079_at	Usp40	ubiquitin specific peptidase 40	-1.11	0.096	-1.16	0.388	-1.33	0.315	-1.7	0.065	-1.33
1439804_at	2310015A10Rik	RIKEN cDNA 2310015A10 gene	-1.69	0.204	-1.05	0.814	-1.03	0.902	-1.24	0.53	-1.25

1422626_at	Mmp16	matrix metallopeptidase 16	-1.46	0.436	-1.13	0.72	-1.05	0.878	-1.28	0.136	-1.23
1436506_a_at	1110008H02Rik	RIKEN cDNA 1110008H02 gene	-1.3	0.026	-1.05	0.534	-1.26	0.154	-1.42	0.003	-1.26
1430245_at	---	---	-1.23	0.262	-1.07	0.64	-1.3	0.116	-1.16	0.632	-1.19
1428495_at	2410003K15Rik	RIKEN cDNA 2410003K15 gene	-1.13	0.126	-1.23	0.023	-1.23	0.153	-1.17	0.368	-1.19
1456702_x_at	Mat2a	methionine adenosyltransferase II, alpha	-1.24	0.523	-1.13	0.479	-1.22	0.189	-1.21	0.11	-1.2
1455073_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.1	0.503	-1.08	0.349	-1.48	0.099	-1.21	0.301	-1.22
1418607_at	Zfp99	zinc finger protein 99	-1.12	0.205	-1.27	0.152	-1.19	0.349	-1.23	0.201	-1.2
1431190_x_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	-1.17	0.156	-1.28	0.107	-1.14	0.262	-1.16	0.379	-1.19
1442715_at	---	---	-1.48	0.124	-1.14	0.859	-1.03	0.887	-1.04	0.907	-1.17
1434596_at	---	PREDICTED: Mus musculus hypothetical protein LOC625568 (LOC625568), mR	-1.09	0.429	-1.08	0.907	-1.49	0.273	-1.88	0.22	-1.38
1452501_at	Cyp2c38	cytochrome P450, family 2, subfamily c, polypeptide 38	-1.13	0.439	-1.11	0.54	-1.37	0.109	-1.92	0.169	-1.38
1445998_at	Prkg1	Protein kinase, cGMP-dependent, type I	-1.01	0.907	-1.1	0.886	-1.61	0.06	-1.36	0.578	-1.27
1430065_at	A930005N03Rik	RIKEN cDNA A930005N03 gene	-1.25	0.743	-1.19	0.759	-1.14	0.588	-2.3	0.122	-1.47
1453158_at	Zfp622	zinc finger protein 622	-1.19	0.814	-1.22	0.749	-1.17	0.579	-1.25	0.658	-1.21
1416841_at	1110059E24Rik	RIKEN cDNA 1110059E24 gene	-1.27	0.113	-1.19	0.001	-1.12	0.374	-1.77	0.11	-1.34
1453804_a_at	Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	-1.09	0.361	-1.29	0.038	-1.21	0.094	-1.21	0.18	-1.2
1416795_at	Cryl1	crystallin, lamda 1	-1.32	0.077	-1.31	0.497	-1	0.985	-1.02	0.925	-1.16
1415970_at	Cox6c	cytochrome c oxidase, subunit VIc	-1.22	0.057	-1.19	0.08	-1.16	0.133	-1.08	0.156	-1.17
1438555_x_at	4933405I11Rik /// M	RIKEN cDNA 4933405I11 gene /// mucin 4	-1.32	0.468	-1.11	0.849	-1.16	0.157	-3.29	0.292	-1.72
1443528_at	Ttbk1	tau tubulin kinase 1	-1.22	0.54	-1.41	0.266	-1.01	0.951	-1.02	0.775	-1.17
1436960_at	Brd3	bromodomain containing 3	-1.1	0.104	-1.18	0.514	-1.32	0.202	-1.09	0.022	-1.17
1433856_at	Hisppd1	histidine acid phosphatase domain containing 1	-1.3	0.067	-1.19	0.434	-1.1	0.185	-1.07	0.328	-1.17
1452961_at	1200009O22Rik	RIKEN cDNA 1200009O22 gene	-1.29	0.278	-1.2	0.434	-1.1	0.541	-1.17	0.218	-1.19
1416446_at	Tmem30a	transmembrane protein 30A	-1.02	0.749	-1.28	0.036	-1.32	0.073	-1.38	0.239	-1.25
1451133_s_at	Tmem168	transmembrane protein 168	-1.07	0.779	-1.11	0.529	-1.45	0.034	-1.48	0.181	-1.28
1452206_at	Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	-1.15	0.24	-1.24	0.026	-1.19	0.181	-1.13	0.08	-1.18
1434485_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	-1.19	0.077	-1.34	0.206	-1.08	0.527	-1.16	0.556	-1.19
1451199_at	Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1	-1.29	0.094	-1.27	0.487	-1.05	0.724	-1.35	0.117	-1.24
1438736_at	Thoc2	THO complex 2	-1.1	0.557	-1.13	0.125	-1.38	0.045	-1.07	0.815	-1.17
1433942_at	Myo6	myosin VI	-1.1	0.299	-1.34	0.01	-1.16	0.491	-1.17	0.015	-1.19
1453776_at	5730407K14Rik	RIKEN cDNA 5730407K14 gene	-1.1	0.399	-1.18	0.449	-1.32	0.176	-1.38	0.002	-1.24
1447423_at	---	---	-1.24	0.46	-1.01	0.98	-1.39	0.145	-1.06	0.906	-1.17
1453701_at	4921515E04Rik	RIKEN cDNA 4921515E04 gene	-1.33	0.693	-1.17	0.789	-1.09	0.667	-3.04	0.02	-1.66
1456761_at	D630030B22Rik	RIKEN cDNA D630030B22 gene	-1.37	0.433	-1.16	0.674	-1.08	0.807	-1.06	0.892	-1.17
1450043_at	Fzd7	frizzled homolog 7 (Drosophila)	-1.04	0.889	-1.51	0.502	-1.12	0.557	-1.5	0.195	-1.29
1441331_at	A230061C15Rik	RIKEN cDNA A230061C15 gene	-1.13	0.256	-1.06	0.595	-1.46	0.077	-1.84	0.172	-1.37
1454822_x_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	-1.35	0.313	-1.01	0.968	-1.27	0.587	-1.24	0.385	-1.22
1458607_at	Tgfbr2	Transforming growth factor, beta receptor II	-1.05	0.933	-1.18	0.754	-1.39	0.088	-1.61	0.136	-1.31
1452708_a_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	-1.16	0.723	-1.13	0.509	-1.29	0.083	-1.13	0.668	-1.18
1427269_at	Sfrs11	splicing factor, arginine/serine-rich 11	-1.21	0.451	-1.24	0.088	-1.13	0.222	-1.14	0.35	-1.18
1424519_at	Mtg1	mitochondrial GTPase 1 homolog (S. cerevisiae)	-1.12	0.354	-1.38	0.009	-1.11	0.462	-1.02	0.788	-1.16
1446483_at	Akr1e1	aldo-keto reductase family 1, member E1	-1.08	0.657	-1.32	0.195	-1.2	0.491	-1.8	0.344	-1.35
1417007_a_at	Vps4b	vacuolar protein sorting 4b (yeast)	-1.2	0.438	-1.25	0.05	-1.13	0.252	-1.48	0.114	-1.26
1416978_at	Fcgrt	Fc receptor, IgG, alpha chain transporter	-1.1	0.437	-1.15	0.096	-1.36	0.204	-1.03	0.932	-1.16
1449055_x_at	Pcbp4	poly(rC) binding protein 4	-1.29	0.119	-1.08	0.645	-1.22	0.002	-1.59	0.121	-1.3
1427484_at	Eml5	echinoderm microtubule associated protein like 5	-1.26	0.004	-1.15	0.476	-1.17	0.726	-1.11	0.594	-1.17
1445163_at	---	---	-1.25	0.808	-1.27	0.416	-1.07	0.655	-1.04	0.964	-1.16
1457082_at	Foxp3	forkhead box P3	-1.38	0.688	-1.05	0.929	-1.19	0.552	-2.4	0.068	-1.5
1457176_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.07	0.521	-1.23	0.382	-1.29	0.238	-1.44	0.18	-1.26
1431638_at	4930592A05Rik	RIKEN cDNA 4930592A05 gene	-1.01	0.824	-1.35	0.194	-1.26	0.552	-1.77	0.247	-1.35
1460411_s_at	AW548124	expressed sequence AW548124	-1.24	0.232	-1.35	0.163	-1.02	0.904	-1.35	0.424	-1.24
1438283_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	-1.39	0.301	-1.05	0.89	-1.18	0.429	-1	0.99	-1.16
1422595_s_at	5730470L24Rik	RIKEN cDNA 5730470L24 gene	-1.06	0.736	-1.13	0.163	-1.44	0.009	-1.52	0.207	-1.29

1460663_at	Cckbr	cholecystokinin B receptor	-1.15	0.109	-1.05	0.677	-1.43	0.554	-1.24	0.487	-1.22
1456548_at	Mtdh	Metadherin	-1.04	0.951	-1.28	0.166	-1.28	0.285	-1.15	0.528	-1.19
1448271_a_at	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	-1.36	0.043	-1.18	0.01	-1.07	0.659	-1.09	0.719	-1.17
1438868_at	D14Ertd668e	DNA segment, Chr 14, ERATO Doi 668, expressed	-1.43	0.052	-1.08	0.317	-1.12	0.497	-1.79	0.053	-1.35
1416056_a_at	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-1.1	0.135	-1.17	0.069	-1.31	0.025	-1.26	0.265	-1.21
1460391_at	2810409H07Rik	RIKEN cDNA 2810409H07 gene	-1.18	0.436	-1.19	0.028	-1.19	0.51	-1.07	0.809	-1.16
1457889_at	AU014972	expressed sequence AU014972	-1.01	0.974	-1.18	0.687	-1.47	0.124	-1.14	0.469	-1.2
1441003_at	Ercc4	excision repair cross-complementing rodent repair deficiency, complementation g	-1.26	0.437	-1.08	0.775	-1.24	0.257	-1.22	0.569	-1.2
1455729_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	-1.11	0.535	-1.08	0.573	-1.44	0.011	-1.2	0.582	-1.21
1455717_s_at	Daam2	dishevelled associated activator of morphogenesis 2	-1.11	0.546	-1.07	0.635	-1.45	0.333	-1.06	0.636	-1.17
1450937_at	Lin7c	lin-7 homolog C (C. elegans)	-1.29	0.12	-1.05	0.659	-1.26	0.128	-1.4	0.132	-1.25
1421852_at	Kcnk5	potassium channel, subfamily K, member 5	-1.31	0.379	-1.31	0.484	-1	0.983	-1.48	0.26	-1.28
1437240_at	Pgm2	phosphoglucomutase 2	-1.16	0.542	-1.38	0.211	-1.06	0.833	-1.67	0.272	-1.32
1456383_at	Rsl1d1	ribosomal L1 domain containing 1	-1.29	0.146	-1.27	0.004	-1.05	0.813	-1.1	0.763	-1.17
1438506_s_at	Pdss1	Prenyl (solanesyl) diphosphate synthase, subunit 1	-1.25	0.49	-1.06	0.708	-1.29	0.224	-1.77	0.113	-1.34
1428921_at	2810021B07Rik	RIKEN cDNA 2810021B07 gene	-1.05	0.625	-1.2	0.348	-1.36	0.023	-1.24	0.382	-1.21
1417766_at	Cyb5b	cytochrome b5 type B	-1.2	0.12	-1.1	0.402	-1.28	0.041	-1.3	0.238	-1.22
1458077_at	Baz2b	Bromodomain adjacent to zinc finger domain, 2B	-1.11	0.678	-1.25	0.134	-1.22	0.353	-1.74	0.192	-1.33
1427097_at	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	-1.21	0.135	-1.17	0.044	-1.18	0.294	-1.17	0.44	-1.18
1418007_at	1810007M14Rik	RIKEN cDNA 1810007M14 gene	-1.33	0.309	-1.15	0.328	-1.11	0.59	-1.23	0.432	-1.2
1447964_at	Ttl	tubulin tyrosine ligase	-1.25	0.436	-1.28	0.541	-1.06	0.873	-1.34	0.582	-1.23
1435106_at	3732412D22Rik	RIKEN cDNA 3732412D22 gene	-1.19	0.19	-1.02	0.912	-1.42	0.102	-1.67	0.168	-1.33
1451495_at	Wac	WW domain containing adaptor with coiled-coil	-1.18	0.292	-1.14	0.242	-1.25	0.125	-1.12	0.106	-1.17
1431467_at	4931402G19Rik	RIKEN cDNA 4931402G19 gene	-1.43	0	-1.16	0.656	-1.04	0.684	-1.73	0.533	-1.34
1435164_s_at	Ube1c	ubiquitin-activating enzyme E1C	-1.32	0.171	-1.08	0.507	-1.2	0.229	-1.19	0.413	-1.19
1438390_s_at	Pttg1	pituitary tumor-transforming 1	-1.09	0.342	-1.28	0.147	-1.21	0.037	-1.17	0.33	-1.19
1427542_at	5330439J01Rik	RIKEN cDNA 5330439J01 gene	-1.08	0.663	-1.4	0.224	-1.14	0.655	-1.24	0.22	-1.21
1448702_at	Ier3ip1	immediate early response 3 interacting protein 1	-1.18	0.087	-1.03	0.642	-1.42	0.001	-1.08	0.618	-1.18
1430318_at	Sat2	spermidine/spermine N1-acetyl transferase 2	-1.24	0.299	-1.11	0.009	-1.22	0.269	-1.23	0.277	-1.2
1418515_at	Mtf2	metal response element binding transcription factor 2	-1.07	0.636	-1.28	0.091	-1.24	0.299	-1.02	0.884	-1.15
1455387_at	Nufip2	nuclear fragile X mental retardation protein interacting protein 2	-1.14	0.352	-1.04	0.695	-1.46	0.078	-1.25	0.576	-1.22
1428826_at	Nr6a1	nuclear receptor subfamily 6, group A, member 1	-1.02	0.705	-1.51	0.051	-1.13	0.375	-1.1	0.843	-1.19
1456729_x_at	Rtel1	regulator of telomere elongation helicase 1	-1.14	0.698	-1.42	0.094	-1.06	0.773	-1.23	0.196	-1.21
1441981_at	Tmprss11f	transmembrane protease, serine 11f	-1.08	0.922	-1.36	0.646	-1.16	0.721	-2.24	0.117	-1.46
1421089_a_at	2610028A01Rik	RIKEN cDNA 2610028A01 gene	-1.11	0.431	-1.24	0.509	-1.22	0.506	-1.26	0.116	-1.21
1455077_a_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// RIKEN cD	-1.14	0.043	-1.07	0.154	-1.4	0.005	-1.24	0.05	-1.21
1423504_at	Jam3	junction adhesion molecule 3	-1.05	0.782	-1.01	0.977	-1.72	0.109	-1.35	0.531	-1.28
1434481_at	4121402D02Rik	RIKEN cDNA 4121402D02 gene	-1.09	0.606	-1.31	0.084	-1.19	0.039	-1.14	0.323	-1.18
1421993_a_at	Tmem134	transmembrane protein 134	-1.23	0.459	-1.25	0.36	-1.09	0.789	-1.24	0.605	-1.2
1418313_at	Zfp276	zinc finger protein (C2H2 type) 276	-1.31	0.375	-1.25	0.344	-1.04	0.729	-1.14	0.704	-1.19
1428282_at	Tbce	tubulin-specific chaperone e	-1.18	0.384	-1.11	0.316	-1.29	0.069	-1.23	0.216	-1.2
1431726_a_at	Tmem80	transmembrane protein 80	-1.12	0.645	-1.25	0.021	-1.19	0.237	-1.06	0.25	-1.16
1445321_at	E430025E21Rik	RIKEN cDNA E430025E21 gene	-1.03	0.907	-1.49	0.01	-1.13	0.47	-1.33	0.426	-1.25
1437322_at	Rbm4	RNA binding motif protein 4	-1.08	0.582	-1.21	0.394	-1.29	0.304	-1.09	0.183	-1.17
1428149_at	Coro7	coronin 7	-1.03	0.93	-1.29	0.04	-1.29	0.137	-1.71	0.121	-1.33
1453518_at	Pdzd11	PDZ domain containing 11	-1.57	0.056	-1.01	0.988	-1.12	0.778	-1.32	0.441	-1.25
1435302_at	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.23	0.607	-1.07	0.775	-1.29	0.101	-1.14	0.303	-1.18
1417285_a_at	Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	-1.11	0.082	-1.15	0.234	-1.32	0.009	-1.11	0.434	-1.17
1443205_at	D5Buc30e	DNA segment, Chr 5, Bucan 30 expressed	-1.5	0.291	-1.06	0.858	-1.09	0.846	-1.18	0.714	-1.21
1438591_at	2610019A05Rik	RIKEN cDNA 2610019A05 gene	-1.33	0.278	-1.11	0.76	-1.14	0.63	-1.32	0.11	-1.23
1436667_at	Slc6a20	solute carrier family 6 (neurotransmitter transporter), member 20	-1.09	0.502	-1.06	0.853	-1.51	0.397	-1.23	0.166	-1.22
1435070_at	Aebp2	AE binding protein 2	-1.1	0.602	-1.1	0.328	-1.41	0.068	-1.28	0.162	-1.22
1443520_at	AU022870	Expressed sequence AU022870	-1.02	0.936	-1.23	0.469	-1.36	0.32	-1.15	0.669	-1.19

1460744_at	2810002I04Rik	RIKEN cDNA 2810002I04 gene	-1.11	0.61	-1.02	0.968	-1.55	0.184	-1.53	0.307	-1.3
1438296_at	C430010C01	hypothetical protein C430010C01	-1.2	0.576	-1.41	0.501	-1.02	0.963	-2.11	0.165	-1.43
1420023_at	Etf1	eukaryotic translation termination factor 1	-1.39	0.03	-1.09	0.739	-1.12	0.566	-1.01	0.958	-1.15
1434941_s_at	2610101J03Rik	RIKEN cDNA 2610101J03 gene	-1.06	0.766	-1.09	0.531	-1.5	0.021	-1.06	0.716	-1.18
1442355_at	LOC546100	hypothetical LOC546100	-1.05	0.653	-1.59	0.535	-1.06	0.823	-1.26	0.053	-1.24
1440909_at	Irgc1	immunity-related GTPase family, cinema 1	-1.07	0.826	-1.47	0.476	-1.1	0.542	-1.01	0.965	-1.16
1416107_at	Nsg2	neuron specific gene family member 2	-1.29	0.255	-1.11	0.857	-1.18	0.685	-2.66	0.037	-1.56
1435689_at	9030025P20Rik	RIKEN cDNA 9030025P20 gene	-1.21	0.269	-1.28	0.059	-1.08	0.632	-1.65	0.075	-1.31
1441613_at	1110033F14Rik	RIKEN cDNA 1110033F14 gene	-1.23	0.458	-1.24	0.724	-1.1	0.714	-1.57	0.304	-1.28
1454945_at	Lrriq2	leucine-rich repeats and IQ motif containing 2	-1.07	0.425	-1.34	0.367	-1.18	0.382	-1.37	0.183	-1.24
1456220_at	Fbxl7	F-box and leucine-rich repeat protein 7	-1.27	0.407	-1.14	0.767	-1.16	0.347	-1.6	0.07	-1.29
1446053_at	Gpkow	G patch domain and KOW motifs	-1.3	0.177	-1.2	0.678	-1.08	0.69	-1.25	0.173	-1.21
1438668_x_at	Atxn2l	ataxin 2-like	-1.35	0.022	-1.19	0.145	-1.06	0.389	-1.04	0.794	-1.16
1449515_at	Zfp292	zinc finger protein 292	-1.18	0.275	-1.05	0.752	-1.37	0.038	-1.69	0.136	-1.32
1428038_at	Gm568	gene model 568, (NCBI)	-1.16	0.872	-1.18	0.745	-1.22	0.651	-1.31	0.313	-1.22
1437131_x_at	Mrpl11	mitochondrial ribosomal protein L11	-1.01	0.892	-1.44	0.089	-1.18	0.716	-1.27	0.228	-1.22
1447689_at	Gprasp1	G protein-coupled receptor associated sorting protein 1	-1.5	0.696	-1.15	0.6	-1.01	0.977	-1.76	0.399	-1.36
1416971_at	Cox7a2	cytochrome c oxidase, subunit VIIa 2	-1.13	0.06	-1.25	0.012	-1.18	0.012	-1.1	0.529	-1.16
1453702_at	Ccdc105	coiled-coil domain containing 105	-1.03	0.971	-1.51	0.482	-1.11	0.865	-1.6	0.465	-1.31
1418390_at	Phf21a	PHD finger protein 21A	-1.07	0.444	-1.29	0.268	-1.22	0.129	-1.81	0.121	-1.35
1443038_at	---	---	-1.31	0.547	-1.05	0.873	-1.22	0.109	-1.35	0.108	-1.23
1453420_at	1700013G10Rik	RIKEN cDNA 1700013G10 gene	-1.15	0.454	-1.06	0.869	-1.4	0.078	-1.53	0.34	-1.28
1448063_at	Iqsec2	IQ motif and Sec7 domain 2	-1.1	0.542	-1.22	0.367	-1.24	0.486	-2.12	0.123	-1.42
1421295_at	Chrdl1	chordin-like 1	-1.27	0.475	-1.34	0.509	-1.01	0.985	-1.42	0.157	-1.26
1431494_at	A930008B05Rik	RIKEN cDNA A930008B05 gene	-1.06	0.885	-1.68	0.366	-1.01	0.953	-1.83	0.122	-1.39
1444638_at	Ttn	titin	-1.59	0.116	-1.02	0.941	-1.09	0.692	-1.21	0.444	-1.23
1435541_at	Btc	betacellulin, epidermal growth factor family member	-1.37	0.295	-1.17	0.661	-1.06	0.714	-1.08	0.845	-1.17
1452867_at	Col4a3bp	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-1.24	0.237	-1.11	0.25	-1.22	0.074	-1.19	0.348	-1.19
1452335_at	2810423E13Rik	RIKEN cDNA 2810423E13 gene	-1.22	0.278	-1.37	0.166	-1.02	0.935	-1.42	0.347	-1.26
1417102_a_at	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	-1.08	0.221	-1.2	0.144	-1.29	0.033	-1.38	0.221	-1.24
1449745_at	---	Transcribed locus	-1.17	0.598	-1.2	0.401	-1.19	0.453	-1.24	0.354	-1.2
1427984_at	Senp6	SUMO/sentrin specific peptidase 6	-1.11	0.774	-1.47	0.499	-1.06	0.794	-1.01	0.965	-1.16
1420608_at	Rbm18	RNA binding motif protein 18	-1.27	0.258	-1.06	0.453	-1.24	0.005	-1.19	0.381	-1.19
1426829_at	Rxrip110	retinoid X receptor interacting protein 110	-1.16	0.514	-1.17	0.058	-1.22	0.099	-1.28	0.184	-1.21
1459080_at	---	---	-1.26	0.611	-1.08	0.761	-1.23	0.646	-1.05	0.901	-1.16
1457746_at	2610028H07Rik	RIKEN cDNA 2610028H07 gene	-1.08	0.6	-1.26	0.022	-1.23	0.406	-1.57	0.044	-1.29
1437158_at	Nipbl	Nipped-B homolog (Drosophila)	-1.11	0.409	-1.17	0.324	-1.29	0.232	-1.16	0.4	-1.18
1451275_at	E030041M21Rik	RIKEN cDNA E030041M21 gene	-1.25	0.124	-1.12	0.385	-1.19	0.103	-1.27	0.358	-1.21
1434106_at	Epm2aip1	EPM2A (laforin) interacting protein 1	-1.13	0.232	-1.14	0.462	-1.3	0.114	-1.31	0.211	-1.22
1451153_a_at	Cyhr1	cysteine and histidine rich 1	-1.17	0.442	-1.19	0.296	-1.19	0.267	-1.31	0.08	-1.22
1416979_at	Pomp	proteasome maturation protein	-1.23	0.031	-1.16	0.019	-1.17	0.278	-1.29	0.147	-1.21
1443942_at	Gabpb2	GA repeat binding protein, beta 2	-1.36	0.306	-1.19	0.663	-1.05	0.841	-1.38	0.25	-1.24
1434796_at	Vamp4	vesicle-associated membrane protein 4	-1.19	0.26	-1.12	0.31	-1.25	0.335	-1.72	0.105	-1.32
1416379_at	Panx1	pannexin 1	-1.33	0.045	-1.23	0.766	-1.04	0.86	-2.11	0.142	-1.43
1433654_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	-1.13	0.557	-1.32	0.14	-1.12	0.391	-1.33	0.285	-1.23
1421022_x_at	Acyp1	acylphosphatase 1, erythrocyte (common) type	-1.39	0.097	-1.14	0.2	-1.07	0.534	-1.2	0.531	-1.2
1459117_at	---	Transcribed locus	-1.11	0.591	-1.35	0.512	-1.12	0.685	-2.14	0.077	-1.43
1444173_at	---	8 days neonate male testis cDNA, RIKEN full-length enriched library, clone:G630	-1.26	0.752	-1.22	0.655	-1.09	0.818	-1.18	0.709	-1.19
1459623_at	---	---	-1.12	0.777	-1.53	0.439	-1.01	0.986	-1.23	0.784	-1.22
1451403_at	BC024868	cDNA sequence BC024868	-1.03	0.905	-1.4	0.01	-1.18	0.443	-1.18	0.592	-1.2
1417555_at	Atad1	ATPase family, AAA domain containing 1	-1.15	0.555	-1.17	0.453	-1.23	0.237	-1.19	0.404	-1.19
1434806_at	Mtx3	metaxin 3	-1.4	0.238	-1.1	0.561	-1.1	0.627	-1.34	0.57	-1.24
1420532_at	Magi2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1.21	0.422	-1.2	0.725	-1.14	0.33	-1.48	0.2	-1.26

1437981_x_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	-1.14	0.581	-1.3	0.61	-1.13	0.254	-1.03	0.94	-1.15
1455502_at	Madd	MAP-kinase activating death domain	-1.14	0.596	-1.46	0.1	-1.03	0.887	-1.67	0.059	-1.32
1433957_at	C030048B08Rik	RIKEN cDNA C030048B08 gene	-1.08	0.573	-1.1	0.597	-1.42	0.237	-1.46	0.061	-1.27
1438971_x_at	Ube2h	ubiquitin-conjugating enzyme E2H	-1.31	0.004	-1.21	0.25	-1.06	0.725	-1.06	0.562	-1.16
1424398_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	-1.01	0.988	-1.36	0.038	-1.24	0.391	-1.14	0.682	-1.19
1456303_at	Phf14	PHD finger protein 14	-1.01	0.954	-1.11	0.311	-1.55	0.026	-1.22	0.071	-1.22
1452986_at	Hgd	homogentisate 1, 2-dioxygenase	-1.16	0.309	-1.24	0.242	-1.15	0.683	-1.13	0.819	-1.17
1455483_at	Zfp148	zinc finger protein 148	-1.23	0.184	-1.08	0.334	-1.26	0.215	-1.07	0.367	-1.16
1428240_at	Nrxn1	neurexin I	-1.17	0.77	-1.17	0.517	-1.21	0.259	-1.16	0.091	-1.18
1459062_x_at	AU041133	Expressed sequence AU041133	-1.1	0.906	-1.18	0.699	-1.29	0.107	-1.35	0.312	-1.23
1440183_x_at	Coq9	Coenzyme Q9 homolog (yeast)	-1.19	0.254	-1.18	0.154	-1.18	0.452	-1.35	0.263	-1.23
1432784_at	4930556A17Rik	RIKEN cDNA 4930556A17 gene	-1.33	0.456	-1.21	0.745	-1.05	0.935	-1.34	0.536	-1.23
1450954_at	Yme1l1	YME1-like 1 (S. cerevisiae)	-1.15	0.256	-1.2	0.185	-1.2	0.117	-1	0.966	-1.14
1436656_at	BC062109	cDNA sequence BC062109	-1.04	0.848	-1.37	0.646	-1.19	0.377	-1.48	0.312	-1.27
1416000_a_at	Prdx1	peroxiredoxin 1	-1.22	0.13	-1.13	0.44	-1.21	0.018	-1.2	0.147	-1.19
1427075_s_at	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-1.34	0.223	-1.04	0.775	-1.21	0.193	-1.28	0.061	-1.22
1436284_s_at	Zfp319	zinc finger protein 319	-1.11	0.377	-1.15	0.502	-1.3	0.111	-1.17	0.466	-1.18
1432403_at	4933402C06Rik	RIKEN cDNA 4933402C06 gene	-1	1	-1.38	0.675	-1.23	0.249	-1.42	0.458	-1.26
1430222_at	9130007G19Rik	RIKEN cDNA 9130007G19 gene	-1.27	0.385	-1	0.998	-1.34	0.153	-2.76	0.001	-1.59
1451442_at	Ccdc104	coiled-coil domain containing 104	-1.1	0.502	-1.34	0.09	-1.14	0.301	-1.05	0.54	-1.16
1433643_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	-1.1	0.603	-1.08	0.665	-1.43	0.219	-1.02	0.952	-1.16
1456204_at	2010107H07Rik	RIKEN cDNA 2010107H07 gene	-1.02	0.527	-1.17	0.385	-1.41	0.077	-1.03	0.892	-1.16
1446481_at	Apbb2	Amyloid beta (A4) precursor protein-binding, family B, member 2	-1.04	0.907	-1.04	0.912	-1.62	0.165	-1.58	0.211	-1.32
1447853_x_at	Kif13a	Kinesin family member 13A	-1.03	0.303	-1.35	0.554	-1.21	0.168	-1.02	0.955	-1.15
1438756_at	Ankrd29	ankyrin repeat domain 29	-1.08	0.749	-1.15	0.605	-1.35	0.278	-1.66	0.178	-1.31
1431701_a_at	Pdzk1	PDZ domain containing 1	-1.12	0.339	-1.26	0.06	-1.18	0.436	-2.05	0.306	-1.4
1448518_at	Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	-1.27	0.388	-1.28	0.423	-1.03	0.766	-1.05	0.741	-1.16
1441796_at	2010309E21Rik	RIKEN cDNA 2010309E21 gene	-1.27	0.576	-1.31	0.004	-1.02	0.959	-1.11	0.76	-1.18
1449664_s_at	Rnf20	ring finger protein 20	-1.33	0.088	-1.04	0.688	-1.21	0.206	-1.1	0.398	-1.17
1457472_at	Tnrc15	trinucleotide repeat containing 15	-1.14	0.476	-1.11	0.536	-1.32	0.155	-1.1	0.61	-1.17
1438080_at	Mrpl11	mitochondrial ribosomal protein L11	-1.13	0.858	-1.53	0.029	-1	1	-1.29	0.354	-1.24
1434732_x_at	Tomm7	Translocase of outer mitochondrial membrane 7 homolog (yeast)	-1.26	0.196	-1.08	0.654	-1.23	0.358	-1.17	0.499	-1.18
1443335_at	Pdzrn3	PDZ domain containing RING finger 3	-1.06	0.792	-1.13	0.589	-1.41	0.088	-1.2	0.549	-1.2
1437924_at	---	---	-1.24	0.143	-1.33	0.045	-1.02	0.856	-1.03	0.653	-1.16
1456120_at	3110001I20Rik	RIKEN cDNA 3110001I20 gene	-1.05	0.757	-1.38	0.452	-1.17	0.724	-1.37	0.495	-1.24
1433597_at	9430010O03Rik	RIKEN cDNA 9430010O03 gene	-1.23	0.386	-1.11	0.525	-1.21	0.401	-1.08	0.724	-1.16
1439210_at	Mrps9	mitochondrial ribosomal protein S9	-1.21	0.062	-1.02	0.861	-1.36	0.335	-1.27	0.318	-1.22
1436115_at	Gm266	gene model 266, (NCBI)	-1.45	0.262	-1.05	0.905	-1.11	0.808	-3.02	0.042	-1.66
1444679_at	Phf21a	PHD finger protein 21A	-1.04	0.901	-1.05	0.739	-1.6	0.07	-1.19	0.439	-1.22
1455664_at	Rtn4rl1	reticulon 4 receptor-like 1	-1.17	0.445	-1.37	0.352	-1.05	0.823	-1.77	0.121	-1.34
1442528_at	Xpo4	exportin 4	-1.28	0.112	-1.13	0.665	-1.14	0.733	-1.16	0.686	-1.18
1457696_at	Rilp	Rab interacting lysosomal protein	-1.17	0.152	-1.24	0.15	-1.14	0.387	-1.43	0.364	-1.24
1450066_at	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	-1.18	0.368	-1.06	0.577	-1.33	0.126	-1.3	0.217	-1.22
1431009_at	B230219D22Rik	RIKEN cDNA B230219D22 gene	-1.03	0.652	-1.21	0.687	-1.35	0.11	-1.1	0.781	-1.17
1419702_at	Taf1a	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, A	-1.21	0.183	-1.26	0.167	-1.09	0.532	-1.48	0.012	-1.26
1419006_s_at	Peli2	pellino 2	-1.46	0.474	-1.03	0.933	-1.14	0.299	-1.74	0.2	-1.34
1422026_at	Pi16	peptidase inhibitor 16	-1.09	0.755	-1.39	0.412	-1.1	0.776	-1.78	0.591	-1.34
1429027_at	0610007N19Rik	RIKEN cDNA 0610007N19 gene	-1.07	0.692	-1.12	0.759	-1.4	0.042	-1.34	0.211	-1.23
1444004_at	Thoc2	THO complex 2	-1.03	0.898	-1.1	0.118	-1.52	0.081	-1.04	0.867	-1.17
1436516_at	Abhd13	abhydrolase domain containing 13	-1.07	0.818	-1.28	0.013	-1.22	0.108	-1.31	0.094	-1.22
1421052_a_at	Sms /// LOC671878	spermine synthase /// similar to Spermine synthase (Spermidine aminopropyltran	-1.26	0.231	-1.15	0.505	-1.15	0.152	-1.28	0.004	-1.21
1447112_s_at	Cryl1	crystallin, lamda 1	-1.29	0.188	-1.16	0.525	-1.1	0.377	-1.11	0.729	-1.17
1454890_at	Amot	angiomotin	-1.02	0.803	-1.17	0.099	-1.42	0.078	-1.28	0.53	-1.22

1419158_a_at	Harsl	histidyl-tRNA synthetase-like	-1.14	0.313	-1.34	0.01	-1.09	0.55	-1.19	0.383	-1.19
1440835_at	Zfp27	zinc finger protein 27	-1.03	0.813	-1.34	0.3	-1.21	0.251	-1.37	0.024	-1.24
1416810_at	Mea1	male enhanced antigen 1	-1.08	0.102	-1.15	0.264	-1.34	0.062	-1.28	0.13	-1.21
1449655_a_at	---	CDNA clone IMAGE:5690974	-1.03	0.532	-1.6	0.171	-1.05	0.867	-1.87	0.155	-1.39
1444366_at	Taok3	TAO kinase 3	-1.11	0.758	-1.17	0.617	-1.28	0.432	-1.26	0.449	-1.2
1457944_at	Etv6	Ets variant gene 6 (TEL oncogene)	-1.03	0.864	-1.06	0.439	-1.59	0.234	-1.51	0.082	-1.3
1421256_at	Gzmc	granzyme C	-1	0.999	-1.02	0.975	-1.79	0.155	-3	0.351	-1.7
1415776_at	Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	-1.01	0.848	-1.41	0.386	-1.19	0.204	-1.51	0.178	-1.28
1459856_at	Mrpl13	Mitochondrial ribosomal protein L13	-1.32	0.278	-1.01	0.971	-1.26	0.523	-1.11	0.101	-1.18
1417842_at	Caml	calcium modulating ligand	-1.29	0.119	-1.09	0.162	-1.18	0.168	-1.14	0.444	-1.17
1456896_at	6720462K09Rik	RIKEN cDNA 6720462K09 gene	-1.02	0.657	-1.02	0.933	-1.73	0.019	-1.04	0.722	-1.2
1424456_at	Pvrl2	poliovirus receptor-related 2	-1.09	0.647	-1.45	0.011	-1.07	0.392	-1.28	0.316	-1.22
1439345_at	Gpnmb	glycoprotein (transmembrane) nmb	-1.26	0.53	-1.32	0.519	-1	0.983	-1.07	0.804	-1.17
1440840_at	D630004K10Rik	RIKEN cDNA D630004K10 gene	-1.12	0.008	-1.15	0.563	-1.28	0.289	-1	0.993	-1.14
1442288_at	Anxa6	Annexin A6	-1.04	0.861	-1.11	0.674	-1.46	0.068	-1.33	0.588	-1.24
1418966_a_at	Dcbld1	discoidin, CUB and LCCL domain containing 1	-1.13	0.61	-1.13	0.368	-1.3	0.149	-1.28	0.071	-1.21
1416471_at	Cept1	choline/ethanolaminephosphotransferase 1	-1.35	0.064	-1.15	0.176	-1.07	0.463	-1.59	0.078	-1.29
1442166_at	Cpne5	copine V	-1.33	0.097	-1.2	0.508	-1.04	0.819	-1.14	0.228	-1.18
1417736_at	Smc6	structural maintenance of chromosomes 6	-1.24	0.134	-1.11	0.593	-1.19	0.076	-1.01	0.968	-1.14
1442784_at	Zfp608	Zinc finger protein 608	-1.03	0.732	-1.19	0.775	-1.37	0.397	-2.78	0.024	-1.59
1416370_at	Zipro1	zinc finger proliferation 1	-1.21	0.201	-1.05	0.719	-1.31	0.093	-1.24	0.493	-1.2
1428919_at	Fgfr1op	Fgfr1 oncogene partner	-1.17	0.081	-1.1	0.464	-1.28	0.122	-1.38	0.251	-1.23
1427978_at	4732418C07Rik	RIKEN cDNA 4732418C07 gene	-1.12	0.501	-1.14	0.509	-1.29	0.274	-1.17	0.533	-1.18
1420590_at	Has1	hyaluronan synthase1	-1.23	0.605	-1.13	0.653	-1.17	0.565	-1.01	0.991	-1.14
1428067_at	Rasl12	RAS-like, family 12	-1.22	0.449	-1.07	0.598	-1.27	0.214	-1	0.994	-1.14
1436222_at	Gas5	growth arrest specific 5	-1.32	0.416	-1.24	0.45	-1.02	0.929	-1.2	0.467	-1.19
1446550_at	Gspt1	G1 to S phase transition 1	-1.06	0.423	-1.07	0.748	-1.5	0.019	-1.12	0.519	-1.19
1456851_at	Foxp1	Forkhead box P1	-1.02	0.974	-1.28	0.354	-1.27	0.376	-2.66	0.1	-1.56
1434175_s_at	2210010N04Rik	RIKEN cDNA 2210010N04 gene	-1.28	0.294	-1.22	0.669	-1.06	0.772	-1.7	0.314	-1.31
1416874_a_at	Paf1	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	-1.39	0.3	-1.07	0.546	-1.13	0.654	-1.64	0.175	-1.3
1433672_at	4732479N06Rik	RIKEN cDNA 4732479N06 gene	-1.15	0.066	-1.33	0.027	-1.09	0.301	-1.2	0.271	-1.19
1456763_at	AA536749	expressed sequence AA536749	-1.01	0.912	-1.15	0.339	-1.45	0.094	-1.22	0.342	-1.21
1420964_at	Enc1	ectodermal-neural cortex 1	-1.27	0.019	-1.2	0.8	-1.09	0.886	-1.22	0.848	-1.19
1426559_at	Sbno1	sno, strawberry notch homolog 1 (Drosophila)	-1.16	0.319	-1.2	0.01	-1.17	0.04	-1.15	0.149	-1.17
1449303_at	Sesn3	sestrin 3	-1.32	0.044	-1.15	0.378	-1.09	0.779	-2.24	0.068	-1.45
1417673_at	Grb14	growth factor receptor bound protein 14	-1.13	0.342	-1.31	0.013	-1.12	0.475	-1.66	0.518	-1.3
1457508_at	C430003N24Rik	RIKEN cDNA C430003N24 gene	-1.03	0.908	-1.08	0.678	-1.54	0.071	-1.36	0.367	-1.25
1450482_a_at	Pitx2	paired-like homeodomain transcription factor 2	-1.14	0.717	-1.15	0.699	-1.25	0.477	-1.04	0.942	-1.15
1452765_at	LOC674308	similar to solute carrier family 39 (zinc transporter), member 9	-1.18	0.249	-1.16	0.226	-1.19	0.077	-1.12	0.453	-1.16
1421478_a_at	Zfp318	zinc finger protein 318	-1.07	0.599	-1.36	0.043	-1.14	0.052	-2.25	0.131	-1.46
1447990_at	C76332	expressed sequence C76332	-1.27	0.487	-1.03	0.954	-1.27	0.622	-3.94	0.023	-1.88
1452333_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.02	0.952	-1.26	0.436	-1.3	0.092	-1.8	0.273	-1.34
1433752_s_at	D030016E14Rik	RIKEN cDNA D030016E14 gene	-1.14	0.315	-1.35	0.007	-1.07	0.649	-1.27	0.094	-1.21
1427475_a_at	LOC669660	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ an	-1.17	0.203	-1.23	0.078	-1.13	0.335	-1.07	0.679	-1.15
1436993_x_at	Pfn2	profilin 2	-1.28	0.137	-1.22	0.507	-1.05	0.754	-1.52	0.175	-1.27
1417390_at	Xab1	XPA binding protein 1	-1.41	0.04	-1.16	0.124	-1.02	0.838	-1.43	0.114	-1.26
1428388_at	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-1.1	0.133	-1.03	0.818	-1.48	0.297	-1.53	0.226	-1.29
1446520_at	Il1rapl2	interleukin 1 receptor accessory protein-like 2	-1.05	0.937	-1.12	0.777	-1.43	0.373	-1.07	0.898	-1.17
1453636_at	Pcgf5	polycomb group ring finger 5	-1.09	0.467	-1.12	0.633	-1.36	0.232	-1.91	0.156	-1.37
1451556_a_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	-1.28	0.044	-1.11	0.704	-1.16	0.094	-1.16	0.055	-1.18
1438104_at	---	---	-1.01	0.898	-1.06	0.678	-1.63	0.275	-1.16	0.03	-1.21
1416281_at	Wdr45l	Wdr45 like	-1.11	0.639	-1.09	0.352	-1.37	0.037	-1.24	0.177	-1.2
1444310_at	Polr3a	polymerase (RNA) III (DNA directed) polypeptide A	-1.13	0.799	-1.23	0.661	-1.18	0.748	-1.01	0.894	-1.14

1434379_at	Mxd4	Max dimerization protein 4	-1.01	0.988	-1.13	0.505	-1.49	0.058	-1.56	0.169	-1.3
1417834_at	Synj2bp	synaptojanin 2 binding protein	-1.1	0.358	-1.19	0.058	-1.24	0.054	-1.18	0.11	-1.18
1436226_at	Tceb1	transcription elongation factor B (SIII), polypeptide 1	-1.06	0.388	-1.07	0.33	-1.48	0	-1.11	0.602	-1.18
1456460_at	BC068281	cDNA sequence BC068281	-1.39	0.431	-1.17	0.492	-1.02	0.949	-1.31	0.412	-1.22
AFFX-MUR_b2_at	---	---	-1.13	0.334	-1.09	0.255	-1.35	0.111	-1.08	0.706	-1.16
1428180_at	2810422J05Rik	RIKEN cDNA 2810422J05 gene	-1.15	0.452	-1.15	0.311	-1.23	0.181	-1.36	0.051	-1.22
1442911_at	Riok2	RIO kinase 2 (yeast)	-1.05	0.809	-1.09	0.801	-1.47	0.073	-1.44	0.098	-1.26
1425892_a_at	Pnoc	prepronociceptin	-1.28	0.716	-1.11	0.744	-1.15	0.699	-1.2	0.552	-1.18
1424873_at	Rnf2	ring finger protein 2	-1.16	0.391	-1.1	0.154	-1.28	0.004	-1.59	0.069	-1.28
1434823_x_at	Myeov2	myeloma overexpressed 2	-1.16	0.209	-1.1	0.026	-1.28	0.176	-1.49	0.117	-1.26
1426861_at	Aftph	aftiphilin	-1.23	0.3	-1.05	0.64	-1.27	0.072	-1.16	0.553	-1.18
1428500_at	2210419D22Rik	RIKEN cDNA 2210419D22 gene	-1.14	0.358	-1.04	0.659	-1.41	0.112	-1.1	0.729	-1.17
1428248_at	Nfx1	nuclear transcription factor, X-box binding 1	-1.13	0.639	-1.15	0.442	-1.26	0.178	-1.34	0.149	-1.22
1439901_at	2610208M17Rik	RIKEN cDNA 2610208M17 gene	-1.12	0.681	-1.05	0.833	-1.42	0.008	-1.34	0.127	-1.23
1460420_a_at	Egfr	epidermal growth factor receptor	-1.28	0.225	-1.16	0.685	-1.1	0.663	-1.1	0.64	-1.16
1446938_at	AA408213	expressed sequence AA408213	-1.07	0.791	-1.06	0.845	-1.48	0.19	-1.44	0.36	-1.26
1423331_a_at	Pvrl3	poliovirus receptor-related 3	-1.11	0.508	-1.13	0.427	-1.32	0.18	-1.4	0.005	-1.24
1428825_at	Nr6a1	nuclear receptor subfamily 6, group A, member 1	-1.29	0.167	-1.18	0.61	-1.08	0.572	-1.69	0.323	-1.31
1428853_at	Ptch1	patched homolog 1	-1.01	0.933	-1.19	0.143	-1.39	0.226	-1.29	0.056	-1.22
1449025_at	Ifit3	interferon-induced protein with tetratricopeptide repeats 3	-1.18	0.43	-1.13	0.681	-1.22	0.444	-1.55	0.3	-1.27
1419660_at	1600012F09Rik	RIKEN cDNA 1600012F09 gene	-1.17	0.038	-1.17	0.205	-1.19	0.122	-1.07	0.748	-1.15
1419007_at	Zp3	zona pellucida glycoprotein 3	-1.05	0.95	-1.25	0.647	-1.25	0.308	-2.79	0.496	-1.59
1450780_s_at	Hmga2	high mobility group AT-hook 2	-1.02	0.939	-1.46	0.053	-1.12	0.595	-1.6	0.219	-1.3
1425577_at	9830124H08Rik	RIKEN cDNA 9830124H08 gene	-1.07	0.437	-1.16	0.112	-1.33	0.067	-1.55	0.119	-1.28
1443001_at	C78344	expressed sequence C78344	-1.07	0.883	-1.16	0.821	-1.32	0.585	-1.03	0.961	-1.15
1432171_at	4933409F18Rik	RIKEN cDNA 4933409F18 gene	-1.15	0.603	-1.09	0.859	-1.31	0.48	-1.27	0.577	-1.2
1440846_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	-1.38	0.406	-1.12	0.481	-1.07	0.797	-1.42	0.027	-1.25
1454422_at	4930456J16Rik	RIKEN cDNA 4930456J16 gene	-1.02	0.842	-1.22	0.573	-1.34	0.011	-1.01	0.975	-1.14
1415872_at	Hnrph1	heterogeneous nuclear ribonucleoprotein H1	-1.07	0.325	-1.17	0.142	-1.3	0.118	-1.15	0.571	-1.17
1427020_at	Scara3	scavenger receptor class A, member 3	-1.03	0.838	-1.43	0.191	-1.14	0.64	-1.42	0.45	-1.25
1426803_at	Rbm26	RNA binding motif protein 26	-1.29	0.315	-1.22	0.102	-1.04	0.754	-1.17	0.588	-1.18
1422532_at	Xpc		-1.21	0.095	-1.22	0.069	-1.11	0.508	-1.38	0.151	-1.23
1438766_at	Pnrc2	proline-rich nuclear receptor coactivator 2	-1.03	0.858	-1.35	0.139	-1.19	0.494	-1.46	0.079	-1.26
1442002_at	7030402D04Rik	RIKEN cDNA 7030402D04 gene	-1.08	0.643	-1.13	0.356	-1.35	0.153	-1.1	0.405	-1.16
1433810_x_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-1.21	0.215	-1.13	0.397	-1.19	0.507	-1.18	0.709	-1.18
1424047_at	Dera	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	-1.28	0.106	-1.22	0.103	-1.05	0.717	-1.17	0.323	-1.18
1460544_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-1.23	0.102	-1.29	0.277	-1.04	0.873	-1.65	0.003	-1.3
1419105_at	Nr1h4	nuclear receptor subfamily 1, group H, member 4	-1.32	0.382	-1.18	0.048	-1.06	0.89	-1.93	0.06	-1.37
1444231_at	Zdhhc6	Zinc finger, DHHC domain containing 6	-1.09	0.3	-1	0.994	-1.56	0.053	-1.15	0.51	-1.2
1416067_at	Ifrd1	interferon-related developmental regulator 1	-1.05	0.878	-1.29	0.156	-1.21	0.116	-1.03	0.696	-1.14
1453123_at	Sf3b2	splicing factor 3b, subunit 2	-1.21	0.072	-1.28	0.207	-1.06	0.67	-1.16	0.234	-1.18
1436248_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330033L	-1.11	0.572	-1.2	0.016	-1.23	0.22	-1.04	0.792	-1.14
1441144_at	Arr3	arrestin 3, retinal	-1.44	0.316	-1.04	0.884	-1.11	0.76	-1.53	0.156	-1.28
1440893_at	---	---	-1.04	0.88	-1.09	0.735	-1.48	0.155	-1.11	0.673	-1.18
1427876_at	2610312B22Rik	RIKEN cDNA 2610312B22 gene	-1.11	0.483	-1.2	0.154	-1.22	0.054	-1.16	0.044	-1.17
1438843_x_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	-1.28	0.117	-1.19	0.041	-1.07	0.758	-1.16	0.318	-1.18
1426429_at	Thap7	THAP domain containing 7	-1.26	0.729	-1.12	0.629	-1.16	0.712	-1.24	0.091	-1.19
1429556_at	2610024B07Rik	RIKEN cDNA 2610024B07 gene	-1.22	0.424	-1	0.986	-1.36	0.411	-1.17	0.546	-1.19
1422806_x_at	Ing3	inhibitor of growth family, member 3	-1.28	0.49	-1.15	0.307	-1.1	0.503	-1.79	0.13	-1.33
1417321_at	D4Wsu132e	DNA segment, Chr 4, Wayne State University 132, expressed	-1.21	0.385	-1.1	0.324	-1.22	0.32	-1.63	0.204	-1.29
1428321_at	Eml1 /// LOC63410	echinoderm microtubule associated protein like 1 /// similar to echinoderm microtu	-1.02	0.955	-1.45	0.618	-1.13	0.602	-1.7	0.144	-1.32
1416154_at	Srp54 /// LOC6651	signal recognition particle 54 /// similar to signal recognition particle 54	-1.32	0.732	-1.18	0.698	-1.05	0.806	-1.1	0.342	-1.16
1429733_at	Ccdc94	coiled-coil domain containing 94	-1.2	0.269	-1.11	0.758	-1.21	0.08	-1.32	0.156	-1.21

1438695_at	C230091D08Rik	RIKEN cDNA C230091D08 gene	-1.06	0.725	-1.1	0.132	-1.42	0.068	-1.13	0.327	-1.18
1418117_at	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	-1.09	0.564	-1.54	0.005	-1.01	0.942	-1.13	0.49	-1.19
1417451_a_at	Ppia	peptidylprolyl isomerase A	-1.17	0.151	-1.13	0.342	-1.22	0.006	-1.23	0.016	-1.19
1434550_at	3830406C13Rik	RIKEN cDNA 3830406C13 gene	-1.12	0.059	-1.1	0.528	-1.32	0.108	-1.46	0.157	-1.25
1429000_at	Phf3	PHD finger protein 3	-1.1	0.454	-1.18	0.313	-1.25	0.157	-1.01	0.968	-1.13
1420626_at	2410016F19Rik	RIKEN cDNA 2410016F19 gene	-1.1	0.276	-1.1	0.386	-1.35	0.017	-1.07	0.653	-1.16
1442231_at	AI616248	expressed sequence AI616248	-1.38	0.562	-1.1	0.837	-1.08	0.669	-1.6	0.424	-1.29
1455958_s_at	Pptc7	PTC7 protein phosphatase homolog (S. cerevisiae)	-1.17	0.345	-1.2	0.449	-1.15	0.304	-1.62	0.124	-1.28
1428556_at	Pigy	phosphatidylinositol glycan anchor biosynthesis, class Y	-1.14	0.293	-1.23	0.034	-1.16	0.061	-1.03	0.75	-1.14
1437538_at	2610002F03Rik	RIKEN cDNA 2610002F03 gene	-1.12	0.526	-1.45	0.083	-1.03	0.814	-1.05	0.914	-1.16
1449800_x_at	Phf7	PHD finger protein 7	-1.13	0.403	-1.1	0.582	-1.32	0.134	-1.48	0.256	-1.26
1435781_at	Cand1	cullin associated and neddylation disassociated 1	-1.03	0.873	-1.15	0.31	-1.38	0.117	-1.19	0.05	-1.19
1439071_at	5430416N02Rik	RIKEN cDNA 5430416N02 gene	-1.09	0.743	-1.12	0.661	-1.33	0.074	-1.34	0.117	-1.22
1417250_at	Rnf12	ring finger protein 12	-1.05	0.716	-1	0.976	-1.65	0.05	-1.06	0.787	-1.19
1426489_s_at	Bfar	bifunctional apoptosis regulator	-1.25	0.077	-1.13	0.264	-1.15	0.148	-1.48	0.112	-1.25
1424489_a_at	Trit1	tRNA isopentenyltransferase 1	-1.26	0.284	-1.19	0.188	-1.09	0.627	-1.86	0.065	-1.35
1423451_at	Pgrmc1	progesterone receptor membrane component 1	-1.19	0.337	-1.22	0.223	-1.11	0.315	-1.18	0.385	-1.18
1443212_at	Large	Like-glycosyltransferase	-1.07	0.579	-1.06	0.875	-1.46	0.249	-1.11	0.825	-1.17
1428022_at	Lcn13	lipocalin 13	-1.11	0.735	-1.26	0.599	-1.15	0.456	-1.37	0.17	-1.22
1428785_at	Amotl1	angiomotin-like 1	-1.09	0.29	-1.23	0.34	-1.2	0.391	-1.12	0.464	-1.16
1452047_at	Cacybp	calcyclin binding protein	-1.12	0.285	-1.18	0.134	-1.22	0.026	-1.16	0.645	-1.17
1434851_s_at	Crb3	crumbs homolog 3 (Drosophila)	-1.03	0.794	-1.18	0.103	-1.34	0.088	-1.46	0.134	-1.25
1438041_at	---	---	-1.01	0.973	-1.14	0.598	-1.45	0.115	-1.93	0.133	-1.38
1445843_at	Chd2	chromodomain helicase DNA binding protein 2	-1.08	0.695	-1.06	0.228	-1.44	0.01	-1.6	0.185	-1.3
1434555_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	-1.06	0.46	-1.17	0.298	-1.31	0.031	-1.37	0.035	-1.23
1458870_x_at	Phr1	pam, highwire, rpm 1	-1.29	0.496	-1.09	0.809	-1.15	0.476	-1.02	0.96	-1.14
1428725_at	Pias2	protein inhibitor of activated STAT 2	-1.12	0.553	-1.19	0.182	-1.21	0.09	-1.26	0.151	-1.2
1449291_a_at	Dcbld1	discoidin, CUB and LCCL domain containing 1	-1.09	0.272	-1.07	0.778	-1.42	0.105	-1.78	0.107	-1.34
1433482_a_at	Fubp1	far upstream element (FUSE) binding protein 1	-1.09	0.684	-1.5	0.13	-1.03	0.871	-1.67	0.2	-1.32
1434180_at	Plekhc1	pleckstrin homology domain containing, family C (with FERM domain) member 1	-1.02	0.608	-1.15	0.351	-1.41	0.062	-1.48	0.216	-1.26
1416278_a_at	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-1.15	0.191	-1.23	0.081	-1.15	0.389	-1.06	0.525	-1.14
1437041_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	-1.19	0.375	-1.14	0.518	-1.18	0.347	-1.37	0.355	-1.22
1418578_at	Dgka	diacylglycerol kinase, alpha	-1.1	0.14	-1.36	0.047	-1.09	0.592	-3.33	0.023	-1.72
1459537_at	4631427C17Rik	RIKEN cDNA 4631427C17 gene	-1.54	0.004	-1.03	0.921	-1.06	0.718	-1.44	0.112	-1.27
1435221_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.15	0.428	-1.27	0.112	-1.11	0.6	-1.98	0.141	-1.38
1445056_at	9230102K24Rik	RIKEN cDNA 9230102K24 gene	-1.36	0.595	-1.06	0.889	-1.14	0.78	-1.18	0.475	-1.18
1436505_at	Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	-1	0.997	-1.22	0.135	-1.35	0.165	-1.13	0.615	-1.17
1426365_at	2810403A07Rik	RIKEN cDNA 2810403A07 gene	-1.22	0.416	-1.27	0.057	-1.04	0.833	-1.24	0.214	-1.19
1416058_s_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	-1.25	0.008	-1.3	0.011	-1.01	0.849	-1.05	0.675	-1.15
1454888_at	Pfdn4	prefoldin 4	-1.02	0.689	-1.14	0.019	-1.42	0.034	-1.23	0.219	-1.2
1438478_a_at	Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	-1.15	0.019	-1.21	0.277	-1.15	0.447	-1.48	0.176	-1.25
1420456_at	Gcm2	glial cells missing homolog 2 (Drosophila)	-1.34	0.341	-1.13	0.712	-1.08	0.723	-1.16	0.79	-1.18
1420628_at	Pura	purine rich element binding protein A	-1.05	0.166	-1.2	0.026	-1.3	0.054	-1.4	0.169	-1.24
1452611_at	Zfp294	zinc finger protein 294	-1.09	0.46	-1.33	0.12	-1.12	0.561	-1.09	0.655	-1.16
1423781_at	Appbp1	amyloid beta precursor protein binding protein 1	-1.17	0.446	-1.03	0.663	-1.36	0.039	-1.43	0.016	-1.25
1442666_at	D9Ertd12e	DNA segment, Chr 9, ERATO Doi 12, expressed	-1.08	0.632	-1.24	0.758	-1.21	0.597	-1.43	0.52	-1.24
1423442_a_at	Fbxw2	F-box and WD-40 domain protein 2	-1.2	0.497	-1.22	0.106	-1.1	0.61	-1.04	0.881	-1.14
1415894_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.25	0.011	-1.02	0.835	-1.27	0.168	-1.14	0.335	-1.17
1458900_at	Slc24a3	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	-1.04	0.907	-1.13	0.764	-1.41	0.044	-1.19	0.588	-1.19
1429202_at	2610019N06Rik	RIKEN cDNA 2610019N06 gene	-1.12	0.135	-1.37	0.374	-1.07	0.722	-1.36	0.095	-1.23
1440348_at	Zfyve9	zinc finger, FYVE domain containing 9	-1.16	0.439	-1.13	0.284	-1.23	0.183	-1.27	0.263	-1.2
1434306_at	Rab3ip	RAB3A interacting protein	-1.07	0.304	-1.13	0.449	-1.35	0.007	-1.65	0.023	-1.3
1457635_s_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	-1.16	0.314	-1.01	0.958	-1.41	0.022	-1.28	0.301	-1.22

1424016_at	2310007F21Rik	RIKEN cDNA 2310007F21 gene	-1.11	0.21	-1.29	0.183	-1.13	0.378	-1.16	0.586	-1.17
1439524_at	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	-1.09	0.807	-1.15	0.667	-1.3	0.445	-1.24	0.253	-1.19
1418407_at	Pde8a	phosphodiesterase 8A	-1.07	0.717	-1.5	0.315	-1.04	0.896	-1.36	0.478	-1.24
1437288_at	Impad1	inositol monophosphatase domain containing 1	-1.03	0.611	-1.07	0.577	-1.53	0.058	-1.08	0.577	-1.18
1453886_a_at	Slc25a26	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 26	-1.23	0.009	-1.22	0.357	-1.08	0.76	-1.3	0.358	-1.21
1422525_at	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	-1.18	0.007	-1.31	0.024	-1.05	0.593	-1.05	0.599	-1.15
1452153_at	Fbxo18	F-box protein 18	-1.12	0.291	-1.2	0.083	-1.19	0.129	-1.22	0.383	-1.18
1442519_at	Ga17	Dendritic cell protein GA17	-1.07	0.687	-1.35	0.079	-1.12	0.427	-1.05	0.776	-1.15
1454852_at	Sp1	trans-acting transcription factor 1	-1.13	0.173	-1.06	0.618	-1.36	0.024	-1.13	0.54	-1.17
1460052_at	Acsm1	Acyl-CoA synthetase medium-chain family member 1	-1.02	0.896	-1.22	0.297	-1.31	0.632	-1.58	0.345	-1.28
1423298_at	Add3	adducin 3 (gamma)	-1.23	0.134	-1.1	0.688	-1.19	0.327	-1.78	0.169	-1.33
1431996_at	---	---	-1.13	0.413	-1.14	0.548	-1.25	0.517	-1.03	0.932	-1.14
1453419_at	2900078C09Rik	RIKEN cDNA 2900078C09 gene	-1.15	0.64	-1.44	0.129	-1	0.972	-1.55	0.201	-1.28
1432519_at	1810059H22Rik	RIKEN cDNA 1810059H22 gene	-1.34	0.207	-1.15	0.746	-1.05	0.919	-1.52	0.118	-1.27
1417280_at	Slc17a1	solute carrier family 17 (sodium phosphate), member 1	-1.05	0.261	-1.2	0.192	-1.28	0.674	-1.28	0.327	-1.2
1441190_at	Arpc5l	actin related protein 2/3 complex, subunit 5-like	-1.01	0.981	-1.53	0.131	-1.09	0.776	-1.11	0.784	-1.19
1441944_s_at	Gpr135	G protein-coupled receptor 135	-1.31	0.448	-1.15	0.789	-1.08	0.896	-1.36	0.332	-1.22
1451287_s_at	2810003C17Rik	RIKEN cDNA 2810003C17 gene	-1.21	0.239	-1.17	0.755	-1.13	0.562	-1.54	0.501	-1.26
1456594_at	---	---	-1.29	0.216	-1.13	0.466	-1.11	0.788	-1.69	0.425	-1.3
1428681_at	Gm608	gene model 608, (NCBI)	-1.08	0.064	-1.13	0.186	-1.33	0.012	-1.19	0.117	-1.18
1460575_at	Eif2a	eukaryotic translation initiation factor 2a	-1.18	0.486	-1.16	0.286	-1.16	0	-1.14	0.297	-1.16
1439979_at	Zfp398	zinc finger protein 398	-1.35	0.185	-1.18	0.587	-1.02	0.891	-1.42	0.351	-1.24
1416624_a_at	Uba52 /// LOC6665	ubiquitin A-52 residue ribosomal protein fusion product 1 /// similar to ubiquitin A-	-1.06	0.271	-1.19	0.395	-1.28	0.007	-1.23	0.058	-1.19
1416482_at	Ttc3	tetratricopeptide repeat domain 3	-1.37	0.327	-1.19	0.367	-1.01	0.981	-1.92	0.067	-1.37
1426760_at	Ipo8	importin 8	-1.02	0.757	-1.31	0.055	-1.21	0.095	-1.06	0.798	-1.15
1429165_at	3110001I22Rik	RIKEN cDNA 3110001I22 gene	-1.06	0.737	-1.37	0.092	-1.12	0.309	-1.34	0.183	-1.22
1424493_s_at	Ugt3a1	UDP glycosyltransferases 3 family, polypeptide A1	-1.03	0.827	-1.22	0.152	-1.29	0.503	-1.02	0.943	-1.14
1458242_at	Gphn	Gephyrin	-1.43	0.521	-1.04	0.943	-1.1	0.786	-1.31	0.759	-1.22
1450897_at	Arhgap5	Rho GTPase activating protein 5	-1.18	0.503	-1.14	0.39	-1.18	0.065	-1.37	0.314	-1.22
1430546_at	Cryzl1	crystallin, zeta (quinone reductase)-like 1	-1.3	0.297	-1.02	0.934	-1.22	0.34	-1.21	0.588	-1.19
1434178_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	-1.08	0.509	-1.1	0.498	-1.36	0.114	-1.06	0.576	-1.15
1435088_at	Nsd1	nuclear receptor-binding SET-domain protein 1	-1.06	0.588	-1.1	0.304	-1.39	0.069	-1.69	0.065	-1.31
1456154_at	Zfp444	Zinc finger protein 444	-1.27	0.773	-1.07	0.924	-1.18	0.526	-1.05	0.862	-1.14
1426709_a_at	Usp33	ubiquitin specific peptidase 33	-1.23	0.458	-1.07	0.473	-1.21	0.185	-1.19	0.281	-1.18
1455646_at	2010004M13Rik	RIKEN cDNA 2010004M13 gene	-1.07	0.485	-1.34	0.525	-1.12	0.501	-1.78	0.066	-1.33
1438986_x_at	Rps17	ribosomal protein S17	-1.11	0.027	-1.06	0.567	-1.38	0	-1.36	0.008	-1.23
1437271_at	Clcf1	cardiotrophin-like cytokine factor 1	-1.06	0.572	-1.16	0.451	-1.31	0.242	-2.04	0.078	-1.39
AFFX-r2-P1-cre-3_a	---	---	-1.01	0.9	-1.17	0.553	-1.38	0.043	-1.23	0.082	-1.2
1428819_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	-1.14	0.358	-1.08	0.769	-1.3	0.289	-1.11	0.815	-1.16
1430703_at	---	---	-1.05	0.869	-1.52	0.378	-1.05	0.806	-1.11	0.877	-1.18
1424324_at	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-1.15	0.065	-1.06	0.438	-1.33	0.026	-1.5	0.04	-1.26
1420967_at	Slc25a15	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	-1.19	0.027	-1.09	0.289	-1.24	0.203	-1.14	0.349	-1.16
1424912_at	Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), m	-1.24	0.003	-1.27	0.047	-1.03	0.857	-1.03	0.576	-1.14
1428845_at	Bclaf1	BCL2-associated transcription factor 1	-1.19	0.318	-1.14	0.246	-1.17	0.353	-1.18	0.233	-1.17
1424526_a_at	Tgds	TDP-glucose 4,6-dehydratase	-1.07	0.149	-1.05	0.654	-1.49	0.026	-1.69	0.106	-1.32
1417720_at	Polr2j	polymerase (RNA) II (DNA directed) polypeptide J	-1.15	0.39	-1.14	0.009	-1.21	0.106	-1.01	0.952	-1.13
1452261_at	Shprh	SNF2 histone linker PHD RING helicase	-1.1	0.417	-1.23	0.229	-1.18	0.034	-1.29	0.108	-1.2
1433649_at	Aof1	amine oxidase, flavin containing 1	-1.18	0.328	-1.07	0.601	-1.27	0.145	-1.77	0.177	-1.32
1425102_a_at	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	-1.08	0.692	-1.22	0.746	-1.22	0.469	-2.01	0.224	-1.38
1424635_at	Eef1a1	eukaryotic translation elongation factor 1 alpha 1	-1.13	0.034	-1.18	0.447	-1.2	0.01	-1.23	0.052	-1.19
1426477_at	Rasa1	RAS p21 protein activator 1	-1.04	0.05	-1.02	0.703	-1.58	0	-1.47	0.132	-1.28
1431689_at	5830400J07Rik	RIKEN cDNA 5830400J07 gene	-1.28	0.169	-1.06	0.864	-1.18	0.604	-1.2	0.167	-1.18
1451649_a_at	Wdr75	WD repeat domain 75	-1.18	0.411	-1.05	0.296	-1.31	0.05	-1.4	0.131	-1.23

1427254_at	Zfp445	zinc finger protein 445	-1.07	0.718	-1.06	0.795	-1.45	0.13	-1.39	0.322	-1.24
1441062_at	Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog,	-1.1	0.747	-1.08	0.891	-1.37	0.461	-1.12	0.72	-1.17
1452101_at	Blmh	bleomycin hydrolase	-1.35	0.113	-1.14	0.297	-1.05	0.749	-1.03	0.919	-1.14
1423112_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-1.23	0.524	-1.27	0.079	-1.03	0.909	-1.09	0.698	-1.15
1455491_at	Hnrph3 /// LOC669	heterogeneous nuclear ribonucleoprotein H3 /// similar to heterogeneous nuclear	-1.25	0.295	-1.18	0.363	-1.08	0.531	-1.38	0.189	-1.22
1457743_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	-1.07	0.928	-1.34	0.718	-1.13	0.674	-1.24	0.534	-1.19
1417981_at	Insig2	insulin induced gene 2	-1.04	0.562	-1.22	0.367	-1.27	0.07	-1.31	0.119	-1.21
1424603_at	Sumf1	sulfatase modifying factor 1	-1.25	0.488	-1.01	0.971	-1.29	0.464	-1.72	0.319	-1.32
1429882_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	-1.1	0.679	-1.16	0.429	-1.25	0.268	-1.74	0.159	-1.31
1428998_at	Phf3	PHD finger protein 3	-1.1	0.135	-1.17	0.145	-1.25	0.11	-1.04	0.77	-1.14
1457751_at	4832420A03Rik	RIKEN cDNA 4832420A03 gene	-1.01	0.54	-1.11	0.553	-1.47	0.019	-1.12	0.474	-1.18
1460207_s_at	E2f5	E2F transcription factor 5	-1.24	0.079	-1.12	0.361	-1.15	0.092	-1.16	0.47	-1.17
1451554_a_at	Aph1a	anterior pharynx defective 1a homolog (C. elegans)	-1.05	0.627	-1.29	0.043	-1.19	0.329	-1.54	0.093	-1.27
1437050_s_at	Angel2	angel homolog 2 (Drosophila)	-1.05	0.494	-1.01	0.939	-1.58	0.043	-1.53	0.003	-1.29
1424564_at	2410001C21Rik	RIKEN cDNA 2410001C21 gene	-1.06	0.537	-1.41	0.113	-1.08	0.608	-1.05	0.221	-1.15
1448248_at	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	-1.07	0.664	-1.14	0.004	-1.33	0.064	-1.39	0.005	-1.23
1452992_at	LOC668450 /// LOC	similar to cell division cycle 26 /// similar to cell division cycle 26 /// similar to cell c	-1.35	0.256	-1.11	0.393	-1.08	0.446	-1.21	0.391	-1.19
1419141_at	Crygd	crystallin, gamma D	-1.04	0.946	-1.18	0.272	-1.3	0.106	-1.15	0.778	-1.17
1436740_at	A430108E01Rik	RIKEN cDNA A430108E01 gene	-1.09	0.357	-1.16	0.03	-1.27	0.182	-1.53	0.097	-1.26
1417465_at	Fnta	farnesyltransferase, CAAX box, alpha	-1.11	0.113	-1.09	0.432	-1.32	0	-1.25	0.108	-1.19
1452422_a_at	Snrpb2	U2 small nuclear ribonucleoprotein B	-1.16	0.15	-1.07	0.497	-1.29	0.008	-1.28	0.21	-1.2
1430398_at	4921517O11Rik	RIKEN cDNA 4921517O11 gene	-1.1	0.733	-1.47	0.45	-1.02	0.895	-1.13	0.869	-1.18
1455273_at	---	---	-1.13	0.732	-1.07	0.736	-1.32	0.142	-1.1	0.727	-1.16
1415788_at	Ublcp1	ubiquitin-like domain containing CTD phosphatase 1	-1.16	0.197	-1.15	0.154	-1.19	0.14	-1.18	0.307	-1.17
1437456_x_at	Ythdf1	YTH domain family 1	-1.11	0.2	-1.22	0.039	-1.18	0.079	-1.05	0.509	-1.14
1455290_at	Znrf2	zinc and ring finger 2	-1.22	0.244	-1.19	0.309	-1.1	0.561	-1.4	0.212	-1.23
1448828_at	Smc6	structural maintenance of chromosomes 6	-1.18	0.231	-1.26	0.135	-1.07	0.636	-1.05	0.766	-1.14
1445440_at	A430106J12Rik	RIKEN cDNA A430106J12 gene	-1.34	0.023	-1.05	0.81	-1.14	0.467	-1.02	0.852	-1.14
1424033_at	Sfrs7	splicing factor, arginine/serine-rich 7	-1.2	0.372	-1.15	0.106	-1.15	0.248	-1.32	0.124	-1.21
1431465_s_at	Fyttd1	forty-two-three domain containing 1	-1.27	0.509	-1.18	0.599	-1.07	0.802	-1.19	0.294	-1.18
1428302_at	Mrpl48	mitochondrial ribosomal protein L48	-1.22	0.016	-1.13	0.122	-1.15	0.25	-1.09	0.683	-1.15
1454989_at	Cspp1	centrosome and spindle pole associated protein 1	-1.35	0.164	-1.14	0.319	-1.04	0.785	-1.1	0.734	-1.16
1431610_at	5330439A09Rik	RIKEN cDNA 5330439A09 gene	-1.06	0.926	-1.1	0.851	-1.39	0.206	-1.07	0.869	-1.16
1434328_at	Rpl15	ribosomal protein L15	-1.15	0.295	-1.05	0.351	-1.34	0.099	-1.58	0.078	-1.28
1435341_at	Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	-1.13	0.452	-1.03	0.832	-1.39	0.065	-1.15	0.325	-1.18
1451325_at	Fyttd1	forty-two-three domain containing 1	-1.21	0.496	-1.06	0.854	-1.25	0.131	-1.25	0.36	-1.19
1423149_at	Skp1a	S-phase kinase-associated protein 1A	-1.02	0.865	-1.11	0.419	-1.43	0.002	-1	0.989	-1.14
1423108_at	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), membe	-1.04	0.921	-1.45	0.186	-1.09	0.568	-1.4	0.271	-1.24
1426954_at	Trim33 /// 8030451I	tripartite motif protein 33 /// RIKEN cDNA 8030451N04 gene	-1.3	0.101	-1.12	0.264	-1.1	0.283	-1.28	0.011	-1.2
1445239_at	Gatad2a	GATA zinc finger domain containing 2A	-1.13	0.682	-1.17	0.442	-1.2	0.417	-1.22	0.109	-1.18
1428589_at	Mrpl41	mitochondrial ribosomal protein L41	-1.13	0.201	-1.16	0.042	-1.21	0.153	-1.12	0.323	-1.15
1436371_at	Recql	RecQ protein-like	-1.19	0.576	-1.1	0.733	-1.22	0.436	-1.5	0.16	-1.25
1452825_at	5330410G16Rik	RIKEN cDNA 5330410G16 gene	-1.2	0.61	-1.29	0.595	-1.03	0.796	-1.02	0.869	-1.14
1427406_at	Trip11	thyroid hormone receptor interactor 11	-1.15	0.707	-1.02	0.942	-1.39	0.232	-1.6	0.26	-1.29
1417557_at	Ubxd1	UBX domain containing 1	-1.09	0.286	-1.18	0.138	-1.23	0.021	-1.6	0.082	-1.28
1435001_at	Plaa	phospholipase A2, activating protein	-1.24	0.167	-1.13	0.508	-1.14	0.037	-1.07	0.793	-1.14
1429633_at	Lcor	ligand dependent nuclear receptor corepressor	-1.05	0.467	-1.16	0.078	-1.31	0.07	-1.17	0.235	-1.17
1454894_at	Smurf2	SMAD specific E3 ubiquitin protein ligase 2	-1.17	0.087	-1.13	0.021	-1.21	0.094	-1.42	0.182	-1.23
1417846_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	-1.08	0.575	-1.17	0.089	-1.26	0.111	-1.4	0.287	-1.23
1436995_a_at	Rpl26	ribosomal protein L26	-1.17	0.094	-1.04	0.635	-1.31	0.004	-1.32	0.013	-1.21
1444049_at	Adat1	adenosine deaminase, tRNA-specific 1	-1.48	0.34	-1.09	0.733	-1.02	0.959	-1.08	0.541	-1.17
1418934_at	Mab21l2	mab-21-like 2 (C. elegans)	-1.04	0.846	-1.26	0.388	-1.22	0.637	-1.06	0.818	-1.14
1437406_x_at	Igfbp4	insulin-like growth factor binding protein 4	-1.08	0.437	-1.13	0.439	-1.31	0.55	-1.17	0.765	-1.17

1416210_at	Imp3	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.09	0.512	-1.26	0.034	-1.16	0.254	-1.36	0.077	-1.22
1457241_at	Lrrc48	Leucine rich repeat containing 48	-1.16	0.406	-1.03	0.898	-1.34	0.207	-1.47	0.223	-1.25
1446306_at	---	---	-1.14	0.531	-1.08	0.861	-1.29	0.56	-1.08	0.819	-1.15
1427088_at	Ccnt2	cyclin T2	-1.17	0.348	-1.18	0.3	-1.15	0.458	-1.21	0.34	-1.18
1446562_at	Sh3kbp1	SH3-domain kinase binding protein 1	-1.41	0.2	-1.09	0.88	-1.05	0.879	-1.5	0.028	-1.26
1429698_at	Mterf	mitochondrial transcription termination factor	-1.31	0.492	-1.03	0.838	-1.19	0.277	-1.37	0.139	-1.22
1457349_at	LOC639426	similar to Tetratricopeptide repeat protein 6 (TPR repeat protein 6)	-1.03	0.953	-1.28	0.387	-1.21	0.12	-3.33	0.036	-1.71
1455538_at	6330403M23Rik	RIKEN cDNA 6330403M23 gene	-1.13	0.2	-1.06	0.525	-1.34	0.024	-1.36	0.182	-1.22
1427949_at	Zfp294	zinc finger protein 294	-1.15	0.096	-1.14	0.049	-1.21	0.109	-1.05	0.593	-1.14
1435531_at	Usp3	ubiquitin specific peptidase 3	-1.11	0.446	-1.28	0.011	-1.12	0.247	-1.71	0.012	-1.3
1454740_at	Mib1	mindbomb homolog 1 (Drosophila)	-1.14	0.637	-1.01	0.925	-1.41	0.044	-1.13	0.676	-1.17
1444585_at	Adc	arginine decarboxylase	-1.17	0.285	-1.06	0.639	-1.28	0.175	-1.1	0.36	-1.15
1436698_x_at	BC054438	cDNA sequence BC054438	-1.07	0.81	-1.01	0.935	-1.54	0.026	-1.77	0.252	-1.35
1429159_at	4631408O11Rik	RIKEN cDNA 4631408O11 gene	-1.16	0.61	-1.26	0.054	-1.09	0.821	-2.06	0.103	-1.39
1424282_at	Pet112l	PET112-like (yeast)	-1.08	0.696	-1.23	0.416	-1.2	0.382	-1.22	0.088	-1.18
1429890_at	A930007D18Rik	RIKEN cDNA A930007D18 gene	-1.12	0.615	-1.07	0.849	-1.32	0.51	-1.7	0.112	-1.3
1435843_x_at	Mrps9	mitochondrial ribosomal protein S9	-1.12	0.186	-1.07	0.28	-1.34	0.247	-1.25	0.014	-1.19
1424197_s_at	Fance	Fanconi anemia, complementation group E	-1.16	0.57	-1.25	0.308	-1.09	0.691	-1.6	0.271	-1.27
1454987_a_at	H2-Ke6	H2-K region expressed gene 6	-1.02	0.904	-1.25	0.247	-1.25	0.053	-1.77	0.215	-1.32
1452692_a_at	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	-1.04	0.649	-1.21	0.114	-1.27	0.064	-1.08	0.499	-1.15
1426841_at	Ythdf3	YTH domain family 3	-1.05	0.013	-1.25	0.008	-1.2	0.04	-1.15	0.342	-1.16
1456803_at	Polr3c	Polymerase (RNA) III (DNA directed) polypeptide C	-1.01	0.977	-1.16	0.535	-1.37	0.287	-1.29	0.211	-1.21
1432458_at	1700011F14Rik	RIKEN cDNA 1700011F14 gene	-1.07	0.178	-1.08	0.654	-1.39	0.111	-1.29	0.185	-1.21
1437055_x_at	Mfsd1	Major facilitator superfamily domain containing 1	-1.52	0.06	-1.04	0.757	-1.04	0.845	-1.26	0.203	-1.21
1418316_a_at	Mark3	MAP/microtubule affinity-regulating kinase 3	-1.07	0.783	-1.22	0.112	-1.22	0.361	-1.01	0.96	-1.13
1416655_at	C1galt1c1	C1GALT1-specific chaperone 1	-1.06	0.095	-1.12	0.248	-1.35	0.008	-1.01	0.889	-1.13
1425482_s_at	Ankmy2	ankyrin repeat and MYND domain containing 2	-1.16	0.033	-1.11	0.459	-1.23	0.191	-1.37	0.164	-1.22
1434718_at	Cul3	cullin 3	-1.19	0.57	-1.21	0.3	-1.1	0.591	-1.15	0.417	-1.16
1418704_at	S100a13	S100 calcium binding protein A13	-1.03	0.714	-1.07	0.638	-1.49	0.025	-1.11	0.677	-1.17
1418101_a_at	Rtn3	reticulon 3	-1.09	0.383	-1.25	0.094	-1.16	0.075	-1.04	0.77	-1.14
1432423_a_at	C530008M17Rik	RIKEN cDNA C530008M17 gene	-1.27	0.468	-1.2	0.349	-1.04	0.778	-1.17	0.382	-1.17
1451901_at	Smarca3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.25	0.023	-1.03	0.937	-1.25	0.15	-1.31	0.331	-1.21
1429709_at	Pmpcb	peptidase (mitochondrial processing) beta	-1.1	0.233	-1.26	0.042	-1.14	0.039	-1.07	0.577	-1.14
1435139_at	Narg1	NMDA receptor-regulated gene 1	-1.19	0.26	-1.15	0.122	-1.15	0.258	-1.02	0.948	-1.13
1448998_at	Lpo	lactoperoxidase	-1.33	0.588	-1.13	0.499	-1.06	0.635	-2	0.12	-1.38
1451902_at	Zfp758	zinc finger protein 758	-1.15	0.011	-1.19	0.019	-1.14	0.066	-1.39	0.061	-1.22
1435901_at	Usp40	ubiquitin specific peptidase 40	-1.06	0.693	-1.14	0.336	-1.32	0.063	-1.34	0.324	-1.21
1423065_at	Dnmt3a	DNA methyltransferase 3A	-1.07	0.575	-1.18	0.344	-1.24	0.386	-1.19	0.274	-1.17
1434099_at	Ppargc1a	Peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	-1.23	0.456	-1.26	0.499	-1.03	0.918	-2.55	0.422	-1.52
1436691_x_at	Prdx1	peroxiredoxin 1	-1.16	0.07	-1.11	0.411	-1.22	0.011	-1.32	0.053	-1.2
1449623_at	Txnrd3	thioredoxin reductase 3	-1.11	0.092	-1.06	0.741	-1.35	0.069	-1.27	0.218	-1.2
1434065_at	Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	-1.27	0.01	-1.17	0.386	-1.07	0.388	-1.17	0.003	-1.17
1418038_s_at	Dusp19	dual specificity phosphatase 19	-1.08	0.021	-1.16	0.186	-1.26	0.063	-1.18	0.385	-1.17
1451968_at	Xrcc5	X-ray repair complementing defective repair in Chinese hamster cells 5	-1.32	0.017	-1.05	0.692	-1.15	0.339	-1.28	0.049	-1.2
1452234_s_at	D16Bwg1494e	DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed	-1.1	0.695	-1.24	0.416	-1.16	0.637	-1.35	0.102	-1.21
1434618_at	---	---	-1.21	0.075	-1.18	0.083	-1.1	0.573	-1.3	0.094	-1.2
1447066_at	---	Adult inner ear cDNA, RIKEN full-length enriched library, clone:F930039H20 proc	-1.35	0.745	-1.07	0.891	-1.11	0.734	-2.69	0.434	-1.55
1455682_at	AA536808	expressed sequence AA536808	-1.17	0.027	-1.16	0.288	-1.16	0.322	-1.35	0.082	-1.21
1433302_at	Cdh10	cadherin 10	-1.23	0.504	-1.1	0.812	-1.17	0.586	-1.48	0.209	-1.24
1428236_at	Acbd5	acyl-Coenzyme A binding domain containing 5	-1.07	0.671	-1.16	0.067	-1.27	0.025	-1.21	0.144	-1.18
1457302_at	Slc20a2	Solute carrier family 20, member 2	-1.23	0.107	-1.17	0.351	-1.09	0.592	-1.39	0.246	-1.22
1457735_at	---	Transcribed locus	-1.16	0.168	-1.03	0.965	-1.34	0.538	-1.02	0.708	-1.14
1444402_at	Zc3h12c	zinc finger CCCH type containing 12C	-1.12	0.125	-1.32	0.029	-1.07	0.698	-1.31	0.149	-1.21

1448488_at	Mrps5	mitochondrial ribosomal protein S5	-1.06	0.738	-1.13	0.132	-1.32	0.019	-1.11	0.515	-1.15
1427031_s_at	Ccdc52	coiled-coil domain containing 52	-1.19	0.44	-1.29	0.213	-1.03	0.53	-1.33	0.054	-1.21
1420870_at	Mllt10	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosop	-1.21	0.401	-1.29	0.048	-1.02	0.918	-1.12	0.41	-1.16
1457070_at	Uhrf2	Ubiquitin-like, containing PHD and RING finger domains 2	-1.1	0.628	-1.18	0.62	-1.21	0.313	-1.2	0.689	-1.17
1423622_a_at	Ccnl1	cyclin L1	-1.04	0.849	-1.13	0.188	-1.37	0.097	-1.31	0.199	-1.21
1453475_at	4930445K14Rik	RIKEN cDNA 4930445K14 gene	-1.18	0.045	-1.08	0.622	-1.23	0.382	-1.26	0.004	-1.19
1424634_at	Tceal1	transcription elongation factor A (SII)-like 1	-1.06	0.808	-1.15	0.623	-1.31	0.115	-1.15	0.346	-1.17
1453774_at	2810002O09Rik	RIKEN cDNA 2810002O09 gene	-1.06	0.63	-1.12	0.597	-1.34	0.209	-1.32	0.371	-1.21
1448858_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	-1.09	0.262	-1.29	0.191	-1.12	0.56	-1.13	0.217	-1.16
1459359_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	-1.09	0.552	-1.26	0.662	-1.14	0.75	-1.76	0.315	-1.31
1434949_at	Armc8	armadillo repeat containing 8	-1.16	0.529	-1.08	0.501	-1.25	0.103	-1.24	0.413	-1.18
1416668_at	4921531G14Rik	RIKEN cDNA 4921531G14 gene	-1.1	0.254	-1.02	0.591	-1.44	0.001	-1.38	0.247	-1.24
1426152_a_at	Kitl	kit ligand	-1.03	0.862	-1.26	0.473	-1.22	0.454	-1.01	0.924	-1.13
1435096_at	Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	-1.13	0.424	-1.28	0.067	-1.09	0.499	-1.37	0.054	-1.22
1449056_at	E330009J07Rik	RIKEN cDNA E330009J07 gene	-1.03	0.846	-1.16	0.236	-1.32	0.145	-1.83	0.013	-1.34
1438821_at	Rfwd2	Ring finger and WD repeat domain 2	-1.22	0.678	-1.07	0.801	-1.2	0.379	-1.26	0.251	-1.19
1425480_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	-1	0.995	-1.25	0.04	-1.27	0.041	-1.26	0.512	-1.2
1423324_at	Pnn	pinin	-1.16	0.453	-1.11	0.543	-1.21	0.468	-1.33	0.414	-1.2
1450973_s_at	Mapkbp1	mitogen activated protein kinase binding protein 1	-1.06	0.738	-1.16	0.256	-1.29	0.207	-1.27	0.29	-1.19
1436436_at	Cnih4	cornichon homolog 4 (Drosophila)	-1.03	0.748	-1.26	0.129	-1.21	0.086	-1.12	0.28	-1.16
1439962_at	2310010J17Rik	RIKEN cDNA 2310010J17 gene	-1.26	0.256	-1.03	0.862	-1.22	0.424	-1.18	0.767	-1.17
1416926_at	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	-1.06	0.784	-1.12	0.478	-1.33	0.287	-1.06	0.883	-1.14
1443534_at	---	---	-1.03	0.629	-1.04	0.831	-1.54	0.099	-1.81	0.129	-1.35
1422126_a_at	Nudt13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	-1.28	0.328	-1.01	0.958	-1.23	0.119	-1.35	0.214	-1.22
1430578_at	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	-1.05	0.943	-1.13	0.598	-1.34	0.076	-1.08	0.804	-1.15
1450840_a_at	Rpl39	ribosomal protein L39	-1.04	0.753	-1.08	0.638	-1.43	0.017	-1.24	0.008	-1.2
1452133_at	Uqcrh	ubiquinol-cytochrome c reductase hinge protein	-1.13	0.094	-1.2	0.029	-1.15	0.381	-1.15	0.39	-1.16
1430344_at	2900064P18Rik	RIKEN cDNA 2900064P18 gene	-1.01	0.949	-1.3	0.474	-1.21	0.72	-1.6	0.385	-1.28
1448032_at	Azi2	5-azacytidine induced gene 2	-1.04	0.851	-1.19	0.104	-1.27	0.234	-1.17	0.185	-1.17
1453160_at	Thrap1	thyroid hormone receptor associated protein 1	-1.06	0.351	-1.06	0.699	-1.43	0.06	-1.12	0.353	-1.17
1441642_at	Large	Like-glycosyltransferase	-1.36	0.328	-1.01	0.976	-1.16	0.669	-1.2	0.412	-1.18
1431198_x_at	9430038I01Rik	RIKEN cDNA 9430038I01 gene	-1.09	0.61	-1.43	0.272	-1.03	0.871	-1.3	0.284	-1.21
1435977_at	Hdgfrp3	hepatoma-derived growth factor, related protein 3	-1.1	0.467	-1.11	0.802	-1.28	0.3	-1.22	0.594	-1.18
1453186_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	-1.09	0.53	-1.12	0.619	-1.29	0.181	-1.19	0.645	-1.17
1437751_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	-1.11	0.362	-1.24	0.36	-1.13	0.195	-1.95	0.146	-1.36
1435462_at	LOC433022	hypothetical LOC433022	-1.05	0.549	-1.27	0.304	-1.17	0.499	-1.62	0.166	-1.28
1442093_at	Adc	Arginine decarboxylase	-1.27	0.68	-1.02	0.962	-1.22	0.364	-1.34	0.529	-1.21
1421560_at	Snai3	snail homolog 3 (Drosophila)	-1.23	0.153	-1.04	0.89	-1.24	0.304	-1.29	0.491	-1.2
1438859_x_at	Rps29 /// LOC6299	ribosomal protein S29 /// similar to 40S ribosomal protein S29 /// similar to 40S rib	-1.18	0.068	-1.03	0.856	-1.29	0.013	-1.22	0.051	-1.18
1448598_at	Mmp17	matrix metallopeptidase 17	-1.24	0.337	-1.17	0.754	-1.08	0.767	-1.13	0.049	-1.15
1426675_at	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	-1.08	0.694	-1.07	0.101	-1.37	0.074	-1.04	0.688	-1.14
1433738_at	5730445M16Rik	RIKEN cDNA 5730445M16 gene	-1.02	0.752	-1.16	0.201	-1.33	0.036	-1.29	0.089	-1.2
1429050_at	Chic2	cysteine-rich hydrophobic domain 2	-1.03	0.709	-1.23	0.25	-1.25	0.077	-1.06	0.509	-1.14
1428161_a_at	Chchd2	coiled-coil-helix-coiled-coil-helix domain containing 2	-1.13	0.045	-1.19	0.163	-1.15	0.033	-1.13	0.027	-1.15
1453229_s_at	Uqcrh	ubiquinol-cytochrome c reductase hinge protein	-1.21	0.046	-1.11	0.191	-1.16	0.207	-1.59	0.083	-1.27
1434041_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.12	0.327	-1.06	0.67	-1.34	0.134	-1.28	0.135	-1.2
1441973_at	Zfp295	zinc finger protein 295	-1.04	0.178	-1.17	0.596	-1.3	0.413	-1.16	0.157	-1.17
1434562_at	Mfap3	microfibrillar-associated protein 3	-1.15	0.305	-1.05	0.639	-1.31	0.03	-1.1	0.505	-1.15
1418544_at	Kcnip3	Kv channel interacting protein 3, calsenilin	-1.26	0.375	-1.12	0.142	-1.11	0.516	-1.24	0.446	-1.18
1457355_at	---	---	-1.23	0.329	-1.19	0.384	-1.07	0.555	-1.19	0.518	-1.17
1441339_at	Chd9	chromodomain helicase DNA binding protein 9	-1.26	0.346	-1.1	0.288	-1.13	0.443	-1.38	0.101	-1.22
1453399_at	Ccnt2	Cyclin T2	-1.1	0.577	-1.09	0.494	-1.31	0.24	-1.55	0.004	-1.26
1426776_at	Wasl	Wiskott-Aldrich syndrome-like (human)	-1.07	0.264	-1.08	0.097	-1.36	0.182	-1	0.995	-1.13

1419945_s_at	Rab2	RAB2, member RAS oncogene family	-1.14	0.194	-1.05	0.207	-1.3	0.019	-1.18	0.383	-1.17
1445317_at	Sdha	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-1	0.909	-1.09	0.547	-1.49	0.065	-1.36	0.224	-1.23
1455036_s_at	Ndufc2 /// LOC675	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 /// similar to NADI	-1.17	0.017	-1.1	0.219	-1.21	0.039	-1.06	0.212	-1.14
1459773_x_at	Snip1	Smad nuclear interacting protein 1	-1.1	0.228	-1.23	0.107	-1.15	0.373	-1.29	0.146	-1.19
1426531_at	Zmynd11	zinc finger, MYND domain containing 11	-1.08	0.258	-1.14	0.329	-1.27	0.075	-1.52	0.242	-1.25
1423696_a_at	Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	-1.18	0.104	-1.04	0.764	-1.27	0.02	-1.19	0.362	-1.17
1435207_at	Dixdc1	DIX domain containing 1	-1.23	0.421	-1.11	0.564	-1.14	0.055	-1.64	0.039	-1.28
1455543_at	Klhl18	kelch-like 18 (Drosophila)	-1.24	0.423	-1.25	0.348	-1.01	0.942	-1.47	0.234	-1.24
1423211_at	Nola3	nucleolar protein family A, member 3	-1.22	0.226	-1.09	0.151	-1.17	0.276	-1.16	0.271	-1.16
1424577_at	Msto1	misato homolog 1 (Drosophila)	-1.13	0.222	-1.13	0.661	-1.22	0	-1.14	0.477	-1.15
1431745_a_at	Zc3h14	zinc finger CCCH type containing 14	-1.21	0.133	-1.27	0.005	-1.02	0.824	-1.02	0.861	-1.13
1428505_at	2310015N07Rik	RIKEN cDNA 2310015N07 gene	-1.17	0.107	-1.07	0.19	-1.25	0.002	-1.18	0.071	-1.17
1422581_at	Pias1	protein inhibitor of activated STAT 1	-1.18	0.223	-1.05	0.648	-1.26	0.152	-1.43	0.048	-1.23
1435803_a_at	Eif4e2	eukaryotic translation initiation factor 4E member 2	-1.16	0.223	-1.18	0.246	-1.14	0.243	-1.1	0.381	-1.14
1428594_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.21	0.08	-1.09	0.452	-1.17	0.247	-1.2	0.353	-1.17
1448689_at	Rras2	related RAS viral (r-ras) oncogene homolog 2	-1.05	0.52	-1.07	0.013	-1.42	0.038	-2.29	0.097	-1.46
1428760_at	Snapc3	small nuclear RNA activating complex, polypeptide 3	-1.3	0.016	-1.09	0.571	-1.1	0.379	-1.24	0.437	-1.18
1443167_at	Rnf12	Ring finger protein 12	-1	0.999	-1.05	0.739	-1.56	0	-1.21	0.071	-1.21
1429512_at	Zpbp2	zona pellucida binding protein 2	-1.11	0.821	-1.37	0.533	-1.04	0.877	-1.24	0.489	-1.19
1428230_at	Prkcn	protein kinase C, nu	-1.12	0.457	-1.24	0.213	-1.12	0.295	-1.89	0.082	-1.34
1424430_at	Mterfd2	MTERF domain containing 2	-1.19	0.215	-1.19	0.171	-1.1	0.615	-1.14	0.438	-1.15
1420139_s_at	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	-1.15	0.38	-1.14	0.133	-1.17	0.059	-1.12	0.169	-1.15
1419188_s_at	Ccl27	chemokine (C-C motif) ligand 27	-1.11	0.188	-1.17	0.343	-1.2	0.317	-1.31	0.511	-1.2
1429087_at	1110054O05Rik	RIKEN cDNA 1110054O05 gene	-1.3	0.625	-1.21	0.329	-1	0.997	-1.06	0.589	-1.14
1458656_at	AW050198	expressed sequence AW050198	-1.13	0.489	-1.08	0.478	-1.28	0.141	-1.32	0.061	-1.2
1446616_at	Gltscr1	Glioma tumor suppressor candidate region gene 1	-1.09	0.872	-1.2	0.512	-1.19	0.272	-1.08	0.831	-1.14
1444315_at	D630024D03Rik	RIKEN cDNA D630024D03 gene	-1.14	0.316	-1.28	0.499	-1.07	0.701	-1.68	0.42	-1.29
1417264_at	Coq5	coenzyme Q5 homolog, methyltransferase (yeast)	-1.07	0.312	-1.15	0.335	-1.27	0.283	-1	0.999	-1.12
1425534_at	Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	-1.06	0.292	-1.22	0.347	-1.2	0.407	-1.61	0.114	-1.27
1453322_at	Wdr33	WD repeat domain 33	-1.14	0.089	-1.04	0.797	-1.32	0.161	-1.18	0.205	-1.17
1449702_at	Zfand2a	zinc finger, AN1-type domain 2A	-1.07	0.629	-1.2	0.364	-1.2	0.118	-1.36	0.105	-1.21
1428086_at	Dnm1l	dynamin 1-like	-1.2	0.443	-1.13	0.205	-1.14	0.324	-1.24	0.153	-1.18
1439738_at	---	---	-1.21	0.488	-1.04	0.84	-1.23	0.571	-1.23	0.623	-1.18
1419489_at	AW049604	expressed sequence AW049604	-1.11	0.04	-1.05	0.897	-1.35	0.42	-1.61	0.368	-1.28
1440384_at	Tmcc1	transmembrane and coiled coil domains 1	-1.32	0.13	-1.04	0.49	-1.15	0.136	-1.01	0.973	-1.13
1422508_at	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	-1.2	0.314	-1.09	0.424	-1.19	0.213	-1.15	0.277	-1.16
1424893_at	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	-1.06	0.796	-1.03	0.724	-1.46	0.209	-1.14	0.456	-1.17
1452632_at	LOC637741	hypothetical protein LOC637741	-1.08	0.531	-1.36	0.141	-1.07	0.786	-1.43	0.103	-1.24
1452056_s_at	Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	-1.09	0.274	-1.1	0.255	-1.3	0.019	-1.5	0.107	-1.25
1436051_at	9630007J19Rik	RIKEN cDNA 9630007J19 gene	-1.31	0.05	-1.14	0.493	-1.05	0.848	-1.41	0.311	-1.23
1434401_at	Zcchc2	zinc finger, CCHC domain containing 2	-1.08	0.492	-1.3	0.094	-1.11	0.459	-1.65	0.058	-1.29
1418312_at	Zfp276	zinc finger protein (C2H2 type) 276	-1.13	0.485	-1.27	0.178	-1.08	0.334	-1.02	0.891	-1.13
1436317_at	D230012E17Rik	RIKEN cDNA D230012E17 gene	-1.1	0.67	-1.15	0.258	-1.22	0.271	-2.35	0.054	-1.46
1432749_at	---	---	-1.51	0.154	-1.06	0.543	-1.01	0.97	-1.47	0.654	-1.26
1441536_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-1.26	0.136	-1.03	0.927	-1.2	0.065	-1.56	0.43	-1.26
1417553_at	Plac1	placental specific protein 1	-1.25	0.663	-1.01	0.964	-1.23	0.401	-1.04	0.844	-1.14
1453145_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	-1.08	0.161	-1.03	0.916	-1.44	0.071	-1.55	0.261	-1.27
1446375_at	Exoc6	Exocyst complex component 6	-1.06	0.91	-1.1	0.149	-1.34	0.628	-1.09	0.871	-1.15
1429923_x_at	Spata3	spermatogenesis associated 3	-1.22	0.715	-1.19	0.329	-1.06	0.525	-2.37	0.124	-1.46
1448337_at	2410003P15Rik	RIKEN cDNA 2410003P15 gene	-1.05	0.717	-1.39	0.13	-1.08	0.576	-1.06	0.532	-1.15
1433478_at	Parl	presenilin associated, rhomboid-like	-1.24	0.161	-1.21	0.024	-1.04	0.745	-1.53	0.056	-1.25
1452256_at	1110002N22Rik	RIKEN cDNA 1110002N22 gene	-1.18	0.146	-1.1	0.21	-1.19	0.238	-1.17	0.253	-1.16
1441203_at	---	CDNA clone IMAGE:30543871	-1.32	0.04	-1.13	0.731	-1.04	0.806	-1.07	0.767	-1.14

1420487_at	Nol7	nucleolar protein 7	-1.25	0.473	-1.13	0.628	-1.1	0.508	-1.37	0.26	-1.21
1447158_at	---	---	-1.23	0.547	-1.1	0.69	-1.15	0.407	-1.55	0.506	-1.25
1437070_at	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	-1.21	0.317	-1.23	0.056	-1.04	0.832	-1.34	0.294	-1.21
1456820_at	---	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030	-1.09	0.701	-1.04	0.933	-1.4	0.47	-1.19	0.592	-1.18
1424001_at	Mki67ip	Mki67 (FHA domain) interacting nucleolar phosphoprotein	-1.07	0.733	-1.12	0.123	-1.3	0.096	-1.03	0.761	-1.13
1417157_at	Actr10	ARP10 actin-related protein 10 homolog (S. cerevisiae)	-1.16	0.093	-1.15	0.245	-1.16	0.102	-1.18	0.375	-1.16
1437446_at	Rab5b	RAB5B, member RAS oncogene family	-1.06	0.565	-1.07	0.802	-1.38	0.11	-1.3	0.059	-1.2
1435557_at	Fhod1	formin homology 2 domain containing 1	-1.42	0.208	-1.06	0.862	-1.05	0.879	-1.14	0.714	-1.17
1443677_at	E030011O05Rik	RIKEN cDNA E030011O05 gene	-1.35	0.441	-1.02	0.962	-1.14	0.623	-1.42	0.081	-1.23
1454705_at	D15Ertd621e	DNA segment, Chr 15, ERATO Doi 621, expressed	-1.21	0.031	-1.08	0.065	-1.18	0.172	-1.15	0.519	-1.16
1456798_at	9330118A15Rik	RIKEN cDNA 9330118A15 gene	-1.02	0.944	-1.05	0.947	-1.5	0.222	-1.45	0.674	-1.26
1425178_s_at	Shmt1	serine hydroxymethyl transferase 1 (soluble)	-1.3	0.093	-1.06	0.725	-1.13	0.487	-1.1	0.358	-1.15
1436117_at	A830010M20Rik	RIKEN cDNA A830010M20 gene	-1.31	0.006	-1.06	0.082	-1.12	0.382	-1.28	0.524	-1.19
1424188_at	Rabgap1	RAB GTPase activating protein 1	-1.04	0.089	-1.13	0.04	-1.33	0.122	-1.22	0.319	-1.18
1436767_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	-1.1	0.536	-1.12	0.305	-1.26	0.19	-1.21	0.246	-1.17
1433562_s_at	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	-1.16	0.267	-1.19	0.071	-1.12	0.121	-1.03	0.745	-1.12
1456975_at	Taok1	TAO kinase 1	-1.08	0.837	-1.14	0.638	-1.26	0.307	-1.33	0.265	-1.2
1421643_at	Zfpn1a2	zinc finger protein, subfamily 1A, 2 (Helios)	-1.38	0.28	-1.02	0.955	-1.12	0.448	-1.57	0.604	-1.27
1455418_at	---	Transcribed locus	-1.04	0.752	-1.05	0.872	-1.47	0.11	-1.29	0.145	-1.21
1417663_a_at	Ndrg3	N-myc downstream regulated gene 3	-1.1	0.31	-1.09	0.414	-1.31	0.104	-1.24	0.038	-1.18
1416212_at	Magoh	mago-nashi homolog, proliferation-associated (Drosophila)	-1.14	0.058	-1.13	0.023	-1.2	0.095	-1.16	0.326	-1.16
1435295_at	Dopey1	dopey family member 1	-1.28	0.152	-1.05	0.748	-1.16	0.515	-1.28	0.196	-1.19
1460123_at	Gpr1	G protein-coupled receptor 1	-1.21	0.561	-1.22	0.699	-1.05	0.837	-1.02	0.915	-1.13
1436040_at	2310005L22Rik	RIKEN cDNA 2310005L22 gene	-1.3	0.298	-1.2	0.265	-1.01	0.954	-1.23	0.152	-1.18
1442086_at	Mta3	Metastasis associated 3	-1.32	0.065	-1.17	0.793	-1.02	0.952	-1.31	0.253	-1.2
1444010_at	LOC668879 /// LOC	hypothetical protein LOC668879 /// hypothetical protein LOC669500	-1.05	0.853	-1.36	0.413	-1.1	0.315	-1.62	0.144	-1.28
1458887_at	Tcf21	transcription factor 21	-1.09	0.718	-1.23	0.658	-1.15	0.529	-1.45	0.172	-1.23
1428258_at	2010107E04Rik	RIKEN cDNA 2010107E04 gene	-1.19	0.079	-1.15	0.123	-1.13	0.473	-1.02	0.91	-1.12
1434839_s_at	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	-1.27	0.103	-1.13	0.221	-1.08	0.496	-1.24	0.371	-1.18
1422893_at	Sfmbt1	Scm-like with four mbt domains 1	-1.07	0.589	-1.35	0.032	-1.08	0.61	-1.11	0.644	-1.15
1436191_at	Arid4a	AT rich interactive domain 4A (Rbp1 like)	-1.16	0.338	-1.04	0.746	-1.3	0.138	-1.29	0.354	-1.19
1428798_s_at	0610039J04Rik	RIKEN cDNA 0610039J04 gene	-1.19	0.361	-1.16	0.438	-1.12	0.497	-1.17	0.376	-1.16
1418983_at	Inadl	InaD-like (Drosophila)	-1.05	0.76	-1.37	0.153	-1.09	0.626	-1.86	0.052	-1.34
1452342_at	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	-1.04	0.705	-1	0.986	-1.55	0.082	-2.02	0.036	-1.4
1416057_at	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-1.15	0.296	-1.24	0.104	-1.09	0.427	-1	0.956	-1.12
1433641_at	Smad5	MAD homolog 5 (Drosophila)	-1.04	0.111	-1.05	0.541	-1.46	0.03	-1.25	0.039	-1.2
1449446_at	Ccdc59	coiled-coil domain containing 59	-1.16	0.349	-1.16	0.177	-1.14	0.407	-1.3	0.241	-1.19
1435161_at	D5Ertd135e	DNA segment, Chr 5, ERATO Doi 135, expressed	-1.08	0.68	-1.24	0.202	-1.15	0.394	-1.03	0.751	-1.13
1434181_at	Plekhc1	pleckstrin homology domain containing, family C (with FERM domain) member 1	-1.05	0.415	-1.19	0.577	-1.23	0.343	-1.77	0.209	-1.31
1418495_at	Zc3h8	zinc finger CCCH type containing 8	-1.45	0.043	-1.06	0.818	-1.03	0.852	-1.39	0.111	-1.23
1436128_at	Plekha8	pleckstrin homology domain containing, family A (phosphoinositide binding specif	-1.05	0.783	-1.07	0.621	-1.4	0.18	-1.03	0.928	-1.14
1422486_a_at	Smad4	MAD homolog 4 (Drosophila)	-1.04	0.752	-1.21	0.002	-1.24	0.014	-2.01	0.057	-1.37
1426879_at	1190005F20Rik	RIKEN cDNA 1190005F20 gene	-1.06	0.394	-1.28	0.095	-1.14	0.458	-1.44	0.023	-1.23
1417733_at	Rnf146	ring finger protein 146	-1.11	0.436	-1.09	0.099	-1.27	0.014	-1.27	0.053	-1.19
1419914_s_at	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	-1.13	0.525	-1.1	0.197	-1.23	0.12	-1.2	0.2	-1.17
1433784_at	AI265322	expressed sequence AI265322	-1.09	0.161	-1.1	0.397	-1.29	0.092	-1.19	0.346	-1.17
1452113_a_at	Rab23	RAB23, member RAS oncogene family	-1.3	0.241	-1.18	0.436	-1.01	0.934	-1.01	0.903	-1.13
1454574_at	C430049A07Rik	RIKEN cDNA C430049A07 gene	-1.47	0.635	-1.06	0.927	-1.02	0.883	-1.19	0.64	-1.18
1427416_x_at	LOC674944	similar to dual specificity phosphatase 7	-1.17	0.572	-1.12	0.692	-1.16	0.458	-1.48	0.244	-1.24
1429504_at	Rnpc3	RNA-binding region (RNP1, RRM) containing 3	-1.3	0.218	-1.1	0.693	-1.08	0.8	-1.32	0.259	-1.2
1420999_at	Cnot4	CCR4-NOT transcription complex, subunit 4	-1.01	0.739	-1.32	0.075	-1.17	0.157	-1.08	0.277	-1.14
1435329_at	Fbxl11	F-box and leucine-rich repeat protein 11	-1.11	0.464	-1.37	0.07	-1.03	0.9	-1.23	0.162	-1.19
1452633_s_at	LOC637741	hypothetical protein LOC637741	-1.19	0.258	-1.05	0.833	-1.24	0.272	-1.23	0.236	-1.18

1452309_at	Cgnl1 /// LOC6774	cingulin-like 1 /// similar to cingulin-like 1 isoform 1	-1.09	0.137	-1.03	0.782	-1.39	0.109	-1.22	0.385	-1.18
1448020_at	Rap1a	RAS-related protein-1a	-1.2	0.107	-1.07	0.575	-1.2	0.233	-1.1	0.703	-1.14
1437987_at	---	---	-1.09	0.47	-1.14	0.748	-1.23	0.315	-1.67	0.097	-1.28
1454880_s_at	Bmf	Bcl2 modifying factor	-1.19	0.497	-1.27	0.322	-1.03	0.899	-2	0.136	-1.37
1434468_at	Otud4	OTU domain containing 4	-1.11	0.544	-1.12	0.229	-1.22	0.029	-1.27	0.296	-1.18
1435927_at	Dennd3	DENN/MADD domain containing 3	-1.28	0.006	-1	0.997	-1.21	0.16	-2.07	0.082	-1.39
1419454_x_at	Pias2	protein inhibitor of activated STAT 2	-1.18	0.341	-1.08	0.634	-1.21	0.059	-1.02	0.909	-1.12
1452627_at	Senp6	SUMO/sentrin specific peptidase 6	-1.08	0.576	-1.09	0.377	-1.32	0.078	-1.19	0.26	-1.17
1443760_at	Dock1	Dedicator of cyto-kinesis 1	-1.24	0.729	-1.08	0.827	-1.15	0.734	-2.01	0.202	-1.37
1418016_at	Pum2	pumilio 2 (Drosophila)	-1.16	0.054	-1	0.97	-1.34	0.086	-1.15	0.175	-1.16
1435470_at	LOC547150	similar to p47 protein isoform a	-1.35	0.034	-1.01	0.977	-1.15	0.25	-1.2	0.487	-1.18
1448753_at	Srp9	signal recognition particle 9	-1.12	0.342	-1.03	0.518	-1.34	0.121	-1.38	0.196	-1.22
1423715_a_at	Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8	-1.07	0.627	-1.14	0.001	-1.25	0.021	-1.36	0.213	-1.21
1439278_at	Zbtb20	zinc finger and BTB domain containing 20	-1.26	0.317	-1	0.95	-1.23	0.392	-1.12	0.782	-1.15
1428631_a_at	Uqcrc2	ubiquinol cytochrome c reductase core protein 2	-1.18	0.017	-1.29	0.079	-1.02	0.901	-1.2	0.289	-1.17
1433527_at	Ireb2	iron responsive element binding protein 2	-1.17	0.367	-1.05	0.354	-1.26	0.075	-1.13	0.496	-1.15
1422925_s_at	Acot3	acyl-CoA thioesterase 3	-1.21	0.583	-1.22	0.788	-1.04	0.827	-1.11	0.833	-1.15
1435966_x_at	Mrpl13	mitochondrial ribosomal protein L13	-1.13	0.51	-1.08	0.642	-1.27	0.066	-1.17	0.437	-1.16
1459677_at	---	---	-1.17	0.67	-1.03	0.892	-1.29	0.246	-1.39	0.246	-1.22
1420374_at	Foxj2	forkhead box J2	-1.09	0.188	-1.06	0.783	-1.33	0.059	-1.3	0.146	-1.2
1423868_at	Txnrd3	thioredoxin reductase 3	-1.07	0.591	-1.23	0.086	-1.17	0.417	-1.47	0.54	-1.23
1422068_at	Pou3f1	POU domain, class 3, transcription factor 1	-1.09	0.481	-1.1	0.822	-1.29	0.29	-1.38	0.558	-1.21
1455911_x_at	Ndufb11	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11	-1.07	0.294	-1.14	0.152	-1.26	0.036	-1.19	0.259	-1.17
1426485_at	Ubxd2	UBX domain containing 2	-1.08	0.638	-1.27	0.254	-1.12	0.457	-1.08	0.78	-1.14
1447919_x_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-1.07	0.52	-1.39	0.07	-1.05	0.655	-1.27	0.435	-1.2
1438069_a_at	Rbm5	RNA binding motif protein 5	-1.06	0.863	-1.04	0.803	-1.43	0.273	-1.1	0.702	-1.16
1434397_at	Zdhhc17	zinc finger, DHHC domain containing 17	-1.08	0.254	-1.05	0.476	-1.37	0.034	-1.32	0.429	-1.21
1442995_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.23	0.088	-1.11	0.617	-1.12	0.719	-1.4	0.278	-1.22
1436681_x_at	0610009D07Rik	RIKEN cDNA 0610009D07 gene	-1.44	0.069	-1.01	0.957	-1.08	0.634	-1.02	0.801	-1.14
1455574_at	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.13	0.652	-1.01	0.97	-1.37	0.087	-1.09	0.526	-1.15
1436122_at	Zfp667	zinc finger protein 667	-1.15	0.442	-1.14	0.622	-1.16	0.26	-1.34	0.129	-1.2
1425134_a_at	Pigx	phosphatidylinositol glycan anchor biosynthesis, class X	-1.11	0.369	-1.2	0.109	-1.14	0.365	-1.66	0.046	-1.28
1434125_at	Utp15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.07	0.444	-1.24	0.016	-1.15	0.367	-1.07	0.719	-1.13
1450505_a_at	1810015C04Rik	RIKEN cDNA 1810015C04 gene	-1.2	0.565	-1.15	0.364	-1.11	0.657	-1.86	0.136	-1.33
1453524_at	5530401D11Rik	RIKEN cDNA 5530401D11 gene	-1.15	0.52	-1.09	0.806	-1.22	0.164	-1.46	0.217	-1.23
1459836_x_at	Sf3b2	splicing factor 3b, subunit 2	-1.21	0.815	-1.04	0.915	-1.22	0.022	-1.24	0.438	-1.18
1423273_at	Polg	polymerase (DNA directed), gamma	-1.16	0.542	-1.12	0.498	-1.17	0.01	-1.34	0.004	-1.2
1455554_at	A830039N20Rik	RIKEN cDNA A830039N20 gene	-1.15	0.705	-1.25	0.491	-1.06	0.86	-1.5	0.446	-1.24
1434994_at	Dedd	death effector domain-containing	-1.13	0.332	-1.21	0.213	-1.12	0.661	-1.11	0.575	-1.14
1428877_at	Srp72	signal recognition particle 72	-1.14	0.33	-1.2	0.004	-1.11	0.137	-1.05	0.53	-1.13
1418244_at	Nat5	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	-1.19	0.042	-1.06	0.46	-1.21	0.178	-1.01	0.792	-1.12
1427342_at	Fastkd1	FAST kinase domains 1	-1.17	0.32	-1.14	0.455	-1.14	0.415	-1.27	0.267	-1.18
1457681_at	2610301F02Rik	RIKEN cDNA 2610301F02 gene	-1.04	0.908	-1.29	0.11	-1.15	0.439	-1.01	0.873	-1.12
1418520_at	Tgoln1	trans-golgi network protein	-1.02	0.822	-1.45	0.018	-1.07	0.791	-1.06	0.784	-1.15
1456343_at	Slc35f1	solute carrier family 35, member F1	-1.19	0.493	-1.07	0.872	-1.2	0.433	-1.36	0.351	-1.2
1435280_at	AI452195	expressed sequence AI452195	-1.07	0.848	-1.05	0.853	-1.38	0.046	-1.23	0.329	-1.18
1441491_at	A330068G13Rik	RIKEN cDNA A330068G13 gene	-1.06	0.865	-1.09	0.854	-1.34	0.435	-1.29	0.185	-1.2
1430251_at	D330022H12Rik	RIKEN cDNA D330022H12 gene	-1.01	0.846	-1.05	0.9	-1.49	0.089	-1.08	0.894	-1.16
1438501_at	Rps17	Ribosomal protein S17	-1.17	0.029	-1.24	0.509	-1.06	0.804	-1.53	0.045	-1.25
1434604_at	Eif5b	eukaryotic translation initiation factor 5B	-1.16	0.452	-1.07	0.444	-1.23	0.182	-1.16	0.259	-1.16
1444057_at	---	Transcribed locus	-1.28	0.131	-1.09	0.142	-1.1	0.704	-1.32	0.163	-1.2
1460303_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	-1.09	0.6	-1.03	0.687	-1.38	0.103	-1.23	0.375	-1.18
1436256_at	Grpel2	GrpE-like 2, mitochondrial	-1.08	0.531	-1.21	0.452	-1.17	0.446	-1.28	0.162	-1.18

1428360_x_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	-1.09	0.19	-1.16	0.291	-1.2	0.098	-1.12	0.341	-1.14
1439780_at	Rpl7l1	ribosomal protein L7-like 1	-1.08	0.649	-1.14	0.217	-1.24	0.22	-1.26	0.133	-1.18
1434126_at	4930402H24Rik	RIKEN cDNA 4930402H24 gene	-1.25	0.429	-1.2	0.221	-1.02	0.937	-1.25	0.542	-1.18
1417674_s_at	Golga4	golgi autoantigen, golgin subfamily a, 4	-1.15	0.266	-1.17	0.148	-1.13	0.261	-1.12	0.404	-1.14
1422475_a_at	Rps3a	ribosomal protein S3a	-1.11	0.156	-1.05	0.202	-1.32	0.001	-1.36	0.024	-1.21
1433502_s_at	Tsr1	TSR1, 20S rRNA accumulation, homolog (yeast)	-1.03	0.884	-1.17	0.421	-1.28	0.062	-1.38	0.533	-1.21
1447936_at	2410006H16Rik	RIKEN cDNA 2410006H16 gene	-1.07	0.591	-1.26	0.111	-1.13	0.66	-2.45	0.034	-1.48
1431972_a_at	Gcap14	granule cell antiserum positive 14	-1.09	0.761	-1.3	0.361	-1.08	0.746	-1.64	0.175	-1.28
1458979_at	---	---	-1.04	0.968	-1.41	0.22	-1.06	0.901	-1.5	0.497	-1.25
1460096_at	Lamp1	Lysosomal membrane glycoprotein 1	-1.1	0.387	-1.08	0.355	-1.29	0.261	-1.04	0.895	-1.13
1449371_at	Harsl	histidyl-tRNA synthetase-like	-1.35	0.171	-1.07	0.595	-1.07	0.775	-1.21	0.183	-1.18
1418118_at	Slc22a1	solute carrier family 22 (organic cation transporter), member 1	-1.18	0.33	-1.26	0.002	-1.03	0.861	-1.39	0.283	-1.22
1424455_at	Gprasp1	G protein-coupled receptor associated sorting protein 1	-1.07	0.605	-1.12	0.376	-1.27	0.178	-1.39	0.322	-1.21
1433895_at	Tmem127	transmembrane protein 127	-1.05	0.825	-1.13	0.334	-1.3	0.222	-1.41	0.066	-1.22
1438560_x_at	Cct4	chaperonin subunit 4 (delta)	-1.2	0.326	-1.03	0.82	-1.24	0.072	-1.22	0.078	-1.17
1419244_a_at	Rab14	RAB14, member RAS oncogene family	-1.06	0.621	-1.21	0.2	-1.19	0.266	-1.62	0.085	-1.27
1428309_s_at	Pdrg1	p53 and DNA damage regulated 1	-1.02	0.806	-1.2	0.385	-1.25	0.19	-1.86	0.084	-1.33
1427078_at	Snx19	sorting nexin 19	-1.15	0.387	-1.26	0.096	-1.05	0.652	-1.13	0.387	-1.15
1451324_s_at	Fyttd1	forty-two-three domain containing 1	-1.28	0.424	-1.08	0.437	-1.1	0.068	-1.39	0.152	-1.21
1454781_x_at	Commd9	COMM domain containing 9	-1.05	0.375	-1.09	0.435	-1.36	0.267	-1.11	0.541	-1.15
1457011_at	---	Transcribed locus	-1.15	0.771	-1.18	0.492	-1.12	0.778	-3.13	0.072	-1.64
1429666_at	Kctd16	potassium channel tetramerisation domain containing 16	-1.16	0.771	-1.09	0.812	-1.2	0.576	-1.01	0.963	-1.11
1417847_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	-1.06	0.752	-1.29	0.007	-1.12	0.362	-1.14	0.609	-1.15
1427997_at	1110007M04Rik	RIKEN cDNA 1110007M04 gene	-1.06	0.778	-1.34	0.035	-1.08	0.347	-1.03	0.879	-1.13
1444403_at	Cbfa2t2h	Core-binding factor, runt domain, alpha subunit 2, translocated to, 2 homolog (hu	-1.15	0.725	-1.15	0.396	-1.14	0.681	-1.31	0.218	-1.19
1452901_at	Creb1	cAMP responsive element binding protein 1	-1.04	0.815	-1.06	0.353	-1.4	0.018	-1.36	0.24	-1.22
1428633_at	Twistnb /// LOC627	TWIST neighbor /// similar to TWIST neighbor /// similar to TWIST neighbor	-1.18	0.31	-1.03	0.935	-1.26	0.228	-1.23	0.375	-1.17
1441139_at	B330003H21	hypothetical protein B330003H21	-1.45	0.227	-1.03	0.92	-1.05	0.841	-1.09	0.74	-1.15
1440332_at	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	-1.01	0.907	-1.13	0.386	-1.36	0.138	-1.32	0.396	-1.2
1436636_at	---	---	-1.03	0.806	-1.37	0.068	-1.1	0.682	-1.07	0.679	-1.14
1422490_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	-1.1	0.287	-1.02	0.81	-1.37	0.032	-1.32	0.141	-1.21
1456758_at	9930017N22Rik	RIKEN cDNA 9930017N22 gene	-1.05	0.199	-1.14	0.215	-1.26	0.167	-1.46	0.095	-1.23
1436924_x_at	Ero1l /// Rpl31 /// LO	ERO1-like (S. cerevisiae) /// ribosomal protein L31 /// similar to ribosomal protein	-1.1	0.186	-1.07	0.449	-1.3	0.003	-1.31	0	-1.19
1424637_s_at	2610204L23Rik	RIKEN cDNA 2610204L23 gene	-1.03	0.919	-1.08	0.254	-1.39	0.043	-1.1	0.741	-1.15
1453741_x_at	Angel2	angel homolog 2 (Drosophila)	-1.16	0.7	-1.1	0.758	-1.19	0.714	-2.14	0.111	-1.4
1416669_s_at	Naca	nascent polypeptide-associated complex alpha polypeptide	-1.07	0.258	-1.22	0.131	-1.16	0.098	-1.32	0.038	-1.19
1451399_at	Pnkd	paroxysmal nonkinesiogenic dyskinesia	-1.03	0.785	-1.2	0.096	-1.22	0.134	-1.34	0.23	-1.2
1415734_at	Rab7	RAB7, member RAS oncogene family	-1.15	0.052	-1.09	0.014	-1.21	0.186	-1.28	0.293	-1.18
1437100_x_at	Pim3	proviral integration site 3	-1.11	0.64	-1.32	0.289	-1.04	0.765	-1.2	0.194	-1.17
1438025_at	Mtrf1l	mitochondrial translational release factor 1-like	-1.11	0.082	-1.12	0.459	-1.21	0.239	-1.01	0.96	-1.11
1456633_at	Trpm3	transient receptor potential cation channel, subfamily M, member 3	-1.08	0.729	-1.3	0.591	-1.08	0.775	-1.48	0.227	-1.24
1454859_a_at	Rpl23	ribosomal protein L23	-1.08	0.476	-1.06	0.646	-1.35	0.001	-1.38	0.026	-1.21
1442886_at	Tra2a	transformer 2 alpha homolog (Drosophila)	-1.09	0.689	-1.06	0.726	-1.32	0.19	-1.17	0.474	-1.16
1451570_a_at	6720467C03Rik	RIKEN cDNA 6720467C03 gene	-1.34	0.032	-1.06	0.43	-1.08	0.427	-1.07	0.385	-1.14
1423142_a_at	Gtpbp4	GTP binding protein 4	-1.26	0.516	-1.11	0.433	-1.08	0.569	-1.32	0.166	-1.19
1451113_a_at	Ik	IK cytokine	-1.15	0.362	-1.03	0.254	-1.28	0.048	-1.32	0.254	-1.2
1456018_at	AL022779	expressed sequence AL022779	-1.15	0.218	-1.15	0.116	-1.14	0.216	-1.14	0.227	-1.14
1448909_a_at	Mrpl39	mitochondrial ribosomal protein L39	-1.03	0.85	-1.35	0.104	-1.1	0.383	-1.37	0.1	-1.21
1441069_at	Zdhhc23	zinc finger, DHHC domain containing 23	-1.15	0.603	-1.2	0.8	-1.09	0.698	-1.28	0.385	-1.18
1443199_at	Lrch3	Leucine-rich repeats and calponin homology (CH) domain containing 3	-1.14	0.555	-1.02	0.949	-1.32	0.247	-1.01	0.973	-1.12
1416577_a_at	Rbx1	ring-box 1	-1.11	0.495	-1.1	0.052	-1.23	0.262	-1.02	0.841	-1.12
1452594_at	Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	-1.1	0.738	-1.05	0.661	-1.32	0.098	-1.76	0.025	-1.31
1437375_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430010E	-1.13	0.686	-1.15	0.645	-1.16	0.307	-1.32	0.358	-1.19

1419805_s_at	Ggps1	geranylgeranyl diphosphate synthase 1	-1.2	0.003	-1.11	0.48	-1.13	0.303	-1.56	0.022	-1.25
1430123_a_at	Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	-1.22	0.053	-1.13	0.576	-1.09	0.16	-1.16	0.212	-1.15
1434681_at	4932441K18Rik	RIKEN cDNA 4932441K18 gene	-1.28	0.169	-1.02	0.878	-1.17	0.359	-1.16	0.54	-1.16
1434793_at	Wdr78	WD repeat domain 78	-1.25	0.263	-1.21	0.572	-1.01	0.968	-1.19	0.579	-1.16
1448050_s_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	-1.25	0.561	-1.13	0.838	-1.07	0.36	-1.94	0.023	-1.35
1454568_at	6030460B20Rik	RIKEN cDNA 6030460B20 gene	-1.14	0.703	-1.13	0.739	-1.17	0.277	-1.47	0.01	-1.23
1449929_at	Dynlt3	dynein light chain Tctex-type 3	-1.07	0.375	-1.06	0.127	-1.35	0.029	-1.17	0.37	-1.16
1450084_s_at	Ivns1abp	influenza virus NS1A binding protein	-1.19	0.052	-1.11	0.603	-1.14	0.402	-1.24	0.438	-1.17
1428033_at	LOC245174	hypothetical protein LOC245174	-1.08	0.55	-1.23	0.654	-1.14	0.447	-1.17	0.5	-1.15
1443074_at	---	---	-1.09	0.075	-1.32	0.444	-1.06	0.768	-1.36	0.626	-1.21
1451494_at	Wac	WW domain containing adaptor with coiled-coil	-1.05	0.436	-1.07	0.327	-1.37	0.016	-1.33	0.052	-1.21
1437413_x_at	Rps29 /// LOC6299	ribosomal protein S29 /// similar to 40S ribosomal protein S29 /// similar to 40S rib	-1.15	0.011	-1.03	0.78	-1.29	0.009	-1.25	0.025	-1.18
1429608_at	Adh6a	alcohol dehydrogenase 6A (class V)	-1.13	0.866	-1.19	0.784	-1.12	0.876	-1.81	0.391	-1.31
1457537_at	Rab1	RAB1, member RAS oncogene family	-1.02	0.945	-1.16	0.677	-1.29	0.227	-1.19	0.233	-1.16
1455749_x_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	-1.05	0.606	-1.13	0.128	-1.27	0.169	-1.03	0.911	-1.12
1428339_at	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	-1.09	0.537	-1.15	0.161	-1.2	0.247	-1.03	0.881	-1.12
1455949_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-1.28	0.002	-1.14	0.829	-1.04	0.795	-1.01	0.988	-1.12
1460543_x_at	Rpl37a	ribosomal protein L37a	-1.11	0.077	-1.04	0.69	-1.33	0.001	-1.32	0.023	-1.2
1423898_a_at	Trip12	thyroid hormone receptor interactor 12	-1.2	0.265	-1.09	0.141	-1.15	0.304	-1.3	0.06	-1.19
1435696_s_at	3110031B13Rik	RIKEN cDNA 3110031B13 gene	-1.24	0.014	-1.04	0.661	-1.17	0.347	-1.02	0.848	-1.12
1426577_a_at	1810054G18Rik	RIKEN cDNA 1810054G18 gene	-1.15	0.539	-1.12	0.189	-1.16	0.137	-1.28	0.324	-1.18
1431202_at	Herc3	hect domain and RLD 3	-1.35	0.346	-1.13	0.838	-1.01	0.979	-1.13	0.483	-1.15
1457658_x_at	Anxa4	annexin A4	-1.22	0.32	-1.15	0.382	-1.07	0.769	-1.4	0.429	-1.21
1455021_at	Gabbr1	gamma-aminobutyric acid (GABA-B) receptor, 1	-1.01	0.901	-1.4	0.322	-1.09	0.682	-1.03	0.948	-1.13
1427916_at	St7l	suppression of tumorigenicity 7-like	-1.19	0.281	-1.06	0.661	-1.19	0.06	-1.08	0.497	-1.13
1426486_at	Ubxd2	UBX domain containing 2	-1.13	0.168	-1.1	0.214	-1.21	0.067	-1.06	0.674	-1.13
1423874_at	Wdr33	WD repeat domain 33	-1.28	0.199	-1.1	0.684	-1.08	0.538	-1.42	0.45	-1.22
1430526_a_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.13	0.475	-1.03	0.881	-1.32	0.19	-1.4	0.342	-1.22
1451276_at	E030041M21Rik	RIKEN cDNA E030041M21 gene	-1.08	0.188	-1.12	0.145	-1.25	0.119	-1.35	0.295	-1.2
1416938_at	Chchd1	coiled-coil-helix-coiled-coil-helix domain containing 1	-1.06	0.124	-1.08	0.087	-1.34	0.01	-1.29	0.324	-1.19
1441351_at	Ankib1	Ankyrin repeat and IBR domain containing 1	-1.28	0.446	-1.02	0.963	-1.17	0.36	-1.56	0.136	-1.26
1424488_a_at	Ppa2	pyrophosphatase (inorganic) 2	-1.08	0.017	-1.14	0.085	-1.21	0.046	-1.03	0.868	-1.12
1453545_at	5730492I20Rik	RIKEN cDNA 5730492I20 gene	-1.08	0.892	-1.1	0.425	-1.28	0.679	-1.68	0.074	-1.28
1438456_at	H13	histocompatibility 13	-1	0.981	-1.41	0.138	-1.09	0.549	-1.23	0.484	-1.18
1439859_at	9630033F20Rik	RIKEN cDNA 9630033F20 gene	-1.18	0.086	-1.11	0.576	-1.14	0.437	-1.14	0.464	-1.14
1436103_at	Rab3ip	RAB3A interacting protein	-1.07	0.563	-1.16	0.417	-1.2	0.118	-1.9	0.1	-1.34
1443496_at	Elmod1	ELMO domain containing 1	-1.53	0.104	-1.01	0.985	-1.02	0.955	-1.46	0.58	-1.26
1436234_at	4732471D19Rik	RIKEN cDNA 4732471D19 gene	-1.12	0.52	-1.36	0.074	-1	0.98	-1.2	0.475	-1.17
1430978_at	Rps25	ribosomal protein S25	-1.14	0.021	-1.2	0.34	-1.1	0.728	-1.47	0.073	-1.23
1425207_at	BC026439	cDNA sequence BC026439	-1.2	0.292	-1.22	0.636	-1.04	0.803	-2.37	0.289	-1.45
1437770_at	AW557046	expressed sequence AW557046	-1.02	0.489	-1.36	0.545	-1.11	0.8	-1	0.986	-1.12
1428503_a_at	Nkiras1	NFKB inhibitor interacting Ras-like protein 1	-1.12	0.381	-1.16	0.099	-1.15	0.399	-1.4	0.17	-1.21
1448584_at	Rsrc1	arginine/serine-rich coiled-coil 1	-1.08	0.549	-1.03	0.651	-1.37	0.064	-1.31	0.062	-1.2
1434919_at	---	Transcribed locus	-1.18	0.597	-1.1	0.767	-1.15	0.484	-1.13	0.707	-1.14
1457323_at	LOC632191	hypothetical protein LOC632191	-1.05	0.109	-1.05	0.726	-1.4	0.466	-1.16	0.644	-1.16
1444268_at	BC004004	cDNA sequence BC004004	-1.14	0.683	-1.28	0.27	-1.04	0.892	-1.24	0.47	-1.17
1452586_at	Anapc13	anaphase promoting complex subunit 13	-1.14	0.148	-1.08	0.084	-1.21	0.172	-1.14	0.318	-1.14
1419081_at	Atg10	autophagy-related 10 (yeast)	-1.1	0.469	-1.18	0.319	-1.15	0.039	-1.33	0.23	-1.19
1428830_at	Atm	ataxia telangiectasia mutated homolog (human)	-1.14	0.201	-1.18	0.093	-1.11	0.636	-1.89	0.143	-1.33
1424578_at	Arrdc1	arrestin domain containing 1	-1.14	0.516	-1.06	0.651	-1.24	0.096	-1.72	0.038	-1.29
1433068_at	6330582A15Rik	RIKEN cDNA 6330582A15 gene	-1.11	0.691	-1.25	0.238	-1.09	0.667	-1.1	0.804	-1.14
1426863_at	Rbmx	RNA binding motif protein, X chromosome	-1.16	0.586	-1	0.964	-1.3	0.385	-1.33	0.37	-1.2
1417704_a_at	Arhgap6	Rho GTPase activating protein 6	-1.2	0.4	-1.15	0.249	-1.09	0.526	-1.07	0.818	-1.13

1429163_at	Dchs1	dachsous 1 (Drosophila)	-1.11	0.725	-1.13	0.661	-1.2	0.395	-1.74	0.032	-1.29
1434070_at	Jag1	jagged 1	-1.22	0.056	-1.19	0.541	-1.04	0.769	-1.66	0.103	-1.28
1451903_at	Kynu	kynureninase (L-kynurenine hydrolase)	-1.18	0.811	-1.08	0.801	-1.17	0.576	-1.34	0.223	-1.19
1418092_s_at	Trip10	thyroid hormone receptor interactor 10	-1.07	0.672	-1.28	0.105	-1.1	0.512	-1.38	0.046	-1.21
1419291_x_at	Gas5	growth arrest specific 5	-1.02	0.715	-1.11	0.426	-1.34	0.158	-1.52	0.008	-1.25
1433594_at	Commd2	COMM domain containing 2	-1.12	0.535	-1.03	0.552	-1.32	0.168	-1.58	0.164	-1.26
1429456_a_at	Polr3e	polymerase (RNA) III (DNA directed) polypeptide E	-1.21	0.722	-1.19	0.322	-1.04	0.784	-1.2	0.13	-1.16
1451217_a_at	Immp1l	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	-1.06	0.231	-1.27	0.031	-1.12	0.377	-1.17	0.457	-1.15
1459630_at	---	Transcribed locus	-1.14	0.658	-1.06	0.8	-1.25	0.218	-1.09	0.52	-1.13
1434474_at	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	-1.09	0.529	-1.06	0.613	-1.31	0.177	-1.5	0.344	-1.24
1438673_at	---	---	-1.13	0.588	-1.17	0.068	-1.13	0.087	-1.51	0.133	-1.24
1446060_at	9230109A22Rik	RIKEN cDNA 9230109A22 gene	-1.2	0.817	-1.06	0.915	-1.18	0.575	-1.38	0.23	-1.2
1460572_a_at	Zfp511	zinc finger protein 511	-1.07	0.763	-1.11	0.571	-1.27	0.315	-1.48	0.034	-1.23
1425159_at	Golt1a	golgi transport 1 homolog A (S. cerevisiae)	-1.42	0.217	-1.04	0.636	-1.04	0.815	-1.35	0.536	-1.21
1418622_at	Rab2	RAB2, member RAS oncogene family	-1.1	0.238	-1.1	0.225	-1.24	0.088	-1.13	0.596	-1.14
1457086_at	LOC434147	hypothetical LOC434147	-1.13	0.509	-1.09	0.788	-1.22	0.622	-1.3	0.597	-1.18
1439049_at	Dph5	DPH5 homolog (S. cerevisiae)	-1.14	0.579	-1.03	0.837	-1.29	0.256	-2.48	0.056	-1.49
1448497_at	Ercc3	excision repair cross-complementing rodent repair deficiency, complementation g	-1.04	0.791	-1.22	0.122	-1.19	0.289	-1.18	0.339	-1.16
1422561_at	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.05	0.216	-1.42	0.153	-1.03	0.739	-1.39	0.269	-1.22
1434410_at	BC043118	cDNA sequence BC043118	-1.18	0.49	-1.18	0.153	-1.08	0.643	-1	0.989	-1.11
1436175_at	A430107N12Rik	RIKEN cDNA A430107N12 gene	-1.09	0.536	-1.02	0.858	-1.36	0.044	-1.43	0.212	-1.23
1423876_at	AI450540	expressed sequence AI450540	-1.1	0.52	-1.08	0.689	-1.26	0.183	-1.18	0.605	-1.16
1416015_s_at	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	-1.1	0.47	-1.11	0.222	-1.23	0.019	-1.02	0.883	-1.11
1456349_x_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	-1.13	0.435	-1.03	0.805	-1.3	0.007	-1.35	0.107	-1.2
1430300_at	Sco1	SCO cytochrome oxidase deficient homolog 1 (yeast)	-1.15	0.386	-1.16	0.292	-1.12	0.257	-1.12	0.469	-1.14
1434392_at	Usp34	ubiquitin specific peptidase 34	-1.08	0.734	-1.09	0.436	-1.28	0.059	-1.13	0.545	-1.14
1419351_a_at	0610007P06Rik	RIKEN cDNA 0610007P06 gene	-1.13	0.041	-1.23	0.204	-1.07	0.639	-1.12	0.41	-1.14
1428115_a_at	Rab2b	RAB2B, member RAS oncogene family	-1.16	0.397	-1.2	0.522	-1.07	0.586	-1.65	0.152	-1.27
1418000_a_at	Itm2b	integral membrane protein 2B	-1.08	0.066	-1.23	0.336	-1.13	0.084	-1.04	0.531	-1.12
1435128_at	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	-1	0.994	-1.5	0.249	-1.04	0.913	-1.09	0.761	-1.16
1441837_at	Chrnb2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	-1.16	0.637	-1.04	0.899	-1.24	0.597	-4.29	0.002	-1.93
1449436_s_at	Ubb /// LOC218963	ubiquitin B /// ubiquitin pseudogene /// gene model 1821, (NCBI) /// similar to poly	-1.08	0.351	-1.15	0.22	-1.2	0.031	-1.11	0.132	-1.14
1417340_at	Txnl2	thioredoxin-like 2	-1.18	0.123	-1.1	0.1	-1.15	0.142	-1.34	0.26	-1.19
1455403_at	Manea	mannosidase, endo-alpha	-1.23	0.041	-1.09	0.165	-1.11	0.163	-1.04	0.877	-1.12
1430575_a_at	Tpp2	tripeptidyl peptidase II	-1.02	0.84	-1.14	0.531	-1.3	0.07	-1.49	0.083	-1.24
1428461_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-1.19	0.587	-1.14	0.35	-1.09	0.224	-1.03	0.774	-1.12
1452970_at	Zmym2	zinc finger, MYM-type 2	-1.17	0.16	-1.09	0.337	-1.16	0.134	-1.2	0.089	-1.16
1446313_at	Zfp30	zinc finger protein 30	-1.05	0.707	-1.35	0.513	-1.07	0.87	-1.71	0.183	-1.3
1428898_at	Mon1a	MON1 homolog A (yeast)	-1.1	0.657	-1.17	0.298	-1.16	0.203	-1.2	0.298	-1.16
1443262_at	Mrps14	mitochondrial ribosomal protein S14	-1.18	0.196	-1.22	0.23	-1.04	0.827	-1.65	0.206	-1.27
1434568_at	---	Transcribed locus	-1.01	0.924	-1.13	0.643	-1.32	0.003	-1.21	0.509	-1.17
1460448_s_at	Ttc14	tetratricopeptide repeat domain 14	-1.06	0.85	-1.18	0.365	-1.2	0.361	-1.23	0.091	-1.17
1439788_at	Ccdc111	coiled-coil domain containing 111	-1.31	0.404	-1.12	0.193	-1.03	0.904	-1.2	0.2	-1.16
1416472_at	Syap1	synapse associated protein 1	-1.1	0.05	-1.12	0.211	-1.22	0.077	-1.08	0.708	-1.13
1454955_at	Ipo7	importin 7	-1.13	0.515	-1.18	0.21	-1.11	0.263	-1.06	0.829	-1.12
1454874_at	Btbd7	BTB (POZ) domain containing 7	-1.14	0.075	-1.1	0.548	-1.18	0.132	-1.21	0.323	-1.16
1427913_at	Rwdd1	RWD domain containing 1	-1.07	0.56	-1.09	0.272	-1.29	0.048	-1.3	0.113	-1.19
1430287_s_at	Hemk1	HemK methyltransferase family member 1	-1.09	0.758	-1.13	0.453	-1.21	0.524	-1.33	0.355	-1.19
1424604_s_at	Sumf1	sulfatase modifying factor 1	-1.04	0.742	-1.1	0.375	-1.32	0.085	-1.11	0.667	-1.14
1455742_x_at	Morf4l1 /// A730098	mortality factor 4 like 1 /// RIKEN cDNA A730098P11 gene /// similar to mortality f	-1.08	0.057	-1.07	0.08	-1.3	0.001	-1.18	0.034	-1.16
1428172_at	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	-1.03	0.725	-1.12	0.633	-1.31	0.147	-1.45	0.314	-1.23
1453520_at	Ttc21b	tetratricopeptide repeat domain 21B	-1.02	0.987	-1.09	0.918	-1.37	0.258	-2.47	0.099	-1.49
1437489_x_at	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	-1.3	0.086	-1.04	0.753	-1.11	0.388	-1.16	0.328	-1.15

1437993_x_at	Qdpr	quininoid dihydropteridine reductase	-1.16	0.035	-1.13	0.44	-1.13	0.191	-1.2	0.461	-1.15
1441980_at	C030007I09Rik	RIKEN cDNA C030007I09 gene	-1.19	0.326	-1.01	0.87	-1.24	0.179	-1.23	0.377	-1.17
1457814_at	1110014D18Rik	RIKEN cDNA 1110014D18 gene	-1.01	0.974	-1.45	0.056	-1.05	0.797	-1.18	0.369	-1.17
1455072_at	Cep350	centrosomal protein 350	-1.2	0.101	-1.07	0.499	-1.16	0.335	-1.12	0.467	-1.14
1435501_at	C030004M05Rik	RIKEN cDNA C030004M05 gene	-1.17	0.597	-1.24	0.222	-1.03	0.909	-1.24	0.417	-1.17
1429116_at	Slc17a5	solute carrier family 17 (anion/sugar transporter), member 5	-1.13	0.401	-1.03	0.873	-1.29	0.231	-1.04	0.91	-1.12
1458453_at	Lmo7	LIM domain only 7	-1.11	0.164	-1.31	0.651	-1.03	0.883	-1.91	0.044	-1.34
1428431_at	2310047A01Rik	RIKEN cDNA 2310047A01 gene	-1.17	0.264	-1.02	0.82	-1.26	0.235	-1.43	0.088	-1.22
1416943_at	Ube2e1 /// LOC631	ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast) /// similar to Ubiqui	-1.26	0	-1.1	0.021	-1.07	0.407	-1.45	0.088	-1.22
1434396_a_at	Myl6 /// LOC43329	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle /// similar to m	-1.01	0.922	-1.02	0.881	-1.53	0.003	-1.27	0.05	-1.21
1437405_a_at	Igfbp4	insulin-like growth factor binding protein 4	-1.13	0.39	-1.17	0.382	-1.12	0.599	-1.21	0.41	-1.16
1426124_a_at	Clk1	CDC-like kinase 1	-1.13	0.333	-1.16	0.377	-1.13	0.411	-1.44	0.182	-1.22
1438348_x_at	Ccbl1	cysteine conjugate-beta lyase 1	-1.06	0.891	-1.03	0.928	-1.39	0.396	-1.37	0.236	-1.21
1431333_at	Hist1h4h	histone 1, H4h	-1.23	0.806	-1.15	0.471	-1.06	0.814	-1.01	0.977	-1.11
1444883_at	Tmem19	transmembrane protein 19	-1	0.989	-1.01	0.977	-1.55	0.043	-1.59	0.23	-1.29
1434659_at	5830411G16Rik	RIKEN cDNA 5830411G16 gene	-1.05	0.535	-1.11	0.083	-1.27	0.065	-1.44	0.17	-1.22
1417935_at	Mkrn2	makorin, ring finger protein, 2	-1.22	0.054	-1.1	0.374	-1.11	0.421	-1.2	0.027	-1.16
1452239_at	Gt(ROSA)26Sor	gene trap ROSA 26, Philippe Soriano	-1.25	0.106	-1.06	0.746	-1.13	0.407	-1.28	0.062	-1.18
1429988_at	Zfp235	zinc finger protein 235	-1.15	0.46	-1.18	0.219	-1.09	0.526	-1	0.998	-1.11
1424681_a_at	Psma5	proteasome (prosome, macropain) subunit, alpha type 5	-1.17	0.025	-1.13	0.137	-1.12	0.299	-1.04	0.879	-1.11
1434162_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	-1.07	0.525	-1.13	0.155	-1.23	0.07	-1.19	0.231	-1.16
1434756_at	5430421B17	hypothetical protein 5430421B17	-1.05	0.632	-1.01	0.954	-1.43	0.132	-1.27	0.229	-1.19
1456540_s_at	Mtmr6	myotubularin related protein 6	-1.17	0.528	-1.06	0.704	-1.19	0.089	-1.42	0.103	-1.21
1459013_at	---	---	-1.16	0.61	-1.15	0.78	-1.11	0.823	-1.01	0.989	-1.11
1435662_at	2610020O08Rik	RIKEN cDNA 2610020O08 gene	-1.08	0.501	-1.1	0.464	-1.25	0.016	-1.28	0.307	-1.18
1434520_at	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	-1.08	0.46	-1.17	0.528	-1.17	0.358	-1.27	0.006	-1.17
1441119_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.21	0.034	-1.06	0.84	-1.15	0.396	-1.09	0.667	-1.13
1426598_at	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	-1.14	0.861	-1.19	0.838	-1.09	0.723	-1.36	0.639	-1.2
1427089_at	Ccnt2	cyclin T2	-1.1	0.564	-1.23	0.155	-1.09	0.59	-1.15	0.551	-1.14
1433669_at	Akap8	A kinase (PRKA) anchor protein 8	-1.12	0.229	-1.13	0.413	-1.17	0.205	-1.28	0.228	-1.17
1429549_at	Col27a1	procollagen, type XXVII, alpha 1	-1.06	0.607	-1.4	0.307	-1.03	0.952	-1.33	0.158	-1.2
1446548_at	Gltscr1	Glioma tumor suppressor candidate region gene 1	-1.04	0.927	-1.37	0.143	-1.06	0.874	-1.2	0.512	-1.17
1425533_a_at	Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	-1.07	0.639	-1.35	0.099	-1.04	0.718	-1.03	0.894	-1.12
1446194_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	-1.24	0.419	-1.04	0.857	-1.15	0.625	-1.17	0.336	-1.15
1447703_x_at	Zfp593	zinc finger protein 593	-1.21	0.083	-1.22	0.144	-1.02	0.953	-1.68	0.236	-1.28
1427319_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	-1.16	0.49	-1.28	0.091	-1	0.987	-1.48	0.271	-1.23
1415833_x_at	Rps29 /// LOC6299	ribosomal protein S29 /// similar to 40S ribosomal protein S29 /// similar to 40S rib	-1.12	0.101	-1.02	0.824	-1.32	0.007	-1.33	0.05	-1.2
1451219_at	Ormdl1	ORM1-like 1 (S. cerevisiae)	-1.03	0.861	-1.38	0.135	-1.07	0.719	-1.24	0.171	-1.18
1448137_at	Aldh7a1	aldehyde dehydrogenase family 7, member A1	-1.16	0.553	-1.15	0.664	-1.1	0.621	-1.24	0.29	-1.16
1455613_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-1.22	0.225	-1.21	0.323	-1	0.966	-1.02	0.857	-1.11
1439704_at	Hdac2	histone deacetylase 2	-1.08	0.814	-1.24	0.62	-1.1	0.61	-1.31	0.4	-1.18
1434078_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	-1.09	0.621	-1.15	0.235	-1.18	0.52	-1.11	0.114	-1.13
1456871_a_at	Phf20l1	PHD finger protein 20-like 1	-1.02	0.792	-1	0.979	-1.51	0.02	-1.12	0.446	-1.16
1417918_at	Mrpl11	mitochondrial ribosomal protein L11	-1.22	0.062	-1.16	0.023	-1.05	0.827	-1.39	0.052	-1.2
1434404_at	C030011O14Rik	RIKEN cDNA C030011O14 gene	-1.11	0.547	-1.19	0.583	-1.11	0.491	-1.26	0.447	-1.17
1456038_at	Fbxl4	F-box and leucine-rich repeat protein 4	-1.24	0.146	-1.08	0.154	-1.11	0.385	-1.11	0.724	-1.13
1436276_at	---	Transcribed locus	-1.01	0.94	-1.52	0.176	-1.01	0.959	-1.13	0.435	-1.17
1426518_at	Tubgcp5	tubulin, gamma complex associated protein 5	-1.12	0.43	-1.16	0.33	-1.13	0.5	-1.26	0.451	-1.17
1428152_a_at	Rpl18a	Ribosomal protein L18A	-1.02	0.887	-1.12	0.065	-1.31	0.007	-1.26	0.034	-1.18
1437704_at	2900024O10Rik	RIKEN cDNA 2900024O10 gene	-1.15	0.301	-1.07	0.685	-1.2	0.013	-1.5	0.072	-1.23
1438430_at	Hbp1	high mobility group box transcription factor 1	-1.05	0.094	-1.1	0.317	-1.29	0.007	-1.36	0.151	-1.2
1426844_a_at	Pdcd2l	programmed cell death 2-like	-1.29	0.139	-1.14	0.371	-1.02	0.915	-1.78	0.012	-1.3
1456429_at	Malt1	mucosa associated lymphoid tissue lymphoma translocation gene 1	-1.23	0.384	-1.13	0.518	-1.06	0.842	-1.84	0.143	-1.32

1426216_at	Cog6	component of oligomeric golgi complex 6	-1.22	0.009	-1.21	0.169	-1.01	0.9	-1.07	0.649	-1.13
1457606_x_at	AU015228	expressed sequence AU015228	-1.02	0.947	-1.07	0.432	-1.38	0.005	-1.42	0.289	-1.22
1442858_at	Phr1	Pam, highwire, rpm 1	-1.17	0.469	-1.05	0.895	-1.2	0.294	-1.53	0.148	-1.24
1459638_at	Ptpre	Protein tyrosine phosphatase, receptor type, E	-1.12	0.673	-1.14	0.649	-1.15	0.535	-1.21	0.532	-1.16
1441982_at	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.1	0.549	-1.27	0.516	-1.07	0.871	-1.28	0.749	-1.18
1425343_at	Hdhd3	haloacid dehalogenase-like hydrolase domain containing 3	-1.24	0.379	-1.04	0.77	-1.15	0.418	-1.27	0.69	-1.17
1425523_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	-1.2	0.12	-1.15	0.095	-1.06	0.5	-1.03	0.857	-1.11
1446239_at	4930444F02Rik	RIKEN cDNA 4930444F02 gene	-1.09	0.878	-1.18	0.472	-1.15	0.702	-1.27	0.348	-1.17
1445796_at	AI315068	Expressed sequence AI315068	-1.32	0.251	-1.02	0.954	-1.11	0.544	-1.08	0.653	-1.13
1447320_x_at	Rpo1-3	RNA polymerase 1-3	-1.08	0.735	-1.1	0.451	-1.25	0.174	-1.2	0.179	-1.16
1423444_at	Rock1	Rho-associated coiled-coil containing protein kinase 1	-1.1	0.561	-1.09	0.207	-1.23	0.062	-1.02	0.866	-1.11
1431150_at	1700110M21Rik	RIKEN cDNA 1700110M21 gene	-1.05	0.889	-1.19	0.729	-1.18	0.696	-1.61	0.494	-1.26
1422886_a_at	Clk4	CDC like kinase 4	-1.14	0.434	-1.08	0.606	-1.2	0.443	-1.12	0.633	-1.13
1451035_a_at	Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	-1.24	0.021	-1.09	0.224	-1.09	0.323	-1.19	0.291	-1.15
1450047_at	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	-1.11	0.725	-1.19	0.675	-1.12	0.538	-1.24	0.501	-1.16
1448853_at	Synj2bp	synaptojanin 2 binding protein	-1.05	0.616	-1.12	0.15	-1.25	0.135	-1.58	0.068	-1.25
1454750_a_at	BC057552	cDNA sequence BC057552	-1.03	0.803	-1.36	0.231	-1.07	0.725	-1.2	0.135	-1.17
1437180_at	6530403A03Rik	RIKEN cDNA 6530403A03 gene	-1.26	0.075	-1	0.991	-1.18	0.328	-1.38	0.185	-1.2
1431784_a_at	Bxdc5	brix domain containing 5	-1.13	0.369	-1.26	0.195	-1.04	0.764	-1.33	0.229	-1.19
1423322_at	Lin7c	lin-7 homolog C (C. elegans)	-1.09	0.026	-1.15	0.097	-1.17	0.009	-1.16	0.393	-1.14
1457219_at	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	-1.04	0.69	-1.21	0.712	-1.16	0.306	-2.12	0.084	-1.39
1445609_at	---	Transcribed locus	-1.02	0.889	-1.15	0.699	-1.26	0.69	-1.63	0.451	-1.27
1428777_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	-1.05	0.564	-1.37	0.149	-1.05	0.829	-1.03	0.86	-1.12
1455916_at	AI931714	expressed sequence AI931714	-1.13	0.517	-1.01	0.887	-1.3	0.197	-1.22	0.257	-1.17
1416174_at	Rbbp9	retinoblastoma binding protein 9	-1.1	0.374	-1.06	0.141	-1.26	0.147	-1.54	0.104	-1.24
1443693_at	AU022332	expressed sequence AU022332	-1.08	0.912	-1.28	0.651	-1.07	0.851	-1.03	0.921	-1.12
1429107_at	1110059H15Rik	RIKEN cDNA 1110059H15 gene	-1.12	0.357	-1.19	0.086	-1.1	0.459	-1.02	0.933	-1.11
1445905_at	C79206	expressed sequence C79206	-1.3	0.693	-1.04	0.928	-1.1	0.77	-1.04	0.935	-1.12
1422485_at	Smad4	MAD homolog 4 (Drosophila)	-1.11	0.057	-1.19	0.121	-1.12	0.451	-1.75	0.152	-1.29
1429193_at	Ankib1	ankyrin repeat and IBR domain containing 1	-1.15	0.144	-1.1	0.39	-1.16	0.313	-1.3	0.076	-1.18
1423756_s_at	Igfbp4	insulin-like growth factor binding protein 4	-1.21	0.453	-1.16	0.392	-1.05	0.87	-1.29	0.441	-1.18
1439100_s_at	---	---	-1.02	0.962	-1.11	0.796	-1.32	0.105	-2.17	0.432	-1.41
1423577_at	Ankrd32	ankyrin repeat domain 32	-1.14	0.591	-1.11	0.306	-1.15	0.176	-1	0.998	-1.1
1448109_a_at	Rpl26	ribosomal protein L26	-1.06	0.167	-1.07	0.499	-1.32	0.025	-1.26	0.001	-1.18
1427599_at	Boll	bol, boule-like (Drosophila)	-1.14	0.749	-1.3	0.416	-1	0.993	-1.1	0.729	-1.14
1451231_a_at	Cul2	cullin 2	-1.1	0.405	-1.14	0.195	-1.17	0.033	-1.02	0.879	-1.11
1433457_s_at	Grsf1	G-rich RNA sequence binding factor 1	-1.1	0.405	-1.22	0.102	-1.09	0.585	-1.04	0.851	-1.11
1430028_at	2210018M11Rik	RIKEN cDNA 2210018M11 gene	-1.01	0.966	-1.35	0.239	-1.1	0.121	-1.05	0.603	-1.13
1434935_at	LOC637741	hypothetical protein LOC637741	-1.12	0.237	-1.1	0.099	-1.18	0.183	-1.72	0.037	-1.28
1417974_at	Kpna4	karyopherin (importin) alpha 4	-1.07	0.662	-1.06	0.598	-1.31	0.053	-1.46	0.131	-1.22
1446868_at	Hcfc1	host cell factor C1	-1.12	0.477	-1.17	0.721	-1.11	0.731	-1.97	0.249	-1.35
1452039_a_at	Bap1	Brca1 associated protein 1	-1.13	0.322	-1.05	0.713	-1.24	0.087	-1.15	0.097	-1.14
1428007_at	Krtap13-1	keratin associated protein 13-1	-1.09	0.893	-1.2	0.617	-1.11	0.768	-1.07	0.846	-1.12
1422266_at	Mycs	myc-like oncogene, s-myc protein	-1.23	0.704	-1.08	0.883	-1.11	0.771	-1.57	0.08	-1.24
1423450_a_at	Hs3st1	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-1.23	0.422	-1.05	0.908	-1.14	0.279	-2.76	0.048	-1.54
1417670_at	Timm44	translocase of inner mitochondrial membrane 44	-1.16	0.405	-1.2	0.205	-1.06	0.149	-1.06	0.706	-1.12
1442161_at	Igbp1	immunoglobulin (CD79A) binding protein 1	-1.21	0.672	-1.21	0.218	-1.01	0.987	-1.26	0.329	-1.17
1445443_at	---	---	-1.05	0.527	-1.05	0.843	-1.35	0.147	-1.11	0.553	-1.14
1456109_a_at	Mrps15	mitochondrial ribosomal protein S15	-1.07	0.499	-1.18	0.014	-1.16	0.232	-1.39	0.059	-1.2
1416270_at	Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	-1.18	0.051	-1.11	0.055	-1.11	0.142	-1.31	0.064	-1.18
1425972_a_at	Zfx	zinc finger protein X-linked	-1.08	0.386	-1	0.982	-1.38	0.074	-1.24	0.249	-1.18
1423757_x_at	Igfbp4	insulin-like growth factor binding protein 4	-1.13	0.759	-1.2	0.401	-1.08	0.684	-1.24	0.45	-1.16
1426457_at	Slmap	sarcolemma associated protein	-1.09	0.595	-1.13	0.07	-1.19	0.12	-1.09	0.589	-1.13

1428911_at	Ttll4	tubulin tyrosine ligase-like family, member 4	-1.15	0.601	-1.18	0.188	-1.08	0.581	-1.2	0.341	-1.15
1436219_at	4933403F05Rik	RIKEN cDNA 4933403F05 gene	-1.17	0.421	-1.02	0.897	-1.23	0.054	-1.01	0.925	-1.11
1436165_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	-1.11	0.031	-1.06	0.459	-1.26	0.15	-1.03	0.867	-1.11
1433781_a_at	Cldn12	claudin 12	-1	0.97	-1.22	0.163	-1.21	0.126	-1.37	0.42	-1.2
1456600_a_at	Rnf7	ring finger protein 7	-1.07	0.659	-1.01	0.939	-1.38	0.02	-1.1	0.706	-1.14
1446508_at	---	---	-1.07	0.553	-1.08	0.749	-1.28	0.446	-1.01	0.937	-1.11
1431507_a_at	Synj2bp /// 181002(	synaptojanin 2 binding protein /// RIKEN cDNA 1810020G14 gene	-1.18	0.382	-1.22	0.143	-1.03	0.757	-1.29	0.488	-1.18
1434476_at	Crtc1	CREB regulated transcription coactivator 1	-1.19	0.246	-1.04	0.652	-1.19	0.1	-1.22	0.417	-1.16
1423195_at	Hiat1	hippocampus abundant gene transcript 1	-1.21	0.243	-1.1	0.42	-1.09	0.259	-1.33	0.204	-1.18
1424311_at	0710008K08Rik	RIKEN cDNA 0710008K08 gene	-1.13	0.498	-1.1	0.105	-1.17	0.533	-1.56	0.094	-1.24
1424800_at	Enah	enabled homolog (Drosophila)	-1.04	0.855	-1.15	0.752	-1.23	0.169	-1.35	0.247	-1.19
1449099_at	Lrba	LPS-responsive beige-like anchor	-1.03	0.802	-1.33	0.015	-1.08	0.399	-1.16	0.028	-1.15
1424517_at	Ccdc12	coiled-coil domain containing 12	-1.25	0.269	-1.16	0.036	-1.02	0.935	-1.43	0.094	-1.21
1418185_at	4733401H18Rik	RIKEN cDNA 4733401H18 gene	-1.16	0.066	-1.2	0.002	-1.06	0.736	-1.09	0.671	-1.13
1425063_at	---	---	-1.42	0.643	-1.04	0.859	-1.02	0.972	-2.92	0.098	-1.6
1456722_at	Chrdl1	chordin-like 1	-1.32	0.198	-1.05	0.9	-1.07	0.835	-1.58	0.319	-1.26
1427894_at	Vasn	vasorin	-1.12	0.563	-1.17	0.313	-1.11	0.674	-1.48	0.335	-1.22
1439722_at	---	---	-1.22	0.377	-1.02	0.924	-1.18	0.358	-1.59	0.086	-1.25
1417594_at	Gkap1	G kinase anchoring protein 1	-1.08	0.69	-1.08	0.681	-1.27	0.246	-1.12	0.765	-1.13
1416217_a_at	Rpl37a	ribosomal protein L37a	-1.01	0.953	-1.14	0.202	-1.29	0.001	-1.25	0.027	-1.17
1434757_at	Cbfa2t2h	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 homolog (hur	-1.11	0.384	-1.02	0.91	-1.31	0.089	-1.13	0.113	-1.14
1443385_at	A930012N16Rik	RIKEN cDNA A930012N16 gene	-1.09	0.916	-1.23	0.582	-1.09	0.865	-1.08	0.914	-1.12
1455596_a_at	BC029214	cDNA sequence BC029214	-1.03	0.81	-1.32	0.108	-1.09	0.374	-1.24	0.313	-1.17
1416765_s_at	Magmas	mitochondria-associated protein involved in granulocyte-macrophage colony-stim	-1.03	0.375	-1.13	0.226	-1.26	0.157	-1.2	0.237	-1.15
1453794_at	Fer1l4	fer-1-like 4 (C. elegans)	-1.14	0.826	-1.01	0.975	-1.28	0.416	-1.09	0.652	-1.13
1448866_at	Senp3	SUMO/sentrin specific peptidase 3	-1.24	0.213	-1	0.994	-1.19	0.032	-1.21	0.248	-1.16
1441440_at	Atg4c	autophagy-related 4C (yeast)	-1.06	0.627	-1.01	0.966	-1.4	0.006	-1.57	0.097	-1.26
1456403_at	Pag1	phosphoprotein associated with glycosphingolipid microdomains 1	-1.17	0.643	-1.24	0.654	-1.02	0.951	-1.39	0.28	-1.2
1442567_at	Zbtb24	zinc finger and BTB domain containing 24	-1.25	0.542	-1.13	0.758	-1.04	0.811	-1.02	0.944	-1.11
1440150_at	Tgm3	Transglutaminase 3, E polypeptide	-1.17	0.63	-1.11	0.777	-1.12	0.803	-1.28	0.737	-1.17
1436555_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	-1.1	0.089	-1.2	0.464	-1.11	0.608	-1.11	0.703	-1.13
1456201_at	4632427E13Rik	RIKEN cDNA 4632427E13 gene	-1.04	0.865	-1.07	0.403	-1.32	0.161	-1.04	0.674	-1.12
1429707_at	Plaa	phospholipase A2, activating protein	-1.18	0.223	-1.14	0.211	-1.08	0.576	-1.06	0.294	-1.12
1437977_at	Sgtb	Small glutamine-rich tetratricopeptide repeat (TPR)-containing, beta	-1.23	0.29	-1.14	0.506	-1.05	0.852	-1.04	0.852	-1.11
1422130_at	Nptx1	neuronal pentraxin 1	-1.16	0.421	-1.08	0.615	-1.16	0.27	-1.67	0.091	-1.27
1450730_at	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	-1.08	0.462	-1.1	0.571	-1.23	0.45	-1.08	0.801	-1.12
1436056_at	Kif13b	kinesin family member 13B	-1.13	0.266	-1.12	0.267	-1.16	0.328	-1.03	0.874	-1.11
1431515_at	4932414N04Rik	RIKEN cDNA 4932414N04 gene	-1.04	0.947	-1.41	0.488	-1.02	0.964	-1.83	0.337	-1.32
1418503_at	Hspa9a	heat shock protein 9A	-1.11	0.373	-1.15	0.206	-1.14	0.169	-1.31	0.267	-1.18
1435250_at	Ints8	integrator complex subunit 8	-1.09	0.593	-1.13	0.282	-1.18	0.268	-1.13	0.572	-1.13
1452770_at	Vkorc1	vitamin K epoxide reductase complex, subunit 1	-1.04	0.625	-1.15	0.004	-1.22	0.03	-1.12	0.387	-1.13
1436008_at	Tpd52	Tumor protein D52	-1.19	0.354	-1.12	0.697	-1.09	0.766	-1.21	0.132	-1.15
1436848_x_at	Impa1	inositol (myo)-1(or 4)-monophosphatase 1	-1.07	0.625	-1.17	0.251	-1.16	0.108	-1.06	0.374	-1.12
1452580_a_at	Mrpl21	mitochondrial ribosomal protein L21	-1.16	0.008	-1.18	0.018	-1.06	0.63	-1.26	0.205	-1.17
1438330_at	BC065397	cDNA sequence BC065397	-1.19	0.375	-1.15	0.307	-1.06	0.812	-1.17	0.554	-1.14
1417510_at	Vps4a	vacuolar protein sorting 4a (yeast)	-1.05	0.573	-1.06	0.2	-1.31	0.046	-1.28	0.201	-1.18
1417538_at	Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member 1	-1.06	0.503	-1.04	0.718	-1.34	0.009	-1.05	0.778	-1.12
1460008_x_at	Ero1l /// Rpl31 /// L(	ERO1-like (S. cerevisiae) /// ribosomal protein L31 /// similar to ribosomal protein	-1.13	0.025	-1.02	0.73	-1.26	0.021	-1.27	0.001	-1.17
1428829_at	6820401H01Rik	RIKEN cDNA 6820401H01 gene	-1.1	0.624	-1.21	0.11	-1.1	0.361	-1.55	0.214	-1.24
1445729_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-1.27	0.072	-1.15	0.316	-1	0.975	-1.05	0.838	-1.12
1445396_at	Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1	-1.12	0.792	-1.03	0.934	-1.26	0.427	-1.61	0.287	-1.26
1437508_at	Sp4	trans-acting transcription factor 4	-1.08	0.766	-1.05	0.858	-1.3	0.067	-1.01	0.963	-1.11
1434921_at	Nr2e1	nuclear receptor subfamily 2, group E, member 1	-1.11	0.887	-1.08	0.838	-1.21	0.772	-1.06	0.815	-1.11

1443830_x_at	Rnf103	ring finger protein 103	-1.08	0.708	-1.1	0.392	-1.22	0.245	-1.17	0.748	-1.14
1429017_at	Smcr8	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)	-1.07	0.634	-1.2	0.245	-1.13	0.404	-1.19	0.119	-1.15
1428421_a_at	2700085E05Rik	RIKEN cDNA 2700085E05 gene	-1.1	0.018	-1.23	0.099	-1.07	0.557	-1.05	0.686	-1.11
1442937_at	C77190	expressed sequence C77190	-1.12	0.889	-1.18	0.779	-1.1	0.836	-1.17	0.844	-1.14
1456358_at	Etv3	Ets variant gene 3	-1.06	0.625	-1.16	0.377	-1.18	0.624	-1.93	0.102	-1.33
1420855_at	Eln	elastin	-1.06	0.514	-1.08	0.534	-1.27	0.138	-1.39	0.291	-1.2
1423654_a_at	Rnf4	ring finger protein 4	-1.17	0.489	-1.09	0.02	-1.14	0.152	-1.07	0.372	-1.12
1445181_at	Eml5	echinoderm microtubule associated protein like 5	-1.08	0.659	-1.02	0.95	-1.34	0.009	-1.15	0.15	-1.15
1450543_at	Myo1h	myosin 1H	-1.19	0.807	-1.11	0.818	-1.09	0.731	-1.25	0.471	-1.16
1455420_at	Rad23b	RAD23b homolog (S. cerevisiae)	-1.2	0.071	-1.02	0.912	-1.19	0.247	-1.25	0.305	-1.17
1446410_at	Cept1	Choline/ethanolaminephosphotransferase 1	-1.05	0.594	-1.07	0.777	-1.31	0.123	-1.57	0.083	-1.25
1450859_s_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-1.1	0.504	-1.06	0.563	-1.25	0.364	-1.31	0.072	-1.18
1419174_at	2410004B18Rik	RIKEN cDNA 2410004B18 gene	-1.09	0.093	-1.11	0.242	-1.2	0.021	-1.27	0.028	-1.17
1434274_at	Phr1	pam, highwire, rpm 1	-1.15	0.194	-1.04	0.76	-1.22	0.134	-1.63	0.09	-1.26
1439271_x_at	Ik	IK cytokine	-1.12	0.482	-1.09	0.288	-1.19	0.067	-1.18	0.292	-1.14
1433101_at	9030419F21Rik	RIKEN cDNA 9030419F21 gene	-1.19	0.193	-1.05	0.735	-1.16	0.44	-1.29	0.389	-1.17
1458095_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.09	0.484	-1.27	0.752	-1.06	0.869	-1.95	0.184	-1.34
1431951_a_at	Usp16	ubiquitin specific peptidase 16	-1.13	0.585	-1.04	0.682	-1.24	0.109	-1.21	0.216	-1.16
1436580_at	---	---	-1.14	0.327	-1.17	0.627	-1.09	0.393	-1.02	0.959	-1.1
1429485_a_at	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	-1.13	0.177	-1.07	0.167	-1.2	0.036	-1.21	0.069	-1.15
1447333_at	Slc11a2	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member	-1.23	0.695	-1.04	0.94	-1.13	0.805	-1.09	0.876	-1.13
1423890_x_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-1.07	0.065	-1.28	0.126	-1.07	0.698	-2.21	0.073	-1.41
1423046_s_at	Ncbp2	nuclear cap binding protein subunit 2	-1.04	0.691	-1.11	0.466	-1.26	0.052	-1.3	0.114	-1.18
1424295_at	Dppa3	developmental pluripotency-associated 3	-1.35	0.614	-1	0.994	-1.09	0.808	-1.09	0.787	-1.13
1427134_at	Sfrs12	splicing factor, arginine/serine-rich 12	-1.02	0.883	-1.13	0.317	-1.27	0.019	-1.02	0.937	-1.11
1456153_at	Ssh2	slingshot homolog 2 (Drosophila)	-1.05	0.866	-1.16	0.334	-1.19	0.068	-1.46	0.118	-1.21
1426556_at	Suhw4	suppressor of hairy wing homolog 4 (Drosophila)	-1.07	0.629	-1.15	0.264	-1.18	0.143	-1.27	0.006	-1.17
1417982_at	Insig2	insulin induced gene 2	-1.02	0.867	-1.35	0.207	-1.07	0.693	-1.17	0.37	-1.15
1425068_a_at	Tex264	testis expressed gene 264	-1.01	0.931	-1.19	0.272	-1.22	0.249	-1.48	0.185	-1.22
1449004_at	Mrpl46	mitochondrial ribosomal protein L46	-1.06	0.577	-1.11	0.284	-1.25	0.047	-1.07	0.738	-1.12
1454851_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	-1.1	0.219	-1.06	0.598	-1.24	0.282	-1.1	0.65	-1.13
1452721_a_at	Ccdc53	coiled-coil domain containing 53	-1.12	0.366	-1.2	0.18	-1.07	0.568	-1.46	0.077	-1.22
1454602_s_at	Cnot2	CCR4-NOT transcription complex, subunit 2	-1.06	0.188	-1.17	0.07	-1.17	0.268	-1.12	0.315	-1.13
1421881_a_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	-1.21	0.808	-1.09	0.858	-1.1	0.73	-1.01	0.971	-1.1
1424052_at	Thap4	THAP domain containing 4	-1.08	0.008	-1.18	0.51	-1.14	0.4	-1.15	0.047	-1.14
1455565_at	Bcl9	B-cell CLL/lymphoma 9	-1.23	0.777	-1.04	0.93	-1.14	0.667	-1.94	0.065	-1.34
1460213_at	Golga4	golgi autoantigen, golgin subfamily a, 4	-1.05	0.718	-1.25	0.125	-1.11	0.744	-1.06	0.828	-1.12
1417405_at	Stard3	START domain containing 3	-1.11	0.157	-1.08	0.435	-1.21	0.127	-1.35	0.206	-1.19
1444456_at	9030425P06Rik	RIKEN cDNA 9030425P06 gene	-1.06	0.661	-1.04	0.761	-1.33	0.149	-1.44	0.146	-1.22
1434192_at	Zzef1	zinc finger, ZZ-type with EF hand domain 1	-1.12	0.3	-1.15	0.297	-1.13	0.462	-1.25	0.305	-1.16
1433882_at	Cnot10	CCR4-NOT transcription complex, subunit 10	-1.12	0.439	-1.09	0.101	-1.18	0.107	-1.04	0.677	-1.11
1426840_at	Ythdf3	YTH domain family 3	-1.15	0.578	-1.03	0.739	-1.23	0.072	-1.38	0.124	-1.2
1419287_at	Hspc171	HSPC171 protein	-1.05	0.041	-1.1	0.176	-1.27	0.139	-1.01	0.925	-1.11
1428448_a_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	-1.19	0.099	-1.13	0.39	-1.07	0.563	-1.08	0.108	-1.12
1430293_a_at	B230118G17Rik	RIKEN cDNA B230118G17 gene	-1.16	0.294	-1.12	0.183	-1.11	0.508	-1.11	0.251	-1.12
1448589_at	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	-1.1	0.158	-1.28	0.043	-1.03	0.788	-1.48	0.144	-1.23
1447507_at	C80406	expressed sequence C80406	-1.2	0.113	-1.1	0.499	-1.1	0.433	-1.38	0.176	-1.19
1416996_at	Tbc1d8	TBC1 domain family, member 8	-1.07	0.8	-1.31	0.39	-1.05	0.595	-1.32	0.091	-1.19
1450785_at	Trip4	thyroid hormone receptor interactor 4	-1.12	0.348	-1.15	0.57	-1.12	0.68	-1.19	0.457	-1.14
1448483_a_at	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	-1.09	0.26	-1.08	0.224	-1.23	0.203	-1.01	0.959	-1.1
1451385_at	2310056P07Rik	RIKEN cDNA 2310056P07 gene	-1.1	0.197	-1.12	0.054	-1.17	0.271	-1.32	0.112	-1.18
1419111_at	Ing2	inhibitor of growth family, member 2	-1.18	0.249	-1.03	0.711	-1.19	0.105	-1.17	0.575	-1.14
1434340_at	---	---	-1.08	0.335	-1.34	0.018	-1.02	0.953	-1.04	0.677	-1.12

1435769_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	-1.08	0.506	-1.12	0.106	-1.19	0.023	-1.24	0.447	-1.16
1455762_at	C330002I19Rik	RIKEN cDNA C330002I19 gene	-1.1	0.287	-1.13	0.423	-1.16	0.503	-1.31	0.504	-1.18
1455189_at	Trim33 /// 8030451I	tripartite motif protein 33 /// RIKEN cDNA 8030451N04 gene	-1.2	0.082	-1.02	0.916	-1.18	0.196	-1.07	0.456	-1.12
1438409_at	Cep63	centrosomal protein 63	-1.01	0.884	-1.02	0.915	-1.45	0.024	-1.38	0.119	-1.22
1416096_at	AI413782	expressed sequence AI413782	-1.19	0.313	-1.05	0.573	-1.16	0.251	-1.19	0.35	-1.15
1427519_at	Adora2a	adenosine A2a receptor	-1.31	0.411	-1.04	0.92	-1.08	0.719	-1.04	0.928	-1.12
1417410_s_at	Prkci	protein kinase C, iota	-1.05	0.629	-1.1	0.289	-1.26	0.196	-1.48	0.17	-1.22
1458404_at	Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	-1.15	0.183	-1.26	0.43	-1.01	0.978	-1.18	0.034	-1.15
1447195_at	Elp4	Elongation protein 4 homolog (S. cerevisiae)	-1.11	0.5	-1	0.997	-1.32	0.282	-1.34	0.092	-1.19
1416721_s_at	Sfrs6	splicing factor, arginine/serine-rich 6	-1	0.983	-1.25	0.018	-1.16	0.162	-1.01	0.967	-1.11
1423070_at	Rpl21	ribosomal protein L21	-1.1	0.694	-1.03	0.879	-1.29	0.245	-1.14	0.532	-1.14
1424017_a_at	Hint1	histidine triad nucleotide binding protein 1	-1.11	0.133	-1.13	0.556	-1.15	0.065	-1.18	0.153	-1.14
1458202_at	6330500D04Rik	RIKEN cDNA 6330500D04 gene	-1.06	0.885	-1.3	0.195	-1.06	0.844	-2.68	0.038	-1.53
1420500_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	-1.04	0.795	-1.05	0.714	-1.35	0.091	-1.5	0.166	-1.24
1416488_at	Ccng2	cyclin G2	-1.11	0.667	-1.12	0.512	-1.15	0.255	-1.57	0.084	-1.24
1454774_at	Zfp445	zinc finger protein 445	-1.18	0.531	-1.05	0.292	-1.16	0.235	-1.44	0.118	-1.21
1416420_a_at	Rpl9 /// LOC63737	ribosomal protein L9 /// similar to ribosomal protein L9	-1.11	0.082	-1.07	0.281	-1.22	0.003	-1.25	0.003	-1.16
1438391_x_at	Hadh2	hydroxyacyl-Coenzyme A dehydrogenase type II	-1.04	0.698	-1.16	0.175	-1.2	0.052	-1.1	0.708	-1.13
1424025_at	BC013529	cDNA sequence BC013529	-1.17	0.014	-1.11	0.491	-1.1	0.251	-1.08	0.556	-1.12
1456063_at	ORF34	open reading frame 34	-1.09	0.338	-1.13	0.519	-1.17	0.316	-1.07	0.837	-1.11
1448442_a_at	Psma3	proteasome (prosome, macropain) subunit, alpha type 3	-1.04	0.51	-1.16	0.007	-1.19	0.027	-1.19	0.049	-1.15
1426924_at	Mnab	membrane associated DNA binding protein	-1.07	0.8	-1.02	0.813	-1.34	0.023	-1.01	0.824	-1.11
1416463_at	Gpiap1	GPI-anchored membrane protein 1	-1.01	0.941	-1.48	0.346	-1	0.993	-1.06	0.709	-1.14
1450357_a_at	Ccr6	chemokine (C-C motif) receptor 6	-1.08	0.814	-1.32	0.575	-1.02	0.795	-3.17	0.046	-1.65
1440020_at	Rlf	Rearranged L-myc fusion sequence	-1.09	0.775	-1.07	0.761	-1.24	0.12	-1.08	0.45	-1.12
1450895_a_at	1810020G14Rik	RIKEN cDNA 1810020G14 gene	-1.25	0.062	-1.06	0.406	-1.09	0.519	-1.63	0.202	-1.26
1438018_at	Hook1	hook homolog 1 (Drosophila)	-1.08	0.586	-1.1	0.203	-1.22	0.122	-1.86	0.087	-1.31
1424251_a_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	-1.07	0.705	-1.25	0.074	-1.08	0.426	-1.11	0.509	-1.13
1425018_at	Mcts1	malignant T cell amplified sequence 1	-1.18	0.007	-1.17	0.041	-1.04	0.669	-1.23	0.25	-1.16
1457248_x_at	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	-1.06	0.631	-1.03	0.872	-1.34	0.001	-1.36	0.307	-1.2
1427073_at	Lace1	lactation elevated 1	-1.12	0.103	-1.22	0.278	-1.05	0.698	-1.21	0.125	-1.15
1459986_a_at	Rps17	ribosomal protein S17	-1.1	0.211	-1.06	0.576	-1.23	0.005	-1.24	0.003	-1.16
1432195_s_at	Ccnl2	cyclin L2	-1.33	0.003	-1.01	0.913	-1.08	0.545	-1.26	0.226	-1.17
1439470_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	-1.19	0.534	-1.06	0.73	-1.14	0.421	-1.15	0.266	-1.14
1434406_at	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	-1.23	0.057	-1.13	0.368	-1.04	0.827	-1.07	0.157	-1.12
1428908_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	-1.16	0.415	-1.12	0.143	-1.1	0.374	-1.1	0.783	-1.12
1430875_a_at	Pak1ip1	PAK1 interacting protein 1	-1.02	0.896	-1.36	0.043	-1.06	0.68	-1.11	0.732	-1.14
1452286_at	5033405K12Rik	RIKEN cDNA 5033405K12 gene	-1.13	0.668	-1.19	0.076	-1.06	0.664	-1.16	0.078	-1.14
1460182_at	Snx4	sorting nexin 4	-1.09	0.347	-1.04	0.267	-1.27	0.028	-1.33	0.204	-1.18
1434009_at	Grlf1	glucocorticoid receptor DNA binding factor 1	-1.04	0.524	-1.21	0.013	-1.14	0.389	-1.56	0.018	-1.24
1437435_at	1700061G19Rik ///	RIKEN cDNA 1700061G19 gene /// similar to gonadotropin-regulated long chain a	-1.08	0.508	-1.24	0.562	-1.07	0.601	-1.73	0.206	-1.28
1454657_s_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-1.13	0.12	-1.16	0.218	-1.09	0.082	-1.19	0.218	-1.14
1418205_at	---	---	-1.2	0.358	-1.17	0.647	-1.02	0.872	-1.39	0.143	-1.2
1453928_a_at	Ssb	Sjogren syndrome antigen B	-1.05	0.725	-1.04	0.544	-1.34	0.088	-1.31	0.205	-1.18
1433472_x_at	Rpl38 /// LOC62564	ribosomal protein L38 /// similar to ribosomal protein L38 /// similar to ribosomal pı	-1.11	0.048	-1.02	0.832	-1.28	0.02	-1.29	0.015	-1.18
1418150_at	Mtmr4	myotubularin related protein 4	-1.07	0.781	-1.26	0.044	-1.07	0.851	-1.03	0.946	-1.11
1419818_x_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	-1.3	0.288	-1.05	0.674	-1.06	0.684	-1.03	0.893	-1.11
1448308_at	Ap3m1	adaptor-related protein complex 3, mu 1 subunit	-1.07	0.279	-1.15	0.481	-1.17	0.139	-1.01	0.917	-1.1
1455152_at	AI462493	expressed sequence AI462493	-1.02	0.854	-1.15	0.072	-1.22	0.092	-1.5	0.128	-1.22
1452749_at	Papd1	PAP associated domain containing 1	-1.17	0.049	-1.1	0.267	-1.12	0.348	-1.37	0.009	-1.19
1443438_at	Ncoa1	Nuclear receptor coactivator 1	-1.02	0.915	-1.11	0.75	-1.28	0.038	-1.83	0.068	-1.31
1449083_at	Ccdc91	coiled-coil domain containing 91	-1.2	0.014	-1.02	0.92	-1.18	0.155	-1.22	0.41	-1.15
1426915_at	Dapk1	death associated protein kinase 1	-1.15	0.046	-1	0.999	-1.25	0.014	-1.16	0.486	-1.14

1451283_at	1810073G14Rik	RIKEN cDNA 1810073G14 gene	-1.08	0.169	-1.24	0.017	-1.07	0.647	-1.32	0.003	-1.18
1425956_a_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.11	0.636	-1.15	0.045	-1.11	0.336	-1.13	0.364	-1.13
1442432_x_at	Atxn7l1	ataxin 7-like 1	-1.13	0.432	-1.22	0.568	-1.04	0.92	-1.12	0.665	-1.13
1435247_at	Ube1dc1	ubiquitin-activating enzyme E1-domain containing 1	-1.09	0.273	-1	0.962	-1.33	0.106	-1.36	0.055	-1.2
1450804_at	Kif5c	kinesin family member 5C	-1.23	0.049	-1.07	0.853	-1.09	0.811	-1	0.986	-1.1
1435347_at	Stau1	staufen (RNA binding protein) homolog 1 (Drosophila)	-1.08	0.425	-1.17	0.123	-1.12	0.475	-1.09	0.732	-1.12
1438082_at	2310028N02Rik	RIKEN cDNA 2310028N02 gene	-1.05	0.789	-1.25	0.206	-1.1	0.755	-1.29	0.214	-1.17
1453723_x_at	Ubb /// Gm1821	ubiquitin B /// gene model 1821, (NCBI)	-1.06	0.065	-1.15	0.222	-1.18	0.031	-1.12	0.035	-1.12
1444028_s_at	Dock9 /// LOC6703	dedicator of cytokinesis 9 /// similar to Dedicator of cytokinesis protein 9 (Cdc42 g	-1.16	0.449	-1.19	0.283	-1.03	0.866	-1.38	0.158	-1.19
1445375_at	Itsn2	intersectin 2	-1.09	0.611	-1.04	0.524	-1.27	0.154	-1.48	0.166	-1.22
1417402_at	1190017O12Rik	RIKEN cDNA 1190017O12 gene	-1.11	0.669	-1.05	0.453	-1.23	0.229	-1.29	0.262	-1.17
1455740_at	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	-1.16	0.808	-1.09	0.711	-1.12	0.648	-1.34	0.595	-1.18
1456467_s_at	Nlk	nemo like kinase	-1.15	0.608	-1.06	0.805	-1.18	0.153	-1.47	0.027	-1.21
1429418_at	Cdc14b	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	-1.1	0.652	-1.14	0.213	-1.14	0.47	-1.29	0.446	-1.17
1452116_s_at	Atf2	activating transcription factor 2	-1.07	0.477	-1.08	0.256	-1.23	0.091	-1.01	0.811	-1.1
1439973_at	Crxos1	Crx opposite strand transcript 1	-1.29	0.085	-1.01	0.965	-1.11	0.55	-1.45	0.104	-1.21
1417369_at	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	-1.05	0.813	-1.36	0.098	-1.03	0.868	-1.13	0.692	-1.14
1443970_at	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	-1.02	0.965	-1.35	0.145	-1.06	0.875	-1.17	0.602	-1.15
1415684_at	Atg5	autophagy-related 5 (yeast)	-1.12	0.436	-1.06	0.721	-1.21	0.491	-1.08	0.231	-1.12
1435099_at	Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	-1.23	0.268	-1.05	0.478	-1.1	0.353	-1.26	0.073	-1.16
1415738_at	Txndc12	thioredoxin domain containing 12 (endoplasmic reticulum)	-1.29	0.076	-1.03	0.701	-1.09	0.596	-1.45	0.101	-1.21
1455252_at	Tsc1	tuberous sclerosis 1	-1.06	0.251	-1.08	0.561	-1.26	0.175	-1.16	0.013	-1.14
1430702_at	5830427D03Rik	RIKEN cDNA 5830427D03 gene	-1.08	0.504	-1.01	0.971	-1.34	0.349	-1.35	0.34	-1.19
1457559_at	Wac	WW domain containing adaptor with coiled-coil	-1.05	0.746	-1.08	0.219	-1.27	0.116	-1.04	0.755	-1.11
1423033_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisia	-1.13	0.528	-1.13	0.578	-1.12	0.542	-1.12	0.615	-1.12
1425554_a_at	Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	-1.17	0.128	-1.07	0.627	-1.14	0.145	-1.1	0.458	-1.12
1427050_at	5730420B22Rik	RIKEN cDNA 5730420B22 gene	-1.09	0.673	-1.24	0.315	-1.06	0.281	-1.87	0.077	-1.32
1420709_s_at	Dao1	D-amino acid oxidase 1	-1.09	0.805	-1.21	0.616	-1.09	0.761	-1.15	0.596	-1.13
1450642_at	3110001I20Rik	RIKEN cDNA 3110001I20 gene	-1.1	0.679	-1.14	0.19	-1.13	0.257	-1.17	0.468	-1.14
1444159_at	Pip5k2a	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	-1.09	0.315	-1.04	0.863	-1.27	0.433	-1.13	0.732	-1.13
1428188_at	2610019A05Rik	RIKEN cDNA 2610019A05 gene	-1.09	0.74	-1.12	0.791	-1.16	0.64	-1.43	0.275	-1.2
1459874_s_at	Mtmr4	myotubularin related protein 4	-1.02	0.934	-1.13	0.51	-1.24	0.013	-1.33	0.07	-1.18
1448958_at	Ifrg15	interferon alpha responsive gene	-1.2	0.205	-1.08	0.729	-1.1	0.676	-1.15	0.57	-1.13
1434215_at	B230308N11Rik	RIKEN cDNA B230308N11 gene	-1.11	0.281	-1.1	0.387	-1.16	0.1	-1.04	0.402	-1.1
1432984_at	1700026H06Rik	RIKEN cDNA 1700026H06 gene	-1.09	0.665	-1.07	0.609	-1.23	0.129	-1.14	0.612	-1.13
1438993_a_at	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	-1.06	0.711	-1.15	0.1	-1.16	0.1	-1.25	0.083	-1.16
1437470_at	Pknox1	Pbx/knotted 1 homeobox	-1.1	0.696	-1.19	0.338	-1.09	0.732	-1.06	0.596	-1.11
1456395_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	-1.11	0.599	-1.29	0.358	-1.01	0.921	-1.68	0.346	-1.27
1451576_at	Prkdc	protein kinase, DNA activated, catalytic polypeptide	-1.14	0.549	-1.18	0.288	-1.05	0.681	-1.07	0.708	-1.11
1426527_at	Toe1	target of EGR1, member 1 (nuclear)	-1.12	0.541	-1.04	0.859	-1.23	0.103	-1.29	0.046	-1.17
1454620_x_at	Rps6 /// LOC43440	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	-1.01	0.88	-1.09	0.368	-1.31	0.002	-1.32	0.006	-1.18
1444031_at	---	---	-1.12	0.756	-1.13	0.525	-1.12	0.682	-1.34	0.522	-1.18
1433768_at	Palld	palladin, cytoskeletal associated protein	-1.06	0.681	-1.31	0.064	-1.04	0.854	-1.27	0.463	-1.17
1460571_at	Dicer1	Dicer1, Dcr-1 homolog (Drosophila)	-1.08	0.03	-1.1	0.124	-1.2	0.31	-1.54	0.153	-1.23
1444858_at	Inoc1	INO80 complex homolog 1 (S. cerevisiae)	-1.11	0.136	-1.11	0.645	-1.15	0.442	-1.5	0.1	-1.22
1420883_at	Sln	sarcolipin	-1.03	0.896	-1.17	0.665	-1.18	0.669	-1.1	0.84	-1.12
1416312_at	Rars	arginyl-tRNA synthetase	-1.1	0.593	-1.17	0.053	-1.11	0.045	-1.08	0.553	-1.11
1448990_a_at	Myo1b	myosin IB	-1.13	0.769	-1.18	0.301	-1.07	0.739	-1.75	0.057	-1.28
1438051_at	Ttc14	tetratricopeptide repeat domain 14	-1.16	0.659	-1.11	0.736	-1.1	0.331	-1.2	0.38	-1.14
1459854_s_at	Dynlt3	dynein light chain Tctex-type 3	-1.14	0.374	-1.05	0.608	-1.19	0.032	-1.14	0.57	-1.13
1446107_at	Stk24	Serine/threonine kinase 24 (STE20 homolog, yeast)	-1.19	0.621	-1.08	0.578	-1.1	0.755	-1.33	0.247	-1.18
1434214_at	0910001L09Rik	RIKEN cDNA 0910001L09 gene	-1.06	0.696	-1.14	0.115	-1.18	0.339	-1.52	0.081	-1.22
1455434_a_at	Ktn1	kinectin 1	-1.1	0.672	-1.16	0.199	-1.11	0.196	-1.47	0.247	-1.21

1418209_a_at	Pfn2	profilin 2	-1.09	0.303	-1.03	0.921	-1.28	0.202	-1.38	0.237	-1.2
1439795_at	Gpr64	G protein-coupled receptor 64	-1.02	0.974	-1.28	0.695	-1.1	0.605	-1.42	0.371	-1.21
1424721_at	Mfap3	microfibrillar-associated protein 3	-1.07	0.759	-1.05	0.769	-1.28	0.061	-1.36	0.037	-1.19
1437791_s_at	Eml5	echinoderm microtubule associated protein like 5	-1.05	0.786	-1.08	0.713	-1.27	0.246	-1.26	0.121	-1.16
1449533_at	Tmem100	transmembrane protein 100	-1.06	0.873	-1.3	0.567	-1.04	0.608	-1.37	0.42	-1.19
1431665_a_at	Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	-1.06	0.593	-1.05	0.596	-1.29	0.012	-1.02	0.946	-1.1
1459457_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	-1.09	0.254	-1.13	0.648	-1.15	0.543	-1	0.989	-1.09
1417791_a_at	Zfml	zinc finger, matrin-like	-1.09	0.599	-1.09	0.623	-1.19	0.369	-1.4	0.174	-1.19
1436539_at	Clmn	calmin	-1.3	0.094	-1.05	0.862	-1.05	0.932	-1.18	0.147	-1.15
1433846_s_at	C430003P19Rik	RIKEN cDNA C430003P19 gene	-1.15	0.019	-1.04	0.477	-1.19	0.09	-1.31	0.103	-1.17
1435011_x_at	Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	-1.23	0.026	-1.07	0.246	-1.08	0.209	-1.2	0.341	-1.15
1428394_at	Phyhd1 /// Lrrc8a	phytanoyl-CoA dioxygenase domain containing 1 /// leucine rich repeat containing	-1.08	0.301	-1.17	0.054	-1.12	0.629	-1.35	0.215	-1.18
1457672_at	Chd9	chromodomain helicase DNA binding protein 9	-1	0.972	-1.23	0.126	-1.16	0.237	-1.41	0.23	-1.2
1423272_at	Polg	polymerase (DNA directed), gamma	-1.1	0.236	-1.21	0.011	-1.07	0.727	-1.32	0.011	-1.17
1435158_at	Rbm12b	RNA binding motif protein 12B	-1.3	0.475	-1.01	0.953	-1.09	0.649	-1.77	0.039	-1.29
1419046_at	Brp16	brain protein 16	-1.06	0.685	-1.23	0.143	-1.09	0.643	-1.32	0.242	-1.18
1455139_at	AI851716	expressed sequence AI851716	-1.08	0.69	-1.3	0.294	-1.02	0.823	-1.1	0.647	-1.13
1448794_s_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	-1.02	0.896	-1.18	0.326	-1.18	0.344	-1.12	0.71	-1.13
1427407_s_at	Trip11	thyroid hormone receptor interactor 11	-1.13	0.333	-1.01	0.894	-1.25	0.075	-1.3	0.263	-1.17
1440966_at	7-Mar	membrane-associated ring finger (C3HC4) 7	-1.01	0.966	-1.08	0.659	-1.33	0.129	-1.58	0.131	-1.25
1434232_a_at	2610030H06Rik	RIKEN cDNA 2610030H06 gene	-1.07	0.675	-1.25	0.151	-1.07	0.703	-1.06	0.847	-1.11
1448448_a_at	Chkb	choline kinase beta	-1.1	0.526	-1.27	0.045	-1.02	0.775	-1.44	0.134	-1.21
1424299_at	Oma1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	-1.13	0.246	-1.1	0.242	-1.14	0.262	-1.39	0.076	-1.19
1438418_at	4932432K03Rik	RIKEN cDNA 4932432K03 gene	-1.12	0.086	-1.06	0.797	-1.19	0.345	-1.32	0.307	-1.17
1426862_at	Aftph	aftiphilin	-1.12	0.308	-1.08	0.333	-1.17	0.205	-1.07	0.642	-1.11
1427881_at	Dnttip2	deoxynucleotidyltransferase, terminal, interacting protein 2	-1.08	0.745	-1.19	0.118	-1.11	0.586	-1.21	0.206	-1.15
1441229_at	D230019N24Rik	RIKEN cDNA D230019N24 gene	-1.03	0.614	-1.32	0.113	-1.06	0.708	-1.59	0.123	-1.25
1434952_at	Cox4nb	COX4 neighbor	-1.03	0.853	-1.24	0.426	-1.12	0.585	-1.08	0.884	-1.12
1446096_at	2310001H17Rik	RIKEN cDNA 2310001H17 gene	-1.14	0.499	-1.19	0.117	-1.04	0.916	-1.43	0.124	-1.2
1416616_s_at	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	-1.1	0.401	-1.09	0.523	-1.18	0.201	-1.03	0.739	-1.1
1434179_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	-1.06	0.374	-1.16	0.093	-1.16	0.431	-1.24	0.273	-1.15
1435568_at	AK129128	cDNA sequence AK129128	-1.16	0.275	-1.09	0.483	-1.11	0.334	-1.03	0.848	-1.1
1428406_s_at	Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	-1.12	0.578	-1.18	0.456	-1.07	0.633	-1.04	0.747	-1.1
1423301_at	Copb1	coatomer protein complex, subunit beta 1	-1.11	0.524	-1.16	0.015	-1.09	0.371	-1.24	0.072	-1.15
1433852_at	C330002I19Rik	RIKEN cDNA C330002I19 gene	-1.15	0.164	-1.03	0.596	-1.2	0.304	-1.25	0.419	-1.16
1459715_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	-1.12	0.71	-1.09	0.48	-1.16	0.597	-1.23	0.494	-1.15
1434884_at	Mtdh	Metadherin	-1.18	0.483	-1.09	0.575	-1.1	0.415	-1.01	0.969	-1.09
1426536_at	Narg2	NMDA receptor-regulated gene 2	-1.12	0.479	-1.03	0.718	-1.23	0.118	-1.42	0.121	-1.2
1445244_at	Tm2d1	TM2 domain containing 1	-1.11	0.808	-1.07	0.914	-1.19	0.484	-1.13	0.778	-1.12
1426741_a_at	Fastkd2	FAST kinase domains 2	-1.23	0.352	-1.12	0.137	-1.03	0.411	-1.04	0.47	-1.1
1422888_at	Rnf5	ring finger protein 5	-1.36	0.207	-1.06	0.709	-1	0.995	-1.03	0.766	-1.11
1428177_at	Trappc6b /// LOC43	trafficking protein particle complex 6B /// similar to Trafficking protein particle com	-1.18	0.066	-1.17	0.017	-1.03	0.764	-1.03	0.847	-1.1
1430678_at	5730457N03Rik	RIKEN cDNA 5730457N03 gene	-1.17	0.843	-1.17	0.604	-1.03	0.945	-2.37	0.284	-1.44
1439558_at	Zfp75	zinc finger protein 75	-1.23	0.735	-1.08	0.784	-1.06	0.489	-1.2	0.568	-1.14
1457787_at	---	---	-1.24	0.341	-1.02	0.917	-1.12	0.531	-1.18	0.238	-1.14
1456058_at	Rbm27	RNA binding motif protein 27	-1.02	0.883	-1.02	0.846	-1.38	0.014	-1.12	0.045	-1.14
1433778_at	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	-1.01	0.916	-1.21	0.059	-1.16	0.42	-1	0.989	-1.1
1454794_at	Spast	spastin	-1.04	0.77	-1.17	0.234	-1.16	0.152	-1.03	0.609	-1.1
1428170_at	Zfp180	zinc finger protein 180	-1.02	0.914	-1.11	0.503	-1.27	0.06	-1.06	0.769	-1.11
1454116_a_at	Mterfd1	MTERF domain containing 1	-1.19	0.412	-1.01	0.898	-1.18	0.074	-1.64	0.062	-1.25
1438972_x_at	2810410L24Rik	RIKEN cDNA 2810410L24 gene	-1.15	0.414	-1.07	0.77	-1.15	0.502	-1.26	0.462	-1.16
1447883_x_at	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	-1.09	0.38	-1.11	0.525	-1.17	0.206	-1.01	0.931	-1.09
1420895_at	Tgfbr1	transforming growth factor, beta receptor I	-1.03	0.751	-1.04	0.698	-1.35	0.014	-1.36	0.192	-1.19

1448641_at	Mbtd1	mbt domain containing 1	-1.05	0.513	-1.08	0.311	-1.25	0.141	-1.26	0.041	-1.16
1456553_at	Zcchc11	Zinc finger, CCHC domain containing 11	-1.02	0.922	-1.15	0.484	-1.21	0.264	-2.37	0.112	-1.44
1448403_at	Lars	leucyl-tRNA synthetase	-1.15	0.467	-1.04	0.32	-1.18	0.256	-1.01	0.953	-1.09
1426432_a_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	-1.08	0.496	-1.03	0.696	-1.28	0.111	-1.09	0.896	-1.12
1448707_at	Taf13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.05	0.712	-1.03	0.661	-1.31	0.042	-1.28	0.167	-1.17
1418479_at	Vps54	vacuolar protein sorting 54 (yeast)	-1.16	0.375	-1.2	0.043	-1.02	0.749	-1.1	0.341	-1.12
1432119_at	4933405I11Rik	RIKEN cDNA 4933405I11 gene	-1.21	0.701	-1.03	0.911	-1.13	0.405	-1.32	0.62	-1.17
1426763_at	Oaz2	ornithine decarboxylase antizyme 2	-1.22	0.081	-1	0.976	-1.16	0.218	-1.26	0.104	-1.16
1448179_at	Usmg5	upregulated during skeletal muscle growth 5	-1.22	0.005	-1.13	0.692	-1.03	0.923	-1.33	0.21	-1.18
1428155_at	Commd9	COMM domain containing 9	-1.12	0.697	-1.09	0.457	-1.16	0.255	-1.05	0.687	-1.1
1422627_a_at	Mkks	McKusick-Kaufman syndrome protein	-1.08	0.55	-1.05	0.63	-1.24	0.016	-1.2	0.345	-1.14
1429473_at	1200003I07Rik	RIKEN cDNA 1200003I07 gene	-1.17	0.499	-1.08	0.057	-1.11	0.172	-1.58	0.063	-1.23
1443932_at	Klhdc1	kelch domain containing 1	-1.27	0.059	-1.03	0.966	-1.09	0.481	-1.66	0.089	-1.26
1437020_at	Ep400	E1A binding protein p400	-1.08	0.665	-1.16	0.716	-1.13	0.433	-1.09	0.75	-1.11
1435637_at	Itfg1	integrin alpha FG-GAP repeat containing 1	-1.11	0.085	-1.12	0.081	-1.13	0.144	-1.16	0.427	-1.13
1437441_at	AA388235	expressed sequence AA388235	-1.3	0.161	-1.03	0.954	-1.07	0.716	-1.51	0.239	-1.23
1428337_at	1810034K20Rik	RIKEN cDNA 1810034K20 gene	-1.15	0.038	-1.06	0.612	-1.16	0.223	-1.53	0.123	-1.22
1427733_a_at	Nfia	nuclear factor I/A	-1.17	0.415	-1.01	0.966	-1.2	0.385	-1.23	0.309	-1.15
1433953_at	Zfp277	zinc finger protein 277	-1.07	0.424	-1.14	0.15	-1.15	0.221	-1.93	0.071	-1.32
1441998_at	---	Transcribed locus	-1.14	0.517	-1.18	0.485	-1.05	0.616	-1.23	0.437	-1.15
1424384_a_at	Znrf1	zinc and ring finger 1	-1.01	0.939	-1.08	0.648	-1.31	0.044	-2.09	0.053	-1.37
1437212_at	B230312I18Rik	RIKEN cDNA B230312I18 gene	-1.14	0.388	-1	0.996	-1.25	0.169	-1.85	0.095	-1.31
1422698_s_at	Jarid2	jumonji, AT rich interactive domain 2	-1.11	0.562	-1.12	0.521	-1.12	0.248	-1.29	0.024	-1.16
1426241_a_at	Scmh1	sex comb on midleg homolog 1	-1.22	0.298	-1.15	0.358	-1.01	0.948	-1.13	0.185	-1.13
1460429_at	Cdc5l	cell division cycle 5-like (S. pombe)	-1.25	0.132	-1.04	0.446	-1.09	0.306	-1.21	0.129	-1.15
1433648_at	Spag9	sperm associated antigen 9	-1.09	0.64	-1.03	0.76	-1.25	0.139	-1.38	0.404	-1.19
1417598_a_at	Fxr1h	fragile X mental retardation gene 1, autosomal homolog	-1.12	0.544	-1.27	0.006	-1	0.983	-1.13	0.399	-1.13
1437447_s_at	Ercc1	excision repair cross-complementing rodent repair deficiency, complementation g	-1.11	0.537	-1.07	0.775	-1.19	0.067	-1.37	0.272	-1.18
1450775_at	Mos	Moloney sarcoma oncogene	-1.25	0.597	-1.11	0.502	-1.02	0.926	-1.51	0.018	-1.22
1415729_at	Pdpk1	3-phosphoinositide dependent protein kinase-1	-1.1	0.482	-1.13	0.302	-1.12	0.37	-1.06	0.672	-1.1
1420731_a_at	Csrp2	cysteine and glycine-rich protein 2	-1.03	0.394	-1.11	0.209	-1.23	0.284	-1.64	0.078	-1.25
1429699_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	-1.01	0.966	-1.33	0.025	-1.07	0.823	-1.04	0.845	-1.11
1452897_at	Cdc2l5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	-1.18	0.002	-1.13	0.278	-1.05	0.643	-1.35	0.056	-1.18
1432902_at	9130414P19Rik	RIKEN cDNA 9130414P19 gene	-1.24	0.669	-1.02	0.901	-1.11	0.549	-1.4	0.653	-1.19
1452710_at	Rpusd4	RNA pseudouridylate synthase domain containing 4	-1.12	0.224	-1.11	0.603	-1.12	0.434	-1.3	0.08	-1.16
1441052_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	-1.06	0.329	-1.09	0.614	-1.22	0.082	-1.37	0.055	-1.19
1435746_at	Srpk2	serine/arginine-rich protein specific kinase 2	-1	0.999	-1.03	0.768	-1.41	0.098	-1.69	0.099	-1.28
1418440_at	Col8a1	procollagen, type VIII, alpha 1	-1.22	0.543	-1.11	0.776	-1.04	0.855	-1.01	0.966	-1.1
1425201_a_at	Hyi	hydroxypyruvate isomerase homolog (E. coli)	-1.02	0.927	-1.28	0.453	-1.09	0.67	-1.7	0.004	-1.27
1426494_at	Rg9mtd3	RNA (guanine-9-) methyltransferase domain containing 3	-1.08	0.593	-1.08	0.355	-1.2	0.134	-1.28	0.211	-1.16
1437196_x_at	Rps16	ribosomal protein S16	-1	0.974	-1.05	0.694	-1.36	0.006	-1.32	0.007	-1.18
1424792_at	Rpp40	ribonuclease P 40 subunit (human)	-1.25	0.184	-1.06	0.765	-1.07	0.538	-1.27	0.369	-1.16
1426424_at	Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	-1.07	0.434	-1.15	0.536	-1.14	0.034	-1.15	0.308	-1.13
1453846_at	2810013C04Rik	RIKEN cDNA 2810013C04 gene	-1.19	0.718	-1.03	0.937	-1.15	0.16	-1.78	0.035	-1.29
1459952_at	Ankrd17	Ankyrin repeat domain 17	-1.04	0.618	-1.04	0.833	-1.32	0.223	-1.5	0.073	-1.22
1446923_at	Ptplb	Protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	-1.09	0.484	-1.11	0.758	-1.16	0.549	-1.41	0.403	-1.19
1455180_at	AA407270	expressed sequence AA407270	-1.01	0.959	-1.16	0.716	-1.21	0.197	-1.48	0.261	-1.21
1449118_at	Dbt	dihydrolipoamide branched chain transacylase E2	-1.14	0.027	-1.17	0.133	-1.06	0.575	-1.14	0.444	-1.13
1437203_at	Cbll1	Casitas B-lineage lymphoma-like 1	-1.12	0.146	-1.07	0.562	-1.16	0.078	-1.3	0.267	-1.16
1417683_at	Diablo	diablo homolog (Drosophila)	-1.14	0.124	-1.09	0.057	-1.12	0.109	-1.09	0.291	-1.11
1455006_at	2310016M24Rik	RIKEN cDNA 2310016M24 gene	-1.06	0.432	-1.17	0.163	-1.13	0.311	-1.27	0.298	-1.16
1426490_at	Bfar	bifunctional apoptosis regulator	-1.03	0.503	-1.19	0.118	-1.16	0.266	-1.37	0.153	-1.18
1423641_s_at	Cnot7	CCR4-NOT transcription complex, subunit 7	-1.13	0.249	-1.06	0.436	-1.17	0.049	-1.12	0.449	-1.12

1419979_s_at	Creb3	cAMP responsive element binding protein 3	-1.05	0.033	-1.03	0.68	-1.3	0.012	-1.06	0.626	-1.11
1422805_a_at	Ing3	inhibitor of growth family, member 3	-1.2	0.018	-1.07	0.547	-1.09	0.641	-1.52	0.177	-1.22
1422697_s_at	---	---	-1.14	0.339	-1.07	0.165	-1.14	0.121	-1.27	0.048	-1.16
1415774_at	Statip1	signal transducer and activator of transcription interacting protein 1	-1.15	0.69	-1.05	0.746	-1.16	0.279	-1.22	0.418	-1.15
1433516_a_at	Myeov2	myeloma overexpressed 2	-1.06	0.524	-1.01	0.879	-1.34	0.097	-1.62	0.106	-1.26
1428083_at	2310043N10Rik	RIKEN cDNA 2310043N10 gene	-1.11	0.597	-1.24	0.386	-1.02	0.918	-1.18	0.48	-1.14
1433726_at	---	---	-1.11	0.397	-1.08	0.548	-1.17	0.004	-1.24	0.368	-1.15
1454785_at	Dusp11	dual specificity phosphatase 11 (RNA/RNP complex 1-interacting)	-1.07	0.689	-1.17	0.08	-1.12	0.31	-1.24	0.238	-1.15
1435174_at	Rsbn1	rosbin, round spermatid basic protein 1	-1.14	0.464	-1.01	0.934	-1.21	0.009	-1.23	0.276	-1.15
1444051_at	5830405N20Rik	RIKEN cDNA 5830405N20 gene	-1.21	0.507	-1.14	0.423	-1.02	0.93	-2.05	0.087	-1.35
1423665_a_at	Rpl5	ribosomal protein L5	-1.11	0.212	-1.05	0.372	-1.19	0.01	-1.21	0.005	-1.14
1448157_s_at	Rpl10	ribosomal protein 10	-1.04	0.239	-1.06	0.65	-1.28	0	-1.24	0.032	-1.15
1429400_at	Clcn5	chloride channel 5	-1.18	0.33	-1.08	0.277	-1.09	0.186	-1.11	0.721	-1.12
1452604_at	Stard13	serologically defined colon cancer antigen 13	-1.3	0.026	-1.04	0.859	-1.04	0.869	-1.68	0.081	-1.27
1454747_a_at	Klhdc3	kelch domain containing 3	-1.22	0.001	-1.12	0.218	-1.03	0.832	-1.07	0.684	-1.11
1424358_at	Ube2e2	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	-1	0.975	-1.05	0.536	-1.35	0.119	-2.41	0.024	-1.45
1452083_a_at	Pja1	praja1, RING-H2 motif containing	-1.12	0.594	-1.11	0.537	-1.12	0.387	-1.25	0.545	-1.15
1448801_a_at	Timm44	translocase of inner mitochondrial membrane 44	-1.19	0.141	-1.12	0.107	-1.05	0.775	-1.09	0.462	-1.11
1450664_at	Gabpa	GA repeat binding protein, alpha	-1.27	0.077	-1.03	0.524	-1.08	0.302	-1.07	0.423	-1.11
1420489_at	Mrps14	mitochondrial ribosomal protein S14	-1.13	0.267	-1.15	0.008	-1.08	0.224	-1.14	0.419	-1.12
1449686_s_at	Scp2	sterol carrier protein 2, liver	-1.09	0.476	-1.09	0.363	-1.18	0.181	-1.53	0.164	-1.22
1434742_s_at	2810401C16Rik	RIKEN cDNA 2810401C16 gene	-1.17	0.599	-1.09	0.719	-1.09	0.788	-1.05	0.931	-1.1
1458501_at	Vapb	vesicle-associated membrane protein, associated protein B and C	-1.04	0.897	-1.06	0.781	-1.28	0.052	-1.04	0.853	-1.1
1426870_at	Fbxo33	F-box only protein 33	-1.15	0.252	-1.08	0.544	-1.12	0.33	-1.06	0.733	-1.1
1448356_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	-1.01	0.818	-1.16	0.02	-1.2	0.002	-1.31	0.132	-1.17
1423893_x_at	Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	-1.07	0.74	-1.26	0.584	-1.04	0.556	-1.34	0.163	-1.18
1437696_at	BC049807	cDNA sequence BC049807	-1.05	0.906	-1.07	0.786	-1.25	0.344	-1.07	0.765	-1.11
1436597_at	Ankhd1	ankyrin repeat and KH domain containing 1	-1.15	0.645	-1.09	0.417	-1.12	0.367	-1.43	0.073	-1.2
1454722_at	Pten	phosphatase and tensin homolog	-1.06	0.635	-1.02	0.085	-1.3	0.132	-1.44	0.278	-1.21
1435317_x_at	Psma6	proteasome (prosome, macropain) subunit, alpha type 6	-1.16	0.258	-1.01	0.938	-1.19	0.379	-1.33	0.252	-1.17
1452878_at	Prkce	protein kinase C, epsilon	-1.26	0.12	-1	0.986	-1.12	0.492	-1.2	0.448	-1.14
1443573_at	Parp1	poly (ADP-ribose) polymerase family, member 1	-1.08	0.817	-1.1	0.748	-1.17	0.468	-1.39	0.289	-1.19
1445960_at	---	---	-1.13	0.813	-1.13	0.768	-1.09	0.627	-1.64	0.303	-1.25
1430060_at	1700034G24Rik	RIKEN cDNA 1700034G24 gene	-1.02	0.922	-1.2	0.384	-1.14	0.339	-1.25	0.262	-1.15
1426558_x_at	3100002L24Rik /// I	RIKEN cDNA 3100002L24 gene /// similar to zinc finger protein 14 /// RIKEN cDN	-1.22	0.218	-1.14	0.11	-1.01	0.946	-1.13	0.468	-1.12
1439108_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5	-1.05	0.859	-1.33	0.022	-1.02	0.946	-1.32	0.243	-1.18
1431500_at	4933406J10Rik	RIKEN cDNA 4933406J10 gene	-1.01	0.962	-1.08	0.708	-1.3	0.345	-1.23	0.202	-1.15
1416244_a_at	Cnbp	cellular nucleic acid binding protein	-1.06	0.224	-1.19	0.108	-1.1	0.228	-1.15	0.074	-1.13
1423911_at	Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	-1.17	0.199	-1.1	0.432	-1.08	0.154	-1.29	0.29	-1.16
1438626_x_at	Rpl14	ribosomal protein L14	-1.19	0.264	-1.05	0.633	-1.12	0.411	-1.31	0.024	-1.17
1430045_at	Tsnax	translin-associated factor X	-1.03	0.884	-1.02	0.828	-1.35	0.139	-1.23	0.247	-1.16
1434332_at	Zzz3	zinc finger, ZZ domain containing 3	-1.05	0.314	-1.17	0.067	-1.12	0.026	-1.1	0.298	-1.11
1437256_at	---	---	-1.1	0.821	-1.26	0.648	-1.02	0.957	-2.06	0.184	-1.36
1449679_s_at	Stx5a	syntaxin 5A	-1.06	0.092	-1.06	0.615	-1.24	0.076	-1.14	0.199	-1.13
1452790_x_at	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	-1.04	0.755	-1.21	0.028	-1.11	0.448	-1.13	0.353	-1.12
1426578_s_at	Snapap	SNAP-associated protein	-1.01	0.932	-1.22	0.344	-1.13	0.639	-1.1	0.596	-1.12
1449585_at	Il1rap	interleukin 1 receptor accessory protein	-1.07	0.903	-1.29	0.104	-1.01	0.961	-1	0.993	-1.1
1454595_at	4930451E06Rik	RIKEN cDNA 4930451E06 gene	-1.1	0.876	-1.13	0.699	-1.11	0.82	-1.39	0.194	-1.18
1434486_x_at	Ugp2	UDP-glucose pyrophosphorylase 2	-1.09	0.263	-1.15	0.404	-1.1	0.334	-1.13	0.681	-1.12
1434402_at	Samd8	sterile alpha motif domain containing 8	-1.19	0.265	-1.09	0.434	-1.07	0.666	-1.22	0.307	-1.14
1438563_s_at	Mrps24	mitochondrial ribosomal protein S24	-1.01	0.944	-1.06	0.646	-1.32	0.131	-1.13	0.532	-1.13
1424862_s_at	Mib2	mindbomb homolog 2 (Drosophila)	-1.04	0.894	-1.19	0.354	-1.13	0.46	-1.21	0.437	-1.14
1435440_at	Pdzd8	PDZ domain containing 8	-1.01	0.932	-1.18	0.017	-1.17	0.186	-1.07	0.255	-1.11

1420583_a_at	Rora	RAR-related orphan receptor alpha	-1.06	0.746	-1.11	0.46	-1.18	0.181	-1.26	0.114	-1.15
1439998_at	Jmjd1c	jumonji domain containing 1C	-1.02	0.943	-1.04	0.773	-1.33	0.214	-1.6	0.11	-1.25
1422517_a_at	Znrd1	zinc ribbon domain containing, 1	-1.03	0.498	-1.01	0.726	-1.36	0.017	-1.58	0.134	-1.25
1452266_at	Las1l	LAS1-like (S. cerevisiae)	-1.05	0.335	-1.17	0.056	-1.13	0.541	-1.13	0.27	-1.12
1454064_a_at	Rnf138	ring finger protein 138	-1.16	0.408	-1.11	0.269	-1.08	0.479	-1.55	0.073	-1.22
1452188_at	Maml1	mastermind like 1 (Drosophila)	-1.19	0.005	-1.14	0.311	-1.02	0.859	-1.38	0.087	-1.18
1423338_at	Ccdc16	coiled-coil domain containing 16	-1.14	0.308	-1.19	0.067	-1.03	0.855	-1.15	0.311	-1.13
1416153_at	Srp54 /// LOC6651	signal recognition particle 54 /// similar to signal recognition particle 54	-1.19	0.032	-1.05	0.348	-1.11	0.396	-1.08	0.37	-1.11
1456726_x_at	Qars	glutaminyl-tRNA synthetase	-1.13	0.158	-1.17	0.16	-1.05	0.688	-1.38	0.043	-1.18
1429351_at	Klhl24	kelch-like 24 (Drosophila)	-1.16	0.477	-1.11	0.13	-1.07	0.65	-1.78	0.229	-1.28
1415942_at	Rpl10 /// LOC2347(	ribosomal protein 10 /// similar to ribosomal protein L10 /// similar to ribosomal pro	-1.02	0.871	-1.14	0.328	-1.2	0.004	-1.18	0.013	-1.13
1448427_at	Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	-1.06	0.394	-1.17	0.099	-1.11	0.181	-1.4	0.128	-1.19
1418815_at	Cdh2	cadherin 2	-1.02	0.795	-1	0.974	-1.39	0.377	-1.2	0.72	-1.15
1424545_at	BC003965	cDNA sequence BC003965	-1.05	0.391	-1.14	0.047	-1.16	0.154	-1.07	0.466	-1.11
1425085_at	6330416L07Rik	RIKEN cDNA 6330416L07 gene	-1.35	0.338	-1.03	0.81	-1.02	0.951	-1	0.992	-1.1
1448760_at	Zfp68	zinc finger protein 68	-1.02	0.885	-1.06	0.143	-1.3	0.067	-1.41	0.214	-1.2
1419374_at	Wbp4	WW domain binding protein 4	-1.08	0.602	-1.08	0.216	-1.18	0.187	-1.02	0.929	-1.09
1419112_at	Nlk	nemo like kinase	-1.16	0.175	-1.06	0.643	-1.12	0.302	-1.74	0.045	-1.27
1417934_at	Dnajc4	DnaJ (Hsp40) homolog, subfamily C, member 4	-1.19	0.052	-1.17	0.184	-1	0.965	-1.34	0.044	-1.17
1419352_at	0610007P06Rik	RIKEN cDNA 0610007P06 gene	-1.17	0.247	-1.15	0.175	-1.03	0.847	-1.05	0.742	-1.1
1451804_a_at	Lrrc16	leucine rich repeat containing 16	-1	0.983	-1.39	0.265	-1.02	0.953	-2.18	0.073	-1.4
1434683_at	Cutl1	Cut-like 1 (Drosophila)	-1.19	0.144	-1.03	0.887	-1.13	0.376	-1.18	0.565	-1.13
1430264_at	2610030P05Rik	RIKEN cDNA 2610030P05 gene	-1.1	0.789	-1.04	0.815	-1.22	0.13	-1.19	0.191	-1.14
1423840_at	Ccdc56	coiled-coil domain containing 56	-1.19	0.325	-1.08	0.52	-1.08	0.782	-1.53	0.209	-1.22
1453491_at	4833409A17Rik	RIKEN cDNA 4833409A17 gene	-1.14	0.689	-1.21	0.646	-1.01	0.984	-2.33	0.048	-1.42
1433831_at	4833418A01Rik	RIKEN cDNA 4833418A01 gene	-1.04	0.718	-1.01	0.928	-1.35	0.044	-1.66	0.021	-1.26
1422858_at	Trip4	thyroid hormone receptor interactor 4	-1.12	0.188	-1.05	0.584	-1.17	0.418	-1.17	0.154	-1.13
1424607_a_at	BC003993 /// LOC5	cDNA sequence BC003993 /// hypothetical LOC544818	-1.04	0.859	-1.14	0.013	-1.17	0.322	-1.05	0.526	-1.1
1416751_a_at	Ddx20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	-1.12	0.535	-1.23	0.22	-1.01	0.859	-1.01	0.955	-1.09
1419360_a_at	Ss18	synovial sarcoma translocation, Chromosome 18	-1.05	0.69	-1.09	0.128	-1.2	0.11	-1.24	0.341	-1.15
1438288_x_at	1110059G02Rik	RIKEN cDNA 1110059G02 gene	-1.24	0.178	-1.11	0.664	-1.01	0.951	-1.27	0.244	-1.16
1460716_a_at	Cbfb	core binding factor beta	-1.04	0.429	-1.11	0.491	-1.2	0.124	-1.53	0.168	-1.22
1439504_s_at	Zfp28	zinc finger protein 28	-1.18	0.562	-1.17	0.803	-1.01	0.986	-1.78	0.303	-1.28
1415722_a_at	1110059P08Rik	RIKEN cDNA 1110059P08 gene	-1.11	0.232	-1.11	0.176	-1.11	0.351	-1.19	0.268	-1.13
1455402_at	Socs7	suppressor of cytokine signaling 7	-1.25	0.102	-1.05	0.659	-1.06	0.637	-1.17	0.183	-1.13
1434551_at	Hnrpul2	heterogeneous nuclear ribonucleoprotein U-like 2	-1.15	0.457	-1.15	0.395	-1.04	0.831	-1.02	0.928	-1.09
1423923_a_at	Wdr8	WD repeat domain 8	-1	0.986	-1.25	0.222	-1.11	0.095	-1.1	0.528	-1.12
1452048_at	Mrpl12	mitochondrial ribosomal protein L12	-1.06	0.455	-1.1	0.1	-1.18	0.029	-1.14	0.472	-1.12
1435442_at	Wdsof1	WD repeats and SOF domain containing 1	-1.09	0.437	-1.16	0.187	-1.09	0.589	-1.17	0.205	-1.13
1433934_at	Sec24a	SEC24 related gene family, member A (S. cerevisiae)	-1.22	0.287	-1.04	0.678	-1.09	0.493	-1.08	0.781	-1.11
1425672_a_at	Trpc2	transient receptor potential cation channel, subfamily C, member 2	-1.06	0.746	-1.1	0.54	-1.18	0.582	-1.35	0.648	-1.17
1429160_at	2810012L14Rik	RIKEN cDNA 2810012L14 gene	-1	0.982	-1.27	0.137	-1.09	0.657	-1.85	0.112	-1.3
1424309_a_at	Mocs2	molybdenum cofactor synthesis 2	-1.06	0.372	-1.18	0.095	-1.09	0.233	-1.12	0.052	-1.12
1424209_at	Rarsl	arginyl-tRNA synthetase-like	-1.26	0.167	-1.09	0.293	-1.01	0.922	-1.04	0.713	-1.1
1454641_at	Cggbp1	CGG triplet repeat binding protein 1	-1.1	0.02	-1.03	0.546	-1.22	0.016	-1.04	0.042	-1.1
1435590_at	D430047L21Rik	RIKEN cDNA D430047L21 gene	-1.02	0.953	-1.09	0.7	-1.26	0.353	-1.18	0.446	-1.14
1448965_at	Inoc1	INO80 complex homolog 1 (S. cerevisiae)	-1.1	0.722	-1.22	0.24	-1.03	0.926	-1.12	0.74	-1.12
1454756_at	Lrch3	leucine-rich repeats and calponin homology (CH) domain containing 3	-1.19	0.357	-1.05	0.629	-1.1	0.652	-1.62	0.081	-1.24
1424703_at	Hemk1	HemK methyltransferase family member 1	-1.07	0.65	-1.26	0.152	-1.03	0.941	-1.62	0.123	-1.24
1460339_at	Psma4	proteasome (prosome, macropain) subunit, alpha type 4	-1.12	0.098	-1.12	0.246	-1.1	0.272	-1.17	0.483	-1.13
1457046_s_at	C77370	expressed sequence C77370	-1.15	0.779	-1.12	0.717	-1.06	0.888	-1.93	0.435	-1.32
1420265_x_at	Cog8	component of oligomeric golgi complex 8	-1.23	0.268	-1.09	0.478	-1.04	0.898	-1.73	0.02	-1.27
1422797_at	Mapbpip	mitogen activated protein binding protein interacting protein	-1.11	0.203	-1.18	0.141	-1.05	0.209	-1.63	0.063	-1.24

1452166_a_at	Krt10	keratin 10	-1.04	0.027	-1.06	0.67	-1.26	0.071	-1.21	0.503	-1.14
1431028_a_at	Pank1	pantothenate kinase 1	-1.06	0.849	-1.09	0.55	-1.19	0.26	-1.24	0.354	-1.15
1433830_at	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	-1.22	0.152	-1.04	0.562	-1.09	0.488	-1.15	0.407	-1.12
1416983_s_at	Foxo1	forkhead box O1	-1.07	0.801	-1.17	0.495	-1.1	0.587	-2.06	0.101	-1.35
1434841_at	BC010584	CDNA sequence BC010584	-1.14	0.259	-1.02	0.905	-1.2	0.255	-1.41	0.143	-1.19
1456253_s_at	Plekhn1 /// Klhl17	pleckstrin homology domain containing, family N member 1 /// kelch-like 17 (Dros	-1.02	0.919	-1.19	0.17	-1.13	0.287	-1.05	0.676	-1.1
1435149_at	Plcg1	phospholipase C, gamma 1	-1.02	0.895	-1.14	0.332	-1.18	0.437	-1.55	0.278	-1.22
1454217_at	4930556N09Rik	RIKEN cDNA 4930556N09 gene	-1.24	0.776	-1.04	0.794	-1.07	0.875	-1.4	0.079	-1.19
1433397_at	9430012M22Rik	RIKEN cDNA 9430012M22 gene	-1.19	0.534	-1.14	0.769	-1.01	0.972	-2.13	0.051	-1.37
1440130_at	BB116930	expressed sequence BB116930	-1.36	0.133	-1.03	0.932	-1	0.994	-1.31	0.346	-1.18
1424839_a_at	Nsun4	NOL1/NOP2/Sun domain family, member 4	-1.21	0.269	-1.11	0.512	-1.03	0.827	-1.11	0.302	-1.11
1460680_a_at	Rpl23	ribosomal protein L23	-1.15	0.237	-1.05	0.381	-1.15	0.087	-1.34	0.011	-1.17
1433824_x_at	Grsf1	G-rich RNA sequence binding factor 1	-1.18	0.298	-1.16	0.057	-1.01	0.857	-1.25	0.127	-1.15
1436121_a_at	Nsmce1	non-SMC element 1 homolog (S. cerevisiae)	-1.08	0.154	-1.09	0.009	-1.16	0.201	-1.31	0.277	-1.16
1454022_at	Ephb2	Eph receptor B2	-1.22	0.434	-1.05	0.722	-1.07	0.534	-1.07	0.719	-1.1
1419636_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	-1.05	0.813	-1.11	0.475	-1.17	0.457	-1.65	0.052	-1.25
1432271_a_at	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	-1.12	0.321	-1.11	0.204	-1.1	0.442	-1.19	0.274	-1.13
1417792_at	Zfml	zinc finger, matrin-like	-1.02	0.829	-1.26	0.272	-1.08	0.679	-1.08	0.749	-1.11
1447923_at	2810013C04Rik	RIKEN cDNA 2810013C04 gene	-1.17	0.543	-1.03	0.744	-1.14	0.206	-2.02	0.063	-1.34
1423625_a_at	Dnajc19	DnaJ (Hsp40) homolog, subfamily C, member 19	-1.08	0.63	-1.11	0.368	-1.14	0.459	-1.23	0.492	-1.14
1436982_at	Tnrc6b	trinucleotide repeat containing 6b	-1.12	0.334	-1.07	0.529	-1.14	0.464	-1.03	0.606	-1.09
1416857_at	Sdf2	stromal cell derived factor 2	-1.06	0.144	-1.09	0.018	-1.19	0.031	-1.24	0.337	-1.14
1416764_at	Fis1	fission 1 (mitochondrial outer membrane) homolog (yeast)	-1.09	0.532	-1.02	0.698	-1.24	0.08	-1.19	0.375	-1.14
1455195_at	Rps24	ribosomal protein S24	-1.16	0.055	-1.07	0.502	-1.1	0.641	-1.49	0.038	-1.21
1437776_at	Tmcc1	transmembrane and coiled coil domains 1	-1.07	0.688	-1.11	0.619	-1.16	0.089	-1.29	0.023	-1.16
1427095_at	Cdcp1	CUB domain containing protein 1	-1.18	0.245	-1.01	0.938	-1.15	0.203	-1.21	0.507	-1.14
1429949_at	6530415H11Rik	RIKEN cDNA 6530415H11 gene	-1.07	0.747	-1.29	0.302	-1.01	0.977	-1.01	0.909	-1.1
1428357_at	2610019F03Rik	RIKEN cDNA 2610019F03 gene	-1.06	0.642	-1.17	0.385	-1.1	0.723	-2.74	0.126	-1.52
1427544_a_at	Papola	poly (A) polymerase alpha	-1.03	0.937	-1.23	0.27	-1.1	0.684	-1.06	0.797	-1.1
1434377_x_at	Rps6 /// LOC66773	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	-1.07	0.14	-1.04	0.574	-1.24	0.003	-1.25	0.004	-1.15
1416981_at	Foxo1	forkhead box O1	-1.03	0.848	-1.2	0.294	-1.1	0.493	-2.31	0.052	-1.41
1450949_at	Katna1	katanin p60 (ATPase-containing) subunit A1	-1.09	0.568	-1.23	0.019	-1.03	0.82	-1.06	0.693	-1.1
1429711_at	Styx	phosphoserine/threonine/tyrosine interaction protein	-1.04	0.547	-1.02	0.838	-1.3	0.099	-1.15	0.122	-1.13
1426810_at	Jmjd1a	jumonji domain containing 1A	-1.15	0.388	-1.09	0.443	-1.09	0.39	-1.15	0.002	-1.12
1420862_at	Dctn4	dynactin 4	-1.07	0.444	-1.2	0.129	-1.07	0.527	-1.11	0.559	-1.11
1428163_at	Sar1b	SAR1 gene homolog B (S. cerevisiae)	-1.05	0.588	-1.14	0.415	-1.14	0.135	-1.03	0.778	-1.09
1448347_a_at	Gpiap1	GPI-anchored membrane protein 1	-1.07	0.679	-1.05	0.708	-1.22	0.085	-1.02	0.742	-1.09
1442243_at	Per3	period homolog 3 (Drosophila)	-1.05	0.903	-1.09	0.865	-1.19	0.733	-1.06	0.376	-1.1
1448286_at	Hadh2	hydroxyacyl-Coenzyme A dehydrogenase type II	-1.13	0.238	-1.12	0.062	-1.08	0.655	-1.11	0.666	-1.11
1417474_at	1500035H01Rik	RIKEN cDNA 1500035H01 gene	-1	0.88	-1.14	0.259	-1.2	0.277	-1.3	0.032	-1.16
1460581_a_at	Rpl13 /// LOC28004	ribosomal protein L13 /// similar to 60S ribosomal protein L13 /// similar to 60S rib	-1.05	0.412	-1.06	0.663	-1.23	0.042	-1.3	0.07	-1.16
1443762_s_at	Sbf2	SET binding factor 2	-1.08	0.526	-1.09	0.535	-1.16	0.253	-1.11	0.527	-1.11
1426845_at	Pdcd2l	programmed cell death 2-like	-1.13	0.273	-1.19	0.028	-1.02	0.866	-1.28	0.095	-1.15
1424105_a_at	Pttg1	pituitary tumor-transforming 1	-1.11	0.229	-1.23	0.035	-1.01	0.94	-1.01	0.946	-1.09
1433927_at	Uspl1	ubiquitin specific peptidase like 1	-1.03	0.731	-1.08	0.401	-1.24	0.178	-1.29	0.019	-1.16
1453929_at	Rnf24	ring finger protein 24	-1.27	0.417	-1.07	0.708	-1.01	0.807	-1.03	0.616	-1.1
1423793_at	D2Ertd391e	DNA segment, Chr 2, ERATO Doi 391, expressed	-1.05	0.564	-1.31	0.183	-1.01	0.964	-1.17	0.481	-1.13
1451076_s_at	Ga17	dendritic cell protein GA17	-1.07	0.604	-1.12	0.017	-1.14	0.068	-1.38	0.112	-1.18
1415699_a_at	Gps1	G protein pathway suppressor 1	-1.01	0.934	-1.08	0.013	-1.26	0.047	-1.13	0.148	-1.12
1442098_at	AU022434	expressed sequence AU022434	-1.17	0.364	-1.14	0.225	-1.02	0.863	-1.83	0.089	-1.29
1426084_a_at	Tor1aip1	torsin A interacting protein 1	-1.11	0.061	-1.19	0.122	-1.03	0.633	-1.29	0.25	-1.16
1419308_at	Invs	inversin	-1.09	0.264	-1.25	0.061	-1.01	0.966	-1.62	0.13	-1.24
1437210_a_at	Brd2	bromodomain containing 2	-1	0.987	-1.23	0.136	-1.11	0.685	-1.14	0.443	-1.12

1445747_at	---	15 days embryo male testis cDNA, RIKEN full-length enriched library, clone:8030	-1.18	0.5	-1	0.998	-1.16	0.47	-1.36	0.307	-1.17
1457432_at	Prox1	prospero-related homeobox 1	-1.09	0.796	-1.05	0.588	-1.2	0.189	-1.33	0.237	-1.16
1422451_at	Mrps21	mitochondrial ribosomal protein S21	-1.04	0.534	-1.12	0.143	-1.17	0.168	-1.25	0.275	-1.14
1427878_at	0610010O12Rik	RIKEN cDNA 0610010O12 gene	-1.15	0.189	-1.02	0.881	-1.15	0.254	-1.21	0.52	-1.14
1432263_a_at	Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	-1.12	0.048	-1.12	0.093	-1.08	0.645	-1.96	0.131	-1.32
1440830_at	Gpr116	G protein-coupled receptor 116	-1.01	0.948	-1.01	0.864	-1.37	0.104	-1.32	0.382	-1.18
1451146_at	Zfp386 /// LOC676	zinc finger protein 386 (Kruppel-like) /// similar to zinc finger protein 386 (Kruppel-	-1.14	0.389	-1.14	0.33	-1.04	0.835	-1.93	0.041	-1.31
1423989_at	2210010N04Rik	RIKEN cDNA 2210010N04 gene	-1.02	0.916	-1.25	0.417	-1.08	0.687	-2.4	0.071	-1.44
1455227_at	Aadacl1	arylacetamide deacetylase-like 1	-1.04	0.486	-1.29	0.178	-1.02	0.889	-1.13	0.668	-1.12
1448398_s_at	Rpl22	ribosomal protein L22	-1.14	0.57	-1.04	0.793	-1.15	0.306	-1.38	0.159	-1.18
1448493_at	Paip2	polyadenylate-binding protein-interacting protein 2	-1.04	0.695	-1.08	0.184	-1.21	0.093	-1.25	0.181	-1.15
1452075_at	4933435A13Rik	RIKEN cDNA 4933435A13 gene	-1.17	0.295	-1.11	0.532	-1.05	0.773	-1.02	0.823	-1.09
1422471_at	Pex13	peroxisomal biogenesis factor 13	-1.1	0.01	-1.14	0.135	-1.09	0.484	-1.17	0.347	-1.12
1424005_at	B230219D22Rik	RIKEN cDNA B230219D22 gene	-1.02	0.644	-1.14	0.109	-1.17	0.388	-1.04	0.76	-1.09
1426830_a_at	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	-1.02	0.875	-1.04	0.176	-1.3	0.071	-1.1	0.493	-1.11
1417885_at	Mapt	microtubule-associated protein tau	-1.07	0.781	-1.15	0.751	-1.1	0.264	-2.25	0.478	-1.39
1439841_at	Zfyve27	zinc finger, FYVE domain containing 27	-1.22	0.288	-1.08	0.805	-1.03	0.879	-1.08	0.729	-1.1
1421212_at	Abcc6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	-1.01	0.954	-1.13	0.416	-1.2	0.111	-1.15	0.686	-1.12
1451294_s_at	Snrpe	small nuclear ribonucleoprotein E	-1.03	0.728	-1.1	0.175	-1.2	0.214	-1.2	0.17	-1.13
1418516_at	Mtf2	metal response element binding transcription factor 2	-1.05	0.767	-1.17	0.227	-1.11	0.362	-1.29	0.227	-1.15
1417113_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	-1.1	0.061	-1.07	0.412	-1.16	0.039	-1.27	0.205	-1.15
1428215_x_at	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	-1.03	0.713	-1.08	0.351	-1.22	0.137	-1.29	0.304	-1.16
1457674_at	Vps13a	vacuolar protein sorting 13A (yeast)	-1.25	0.289	-1.02	0.947	-1.08	0.582	-1.43	0.004	-1.19
1424463_at	2210010L05Rik	RIKEN cDNA 2210010L05 gene	-1.03	0.554	-1.11	0.699	-1.2	0.016	-1.24	0.186	-1.14
1459433_at	C130051F05Rik	RIKEN cDNA C130051F05 gene	-1.06	0.847	-1.02	0.891	-1.27	0.159	-1.68	0.056	-1.26
1416439_at	2410015N17Rik	RIKEN cDNA 2410015N17 gene	-1.1	0.682	-1.15	0.333	-1.07	0.741	-1.28	0.5	-1.15
1449386_at	Hsd17b9	hydroxysteroid (17-beta) dehydrogenase 9	-1.07	0.938	-1.15	0.703	-1.1	0.504	-2.08	0.25	-1.35
1430417_s_at	0610025P10Rik	RIKEN cDNA 0610025P10 gene	-1.02	0.782	-1.14	0.318	-1.17	0.267	-1.1	0.616	-1.11
1433570_s_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-1.06	0.751	-1.27	0.03	-1.02	0.904	-1.14	0.384	-1.12
1416762_at	S100a10	S100 calcium binding protein A10 (calpactin)	-1.02	0.638	-1.09	0.425	-1.24	0.046	-1.57	0.302	-1.23
1434344_at	Gpkow	G patch domain and KOW motifs	-1.13	0.268	-1.17	0.01	-1.03	0.473	-1.07	0.557	-1.1
1426820_at	2610507B11Rik	RIKEN cDNA 2610507B11 gene	-1.01	0.728	-1.23	0.08	-1.1	0.406	-1.23	0.138	-1.14
1455153_at	Zfp236	zinc finger protein 236	-1.11	0.435	-1.21	0.117	-1.02	0.859	-1.31	0.092	-1.16
1416465_a_at	Vapa	vesicle-associated membrane protein, associated protein A	-1.04	0.801	-1.29	0.037	-1.03	0.791	-1.13	0.291	-1.12
1422613_a_at	Rpl7a	ribosomal protein L7a	-1.08	0.146	-1.1	0.204	-1.14	0.088	-1.29	0.002	-1.15
1433464_at	Ipo13	importin 13	-1.12	0.248	-1.13	0.224	-1.07	0.662	-1.17	0.2	-1.12
1426724_at	Cnn3	calponin 3, acidic	-1.03	0.606	-1.08	0.531	-1.22	0.225	-2.32	0.04	-1.41
1453032_at	2610109B12Rik	RIKEN cDNA 2610109B12 gene	-1.04	0.412	-1.02	0.744	-1.29	0.012	-1.18	0.024	-1.13
1416171_at	2310037I24Rik	RIKEN cDNA 2310037I24 gene	-1.03	0.759	-1.15	0.224	-1.14	0.377	-1.26	0.013	-1.15
1447483_s_at	2610002F03Rik	RIKEN cDNA 2610002F03 gene	-1.02	0.898	-1.27	0.392	-1.05	0.642	-1	0.993	-1.09
1427898_at	Rnf6	ring finger protein (C3H2C3 type) 6	-1.05	0.413	-1.08	0.452	-1.2	0.156	-1.17	0.034	-1.12
1437657_at	Zfp291	zinc finger protein 291	-1.03	0.917	-1.15	0.675	-1.14	0.598	-1.48	0.283	-1.2
1417590_at	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	-1.01	0.946	-1.21	0.174	-1.11	0.637	-2.13	0.123	-1.36
1424706_at	Zfp51	zinc finger protein 51	-1.11	0.683	-1.1	0.476	-1.1	0.469	-1.73	0.083	-1.26
1453729_a_at	Rpl37	ribosomal protein L37	-1.06	0.076	-1	0.906	-1.29	0.018	-1.22	0.012	-1.14
1428449_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	-1.14	0.312	-1.13	0.417	-1.05	0.806	-1.03	0.93	-1.09
1448921_a_at	Mrps9	mitochondrial ribosomal protein S9	-1.1	0.643	-1.11	0.526	-1.1	0.031	-1.14	0.191	-1.11
1451388_a_at	Atp11b	ATPase, Class VI, type 11B	-1.06	0.574	-1.22	0.276	-1.05	0.696	-1.02	0.909	-1.09
1443089_at	4930506C02Rik	RIKEN cDNA 4930506C02 gene	-1.02	0.919	-1.32	0.27	-1.02	0.974	-1.46	0.365	-1.21
1443453_at	Zfp651	zinc finger protein 651	-1	0.994	-1.13	0.876	-1.19	0.649	-1.56	0.396	-1.22
1451096_at	Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	-1.11	0.401	-1.16	0.234	-1.05	0.734	-1.43	0.068	-1.19
1436936_s_at	Xist	inactive X specific transcripts	-1.05	0.792	-1.15	0.26	-1.12	0.425	-1.07	0.615	-1.1
1424782_at	Tmem77	transmembrane protein 77	-1.13	0.364	-1.03	0.613	-1.16	0.036	-1.28	0.102	-1.15

1451905_a_at	Mx1	myxovirus (influenza virus) resistance 1	-1.13	0.737	-1.02	0.965	-1.18	0.523	-2.34	0.147	-1.42
1452701_x_at	Uba52 /// LOC6665	ubiquitin A-52 residue ribosomal protein fusion product 1 /// similar to ubiquitin A-	-1.07	0.049	-1.04	0.723	-1.21	0.024	-1.28	0.017	-1.15
1450601_at	V1rb8	vomeronasal 1 receptor, B8	-1.14	0.519	-1.05	0.902	-1.13	0.854	-1.19	0.766	-1.13
1424218_a_at	Creb3l4	cAMP responsive element binding protein 3-like 4	-1.02	0.967	-1.24	0.56	-1.07	0.895	-1.95	0.443	-1.32
1433550_at	Chfr	checkpoint with forkhead and ring finger domains	-1.27	0.149	-1.04	0.481	-1.03	0.726	-1.14	0.125	-1.12
1429043_at	Smndc1	survival motor neuron domain containing 1	-1.17	0.275	-1.08	0.453	-1.06	0.554	-1.11	0.422	-1.11
1422608_at	Arpp19 /// 2700024	cAMP-regulated phosphoprotein 19 /// RIKEN cDNA 2700024H10 gene	-1.03	0.753	-1.01	0.902	-1.33	0.205	-1.04	0.804	-1.1
1428709_a_at	Mrpl24	mitochondrial ribosomal protein L24	-1.12	0.133	-1.16	0.002	-1.04	0.598	-1.63	0.073	-1.24
1435171_at	2810416G20Rik	RIKEN cDNA 2810416G20 gene	-1.16	0.413	-1.08	0.751	-1.07	0.76	-1.27	0.113	-1.15
1422601_at	Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	-1.01	0.956	-1.1	0.418	-1.22	0.006	-1.05	0.428	-1.1
1415841_at	Dync1i2	dynein cytoplasmic 1 intermediate chain 2	-1.03	0.817	-1.08	0.355	-1.21	0.012	-1.12	0.074	-1.11
1451302_at	1110012L19Rik	RIKEN cDNA 1110012L19 gene	-1.07	0.666	-1.04	0.711	-1.22	0.234	-1.12	0.568	-1.11
1415711_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibite	-1.11	0.342	-1.09	0.195	-1.1	0.406	-1.28	0.119	-1.15
1416447_at	Tmem30a	transmembrane protein 30A	-1.09	0.499	-1.16	0.446	-1.07	0.655	-1.37	0.149	-1.17
1430171_at	Fibp	fibroblast growth factor (acidic) intracellular binding protein	-1.15	0.478	-1.05	0.66	-1.12	0.52	-1.4	0.22	-1.18
1457304_at	D13Ertd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	-1.06	0.902	-1.02	0.932	-1.26	0.468	-1.52	0.122	-1.21
1428327_at	Trak1	trafficking protein, kinesin binding 1	-1.11	0.672	-1.18	0.345	-1.03	0.859	-1.14	0.392	-1.12
1434127_a_at	H3f3a /// LOC54497	H3 histone, family 3A /// similar to H3 histone, family 3B /// similar to H3 histone, f	-1.06	0.701	-1.05	0.334	-1.21	0.043	-1.12	0.152	-1.11
1426290_at	Dimt1	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	-1.18	0.422	-1.07	0.829	-1.06	0.532	-1.13	0.498	-1.11
1436079_s_at	Vapb	vesicle-associated membrane protein, associated protein B and C	-1.04	0.881	-1.11	0.235	-1.16	0.292	-1.33	0.389	-1.16
1425781_a_at	Plcb1	phospholipase C, beta 1	-1.15	0.476	-1.13	0.372	-1.04	0.875	-1.21	0.323	-1.13
1455662_x_at	Rps17	ribosomal protein S17	-1.11	0.123	-1.01	0.802	-1.2	0.017	-1.31	0.003	-1.16
1444167_at	---	Transcribed locus	-1.15	0.432	-1.16	0.64	-1.01	0.945	-1.07	0.678	-1.1
1455429_at	AI450540	expressed sequence AI450540	-1.01	0.939	-1.15	0.407	-1.16	0.199	-1.26	0.021	-1.15
1444507_at	Usp53	ubiquitin specific peptidase 53	-1.09	0.553	-1.04	0.814	-1.18	0.204	-1.82	0.112	-1.28
1418564_s_at	Serbp1	Serpine1 mRNA binding protein 1	-1.06	0.276	-1.05	0.262	-1.22	0.104	-1.1	0.356	-1.1
1429436_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	-1.02	0.712	-1.03	0.795	-1.29	0.082	-1.08	0.718	-1.11
1418501_a_at	Oxr1	oxidation resistance 1	-1.05	0.604	-1.08	0.106	-1.19	0.129	-1.14	0.456	-1.11
1433723_s_at	Serf2	small EDRK-rich factor 2	-1.15	0.236	-1.09	0.02	-1.06	0.542	-1.37	0.04	-1.17
1453207_at	2900053A13Rik	RIKEN cDNA 2900053A13 gene	-1.08	0.462	-1.02	0.786	-1.23	0.331	-1.05	0.802	-1.09
1433603_at	Ndufs6	NADH dehydrogenase (ubiquinone) Fe-S protein 6	-1.08	0.376	-1.1	0.211	-1.13	0.328	-1.05	0.816	-1.09
1416372_at	Ptdss1	phosphatidylserine synthase 1	-1.02	0.391	-1.09	0.48	-1.2	0.033	-1.06	0.343	-1.1
1419013_at	Gpatc1	G patch domain containing 1	-1.18	0.293	-1.05	0.445	-1.08	0.629	-1.04	0.777	-1.09
1438386_x_at	Mat2a	methionine adenosyltransferase II, alpha	-1.02	0.94	-1.07	0.681	-1.23	0.125	-1.18	0.136	-1.13
1416344_at	Lamp2	lysosomal membrane glycoprotein 2	-1.07	0.43	-1.03	0.484	-1.22	0.086	-1.03	0.829	-1.09
1450444_a_at	Nr1h3	nuclear receptor subfamily 1, group H, member 3	-1.08	0.523	-1.01	0.884	-1.23	0.127	-1.04	0.891	-1.09
1451135_at	Gtf2b	general transcription factor IIB	-1.2	0.015	-1.03	0.708	-1.09	0.426	-1.27	0.075	-1.15
1436967_at	Ankrd11	ankyrin repeat domain 11	-1.07	0.454	-1.07	0.597	-1.17	0.55	-1.43	0.299	-1.18
1449973_a_at	Pelp1	proline, glutamic acid and leucine rich protein 1	-1.31	0.463	-1.04	0.948	-1	0.991	-1.77	0.311	-1.28
1431544_at	4930524B17Rik	RIKEN cDNA 4930524B17 gene	-1.15	0.837	-1.04	0.932	-1.12	0.664	-1.26	0.232	-1.14
1455500_at	D11Ertd759e /// LO	DNA segment, Chr 11, ERATO Doi 759, expressed /// similar to chromosome 17	-1.09	0.629	-1.11	0.28	-1.11	0.59	-1.27	0.318	-1.14
1431428_a_at	Nosip	nitric oxide synthase interacting protein	-1.01	0.934	-1.15	0.282	-1.16	0.213	-1.11	0.66	-1.11
1425354_a_at	Aggf1	angiogenic factor with G patch and FHA domains 1	-1.04	0.776	-1.03	0.723	-1.26	0.016	-1.04	0.775	-1.09
1418715_at	Pank1	pantothenate kinase 1	-1.05	0.87	-1.04	0.752	-1.24	0.091	-1.06	0.412	-1.1
1432444_a_at	1810011O16Rik	RIKEN cDNA 1810011O16 gene	-1.01	0.916	-1.21	0.026	-1.09	0.477	-1.33	0.281	-1.16
1417075_at	2010309E21Rik	RIKEN cDNA 2010309E21 gene	-1.08	0.545	-1.04	0.493	-1.2	0.312	-1.04	0.815	-1.09
1416356_at	Gmpr2	guanosine monophosphate reductase 2	-1.07	0.245	-1.11	0.141	-1.12	0.317	-1.21	0.028	-1.13
1433537_at	4833408C14Rik	RIKEN cDNA 4833408C14 gene	-1.02	0.94	-1.01	0.881	-1.33	0.024	-1.12	0.661	-1.12
1425266_a_at	Rap1gds1	RAP1, GTP-GDP dissociation stimulator 1	-1.05	0.477	-1.16	0.285	-1.1	0.488	-1.43	0.248	-1.18
1454301_at	2900073C17Rik	RIKEN cDNA 2900073C17 gene	-1.03	0.964	-1.13	0.811	-1.16	0.803	-2.17	0.074	-1.37
1447388_at	5830484A20Rik	RIKEN cDNA 5830484A20 gene	-1.15	0.804	-1.1	0.864	-1.05	0.893	-1.01	0.972	-1.08
1422994_at	Pip5k3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	-1.21	0.55	-1.08	0.881	-1.03	0.919	-2.24	0.032	-1.39
1418319_at	1810047C23Rik	RIKEN cDNA 1810047C23 gene	-1.09	0.446	-1.08	0.04	-1.14	0.366	-1.21	0.066	-1.13

1429421_at	2610203E10Rik	RIKEN cDNA 2610203E10 gene	-1.14	0.588	-1.17	0.525	-1.01	0.957	-1.05	0.809	-1.09
1460578_at	Fgd5	FYVE, RhoGEF and PH domain containing 5	-1.18	0.433	-1.05	0.827	-1.08	0.494	-1.07	0.592	-1.1
1455693_x_at	Rps6 /// LOC43440	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	-1.04	0.753	-1.07	0.561	-1.21	0.014	-1.28	0.006	-1.15
1415688_at	Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	-1.12	0.297	-1.14	0.076	-1.05	0.343	-1.02	0.781	-1.08
1427074_at	Pcmtd2	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-1.18	0.416	-1.07	0.345	-1.06	0.644	-1.03	0.821	-1.09
1452583_s_at	Galm	galactose mutarotase	-1.13	0.132	-1.17	0.43	-1.02	0.92	-1.61	0.196	-1.23
1452249_at	Prickle1	prickle like 1 (Drosophila)	-1.06	0.171	-1.05	0.725	-1.2	0.546	-1.2	0.247	-1.13
1450858_a_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-1.06	0.438	-1.15	0.001	-1.09	0.321	-1.16	0.201	-1.11
1426513_at	Rbm28	RNA binding motif protein 28	-1	0.972	-1.13	0.326	-1.18	0.556	-1.2	0.493	-1.13
1436187_at	1110054M08Rik	RIKEN cDNA 1110054M08 gene	-1.11	0.37	-1.18	0.101	-1.03	0.844	-1.45	0.305	-1.19
1451645_at	Fbs1	fibrosin 1	-1	0.989	-1.37	0.017	-1	0.968	-1.38	0.017	-1.19
1450921_at	Aptx	aprataxin	-1.11	0.262	-1.08	0.529	-1.11	0.372	-1.29	0.254	-1.15
1448373_at	Mrpl18	mitochondrial ribosomal protein L18	-1.09	0.251	-1.12	0.278	-1.09	0.24	-1.01	0.945	-1.08
1432158_a_at	Trappc2	trafficking protein particle complex 2	-1.1	0.112	-1.04	0.505	-1.17	0.01	-1.21	0.027	-1.13
1417999_at	Itm2b	integral membrane protein 2B	-1.1	0.588	-1.08	0.513	-1.13	0.05	-1.08	0.368	-1.09
1419803_s_at	Ccdc12	coiled-coil domain containing 12	-1.14	0.402	-1.03	0.779	-1.14	0.174	-1.62	0.019	-1.23
1451238_at	1200003C05Rik	RIKEN cDNA 1200003C05 gene	-1.1	0.549	-1.11	0.238	-1.09	0.436	-1.13	0.18	-1.11
1436163_at	Kcnj16	potassium inwardly-rectifying channel, subfamily J, member 16	-1.03	0.74	-1.26	0.255	-1.04	0.777	-1.29	0.564	-1.15
1440044_at	Ttf1	Transcription termination factor 1	-1.06	0.657	-1.28	0.432	-1	0.988	-1.36	0.486	-1.17
1420668_a_at	Yipf2	Yip1 domain family, member 2	-1.06	0.797	-1.15	0.49	-1.1	0.771	-1.02	0.937	-1.08
1422996_at	Acot2	acyl-CoA thioesterase 2	-1	0.995	-1.14	0.809	-1.17	0.538	-1.12	0.672	-1.11
1455283_x_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	-1.05	0.636	-1.07	0.23	-1.2	0.056	-1.04	0.691	-1.09
1437013_x_at	Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	-1.02	0.853	-1.19	0.052	-1.1	0.477	-1.29	0.025	-1.15
1436153_a_at	Zmynd11	zinc finger, MYND domain containing 11	-1.13	0.518	-1.08	0.421	-1.09	0.674	-2.18	0.161	-1.37
1418255_s_at	Srf	serum response factor	-1.2	0.496	-1.06	0.803	-1.05	0.833	-1.66	0.09	-1.24
1455312_at	Phc3	polyhomeotic-like 3 (Drosophila)	-1.01	0.793	-1.01	0.957	-1.33	0.119	-1.28	0.257	-1.16
1452312_at	2810002D19Rik	RIKEN cDNA 2810002D19 gene	-1.07	0.376	-1.02	0.802	-1.22	0.016	-1.42	0.126	-1.18
1455700_at	Mterfd3	MTERF domain containing 3	-1.12	0.717	-1.05	0.856	-1.14	0.428	-2.11	0.11	-1.35
1416095_x_at	1110005A23Rik	RIKEN cDNA 1110005A23 gene	-1.1	0.032	-1.01	0.908	-1.2	0.094	-1.03	0.795	-1.09
1419077_at	Mpp3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	-1.16	0.316	-1.07	0.891	-1.07	0.728	-1.23	0.611	-1.13
1423127_at	Impa1	inositol (myo)-1(or 4)-monophosphatase 1	-1.03	0.713	-1.13	0.028	-1.15	0.155	-1.15	0.251	-1.11
1449014_at	Lactb	lactamase, beta	-1.02	0.832	-1.15	0.237	-1.15	0.397	-1.7	0.049	-1.25
1433463_at	0610010K06Rik	RIKEN cDNA 0610010K06 gene	-1.06	0.287	-1.01	0.744	-1.26	0.119	-1.1	0.386	-1.11
1424458_at	Jmjd2c	jumonji domain containing 2C	-1.16	0.48	-1.01	0.91	-1.15	0.291	-1.27	0.192	-1.15
1417002_at	0610012G03Rik	RIKEN cDNA 0610012G03 gene	-1.08	0.452	-1.2	0.046	-1.03	0.708	-1.06	0.503	-1.09
1449444_a_at	Mfap1	microfibrillar-associated protein 1	-1	0.978	-1.2	0.181	-1.11	0.113	-1.13	0.45	-1.11
1428954_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	-1.09	0.802	-1.09	0.789	-1.12	0.653	-1.41	0.204	-1.18
1424496_at	5133401N09Rik	RIKEN cDNA 5133401N09 gene	-1.06	0.694	-1.19	0.034	-1.06	0.545	-1.5	0.048	-1.2
1435717_at	4833428C12Rik	RIKEN cDNA 4833428C12 gene	-1.06	0.83	-1.03	0.779	-1.23	0.36	-1.44	0.303	-1.19
1451783_a_at	Kifap3	kinesin-associated protein 3	-1.15	0.4	-1.02	0.837	-1.13	0.238	-1.07	0.827	-1.09
1437306_at	C130092O11Rik	RIKEN cDNA C130092O11 gene	-1.01	0.913	-1.14	0.805	-1.15	0.19	-1.37	0.356	-1.17
1428708_x_at	Ptms	parathymosin	-1.07	0.86	-1.07	0.76	-1.17	0.246	-1.05	0.896	-1.09
1427173_a_at	Mrps33	mitochondrial ribosomal protein S33	-1.23	0.079	-1.05	0.532	-1.03	0.737	-1.28	0.103	-1.15
1450900_at	AW011752	expressed sequence AW011752	-1.01	0.884	-1.09	0.491	-1.21	0.182	-1.34	0.056	-1.16
1448762_at	Rad17	RAD17 homolog (S. pombe)	-1.27	0.311	-1	0.96	-1.06	0.695	-1.25	0.104	-1.15
1417344_at	2900064A13Rik	RIKEN cDNA 2900064A13 gene	-1.06	0.121	-1.03	0.634	-1.23	0.006	-1	0.976	-1.08
1424104_at	Syf2	SYF2 homolog, RNA splicing factor (S. cerevisiae)	-1.13	0.207	-1.07	0.34	-1.09	0.26	-1.12	0.151	-1.1
1442446_at	Zfp523	Zinc finger protein 523	-1.04	0.911	-1.09	0.756	-1.17	0.525	-1.29	0.603	-1.15
1451244_a_at	Zfp422	zinc finger protein 422	-1.16	0.372	-1.11	0.238	-1.03	0.807	-1.19	0.35	-1.12
1424821_at	Ndfip1	Nedd4 family interacting protein 1	-1.07	0.414	-1.14	0.123	-1.09	0.343	-1.34	0.344	-1.16
1443203_at	Zfhx1a	Zinc finger homeobox 1a	-1.05	0.949	-1.05	0.796	-1.22	0.053	-1.07	0.701	-1.1
1435757_a_at	Uqcrc2	ubiquinol cytochrome c reductase core protein 2	-1.05	0.245	-1.11	0.357	-1.14	0.152	-1.43	0.216	-1.18
1418100_at	A030009H04Rik	RIKEN cDNA A030009H04 gene	-1.11	0.378	-1.16	0.847	-1.03	0.898	-1.13	0.657	-1.11

1448425_at	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)	-1.02	0.925	-1.1	0.121	-1.19	0.297	-1.02	0.782	-1.08
1416277_a_at	Rplp1	ribosomal protein, large, P1	-1.08	0.231	-1.03	0.714	-1.2	0.095	-1.3	0.029	-1.15
1455727_at	U2af1-rs2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 2	-1.08	0.525	-1.05	0.715	-1.17	0.238	-1	0.998	-1.08
1416280_at	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B	-1.13	0.182	-1.13	0.464	-1.04	0.524	-1.04	0.752	-1.08
1423773_at	Gpbp1	GC-rich promoter binding protein 1	-1.02	0.84	-1.03	0.461	-1.29	0.074	-1.09	0.394	-1.1
1419512_at	Prpf40b	PRP40 pre-mRNA processing factor 40 homolog B (yeast)	-1.06	0.781	-1.04	0.693	-1.21	0.34	-1.51	0.173	-1.2
1448799_s_at	Mrps12	mitochondrial ribosomal protein S12	-1.1	0.141	-1.03	0.687	-1.17	0.165	-1.15	0.484	-1.11
1427941_at	Dicer1	Dicer1, Dcr-1 homolog (Drosophila)	-1.11	0.798	-1.11	0.642	-1.08	0.662	-1.16	0.628	-1.11
1424241_at	Slc30a6	solute carrier family 30 (zinc transporter), member 6	-1.05	0.676	-1.16	0.011	-1.09	0.433	-1.03	0.369	-1.08
1420113_s_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	-1	0.959	-1	0.989	-1.36	0.003	-1.28	0.044	-1.16
1435571_at	A530065I17Rik	RIKEN cDNA A530065I17 gene	-1.04	0.921	-1.2	0.265	-1.07	0.745	-1.02	0.872	-1.08
1455291_s_at	Znrf2	zinc and ring finger 2	-1.1	0.542	-1.04	0.734	-1.16	0.268	-1.68	0.163	-1.24
1434493_at	1810022K09Rik	RIKEN cDNA 1810022K09 gene	-1.01	0.964	-1.28	0.063	-1.04	0.572	-1.63	0.146	-1.24
1430992_s_at	1500009M05Rik	RIKEN cDNA 1500009M05 gene	-1.16	0.189	-1.04	0.684	-1.1	0.755	-1.1	0.689	-1.1
1435680_a_at	Dpp7	dipeptidylpeptidase 7	-1.17	0.228	-1.02	0.932	-1.12	0.374	-1.27	0.13	-1.14
1423707_at	Tmem50b	transmembrane protein 50B	-1.07	0.469	-1.06	0.201	-1.17	0.072	-1.1	0.549	-1.1
1455941_s_at	Map2k5	mitogen activated protein kinase kinase 5	-1	0.995	-1.3	0.198	-1.03	0.871	-1.39	0.257	-1.18
1429255_at	2010007H12Rik	RIKEN cDNA 2010007H12 gene	-1.07	0.682	-1.05	0.708	-1.18	0.312	-1.24	0.441	-1.14
1452451_at	Bean	brain expressed, associated with Nedd4	-1.01	0.989	-1.14	0.684	-1.16	0.519	-3.12	0.091	-1.61
1427108_at	9530068E07Rik	RIKEN cDNA 9530068E07 gene	-1	0.946	-1.26	0.008	-1.06	0.661	-1.18	0.226	-1.13
1416858_a_at	Fkbp3	FK506 binding protein 3	-1.11	0.284	-1.04	0.735	-1.15	0.136	-1.65	0.065	-1.24
1428619_at	2310005N03Rik	RIKEN cDNA 2310005N03 gene	-1.1	0.156	-1	0.999	-1.21	0.019	-1.14	0.263	-1.11
1423197_a_at	AW011752	expressed sequence AW011752	-1	0.965	-1.01	0.913	-1.34	0.175	-1.39	0.084	-1.19
1452775_at	Csrp2bp	cysteine and glycine-rich protein 2 binding protein	-1.18	0.368	-1.11	0.145	-1.01	0.957	-1.07	0.575	-1.09
1452186_at	Rbm5	RNA binding motif protein 5	-1.23	0.154	-1.05	0.628	-1.03	0.852	-1.41	0.171	-1.18
1423131_at	LOC433230	similar to TGF beta-inducible nuclear protein 1 (L-name-related protein 42) (LNR4	-1.05	0.33	-1.11	0.509	-1.12	0.222	-1.45	0.157	-1.19
1454863_at	Ankrd11	ankyrin repeat domain 11	-1.02	0.937	-1.17	0.135	-1.11	0.19	-1.18	0.4	-1.12
1455507_s_at	D8Ertd587e	DNA segment, Chr 8, ERATO Doi 587, expressed	-1.01	0.929	-1.03	0.635	-1.28	0.152	-1.34	0.329	-1.17
1428539_at	2610207I05Rik	RIKEN cDNA 2610207I05 gene	-1.06	0.776	-1.06	0.824	-1.19	0.579	-1.26	0.607	-1.14
1425486_s_at	Mtmr6	myotubularin related protein 6	-1.11	0.522	-1.01	0.834	-1.18	0.243	-1.29	0.193	-1.15
1424189_at	Pigc	phosphatidylinositol glycan anchor biosynthesis, class C	-1.07	0.416	-1.1	0.384	-1.12	0.202	-1.28	0.037	-1.14
1456194_a_at	Park7	Parkinson disease (autosomal recessive, early onset) 7	-1.1	0.097	-1.07	0.564	-1.12	0.024	-1.2	0.315	-1.12
1456332_at	Tmem17	transmembrane protein 17	-1.03	0.963	-1.28	0.136	-1.02	0.929	-1.57	0.492	-1.22
1426087_at	Icosl	icos ligand	-1.05	0.661	-1.15	0.662	-1.09	0.459	-1.15	0.59	-1.11
1436545_at	Dtx4	deltex 4 homolog (Drosophila)	-1.08	0.844	-1.07	0.696	-1.14	0.432	-1.05	0.706	-1.09
1445499_at	Zc3h13	zinc finger CCCH type containing 13	-1.1	0.75	-1.13	0.656	-1.06	0.776	-1.23	0.409	-1.13
1448505_at	C1d	nuclear DNA binding protein	-1.15	0.099	-1.07	0.338	-1.07	0.645	-1.05	0.444	-1.08
1454772_at	Ascc3l1	activating signal cointegrator 1 complex subunit 3-like 1	-1.04	0.614	-1.19	0.327	-1.07	0.488	-1.42	0.139	-1.18
1428466_at	Chd3	chromodomain helicase DNA binding protein 3	-1.13	0.441	-1.07	0.688	-1.09	0.669	-1.41	0.162	-1.17
1420631_a_at	Blcap	bladder cancer associated protein homolog (human)	-1.04	0.846	-1.1	0.177	-1.15	0.261	-1.36	0.406	-1.16
1450934_at	Eif4a2	eukaryotic translation initiation factor 4A2	-1.04	0.415	-1.14	0.017	-1.11	0.307	-1.45	0.22	-1.19
1451223_a_at	Btf3l4	basic transcription factor 3-like 4	-1.06	0.698	-1.06	0.325	-1.17	0.374	-1.18	0.194	-1.12
1448251_at	9030425E11Rik	RIKEN cDNA 9030425E11 gene	-1.05	0.772	-1.07	0.923	-1.17	0.264	-1.23	0.219	-1.13
1460621_x_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	-1.03	0.656	-1.08	0.163	-1.18	0.044	-1.18	0.316	-1.12
1416911_a_at	6330407G11Rik	RIKEN cDNA 6330407G11 gene	-1.21	0.526	-1.03	0.874	-1.06	0.664	-1.32	0.094	-1.16
1427212_at	Mapkap1	mitogen-activated protein kinase associated protein 1	-1.02	0.917	-1.2	0.137	-1.09	0.379	-1.06	0.307	-1.09
1419635_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	-1	0.974	-1.25	0.331	-1.06	0.539	-1.57	0.003	-1.22
1428218_a_at	1600012H06Rik	RIKEN cDNA 1600012H06 gene	-1.03	0.829	-1.13	0.391	-1.12	0.453	-1.21	0.213	-1.12
1420530_at	Neud4	neuronal d4 domain family member	-1.07	0.908	-1.01	0.984	-1.23	0.516	-1.15	0.016	-1.11
1418223_at	Sec11l1	Sec11-like 1 (S. cerevisiae)	-1.13	0.501	-1.05	0.468	-1.1	0.329	-1.14	0.098	-1.11
1456873_at	Clic5	chloride intracellular channel 5	-1.04	0.728	-1.12	0.858	-1.13	0.531	-1.63	0.13	-1.23
1427132_at	Sbf2	SET binding factor 2	-1.09	0.477	-1.05	0.487	-1.15	0.639	-1.01	0.947	-1.08
1448697_s_at	Rpl36al	ribosomal protein L36a-like	-1.03	0.606	-1.04	0.611	-1.24	0.02	-1.44	0.028	-1.19

1423043_s_at	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	-1.04	0.395	-1.04	0.642	-1.22	0.008	-1.07	0.314	-1.09
1433039_at	4930555B11Rik	RIKEN cDNA 4930555B11 gene	-1.11	0.543	-1.03	0.924	-1.15	0.815	-1.05	0.942	-1.08
1450778_a_at	Rnuxa	RNA U, small nuclear RNA export adaptor	-1.1	0.711	-1.07	0.435	-1.11	0.551	-1.41	0.032	-1.17
1428441_at	1500009M05Rik	RIKEN cDNA 1500009M05 gene	-1.03	0.761	-1.05	0.496	-1.22	0	-1.21	0.288	-1.13
1417098_s_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	-1.15	0.597	-1.1	0.083	-1.03	0.845	-1.03	0.863	-1.08
1435900_at	Zfp297b	zinc finger protein 297B	-1.11	0.338	-1.03	0.82	-1.15	0.134	-1.2	0.021	-1.12
1415701_x_at	Rpl23	ribosomal protein L23	-1.08	0.444	-1.02	0.591	-1.2	0.019	-1.25	0.009	-1.14
1425462_at	Fbxw11	F-box and WD-40 domain protein 11	-1.14	0.156	-1.03	0.78	-1.12	0.371	-1.13	0.188	-1.11
1438491_x_at	A530054K11Rik	RIKEN cDNA A530054K11 gene	-1.11	0.326	-1.03	0.93	-1.15	0.688	-1.73	0.267	-1.25
1439452_x_at	Dnpep	aspartyl aminopeptidase	-1.21	0.19	-1.08	0.19	-1.01	0.962	-1.09	0.262	-1.1
1438983_x_at	AI413782	expressed sequence AI413782	-1.11	0.481	-1.08	0.076	-1.08	0.15	-1.46	0.133	-1.19
1450818_a_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	-1.07	0.474	-1.09	0.287	-1.12	0.46	-1.16	0.34	-1.11
1426219_at	Scp2	sterol carrier protein 2, liver	-1.03	0.64	-1.27	0.221	-1.02	0.9	-1.33	0.076	-1.16
1415736_at	Pfdn5	prefoldin 5	-1.06	0.691	-1.01	0.827	-1.23	0.058	-2.28	0.205	-1.4
1448712_at	Chm	choroidermia	-1.11	0.241	-1.08	0.033	-1.09	0.033	-1.19	0.604	-1.12
1436949_a_at	Tceb2 /// LOC6685	transcription elongation factor B (SIII), polypeptide 2 /// similar to transcription elo	-1.01	0.877	-1.05	0.13	-1.25	0.056	-1.09	0.638	-1.1
1437005_a_at	Rpl18	ribosomal protein L18	-1	0.977	-1.06	0.446	-1.25	0.012	-1.26	0.008	-1.14
1418077_at	Trim21	tripartite motif protein 21	-1.14	0.528	-1.09	0.552	-1.05	0.628	-1.43	0.209	-1.18
1446371_at	---	---	-1.02	0.957	-1.04	0.868	-1.25	0.146	-1.23	0.309	-1.14
1448540_a_at	0610012G03Rik ///	RIKEN cDNA 0610012G03 gene /// hypothetical protein LOC638521	-1.06	0.503	-1.14	0.056	-1.08	0.542	-1.38	0.331	-1.17
1436034_at	Cep68	centrosomal protein 68	-1.09	0.428	-1.09	0.571	-1.1	0.087	-1.43	0.097	-1.18
1440500_at	Map3k10	Mitogen activated protein kinase kinase kinase 10	-1.01	0.923	-1.2	0.542	-1.09	0.585	-1.07	0.653	-1.09
1445693_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	-1.09	0.713	-1.02	0.917	-1.19	0.397	-1.13	0.632	-1.11
1449956_at	Prkce	protein kinase C, epsilon	-1.17	0.37	-1.04	0.783	-1.07	0.479	-1.3	0.119	-1.15
1448763_at	Atad1	ATPase family, AAA domain containing 1	-1.11	0.038	-1.08	0.23	-1.09	0.242	-1.22	0.147	-1.13
1455976_x_at	Dbi	diazepam binding inhibitor	-1.16	0.243	-1.03	0.798	-1.1	0.405	-1.06	0.621	-1.09
1434703_at	Extl3	exostoses (multiple)-like 3	-1.02	0.887	-1.14	0.177	-1.13	0.392	-1.02	0.847	-1.08
1459749_s_at	Fat4	FAT tumor suppressor homolog 4 (Drosophila)	-1.05	0.926	-1.06	0.672	-1.18	0.396	-1.26	0.463	-1.14
1434219_at	Stim2	stromal interaction molecule 2	-1.06	0.77	-1.12	0.12	-1.1	0.258	-1.4	0.108	-1.17
1425321_a_at	Clmn	calmin	-1.08	0.603	-1.16	0.411	-1.05	0.772	-1.57	0.164	-1.21
1424355_a_at	Sin3b	transcriptional regulator, SIN3B (yeast)	-1.11	0.341	-1.17	0.192	-1.01	0.926	-1.22	0.124	-1.13
1435862_at	Son	Son cell proliferation protein	-1.02	0.869	-1.07	0.509	-1.21	0.387	-1.43	0.107	-1.18
1417684_at	Thumpd3	THUMP domain containing 3	-1.1	0.17	-1.09	0.354	-1.09	0.53	-1.21	0.141	-1.12
1424277_at	1110020L19Rik	RIKEN cDNA 1110020L19 gene	-1.14	0.66	-1.13	0.661	-1.02	0.749	-1.08	0.673	-1.09
1428303_at	1500005I02Rik	RIKEN cDNA 1500005I02 gene	-1	0.997	-1.14	0.865	-1.15	0.73	-1.32	0.728	-1.15
1426978_at	Klhl2	kelch-like 2, Mayven (Drosophila)	-1.07	0.643	-1.08	0.402	-1.13	0.586	-1.09	0.818	-1.09
1449272_at	Igsf4b	immunoglobulin superfamily, member 4B	-1.03	0.969	-1.06	0.913	-1.2	0.609	-1.18	0.686	-1.12
1459227_at	---	Transcribed locus	-1.02	0.895	-1.07	0.734	-1.19	0.558	-1.23	0.293	-1.13
1417317_s_at	Rpl35a	ribosomal protein L35a	-1.03	0.304	-1.01	0.83	-1.27	0.001	-1.42	0.016	-1.18
1428465_at	Tmem147	transmembrane protein 147	-1.06	0.668	-1.13	0.122	-1.1	0.452	-1.01	0.928	-1.07
1439455_x_at	Capza1	capping protein (actin filament) muscle Z-line, alpha 1	-1.06	0.588	-1.16	0.16	-1.07	0.621	-1.34	0.091	-1.16
1415761_at	Mrpl52	mitochondrial ribosomal protein L52	-1.03	0.652	-1.01	0.865	-1.26	0.162	-1.22	0.445	-1.13
1426660_x_at	Rpl23a	ribosomal protein L23a	-1.02	0.679	-1	0.914	-1.3	0.006	-1.28	0.005	-1.15
1450889_at	Smarca3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.1	0.48	-1.13	0.292	-1.05	0.671	-1.75	0.064	-1.26
1437773_x_at	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-1.14	0.348	-1.02	0.852	-1.12	0.273	-1.28	0.117	-1.14
1437016_x_at	Rap2c	RAP2C, member of RAS oncogene family	-1.12	0.703	-1.15	0.344	-1.02	0.78	-1.09	0.711	-1.09
1436272_at	Rab3gap2	RAB3 GTPase activating protein subunit 2	-1.15	0.062	-1.01	0.979	-1.13	0.384	-1.02	0.769	-1.08
1431614_at	2810049E08Rik	RIKEN cDNA 2810049E08 gene	-1.06	0.835	-1.03	0.87	-1.2	0.32	-1.2	0.36	-1.12
1450031_at	Aff4	AF4/FMR2 family, member 4	-1.12	0.176	-1.04	0.733	-1.12	0.066	-1.35	0.096	-1.16
1426484_at	Ubxd2	UBX domain containing 2	-1.1	0.315	-1.07	0.426	-1.11	0.098	-1.14	0.342	-1.1
1426487_a_at	Rbbp6	retinoblastoma binding protein 6	-1.08	0.689	-1	0.985	-1.21	0.144	-1.33	0.041	-1.16
1418134_at	1200007B05Rik	RIKEN cDNA 1200007B05 gene	-1.08	0.648	-1.16	0.047	-1.04	0.736	-1.02	0.889	-1.08
1444433_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	-1.07	0.742	-1.12	0.564	-1.09	0.529	-1.02	0.913	-1.07

1426968_a_at	Rdh10	retinol dehydrogenase 10 (all-trans)	-1.13	0.513	-1.11	0.078	-1.04	0.808	-1.03	0.898	-1.08
1422340_a_at	Actg2	actin, gamma 2, smooth muscle, enteric	-1.24	0.606	-1.01	0.958	-1.04	0.87	-1.46	0.057	-1.19
1418419_at	Fbxl20	F-box and leucine-rich repeat protein 20	-1.15	0.189	-1.1	0.012	-1.03	0.58	-1.16	0.393	-1.11
1425262_at	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	-1.05	0.753	-1.01	0.846	-1.23	0.228	-1.06	0.389	-1.09
1451005_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	-1.06	0.554	-1.01	0.905	-1.23	0.105	-1.21	0.15	-1.13
1452985_at	Uaca	uveal autoantigen with coiled-coil domains and ankyrin repeats	-1.05	0.75	-1.11	0.572	-1.11	0.722	-1.05	0.912	-1.08
1417526_at	Pcbp3	poly(rC) binding protein 3	-1.08	0.635	-1.03	0.933	-1.17	0.536	-1.19	0.561	-1.12
1434516_at	Pstk	phosphoseryl-tRNA kinase	-1.17	0.018	-1.1	0.467	-1.02	0.909	-1.07	0.337	-1.09
1438684_at	Nuak1	NUAK family, SNF1-like kinase, 1	-1.18	0.041	-1.02	0.936	-1.08	0.774	-1.25	0.334	-1.13
1433879_a_at	C130032J12Rik	RIKEN cDNA C130032J12 gene	-1.1	0.512	-1.15	0.124	-1.03	0.895	-1.03	0.576	-1.08
1441878_s_at	1810049H13Rik	RIKEN cDNA 1810049H13 gene	-1.02	0.887	-1.14	0.441	-1.12	0.316	-1.41	0.035	-1.17
1437253_at	A630054L15Rik	RIKEN cDNA A630054L15 gene	-1.14	0.353	-1.02	0.793	-1.11	0.4	-1.08	0.499	-1.09
1457594_at	---	Transcribed locus	-1.07	0.843	-1.07	0.791	-1.13	0.191	-1.27	0.478	-1.14
1428985_at	Ints12	integrator complex subunit 12	-1.06	0.567	-1.08	0.516	-1.13	0.127	-1.31	0.045	-1.15
1418040_at	4432406C05Rik	RIKEN cDNA 4432406C05 gene	-1.04	0.885	-1.18	0.47	-1.06	0.506	-1.13	0.622	-1.1
1455323_at	Rbak	RB-associated KRAB repressor	-1.07	0.814	-1.02	0.848	-1.2	0.389	-1.08	0.768	-1.09
1418401_a_at	Dusp16	dual specificity phosphatase 16	-1.06	0.87	-1	0.976	-1.23	0.166	-1.72	0.021	-1.26
1448430_a_at	Naca /// LOC62827	nascent polypeptide-associated complex alpha polypeptide /// similar to nascent p	-1.09	0.476	-1.11	0.068	-1.07	0.091	-1.41	0.027	-1.17
1416103_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	-1.01	0.816	-1.29	0.247	-1.02	0.911	-1.05	0.644	-1.09
1434521_at	Rfxdc2	regulatory factor X domain containing 2 homolog (human)	-1.15	0.296	-1.11	0.201	-1.02	0.927	-1.53	0.163	-1.2
1434301_at	D330050I23Rik	RIKEN cDNA D330050I23 gene	-1.09	0.513	-1.19	0.321	-1	0.965	-2.04	0.056	-1.33
1420129_s_at	D10Wsu52e	DNA segment, Chr 10, Wayne State University 52, expressed	-1.1	0.475	-1.15	0.16	-1.03	0.791	-1.53	0.041	-1.2
1450668_s_at	Hspe1	heat shock protein 1 (chaperonin 10)	-1.11	0.065	-1.13	0.186	-1.03	0.816	-1.47	0.005	-1.19
1446865_at	Sema5a	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmem	-1.1	0.659	-1	0.997	-1.18	0.753	-2.66	0.043	-1.49
1449951_at	Nfkbil1	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	-1.14	0.268	-1.09	0.713	-1.05	0.738	-1.68	0.127	-1.24
1415867_at	Cct4	chaperonin subunit 4 (delta)	-1.12	0.097	-1.09	0.275	-1.06	0.736	-1.12	0.352	-1.1
1427236_a_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5	-1.06	0.51	-1.18	0.087	-1.04	0.773	-1.43	0.206	-1.18
1422059_at	Cbx2	chromobox homolog 2 (Drosophila Pc class)	-1.01	0.99	-1.16	0.799	-1.11	0.65	-1.52	0.736	-1.2
1427321_s_at	Cxadr	coxsackievirus and adenovirus receptor	-1.06	0.718	-1.1	0.794	-1.11	0.6	-1.14	0.663	-1.1
1437521_s_at	E230022H04Rik	RIKEN cDNA E230022H04 gene	-1.02	0.905	-1.01	0.777	-1.28	0.132	-1.34	0.044	-1.16
1428293_at	2310022M17Rik	RIKEN cDNA 2310022M17 gene	-1.05	0.295	-1.03	0.664	-1.2	0.056	-1.6	0.113	-1.22
1433690_at	2210016L21Rik	RIKEN cDNA 2210016L21 gene	-1.17	0.292	-1.08	0.565	-1.03	0.754	-1.48	0.112	-1.19
1448645_at	Msl31	male-specific lethal-3 homolog 1 (Drosophila)	-1.01	0.943	-1.06	0.585	-1.22	0.063	-1.12	0.452	-1.1
1429141_at	Neurl2	neuralized-like 2 (Drosophila)	-1.27	0.068	-1.01	0.953	-1.02	0.882	-1.66	0.028	-1.24
1428944_at	Ube1l2	ubiquitin-activating enzyme E1-like 2	-1.02	0.843	-1.05	0.715	-1.22	0.247	-1.17	0.344	-1.11
1455320_at	---	---	-1.04	0.871	-1.04	0.817	-1.21	0.341	-1.02	0.88	-1.08
1451200_at	Kif1b	kinesin family member 1B	-1.05	0.292	-1.19	0.109	-1.03	0.819	-1.32	0.162	-1.15
1450892_a_at	Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	-1.05	0.586	-1.09	0.079	-1.13	0.293	-1.07	0.647	-1.09
1423568_at	Psma7	proteasome (prosome, macropain) subunit, alpha type 7	-1.07	0.358	-1.15	0.014	-1.05	0.701	-1.34	0.196	-1.15
1415818_at	Anxa6	annexin A6	-1.08	0.753	-1.09	0.375	-1.1	0.457	-1.59	0.255	-1.21
1416207_at	Taz	tafazzin	-1.14	0.085	-1.09	0.411	-1.04	0.328	-1.41	0.22	-1.17
1427162_a_at	Elk4	ELK4, member of ETS oncogene family	-1.07	0.64	-1.01	0.917	-1.2	0.256	-1.37	0.144	-1.16
1425058_at	Zfp472	zinc finger protein 472	-1.17	0.305	-1.02	0.932	-1.09	0.592	-1.9	0.088	-1.29
1416393_at	Emg1	EMG1 nucleolar protein homolog (S. cerevisiae)	-1.04	0.51	-1.04	0.387	-1.2	0.308	-1.05	0.604	-1.08
1446661_at	---	---	-1.06	0.923	-1.08	0.834	-1.13	0.624	-1.61	0.32	-1.22
1453833_a_at	Rnaseh1	ribonuclease H1	-1.2	0.625	-1.06	0.706	-1.02	0.917	-1.28	0.114	-1.14
1423202_a_at	Ncor1	nuclear receptor co-repressor 1	-1.05	0.482	-1.12	0.054	-1.09	0.501	-1.14	0.231	-1.1
1419760_a_at	ORF5	open reading frame 5	-1.03	0.811	-1.11	0.193	-1.14	0.503	-1.04	0.643	-1.08
1419041_at	Itfg1	integrin alpha FG-GAP repeat containing 1	-1.02	0.766	-1.08	0.124	-1.17	0.134	-1.09	0.606	-1.09
1422569_at	Yy1	YY1 transcription factor	-1.15	0.186	-1.02	0.514	-1.1	0.169	-1.09	0.277	-1.09
1434018_at	BC043098	cDNA sequence BC043098	-1.02	0.951	-1.12	0.463	-1.14	0.667	-1.72	0.058	-1.25
1416245_at	Aurkaip1	aurora kinase A interacting protein 1	-1.07	0.451	-1.11	0.194	-1.09	0.454	-1.04	0.77	-1.08
1451089_a_at	Arcn1	archain 1	-1.1	0.107	-1	0.946	-1.18	0.009	-1.21	0.048	-1.12

1428428_at	Abhd11	abhydrolase domain containing 11	-1.1	0.123	-1.09	0.209	-1.07	0.672	-1.31	0.043	-1.14
1427877_at	2610312B22Rik	RIKEN cDNA 2610312B22 gene	-1.05	0.557	-1.07	0.667	-1.14	0.432	-1.23	0.417	-1.12
1440281_at	0610042C05Rik	RIKEN cDNA 0610042C05 gene	-1.03	0.853	-1.2	0.236	-1.04	0.855	-1.68	0.081	-1.24
1454853_s_at	AW146154 /// AI987	expressed sequence AW146154 /// expressed sequence AI987944	-1.13	0.432	-1.08	0.491	-1.06	0.82	-1.51	0.152	-1.19
1452621_at	Pcbd2	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuc	-1.04	0.72	-1.18	0.252	-1.06	0.472	-1.06	0.054	-1.08
1418125_at	Inoc1	INO80 complex homolog 1 (S. cerevisiae)	-1.15	0.514	-1.08	0.613	-1.03	0.77	-1.15	0.259	-1.1
1428470_at	Exoc2	exocyst complex component 2	-1.05	0.516	-1.16	0.264	-1.05	0.651	-1.08	0.409	-1.09
1438208_at	Taok2	TAO kinase 2	-1.04	0.829	-1.23	0.239	-1.01	0.941	-1.07	0.852	-1.09
1439235_x_at	Tm2d2	TM2 domain containing 2	-1.07	0.676	-1.06	0.607	-1.13	0.037	-1.06	0.316	-1.08
1416821_at	Es2el	expressed sequence 2 embryonic lethal	-1.08	0.666	-1.19	0.69	-1	0.989	-1.21	0.198	-1.12
1424095_at	Rtcd1	RNA terminal phosphate cyclase domain 1	-1.04	0.742	-1.18	0.001	-1.06	0.564	-1.05	0.67	-1.08
1422498_at	Mageh1	melanoma antigen, family H, 1	-1.12	0.518	-1.05	0.725	-1.09	0.761	-1.12	0.748	-1.1
1448808_a_at	Nme2	expressed in non-metastatic cells 2, protein	-1.17	0.035	-1.04	0.687	-1.06	0.427	-1.54	0.139	-1.2
1421914_s_at	Mrpl19	mitochondrial ribosomal protein L19	-1.06	0.506	-1.13	0.15	-1.07	0.542	-1.06	0.67	-1.08
1457002_at	Zfp408	zinc finger protein 408	-1.18	0.24	-1.06	0.716	-1.03	0.818	-1.25	0.288	-1.13
1426748_s_at	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	-1.14	0.484	-1.02	0.929	-1.11	0.062	-1.07	0.47	-1.09
1424319_at	Oraov1	oral cancer overexpressed 1	-1.05	0.627	-1.17	0.242	-1.06	0.786	-1.35	0.017	-1.15
1452798_s_at	Mapk1ip1	mitogen activated protein kinase 1 interacting protein 1	-1.1	0.454	-1.11	0.18	-1.05	0.732	-1.6	0.071	-1.22
1416775_at	2310004L02Rik	RIKEN cDNA 2310004L02 gene	-1.16	0.622	-1.09	0.669	-1.02	0.898	-2.04	0.078	-1.33
1435232_x_at	---	---	-1.11	0.069	-1.05	0.41	-1.09	0.543	-1.07	0.615	-1.08
1437976_x_at	Rpl23a	ribosomal protein L23a	-1.03	0.306	-1	0.957	-1.26	0.017	-1.23	0	-1.13
1418737_at	Nudt2	nudix (nucleoside diphosphate linked moiety X)-type motif 2	-1.23	0.385	-1.03	0.842	-1.02	0.781	-1.26	0.143	-1.14
1454690_at	Ikbkg	inhibitor of kappaB kinase gamma	-1.01	0.923	-1.2	0.072	-1.07	0.401	-1.08	0.755	-1.09
1435437_at	Setd7	SET domain containing (lysine methyltransferase) 7	-1.18	0.249	-1.05	0.81	-1.04	0.855	-1.4	0.195	-1.17
1419002_s_at	Baat	bile acid-Coenzyme A: amino acid N-acyltransferase	-1.03	0.108	-1.22	0.098	-1.03	0.893	-1.77	0.321	-1.26
1418462_at	Exosc9	exosome component 9	-1.18	0.338	-1.03	0.785	-1.06	0.45	-1.11	0.467	-1.1
1422356_at	V1rb10	vomeronasal 1 receptor, B10	-1.18	0.462	-1.02	0.863	-1.07	0.338	-1.18	0.507	-1.11
1426515_a_at	Tor1a	torsin family 1, member A (torsin A)	-1.09	0.524	-1.14	0.336	-1.03	0.745	-1.46	0.002	-1.18
1455110_at	Gabpb2	GA repeat binding protein, beta 2	-1.01	0.926	-1.09	0.152	-1.17	0.254	-1.06	0.724	-1.08
1455169_at	Rab11fip2	RAB11 family interacting protein 2 (class I)	-1.05	0.739	-1.13	0.034	-1.08	0.309	-1.2	0.34	-1.11
1452462_a_at	Banp	Btg3 associated nuclear protein	-1.12	0.244	-1.06	0.697	-1.08	0.655	-1.22	0.46	-1.12
1441239_at	Kctd18	potassium channel tetramerisation domain containing 18	-1	0.999	-1.14	0.417	-1.13	0.581	-1.44	0.22	-1.18
1455284_x_at	Pigx	phosphatidylinositol glycan anchor biosynthesis, class X	-1.02	0.958	-1.03	0.938	-1.23	0.368	-1.09	0.781	-1.09
1437181_at	Peli2	pellino 2	-1.17	0.578	-1.05	0.454	-1.05	0.825	-1.57	0.288	-1.21
1435002_at	zfp507	zinc finger protein 507	-1.09	0.641	-1.06	0.531	-1.12	0.384	-1.26	0.092	-1.13
1426853_at	Set	SET translocation	-1.05	0.775	-1.01	0.881	-1.22	0.106	-1.19	0.313	-1.12
1420497_a_at	Cebpz	CCAAT/enhancer binding protein zeta	-1.03	0.885	-1.07	0.24	-1.17	0.334	-1.37	0.191	-1.16
1415759_a_at	Hbxip	hepatitis B virus x interacting protein	-1.12	0.359	-1.08	0.383	-1.06	0.631	-1.38	0.081	-1.16
1419976_s_at	Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	-1.1	0.246	-1.01	0.901	-1.16	0.113	-1.62	0.06	-1.22
1451448_a_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	-1.08	0.323	-1.03	0.657	-1.16	0.397	-1.96	0.101	-1.31
1433666_s_at	Vps41	vacuolar protein sorting 41 (yeast)	-1.08	0.497	-1.08	0.039	-1.09	0.153	-1.19	0.43	-1.11
1438568_at	Mrgpre	MAS-related GPR, member E	-1.02	0.985	-1.06	0.818	-1.2	0.368	-1.21	0.037	-1.12
1448480_at	Nip7	nuclear import 7 homolog (S. cerevisiae)	-1.13	0.241	-1.04	0.759	-1.09	0.497	-1.21	0.441	-1.12
1448387_at	Rbx1	ring-box 1	-1.1	0.149	-1.1	0.043	-1.05	0.553	-1.1	0.331	-1.09
1436804_s_at	Scyl1	SCY1-like 1 (S. cerevisiae)	-1.04	0.827	-1.14	0.273	-1.08	0.701	-1.28	0.045	-1.14
1428746_a_at	Trspap1	tRNA selenocysteine associated protein 1	-1.04	0.758	-1.01	0.813	-1.23	0.24	-1.32	0.248	-1.15
1434254_at	Gna11	guanine nucleotide binding protein, alpha 11	-1	0.978	-1.02	0.77	-1.26	0.028	-1.38	0.139	-1.17
1438610_a_at	Cryz	Crystallin, zeta	-1.04	0.491	-1.08	0.631	-1.14	0.386	-1.02	0.829	-1.07
1424106_at	1200003C05Rik	RIKEN cDNA 1200003C05 gene	-1.03	0.634	-1.03	0.55	-1.22	0.071	-1.14	0.359	-1.1
1444998_at	---	Transcribed locus	-1.04	0.234	-1.22	0.146	-1.02	0.893	-1.29	0.494	-1.14
1433794_at	Setx	senataxin	-1.09	0.585	-1.01	0.811	-1.17	0.173	-1.51	0.082	-1.19
1455474_at	D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-1.19	0.22	-1.02	0.925	-1.05	0.789	-1.46	0.455	-1.18
1417823_at	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	-1.23	0.53	-1.05	0.875	-1	0.985	-1.59	0.415	-1.22

1452756_at	0610009J22Rik	RIKEN cDNA 0610009J22 gene	-1.07	0.71	-1.14	0.396	-1.04	0.758	-1.16	0.569	-1.1
1457285_at	Zfp187	zinc finger protein 187	-1.02	0.613	-1.09	0.337	-1.15	0.23	-1.28	0.474	-1.13
1433976_at	D10Ucla1	DNA segment, Chr 10, University of California at Los Angeles 1	-1.04	0.241	-1.13	0.208	-1.09	0.35	-1.19	0.487	-1.11
1436899_at	2700019D07Rik	RIKEN cDNA 2700019D07 gene	-1.1	0.747	-1.01	0.881	-1.15	0.115	-1.81	0.027	-1.27
1435734_x_at	Dus1l	dihydrouridine synthase 1-like (S. cerevisiae)	-1.02	0.467	-1.17	0.086	-1.07	0.667	-1.07	0.628	-1.08
1428667_at	Maoa	monoamine oxidase A	-1.03	0.846	-1.07	0.004	-1.16	0.341	-1.01	0.953	-1.07
1434213_x_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	-1.11	0.501	-1.03	0.721	-1.11	0.267	-1.35	0.175	-1.15
1416486_at	Scye1	small inducible cytokine subfamily E, member 1	-1.01	0.967	-1.14	0.154	-1.12	0.24	-1.28	0.053	-1.14
1417372_a_at	Peli1	pellino 1	-1.14	0.555	-1.01	0.922	-1.11	0.354	-2.02	0.073	-1.32
1455042_at	Tbl1x	Transducin (beta)-like 1 X-linked	-1.09	0.524	-1.13	0.241	-1.04	0.723	-1.14	0.388	-1.1
1434617_x_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	-1.07	0.661	-1	0.97	-1.2	0.643	-1.26	0.229	-1.13
1434145_s_at	Serhl	serine hydrolase-like	-1.02	0.906	-1.17	0.41	-1.07	0.767	-1.31	0.117	-1.14
1420850_at	Crnkl1	Crn, crooked neck-like 1 (Drosophila)	-1.05	0.347	-1.18	0.293	-1.04	0.814	-1.15	0.615	-1.1
1435205_at	Tcfap2e	transcription factor AP-2, epsilon	-1.01	0.942	-1.18	0.532	-1.07	0.304	-1.29	0.233	-1.14
1427136_s_at	Sfrs12	splicing factor, arginine/serine-rich 12	-1.08	0.819	-1.02	0.924	-1.16	0.463	-1.19	0.404	-1.11
1433677_at	Sfrs8	splicing factor, arginine/serine-rich 8	-1.15	0.206	-1.04	0.678	-1.06	0.432	-1.03	0.796	-1.07
1435377_at	---	---	-1.03	0.882	-1.08	0.348	-1.15	0.317	-1.11	0.279	-1.09
1459396_at	6030446N20Rik	RIKEN cDNA 6030446N20 gene	-1.07	0.897	-1.17	0.69	-1.02	0.972	-2.11	0.114	-1.34
1452155_a_at	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-1.06	0.712	-1.03	0.519	-1.16	0.386	-1.33	0.19	-1.15
1427192_a_at	Brd8	bromodomain containing 8	-1.12	0.476	-1.01	0.927	-1.13	0.274	-1.15	0.232	-1.1
1440689_at	Foxk2	forkhead box K2	-1.1	0.665	-1.04	0.573	-1.12	0.422	-1.25	0.155	-1.12
1430401_at	3110045C21Rik	RIKEN cDNA 3110045C21 gene	-1.14	0.51	-1.02	0.975	-1.09	0.857	-1.37	0.616	-1.16
1425183_a_at	Rpl4	ribosomal protein L4	-1.06	0.476	-1.05	0.171	-1.14	0.013	-1.31	0.004	-1.14
1455268_at	Zcsl2	zinc finger, CSL domain containing 2	-1.02	0.905	-1.01	0.954	-1.24	0.065	-1.14	0.676	-1.11
1437984_x_at	Bat1a	HLA-B-associated transcript 1A	-1.13	0.016	-1.09	0.537	-1.04	0.805	-1.3	0.087	-1.14
1434571_at	Vps13b /// LOC666	vacuolar protein sorting 13B (yeast) /// similar to vacuolar protein sorting 13B isof	-1.21	0.339	-1.04	0.689	-1.02	0.695	-1.12	0.309	-1.1
1460338_a_at	Crlf3	cytokine receptor-like factor 3	-1.16	0.025	-1.08	0.314	-1.02	0.888	-1.68	0.017	-1.24
1436315_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	-1.04	0.482	-1	0.983	-1.23	0.106	-1.09	0.311	-1.09
1453379_at	4930519P11Rik	RIKEN cDNA 4930519P11 gene	-1.18	0.846	-1.04	0.921	-1.04	0.926	-2.25	0.291	-1.38
1428464_at	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	-1.01	0.97	-1.17	0.121	-1.09	0.525	-1.14	0.38	-1.1
1456581_x_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	-1.03	0.529	-1.07	0.01	-1.16	0.027	-1.3	0.161	-1.14
1420611_at	Prkacb	protein kinase, cAMP dependent, catalytic, beta	-1.11	0.3	-1.09	0.461	-1.05	0.73	-1.43	0.224	-1.17
1426949_s_at	Tpr	translocated promoter region	-1.08	0.485	-1.03	0.615	-1.13	0.349	-1	0.974	-1.06
1433591_at	Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	-1.06	0.823	-1.05	0.674	-1.13	0.359	-1.02	0.904	-1.07
1423099_a_at	Mettl3	methyltransferase-like 3	-1.09	0.309	-1.01	0.81	-1.15	0.113	-1.41	0.1	-1.17
1418850_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	-1.05	0.57	-1.06	0.33	-1.14	0.468	-1.29	0.253	-1.13
1449445_x_at	Mfap1	microfibrillar-associated protein 1	-1.06	0.552	-1.07	0.323	-1.12	0.007	-1.2	0.127	-1.11
1452169_a_at	Dgkz	diacylglycerol kinase zeta	-1.05	0.804	-1.13	0.399	-1.07	0.755	-2.36	0.026	-1.4
1435186_s_at	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	-1.03	0.817	-1.16	0.532	-1.06	0.499	-1.19	0.165	-1.11
1436113_a_at	St13	suppression of tumorigenicity 13	-1.07	0.408	-1.16	0.337	-1.02	0.881	-1.13	0.435	-1.09
1424080_at	Dcps	decapping enzyme, scavenger	-1.11	0.541	-1.12	0.293	-1.02	0.922	-1.07	0.592	-1.08
1424388_at	Cluap1	clusterin associated protein 1	-1.02	0.936	-1.16	0.16	-1.07	0.689	-1.36	0.19	-1.15
1441940_x_at	Klhdc8a	kelch domain containing 8A	-1.1	0.658	-1.08	0.88	-1.06	0.774	-1.37	0.552	-1.15
1417794_at	Zmym3	zinc finger, MYM-type 3	-1.18	0.199	-1	0.997	-1.07	0.623	-1.13	0.375	-1.1
1423763_x_at	Tia1	Cytotoxic granule-associated RNA binding protein 1	-1.02	0.685	-1.01	0.89	-1.23	0.06	-1.21	0.044	-1.12
1416327_at	Ufc1	ubiquitin-fold modifier conjugating enzyme 1	-1.11	0.369	-1.09	0.064	-1.05	0.713	-1.09	0.373	-1.08
1440151_s_at	Edf1	endothelial differentiation-related factor 1	-1.05	0.045	-1.13	0.268	-1.07	0.169	-1.29	0.19	-1.13
1416506_at	Psma6	proteasome (prosome, macropain) subunit, alpha type 6	-1.09	0.04	-1.09	0.041	-1.06	0.644	-1.11	0.507	-1.09
1436546_at	Lix1l	Lix1-like	-1.21	0.064	-1.03	0.862	-1.03	0.892	-1.12	0.62	-1.09
1431289_at	Tspan32	tetraspanin 32	-1.22	0.726	-1	0.999	-1.04	0.906	-1.1	0.501	-1.09
1448722_s_at	Ppcs	phosphopantothenoylcysteine synthetase	-1.05	0.428	-1.19	0.118	-1.01	0.881	-1.56	0.122	-1.2
1430605_at	Ccdc101	coiled-coil domain containing 101	-1.08	0.724	-1.05	0.796	-1.12	0.355	-1.02	0.946	-1.07
1452625_at	Kctd2	potassium channel tetramerisation domain containing 2	-1.1	0.319	-1.08	0.639	-1.06	0.738	-1.35	0.268	-1.15

1434085_at	Zfp523	zinc finger protein 523	-1.14	0.463	-1.04	0.645	-1.06	0.556	-1.25	0.321	-1.12
1449323_a_at	Rpl3 /// LOC66821	ribosomal protein L3 /// similar to ribosomal protein L3 isoform b /// similar to 60S	-1.03	0.606	-1.04	0.573	-1.18	0.057	-1.26	0.015	-1.13
1440235_at	Itga10	integrin, alpha 10	-1.09	0.596	-1.15	0.752	-1.01	0.977	-1.09	0.621	-1.09
1460352_s_at	Pik3r4	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 4, p150	-1.05	0.573	-1.09	0.125	-1.1	0.59	-2.89	0.021	-1.53
1420089_at	Nfkbia	Nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	-1.06	0.679	-1.01	0.923	-1.18	0.275	-1.34	0.157	-1.15
1427966_at	BC087945	cDNA sequence BC087945	-1.03	0.779	-1.15	0.307	-1.06	0.67	-1.73	0.145	-1.24
1427442_a_at	App	amyloid beta (A4) precursor protein	-1.05	0.207	-1.08	0.345	-1.11	0.345	-1.07	0.673	-1.08
1424342_at	Fyttd1	forty-two-three domain containing 1	-1.05	0.768	-1.08	0.384	-1.1	0.703	-1.31	0.216	-1.14
1439799_at	---	Transcribed locus	-1.13	0.211	-1.07	0.78	-1.04	0.88	-1.54	0.306	-1.2
1422669_at	Ebag9	estrogen receptor-binding fragment-associated gene 9	-1.13	0.021	-1.11	0.046	-1.01	0.918	-1.14	0.2	-1.1
1435739_at	AW208599	expressed sequence AW208599	-1.03	0.555	-1.11	0.321	-1.1	0.412	-1.04	0.687	-1.07
1451550_at	Ephb3	Eph receptor B3	-1.22	0.661	-1.03	0.94	-1.01	0.932	-1.2	0.709	-1.12
1416883_at	Clptm1	cleft lip and palate associated transmembrane protein 1	-1.09	0.543	-1.06	0.434	-1.09	0.563	-1.06	0.468	-1.07
1418628_at	Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1	-1.01	0.959	-1.18	0.134	-1.06	0.722	-1.02	0.922	-1.07
1438318_x_at	Ngdn	neuroguidin, EIF4E binding protein	-1.01	0.895	-1.04	0.601	-1.21	0.212	-1.39	0.019	-1.16
1426296_at	Rad52	RAD52 homolog (S. cerevisiae)	-1.04	0.828	-1.03	0.85	-1.18	0.022	-1.11	0.658	-1.09
1420119_s_at	Phf3	PHD finger protein 3	-1.12	0.732	-1.11	0.683	-1.01	0.894	-1.13	0.606	-1.09
1439531_at	E130311K13Rik	RIKEN cDNA E130311K13 gene	-1.02	0.841	-1.04	0.638	-1.19	0.306	-1.45	0.211	-1.18
1438032_at	Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1	-1.02	0.949	-1.04	0.757	-1.19	0.181	-1.43	0.02	-1.17
1439563_at	Zfp3	zinc finger protein 3	-1.08	0.85	-1.11	0.638	-1.05	0.563	-1.23	0.471	-1.12
1418960_at	Phf20l1	PHD finger protein 20-like 1	-1.11	0.517	-1.02	0.931	-1.12	0.416	-1.45	0.031	-1.17
1416647_at	Bckdha	branched chain ketoacid dehydrogenase E1, alpha polypeptide	-1.05	0.798	-1.2	0.23	-1.01	0.96	-1.29	0.309	-1.14
1454350_at	Pdzd6	PDZ domain containing 6	-1.04	0.894	-1.14	0.378	-1.06	0.753	-1.28	0.225	-1.13
1426789_s_at	Ssrp1	structure specific recognition protein 1	-1.21	0.04	-1.03	0.657	-1.01	0.938	-1	0.987	-1.06
1423130_a_at	Sfrs5 /// LOC62246	splicing factor, arginine/serine-rich 5 (SRp40, HRS) /// similar to Splicing factor, a	-1.1	0.747	-1.05	0.746	-1.08	0.556	-1.17	0.581	-1.1
1429103_at	Tomm22	translocase of outer mitochondrial membrane 22 homolog (yeast)	-1.01	0.956	-1.22	0.049	-1.03	0.809	-1.01	0.966	-1.07
1434251_at	Cnot1	CCR4-NOT transcription complex, subunit 1	-1.06	0.363	-1.03	0.798	-1.15	0.079	-1.19	0.111	-1.11
1423045_at	Ncbp2	nuclear cap binding protein subunit 2	-1.05	0.134	-1.04	0.694	-1.15	0.203	-1.17	0.199	-1.1
1432629_at	---	---	-1.08	0.92	-1.14	0.232	-1.02	0.953	-1.32	0.258	-1.14
1416708_a_at	Gramd1a	GRAM domain containing 1A	-1.18	0.156	-1.03	0.855	-1.04	0.757	-2.39	0.023	-1.41
1440076_at	Sqstm1	Sequestosome 1	-1.06	0.132	-1.09	0.496	-1.08	0.522	-1.12	0.699	-1.09
1422555_s_at	Gna13	guanine nucleotide binding protein, alpha 13	-1.02	0.744	-1	0.96	-1.23	0.076	-1.28	0.435	-1.13
1416291_at	Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	-1.07	0.33	-1.11	0.02	-1.05	0.659	-1.17	0.372	-1.1
1428950_s_at	Nol8	nucleolar protein 8	-1.05	0.912	-1.07	0.565	-1.12	0.63	-1.05	0.77	-1.07
1434019_at	Pdap1	PDGFA associated protein 1	-1.09	0.124	-1.1	0.401	-1.05	0.768	-1.02	0.904	-1.06
1451134_a_at	Tm2d2	TM2 domain containing 2	-1.12	0.437	-1.05	0.598	-1.06	0.557	-1.2	0.301	-1.11
1436595_at	Rbm34	RNA binding motif protein 34	-1.08	0.603	-1.07	0.329	-1.08	0.554	-1.12	0.122	-1.09
1449294_at	Mrps15	mitochondrial ribosomal protein S15	-1.04	0.644	-1.02	0.887	-1.19	0.077	-1.32	0.384	-1.14
1428367_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.13	0.678	-1.01	0.954	-1.09	0.825	-1.37	0.47	-1.15
1460726_at	Adss	adenylosuccinate synthetase, non muscle	-1.01	0.926	-1.22	0.022	-1.02	0.881	-1.04	0.683	-1.07
1415751_at	Hp1bp3	heterochromatin protein 1, binding protein 3	-1.04	0.666	-1.16	0.079	-1.04	0.709	-1.08	0.522	-1.08
1423361_at	Yme1l1	YME1-like 1 (S. cerevisiae)	-1.08	0.718	-1.07	0.313	-1.08	0.484	-1.12	0.539	-1.09
1433761_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	-1.21	0.521	-1.02	0.902	-1.02	0.946	-1.63	0.161	-1.22
1428855_at	H13	histocompatibility 13	-1.12	0.638	-1.09	0.885	-1.02	0.929	-3.5	0.096	-1.68
1429194_at	Tigd2	tigger transposable element derived 2	-1.04	0.751	-1	0.971	-1.21	0.183	-1.9	0.095	-1.29
1417979_at	Tnmd	tenomodulin	-1.04	0.936	-1.02	0.947	-1.18	0.697	-1.22	0.699	-1.12
1441089_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	-1.05	0.915	-1.04	0.863	-1.14	0.416	-1.31	0.438	-1.14
1418568_x_at	Srp14	signal recognition particle 14	-1.02	0.702	-1.04	0.216	-1.18	0.026	-1.28	0.081	-1.13
1428520_at	1110032A13Rik	RIKEN cDNA 1110032A13 gene	-1.05	0.556	-1.13	0.088	-1.05	0.764	-1.08	0.315	-1.08
1454947_a_at	Ublcp1 /// LOC665	ubiquitin-like domain containing CTD phosphatase 1 /// similar to ubiquitin-like do	-1.07	0.784	-1.04	0.845	-1.12	0.543	-1.19	0.253	-1.11
1435278_at	Sft2d3	SFT2 domain containing 3	-1.02	0.902	-1.15	0.263	-1.06	0.705	-1.27	0.284	-1.13
1416500_at	Sacm1l	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cerevisiae)	-1.04	0.545	-1.03	0.653	-1.17	0.125	-1.08	0.177	-1.08
1417812_a_at	Lamb3	laminin, beta 3	-1.06	0.925	-1.15	0.881	-1.03	0.944	-1.47	0.295	-1.18

1451185_at	Sf3b5	splicing factor 3b, subunit 5	-1.04	0.444	-1.09	0.144	-1.1	0.501	-1.06	0.667	-1.07
1423441_at	Tfb2m	transcription factor B2, mitochondrial	-1.07	0.066	-1.06	0.409	-1.1	0.355	-1.11	0.574	-1.08
1426890_a_at	Rpap1	RNA polymerase II associated protein 1	-1.1	0.496	-1.09	0.598	-1.03	0.9	-1.19	0.209	-1.1
1451487_at	Rabepk	Rab9 effector protein with kelch motifs	-1.03	0.698	-1.02	0.878	-1.19	0.406	-1.25	0.362	-1.12
1423567_a_at	Psma7	proteasome (prosome, macropain) subunit, alpha type 7	-1.16	0.022	-1.05	0.438	-1.03	0.778	-1.16	0.442	-1.1
1443955_at	---	---	-1.13	0.467	-1.01	0.835	-1.1	0.723	-1.18	0.333	-1.1
1416495_s_at	Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	-1.02	0.716	-1.12	0.03	-1.09	0.189	-1.12	0.554	-1.09
1457501_at	LOC622665	hypothetical protein LOC622665	-1.05	0.896	-1.15	0.738	-1.03	0.907	-1.55	0.177	-1.2
1424078_s_at	Pex6	peroxisomal biogenesis factor 6	-1	0.986	-1.21	0.168	-1.03	0.599	-1.33	0.152	-1.14
1452953_at	Fam18b	family with sequence similarity 18, member B	-1.08	0.22	-1.01	0.873	-1.15	0.192	-1.04	0.794	-1.07
1417827_at	Ngly1	N-glycanase 1	-1.21	0.076	-1.03	0.66	-1	0.959	-1.1	0.278	-1.09
1434057_at	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-1.03	0.802	-1.17	0.12	-1.03	0.435	-1.02	0.909	-1.06
1435017_at	Mel13	melanoma nuclear protein 13	-1.04	0.483	-1.05	0.492	-1.14	0.141	-1.53	0.142	-1.19
1437391_x_at	Mrpl44	mitochondrial ribosomal protein L44	-1.01	0.837	-1.19	0.063	-1.04	0.782	-1.17	0.195	-1.1
1448027_at	2010305B15Rik	RIKEN cDNA 2010305B15 gene	-1.02	0.904	-1.13	0.454	-1.08	0.632	-1.42	0.372	-1.16
1455175_at	Phf13	PHD finger protein 13	-1.06	0.363	-1.1	0.658	-1.07	0.476	-1.52	0.246	-1.19
1460436_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.07	0.464	-1.13	0.148	-1.02	0.945	-1.93	0.085	-1.29
1420088_at	Nfkbia	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	-1.07	0.845	-1.03	0.783	-1.13	0.069	-1.51	0.096	-1.18
1423791_at	Ik	IK cytokine	-1.1	0.6	-1.03	0.576	-1.1	0.425	-1.13	0.605	-1.09
1419490_at	AW049604	expressed sequence AW049604	-1.22	0.338	-1.01	0.974	-1.02	0.914	-1.4	0.651	-1.16
1430969_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	-1.05	0.926	-1.09	0.843	-1.09	0.77	-1.05	0.892	-1.07
1426716_at	Tdrd7	tudor domain containing 7	-1.05	0.735	-1.15	0.224	-1.03	0.804	-1.36	0.049	-1.15
1425023_at	Usp3	ubiquitin specific peptidase 3	-1.08	0.552	-1.15	0.357	-1	0.99	-1.7	0.041	-1.23
1442593_at	---	---	-1.05	0.857	-1.15	0.184	-1.02	0.949	-2.13	0.109	-1.34
1448241_at	Gm2a	GM2 ganglioside activator protein	-1.1	0.022	-1.01	0.92	-1.12	0.352	-1.38	0.322	-1.15
1434946_at	C330021A05Rik	RIKEN cDNA C330021A05 gene	-1.22	0.448	-1.01	0.983	-1.02	0.925	-1.15	0.521	-1.1
1452066_a_at	Ndfip2	Nedd4 family interacting protein 2	-1.07	0.318	-1.1	0.12	-1.05	0.649	-1.36	0.155	-1.15
1435617_at	AI480743	expressed sequence AI480743	-1	0.999	-1.19	0.226	-1.05	0.765	-1.44	0.111	-1.17
1433447_x_at	Cct4	chaperonin subunit 4 (delta)	-1.05	0.594	-1.07	0.552	-1.1	0.405	-1.22	0.022	-1.11
1447805_s_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	-1.02	0.664	-1.08	0.469	-1.12	0.496	-1.16	0.244	-1.1
1448639_a_at	Spata5	spermatogenesis associated 5	-1	0.968	-1.2	0.406	-1.03	0.648	-1.1	0.611	-1.09
1436178_at	Leprel1	leprecan-like 1	-1.05	0.677	-1.02	0.975	-1.16	0.607	-1.27	0.172	-1.12
1454704_at	Scarb2	scavenger receptor class B, member 2	-1.01	0.95	-1.02	0.849	-1.2	0.46	-1.25	0.481	-1.12
1423335_at	1110004F10Rik	RIKEN cDNA 1110004F10 gene	-1.11	0.256	-1.07	0.564	-1.03	0.711	-1.01	0.946	-1.06
1448867_at	Tmem9b	TMEM9 domain family, member B	-1	0.971	-1.02	0.805	-1.22	0.106	-1.15	0.274	-1.1
1424616_s_at	Frag1	FGF receptor activating protein 1	-1.13	0.13	-1.01	0.865	-1.08	0.426	-1.57	0.083	-1.2
1451049_at	Bcap31	B-cell receptor-associated protein 31	-1.03	0.544	-1.08	0.266	-1.11	0.153	-1.03	0.862	-1.06
1448178_a_at	Cct3	chaperonin subunit 3 (gamma)	-1.13	0.243	-1.08	0.437	-1.01	0.91	-1.13	0.1	-1.09
1438289_a_at	Sumo1	SMT3 suppressor of mif two 3 homolog 1 (yeast)	-1.01	0.938	-1.02	0.858	-1.22	0.028	-1.39	0.092	-1.16
1454776_at	Ehmt1	euchromatic histone methyltransferase 1	-1.08	0.392	-1.14	0.129	-1.01	0.915	-1.05	0.615	-1.07
1436004_at	Usp27x	ubiquitin specific peptidase 27, X chromosome	-1.19	0.546	-1.02	0.947	-1.03	0.849	-1.08	0.714	-1.08
1434056_a_at	Ndufb6	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6	-1.1	0.11	-1.07	0.277	-1.04	0.605	-1.16	0.228	-1.1
1454480_at	4933439N06Rik	RIKEN cDNA 4933439N06 gene	-1.02	0.949	-1.16	0.787	-1.05	0.845	-1.26	0.653	-1.12
1451051_a_at	Scyl1	SCY1-like 1 (S. cerevisiae)	-1.11	0.161	-1.09	0.234	-1.02	0.901	-1.18	0.179	-1.1
1460235_at	Scarb2	scavenger receptor class B, member 2	-1.04	0.884	-1.07	0.626	-1.12	0.346	-1.16	0.535	-1.09
1430594_at	Rab11fip1	RAB11 family interacting protein 1 (class I)	-1.11	0.474	-1.09	0.618	-1.02	0.944	-1.33	0.533	-1.14
1416179_a_at	Rdx	radixin	-1.06	0.489	-1.04	0.561	-1.12	0.151	-1.08	0.168	-1.07
1428078_at	0610013E23Rik	RIKEN cDNA 0610013E23 gene	-1.18	0.459	-1.05	0.727	-1	1	-1.33	0.171	-1.14
1439268_x_at	Eif3s6	eukaryotic translation initiation factor 3, subunit 6	-1.03	0.763	-1.05	0.491	-1.15	0.381	-1.36	0.073	-1.15
1421446_at	Prkcc	protein kinase C, gamma	-1	0.996	-1.16	0.67	-1.06	0.798	-1.22	0.693	-1.11
1433712_at	AW555464	expressed sequence AW555464	-1.05	0.787	-1.09	0.348	-1.07	0.342	-1.04	0.79	-1.06
1416522_a_at	Grcc10	gene rich cluster, C10 gene	-1	0.977	-1.1	0.234	-1.12	0.46	-1.7	0.194	-1.23
1426307_at	Cyb5r4	cytochrome b5 reductase 4	-1.15	0.35	-1.04	0.48	-1.03	0.786	-1.29	0.012	-1.13

1460135_at	A930005H10Rik	RIKEN cDNA A930005H10 gene	-1.01	0.977	-1.23	0.294	-1	0.998	-2.65	0.06	-1.47
1424313_a_at	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	-1.02	0.764	-1.14	0.3	-1.06	0.52	-1.12	0.089	-1.09
1442278_at	Jarid1b	Jumonji, AT rich interactive domain 1B (Rbp2 like)	-1.12	0.811	-1.01	0.968	-1.09	0.861	-1.04	0.885	-1.07
1460432_a_at	Eif3s6	eukaryotic translation initiation factor 3, subunit 6	-1.1	0.002	-1.01	0.847	-1.11	0.446	-1.29	0.155	-1.13
1415920_at	Cstf2t	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	-1.1	0.18	-1.01	0.86	-1.1	0.024	-1.56	0.048	-1.19
1418521_a_at	Mtx1	metaxin 1	-1.14	0.127	-1.07	0.411	-1.01	0.937	-1.11	0.218	-1.08
1432487_at	4930405H06Rik	RIKEN cDNA 4930405H06 gene	-1.02	0.958	-1.06	0.873	-1.13	0.576	-1.31	0.317	-1.13
1456324_at	Zfp748	zinc finger protein 748	-1.03	0.847	-1.05	0.793	-1.13	0.087	-1.63	0.059	-1.21
1460308_a_at	Ict1	immature colon carcinoma transcript 1	-1.03	0.826	-1.11	0.02	-1.07	0.67	-1.37	0.146	-1.14
1448363_at	Yap1	yes-associated protein 1	-1.02	0.494	-1.18	0.068	-1.02	0.859	-1.15	0.643	-1.09
1420473_at	Mtpn	myotrophin	-1.02	0.902	-1.03	0.7	-1.17	0.135	-1.37	0.195	-1.15
1426111_x_at	Irf3	interferon regulatory factor 3	-1.09	0.556	-1.12	0.05	-1.01	0.931	-1.55	0.167	-1.19
1457259_at	---	---	-1.12	0.452	-1.07	0.76	-1.02	0.85	-1.22	0.399	-1.11
1436400_at	---	---	-1.04	0.845	-1.08	0.717	-1.08	0.707	-1.11	0.388	-1.08
1433753_x_at	Eral1	Era (G-protein)-like 1 (E. coli)	-1.03	0.831	-1.09	0.502	-1.09	0.609	-1.38	0.147	-1.15
1452852_at	Twistnb	TWIST neighbor	-1.06	0.213	-1.04	0.422	-1.11	0.414	-1.24	0.325	-1.11
1437734_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	-1.16	0.186	-1	0.992	-1.06	0.566	-1.08	0.509	-1.07
1426289_at	2610028H07Rik	RIKEN cDNA 2610028H07 gene	-1.07	0.492	-1.1	0.348	-1.04	0.82	-1.1	0.567	-1.08
1420834_at	Vamp2	vesicle-associated membrane protein 2	-1.03	0.894	-1.13	0.573	-1.05	0.849	-1.11	0.629	-1.08
1454074_a_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	-1.03	0.885	-1.03	0.715	-1.15	0.087	-1.14	0.162	-1.09
1418841_s_at	Cdc2l1	cell division cycle 2-like 1	-1.06	0.73	-1.12	0.03	-1.03	0.753	-1.29	0.089	-1.12
1417844_at	Med4	mediator of RNA polymerase II transcription, subunit 4 homolog (yeast)	-1.01	0.797	-1.08	0.402	-1.11	0.424	-1.15	0.134	-1.09
1455942_at	Fbxl11	F-box and leucine-rich repeat protein 11	-1.01	0.927	-1.09	0.6	-1.11	0.552	-1.13	0.221	-1.09
1434844_at	Hexdc	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	-1.13	0.551	-1.08	0.515	-1	0.982	-1.54	0.188	-1.19
1426537_at	Narg2	NMDA receptor-regulated gene 2	-1.04	0.918	-1.09	0.617	-1.07	0.712	-1.75	0.085	-1.24
1423096_at	Capn7	calpain 7	-1.05	0.792	-1.09	0.274	-1.06	0.608	-1.21	0.197	-1.1
1456011_x_at	Acaa1a	acetyl-Coenzyme A acyltransferase 1A	-1.07	0.878	-1.05	0.874	-1.08	0.709	-1.8	0.088	-1.25
1454765_at	Gtf3c3	general transcription factor IIIC, polypeptide 3	-1.11	0.546	-1.09	0.591	-1.01	0.984	-1.05	0.352	-1.06
1444607_at	Cdsn	Corneodesmosin	-1	0.985	-1.1	0.657	-1.1	0.661	-1.43	0.315	-1.16
1424196_at	Yipf1	Yip1 domain family, member 1	-1.01	0.858	-1.04	0.393	-1.16	0.35	-1.18	0.24	-1.1
1436179_a_at	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	-1.1	0.579	-1.03	0.688	-1.08	0.775	-1.27	0.214	-1.12
1455211_a_at	Timm13	translocase of inner mitochondrial membrane 13 homolog (yeast)	-1	0.963	-1.17	0.065	-1.04	0.653	-1.18	0.45	-1.1
1451573_a_at	Stx4a	syntaxin 4A (placental)	-1.1	0.641	-1.01	0.947	-1.1	0.486	-1.3	0.222	-1.12
1449842_at	1810059G22Rik	RIKEN cDNA 1810059G22 gene	-1.09	0.41	-1.1	0.499	-1.01	0.879	-1.02	0.797	-1.05
1416867_at	Bet1	blocked early in transport 1 homolog (S. cerevisiae)	-1.06	0.597	-1.06	0.742	-1.07	0.724	-1.07	0.756	-1.07
1435271_at	Irf3	interferon regulatory factor 3	-1.04	0.753	-1.04	0.891	-1.13	0.773	-1.7	0.259	-1.23
1452973_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	-1.05	0.616	-1.05	0.523	-1.1	0.558	-1.85	0.154	-1.26
1455022_at	Strn	striatin, calmodulin binding protein	-1.03	0.667	-1.01	0.872	-1.17	0.243	-1.03	0.889	-1.06
1418577_at	Trim8	tripartite motif protein 8	-1.1	0.68	-1.07	0.767	-1.03	0.856	-1.3	0.23	-1.12
1434441_at	1110018J18Rik	RIKEN cDNA 1110018J18 gene	-1.04	0.598	-1.01	0.919	-1.15	0.035	-1.35	0.127	-1.14
1428405_at	Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	-1.07	0.269	-1.06	0.479	-1.07	0.238	-1.18	0.434	-1.09
1430292_a_at	1810030N24Rik	RIKEN cDNA 1810030N24 gene	-1.13	0.054	-1.01	0.896	-1.07	0.554	-1.01	0.935	-1.05
1423958_a_at	2900001O04Rik	RIKEN cDNA 2900001O04 gene	-1.07	0.516	-1.03	0.674	-1.1	0.426	-1.16	0.139	-1.09
1436069_at	Ing5	inhibitor of growth family, member 5	-1.16	0.416	-1.04	0.775	-1.01	0.91	-1.03	0.839	-1.06
1438631_x_at	Ttc13	tetratricopeptide repeat domain 13	-1.01	0.965	-1	0.998	-1.21	0.285	-1.53	0.02	-1.19
1418502_a_at	Oxr1	oxidation resistance 1	-1.14	0.372	-1.05	0.629	-1.01	0.9	-1.12	0.272	-1.08
1434791_at	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	-1.08	0.53	-1.11	0.404	-1.02	0.932	-1.03	0.901	-1.06
1445059_at	C80435	expressed sequence C80435	-1.13	0.811	-1.01	0.987	-1.07	0.86	-2.04	0.072	-1.31
1460637_s_at	Pfdn5	prefoldin 5	-1.03	0.745	-1.06	0.352	-1.12	0.279	-1.75	0.129	-1.24
1437297_at	Chd8	chromodomain helicase DNA binding protein 8	-1.02	0.873	-1.03	0.769	-1.16	0.237	-1.39	0.159	-1.15
1437730_at	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	-1.05	0.287	-1.05	0.637	-1.09	0.137	-1.17	0.219	-1.09
1433511_at	6330549H03Rik	RIKEN cDNA 6330549H03 gene	-1.08	0.726	-1.11	0.757	-1.01	0.922	-1.16	0.326	-1.09
1434022_at	Zbtb33	zinc finger and BTB domain containing 33	-1.02	0.807	-1.05	0.47	-1.13	0.045	-1.24	0.331	-1.11

1423486_at	Cript	cysteine-rich PDZ-binding protein	-1.07	0.231	-1.11	0.214	-1.02	0.891	-1.17	0.447	-1.09
1428634_at	Twistnb	TWIST neighbor	-1.05	0.563	-1.08	0.551	-1.07	0.687	-1.12	0.426	-1.08
1450904_at	Tmem167	transmembrane protein 167	-1.09	0.619	-1.01	0.975	-1.11	0.626	-1.2	0.525	-1.1
1418742_at	Krt34	keratin 34	-1.01	0.959	-1.16	0.669	-1.03	0.835	-1.16	0.549	-1.09
1438071_at	Pms1	postmeiotic segregation increased 1 (S. cerevisiae)	-1.03	0.038	-1.17	0.638	-1	0.992	-1.4	0.062	-1.15
1421870_at	Trim44	tripartite motif-containing 44	-1.04	0.507	-1.13	0.085	-1.03	0.809	-1.02	0.901	-1.05
1423167_at	Prei3	preimplantation protein 3	-1.05	0.765	-1.04	0.833	-1.1	0.634	-1.2	0.492	-1.1
1444113_at	---	Transcribed locus	-1.06	0.796	-1.05	0.734	-1.09	0.587	-1.57	0.044	-1.19
1440268_at	Trim41	tripartite motif-containing 41	-1.1	0.49	-1.01	0.97	-1.09	0.602	-1.03	0.892	-1.06
1416813_at	Tia1	cytotoxic granule-associated RNA binding protein 1	-1.06	0.604	-1.08	0.599	-1.05	0.661	-1.49	0.208	-1.17
1443382_s_at	Btbd14b	BTB (POZ) domain containing 14B	-1.03	0.846	-1.17	0.757	-1.01	0.966	-1	0.984	-1.05
1415980_at	Atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), i	-1.03	0.899	-1.05	0.689	-1.11	0.55	-1.29	0.271	-1.12
1426995_a_at	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	-1.02	0.907	-1.1	0.183	-1.07	0.653	-1.01	0.908	-1.05
1436027_at	Osbpl11	oxysterol binding protein-like 11	-1.1	0.705	-1.01	0.942	-1.09	0.583	-1.37	0.054	-1.14
1451020_at	Gsk3b	glycogen synthase kinase 3 beta	-1.11	0.581	-1.05	0.649	-1.03	0.779	-1	0.992	-1.05
1454614_at	1810013D10Rik	RIKEN cDNA 1810013D10 gene	-1.09	0.271	-1.01	0.921	-1.09	0.471	-1.19	0.169	-1.09
1424883_s_at	Sfrs7	splicing factor, arginine/serine-rich 7	-1.05	0.827	-1.07	0.55	-1.07	0.636	-1.19	0.123	-1.09
1428178_s_at	Trappc6b	trafficking protein particle complex 6B	-1.15	0.086	-1.01	0.815	-1.04	0.672	-1.21	0.209	-1.1
1426602_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	-1.01	0.96	-1.07	0.575	-1.11	0.348	-1.08	0.671	-1.07
1416538_at	Siae	sialic acid acetylesterase	-1.1	0.232	-1.08	0.521	-1.02	0.932	-1.05	0.798	-1.06
1421859_at	Adam17	a disintegrin and metallopeptidase domain 17	-1.11	0.188	-1.03	0.841	-1.05	0.819	-1.36	0.107	-1.14
1422849_a_at	Pabpn1	poly(A) binding protein, nuclear 1	-1.03	0.862	-1.03	0.859	-1.13	0.297	-1.16	0.236	-1.09
1417010_at	Zfp238	zinc finger protein 238	-1.03	0.491	-1.02	0.862	-1.15	0.049	-1.75	0.051	-1.24
1416526_a_at	Park7	Parkinson disease (autosomal recessive, early onset) 7	-1.05	0.36	-1.13	0.252	-1.01	0.803	-1.12	0.407	-1.08
1417054_a_at	0610009D07Rik	RIKEN cDNA 0610009D07 gene	-1.09	0.036	-1.07	0.187	-1.03	0.854	-1.11	0.35	-1.07
1451525_at	Arhgap12	Rho GTPase activating protein 12	-1.06	0.42	-1.04	0.711	-1.09	0.516	-1.21	0.603	-1.1
1450865_s_at	Mrps24	mitochondrial ribosomal protein S24	-1.08	0.5	-1.01	0.77	-1.1	0.618	-1.04	0.788	-1.06
1417029_a_at	Trim2	tripartite motif protein 2	-1.16	0.603	-1.01	0.981	-1.02	0.918	-1.08	0.818	-1.07
1440799_s_at	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	-1.03	0.89	-1.05	0.741	-1.11	0.662	-1.09	0.815	-1.07
1449343_s_at	Sin3a	transcriptional regulator, SIN3A (yeast)	-1.02	0.828	-1.09	0.489	-1.07	0.636	-1.17	0.25	-1.09
1450811_at	Sprr2j	small proline-rich protein 2J	-1.03	0.704	-1.04	0.906	-1.12	0.536	-1.3	0.496	-1.12
1421261_at	Lipg	lipase, endothelial	-1.02	0.961	-1.04	0.847	-1.12	0.697	-1.27	0.231	-1.11
1455141_at	Tnrc6a	trinucleotide repeat containing 6a	-1.11	0.094	-1.01	0.913	-1.06	0.605	-1.59	0.063	-1.19
1447960_at	9630017O17	hypothetical protein 9630017O17	-1.09	0.418	-1.04	0.887	-1.05	0.829	-1.17	0.276	-1.09
1448993_at	Atg3	autophagy-related 3 (yeast)	-1.07	0.243	-1.11	0.262	-1	0.979	-1.29	0.262	-1.12
1426999_at	Zc3h14	zinc finger CCCH type containing 14	-1.06	0.529	-1.08	0.081	-1.04	0.81	-1.11	0.439	-1.07
1428874_at	1110019N10Rik	RIKEN cDNA 1110019N10 gene	-1.05	0.835	-1.13	0.312	-1	0.98	-1.11	0.507	-1.07
1451220_at	2310040A13Rik	RIKEN cDNA 2310040A13 gene	-1.08	0.575	-1.09	0.258	-1.01	0.835	-1.34	0.095	-1.13
1428645_at	Gnai3	guanine nucleotide binding protein, alpha inhibiting 3	-1.06	0.164	-1.07	0.235	-1.05	0.658	-1.45	0.074	-1.16
1417452_a_at	Fau	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fo	-1.04	0.703	-1.03	0.756	-1.11	0.417	-1.46	0.052	-1.16
1426749_at	Prmt3	protein arginine N-methyltransferase 3	-1.03	0.709	-1.06	0.38	-1.09	0.306	-1.34	0.146	-1.13
1418017_at	Pum2	pumilio 2 (Drosophila)	-1.12	0.146	-1.01	0.952	-1.05	0.681	-1.05	0.597	-1.06
1451520_at	---	---	-1.02	0.869	-1.09	0.394	-1.07	0.836	-1.32	0.435	-1.12
1442830_at	Nusap1	Nucleolar and spindle associated protein 1	-1.02	0.893	-1.06	0.937	-1.1	0.801	-1.97	0.171	-1.29
1427449_a_at	Adprhl2	ADP-ribosylhydrolase like 2	-1.03	0.849	-1.11	0.574	-1.03	0.846	-1.15	0.135	-1.08
1455534_s_at	Osbpl11	oxysterol binding protein-like 11	-1.08	0.542	-1.05	0.676	-1.05	0.747	-1.31	0.042	-1.12
1417348_at	2310039H08Rik	RIKEN cDNA 2310039H08 gene	-1.05	0.516	-1.04	0.537	-1.08	0.567	-1.17	0.391	-1.09
1452044_at	Arpc5l	actin related protein 2/3 complex, subunit 5-like	-1.01	0.924	-1.13	0.087	-1.04	0.715	-1.81	0.104	-1.25
1436016_x_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	-1.04	0.163	-1	0.934	-1.15	0.129	-1.3	0.122	-1.12
1449642_at	Phgdhl1	Phosphoglycerate dehydrogenase like 1	-1.06	0.708	-1.03	0.936	-1.08	0.837	-1.3	0.529	-1.12
1424541_at	Tmem70	transmembrane protein 70	-1.1	0.168	-1.02	0.805	-1.05	0.592	-1.01	0.929	-1.05
1448224_at	Tfam	transcription factor A, mitochondrial	-1.04	0.887	-1.04	0.772	-1.1	0.004	-1.78	0.069	-1.24
1417798_at	1810019J16Rik	RIKEN cDNA 1810019J16 gene	-1.01	0.966	-1.02	0.951	-1.16	0.278	-1.45	0.535	-1.16

1436783_x_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	-1.05	0.428	-1	0.958	-1.12	0.429	-1.07	0.512	-1.06
1442372_at	---	Transcribed locus	-1.06	0.758	-1.03	0.825	-1.08	0.547	-1.05	0.831	-1.05
1436652_at	5830418K08Rik	RIKEN cDNA 5830418K08 gene	-1.03	0.669	-1.12	0.717	-1.02	0.959	-1.01	0.942	-1.05
1426643_at	Elp3	elongation protein 3 homolog (S. cerevisiae)	-1.11	0.13	-1.02	0.701	-1.04	0.525	-1.28	0.04	-1.11
1435865_at	Hist3h2a	histone 3, H2a	-1.15	0.463	-1.02	0.882	-1.01	0.866	-1.06	0.711	-1.06
1428526_at	Lsmd1	LSM domain containing 1	-1.1	0.582	-1.01	0.884	-1.06	0.634	-1.03	0.87	-1.05
1424018_at	Hint1	histidine triad nucleotide binding protein 1	-1.03	0.825	-1.03	0.686	-1.1	0.482	-1.12	0.37	-1.07
1450726_at	Asah2	N-acylsphingosine amidohydrolase 2	-1.03	0.777	-1.06	0.593	-1.08	0.626	-1.04	0.775	-1.05
1448240_at	Mbtps1	membrane-bound transcription factor peptidase, site 1	-1.07	0.351	-1.04	0.318	-1.06	0.66	-1.35	0.046	-1.13
1454964_at	BC021395	cDNA sequence BC021395	-1.1	0.413	-1.01	0.908	-1.06	0.641	-1.04	0.894	-1.05
1435085_at	Crebl2	cAMP responsive element binding protein-like 2	-1.04	0.867	-1.08	0.646	-1.05	0.622	-1.23	0.501	-1.1
1417032_at	Ube2g2	ubiquitin-conjugating enzyme E2G 2	-1.01	0.862	-1.08	0.508	-1.07	0.166	-1.02	0.859	-1.05
1426762_s_at	Aof2	amine oxidase (flavin containing) domain 2	-1.13	0.169	-1.02	0.601	-1.02	0.7	-1.2	0.184	-1.09
1426979_at	Mlxip	MLX interacting protein	-1.09	0.792	-1.06	0.584	-1.01	0.953	-1.58	0.247	-1.19
1448917_at	Thrap6	thyroid hormone receptor associated protein 6	-1.04	0.648	-1.08	0.57	-1.05	0.698	-1.06	0.263	-1.06
1425719_a_at	Nmi	N-myc (and STAT) interactor	-1.07	0.499	-1.02	0.839	-1.08	0.349	-1.52	0.19	-1.17
1417136_s_at	Srpk2	serine/arginine-rich protein specific kinase 2	-1.06	0.511	-1.06	0.747	-1.04	0.657	-1.47	0.397	-1.16
1432094_a_at	1700034M03Rik	RIKEN cDNA 1700034M03 gene	-1.12	0.379	-1	0.939	-1.04	0.828	-1.07	0.665	-1.06
1423645_a_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-1.07	0.782	-1.01	0.908	-1.08	0.353	-1.33	0.253	-1.12
1455058_at	Mtmr9	myotubularin related protein 9	-1.05	0.649	-1.05	0.605	-1.06	0.541	-1.26	0.288	-1.11
1420609_at	7-Mar	membrane-associated ring finger (C3HC4) 7	-1.08	0.741	-1.08	0.336	-1	0.989	-1.37	0.21	-1.13
1451184_at	Hnrpa3 /// LOC545	heterogeneous nuclear ribonucleoprotein A3 /// similar to heterogeneous nuclear	-1.05	0.259	-1.03	0.677	-1.09	0.336	-1.2	0.038	-1.09
1453342_at	Cdc40	cell division cycle 40 homolog (yeast)	-1.06	0.076	-1.09	0.267	-1.02	0.865	-1.34	0.068	-1.13
1417468_at	Nit1	nitrilase 1	-1.06	0.412	-1.07	0.403	-1.03	0.748	-1.11	0.404	-1.07
1428769_at	Tatdn3	TatD DNase domain containing 3	-1.12	0.268	-1.02	0.899	-1.02	0.875	-1.03	0.88	-1.05
1451025_at	Arl1	ADP-ribosylation factor-like 1	-1.08	0.225	-1.03	0.424	-1.05	0.485	-1.31	0.16	-1.12
1426481_at	Klhl22	kelch-like 22 (Drosophila)	-1.1	0.022	-1.02	0.803	-1.05	0.595	-1.06	0.571	-1.05
1429429_s_at	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-1	0.99	-1.09	0.098	-1.07	0.615	-1.17	0.491	-1.08
1438030_at	Rasgrp3	RAS, guanyl releasing protein 3	-1.07	0.607	-1.03	0.904	-1.06	0.847	-1.5	0.294	-1.16
1415727_at	Apoa1bp	apolipoprotein A-I binding protein	-1	0.996	-1.08	0.61	-1.08	0.492	-1.14	0.573	-1.08
1452023_at	Asb16	ankyrin repeat and SOCS box-containing 16	-1.02	0.839	-1.04	0.927	-1.1	0.634	-1.54	0.202	-1.17
1435153_at	Btbd6	BTB (POZ) domain containing 6	-1.12	0.358	-1.01	0.936	-1.04	0.682	-1.18	0.519	-1.09
1434680_at	Plekhg3	pleckstrin homology domain containing, family G (with RhoGef domain) member	-1.06	0.463	-1.02	0.886	-1.08	0.565	-1.2	0.22	-1.09
1455340_at	AI852444	Expressed sequence AI852444	-1.09	0.616	-1.06	0.522	-1.01	0.92	-1.12	0.748	-1.07
1437284_at	Fzd1	frizzled homolog 1 (Drosophila)	-1.09	0.257	-1.07	0.691	-1	0.995	-1.1	0.769	-1.06
1448287_at	Rpo1-3	RNA polymerase 1-3	-1.12	0.444	-1.02	0.716	-1.02	0.907	-1.15	0.468	-1.08
1431766_x_at	Rps2	ribosomal protein S2	-1.1	0.218	-1.03	0.859	-1.03	0.486	-1.2	0.003	-1.09
1433475_a_at	C78339	expressed sequence C78339	-1.01	0.703	-1.01	0.941	-1.15	0.146	-1.38	0.013	-1.14
1453206_at	Acad9	acyl-Coenzyme A dehydrogenase family, member 9	-1.08	0.428	-1.04	0.756	-1.03	0.666	-1.2	0.461	-1.09
1431825_at	Srpk3	serine/arginine-rich protein specific kinase 3	-1.04	0.73	-1.04	0.91	-1.07	0.746	-1.93	0.151	-1.27
1423789_at	BC005624	cDNA sequence BC005624	-1.06	0.65	-1.03	0.642	-1.06	0.667	-1.41	0.031	-1.14
1455348_x_at	Rpl29 /// LOC4333	ribosomal protein L29 /// similar to 60S ribosomal protein L29 /// similar to 60S rib	-1	0.968	-1.01	0.87	-1.15	0.063	-1.31	0.044	-1.12
1425459_at	Mtmr2	myotubularin related protein 2	-1.08	0.715	-1.02	0.885	-1.05	0.776	-1.08	0.695	-1.06
1428080_at	Pgam5	phosphoglycerate mutase family member 5	-1.04	0.686	-1.04	0.48	-1.06	0.607	-1.14	0.294	-1.07
1429596_at	Slc7a6os	solute carrier family 7, member 6 opposite strand	-1.03	0.848	-1.03	0.805	-1.09	0.687	-1.72	0.04	-1.22
1454922_at	AI553587	expressed sequence AI553587	-1.01	0.848	-1.11	0.294	-1.04	0.855	-1.03	0.802	-1.05
1424275_s_at	Trim41	tripartite motif-containing 41	-1.11	0.57	-1.01	0.935	-1.03	0.292	-1.18	0.481	-1.08
1421773_at	Etv2	ets variant gene 2	-1.03	0.934	-1.1	0.801	-1.02	0.92	-1.81	0.298	-1.24
1418695_a_at	Kcmf1	potassium channel modulatory factor 1	-1.02	0.817	-1	0.858	-1.13	0.054	-1.04	0.48	-1.05
1452971_at	Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	-1.02	0.929	-1.1	0.706	-1.03	0.867	-1.14	0.269	-1.07
1427022_at	Ddx42	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42	-1.01	0.944	-1.02	0.898	-1.12	0.387	-1.04	0.825	-1.05
1448295_at	D13Wsu50e	DNA segment, Chr 13, Wayne State University 50, expressed	-1.06	0.332	-1.01	0.945	-1.08	0.025	-1.37	0.123	-1.13
1421810_at	Dgcr2	DiGeorge syndrome critical region gene 2	-1.15	0.264	-1.01	0.936	-1	0.994	-1.21	0.292	-1.09

1423838_s_at	2400003C14Rik	RIKEN cDNA 2400003C14 gene	-1.01	0.728	-1.02	0.755	-1.12	0.161	-1.32	0.203	-1.12
1420829_a_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	-1.04	0.685	-1.02	0.84	-1.09	0.204	-1.08	0.621	-1.06
1427185_at	Mef2a	myocyte enhancer factor 2A	-1.05	0.791	-1.02	0.659	-1.07	0.703	-1.31	0.292	-1.11
1437852_x_at	Cpsf3	cleavage and polyadenylation specificity factor 3	-1.02	0.928	-1.1	0.202	-1.02	0.846	-1.68	0.133	-1.21
1424473_at	Polr2h	polymerase (RNA) II (DNA directed) polypeptide H	-1.09	0.626	-1.01	0.952	-1.05	0.817	-1.03	0.896	-1.04
1456538_at	Sdccag8	serologically defined colon cancer antigen 8	-1.01	0.933	-1.06	0.534	-1.08	0.568	-1.5	0.088	-1.16
1456748_a_at	Nipsnap1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolo	-1.01	0.454	-1.13	0.377	-1.01	0.875	-1.24	0.039	-1.1
1433823_at	AW456874	expressed sequence AW456874	-1.02	0.872	-1	1	-1.13	0.726	-1.13	0.708	-1.07
1453380_a_at	Xrcc6bp1	XRCC6 binding protein 1	-1.05	0.702	-1.08	0.454	-1.01	0.957	-1.34	0.045	-1.12
1437225_x_at	Gnai3	guanine nucleotide binding protein, alpha inhibiting 3	-1.13	0.619	-1	0.976	-1.02	0.871	-1.34	0.039	-1.12
1460547_a_at	Hnrpk	heterogeneous nuclear ribonucleoprotein K	-1.02	0.747	-1.01	0.896	-1.12	0.014	-1.05	0.128	-1.05
1448115_at	Htf9c	HpaII tiny fragments locus 9c	-1.02	0.381	-1.01	0.926	-1.12	0.498	-1.18	0.086	-1.08
1435230_at	Ankrd12	ankyrin repeat domain 12	-1.07	0.681	-1.01	0.964	-1.05	0.849	-1.18	0.402	-1.08
1441121_at	Pcid2	PCI domain containing 2	-1.01	0.985	-1.01	0.902	-1.13	0.505	-1.1	0.562	-1.06
1417174_at	1810021J13Rik	RIKEN cDNA 1810021J13 gene	-1.01	0.893	-1.03	0.795	-1.09	0.626	-1.46	0.168	-1.15
1450816_at	Polg2	polymerase (DNA directed), gamma 2, accessory subunit	-1.01	0.976	-1.04	0.812	-1.1	0.492	-1.57	0.02	-1.18
1460363_at	Tnrc6c	trinucleotide repeat containing 6C	-1.04	0.729	-1	0.987	-1.1	0.622	-1.56	0.082	-1.18
1448495_at	Tsta3	tissue specific transplantation antigen P35B	-1.02	0.87	-1.02	0.803	-1.09	0.479	-1.33	0.086	-1.12
1426903_at	Fndc3a	fibronectin type III domain containing 3a	-1.01	0.952	-1.05	0.569	-1.08	0.559	-1.43	0.383	-1.14
1425323_a_at	BC008155	cDNA sequence BC008155	-1.02	0.666	-1.02	0.73	-1.1	0.375	-1.29	0.129	-1.11
1426347_at	2010321M09Rik	RIKEN cDNA 2010321M09 gene	-1.03	0.87	-1.08	0.155	-1.03	0.708	-1.15	0.178	-1.07
1448345_at	Tomm34	translocase of outer mitochondrial membrane 34	-1.12	0.022	-1	0.992	-1.02	0.705	-1.37	0.249	-1.13
1451728_at	Wdr13	WD repeat domain 13	-1.08	0.427	-1.01	0.908	-1.04	0.795	-1.14	0.546	-1.07
1454998_at	1200011I18Rik	RIKEN cDNA 1200011I18 gene	-1.06	0.568	-1	0.999	-1.07	0.645	-1.07	0.496	-1.05
1431704_a_at	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	-1.07	0.768	-1.06	0.557	-1	0.988	-2.48	0.143	-1.4
1429476_s_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	-1.08	0.227	-1.04	0.465	-1.01	0.874	-1.1	0.223	-1.06
1452587_at	Actr2	ARP2 actin-related protein 2 homolog (yeast)	-1.06	0.484	-1.04	0.515	-1.03	0.726	-1.43	0.15	-1.14
1420633_a_at	Csn1s2a	casein alpha s2-like A	-1	0.985	-1.03	0.943	-1.1	0.561	-1.08	0.671	-1.05
1439105_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.08	0.609	-1.04	0.91	-1.01	0.964	-1.18	0.382	-1.08
1437838_x_at	Grsf1	G-rich RNA sequence binding factor 1	-1.06	0.684	-1.05	0.309	-1.01	0.738	-1.04	0.568	-1.04
1424652_at	Tmem166	transmembrane protein 166	-1.1	0.549	-1	0.992	-1.03	0.843	-1.18	0.761	-1.08
1422184_a_at	Ak1	adenylate kinase 1	-1.06	0.818	-1.03	0.901	-1.03	0.846	-1.59	0.053	-1.18
1452084_at	Zcchc17	zinc finger, CCHC domain containing 17	-1.05	0.381	-1.02	0.799	-1.05	0.798	-1.08	0.54	-1.05
1429155_at	4933411K20Rik	RIKEN cDNA 4933411K20 gene	-1	0.976	-1.03	0.429	-1.09	0.541	-1.09	0.644	-1.05
1448418_s_at	Wdr23	WD repeat domain 23	-1.06	0.5	-1.06	0.611	-1	0.966	-1.27	0.01	-1.1
1426700_a_at	Usp52	ubiquitin specific peptidase 52	-1.04	0.015	-1.04	0.623	-1.04	0.9	-1.11	0.544	-1.06
1425936_a_at	Ankmy2	ankyrin repeat and MYND domain containing 2	-1.01	0.977	-1.06	0.867	-1.05	0.737	-1.21	0.309	-1.08
1434082_at	---	---	-1.07	0.631	-1.04	0.371	-1	0.979	-1.05	0.578	-1.04
1455357_x_at	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.01	0.939	-1.01	0.818	-1.1	0.52	-1.32	0.232	-1.11
1431112_at	Ulk3	unc-51-like kinase 3 (C. elegans)	-1.01	0.979	-1.09	0.697	-1.01	0.944	-1.18	0.2	-1.08
1433476_at	C78339	expressed sequence C78339	-1	0.999	-1.04	0.135	-1.08	0.478	-1.38	0.033	-1.12
1423455_at	Ptma	prothymosin alpha	-1.02	0.878	-1.02	0.816	-1.07	0.417	-1.07	0.013	-1.05
1441276_at	Ptprk	protein tyrosine phosphatase, receptor type, K	-1.06	0.865	-1.04	0.881	-1.02	0.953	-1.61	0.402	-1.18
1419435_at	Aox1	aldehyde oxidase 1	-1.04	0.911	-1.07	0.688	-1.01	0.941	-1.51	0.437	-1.15
1426426_at	Rbm13	RNA binding motif protein 13	-1.02	0.533	-1.03	0.779	-1.06	0.635	-1.25	0.125	-1.09
1432430_a_at	1700081L11Rik	RIKEN cDNA 1700081L11 gene	-1.03	0.947	-1.02	0.95	-1.06	0.89	-1.44	0.025	-1.14
1424753_at	Nudt14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	-1.01	0.957	-1.09	0.329	-1.01	0.962	-1.55	0.177	-1.16
1437423_a_at	Sra1	steroid receptor RNA activator 1	-1.04	0.059	-1.02	0.862	-1.05	0.664	-1.18	0.26	-1.07
1423181_s_at	Clns1a	chloride channel, nucleotide-sensitive, 1A	-1.05	0.671	-1.01	0.903	-1.05	0.155	-1.12	0.045	-1.06
1436710_at	Zswim4	zinc finger, SWIM domain containing 4	-1.05	0.864	-1.03	0.823	-1.02	0.904	-1.04	0.723	-1.04
1423114_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-1.04	0.697	-1.06	0.533	-1.01	0.959	-1.08	0.292	-1.05
1433040_at	2900018E21Rik	RIKEN cDNA 2900018E21 gene	-1.01	0.971	-1.04	0.852	-1.05	0.756	-1.01	0.963	-1.03
1418583_at	Hint3	histidine triad nucleotide binding protein 3	-1.05	0.56	-1.05	0.706	-1.01	0.93	-1.51	0.174	-1.15

1447302_at	---	Transcribed locus	-1.01	0.929	-1.03	0.939	-1.06	0.889	-1.77	0.394	-1.22
1425528_at	Prrx1	paired related homeobox 1	-1.05	0.875	-1	0.993	-1.05	0.86	-1.46	0.34	-1.14
1425674_a_at	Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	-1.03	0.515	-1.07	0.411	-1	1	-1.48	0.135	-1.15
1458181_at	9030624J02Rik	RIKEN cDNA 9030624J02 gene	-1.09	0.151	-1	0.99	-1.01	0.969	-1.16	0.235	-1.07
1454669_at	Tmem11	transmembrane protein 11	-1.04	0.735	-1.05	0.513	-1	0.988	-1.13	0.315	-1.06
1416440_at	Cd164	CD164 antigen	-1.08	0.422	-1.01	0.945	-1.01	0.748	-1.06	0.779	-1.04
1452734_at	Rnaset2	ribonuclease T2	-1.05	0.445	-1.04	0.696	-1.01	0.898	-1.37	0.149	-1.12
1450988_at	Lgr5	leucine rich repeat containing G protein coupled receptor 5	-1.05	0.101	-1.01	0.966	-1.04	0.825	-1.16	0.709	-1.06
1422449_s_at	Rcn2	reticulocalbin 2	-1.06	0.572	-1.03	0.684	-1	0.973	-1.42	0.143	-1.13
1449138_at	Sf3b1	splicing factor 3b, subunit 1	-1.07	0.254	-1.01	0.939	-1.02	0.931	-1.28	0.307	-1.09
1455581_x_at	9530028C05	hypothetical protein 9530028C05	-1.06	0.735	-1.02	0.894	-1.01	0.885	-2.56	0.057	-1.41
1452009_at	9130422G05Rik	RIKEN cDNA 9130422G05 gene	-1	0.999	-1.02	0.742	-1.06	0.688	-1.28	0.372	-1.09
1419317_x_at	2310002A05Rik ///	RIKEN cDNA 2310002A05 gene /// small proline rich-like 1 /// similar to late cornil	-1	0.998	-1.07	0.621	-1.01	0.906	-2.2	0.47	-1.32
1429690_at	1300003B13Rik	RIKEN cDNA 1300003B13 gene	-1.06	0.69	-1.01	0.964	-1.01	0.933	-1.99	0.144	-1.27
1448353_x_at	Rpn1	ribophorin I	-1.03	0.845	-1.03	0.805	-1.02	0.774	-1.04	0.725	-1.03
1423880_at	D10Wsu52e	DNA segment, Chr 10, Wayne State University 52, expressed	-1.02	0.821	-1.06	0.307	-1	0.977	-1.65	0.057	-1.18
1423132_a_at	5730427N09Rik ///	RIKEN cDNA 5730427N09 gene /// similar to TGF beta-inducible nuclear protein	-1.07	0.688	-1.01	0.852	-1	0.987	-1.97	0.108	-1.26
1429311_at	Ube2q	ubiquitin-conjugating enzyme E2Q (putative)	-1.02	0.795	-1.03	0.614	-1.03	0.663	-1.48	0.057	-1.14
1430995_at	---	---	-1.06	0.775	-1	0.994	-1.02	0.922	-1.26	0.141	-1.09
1416466_at	Vapa	vesicle-associated membrane protein, associated protein A	-1.06	0.282	-1	0.975	-1.02	0.873	-1.03	0.787	-1.03
1451216_at	Zfp330	zinc finger protein 330	-1	0.965	-1.06	0.57	-1.02	0.849	-1.33	0.079	-1.1
1435223_at	Spfh2	SPFH domain family, member 2	-1.02	0.795	-1.02	0.782	-1.04	0.61	-1.03	0.841	-1.03
1416796_at	Nck2	non-catalytic region of tyrosine kinase adaptor protein 2	-1.01	0.889	-1.04	0.836	-1.03	0.752	-1.29	0.116	-1.09
1424139_at	Rap1a	RAS-related protein-1a	-1.04	0.746	-1.03	0.559	-1.01	0.93	-1	0.962	-1.02
1420321_at	Rsad1	Radical S-adenosyl methionine domain containing 1	-1.07	0.84	-1	0.994	-1.01	0.986	-1.24	0.266	-1.08
1435273_at	Wars2	tryptophanyl tRNA synthetase 2 (mitochondrial)	-1.01	0.973	-1.01	0.925	-1.05	0.718	-1.05	0.662	-1.03
1433542_at	Inpp5f	inositol polyphosphate-5-phosphatase F	-1.01	0.869	-1.04	0.692	-1.02	0.771	-2	0.027	-1.27
1436956_at	Bace1	Beta-site APP cleaving enzyme 1	-1.02	0.672	-1.04	0.69	-1.01	0.95	-1.08	0.494	-1.04
1415737_at	Rfk	riboflavin kinase	-1.02	0.745	-1.02	0.718	-1.03	0.738	-1.01	0.969	-1.02
1415796_at	Dazap2	DAZ associated protein 2	-1.02	0.783	-1.02	0.776	-1.01	0.885	-1.29	0.071	-1.09
1451036_at	Spg21	spastic paraplegia 21 homolog (human)	-1.01	0.758	-1.02	0.856	-1.01	0.941	-1.27	0.408	-1.08
1455435_s_at	---	---	-1	0.995	-1.03	0.562	-1	0.997	-1.37	0.199	-1.1
1423262_a_at	H3f3a /// LOC6233(	H3 histone, family 3A /// similar to H3 histone, family 3B /// similar to H3 histone, f	-1.01	0.946	-1	0.886	-1.02	0.822	-1.03	0.834	-1.02
1416094_at	Adam9	a disintegrin and metallopeptidase domain 9 (meltrin gamma)	-1.01	0.95	-1.01	0.778	-1	0.997	-1.22	0.248	-1.06
1437952_at	AU040096	expressed sequence AU040096	-3.88	0.026	-2.67	0.016	-2.28	0.229	1.21	0.676	-1.9
1441825_x_at	Ighmbp2	Immunoglobulin mu binding protein 2	-2.78	0.041	-3.42	0.02	-2.36	0.079	1.32	0.594	-1.81
1444636_at	4930592I03Rik	RIKEN cDNA 4930592I03 gene	-3.53	0.386	-3.32	0.354	-1.92	0.098	1.44	0.46	-1.83
1454342_at	C030007D22Rik	RIKEN cDNA C030007D22 gene	-3.06	0.064	-3.29	0.111	-2.08	0.142	1.56	0.489	-1.72
1458434_at	A730009L09Rik	RIKEN cDNA A730009L09 gene	-2.39	0.347	-2.49	0.246	-3.36	0.094	1.26	0.348	-1.75
1421554_at	Lmx1a	LIM homeobox transcription factor 1 alpha	-2.52	0.339	-3.31	0.365	-2.08	0.2	2.04	0.214	-1.47
1432648_at	4930466F19Rik	RIKEN cDNA 4930466F19 gene	-4.79	0.161	-1.85	0.233	-2.26	0.29	1.29	0.745	-1.9
1446030_at	---	Transcribed locus	-1.98	0.162	-2.62	0.019	-2.92	0.001	3.54	0	-1
1459633_at	---	---	-2.29	0.394	-3.99	0.072	-1.81	0.229	2.03	0.255	-1.51
1433153_at	9030201C23Rik	RIKEN cDNA 9030201C23 gene	-3.07	0.034	-1.59	0.16	-3.44	0.009	1.2	0.794	-1.72
1450839_at	D0H4S114	DNA segment, human D4S114	-1.16	0.748	-4.7	0.021	-5.42	0.005	1.06	0.729	-2.56
1440705_at	AU021720	expressed sequence AU021720	-3.05	0.029	-4.24	0.009	-1.44	0.499	1.73	0.464	-1.75
1445454_at	D2Ertd282e	DNA segment, Chr 2, ERATO Doi 282, expressed	-2.22	0.107	-2.94	0.17	-2.14	0.114	1.68	0.147	-1.4
1432680_at	9130009M17Rik	RIKEN cDNA 9130009M17 gene	-2.48	0.008	-2	0.336	-2.78	0.064	2.83	0.339	-1.11
1457261_at	A930025H08Rik	RIKEN cDNA A930025H08 gene	-2.49	0.413	-2.52	0.046	-2.07	0.226	3.84	0.002	-0.81
1458612_at	A930006A01Rik	RIKEN cDNA A930006A01 gene	-4.1	0.009	-2.92	0.021	-1.4	0.493	1.23	0.566	-1.8
1445496_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	-2.12	0.015	-2.36	0.031	-2.39	0.032	1.19	0.254	-1.42
1457104_at	D930036F22Rik	RIKEN cDNA D930036F22 gene	-2.66	0.154	-2.38	0.028	-1.92	0.149	1.04	0.918	-1.48
1422328_at	Gja10	gap junction membrane channel protein alpha 10	-3.43	0.01	-1.6	0.507	-2.38	0.12	1.65	0.165	-1.44

1454228_a_at	Ccdc77	coiled-coil domain containing 77	-2.51	0.009	-3.06	0.137	-1.63	0.485	1.31	0.441	-1.47
1441012_at	Hip2	Huntingtin interacting protein 2	-4.03	0.092	-2.13	0.519	-1.6	0.197	2.54	0.326	-1.3
1453503_at	9230117E20Rik	RIKEN cDNA 9230117E20 gene	-3.09	0.052	-2.84	0.097	-1.48	0.149	1.14	0.572	-1.57
1417899_at	Zp3r	zona pellucida 3 receptor	-2.52	0.065	-4.09	0.087	-1.4	0.43	3.65	0.004	-1.09
1442589_at	Trpc5	Transient receptor potential cation channel, subfamily C, member 5	-3.2	0.096	-3.74	0.024	-1.28	0.474	1.38	0.419	-1.71
1458699_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	-2.98	0.38	-2	0.221	-1.89	0.123	4.28	0.168	-0.65
1442097_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630011L(	-2.29	0.128	-3.07	0.002	-1.65	0.5	1.15	0.814	-1.46
1446492_at	Tmem132d	transmembrane protein 132D	-3.38	0.095	-1.86	0.344	-1.86	0.03	1.29	0.211	-1.45
1421984_at	Stc1	stanniocalcin 1	-2.07	0.102	-2.55	0.012	-1.99	0.101	3.82	0.008	-0.7
1444327_at	Edd1	E3 ubiquitin protein ligase, HECT domain containing, 1	-2.41	0.43	-3.91	0.001	-1.4	0.278	1.27	0.712	-1.61
1430973_at	Zfp558	zinc finger protein 558	-3.82	0.002	-1.66	0.331	-1.89	0.246	1.37	0.664	-1.5
1453935_a_at	Ccdc7	coiled-coil domain containing 7	-2.07	0.156	-2.1	0.413	-2.32	0.017	2.02	0.121	-1.12
1432980_at	5730420F10Rik	RIKEN cDNA 5730420F10 gene	-1.39	0.526	-2.37	0.242	-3.97	0.055	2.22	0.265	-1.38
1451898_a_at	Sema6c	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-4.47	0.002	-1.58	0.233	-1.87	0.169	2.39	0.064	-1.38
1449493_at	Insl5	insulin-like 5	-1.96	0.126	-2.49	0.004	-2.05	0.395	1.29	0.58	-1.3
1447769_x_at	Amigo2	adhesion molecule with Ig like domain 2	-1.37	0.282	-1.89	0.348	-7.1	0.067	1.12	0.759	-2.31
1419229_at	Rhox4b /// Rhox4e	reproductive homeobox 4B /// reproductive homeobox 4E /// reproductive homeot	-3.61	0.054	-2.39	0.039	-1.41	0.119	1.15	0.796	-1.56
1433276_at	4930556A12Rik	RIKEN cDNA 4930556A12 gene	-4.14	0.341	-2.09	0.099	-1.44	0.461	1.06	0.904	-1.65
1421591_at	Cylc1	cylicin, basic protein of sperm head cytoskeleton 1	-2.27	0.471	-2.19	0.178	-1.93	0.297	1.38	0.567	-1.25
1433346_at	5830432F11Rik	RIKEN cDNA 5830432F11 gene	-2.24	0.449	-1.87	0.067	-2.26	0.388	1.72	0.23	-1.16
1438909_at	Sccpdh	saccharopine dehydrogenase (putative)	-1.79	0.269	-2.44	0.171	-2.19	0.037	1.78	0.101	-1.16
1422248_at	Irs4 /// LOC669982	insulin receptor substrate 4 /// similar to insulin receptor substrate 4	-2.35	0.344	-2.05	0.088	-1.95	0.172	2.78	0.375	-0.89
1439720_at	Ralgps1	Ral GEF with PH domain and SH3 binding motif 1	-3.83	0.393	-2.39	0.2	-1.33	0.563	1.56	0.373	-1.5
1454190_at	9630013K17Rik	RIKEN cDNA 9630013K17 gene	-1.66	0.055	-2.79	0.026	-2.13	0.258	1.03	0.943	-1.39
1460368_at	Mpp4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)	-2.42	0.171	-2.2	0.187	-1.77	0.389	1.84	0.282	-1.14
1442559_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-2.78	0.26	-1.4	0.299	-2.78	0	1.12	0.828	-1.46
1431373_at	Pop5	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)	-5.01	0.005	-1.57	0.608	-1.67	0.172	2.73	0.287	-1.38
1436643_x_at	Hamp2	hepcidin antimicrobial peptide 2	-2.77	0.027	-2.13	0.321	-1.65	0.034	16.19	0.142	2.41
1445262_at	---	---	-2.97	0.064	-1.45	0.572	-2.43	0.03	1.64	0.573	-1.3
1442565_at	Pcdh10	protocadherin 10	-1.97	0.312	-2.25	0.113	-2.03	0.298	2.56	0.223	-0.92
1417746_at	Cplx1	complexin 1	-1.34	0.532	-4.87	0.001	-2	0.392	1.09	0.726	-1.78
1439409_x_at	Tyrp1	tyrosinase-related protein 1	-1.44	0.316	-3.14	0.035	-2.28	0.267	1.27	0.336	-1.4
1419904_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-2.07	0.24	-1.93	0.174	-2.18	0.016	1.9	0.13	-1.07
1447044_at	---	---	-2.2	0.123	-2.11	0.38	-1.87	0.371	2.25	0.345	-0.98
1440118_at	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed	-3.82	0.443	-2.72	0.138	-1.2	0.134	1.2	0.524	-1.63
1459081_at	1700007B14Rik	RIKEN cDNA 1700007B14 gene	-3.23	0.068	-3.54	0.024	-1.15	0.764	2.49	0.294	-1.36
1431438_at	C530001K22Rik	RIKEN cDNA C530001K22 gene	-1.72	0.191	-2.52	0.057	-2.05	0.231	1.18	0.281	-1.28
1440232_at	LOC622645 /// LOC	similar to KIAA1913 /// similar to KIAA1913	-3.39	0.014	-1.82	0.072	-1.6	0.226	1.64	0.041	-1.29
1446263_at	AU015619	expressed sequence AU015619	-2.77	0.38	-1.29	0.66	-2.91	0.151	1.27	0.61	-1.43
1460470_at	Acoxl	acyl-Coenzyme A oxidase-like	-1.56	0.569	-2.68	0.031	-2.15	0.005	1.07	0.918	-1.33
1446686_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.75	0.374	-2.45	0.161	-1.98	0.074	1.54	0.339	-1.16
1454308_at	LOC385154 /// LOC	similar to development- and differentiation-enhancing factor 2; PYK2 C terminus-a	-3.63	0.136	-1.19	0.627	-2.7	0.048	1.32	0.411	-1.55
1431581_at	4922502B01Rik	RIKEN cDNA 4922502B01 gene	-1.59	0.12	-2.7	0.08	-2.03	0.279	1.92	0.069	-1.1
1428055_at	Rian	RNA imprinted and accumulated in nucleus	-1.85	0.504	-4.59	0.145	-1.35	0.627	1.51	0.615	-1.57
1442081_at	AU017455	Expressed sequence AU017455	-2.27	0.116	-2.04	0.239	-1.74	0.201	2.03	0.097	-1
1456268_at	Cks1b	CDC28 protein kinase 1b	-2.68	0.054	-1.39	0.419	-2.42	0.225	1.12	0.776	-1.34
1429997_at	4832441B07Rik	RIKEN cDNA 4832441B07 gene	-2.1	0.101	-1.96	0.479	-1.93	0.042	1.48	0.507	-1.13
1420137_at	---	---	-2.56	0.17	-2.14	0.047	-1.53	0.365	2.04	0.249	-1.05
1420759_s_at	Zfy1 /// Zfy2	zinc finger protein 1, Y linked /// zinc finger protein 2, Y linked	-2.35	0.488	-2.72	0.205	-1.39	0.275	1.18	0.631	-1.32
1442091_at	---	Transcribed locus	-3.53	0.028	-1.42	0.467	-1.9	0.032	1.36	0.424	-1.37
1442318_at	---	Transcribed locus	-2.39	0.293	-2.73	0.085	-1.37	0.381	1.35	0.62	-1.28
1439854_at	Hrk	harakiri, BCL2 interacting protein (contains only BH3 domain)	-2.6	0.473	-1.9	0.143	-1.65	0.415	1.85	0.521	-1.07
1449703_at	Zfand2a	Zinc finger, AN1-type domain 2A	-1.93	0.512	-1.54	0.471	-2.85	0.138	2.08	0.032	-1.06

1433323_at	4930529F21Rik	RIKEN cDNA 4930529F21 gene	-1.48	0.108	-3.04	0.166	-1.94	0.164	1.45	0.46	-1.25
1453637_at	5430410E06Rik	RIKEN cDNA 5430410E06 gene	-1.74	0.255	-2.53	0.048	-1.79	0.183	1.7	0.267	-1.09
1440949_at	---	---	-2.51	0.2	-1.85	0.161	-1.69	0.088	1.02	0.974	-1.26
1442600_at	---	---	-2.81	0.069	-2.19	0.125	-1.39	0.33	1.07	0.615	-1.33
1458687_at	LOC668172 /// LOC	hypothetical protein LOC668172 /// hypothetical protein LOC672498 /// hypothetic	-3.63	0.299	-1.84	0.406	-1.4	0.347	1.05	0.871	-1.46
1454600_at	9530086P17Rik	RIKEN cDNA 9530086P17 gene	-3.06	0.026	-2.71	0.18	-1.19	0.665	1.18	0.776	-1.44
1441602_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	-4.24	0.022	-3.05	0.187	-1.03	0.943	1.13	0.841	-1.8
1446009_at	LOC240444	Similar to Potassium voltage-gated channel subfamily G member 2 (Voltage-gate	-2.58	0.163	-1.91	0.028	-1.59	0.334	1.27	0.423	-1.2
1432175_at	5430434I15Rik	RIKEN cDNA 5430434I15 gene	-1.43	0.467	-3.21	0.006	-1.89	0.133	1.83	0.028	-1.17
1432364_at	4930556N13Rik	RIKEN cDNA 4930556N13 gene	-1.35	0.75	-2.2	0.002	-2.84	0.148	1.36	0.642	-1.26
1444964_at	Csnk1g1	casein kinase 1, gamma 1	-5.44	0.054	-1.24	0.738	-1.79	0.043	1.55	0.157	-1.73
1444957_at	Pspc1	Paraspeckle protein 1	-3.47	0.123	-1.08	0.908	-2.95	0.077	1.3	0.618	-1.55
1445851_at	---	---	-2.23	0.092	-1.88	0.103	-1.75	0.258	1.27	0.679	-1.15
1456982_at	6430562O15Rik	RIKEN cDNA 6430562O15 gene	-2.01	0.219	-1.5	0.031	-2.53	0.085	1.08	0.896	-1.24
1444146_at	Rnf20	ring finger protein 20	-2.26	0.182	-2.42	0.005	-1.42	0.503	1.1	0.75	-1.25
1437011_x_at	Oaz3	ornithine decarboxylase antizyme 3	-1.7	0.446	-2.27	0.174	-1.88	0.271	1.71	0.513	-1.03
1457778_at	Stox2	storkhead box 2	-2.68	0.062	-2.16	0.302	-1.38	0.607	1.01	0.989	-1.3
1431483_at	4930544M13Rik	RIKEN cDNA 4930544M13 gene	-1.72	0.574	-1.7	0.351	-2.54	0.273	1.41	0.614	-1.14
1435215_at	Ap1gbp1	AP1 gamma subunit binding protein 1	-4.08	0.067	-1.54	0.396	-1.49	0.388	1.46	0.331	-1.41
1451808_at	Kcnj4	potassium inwardly-rectifying channel, subfamily J, member 4	-3.12	0.35	-1.6	0.472	-1.6	0.075	1.56	0.435	-1.19
1442345_at	1700031L13Rik	RIKEN cDNA 1700031L13 gene	-2.07	0.531	-2.01	0.431	-1.7	0.371	1.26	0.692	-1.13
1440749_at	Map3k13	Mitogen-activated protein kinase kinase kinase 13	-2.44	0.085	-1.96	0.019	-1.53	0.428	1.12	0.876	-1.2
1429388_at	Nanog	Nanog homeobox	-1.51	0.562	-1.72	0.231	-3.01	0	1.06	0.758	-1.29
1419411_at	Tac2	tachykinin 2	-2.12	0.358	-1.59	0.071	-2.08	0.24	11.54	0.237	1.43
1456725_x_at	Vil2	villin 2	-6.99	0.019	-1.65	0.147	-1.2	0.579	2.07	0.077	-1.94
1430760_a_at	Usp50	ubiquitin specific peptidase 50	-2.42	0.046	-2.12	0.172	-1.43	0.538	1.47	0.598	-1.13
1420805_at	Mylc2pl	myosin light chain 2, precursor lymphocyte-specific	-3.46	0.407	-1.09	0.486	-2.68	0.015	1.65	0.101	-1.39
1445754_at	Acacb	Acetyl-Coenzyme A carboxylase beta	-1.45	0.08	-1.89	0.149	-2.73	0.044	1.35	0.512	-1.18
1432702_at	2810403G07Rik	RIKEN cDNA 2810403G07 gene	-2.76	0.078	-1.52	0.507	-1.76	0.127	1.32	0.592	-1.18
1428525_at	4930488B01Rik	RIKEN cDNA 4930488B01 gene	-4.63	0.004	-1.11	0.734	-2.11	0.156	1.18	0.803	-1.67
1440109_at	D7Ertd413e	DNA segment, Chr 7, ERATO Doi 413, expressed	-1.43	0.642	-3.41	0.071	-1.67	0.24	1.71	0.202	-1.2
1449540_at	Rhox9	reproductive homeobox 9	-3.32	0.023	-1.44	0.24	-1.69	0.301	1.03	0.958	-1.35
1451772_at	Tpcn1	two pore channel 1	-3.08	0.271	-1.76	0.444	-1.42	0.378	2.5	0.036	-0.94
1449873_at	Bmp8a	bone morphogenetic protein 8a	-1.45	0.29	-1.6	0.597	-3.6	0.099	1.07	0.93	-1.39
1446777_at	Spp2	Secreted phosphoprotein 2	-2.24	0.313	-1.96	0.309	-1.55	0.231	2.8	0.001	-0.74
1437081_at	Timp2	Tissue inhibitor of metalloproteinase 2	-1.78	0.26	-2.61	0.361	-1.52	0.325	2.04	0.012	-0.97
1432979_at	Gatad2b	GATA zinc finger domain containing 2B	-2.48	0.457	-2.6	0.112	-1.23	0.748	1.51	0.61	-1.2
1460059_at	Upp2	uridine phosphorylase 2	-1.36	0.018	-2.46	0.27	-2.17	0.288	1.16	0.088	-1.21
1447482_at	5830457H20Rik	RIKEN cDNA 5830457H20 gene	-2.23	0.046	-2.63	0.139	-1.29	0.615	1.06	0.926	-1.27
1446401_at	Atrnl1	Attractin like 1	-2	0.459	-1.77	0.175	-1.85	0.42	2.78	0.037	-0.71
1460504_at	---	---	-2.19	0.463	-1.6	0.523	-1.91	0.161	1.12	0.732	-1.15
1447607_at	---	---	-2.41	0.228	-1.57	0.163	-1.79	0.086	1.39	0.373	-1.1
1439756_at	4933406J04Rik	RIKEN cDNA 4933406J04 gene	-1.71	0.425	-1.79	0.421	-2.16	0.217	1.72	0.377	-0.98
1446629_at	C85938	expressed sequence C85938	-1.29	0.63	-2.52	0.181	-2.27	0.068	1.5	0.629	-1.14
1441000_at	---	PREDICTED: Mus musculus similar to T-cell immunoglobulin and mucin domain	-2.06	0.158	-1.81	0.227	-1.72	0.181	1.03	0.843	-1.14
1442670_at	6430517E21Rik	RIKEN cDNA 6430517E21 gene	-2.09	0.033	-3.82	0.262	-1.14	0.815	1.73	0.25	-1.33
1420955_at	Vsnl1	visinin-like 1	-1.73	0.472	-1.47	0.05	-2.74	0.012	1.55	0.195	-1.1
1450352_at	Mtnr1a	melatonin receptor 1A	-2.13	0.45	-1.98	0.237	-1.53	0.343	1.46	0.527	-1.05
1443548_at	Ank2	Ankyrin 2, brain	-2.1	0.138	-1.81	0.415	-1.67	0.018	1.51	0.526	-1.02
1420145_at	---	Transcribed locus	-2.92	0.106	-1.51	0.254	-1.6	0.097	1.04	0.969	-1.25
1430240_a_at	Clgn	calmegin	-3.03	0.013	-2.11	0.314	-1.21	0.201	1.68	0.535	-1.17
1457103_at	AU046084	expressed sequence AU046084	-1.87	0.351	-1.7	0.194	-1.97	0.193	1.41	0.219	-1.03
1460038_at	Pou3f1	POU domain, class 3, transcription factor 1	-1.82	0.278	-3.27	0.022	-1.29	0.717	1.45	0.485	-1.23

1459183_at	---	PREDICTED: Mus musculus similar to C05G5.5 (LOC230628), mRNA	-1.41	0.38	-2.43	0.109	-1.97	0.032	1.14	0.666	-1.16
1443364_at	---	Transcribed locus	-1.19	0.011	-2.35	0.158	-2.71	0.013	1.41	0.235	-1.21
1459565_at	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	-3.21	0.008	-1.76	0.245	-1.33	0.065	1.65	0.415	-1.16
1441777_at	Emx1	empty spiracles homolog 1 (Drosophila)	-1.43	0.027	-1.8	0.147	-2.64	0.116	1.17	0.785	-1.18
1445472_at	2210412E05Rik ///	RIKEN cDNA 2210412E05 gene /// similar to Carcinoembryonic antigen-related c	-3.69	0.005	-1.9	0.135	-1.19	0.641	1.01	0.985	-1.44
1441961_at	Mtap9	microtubule-associated protein 9	-1.92	0.252	-1.95	0.096	-1.65	0.205	1.66	0.067	-0.97
1442515_at	---	---	-2.54	0.234	-1.67	0.438	-1.55	0.368	1.29	0.501	-1.12
1441421_at	C530030P08Rik	RIKEN cDNA C530030P08 gene	-1.97	0.421	-1.72	0.331	-1.83	0.078	1.74	0.495	-0.94
1419958_at	C330003B14Rik	RIKEN cDNA C330003B14 gene	-3.01	0.295	-1.84	0.494	-1.31	0.4	1.04	0.915	-1.28
1420432_at	Tas1r1	taste receptor, type 1, member 1	-1.47	0.241	-3.26	0.284	-1.52	0.355	1.39	0.384	-1.22
1454508_at	4930485E13Rik	RIKEN cDNA 4930485E13 gene	-2.74	0.102	-1.35	0.646	-1.87	0.246	1.15	0.774	-1.2
1441628_at	Diap3	Diaphanous homolog 3 (Drosophila)	-3.56	0.05	-1.64	0.476	-1.33	0.491	3.57	0.197	-0.74
1454293_at	Rbl1	retinoblastoma-like 1 (p107)	-1.27	0.802	-2.6	0.24	-2.11	0.186	1.12	0.86	-1.22
1433286_at	4833417J16Rik	RIKEN cDNA 4833417J16 gene	-1.43	0.166	-2.01	0.099	-2.22	0.028	1.49	0.236	-1.04
1418306_at	Crybb1	crystallin, beta B1	-1.96	0.531	-1.64	0.457	-1.9	0.155	1.34	0.665	-1.04
1420468_at	Asb17	ankyrin repeat and SOCS box-containing protein 17	-1.65	0.176	-2.38	0.022	-1.61	0.204	5.42	0.158	-0.05
1437700_at	Schip1	Schwannomin interacting protein 1	-1.63	0.03	-2.09	0.132	-1.79	0.044	1.35	0.093	-1.04
1435308_at	Fut9	fucosyltransferase 9	-1.28	0.025	-4.33	0.01	-1.57	0.291	1.21	0.494	-1.49
1459620_at	9130004C02Rik	RIKEN cDNA 9130004C02 gene	-2.59	0.457	-1.76	0.286	-1.43	0.397	1.86	0.144	-0.98
1443211_at	---	---	-1.87	0.634	-4.69	0	-1.1	0.377	1.84	0.401	-1.45
1431297_a_at	4933436C20Rik	RIKEN cDNA 4933436C20 gene	-1.58	0.219	-3.04	0.083	-1.44	0.072	1.58	0.238	-1.12
1444069_at	Auts2	Autism susceptibility candidate 2	-1.19	0.709	-4.63	0.191	-1.68	0.464	1.28	0.493	-1.55
1442713_at	Osbpl10	Oxysterol binding protein-like 10	-2.28	0.27	-1.6	0.043	-1.69	0.246	1.01	0.972	-1.14
1454520_at	5830415B17Rik	RIKEN cDNA 5830415B17 gene	-2.49	0.141	-2.38	0.06	-1.2	0.469	1.11	0.764	-1.24
1432441_at	4933413J09Rik	RIKEN cDNA 4933413J09 gene	-2.13	0.092	-1.62	0.114	-1.76	0.104	1	0.999	-1.13
1419930_at	D15Ertd55e	DNA segment, Chr 15, ERATO Doi 55, expressed	-1.92	0.523	-2.49	0.04	-1.36	0.581	1.96	0.22	-0.95
1444470_x_at	Bmp5	Bone morphogenetic protein 5	-4.18	0.07	1.1	0.838	-3.1	0.003	-3.45	0.091	-2.41
1456838_at	BC072620	cDNA sequence BC072620	-1.88	0.319	-1.57	0.434	-2.03	0.432	2.62	0.057	-0.72
1444649_at	Prkce	Protein kinase C, epsilon	-1.62	0.646	-1.63	0.438	-2.32	0.117	1.51	0.559	-1.02
1460232_s_at	Hsd3b2 /// Hsd3b3	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 ///	-1.19	0.127	-2.2	0.004	-2.71	0.064	1.29	0.71	-1.2
1431379_a_at	Slc13a1	solute carrier family 13 (sodium/sulphate symporters), member 1	-1.03	0.833	-5.14	0.115	-2.04	0.254	1.49	0.461	-1.68
1449064_at	Tdh	L-threonine dehydrogenase	-1.65	0.372	-2.49	0.08	-1.53	0.469	1.42	0.419	-1.06
1430709_at	4833405L11Rik	RIKEN cDNA 4833405L11 gene	-2.42	0.002	-2.68	0.188	-1.14	0.822	2.86	0.223	-0.84
1431695_at	Rph3al	rabphilin 3A-like (without C2 domains)	-1.7	0.11	-1.63	0.407	-2.16	0.245	1.25	0.622	-1.06
1433123_at	2900069G24Rik	RIKEN cDNA 2900069G24 gene	-1.82	0.291	-1.76	0.382	-1.82	0.334	1.85	0.216	-0.89
1432690_at	9030407C09Rik	RIKEN cDNA 9030407C09 gene	-2.16	0.451	-2.15	0.083	-1.35	0.445	1.9	0.047	-0.94
1429231_at	---	---	-1.82	0.041	-1.27	0.542	-3.01	0.155	1.11	0.858	-1.24
1450302_at	4930470P17Rik	RIKEN cDNA 4930470P17 gene	-1.31	0.105	-3.32	0.028	-1.64	0.115	1.81	0.165	-1.12
1446026_at	Kif13a	Kinesin family member 13A	-1.66	0.439	-1.18	0.767	-4.5	0.012	1.79	0.078	-1.39
1460383_at	Gnao1	guanine nucleotide binding protein, alpha o	-3.17	0.466	-1.12	0.875	-2.12	0.183	1.18	0.208	-1.31
1426028_a_at	Cit	citron	-1.91	0.405	-2.34	0.287	-1.37	0.471	2.53	0.307	-0.77
1426203_at	Krtap16-4	keratin associated protein 16-4	-4.42	0.12	-1.23	0.699	-1.56	0.3	1.84	0.202	-1.34
1457221_at	Igsf11	Immunoglobulin superfamily, member 11	-1.22	0.51	-3.05	0.013	-1.88	0.141	1.23	0.633	-1.23
1449559_at	Msx2	homeo box, msh-like 2	-2.5	0.212	-1.28	0.679	-2	0.031	1.07	0.895	-1.18
1444540_at	---	---	-1.46	0.468	-2.82	0.252	-1.56	0.31	1.02	0.931	-1.2
1432005_at	Dnm2	dynamin 2	-2.11	0.156	-2.3	0	-1.29	0.651	1.57	0.515	-1.03
1441256_at	Wdr45l	Wdr45 like	-2.32	0.031	-1.52	0.534	-1.68	0.383	1.49	0.45	-1.01
1441775_at	Wdr7	WD repeat domain 7	-2.14	0.149	-1.26	0.485	-2.34	0.013	1.25	0.362	-1.12
1443705_at	D14Ertd171e	DNA segment, Chr 14, ERATO Doi 171, expressed	-1.76	0.276	-2.2	0.006	-1.51	0.318	1.81	0.382	-0.91
1458728_at	---	---	-1.55	0.482	-2.45	0.35	-1.57	0.106	1.19	0.531	-1.1
1420672_at	Kcne1	potassium voltage-gated channel, Isk-related subfamily, member 1	-2.79	0.065	-2.06	0.387	-1.18	0.415	1.01	0.986	-1.26
1424561_at	Ece2	endothelin converting enzyme 2	-1.97	0.267	-1.43	0.503	-2.06	0.171	1.24	0.738	-1.06
1442650_at	---	Transcribed locus	-3.08	0.014	-1.32	0.487	-1.63	0.137	1.1	0.701	-1.23

1458539_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	-1.18	0.485	-2.56	0.048	-2.2	0.096	2.06	0.201	-0.97
1439990_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.45	0.348	-1.87	0.356	-2.12	0.313	1.01	0.98	-1.11
1453088_at	6430628N08Rik	RIKEN cDNA 6430628N08 gene	-1.9	0.066	-1.59	0.202	-1.84	0.182	1.06	0.86	-1.07
1427669_a_at	Cit	citron	-2.11	0.113	-2.47	0.208	-1.22	0.504	3.26	0.077	-0.64
1426139_a_at	Ccrl1	chemokine (C-C motif) receptor-like 1	-1.27	0.723	-1.69	0.111	-3.1	0.237	1.13	0.804	-1.23
1433240_at	9430013L17Rik	RIKEN cDNA 9430013L17 gene	-3.79	0.063	1.05	0.92	-2.62	0.017	-3.01	0.06	-2.09
1456035_at	Nxf3	nuclear RNA export factor 3	-1.43	0.608	-2.25	0.256	-1.81	0.107	1.31	0.7	-1.05
1439265_at	Xkr6	X Kell blood group precursor related family member 6 homolog	-1.54	0.137	-1.34	0.72	-3.3	0.049	1.16	0.832	-1.26
1427751_a_at	Krt36	keratin 36	-1.82	0.206	-1.5	0.411	-2.07	0.002	1.12	0.829	-1.07
1424606_at	Cplx3	complexin 3	-3.58	0.166	-3.58	0.007	1.14	0.652	-1.53	0.235	-1.89
1446065_at	Kcnd2	Potassium voltage-gated channel, Shal-related family, member 2	-1.02	0.953	-2.84	0.053	-2.7	0.056	1.69	0.503	-1.22
1446287_at	4931440B09Rik	RIKEN cDNA 4931440B09 gene	-1.2	0.237	-3.64	0.001	-1.69	0.211	1.6	0.38	-1.23
1436202_at	---	---	-1.76	0.129	-1.79	0.053	-1.73	0.025	1.16	0.382	-1.03
1436437_at	Gm97	gene model 97, (NCBI)	-4.09	0.047	-1.85	0.099	-1.09	0.754	1.38	0.52	-1.41
1419576_at	Hoxb13	homeo box B13	-1.57	0.486	-1.73	0.271	-2.04	0.071	1.01	0.989	-1.08
1452570_at	D0Kist5	DNA segment, KIST 5	-2.18	0.225	-1.82	0.227	-1.43	0.384	1.2	0.791	-1.06
1454100_at	4930480E11Rik	RIKEN cDNA 4930480E11 gene	-1.73	0.411	-1.63	0.4	-1.93	0.136	1.59	0.304	-0.93
1434074_x_at	Arf4	ADP-ribosylation factor 4	-3.04	0.145	-1.62	0.63	-1.32	0.278	1.28	0.666	-1.17
1456123_at	AI481121	expressed sequence AI481121	-1.35	0.232	-1.52	0.491	-3.26	0.004	2.01	0.1	-1.03
1429020_at	Pon2	paraoxonase 2	-2.41	0.259	-1.36	0.404	-1.8	0.005	1.56	0.362	-1
1446528_at	Scyl2	SCY1-like 2 (S. cerevisiae)	-1.59	0.272	-2.01	0.073	-1.72	0.226	1.12	0.493	-1.05
1422108_at	Ppp1r3a	protein phosphatase 1, regulatory (inhibitor) subunit 3A	-3.23	0.143	-1.48	0.29	-1.38	0.27	1.55	0.446	-1.13
1419432_at	Spam1	sperm adhesion molecule 1	-2.29	0.059	-1.38	0.366	-1.82	0.252	1.1	0.836	-1.1
1460512_a_at	4930558O21Rik	RIKEN cDNA 4930558O21 gene	-3.06	0.347	1.03	0.919	-2.85	0.025	-1.08	0.893	-1.49
1453900_at	1700018A14Rik	RIKEN cDNA 1700018A14 gene	-2.41	0.098	-1.8	0.458	-1.35	0.668	2.67	0.046	-0.72
1430493_at	2310061G22Rik	RIKEN cDNA 2310061G22 gene	-2.27	0.146	-1.2	0.539	-2.29	0.035	1.16	0.524	-1.15
1430420_at	Alg9	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase	-2.73	0.06	-2.19	0.293	-1.12	0.807	1.77	0.302	-1.07
1440618_at	9130416B15	hypothetical protein 9130416B15	-1.57	0.541	-1.33	0.467	-3.13	0.07	1.11	0.832	-1.23
1443317_at	D6Ertd47e	DNA segment, Chr 6, ERATO Doi 47, expressed	-4.07	0.259	-1.12	0.885	-1.74	0.121	1.47	0.182	-1.37
1432890_at	2610011E03Rik	RIKEN cDNA 2610011E03 gene	-2.1	0.365	-1.29	0.586	-2.17	0.28	1.02	0.973	-1.13
1439003_s_at	1700008F21Rik /// I	RIKEN cDNA 1700008F21 gene /// similar to coiled-coil domain containing 7	-1.47	0.579	-1.81	0.376	-2.09	0.372	1.33	0.53	-1.01
1427547_a_at	Slc26a3	solute carrier family 26, member 3	-1.6	0.15	-1.78	0.348	-1.9	0.064	1.71	0.287	-0.89
1456391_at	Tdrd5	tudor domain containing 5	-1.07	0.836	-3.55	0.091	-1.97	0.129	1.12	0.767	-1.37
1436612_at	2410004I01Rik	RIKEN cDNA 2410004I01 gene	-4.42	0.011	-1.3	0.762	-1.37	0.233	1.25	0.763	-1.46
1442545_at	---	---	-3.05	0.064	-2.32	0.307	-1.04	0.943	1.38	0.373	-1.26
1458498_at	---	---	-1.52	0.519	-1.75	0.409	-2.02	0.169	1.06	0.896	-1.06
1442552_at	Thsd4	thrombospondin, type I, domain containing 4	-2.63	0.359	-1.25	0.368	-1.84	0.077	2.8	0.282	-0.73
1431451_at	Glt6d1	glycosyltransferase 6 domain containing 1	-3.42	0.04	-2.15	0.123	-1.03	0.934	1.05	0.895	-1.39
1438086_at	Npy6r	neuropeptide Y receptor Y6	-1.82	0.187	-3.63	0.071	-1.11	0.889	2.94	0.021	-0.9
1447768_at	Got2 /// LOC64084	glutamate oxaloacetate transaminase 2, mitochondrial /// similar to Aspartate ami	-1.67	0.058	-2.12	0.074	-1.53	0.059	1.39	0.58	-0.98
1440945_at	---	---	-1.26	0.694	-2.72	0.023	-1.74	0.15	1.41	0.299	-1.08
1459421_at	Hkdc1	hexokinase domain containing 1	-1.68	0.539	-1.92	0.298	-1.62	0.263	1.63	0.437	-0.9
1450636_s_at	Akp5	alkaline phosphatase 5	-2.07	0.146	-1.81	0.166	-1.43	0.421	1.65	0.221	-0.92
1443812_x_at	Prkg1	Protein kinase, cGMP-dependent, type I	-1.91	0.193	-1.67	0.157	-1.63	0.15	1.5	0.324	-0.93
1442729_at	D12Ertd553e	DNA segment, Chr 12, ERATO Doi 553, expressed	-5.96	0.003	-1.76	0.468	1	0.996	-1.2	0.364	-1.98
1457853_at	BC021785	CDNA sequence BC021785	-1.25	0.123	-2.27	0.383	-2.02	0.291	1.23	0.317	-1.08
1459577_at	---	---	-2.07	0.011	-1.67	0.288	-1.52	0.329	1.16	0.809	-1.03
1450188_s_at	Lipg	lipase, endothelial	-1.29	0.704	-2.07	0.198	-2.07	0.005	5	0.276	-0.11
1446753_at	---	---	-2.28	0.169	-1.81	0.167	-1.34	0.686	1.09	0.891	-1.08
1440453_at	1700012C15Rik	RIKEN cDNA 1700012C15 gene	-1.83	0.453	-2.52	0.348	-1.25	0.064	1.19	0.401	-1.1
1432675_at	Mdn1	midasin homolog (yeast)	-1.92	0.048	-1.56	0.556	-1.72	0.213	1.54	0.142	-0.92
1450162_at	Dpf3	D4, zinc and double PHD fingers, family 3	-3.23	0.082	-1.26	0.596	-1.56	0.282	2.39	0.126	-0.92
1438997_at	Ern1	Endoplasmic reticulum (ER) to nucleus signalling 1	-1.88	0.179	-1.99	0.189	-1.41	0.485	1.47	0.121	-0.95

1432354_at	1700003H04Rik	RIKEN cDNA 1700003H04 gene	-1.52	0.346	-2.27	0.203	-1.55	0.259	1.52	0.464	-0.96
1453383_at	1700022F17Rik	RIKEN cDNA 1700022F17 gene	-1.19	0.677	-2.91	0.097	-1.77	0.501	1.35	0.593	-1.13
1445287_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330010P	-1.14	0.882	-1.98	0.228	-2.71	0.149	1.59	0.439	-1.06
1432148_at	4930533K18Rik	RIKEN cDNA 4930533K18 gene	-2.23	0.364	-2.09	0.36	-1.22	0.609	1.27	0.09	-1.07
1439139_at	D2Ertd640e	DNA segment, Chr 2, ERATO Doi 640, expressed	-1.33	0.37	-1.58	0.202	-2.76	0.007	1.72	0.034	-0.99
1444423_at	---	Transcribed locus	-2.77	0.472	-1.67	0.229	-1.27	0.602	1.88	0.338	-0.96
1453856_at	Btbd4	BTB (POZ) domain containing 4	-2.07	0.369	-3.36	0.004	-1.03	0.959	2.75	0.02	-0.93
1442794_at	Col8a1	procollagen, type VIII, alpha 1	-1.35	0.569	-1.89	0.311	-2.09	0.057	1.16	0.839	-1.04
1458954_at	---	---	-2.38	0.059	-2.31	0.266	-1.12	0.802	1.02	0.977	-1.2
1437753_at	AW742931	Expressed sequence AW742931	-1.72	0.395	-1.6	0.041	-1.85	0.121	1.21	0.647	-0.99
1421483_at	Lhx4	LIM homeobox protein 4	-2.48	0.348	-1.29	0.426	-1.74	0.284	1.05	0.947	-1.12
1447129_at	---	---	-1.25	0.425	-2.13	0.261	-2.06	0.143	1.02	0.936	-1.11
1438613_at	Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	-1.49	0.541	-1.62	0.312	-2.16	0.122	1.41	0.624	-0.96
1438341_at	Tgm4	transglutaminase 4 (prostate)	-2.67	0.083	-1.33	0.644	-1.6	0.423	1.04	0.946	-1.14
1441189_at	---	Transcribed locus	-1.39	0.679	-1.83	0.181	-2.05	0.114	1.29	0.751	-0.99
1426704_at	Gak	cyclin G associated kinase	-2.17	0.173	-1.3	0.454	-1.91	0.012	1.32	0.736	-1.01
1431122_at	Armc9	armadillo repeat containing 9	-1.74	0.376	-2.49	0.173	-1.28	0.435	1.84	0.3	-0.92
1456508_at	A030001H23Rik	RIKEN cDNA A030001H23 gene	-1.21	0.594	-2.22	0.1	-2.08	0.379	3.93	0.315	-0.4
1444142_at	LOC432591 /// LOC	hypothetical LOC432591 /// hypothetical protein LOC639155	-1.26	0.543	-1.81	0.24	-2.45	0.082	1.6	0.398	-0.98
1433254_at	5033423K11Rik	RIKEN cDNA 5033423K11 gene	-2.24	0.396	-1.05	0.946	-2.76	0.181	2.49	0.045	-0.89
1446734_at	C77438	expressed sequence C77438	-1.97	0.071	-1.4	0.494	-1.86	0.151	2.11	0.102	-0.78
1432529_at	Boll	bol, boule-like (Drosophila)	-1.95	0.029	-1.29	0.603	-2.14	0.016	1.35	0.535	-1.01
1442211_at	C78893	expressed sequence C78893	-1.92	0.166	-2.49	0.169	-1.19	0.674	1.1	0.809	-1.13
1418093_a_at	Egf	epidermal growth factor	-1.36	0.12	-4.43	0.077	-1.25	0.263	1.16	0.564	-1.47
1430203_at	Usp16	ubiquitin specific peptidase 16	-2.09	0.054	-2.71	0.03	-1.1	0.757	1.12	0.703	-1.19
1446170_at	Abcc12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	-1.35	0.168	-2.26	0.377	-1.72	0.264	1.05	0.956	-1.07
1456570_at	---	---	-1.92	0.247	-1.82	0.265	-1.44	0.502	1.32	0.734	-0.97
1437575_at	Mcmdc1	minichromosome maintenance deficient domain containing 1	-1.35	0.695	-1.42	0.426	-3.09	0.027	1.14	0.803	-1.18
1442285_at	Syne2	synaptic nuclear envelope 2	1.01	0.917	-1.79	0.095	-5.07	0.085	-1.17	0.622	-1.76
1421443_at	Gpr110	G protein-coupled receptor 110	-1.03	0.965	-2.99	0.156	-2.18	0.112	1.81	0.076	-1.1
1430174_at	A930010G16Rik	RIKEN cDNA A930010G16 gene	-1.68	0.37	-1.68	0.616	-1.74	0.049	2.86	0.094	-0.56
1428053_at	Gprc6a	G protein-coupled receptor, family C, group 6, member A	-1.25	0.666	-1.41	0.575	-3.88	0.014	1.53	0.182	-1.25
1447875_x_at	AA407452	EST AA407452	-1.32	0.698	-1.42	0.507	-3.29	0.011	1.42	0.509	-1.15
1445409_at	Lrba	LPS-responsive beige-like anchor	-1.42	0.277	-3.91	0.03	-1.24	0.709	1.4	0.653	-1.29
1428363_at	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	-1.27	0.632	-3.94	0.168	-1.38	0.489	1.2	0.591	-1.34
1430904_at	Arfgap3	ADP-ribosylation factor GTPase activating protein 3	-1.34	0.137	-2.09	0.291	-1.84	0.016	1.34	0.108	-0.98
1445908_at	Eif2b5	Eukaryotic translation initiation factor 2B, subunit 5 epsilon	-1.18	0.219	-2.44	0.194	-1.96	0.038	1.3	0.588	-1.07
1445202_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	-3.04	0.266	-1.7	0.267	-1.17	0.83	2.03	0.023	-0.97
1453705_at	B230110C06Rik	RIKEN cDNA B230110C06 gene	-2.15	0.457	-1.35	0.57	-1.78	0.004	1.12	0.706	-1.04
1449739_at	Ptdss1	Phosphatidylserine synthase 1	1.23	0.638	-2.71	0.058	-5.7	0.012	-2.11	0.098	-2.32
1418697_at	Inmt	indolethylamine N-methyltransferase	-2.02	0.225	-1.95	0.161	-1.31	0.003	2.6	0.314	-0.67
1458942_at	C230037E05Rik	RIKEN cDNA C230037E05 gene	-1.47	0.168	-1.85	0.318	-1.81	0.057	1.43	0.462	-0.93
1445887_at	---	---	-1.7	0.08	-1.28	0.587	-2.49	0.008	1.65	0.114	-0.95
1421428_at	Slc5a7	solute carrier family 5 (choline transporter), member 7	-3.19	0.302	-1.41	0.394	-1.34	0.105	1.27	0.622	-1.17
1453697_at	6530402F18Rik	RIKEN cDNA 6530402F18 gene	-3.28	0.059	-2.18	0.014	1.01	0.981	-1.74	0.177	-1.55
1419895_at	AA536748	expressed sequence AA536748	-1.55	0.445	-2.89	0.11	-1.27	0.499	1.23	0.671	-1.12
1436010_at	BC036313	cDNA sequence BC036313	-1.77	0.17	-1.89	0.085	-1.47	0.144	1.14	0.663	-1
1445352_at	---	Transcribed locus	-1.35	0.18	-6.02	0.024	-1.15	0.579	2.56	0.047	-1.49
1420169_at	AA517841	expressed sequence AA517841	-2.51	0.352	-1.34	0.214	-1.58	0.276	1.18	0.27	-1.06
1442220_at	---	---	-2.46	0.153	-1.16	0.619	-1.96	0.306	1.69	0.257	-0.97
1419919_at	4833422M21Rik	RIKEN cDNA 4833422M21 gene	-2.66	0.091	-1.9	0.141	-1.14	0.789	1.82	0.155	-0.97
1440621_at	Kitl	Kit ligand	-1.02	0.851	-2.2	0.127	-2.94	0.002	1.16	0.522	-1.25
1459470_at	Runx1	Runt related transcription factor 1	-1.74	0.076	-1.78	0.087	-1.56	0.137	1.16	0.252	-0.98

1457651_x_at	Rem2	rad and gem related GTP binding protein 2	-2.04	0.532	-1.23	0.562	-2.11	0.227	1.33	0.547	-1.01
1423562_at	Prrt1	proline-rich transmembrane protein 1	-3.27	0.097	-1.49	0.015	-1.25	0.604	1.19	0.757	-1.21
1439877_at	Ext1	Exostoses (multiple) 1	-1.65	0.188	-1.46	0.082	-2.05	0.001	1.24	0.398	-0.98
1441425_at	---	Transcribed locus	-1.34	0.219	-2.05	0.106	-1.84	0.141	1.13	0.247	-1.02
1441283_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	1.04	0.723	-4.38	0.089	-1.95	0.108	-2.16	0.129	-1.86
1421979_at	Phex	phosphate regulating gene with homologies to endopeptidases on the X chromos	-1.35	0.711	-1.23	0.748	-4.44	0.002	1	0.996	-1.5
1417429_at	Fmo1	flavin containing monooxygenase 1	-1.58	0.124	-1.6	0.01	-1.92	0.006	1.38	0.257	-0.93
1445328_at	Col4a4	procollagen, type IV, alpha 4	-1.23	0.419	-2.18	0.452	-1.96	0.039	1.02	0.961	-1.09
1447819_x_at	Col8a1	procollagen, type VIII, alpha 1	-1.52	0.135	-4.58	0.042	-1.11	0.625	1.86	0.208	-1.34
1449792_at	---	---	-1.12	0.858	-2.27	0.282	-2.23	0.208	1.2	0.19	-1.11
1425758_a_at	Impg1	interphotoreceptor matrix proteoglycan 1	-1.42	0.184	-1.44	0.014	-2.58	0.113	1.14	0.403	-1.08
1431918_at	1700036A12Rik	RIKEN cDNA 1700036A12 gene	-2.08	0.137	-1.11	0.856	-2.47	0.055	1.48	0.395	-1.05
1443075_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	-1.28	0.319	-2.27	0.105	-1.78	0.223	1.2	0.808	-1.03
1455034_at	Nr4a2	Nuclear receptor subfamily 4, group A, member 2	-1.53	0.055	-2.2	0.103	-1.47	0.367	2.35	0.053	-0.71
1447684_at	Lzic	Leucine zipper and CTNNBIP1 domain containing	-1.67	0.403	-1.62	0.379	-1.74	0.052	1.49	0.301	-0.89
1446264_at	---	---	-1.44	0.256	-2.47	0.01	-1.45	0.095	1.55	0.32	-0.95
1432071_at	6330437I11Rik	RIKEN cDNA 6330437I11 gene	-1.15	0.452	-2.83	0.259	-1.77	0.226	1.44	0.319	-1.08
1449654_s_at	C77545	expressed sequence C77545	-1.61	0.003	-1.82	0.412	-1.61	0.215	1.08	0.859	-0.99
1459468_at	C79743	expressed sequence C79743	-2.08	0.189	-1.88	0.101	-1.28	0.582	1.26	0.434	-0.99
1432956_at	4930444K16Rik	RIKEN cDNA 4930444K16 gene	-1.53	0.636	-2.66	0.306	-1.31	0.178	1.1	0.923	-1.1
1453465_x_at	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	-1.44	0.153	-2.46	0.004	-1.44	0.202	1.26	0.572	-1.02
1446929_at	Bach2	BTB and CNC homology 2	1.05	0.942	-3.44	0.019	-2.21	0.012	-3.06	0.05	-1.91
1416193_at	Car1	carbonic anhydrase 1	-2.32	0.173	-1.53	0.394	-1.41	0.602	4.83	0.089	-0.11
1444901_at	---	---	1.01	0.991	-2.26	0.199	-2.94	0.122	-1.79	0.258	-1.49
1432412_at	9530004P13Rik	RIKEN cDNA 9530004P13 gene	-2.55	0.089	-1.58	0.363	-1.3	0.359	1.58	0.215	-0.96
1443239_at	Mtap2	Microtubule-associated protein 2	-2.14	0.317	-2.75	0.141	-1.04	0.934	1.38	0.494	-1.14
1453644_at	Obp1a	odorant binding protein Ia	-1.71	0.506	-2.83	0.135	-1.17	0.292	1.96	0.083	-0.94
1453624_at	C430046K18Rik	RIKEN cDNA C430046K18 gene	-1.48	0.169	-1.39	0.544	-2.5	0.051	1.68	0.302	-0.92
1435849_at	6330417G02Rik	RIKEN cDNA 6330417G02 gene	-1.56	0.513	-1.3	0.696	-2.59	0.252	1.12	0.829	-1.08
1444975_at	Chchd6	Coiled-coil-helix-coiled-coil-helix domain containing 6	-1.77	0.18	-1.77	0.321	-1.5	0.164	1.16	0.626	-0.97
1430941_at	Bbs7	Bardet-Biedl syndrome 7	-1.93	0.387	-1.19	0.747	-2.3	0.195	1.3	0.742	-1.03
1446469_at	A030008J09	hypothetical protein A030008J09	-2.56	0.028	-1.2	0.754	-1.74	0.358	1.49	0.574	-1
1430717_at	4930403C10Rik	RIKEN cDNA 4930403C10 gene	-2.19	0.103	-1.9	0.19	-1.23	0.312	1.34	0.707	-0.99
1435310_at	Fbxo7	F-box only protein 7	-1.78	0.312	-1.56	0.286	-1.68	0.067	1.14	0.781	-0.97
1453334_at	B230216N24Rik	RIKEN cDNA B230216N24 gene	-1.71	0.186	-1.46	0.439	-1.88	0.001	1.36	0.601	-0.93
1440541_at	2810442I21Rik	RIKEN cDNA 2810442I21 gene	-1.27	0.524	-2.12	0.24	-1.84	0.264	1.6	0.322	-0.91
1420536_at	Crybb2	crystallin, beta B2	-1.92	0.294	-1.86	0.152	-1.35	0.389	1.36	0.462	-0.94
1453573_at	Hist1h3d	histone1, H3d	-1.96	0.003	-1.84	0.123	-1.34	0.173	1.57	0.223	-0.89
1432393_a_at	5730409G07Rik	RIKEN cDNA 5730409G07 gene	-1.2	0.608	-2.69	0.018	-1.68	0.014	1.07	0.9	-1.12
1432408_a_at	D0Kist2	DNA segment, KIST 2	-2.25	0.155	-1.5	0.192	-1.45	0.555	1.33	0.452	-0.97
1439996_at	Tatdn1	TatD DNase domain containing 1	-2	0.013	-1.52	0.194	-1.54	0.181	1.4	0.004	-0.92
1438210_at	Gpr149	G protein-coupled receptor 149	-3.9	0.007	-1.88	0.063	1.02	0.979	-1.17	0.336	-1.49
1425952_a_at	Gcg	glucagon	-3.72	0.348	-1.91	0.321	1.01	0.983	-2.78	0.155	-1.85
1425056_s_at	Saps2	SAPS domain family, member 2	-1.66	0.021	-1.73	0.156	-1.59	0.145	1.72	0.281	-0.82
1432928_at	4921507K24Rik	RIKEN cDNA 4921507K24 gene	-3.35	0.043	-1.5	0.467	-1.18	0.684	1.32	0.127	-1.18
1443443_at	---	---	-1.51	0.281	-3.16	0.033	-1.2	0.139	1.37	0.61	-1.13
1449458_at	Foxi1	forkhead box I1	-1.63	0.182	-2.16	0.375	-1.37	0.454	2.14	0.004	-0.75
1431300_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	-1.36	0.215	-1.67	0.21	-2.11	0.018	1.91	0.158	-0.81
1446884_at	AU022554	expressed sequence AU022554	-2.57	0.067	-1.16	0.68	-1.8	0.15	1.12	0.836	-1.1
1431489_at	4933432K03Rik	RIKEN cDNA 4933432K03 gene	-2.71	0.094	-1.79	0.438	-1.13	0.815	2.22	0.14	-0.85
1419995_at	D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	-1.4	0.283	-2.04	0.411	-1.64	0.11	1.16	0.773	-0.98
1433119_at	4930456G14Rik	RIKEN cDNA 4930456G14 gene	-3.13	0.013	-1.38	0.462	-1.3	0.562	1.85	0.114	-0.99
1420689_at	4933415F23Rik	RIKEN cDNA 4933415F23 gene	-1.96	0.43	-1.53	0.581	-1.54	0.335	1.09	0.887	-0.99

1426150_at	Gipc3	GIPC PDZ domain containing family, member 3	-1.43	0.564	-1.66	0.078	-1.95	0.173	1.37	0.373	-0.92
1420252_at	---	---	-1.56	0.442	-1.64	0.208	-1.78	0.136	1.65	0.12	-0.83
1431877_a_at	Grhl2	grainyhead-like 2 (Drosophila)	-1.79	0.375	-1.35	0.275	-1.93	0	2.3	0.286	-0.69
1458356_at	---	---	-1.24	0.033	-4.28	0.095	-1.29	0.596	1.03	0.676	-1.44
1425013_at	Slc25a2	solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 2	-1.67	0.216	-2.06	0.024	-1.36	0.29	1.09	0.798	-1
1444778_at	3-Sep	septin 3	-2.06	0.238	-1.02	0.96	-2.83	0.016	1.02	0.966	-1.22
1450584_at	Hoxd11	homeo box D11	-1.83	0.01	-2.05	0.085	-1.28	0.639	1.03	0.972	-1.03
1455907_x_at	Phox2b	paired-like homeobox 2b	-2.34	0.249	-1.21	0.51	-1.76	0.265	1.45	0.492	-0.97
1440425_at	---	---	-2.72	0.027	-1.62	0.031	-1.2	0.741	1.84	0.443	-0.92
1432808_at	5830426K05Rik	RIKEN cDNA 5830426K05 gene	-1.43	0.634	-2.39	0.18	-1.42	0.464	4.19	0.357	-0.26
1430666_at	LOC665270	similar to phospholipase B	-2.01	0.351	-1.46	0.494	-1.57	0.204	1.32	0.199	-0.93
1440009_at	Olfr78	olfactory receptor 78	-2.96	0.342	1.13	0.814	-2.85	0.297	-1.65	0.566	-1.58
1433175_at	---	---	-1.84	0.184	-1.16	0.823	-2.39	0.236	1.92	0.179	-0.87
1442904_at	LOC622118	similar to RNA (guanine-9-) methyltransferase domain containing 2	-1.82	0.496	-2.37	0.406	-1.17	0.339	1.43	0.526	-0.98
1444639_at	Nphp4	Nephronophthisis 4 (juvenile) homolog (human)	-4.13	0.012	-2.34	0.406	1.15	0.776	-1.52	0.529	-1.71
1418917_at	Hebp2	heme binding protein 2	-1.28	0.659	-2.47	0.23	-1.57	0.152	1.15	0.692	-1.04
1421218_at	Bche	butyrylcholinesterase	-1.51	0.382	-1.96	0.188	-1.53	0.344	1.16	0.681	-0.96
1449605_at	---	Transcribed locus	-1.93	0.248	-1.45	0.224	-1.62	0.51	1.03	0.86	-0.99
1456364_at	C230057M02Rik	RIKEN cDNA C230057M02 gene	-2.75	0.118	-2.56	0.117	1.07	0.87	-2.51	0.067	-1.69
1446742_at	Nfia	Nuclear factor I/A	-2.24	0.539	-2.42	0.034	-1.04	0.907	1.62	0.423	-1.02
1456417_at	Zic4	zinc finger protein of the cerebellum 4	-1.73	0.173	-1.73	0.475	-1.5	0.508	4.62	0.011	-0.08
1424437_s_at	Abcg4	ATP-binding cassette, sub-family G (WHITE), member 4	-2.96	0.037	-1.2	0.49	-1.52	0.377	7	0.162	0.33
1450979_at	Ceacam14	CEA-related cell adhesion molecule 14	-1.7	0.169	-2.63	0.118	-1.16	0.801	1	0.995	-1.12
1457798_at	C130039O16Rik	RIKEN cDNA C130039O16 gene	-1.5	0.275	-2.55	0.002	-1.29	0.594	1.22	0.716	-1.03
1438779_at	Col4a3	procollagen, type IV, alpha 3	-1.37	0.284	-1.82	0.009	-1.8	0.095	1.28	0.294	-0.93
1458775_at	1700041E20Rik	RIKEN cDNA 1700041E20 gene	-1.75	0.44	-1.18	0.791	-2.39	0.149	2.29	0.31	-0.76
1437778_at	Rbm15b	RNA binding motif protein 15B	-3.42	0.029	-1.29	0.58	-1.3	0.393	1.67	0.406	-1.08
1445675_at	---	Transcribed locus	-2.09	0.448	-1.81	0.197	-1.24	0.29	1.46	0.471	-0.92
1446181_at	C85699	expressed sequence C85699	-3.7	0.462	-1.07	0.733	-1.58	0.084	1.52	0.49	-1.21
1420988_at	Polh	polymerase (DNA directed), eta (RAD 30 related)	-1.86	0.311	-1.42	0.606	-1.68	0.166	2.65	0.134	-0.58
1444481_at	---	---	-1.8	0.569	-1.62	0.182	-1.5	0.188	1.45	0.357	-0.87
1450794_at	Avp	arginine vasopressin	-2.43	0.13	-1.14	0.758	-1.82	0.164	1.3	0.505	-1.02
1433217_at	4930566N20Rik	RIKEN cDNA 4930566N20 gene	-1.79	0.549	-2.11	0.515	-1.24	0.696	1.22	0.636	-0.98
1453610_at	4931406B18Rik	RIKEN cDNA 4931406B18 gene	-1.43	0.085	-1.82	0.114	-1.69	0.239	1.39	0.091	-0.89
1445633_at	Rex2	Reduced expression 2	-1.81	0.315	-2.45	0.05	-1.13	0.797	1.51	0.226	-0.97
1448000_at	Cdca3	cell division cycle associated 3	-1.7	0.202	-1.97	0.223	-1.34	0.154	1.81	0.188	-0.8
1446665_at	C80918	expressed sequence C80918	-1.12	0.517	-2.12	0.102	-2.09	0.122	1.02	0.969	-1.08
1432166_at	E130018N17Rik	RIKEN cDNA E130018N17 gene	-4.48	0.066	-1.15	0.672	-1.32	0.468	3.2	0.219	-0.94
1420358_at	Krtap13	keratin associated protein 13	-4.46	0.008	-3.2	0.003	1.31	0.701	-2.05	0.109	-2.1
1417518_at	Plagl2	pleiomorphic adenoma gene-like 2	-2.87	0.015	-1.31	0.524	-1.35	0.502	1.08	0.782	-1.11
1445873_at	Tfdp2	Transcription factor Dp 2	-2.07	0.132	-1.34	0.269	-1.62	0.097	3.8	0.158	-0.31
1443332_at	Slc12a2	Solute carrier family 12, member 2	-1.33	0.225	-1.95	0.482	-1.71	0.179	1.33	0.523	-0.91
1425741_at	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	-2.05	0.191	-1.02	0.958	-2.63	0.182	1.01	0.99	-1.17
1425563_s_at	Pcdh10	protocadherin 10	-2.8	0.031	-3.63	0.277	1.22	0.659	-1.33	0.297	-1.63
1422100_at	Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	-3.16	0.414	-1.34	0.473	-1.27	0.702	2.46	0.098	-0.83
1441205_at	---	---	-1.56	0.298	-1.02	0.942	-4.25	0.027	1.19	0.683	-1.41
1423001_at	Spred2	sprouty-related, EVH1 domain containing 2	-1.28	0.65	-1.93	0.408	-1.8	0.445	2.03	0.191	-0.75
1459075_at	AU022479	expressed sequence AU022479	-1.14	0.676	-1.42	0.312	-3.69	0.031	1.38	0.678	-1.22
1418754_at	Adcy8	adenylate cyclase 8	-1.37	0.375	-1.49	0.439	-2.2	0.025	2.92	0.134	-0.54
1444874_at	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), i	-1.27	0.122	-2.47	0.137	-1.51	0.109	2.09	0.084	-0.79
1444047_at	Kctd8	Potassium channel tetramerisation domain containing 8	-1.81	0.284	-1.11	0.644	-2.48	0.023	1.04	0.94	-1.09
1458725_at	---	---	-1.89	0.498	-2.09	0.192	-1.18	0.753	2.89	0	-0.57
1423434_at	Tead1	TEA domain family member 1	-3.22	0.085	-1.69	0.343	-1.05	0.912	1.93	0.362	-1.01

1433284_at	4921522E08Rik	RIKEN cDNA 4921522E08 gene	-3.29	0.002	-2.04	0.027	1.06	0.886	-1.32	0.564	-1.4
1429744_at	4931407G18Rik	RIKEN cDNA 4931407G18 gene	-1.48	0.297	-2.49	0.337	-1.29	0.396	1.1	0.715	-1.04
1418094_s_at	Car4	carbonic anhydrase 4	-1.27	0.078	-1.92	0.09	-1.82	0.006	1.41	0.213	-0.9
1418139_at	Dcx	doublecortin	-1.52	0.607	-1.64	0.421	-1.7	0.525	1.04	0.936	-0.95
1432319_at	1700085C21Rik	RIKEN cDNA 1700085C21 gene	-4.18	0.002	1.34	0.523	-3.54	0.07	-1.02	0.953	-1.85
1457979_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A23001	-2.39	0.503	-3.36	0.198	1.14	0.741	-1.06	0.922	-1.42
1426603_at	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	-1.94	0.302	-1.63	0.428	-1.36	0.331	1.55	0.134	-0.85
1431486_at	4930503E24Rik	RIKEN cDNA 4930503E24 gene	-1.37	0.681	-2.46	0.247	-1.37	0.59	1.07	0.928	-1.03
1422361_at	Tlm	T lymphoma oncogene	-1.44	0.588	-1.5	0.389	-1.97	0.01	1.5	0.139	-0.85
1457804_at	Stx8	Syntaxin 8	-1.34	0.004	-1.19	0.722	-3.61	0.008	1.71	0.43	-1.11
1445089_at	D16Ertd778e	DNA segment, Chr 16, ERATO Doi 778, expressed	-2.03	0.334	-1.45	0.05	-1.47	0.185	2.04	0.045	-0.73
1432812_at	4930554P06Rik	RIKEN cDNA 4930554P06 gene	-1.96	0.46	-1.13	0.441	-2.12	0.213	1.41	0.433	-0.95
1445548_at	Rdx	Radixin	-2.69	0.034	-1.67	0.492	-1.12	0.552	1.72	0.269	-0.94
1440601_at	---	Transcribed locus	-1.19	0.337	-1.72	0.144	-2.23	0.216	1.14	0.831	-1
1449717_at	---	---	-1.38	0.57	-1.41	0.069	-2.31	0.226	1.16	0.331	-0.98
1456190_a_at	Acsm2	Acyl-CoA synthetase medium-chain family member 2	-1.16	0.043	-3.01	0.059	-1.48	0.104	1.16	0.566	-1.12
1436238_at	Lgi3	leucine-rich repeat LGI family, member 3	-2.34	0.484	-1.39	0.518	-1.39	0.332	1.01	0.97	-1.03
1445139_at	AV312086	Expressed sequence AV312086	-4.17	0.231	-1.37	0.256	-1.11	0.731	1.08	0.9	-1.39
1452229_at	Camta2	Calmodulin binding transcription activator 2	-1.62	0.346	-1.61	0.384	-1.59	0.233	1.08	0.913	-0.93
1420437_at	Indo	indoleamine-pyrrole 2,3 dioxygenase	-1.36	0.384	-2.63	0.007	-1.33	0.34	1.03	0.932	-1.07
1426034_a_at	Runx2	runt related transcription factor 2	-1.14	0.863	-3.42	0.21	-1.43	0.306	1.31	0.483	-1.17
1443828_x_at	Herpud2	HERPUD family member 2	-1.67	0.207	-1.99	0.138	-1.3	0.667	1.6	0.53	-0.84
1428209_at	Bex4	brain expressed gene 4	-1.45	0.068	-1.36	0.277	-2.23	0.013	5.13	0.218	0.02
1444515_at	Myo1d	Myosin ID	-1.71	0.159	-1.45	0.185	-1.67	0.036	3.16	0.14	-0.42
1457640_x_at	---	Transcribed locus	-1.8	0.153	-1.73	0.267	-1.35	0.265	1.41	0.433	-0.87
1438077_at	Nalp4a	NACHT, leucine rich repeat and PYD containing 4A	-1.95	0.402	-1.12	0.863	-2.13	0.088	1.18	0.792	-1
1443374_at	---	Transcribed locus	-1.21	0.739	-2.4	0.207	-1.59	0.012	1.18	0.158	-1
1417504_at	Calb1	calbindin-28K	-1.43	0.039	-6.69	0.123	1.03	0.944	-1.21	0.619	-2.07
1457931_at	---	---	-1.84	0.367	-1.27	0.361	-1.85	0.192	1.77	0.242	-0.79
1442696_at	Dhcr7	7-dehydrocholesterol reductase	1.17	0.773	-2.89	0.028	-2.76	0.12	-1.03	0.948	-1.38
1428002_at	Saal1	serum amyloid A-like 1	-2.1	0.078	-1.26	0.651	-1.65	0.227	1.39	0.419	-0.9
1458670_at	Adarb2	Adenosine deaminase, RNA-specific, B2	-2.03	0.064	1.09	0.919	-3.46	0	-1.56	0.593	-1.49
1421696_at	Pkhd1l1	polycystic kidney and hepatic disease 1-like 1	-1.16	0.668	-1.72	0.426	-2.3	0.196	4.78	0.157	-0.1
1460531_at	2900069M18Rik	RIKEN cDNA 2900069M18 gene	-1.19	0.54	-2.07	0.248	-1.8	0.019	1.4	0.384	-0.92
1446675_at	Adk	adenosine kinase	-1.68	0.51	-1.42	0.314	-1.73	0.383	1.19	0.771	-0.91
1418875_at	Syngr4	synaptogyrin 4	-2.35	0.187	-1.04	0.94	-2.02	0.014	1.22	0.627	-1.05
1430859_at	5330427O13Rik	RIKEN cDNA 5330427O13 gene	-1.57	0.339	-1.41	0.495	-1.89	0.176	1.32	0.492	-0.89
1441114_at	9330156P08Rik	RIKEN cDNA 9330156P08 gene	-1.1	0.385	-1.8	0.011	-2.39	0.031	2.43	0.252	-0.72
1438332_at	Slc22a6	solute carrier family 22 (organic anion transporter), member 6	-1.19	0.445	-1.62	0.482	-2.37	0.219	2.14	0.19	-0.76
1450550_at	Il5	interleukin 5	-1.83	0.229	-1.39	0.23	-1.62	0.344	1.89	0.188	-0.74
1447216_at	Nrxn1	neurexin I	-1.51	0.722	-1.42	0.419	-1.95	0.009	1.23	0.393	-0.91
1458341_x_at	---	---	1.04	0.732	-1.85	0.047	-3.38	0.033	-2.18	0.153	-1.59
1444694_at	Tuft1	Tuftelin 1	-1.37	0.705	-2.46	0.174	-1.35	0.615	1.38	0.413	-0.95
1458348_at	---	Transcribed locus	-1.42	0.15	-1.5	0.326	-1.97	0.167	1.09	0.823	-0.95
1458272_at	---	Transcribed locus	-1.53	0.448	-5.25	0.002	1.04	0.945	-1.35	0.342	-1.77
1420019_at	Tspan8	Tetraspanin 8	-1.12	0.717	-2.06	0.208	-1.97	0.017	2.14	0.219	-0.75
1454158_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-1.46	0.526	-1.64	0.011	-1.7	0.033	1.83	0.314	-0.74
1456823_at	Gm70	gene model 70, (NCBI)	-2.22	0.259	-2.4	0.146	1.02	0.961	-1.49	0.124	-1.27
1439809_at	Pramel7	preferentially expressed antigen in melanoma like 7	-1.7	0.305	-2.43	0.08	-1.13	0.85	1.65	0.218	-0.9
1441715_at	B130055D15Rik	RIKEN cDNA B130055D15 gene	-1.85	0.209	-2.06	0.341	-1.16	0.413	1.07	0.829	-1
1449989_at	Mcpt2	mast cell protease 2	-3.39	0.001	-1.05	0.954	-1.58	0.483	1.25	0.69	-1.19
1420211_at	---	---	-1.64	0.475	-1.81	0.255	-1.38	0.441	1.35	0.246	-0.87
1444295_at	Neo1	neogenin	-1.15	0.739	-2.07	0.229	-1.88	0.132	1.6	0.036	-0.87

1445811_at	Nedd8	Neural precursor cell expressed, developmentally down-regulated gene 8	-1.37	0.369	-1.77	0.086	-1.69	0.388	1.21	0.553	-0.91
1441179_at	9530020O07Rik	RIKEN cDNA 9530020O07 gene	-1.36	0.538	-1.58	0.287	-1.93	0.205	1.41	0.648	-0.86
1460296_a_at	Fgf22	fibroblast growth factor 22	-1.54	0.674	-1.36	0.658	-1.99	0.165	1.02	0.935	-0.97
1444225_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	-1.22	0.457	-2.92	0.21	-1.38	0.438	1.18	0.734	-1.08
1418882_at	Nalp5	NACHT, leucine rich repeat and PYD containing 5	-3.05	0.329	-2.17	0.249	1.1	0.685	-1.1	0.816	-1.3
1429263_at	4933425D22Rik	RIKEN cDNA 4933425D22 gene	-1.88	0.108	-2.05	0.12	-1.15	0.135	1.34	0.608	-0.94
1429975_at	4931432M23Rik ///	RIKEN cDNA 4931432M23 gene /// similar to plasma kallikrein-like protein 4	-1.18	0.605	-3.7	0.001	-1.3	0.626	1.48	0.07	-1.17
1430803_at	Lin28b	lin-28 homolog B (C. elegans)	-1.11	0.901	-2.39	0.123	-1.76	0.228	2.45	0.098	-0.7
1420146_at	---	---	-2.03	0.348	-1.55	0.392	-1.33	0.141	1.34	0.565	-0.89
1447661_at	---	Transcribed locus	-1.37	0.704	-1.94	0.337	-1.56	0.251	2.23	0.012	-0.66
1438851_x_at	Cldn1	claudin 1	-1.39	0.632	-3.07	0.018	-1.18	0.725	2.32	0.023	-0.83
1420698_at	Gpx5	glutathione peroxidase 5	-1.76	0.455	-3.73	0.297	1.05	0.663	-1.22	0.185	-1.42
1422890_at	Pcdh18	protocadherin 18	-1.51	0.026	-1.39	0.266	-1.97	0.278	1.11	0.802	-0.94
1434136_at	6332401O19Rik	RIKEN cDNA 6332401O19 gene	-1.27	0.31	-1.47	0.448	-2.35	0.139	1.78	0.255	-0.83
1443652_x_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	-2.47	0.244	-1.56	0.179	-1.18	0.816	2.32	0.344	-0.72
1444630_at	D2Ertd127e	DNA segment, Chr 2, ERATO Doi 127, expressed	-1.52	0.334	-2.3	0.246	-1.25	0.511	1.51	0.058	-0.89
1446197_at	Lphn3	Latrophilin 3	-1.16	0.532	-4.48	0.034	-1.24	0.688	1.29	0.776	-1.4
1446763_at	Kcnh1	Potassium voltage-gated channel, subfamily H (eag-related), member 1	-1.99	0.348	-1.49	0.467	-1.39	0.117	1.1	0.647	-0.94
1446104_at	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	-1.58	0.205	-1.4	0.121	-1.84	0.198	1.03	0.78	-0.95
1445190_at	Golph4	golgi phosphoprotein 4	-1.79	0.563	-2.11	0.117	-1.16	0.661	1.06	0.939	-1
1445309_at	---	---	-2.4	0.015	-2.16	0.013	1.01	0.966	-1.51	0.417	-1.26
1444953_at	Nucks1	Nuclear casein kinase and cyclin-dependent kinase substrate 1	-2.72	0.098	-1.21	0.728	-1.43	0.337	1.1	0.847	-1.07
1458492_x_at	Hnt	neurotrimin	-1.58	0.543	-1.83	0.084	-1.4	0.242	1.29	0.569	-0.88
1458244_at	Tmco5	transmembrane and coiled-coil domains 5	-1.25	0.716	-1.91	0.069	-1.75	0.174	1.78	0.23	-0.78
1444168_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	-1.1	0.876	-2.68	0.051	-1.63	0.168	1.01	0.97	-1.1
1429697_at	1700023D19Rik	RIKEN cDNA 1700023D19 gene	-1.51	0.434	-1.45	0.188	-1.85	0.213	1.7	0.465	-0.78
1446419_at	---	---	1.16	0.548	-3.41	0.168	-2.28	0.367	-1.57	0.187	-1.52
1443912_at	---	---	-2.4	0.089	-1.3	0.606	-1.41	0.41	2.81	0.188	-0.58
1433483_s_at	C86187	expressed sequence C86187	-1.07	0.866	-1.79	0.268	-2.46	0.035	1.11	0.343	-1.05
1459149_at	---	---	-1.37	0.141	-1.84	0.23	-1.6	0.15	1.65	0.355	-0.79
1447572_at	1700052I22Rik	RIKEN cDNA 1700052I22 gene	-3.33	0.027	-1.01	0.981	-1.63	0.325	1.51	0.61	-1.12
1442632_at	Centg2	Centaurin, gamma 2	-1.66	0.166	-1.44	0.189	-1.66	0.148	1.25	0.375	-0.88
1460746_at	Fignl1	fidgetin-like 1	-1.49	0.002	-2.01	0.049	-1.37	0.156	1.73	0.335	-0.79
1454513_at	9430031J08Rik	RIKEN cDNA 9430031J08 gene	-2.39	0.174	-1.29	0.616	-1.41	0.123	1.41	0.49	-0.92
1422722_at	1700001K19Rik	RIKEN cDNA 1700001K19 gene	-1.76	0.466	-1.57	0.386	-1.44	0.452	1.07	0.836	-0.92
1458930_at	A4gnt	alpha-1,4-N-acetylglucosaminyltransferase	-1.31	0.094	-1.83	0.168	-1.7	0.184	1.41	0.14	-0.86
1425770_at	A730028G07Rik	RIKEN cDNA A730028G07 gene	-4.91	0.359	-1.86	0.248	1.16	0.283	-1.06	0.777	-1.67
1442742_at	Atp2c1	ATPase, Ca++-sequestering	-1.27	0.222	-3.17	0.113	-1.26	0.249	1.25	0.325	-1.11
1441752_at	Art3	ADP-ribosyltransferase 3	-1.7	0.481	-1.52	0.437	-1.53	0.182	1.74	0.259	-0.75
1445795_at	Chka	choline kinase alpha	-3.08	0.246	1.15	0.646	-2.33	0.034	-1.12	0.857	-1.34
1443725_at	---	---	-2.31	0.12	-1.22	0.606	-1.54	0.35	2.56	0.154	-0.62
1421764_at	V1rd9	vomeronasal 1 receptor, D9	-2.02	0.472	-1.7	0.122	-1.22	0.239	1.76	0.244	-0.79
1425218_a_at	Scgb3a2	secretoglobin, family 3A, member 2	-1.94	0.006	-1.53	0.344	-1.36	0.005	1.2	0.303	-0.91
1429663_at	Katnal2	katanin p60 subunit A-like 2	-2.43	0.209	-1.72	0.161	-1.1	0.593	1.15	0.764	-1.02
1458982_at	AU014965	expressed sequence AU014965	-2.24	0.034	-2.13	0.081	-1.01	0.985	2.85	0.324	-0.63
1456549_at	Gm550	gene model 550, (NCBI)	-1.27	0.614	-1.47	0.33	-2.28	0.013	1.42	0.313	-0.9
1443865_at	Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	1.07	0.931	-3.79	0.016	-1.76	0.043	-3.58	0.011	-2.01
1447899_x_at	Tacstd1	tumor-associated calcium signal transducer 1	-1.5	0.136	-1.85	0.178	-1.43	0.095	1.11	0.743	-0.92
1446656_at	Angpt1	Angiopoietin 1	-1.64	0.05	-1.44	0.035	-1.66	0.05	1.02	0.961	-0.93
1429200_at	Saal1	serum amyloid A-like 1	-1.09	0.927	-2.55	0.151	-1.67	0.012	1.04	0.931	-1.07
1419822_at	Eif3s6	Eukaryotic translation initiation factor 3, subunit 6	-1.55	0.161	-1.33	0.587	-1.96	0.043	1.11	0.886	-0.93
1430765_at	5730521K06Rik	RIKEN cDNA 5730521K06 gene	-1.69	0.535	-2.13	0.052	-1.18	0.613	1.01	0.948	-1
1443194_at	---	---	-1.09	0.919	-1.56	0.514	-2.84	0.015	1.04	0.929	-1.11

1421293_at	Hdgfl1	hepatoma derived growth factor-like 1	1.02	0.976	-2.29	0.034	-2.19	0.045	-1.05	0.944	-1.13
1430877_at	8030425K09Rik	RIKEN cDNA 8030425K09 gene	-2.25	0.477	-1.33	0.052	-1.4	0.471	1.3	0.069	-0.92
1443876_at	Camk2a	Calcium/calmodulin-dependent protein kinase II alpha	-1.45	0.528	-3.95	0.027	-1.03	0.921	1.82	0.28	-1.15
1444990_at	Hivep2	Human immunodeficiency virus type I enhancer binding protein 2	-1.72	0.255	-1.38	0.347	-1.65	0.051	1.41	0.462	-0.83
1442936_at	Dsg3	Desmoglein 3	-3.46	0.028	-1.8	0.069	1.07	0.743	-1.68	0.481	-1.47
1429791_at	A930004D18Rik	RIKEN cDNA A930004D18 gene	-1.86	0.299	-1.01	0.947	-2.56	0.038	1.05	0.932	-1.1
1450094_at	Ranbp17	RAN binding protein 17	-3.13	0.447	-1.37	0.401	-1.16	0.785	1.69	0.447	-0.99
1460111_at	Myt1l	myelin transcription factor 1-like	-2.87	0.002	1.03	0.948	-1.86	0.051	-2.73	0.069	-1.61
1442457_at	---	---	-2.98	0.334	-1.1	0.803	-1.48	0.397	1.57	0.413	-1
1435054_at	Eme1	essential meiotic endonuclease 1 homolog 1 (S. pombe)	-1.6	0.606	-1.48	0.488	-1.62	0.223	2.47	0.276	-0.56
1426309_at	Asb9	ankyrin repeat and SOCS box-containing protein 9	-1.47	0.033	-1.38	0.102	-1.97	0.297	1.1	0.846	-0.93
1435895_at	D930023J12Rik	RIKEN cDNA D930023J12 gene	-2.57	0.165	-1.35	0.556	-1.27	0.376	1.14	0.691	-1.01
1440212_at	---	---	-1.23	0.287	-2.27	0.339	-1.5	0.483	1.04	0.961	-0.99
1439598_at	Foxo3a	Forkhead box O3a	-1.61	0.181	-1.28	0.031	-1.94	0.05	1.64	0.254	-0.8
1458635_at	4832428D23Rik	RIKEN cDNA 4832428D23 gene	-1.92	0.516	1	0.999	-2.53	0.148	-1.39	0.678	-1.21
1454417_at	4933408M05Rik	RIKEN cDNA 4933408M05 gene	-1.79	0.495	-2	0.262	-1.17	0.638	1.01	0.983	-0.98
1429657_at	Zfand5	zinc finger, AN1-type domain 5	-2.75	0.051	-1.16	0.832	-1.45	0.188	1.76	0.317	-0.9
1430824_at	Arhgap23	Rho GTPase activating protein 23	-1.76	0.055	-1.09	0.749	-2.32	0.042	1.85	0.396	-0.83
1430874_at	9430085M18Rik	RIKEN cDNA 9430085M18 gene	-1.14	0.663	-2.03	0.504	-1.82	0.19	1.49	0.191	-0.87
1449479_at	Cyp2b13	cytochrome P450, family 2, subfamily b, polypeptide 13	-2.74	0.07	-1.55	0.471	-1.1	0.681	1.93	0.017	-0.87
1443658_at	D8Ertd457e	DNA segment, Chr 8, ERATO Doi 457, expressed	1.17	0.741	-2.54	0.016	-2.85	0.047	-1.05	0.163	-1.32
1459692_at	AI661323	expressed sequence AI661323	-2.27	0.025	-1.26	0.757	-1.45	0.115	8.85	0.156	0.97
1444631_at	Zfp410	Zinc finger protein 410	-1.54	0.575	-1.59	0.443	-1.56	0.403	2.31	0.327	-0.59
1429992_at	Speer4b	spermatogenesis associated glutamate (E)-rich protein 4b	-1.88	0.538	-2.09	0.233	-1.1	0.653	1.11	0.859	-0.99
1446202_at	---	Transcribed locus	-2.56	0.155	-1.07	0.931	-1.69	0.357	1.23	0.656	-1.02
1423915_at	Olfml2b	olfactomedin-like 2B	-2.36	0.266	-1.33	0.376	-1.34	0.154	1.8	0.284	-0.81
1456456_x_at	Mela	Melanoma antigen	-1.84	0.329	-1.25	0.635	-1.73	0.388	1.97	0.499	-0.71
1424146_at	Gpr37l1	G protein-coupled receptor 37-like 1	-1.18	0.528	-2.14	0.152	-1.64	0.381	1.15	0.678	-0.95
1448911_at	Atp4b	ATPase, H+/K+ exchanging, beta polypeptide	-5.87	0.006	-1.68	0.074	1.16	0.427	-1.7	0.41	-2.02
1420354_at	Cnnm1	cyclin M1	-1.43	0.462	-1.94	0.342	-1.41	0.566	1.21	0.803	-0.89
1420418_at	Syt2	synaptotagmin II	-1.79	0.425	-1.89	0.337	-1.2	0.604	1.42	0.57	-0.86
1428460_at	Syn2	synapsin II	-1.45	0.224	-3.47	0.327	-1.06	0.885	1.12	0.836	-1.21
1444262_at	1110017F19Rik	RIKEN cDNA 1110017F19 gene	-1.21	0.286	-1.9	0.072	-1.74	0.021	3.08	0.295	-0.44
1441398_at	---	---	-1.97	0.339	-1.04	0.93	-2.19	0.05	1.28	0.364	-0.98
1440256_at	Rgs9bp	regulator of G-protein signalling 9 binding protein	-1.22	0.727	-1.82	0.15	-1.8	0.368	1.21	0.106	-0.91
1433186_at	2610019A05Rik	RIKEN cDNA 2610019A05 gene	-2.17	0.182	-1.35	0.357	-1.38	0.335	1.41	0.229	-0.87
1456289_at	Hamp2 /// Hamp1	hepcidin antimicrobial peptide 2 /// hepcidin antimicrobial peptide 1	-1.86	0.315	-1.32	0.355	-1.58	0.21	2.61	0.376	-0.54
1460480_at	1600014E20Rik	RIKEN cDNA 1600014E20 gene	-1.26	0.743	-1.73	0.018	-1.79	0.037	1.34	0.657	-0.86
1447110_at	4921513D23Rik	RIKEN cDNA 4921513D23 gene	-2.55	0.011	-1.03	0.933	-1.77	0.181	1.15	0.493	-1.05
1419214_at	Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a	-1.83	0.32	-1.49	0.204	-1.41	0.189	1.83	0.12	-0.72
1447714_x_at	---	Transcribed locus	-2.35	0.127	-2.1	0.298	1.03	0.958	-2.17	0.097	-1.4
1460683_at	Tead4	TEA domain family member 4	-1.26	0.32	-1.37	0.281	-2.46	0.232	1.44	0.135	-0.91
1434324_x_at	Eif3s3 /// LOC6250	eukaryotic translation initiation factor 3, subunit 3 (gamma) /// similar to eukaryoti	-2.08	0.219	-1.18	0.42	-1.66	0.38	1.03	0.93	-0.97
1448039_at	LOC622175	Similar to gonadotropin inducible ovarian transcription factor 2	-3.06	0.444	1.07	0.928	-1.87	0.292	-1.04	0.878	-1.23
1445679_at	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	-2.48	0.124	1.11	0.527	-2.41	0.015	-2.09	0.255	-1.47
1446668_at	---	PREDICTED: Mus musculus similar to sidekick homolog 1 (LOC620969), mRNA	-3.6	0.255	-2.02	0.335	1.16	0.801	-1.41	0.366	-1.47
1443580_at	Stxbp6	Syntaxin binding protein 6 (amisyn)	-1.98	0.467	-1.33	0.662	-1.49	0.546	2.22	0.055	-0.65
1441847_at	Mast2	Microtubule associated serine/threonine kinase 2	-1.2	0.831	-1.96	0.047	-1.72	0.337	2.81	0.313	-0.51
1439865_at	Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	-2.72	0.337	-1.4	0.005	-1.18	0.063	1.46	0.43	-0.96
1421975_a_at	Add2	adducin 2 (beta)	-1.74	0.269	-1.11	0.863	-2.18	0.331	5.63	0.172	0.15
1446355_at	9530085L11Rik	RIKEN cDNA 9530085L11 gene	-2.01	0.319	-1.82	0.25	-1.13	0.606	1.55	0.447	-0.85
1457830_at	Net1	Neuroepithelial cell transforming gene 1	-1.74	0.058	-1.3	0.287	-1.71	0.039	1.75	0.322	-0.75
1436786_at	1110069O07Rik	RIKEN cDNA 1110069O07 gene	-1.95	0.243	-1.61	0.324	-1.26	0.007	1.16	0.794	-0.91

1441776_at	Tspan11	tetraspanin 11	-1.79	0.381	-1.54	0.056	-1.38	0.401	1.1	0.836	-0.9
1456931_at	C85363	expressed sequence C85363	-1.22	0.061	-1.71	0.264	-1.89	0.093	1.02	0.942	-0.95
1424679_at	Mab21l1	mab-21-like 1 (C. elegans)	-1.59	0.496	-3.21	0.137	-1.01	0.987	1.59	0.118	-1.05
1420807_a_at	Egfl9	EGF-like-domain, multiple 9	-1.54	0.088	-2.09	0.196	-1.25	0.625	1.64	0.563	-0.81
1421349_x_at	Cend1	cell cycle exit and neuronal differentiation 1	-1.08	0.829	-2.36	0.217	-1.7	0.357	1.01	0.99	-1.04
1457409_at	Fut9	fucosyltransferase 9	-1.05	0.912	-3.3	0.152	-1.47	0.576	1.04	0.902	-1.2
1444784_at	4930564K09Rik	RIKEN cDNA 4930564K09 gene	-1.81	0.141	-1.18	0.805	-1.88	0.139	1.24	0.467	-0.91
1444190_at	E030049G20Rik	RIKEN cDNA E030049G20 gene	-1.79	0.012	-1.26	0.491	-1.73	0.088	1.03	0.953	-0.94
1446920_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-1.49	0.096	-1.37	0.324	-1.88	0.005	1.75	0.271	-0.75
1446641_at	Syt7	Synaptotagmin VII	-2.22	0.139	-1.67	0.033	-1.13	0.778	1.16	0.722	-0.97
1445614_at	---	---	-1.81	0.177	-1.28	0.678	-1.67	0.23	1.29	0.692	-0.87
1427122_at	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2	-2.43	0.454	-1.17	0.766	-1.49	0.116	1.28	0.762	-0.95
1447269_at	9630031F12Rik	RIKEN cDNA 9630031F12 gene	-1.09	0.727	-2.88	0.087	-1.49	0.139	1.04	0.934	-1.11
1445977_at	AU022793	expressed sequence AU022793	-1.21	0.798	-1.7	0.202	-1.9	0.403	1.64	0.227	-0.79
1426252_a_at	Umod	uromodulin	-1.13	0.049	-11.04	0.133	-1.04	0.95	1.73	0.23	-2.87
1446926_at	Pycard	PYD and CARD domain containing	-1.27	0.445	-2.56	0.01	-1.31	0.103	1.11	0.609	-1.01
1432045_at	Tssk5	testis-specific serine kinase 5	-1.83	0.323	-2.09	0.366	-1.1	0.765	2.34	0.005	-0.67
1449522_at	Unc5c	unc-5 homolog C (C. elegans)	-1.59	0.004	-1.49	0.428	-1.57	0.054	1.05	0.786	-0.9
1426166_at	Mup5	major urinary protein 5	-1.44	0.496	-1.56	0.087	-1.66	0.047	1.37	0.58	-0.82
1430470_at	5730411F24Rik	RIKEN cDNA 5730411F24 gene	-1.63	0.236	-1.64	0.062	-1.4	0.008	1.08	0.617	-0.9
1433347_at	A930036A04Rik	RIKEN cDNA A930036A04 gene	-1.5	0.553	-1.08	0.893	-2.89	0.04	1.33	0.659	-1.04
1428089_at	Slitrk1	SLIT and NTRK-like family, member 1	-2.4	0.155	-1.93	0.293	1	0.996	-1.39	0.245	-1.18
1457546_at	Cnot1	CCR4-NOT transcription complex, subunit 1	-1.56	0.403	-1.26	0.634	-1.99	0.11	1.43	0.271	-0.84
1457894_at	---	---	-2.29	0.026	-1.08	0.852	-1.72	0.209	2.31	0.141	-0.69
1444707_at	---	Transcribed locus	1.01	0.987	-3.16	0.056	-1.62	0.351	-1.26	0.412	-1.26
1432838_at	6430598H11Rik	RIKEN cDNA 6430598H11 gene	1	0.99	-3.08	0.091	-1.63	0.412	-2.5	0.299	-1.55
1431683_at	4930473H19Rik	RIKEN cDNA 4930473H19 gene	1.08	0.893	-2.01	0.349	-2.72	0.07	-1.22	0.622	-1.22
1453660_at	5430420F09Rik	RIKEN cDNA 5430420F09 gene	-1.02	0.919	-2.53	0.005	-1.76	0.067	1.26	0.604	-1.01
1439385_x_at	Slc13a3	Solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-1.87	0.377	-1.44	0.355	-1.4	0.325	3.19	0.004	-0.38
1424855_at	Olah	oleoyl-ACP hydrolase	-1.87	0.074	-1.84	0.525	-1.15	0.752	1.06	0.731	-0.95
1422312_a_at	Neurog3	neurogenin 3	-1.44	0.34	-1.73	0.436	-1.48	0.431	1.52	0.465	-0.78
1437219_at	Igf1r	Insulin-like growth factor I receptor	-1.5	0.028	-1.41	0.29	-1.75	0.02	1.09	0.706	-0.89
1449378_at	Krt27	keratin 27	-3.08	0.351	1.1	0.107	-1.91	0.2	-1.22	0.74	-1.28
1444756_at	---	Transcribed locus	-1.18	0.532	-1.54	0.44	-2.2	0.353	1.02	0.946	-0.98
1421711_at	Zfp109	zinc finger protein 109	-2.59	0.218	-1.77	0.067	-1	0.988	1.15	0.768	-1.05
1432294_at	9330177L23Rik	RIKEN cDNA 9330177L23 gene	-1.23	0.58	-2.6	0.292	-1.34	0.277	1.19	0.829	-0.99
1438387_x_at	Top3b	topoisomerase (DNA) III beta	-1.75	0.078	-1.5	0.066	-1.41	0.444	1.73	0.27	-0.73
1444414_at	Apod	Apolipoprotein D	-2.28	0.356	-1.02	0.961	-1.88	0.121	1.26	0.738	-0.98
1424848_at	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha men	-1.05	0.938	-1.69	0.381	-2.49	0.03	2.55	0.062	-0.67
1449513_at	Adam24	a disintegrin and metallopeptidase domain 24 (testase 1)	-1.7	0.248	-1.17	0.487	-1.98	0.31	1.01	0.95	-0.96
1450553_at	Hoxd12	homeo box D12	-1.17	0.65	-2.99	0.259	-1.32	0.421	1.01	0.977	-1.12
1444565_at	BB166591	expressed sequence BB166591	-1.29	0.093	-1.3	0.227	-2.45	0.013	2.6	0.238	-0.61
1438333_at	Prtg	protogenin homolog (Gallus gallus)	-2.36	0.431	-2.86	0.041	1.18	0.783	-1.51	0.341	-1.39
1434501_at	---	---	-1.51	0.316	-1.11	0.872	-2.61	0.101	5.44	0.191	0.05
1447487_at	---	---	-3.59	0.322	-2.24	0.129	1.22	0.648	-1.03	0.962	-1.41
1425976_x_at	Zfp353	zinc finger protein 353	-3.27	0.081	1.04	0.953	-1.67	0.465	-1.06	0.849	-1.24
1432945_at	5230400M06Rik	RIKEN cDNA 5230400M06 gene	-3.04	0.12	-2.42	0.141	1.21	0.639	-1.29	0.354	-1.39
1444297_at	Serpina4-ps1	serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1	1.39	0.597	-24.88	0.181	-1.91	0.278	-1.08	0.538	-6.62
1453094_at	Ches1	checkpoint suppressor 1	-1.47	0.06	-2.41	0	-1.17	0.323	1.24	0.634	-0.95
1456305_x_at	LOC666466	similar to oocyte specific homeobox 2	-1.4	0.355	-1.53	0.208	-1.71	0.559	1.43	0.536	-0.8
1433578_at	Slc10a4	solute carrier family 10 (sodium/bile acid cotransporter family), member 4	-1.44	0.722	-2.79	0.017	-1.11	0.276	1.02	0.912	-1.08
1459222_x_at	---	---	-2.45	0.029	-1.02	0.957	-1.78	0.229	1.5	0.428	-0.94
1428804_at	Mfap3l	microfibrillar-associated protein 3-like	-1.13	0.513	-1.61	0.256	-2.23	0.001	1.65	0.414	-0.83

1440199_at	AU042651	expressed sequence AU042651	-1.46	0.245	-1.11	0.844	-2.73	0.085	1.1	0.902	-1.05
1421695_at	Strc	stereocilin	-1.26	0.636	-1.93	0.256	-1.56	0.226	1.69	0.257	-0.76
1446382_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	-1.86	0.32	-1.48	0.209	-1.35	0.06	1	0.996	-0.92
1458102_at	Plxna2	Plexin A2	-1.1	0.62	-1.68	0.231	-2.24	0.002	1.93	0.098	-0.77
1421202_at	Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4	-1.16	0.765	-1.71	0.333	-1.97	0.276	2.09	0.055	-0.69
1439627_at	Zic1	zinc finger protein of the cerebellum 1	-1.2	0.718	-1.68	0.56	-1.9	0.305	1.22	0.729	-0.89
1423012_at	Syt7	synaptotagmin VII	-3.29	0.029	-1.28	0.507	-1.15	0.804	1.08	0.414	-1.16
1441527_at	4930558J18Rik	RIKEN cDNA 4930558J18 gene	-1.25	0.603	-1.73	0.379	-1.73	0.355	1.71	0.065	-0.75
1456239_at	Fgf17	fibroblast growth factor 17	-2.45	0.507	1.05	0.776	-1.99	0.081	-2.12	0.449	-1.38
1418297_at	Dpysl4	dihydropyrimidinase-like 4	-1.75	0.417	-1.44	0.348	-1.44	0.499	1.16	0.405	-0.87
1458732_at	---	---	-2.73	0.331	1.02	0.975	-1.75	0.127	-1.55	0.358	-1.25
1425564_at	Rest	RE1-silencing transcription factor	-1.33	0.389	-2.31	0.256	-1.3	0.498	1.18	0.718	-0.94
1432362_at	Cenpp	centromere protein P	-1.38	0.404	-1.96	0.119	-1.39	0.444	2.48	0.299	-0.56
1432340_at	1700121N20Rik	RIKEN cDNA 1700121N20 gene	-1.86	0.54	-1.67	0.55	-1.21	0.417	1.16	0.191	-0.9
1458046_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630027M	-1.05	0.819	-2.1	0.033	-1.88	0.005	1.53	0.073	-0.87
1421806_at	Defb3	defensin beta 3	-1.16	0.6	-3.55	0.132	-1.22	0.707	1.24	0.696	-1.18
1439728_at	D330027H18Rik	RIKEN cDNA D330027H18 gene	-2.24	0.116	-1.88	0.207	-1.02	0.892	1.1	0.746	-1.01
1435963_at	---	---	-1.74	0.358	-2.19	0.065	-1.08	0.733	1.27	0.266	-0.93
1425541_at	Ddx27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	-2.26	0.339	-1.17	0.5	-1.5	0.125	2.48	0.105	-0.61
1440960_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630060	-2.74	0.464	-2.96	0.256	1.26	0.634	-2.22	0.405	-1.66
1441125_at	Setd5	SET domain containing 5	-1.65	0.525	-2.93	0.045	1.02	0.981	-2.03	0.559	-1.4
1444265_at	---	---	-1.43	0.51	-7.62	0	1.13	0.276	-1.65	0.486	-2.39
1431585_at	1700034P13Rik	RIKEN cDNA 1700034P13 gene	-1.53	0.267	-2.13	0.005	-1.19	0.714	1.31	0.514	-0.88
1420268_x_at	Npm1	Nucleophosmin 1	-1.1	0.86	-1.36	0.599	-3.18	0.006	1.18	0.658	-1.11
1455272_at	Grm5	glutamate receptor, metabotropic 5	-2.07	0.426	-2.56	0.318	1.09	0.807	-1.06	0.819	-1.15
1421382_at	Prlr	prolactin receptor	-1.62	0.017	-1.1	0.481	-2.29	0.233	1.13	0.701	-0.97
1460459_at	Paqr5	progestin and adipoQ receptor family member V	1.02	0.954	-2.59	0.172	-1.77	0.208	-2.51	0.011	-1.47
1432277_at	4930565D16Rik	RIKEN cDNA 4930565D16 gene	-1.87	0.021	-1.24	0.634	-1.6	0.383	1.22	0.439	-0.87
1459562_at	---	---	-1.12	0.779	-1.83	0.095	-1.9	0.047	1.29	0.396	-0.89
1423477_at	Zic1	zinc finger protein of the cerebellum 1	-4.35	0.029	1.03	0.972	-1.41	0.552	-2.83	0.259	-1.89
1440100_at	4930527D15Rik	RIKEN cDNA 4930527D15 gene	-1.42	0.644	-1.8	0.509	-1.41	0.571	1.17	0.755	-0.87
1438189_s_at	Epb4.9	erythrocyte protein band 4.9	-1.01	0.994	-1.75	0.119	-2.51	0.228	8.82	0.263	0.89
1449249_at	Pcdh7	protocadherin 7	-1.8	0.056	-1.54	0.466	-1.32	0.422	2.1	0.074	-0.64
1447702_x_at	Igsf1	immunoglobulin superfamily, member 1	-1.5	0.535	-1.62	0.436	-1.47	0.178	1.54	0.408	-0.76
1429833_at	Ly6g6e	lymphocyte antigen 6 complex, locus G6E	-1.88	0.218	-1.3	0.473	-1.49	0.145	1.08	0.708	-0.9
1424941_at	BC016579	cDNA sequence, BC016579	-1.14	0.733	-2.4	0.212	-1.48	0.476	3.35	0.027	-0.42
1459181_at	---	PREDICTED: Mus musculus similar to Tubulin alpha-1 chain (LOC629601), mRN	-1.46	0.625	-1.29	0.635	-1.96	0.08	2.04	0.284	-0.67
1433418_at	---	---	-1.54	0.461	-1.63	0.304	-1.41	0.308	1	1	-0.9
1426189_at	Dusp15	dual specificity phosphatase-like 15	-1.06	0.512	-2.74	0.125	-1.52	0.187	1.85	0.378	-0.87
1454150_at	4930453O03Rik	RIKEN cDNA 4930453O03 gene	-1.7	0.22	-1.6	0.423	-1.31	0.154	1.09	0.82	-0.88
1444854_at	---	PREDICTED: Mus musculus similar to gonadotropin inducible ovarian transcriptic	-1.44	0.265	-2.07	0.146	-1.26	0.19	1.56	0.31	-0.8
1444968_at	---	---	-1.45	0.623	-2.34	0.324	-1.17	0.581	1.12	0.673	-0.96
1430712_at	Arhgap24	Rho GTPase activating protein 24	-1.33	0.464	-2.34	0.092	-1.26	0.316	1.07	0.775	-0.97
1432063_at	4833427F10Rik	RIKEN cDNA 4833427F10 gene	-1.99	0.08	-1.16	0.747	-1.65	0.378	2.01	0.194	-0.7
1439172_at	Atp13a5	ATPase type 13A5	-2.62	0.255	-1.41	0.604	-1.14	0.705	1.41	0.462	-0.94
1418065_at	Rag2	recombination activating gene 2	-1.19	0.199	-1.63	0.359	-1.92	0.247	1.1	0.685	-0.91
1432961_at	2610024D14Rik	RIKEN cDNA 2610024D14 gene	-1.84	0.256	-1.51	0.4	-1.3	0.443	1.32	0.45	-0.83
1438357_at	Pfdn5 /// LOC43486	prefoldin 5 /// prefoldin 5 pseudogene	-2.32	0.004	1.1	0.857	-2.26	0.141	-1.48	0.33	-1.24
1433274_at	2610200G18Rik	RIKEN cDNA 2610200G18 gene	-1.37	0.597	-2.15	0.038	-1.28	0.741	2.62	0.225	-0.55
1451900_at	Mfn2	mitofusin 2	-1.37	0.243	-1.74	0.283	-1.49	0.12	1.14	0.727	-0.86
1440108_at	Foxp2	forkhead box P2	-1.38	0.495	-1.6	0.027	-1.59	0.008	1.35	0.361	-0.81
1438307_at	Hmgb2	High mobility group box 2	-1.91	0.177	-1.39	0.595	-1.36	0.201	2.48	0.249	-0.55
1459169_at	Coro1c	Coronin, actin binding protein 1C	-1.77	0.439	-1.39	0.668	-1.44	0.496	1.45	0.391	-0.79

1442443_at	Rbbp4	Retinoblastoma binding protein 4	-1.04	0.285	-1.77	0.121	-2.19	0.032	1.09	0.539	-0.98
1432449_at	4930564B18Rik	RIKEN cDNA 4930564B18 gene	-2.49	0.216	-1.99	0.019	1.07	0.796	-2.05	0.317	-1.36
1445179_at	D10Ertd494e	DNA segment, Chr 10, ERATO Doi 494, expressed	-1.19	0.791	-1.29	0.682	-2.75	0.034	1.16	0.79	-1.02
1446482_at	Cep63	centrosomal protein 63	-1.83	0.354	-1.65	0.601	-1.21	0.636	1.25	0.698	-0.86
1444490_at	---	---	-1.63	0.198	-2.68	0.078	-1.01	0.977	1.73	0.376	-0.9
1453542_at	2610007B07Rik	RIKEN cDNA 2610007B07 gene	-1.36	0.479	-1.56	0.225	-1.65	0.074	1.78	0.008	-0.7
1431508_at	4930423M02Rik	RIKEN cDNA 4930423M02 gene	-1.57	0.206	-2.8	0.037	-1.01	0.964	1.04	0.954	-1.09
1447123_at	---	---	-1.08	0.937	-1.7	0.23	-2.15	0.199	1.37	0.589	-0.89
1432018_at	Ascl2	achaete-scute complex homolog-like 2 (Drosophila)	-1.5	0.226	-1.63	0.4	-1.43	0.306	1.15	0.698	-0.85
1449610_at	Ep400	E1A binding protein p400	-2.62	0.055	-1.4	0.357	-1.13	0.798	1.18	0.455	-0.99
1445643_at	---	PREDICTED: Mus musculus similar to spindle assembly associated Sfi1 homolog	-1.87	0.337	-1.86	0.081	-1.1	0.479	1.17	0.543	-0.92
1458893_at	---	Transcribed locus	-2.2	0.022	-1.94	0.122	1.01	0.977	-1.76	0.545	-1.22
1439437_x_at	Cpe /// LOC677374	carboxypeptidase E /// similar to carboxypeptidase E	-1.99	0.237	1.01	0.982	-2.14	0	-1.86	0.4	-1.24
1447921_at	---	Transcribed locus	-1.24	0.782	-3.34	0.173	-1.14	0.73	1.62	0.273	-1.03
1435743_at	Klhl23	kelch-like 23 (Drosophila)	-1.48	0.199	-1.23	0.661	-2.03	0.005	3.11	0.185	-0.41
1432389_at	4933438A12Rik	RIKEN cDNA 4933438A12 gene	-1.67	0.097	-2.39	0.09	-1.03	0.936	1.04	0.947	-1.02
1438537_at	---	---	1.2	0.365	-2.66	0.053	-2.48	0.32	-1.33	0.615	-1.32
1458561_at	Neurl	neuralized-like homolog (Drosophila)	-1.62	0.311	-1.32	0.102	-1.65	0.23	1.35	0.185	-0.81
1447429_at	---	Transcribed locus	1.08	0.912	-2.32	0.205	-2.14	0.287	-1.05	0.921	-1.1
1418507_s_at	Socs2	suppressor of cytokine signaling 2	-1.19	0.763	-1.93	0.269	-1.6	0.003	1.03	0.904	-0.92
1432936_at	5330433J24Rik	RIKEN cDNA 5330433J24 gene	-1.16	0.387	-1.44	0.133	-2.33	0.231	1.1	0.721	-0.96
1450207_at	Lifr	leukemia inhibitory factor receptor	-1.05	0.71	-5.04	0.006	-1.2	0.661	1.05	0.925	-1.56
1459124_at	Pcsk5	Proprotein convertase subtilisin/kexin type 5	-2.12	0.225	-1.32	0.557	-1.32	0.158	1.32	0.325	-0.86
1456690_at	---	---	-3.2	0.446	-2.75	0.157	1.31	0.245	-1.38	0.68	-1.51
1458058_at	7030407E18Rik	RIKEN cDNA 7030407E18 gene	-1.27	0.619	-1.86	0.011	-1.51	0.016	1.09	0.394	-0.89
1439227_at	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	-1.82	0.084	-1.79	0.078	-1.14	0.196	2.01	0.308	-0.68
1457160_at	Fjx1	four jointed box 1 (Drosophila)	-1.8	0.559	-2.03	0.239	-1.06	0.907	1.4	0.456	-0.87
1420228_at	---	---	-1.26	0.033	-3.61	0.035	-1.09	0.777	1.27	0.486	-1.17
1454744_at	F630043A04Rik	RIKEN cDNA F630043A04 gene	-1.95	0.194	-1.89	0.371	-1.06	0.866	2.38	0.198	-0.63
1439822_at	---	---	-1.12	0.314	-1.25	0.406	-3.34	0.075	1.28	0.453	-1.11
1438589_at	Igsf1	immunoglobulin superfamily, member 1	1.02	0.95	-1.99	0.153	-2.15	0.257	-1.13	0.797	-1.06
1438158_at	---	---	-1.94	0.301	-1.58	0.49	-1.19	0.728	1.09	0.659	-0.91
1440535_at	Uros	uroporphyrinogen III synthase	-1.76	0.231	-1.6	0.409	-1.26	0.542	3.58	0.244	-0.26
1418425_at	Sp7	trans-acting transcription factor 7	-1.68	0.27	-1.74	0.009	-1.22	0.644	1.1	0.694	-0.88
1433146_at	Cald1	caldesmon 1	-1.28	0.455	-1.79	0.059	-1.53	0.08	1.03	0.942	-0.89
1422448_at	Tff2	trefoil factor 2 (spasmolytic protein 1)	-1.3	0.756	-2	0.205	-1.39	0.337	1.13	0.575	-0.89
1437401_at	---	---	-1.32	0.38	-1.18	0.026	-2.56	0.041	1.32	0.368	-0.94
1431856_a_at	C1qtnf6	C1q and tumor necrosis factor related protein 6	-2.1	0.47	-1.67	0.551	-1.09	0.831	1.11	0.328	-0.94
1423412_at	BC013481	cDNA sequence BC013481	-1.92	0.313	-1.51	0.294	-1.24	0.257	1.01	0.989	-0.91
1421458_at	Zfp112	zinc finger protein 112	-1.99	0.231	-2.11	0.191	1.01	0.956	-1.02	0.916	-1.02
1438651_a_at	Agtrl1	angiotensin receptor-like 1	-1.37	0.443	1.05	0.942	-4.79	0.035	-1.98	0.098	-1.77
1440843_at	A230051N06Rik	RIKEN cDNA A230051N06 gene	-1.9	0.024	-1.79	0.01	-1.1	0.601	1.11	0.696	-0.92
1442963_at	Zhx3	zinc fingers and homeoboxes 3	-1.13	0.456	-1.59	0.006	-2.09	0.038	1.47	0.174	-0.83
1427676_a_at	Grik1	glutamate receptor, ionotropic, kainate 1	-1.32	0.714	-1.94	0.148	-1.38	0.595	3.05	0.002	-0.4
1430362_at	5730409N24Rik	RIKEN cDNA 5730409N24 gene	-1.64	0.083	-1.23	0.64	-1.75	0.146	1.58	0.32	-0.76
1444296_a_at	Serpina4-ps1	serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1	1.39	0.56	-22.47	0.142	-1.77	0.019	-1.07	0.9	-5.98
1445019_at	---	---	-1.2	0.822	-1.41	0.511	-2.22	0.244	1.87	0.502	-0.74
1446471_at	---	---	1.02	0.901	-1.84	0.533	-2.3	0.026	-1.81	0.316	-1.23
1416623_at	Thbs3	thrombospondin 3	1.06	0.872	-1.85	0.041	-2.53	0.029	-1.32	0.095	-1.16
1458211_at	Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	-1.13	0.765	-1.45	0.631	-2.36	0.01	1.18	0.83	-0.94
1428208_at	Bcl7a	B-cell CLL/lymphoma 7A	-1.62	0.29	-1.67	0.127	-1.28	0.067	1.02	0.922	-0.89
1444654_at	Trerf1	Transcriptional regulating factor 1	-3.31	0.024	-1.18	0.728	-1.18	0.66	1.09	0.806	-1.14
1429790_at	Brunol6 /// LOC669	bruno-like 6, RNA binding protein (Drosophila) /// similar to bruno-like 6, RNA bin	-2.52	0.137	-1.03	0.948	-1.58	0.1	1.21	0.822	-0.98

1459912_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	-1.75	0.323	-1.2	0.686	-1.68	0.325	1.69	0.175	-0.74
1440415_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430095E	-1.4	0.533	-1.54	0.037	-1.58	0.213	1.29	0.508	-0.81
1446588_at	---	---	-4.2	0.006	-1.1	0.807	-1.17	0.739	1.15	0.721	-1.33
1422984_at	Cyln2	cytoplasmic linker 2	-1.25	0.811	-2.21	0.304	-1.34	0.672	1.59	0.099	-0.8
1417898_a_at	Gzma	granzyme A	-1.81	0.521	1.09	0.749	-2.78	0.054	-5.15	0.032	-2.16
1431946_a_at	Apba2bp	amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein	-1.47	0.382	-2.01	0.009	-1.22	0.497	1.7	0.144	-0.75
1446320_at	2310010I16Rik	RIKEN cDNA 2310010I16 gene	-1.95	0.249	-1.69	0.163	-1.12	0.455	1.05	0.893	-0.93
1448992_at	Ina	internexin neuronal intermediate filament protein, alpha	-1.01	0.994	-1.6	0.246	-2.64	0.065	4.75	0.079	-0.12
1444807_at	---	---	-2.11	0.035	-1.24	0.594	-1.39	0.499	1.57	0.403	-0.79
1419707_at	Krtap14	keratin associated protein 14	-1.49	0.508	-1.42	0.339	-1.59	0.311	1.08	0.883	-0.86
1440468_at	D630023F18Rik	RIKEN cDNA D630023F18 gene	-1.45	0.081	-1.11	0.862	-2.43	0.149	1.03	0.959	-0.99
1441103_at	D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed	-3.29	0.066	-1.03	0.964	-1.39	0.262	1.7	0.204	-1
1441269_at	Hydin	Hydrocephalus inducing	-1.4	0.698	-1.29	0.649	-1.96	0.147	1.4	0.43	-0.81
1439889_at	Scn8a	sodium channel, voltage-gated, type VIII, alpha	-1.83	0.042	-1.42	0.308	-1.33	0.016	1.28	0.08	-0.82
1429886_at	Zfp294	zinc finger protein 294	-2.54	0.156	-1.88	0.036	1.08	0.879	-1.34	0.538	-1.17
1450797_a_at	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	-1.58	0.388	-1.79	0.334	-1.23	0.347	1.38	0.654	-0.81
1444055_at	Hs3st3b1	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	-1.54	0.511	-1.51	0.129	-1.45	0.454	1.68	0.052	-0.7
1441655_at	Gm884	gene model 884, (NCBI)	-2.03	0.446	-1.68	0.524	-1.09	0.885	1.68	0.435	-0.78
1456075_at	Prkd2	protein kinase D2	-2	0.225	-1.27	0.656	-1.39	0.513	1.2	0.769	-0.87
1445102_at	B930096M23Rik	RIKEN cDNA B930096M23 gene	-3.17	0.028	-1.35	0.517	-1.06	0.908	1.9	0.229	-0.92
1438854_x_at	Pitpnm1	phosphatidylinositol membrane-associated 1	-3.36	0.43	-1.64	0.268	1.1	0.646	-1	0.944	-1.23
1459535_at	Cdh13	Cadherin 13	-1.74	0.377	-1.37	0.551	-1.43	0.459	1.26	0.62	-0.82
1432193_at	4930412L05Rik	RIKEN cDNA 4930412L05 gene	-1.55	0.027	-1.83	0.27	-1.23	0.462	1.13	0.795	-0.87
1458700_at	Lrrc8c	Leucine rich repeat containing 8 family, member C	-1.23	0.355	-1.64	0.15	-1.71	0.166	1.03	0.803	-0.89
1415969_s_at	Kap	kidney androgen regulated protein	-1.27	0.008	-27.5	0.13	1.19	0.864	-3.01	0.211	-7.65
1432219_at	Nol9	nucleolar protein 9	-3.39	0.06	-1.76	0.28	1.14	0.788	-1.25	0.569	-1.31
1440473_at	Rap2a	RAS related protein 2a	-1.67	0.49	-1.33	0.424	-1.52	0.335	1.27	0.72	-0.81
1458570_at	Aspscr1	Alveolar soft part sarcoma chromosome region, candidate 1 (human)	-1.32	0.387	-1.28	0.777	-2.11	0.152	1.58	0.065	-0.78
1441735_at	---	---	-2.57	0.008	-1.06	0.893	-1.48	0.355	1.52	0.348	-0.9
1424939_at	Asz1	ankyrin repeat, SAM and basic leucine zipper domain containing 1	-1.62	0.405	-1.87	0.069	-1.17	0.648	1.06	0.848	-0.9
1448068_at	Soat1	sterol O-acyltransferase 1	-1.41	0.271	-2.07	0.166	-1.23	0.416	1.75	0.017	-0.74
1438707_at	Atp13a4	ATPase type 13A4	-1.11	0.748	-1.69	0.584	-1.95	0.04	1.14	0.848	-0.9
1431816_at	Tex9	testis expressed gene 9	-3.16	0.097	-1.71	0.289	1.11	0.59	-1.35	0.421	-1.28
1441353_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	1.11	0.205	-1.9	0.26	-2.67	0.094	-1.16	0.475	-1.15
1432346_a_at	Cdh23	cadherin 23 (otocadherin)	-5.22	0.021	-1.48	0.486	1.14	0.329	-1.39	0.264	-1.73
1437145_s_at	2310002J15Rik	RIKEN cDNA 2310002J15 gene	-3.77	0.131	-1.5	0.167	1.08	0.612	-1.14	0.376	-1.33
1444922_at	---	PREDICTED: Mus musculus similar to microtubule-associated protein, RP/EB far	1.08	0.832	-2.38	0.043	-1.97	0.293	-2.06	0.449	-1.33
1432923_at	2810404I24Rik	RIKEN cDNA 2810404I24 gene	-1.14	0.617	-1.97	0.274	-1.59	0.316	1.11	0.788	-0.9
1419379_x_at	Fxyd2	FXYD domain-containing ion transport regulator 2	-1.26	0.01	-4.69	0.201	1.01	0.986	-1.61	0.392	-1.64
1419395_at	Acot12	acyl-CoA thioesterase 12	-1.14	0.423	-1.44	0.033	-2.25	0.185	1.76	0.112	-0.77
1416689_at	Tuft1	tuftelin 1	-1.5	0.136	-1.9	0.102	-1.22	0.149	1.42	0.31	-0.8
1418475_at	Scnn1b	sodium channel, nonvoltage-gated 1 beta	-1.52	0.115	-2.52	0.002	-1.04	0.795	1.23	0.309	-0.96
1446084_at	Nexn	Nexilin	-2.26	0.243	-1.89	0.289	1.04	0.916	-1.46	0.33	-1.14
1452851_at	Tnrc4	trinucleotide repeat containing 4	-1.46	0.063	-1.74	0.291	-1.33	0.349	1.3	0.427	-0.81
1452460_at	Ankrd26 /// LOC669	ankyrin repeat domain 26 /// similar to ankyrin repeat domain 26	-1.56	0.305	-1.51	0.055	-1.41	0.238	1.43	0.025	-0.76
1457801_at	9930024M15Rik	RIKEN cDNA 9930024M15 gene	-1.51	0.028	-1.5	0.229	-1.46	0.146	1.04	0.888	-0.86
1444813_at	Mast2	Microtubule associated serine/threonine kinase 2	-2.38	0.017	-1.4	0.63	-1.13	0.677	1.29	0.619	-0.91
1447030_at	---	---	1.16	0.427	-2.52	0.08	-2.18	0.224	-1.01	0.982	-1.14
1453930_at	1110015M06Rik	RIKEN cDNA 1110015M06 gene	-2.98	0.01	-1.5	0.139	1.01	0.939	-2.11	0.206	-1.39
1446246_at	Gm438	gene model 438, (NCBI)	-1.31	0.66	-1.86	0.018	-1.39	0.099	1	0.992	-0.89
1445936_at	Skiv2l2	Superkiller viralicidic activity 2-like 2 (S. cerevisiae)	-1.69	0.063	-1.74	0.027	-1.17	0.518	1.03	0.89	-0.89
1433673_at	E130309D14Rik	RIKEN cDNA E130309D14 gene	-1.84	0.291	-1.84	0.005	-1.07	0.744	4.53	0.112	-0.06
1442556_at	---	---	1	0.976	-1.67	0.185	-2.42	0.024	-1.11	0.342	-1.05

1419928_at	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	-1.36	0.288	-1.9	0.075	-1.33	0.423	1.02	0.933	-0.89
1430269_at	Mybphl	myosin binding protein H-like	-5.5	0.027	-1.79	0.144	1.28	0.379	-1.79	0.388	-1.95
1441279_at	C430002E04Rik	RIKEN cDNA C430002E04 gene	-1.5	0.458	-2.11	0.001	-1.14	0.735	1.02	0.969	-0.93
1453706_at	2900042A17Rik	RIKEN cDNA 2900042A17 gene	-1.45	0.443	-1.7	0.237	-1.35	0.576	1.04	0.895	-0.87
1454429_at	5830462O15Rik	RIKEN cDNA 5830462O15 gene	-1.45	0.346	-1.68	0.161	-1.36	0.289	1.16	0.706	-0.83
1430224_at	Wfdc3	WAP four-disulfide core domain 3	-1.7	0.145	-1.95	0.045	-1.09	0.784	2.26	0.183	-0.62
1442602_at	---	---	-1.5	0.335	-1.02	0.977	-2.67	0	1.57	0.609	-0.91
1440789_at	Neo1	neogenin	-1.45	0.287	-1.55	0.379	-1.45	0.055	1.26	0.721	-0.8
1443053_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	-1.09	0.769	-2.79	0.026	-1.34	0.354	1.76	0.216	-0.87
1420111_at	Zfp334	Zinc finger protein 334	-1.6	0.355	-1.82	0.145	-1.18	0.431	1.62	0.2	-0.74
1445377_at	Als2cr19	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (hum	-1.49	0.086	-1.24	0.344	-1.82	0.001	1.27	0.016	-0.82
1456965_at	---	---	-2.58	0.162	1.05	0.911	-1.72	0.117	-1.24	0.552	-1.12
1431762_at	Htra3	HtrA serine peptidase 3	-2.04	0.253	-1.46	0.161	-1.18	0.467	1.63	0.212	-0.76
1434428_at	D330028D13Rik	RIKEN cDNA D330028D13 gene	-1.41	0.382	-1.57	0.026	-1.47	0.021	1.01	0.975	-0.86
1453410_at	Angptl4	angiopoietin-like 4	-1.14	0.804	-1.95	0.038	-1.57	0.218	1.75	0.111	-0.73
1455344_at	Efna3	ephrin A3	-2.09	0.219	-1.99	0.082	1.04	0.834	-1.94	0.291	-1.25
1437966_at	Prrt3	proline-rich transmembrane protein 3	-2.53	0.014	-1.22	0.554	-1.24	0.615	1.21	0.81	-0.95
1443336_at	Fbxl11	F-box and leucine-rich repeat protein 11	-2.1	0.472	1.15	0.783	-2.55	0.178	-1.26	0.797	-1.19
1428371_at	2610507N02Rik	RIKEN cDNA 2610507N02 gene	-1.41	0.224	-1.45	0.014	-1.59	0.146	1.2	0.261	-0.81
1446254_at	Depdc6	DEP domain containing 6	-1.23	0.252	-1.51	0.019	-1.83	0.074	1.43	0.548	-0.78
1440652_at	Ankrd44	ankyrin repeat domain 44	1.06	0.942	-2.79	0.256	-1.66	0.151	-2.05	0.228	-1.36
1456072_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	-1.34	0.06	-1.42	0.058	-1.75	0.004	1.31	0.597	-0.8
1441158_at	Chn2	Chimerin (chimaerin) 2	-1.27	0.489	-2.03	0.005	-1.34	0.49	1.39	0.228	-0.81
1441078_at	1700023F02Rik	RIKEN cDNA 1700023F02 gene	-3.22	0.298	-1.96	0.486	1.21	0.622	-1.04	0.948	-1.26
1454443_at	4833411I10Rik	RIKEN cDNA 4833411I10 gene	-1.98	0.062	-1.17	0.763	-1.51	0.01	1.41	0.345	-0.81
1447087_at	Cgrrf1	Cell growth regulator with ring finger domain 1	-2.22	0.006	-1.39	0.17	-1.17	0.526	1.13	0.683	-0.91
1459581_at	Trp63	transformation related protein 63	1.25	0.679	-2.2	0.036	-3.07	0.034	-1.03	0.963	-1.26
1421473_at	Il1a	interleukin 1 alpha	-1.84	0.023	-1.48	0.465	-1.24	0.464	1.14	0.639	-0.85
1444794_at	---	---	-1.53	0.158	-1.2	0.781	-1.85	0.002	1.19	0.517	-0.85
1431534_at	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	-2.45	0.11	-1.03	0.952	-1.53	0.442	1.31	0.582	-0.93
1447630_x_at	Gnb5	guanine nucleotide binding protein, beta 5	-1.18	0.402	-2.36	0.121	-1.32	0.224	1.88	0.05	-0.74
1417701_at	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	-1.36	0.31	-1.52	0.21	-1.57	0.044	1.1	0.585	-0.84
1433371_at	5430427N15Rik	RIKEN cDNA 5430427N15 gene	-1.18	0.495	-1.38	0.66	-2.18	0.279	1.05	0.945	-0.92
1432611_at	4932430A15Rik	RIKEN cDNA 4932430A15 gene	-1.13	0.77	-2.2	0.128	-1.44	0.352	1.15	0.799	-0.91
1445830_at	Ctnnd1	catenin (cadherin associated protein), delta 1	1	0.991	-1.95	0.074	-1.94	0.09	-1.07	0.901	-0.99
1447793_x_at	Rbx1	Ring-box 1	-1.45	0.426	-1.48	0.006	-1.5	0.115	1.1	0.77	-0.83
1431172_at	Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	1.03	0.743	-1.84	0.131	-2.17	0.012	-1.15	0.504	-1.03
1447642_x_at	Dmwd	dystrophia myotonica-containing WD repeat motif	-1.38	0.64	-1.41	0.595	-1.67	0.234	1.5	0.206	-0.74
1450469_at	Ddc8	testis specific protein, Ddc8	-1.1	0.922	-2.42	0.102	-1.42	0.307	1.39	0.317	-0.89
1433326_at	4930488N24Rik	RIKEN cDNA 4930488N24 gene	-3.98	0.425	1.19	0.663	-1.7	0.532	-2.23	0.033	-1.68
1442550_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	-3.07	0.255	-1.33	0.649	-1.04	0.895	1	0.998	-1.11
1453801_at	Them5	thioesterase superfamily member 5	-1.98	0.268	-1.47	0.432	-1.18	0.543	1.9	0.428	-0.68
1429343_at	1700012H05Rik	RIKEN cDNA 1700012H05 gene	-1.36	0.457	-1.49	0.121	-1.59	0.126	1.1	0.712	-0.84
1440809_at	Swap70	SWA-70 protein	-3.03	0.229	-1.48	0.383	1.03	0.959	-1.44	0.392	-1.23
1438891_at	Ctnnd2	Catenin (cadherin associated protein), delta 2	-1.12	0.756	-2.32	0.148	-1.4	0.382	1.57	0.108	-0.82
1420746_at	Prlpi	prolactin-like protein I	-2.22	0.017	-1.76	0.222	1.02	0.879	-1.08	0.81	-1.01
1432535_at	5530400C23Rik	RIKEN cDNA 5530400C23 gene	-1.14	0.533	-2.19	0.28	-1.44	0.104	1.6	0.453	-0.79
1456327_at	---	Transcribed locus	-2.03	0.006	-1.06	0.882	-1.66	0.048	1.35	0.654	-0.85
1458215_at	Setdb1	SET domain, bifurcated 1	-1.23	0.752	-1.65	0.194	-1.61	0.025	1.32	0.038	-0.79
1457318_at	A330008L17Rik	RIKEN cDNA A330008L17 gene	-2.84	0.017	-1.27	0.313	-1.11	0.777	1.99	0.098	-0.81
1457767_at	Nisch	Nischarin	-2.38	0.204	-1.51	0.348	-1.05	0.92	1.34	0.366	-0.9
1443744_at	Dcc	Deleted in colorectal carcinoma	-1.7	0.358	-1.19	0.693	-1.64	0.501	1.28	0.52	-0.81
1443315_at	---	---	-2.8	0.216	-1.68	0.162	1.08	0.443	-1.05	0.691	-1.11

1442842_at	Hspbap1	Hspb associated protein 1	-1.24	0.815	-1.93	0.073	-1.4	0.575	1.96	0.294	-0.65
1417554_at	Hsd3b4	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 4	-1.02	0.725	-12.17	0.124	-1.02	0.832	1.15	0.656	-3.26
1437967_at	---	Transcribed locus	-1.4	0.033	-1.36	0.097	-1.7	0.063	1.3	0.396	-0.79
1458540_at	---	Transcribed locus	-1.75	0.252	-1.39	0.583	-1.34	0.242	1.15	0.801	-0.83
1457004_at	D15Wsu169e	DNA segment, Chr 15, Wayne State University 169, expressed	-2.95	0.002	-1.42	0.315	-1	0.994	2.3	0.012	-0.77
1435770_at	Txndc13	thioredoxin domain containing 13	-1.26	0.529	-1.96	0.151	-1.36	0.301	1.34	0.589	-0.81
1426758_s_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.18	0.34	-2.38	0.192	-1.29	0.427	1.29	0.398	-0.89
1446080_at	Cutl2	Cut-like 2 (Drosophila)	-1.54	0.299	-1.55	0.388	-1.34	0.329	1.02	0.889	-0.85
1425181_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	-1.22	0.725	-2.38	0.104	-1.25	0.395	2.04	0.045	-0.7
1446859_at	---	---	-1.51	0.407	-1.5	0.439	-1.4	0.039	1.74	0.109	-0.67
1440285_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	-1.41	0.012	-1.39	0.098	-1.63	0.029	1.55	0.228	-0.72
1458495_at	Ppp3ca	Protein phosphatase 3, catalytic subunit, alpha isoform	-1.21	0.346	-1.53	0.216	-1.77	0.201	1	0.909	-0.88
1430920_at	2410075D05Rik	RIKEN cDNA 2410075D05 gene	-1.34	0.469	-1.89	0.035	-1.31	0.397	1.06	0.53	-0.87
1421549_at	Pcdhb15	protocadherin beta 15	-1.38	0.298	-1.74	0.127	-1.35	0.561	2.01	0.399	-0.61
1423671_at	Dner	delta/notch-like EGF-related receptor	-1.96	0.237	-1.17	0.707	-1.47	0.086	1.36	0.411	-0.81
1442028_at	AI593864	expressed sequence AI593864	-1.96	0.177	-1.37	0.101	-1.24	0.679	1.03	0.943	-0.89
1441563_at	2410017P07Rik	RIKEN cDNA 2410017P07 gene	-1.26	0.333	-1.35	0.333	-1.95	0.116	1.2	0.737	-0.84
1443363_at	A430107O13Rik	RIKEN cDNA A430107O13 gene	-1.46	0.447	-1.13	0.784	-2.12	0.072	1.03	0.95	-0.92
1436550_at	Fbxo30	F-box protein 30	-1.14	0.511	-1.59	0.07	-1.87	0.014	2.65	0.264	-0.49
1442952_at	Shrm	Shroom	1.13	0.377	-2.43	0.058	-1.98	0.005	-1.95	0.069	-1.31
1446316_at	Lpin2	Lipin 2	-1	0.995	-2.12	0.095	-1.74	0.227	2.59	0.147	-0.57
1431867_a_at	1700007B13Rik	RIKEN cDNA 1700007B13 gene	-1.64	0.089	-1.85	0.193	-1.12	0.6	1.38	0.611	-0.81
1435012_x_at	Ela3 /// LOC638418	elastase 3, pancreatic /// similar to elastase 3B, pancreatic	-3.75	0.043	-1.36	0.583	1.04	0.909	-1.9	0.644	-1.49
1459485_at	Neo1	Neogenin	-1.23	0.619	-1.51	0.239	-1.76	0.004	1.14	0.8	-0.84
1444384_at	AI591476	Expressed sequence AI591476	-2.42	0.353	1.02	0.977	-1.63	0.005	-1.26	0.322	-1.07
1460274_at	4921530G04Rik	RIKEN cDNA 4921530G04 gene	-1.18	0.575	-1.83	0.234	-1.54	0.45	1.16	0.618	-0.85
1437233_x_at	1110049F12Rik	RIKEN cDNA 1110049F12 gene	-1.87	0.318	-1.28	0.705	-1.38	0.588	1.34	0.348	-0.8
1438726_at	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2	-1.53	0.073	-1.3	0.324	-1.6	0.152	1.41	0.242	-0.76
1456249_x_at	Syp	Synaptophysin	-1.41	0.605	-1.45	0.261	-1.55	0.315	1.07	0.778	-0.83
1454618_at	---	---	-1.5	0.701	-3.48	0.137	1.09	0.855	-1.21	0.004	-1.28
1458520_at	Hipk2	Homeodomain interacting protein kinase 2	-1.4	0.144	-1.27	0.446	-1.84	0.055	1.79	0.397	-0.68
1453245_at	9130024F11Rik	RIKEN cDNA 9130024F11 gene	-1.17	0.713	-1.78	0.312	-1.6	0.397	1.4	0.495	-0.79
1431231_at	Hist2h3c1 /// Hist1h	histone 2, H3c1 /// histone 1, H3f /// histone1, H3d /// histone 1, H3b /// histone 1,	-1.32	0.567	-2.2	0.035	-1.2	0.381	1.76	0.037	-0.74
1441585_at	Spg7	Spastic paraplegia 7 homolog (human)	-1.19	0.779	-1.5	0.064	-1.84	0.337	1.52	0.487	-0.75
1443938_at	---	Transcribed locus	-1.97	0.48	-1.16	0.272	-1.48	0.233	1.5	0.217	-0.78
1430916_at	Fancd2	Fanconi anemia, complementation group D2	-3.34	0.062	-1.12	0.699	-1.17	0.509	1.23	0.085	-1.1
1447574_s_at	Slc32a1	Solute carrier family 32 (GABA vesicular transporter), member 1	-1.74	0.133	-1.08	0.779	-1.83	0.155	1.39	0.435	-0.82
1453957_a_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	1.01	0.974	-1.73	0.353	-2.19	0.282	-1.18	0.746	-1.02
1436201_x_at	Mbp	myelin basic protein	-1.28	0.28	-2.7	0.147	-1.11	0.841	1.81	0.522	-0.82
1432247_at	4633402D09Rik	RIKEN cDNA 4633402D09 gene	1.16	0.689	-2.15	0.163	-2.37	0.294	-1.07	0.804	-1.11
1429368_at	Lrig3	leucine-rich repeats and immunoglobulin-like domains 3	-1.17	0.227	-1.4	0.265	-2.07	0.1	1.18	0.731	-0.86
1440648_at	Coq10a	Coenzyme Q10 homolog A (yeast)	-1.51	0.393	-1.56	0.279	-1.34	0.438	1.04	0.78	-0.84
1439280_at	B230396O12Rik	RIKEN cDNA B230396O12 gene	-1.83	0.463	-2.03	0.22	1.01	0.961	-1.19	0.418	-1.01
1419378_a_at	Fxyd2	FXYD domain-containing ion transport regulator 2	-1.24	0.015	-4.83	0.168	1.04	0.888	-1.64	0.292	-1.67
1438485_at	E130112L23Rik	RIKEN cDNA E130112L23 gene	-1.43	0.421	-1.97	0.105	-1.19	0.653	1.5	0.444	-0.77
1424543_at	Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	-1.81	0.052	-1.17	0.556	-1.55	0.148	1.17	0.519	-0.84
1439929_at	Mfhas1	Malignant fibrous histiocytoma amplified sequence 1	-1.25	0.082	-1.32	0.037	-2.01	0.042	1.2	0.478	-0.85
1454465_at	5830435N06Rik	RIKEN cDNA 5830435N06 gene	-1.91	0.044	-2.09	0.058	1.05	0.877	-1.04	0.945	-1
1416492_at	Ccne1	cyclin E1	-2.22	0.4	-1.2	0.772	-1.31	0.579	4.06	0.152	-0.16
1438911_at	7-Sep	Septin 7	-1.46	0.108	-1.41	0.044	-1.52	0.121	1.09	0.772	-0.82
1419986_at	Ccdc69	Coiled-coil domain containing 69	-2.56	0.069	-1.79	0.369	1.1	0.874	-3.12	0.022	-1.59
1419510_at	Es22	esterase 22	-1.96	0.106	-1.17	0.719	-1.46	0.125	2.59	0.017	-0.5
1458707_at	E430016F16Rik	RIKEN cDNA E430016F16 gene	-1.85	0.45	-1.34	0.212	-1.3	0.4	3.29	0.012	-0.3

1422239_at	Hoxd13	homeo box D13	-1.1	0.171	-1.93	0.098	-1.59	0.422	1.29	0.741	-0.83
1458841_at	Nudcd1	NudC domain containing 1	-1.36	0.415	-1.51	0.195	-1.53	0.187	1	0.992	-0.85
1425818_at	---	---	-1.26	0.113	-1.53	0.009	-1.65	0.203	1.34	0.495	-0.77
1431550_at	4930488B22Rik	RIKEN cDNA 4930488B22 gene	1.23	0.697	-1.98	0.232	-3.18	0.231	-1.34	0.744	-1.32
1427223_a_at	Acsm2	acyl-CoA synthetase medium-chain family member 2	-1.31	0.085	-1.3	0.584	-1.9	0.004	1.48	0.293	-0.76
1425167_a_at	Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polype	-1.63	0.515	-1.56	0.309	-1.25	0.634	1.02	0.973	-0.86
1459401_at	LOC545191	Similar to zinc finger protein 616	-1.8	0.378	-1.24	0.759	-1.44	0.231	1.06	0.85	-0.86
1456655_at	Ext1	Exostoses (multiple) 1	-1.3	0.315	-1.28	0.047	-1.98	0.037	1.47	0.143	-0.77
1433380_at	4921509A06Rik	RIKEN cDNA 4921509A06 gene	-2.18	0.201	-1.6	0.266	-1.03	0.939	1.23	0.687	-0.89
1426273_at	Lmbr1	limb region 1	-1.64	0.067	-1.64	0.009	-1.2	0.284	1.64	0.053	-0.71
1439291_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030(	-1.64	0.514	-1.63	0.093	-1.21	0.643	1.36	0.52	-0.78
1438374_x_at	App	amyloid beta (A4) precursor protein	-1.45	0.286	-1.99	0.363	-1.16	0.516	1.7	0.298	-0.73
1459578_at	AA407175	expressed sequence AA407175	-1.4	0.577	-1.88	0.132	-1.24	0.549	3.12	0.246	-0.35
1427023_at	Phyhipl	phytanoyl-CoA hydroxylase interacting protein-like	-1.43	0.117	-4.29	0.161	1.13	0.616	-4.32	0.184	-2.23
1428665_at	---	---	-3.23	0.019	-1.12	0.852	-1.17	0.686	1.16	0.793	-1.09
1423072_at	6720475J19Rik /// I	RIKEN cDNA 6720475J19 gene /// similar to putative retrovirus-related gag protei	-1.5	0.346	-2.57	0.005	1	0.996	-1.18	0.593	-1.06
1457114_at	Tor1b	torsin family 1, member B	-1.25	0.838	-1.41	0.628	-1.82	0.106	1.17	0.72	-0.83
1437562_at	4932422M17Rik	RIKEN cDNA 4932422M17 gene	-2.32	0.332	-1.34	0.749	-1.13	0.829	2.09	0.118	-0.68
1430572_at	1810042K04Rik	RIKEN cDNA 1810042K04 gene	-1.28	0.237	-1.45	0.337	-1.71	0.204	1.28	0.422	-0.79
1459511_at	3110004L20Rik	RIKEN cDNA 3110004L20 gene	-1.31	0.155	-1.42	0.23	-1.68	0.009	3.97	0.135	-0.11
1433085_at	5930427J20Rik	RIKEN cDNA 5930427J20 gene	-5.21	0.01	1.19	0.588	-1.48	0.276	-1.97	0.37	-1.86
1425752_at	BC014805	cDNA sequence BC014805	-4.16	0.035	1.04	0.827	-1.28	0.516	-1.3	0.19	-1.43
1447746_at	Lrch1	Leucine-rich repeats and calponin homology (CH) domain containing 1	-1.37	0.115	-2.56	0.363	-1.07	0.793	1.63	0.294	-0.84
1429406_at	Slco6c1	solute carrier organic anion transporter family, member 6c1	-1.5	0.668	-1.06	0.906	-2.21	0.137	1.09	0.879	-0.92
1437897_at	Klhl21	kelch-like 21 (Drosophila)	-2.02	0.467	-1.79	0.242	1.01	0.987	-1.22	0.663	-1.01
1446216_at	---	Adult male cecum cDNA, RIKEN full-length enriched library, clone:9130202G13 p	-1.78	0.2	-1.24	0.616	-1.44	0.465	1.24	0.688	-0.81
1440452_at	Drp2	dystrophin related protein 2	-1.33	0.491	-1.46	0.557	-1.59	0.338	1.1	0.62	-0.82
1460263_at	Pdcd6ip	Programmed cell death 6 interacting protein	-1.08	0.44	-2.17	0.166	-1.49	0.215	1.28	0.144	-0.86
1436754_at	AI839735 /// LOC63	expressed sequence AI839735 /// hypothetical protein LOC638311	-1.89	0.001	-1.48	0.149	-1.17	0.606	1.91	0.172	-0.66
1419579_at	Slc7a12	solute carrier family 7 (cationic amino acid transporter, y+ system), member 12	-1.07	0.822	-7.37	0.145	-1.01	0.977	1.29	0.501	-2.04
1458180_at	---	---	-1.7	0.091	-1.44	0.032	-1.28	0.038	1.07	0.781	-0.84
1419496_at	Slco1a6	solute carrier organic anion transporter family, member 1a6	1.08	0.728	-5.64	0.156	-1.24	0.707	-1.3	0.559	-1.78
1430708_a_at	Usp45	ubiquitin specific petidase 45	-1.32	0.324	-2.27	0.144	-1.16	0.721	1.08	0.761	-0.92
1445099_at	---	Transcribed locus	-2.09	0.47	-1.4	0.215	-1.15	0.14	1.32	0.62	-0.83
1453477_at	Zc3h6	zinc finger CCCH type containing 6	-1.8	0.099	-1.45	0.484	-1.22	0.638	1.12	0.79	-0.84
1432342_at	Nmnat3	nicotinamide nucleotide adenylyltransferase 3	-4.04	0.008	1.45	0.336	-2.75	0.135	-1.05	0.921	-1.59
1455709_at	4930422I22Rik	RIKEN cDNA 4930422I22 gene	-1.19	0.689	-1.45	0.528	-1.88	0.202	2.71	0.104	-0.45
1449759_at	D11Ertd326e	DNA segment, Chr 11, ERATO Doi 326, expressed	-2.17	0.207	-1.36	0.662	-1.16	0.846	1.42	0.457	-0.82
1453549_at	4930500G05Rik	RIKEN cDNA 4930500G05 gene	-1.55	0.064	-1.45	0.199	-1.37	0.124	1.48	0.557	-0.72
1439632_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	1.06	0.729	-1.82	0.12	-2.18	0.017	-1.5	0.346	-1.11
1453478_at	Pou3f2	POU domain, class 3, transcription factor 2	-1.38	0.369	-2.75	0.084	-1.03	0.935	1.06	0.91	-1.02
1455501_at	Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	-1.35	0.133	-2.37	0.245	-1.11	0.726	1.03	0.975	-0.95
1435506_at	---	---	-1.81	0.47	-1.21	0.32	-1.46	0.487	1.12	0.858	-0.84
1458765_at	Rbm10	RNA binding motif protein 10	1.02	0.897	-1.85	0.377	-1.98	0.159	-1.25	0.157	-1.02
1451438_s_at	Clec2h	C-type lectin domain family 2, member h	-1.13	0.767	-3.04	0.032	-1.17	0.647	1.23	0.301	-1.03
1445516_at	---	---	-1.16	0.549	-1.81	0.077	-1.53	0.306	1.25	0.663	-0.81
1458902_at	---	---	-2.33	0.136	-1.17	0.54	-1.28	0.382	2.2	0.237	-0.64
1444768_at	---	Transcribed locus	-1.09	0.914	-3.44	0.078	-1.16	0.693	1.5	0.092	-1.05
1447399_at	A330019N05Rik	RIKEN cDNA A330019N05 gene	-1.58	0.149	-1.21	0.395	-1.65	0.038	1.07	0.705	-0.84
1450278_at	Tacr3	tachykinin receptor 3	-1.28	0.803	-1.01	0.986	-3.38	0.126	1.56	0.433	-1.03
1449166_at	S100a14	S100 calcium binding protein A14	-3.56	0.055	-1.22	0.735	-1.03	0.81	1.15	0.68	-1.17
1449908_at	Gip	gastric inhibitory polypeptide	-2.14	0.042	1.16	0.685	-2.27	0.309	-3.35	0.182	-1.65
1418055_at	Neurod4	neurogenic differentiation 4	-1.28	0.721	-1.36	0.521	-1.81	0.228	1.31	0.396	-0.79

1433219_at	6720482G16Rik	RIKEN cDNA 6720482G16 gene	-1.42	0.576	-1.42	0.205	-1.52	0.348	1.9	0.291	-0.61
1456140_at	LOC624168	similar to zinc finger protein of the cerebellum 5	-1.61	0.159	-2.62	0.273	1.07	0.91	-2.51	0.323	-1.42
1458296_at	Ext1	Exostoses (multiple) 1	-1.34	0.162	-1.17	0.062	-2.14	0.063	1.15	0.089	-0.87
1431572_at	2310015K22Rik	RIKEN cDNA 2310015K22 gene	-4.87	0.123	1.03	0.874	-1.2	0.657	-1.83	0.339	-1.72
1458630_at	Vav3	Vav 3 oncogene	1.15	0.861	-2.11	0.242	-2.27	0.127	-1.72	0.22	-1.24
1444875_at	Ppp2ca	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	-1.95	0.028	1.06	0.879	-2.03	0.045	-1.14	0.638	-1.01
1421085_at	Rs1h	retinoschisis 1 homolog (human)	-7.02	0.001	-1.16	0.557	1.07	0.624	-1.07	0.83	-2.05
1441481_at	Mfap3l	microfibrillar-associated protein 3-like	-1.13	0.65	-3.17	0.147	-1.15	0.442	1.18	0.579	-1.07
1427594_at	Zfp697	zinc finger protein 697	-1.56	0.387	-1.12	0.69	-1.87	0.113	1.27	0.622	-0.82
1440422_at	Htr1f	5-hydroxytryptamine (serotonin) receptor 1F	-1.45	0.527	-1.12	0.695	-2.05	0.356	1.3	0.402	-0.83
1450995_at	Folr1	folate receptor 1 (adult)	-1.07	0.572	-2.35	0.303	-1.4	0.296	1.59	0.251	-0.81
1431235_at	---	---	-1.08	0.86	-2.6	0.208	-1.32	0.338	1.44	0.48	-0.89
1446333_at	---	---	-2.77	0.307	-1.17	0.363	-1.16	0.781	1.54	0.472	-0.89
1442451_at	Ttc15	Tetratricopeptide repeat domain 15	1.02	0.925	-1.71	0.166	-2.16	0.011	-2.22	0.048	-1.27
1446167_at	Hipk2	Homeodomain interacting protein kinase 2	-1.28	0.044	-1.22	0.308	-2.12	0.014	2.44	0.247	-0.55
1425841_at	Slc26a7	solute carrier family 26, member 7	-1.8	0.591	-2.52	0.192	1.12	0.583	-1.1	0.872	-1.08
1457561_at	Itga5	integrin alpha 5 (fibronectin receptor alpha)	-1.41	0.399	-1.71	0.21	-1.29	0.25	1.18	0.691	-0.81
1431078_at	Fbxo3	F-box only protein 3	-1.56	0.309	-1.28	0.405	-1.53	0.212	1.39	0.577	-0.75
1442439_at	W91776	expressed sequence W91776	1.01	0.97	-2.02	0.333	-1.77	0.136	-1.74	0.296	-1.13
1424592_a_at	Dnase1	deoxyribonuclease I	1.17	0.545	-2.22	0.293	-2.22	0.227	-1.86	0.141	-1.28
1432990_at	5830495A06Rik	RIKEN cDNA 5830495A06 gene	1.08	0.876	-3.28	0.009	-1.45	0.047	-1.13	0.798	-1.2
1453069_at	Pik3cb	phosphatidylinositol 3-kinase, catalytic, beta polypeptide	-1.58	0.02	-1.35	0.177	-1.42	0.064	1.52	0.283	-0.71
1446867_at	---	---	1.01	0.99	-3	0.087	-1.36	0.519	-1.82	0.023	-1.29
1442815_at	Pex19	Peroxisome biogenesis factor 19	-1.94	0.092	-1.26	0.303	-1.3	0.381	1.01	0.974	-0.87
1447524_at	Ap3m2	adaptor-related protein complex 3, mu 2 subunit	-1.35	0.642	-1.32	0.586	-1.74	0.078	1.78	0.183	-0.66
1450292_a_at	Hormad1	HORMA domain containing 1	-1.6	0.377	-2.02	0.154	-1.05	0.948	1.09	0.858	-0.89
1443810_at	Tssk4	testis-specific serine kinase 4	-1.33	0.743	-1.15	0.51	-2.21	0.006	1.05	0.945	-0.91
1429736_at	1110003F05Rik	RIKEN cDNA 1110003F05 gene	-1.44	0.367	-1.47	0.082	-1.43	0.125	1.53	0.18	-0.7
1424659_at	Slit2	slit homolog 2 (Drosophila)	-1.26	0.222	-1.88	0.288	-1.33	0.285	1.59	0.129	-0.72
1442450_at	D2Ertd501e	DNA segment, Chr 2, ERATO Doi 501, expressed	-1.78	0.515	-2.23	0.314	1.07	0.876	-1.9	0.062	-1.21
1436978_at	Wnt9a	wingless-type MMTV integration site 9A	-1.56	0.217	-3.14	0.056	1.12	0.753	-1.32	0.701	-1.23
1438137_at	2810055G22Rik	RIKEN cDNA 2810055G22 gene	-1.64	0.376	-1.67	0.155	-1.15	0.723	1.1	0.843	-0.84
1459425_at	---	---	-2.11	0.047	-1.16	0.616	-1.35	0.137	1.08	0.66	-0.89
1442875_at	---	---	-1.92	0.455	-2.18	0.06	1.1	0.83	-1.76	0.11	-1.19
1432633_at	9430063H18Rik	RIKEN cDNA 9430063H18 gene	-1.01	0.979	-1.82	0.088	-1.86	0.324	2.92	0.006	-0.44
1435983_at	1700019P01Rik	RIKEN cDNA 1700019P01 gene	-2.82	0.303	-2.7	0.116	1.35	0.408	-1.31	0.613	-1.37
1451440_at	Chodl	chondrolectin	-1.23	0.433	-1.87	0.295	-1.37	0.476	2.17	0.007	-0.57
1453501_at	Hoxb1	homeo box B1	-2.04	0.148	1.03	0.929	-1.8	0.093	-1.22	0.693	-1.01
1440000_at	E330013P04Rik	RIKEN cDNA E330013P04 gene	-2.76	0.065	-1.34	0.615	-1.03	0.954	1.01	0.982	-1.03
1458859_at	---	---	-1.06	0.906	-1.38	0.525	-2.41	0.068	1.94	0.457	-0.73
1427616_at	---	Mus musculus, clone IMAGE:5362978	-2.32	0.138	-1.32	0.681	-1.12	0.805	1.22	0.337	-0.89
1444992_at	AI120166	expressed sequence AI120166	-1.24	0.058	-1.49	0.434	-1.67	0.019	1.65	0.075	-0.69
1457822_at	---	---	-1.04	0.684	-2.24	0.034	-1.49	0.074	1.76	0.1	-0.75
1445793_at	1700011I03Rik	RIKEN cDNA 1700011I03 gene	-1.58	0.652	-1.6	0.404	-1.22	0.748	1.44	0.618	-0.74
1437191_at	BC050789	cDNA sequence BC050789	-1.89	0.548	-3.45	0.109	1.26	0.316	-2	0.101	-1.52
1432120_at	4921513D11Rik	RIKEN cDNA 4921513D11 gene	-1.4	0.187	-1.8	0.226	-1.23	0.152	1.6	0.221	-0.71
1432014_at	6530409C15Rik	RIKEN cDNA 6530409C15 gene	-1.49	0.476	-1.41	0.566	-1.42	0.181	1.23	0.338	-0.77
1445257_at	AU022531	expressed sequence AU022531	-2.45	0.062	-2.69	0.139	1.3	0.73	-2.73	0.21	-1.64
1426339_at	Ak5	adenylate kinase 5	1.14	0.601	-2.44	0.025	-1.87	0.123	-1.66	0.309	-1.21
1446157_at	A330019N05Rik	RIKEN cDNA A330019N05 gene	-2.51	0.11	-1.53	0.482	1.03	0.949	-1.39	0.485	-1.1
1433283_s_at	---	---	-1.29	0.56	-1.22	0.653	-2.05	0.116	1.76	0.249	-0.7
1429410_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	-1.25	0.088	-1.32	0.261	-1.89	0.009	1.33	0.234	-0.78
1437739_a_at	5430432N15Rik	RIKEN cDNA 5430432N15 gene	-1.9	0.336	-1.45	0.34	-1.15	0.748	1.05	0.949	-0.87

1459477_at	Gabarapl2	Gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	-4.63	0.075	-1.02	0.916	-1.12	0.457	1.16	0.763	-1.4
1447407_at	Centd3	centaurin, delta 3	-1.21	0.743	-1.57	0.437	-1.6	0.119	1.16	0.692	-0.81
1443583_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	-1.29	0.051	-1.53	0.045	-1.53	0.15	1.49	0.057	-0.71
1442895_at	---	PREDICTED: Mus musculus similar to zinc finger protein 547 (LOC628043), mRN	-1.26	0.72	-1.36	0.371	-1.79	0.17	1.83	0.117	-0.65
1427638_at	Zbtb16	zinc finger and BTB domain containing 16	-1.59	0.532	-1.45	0.513	-1.3	0.696	1.16	0.883	-0.8
1441161_at	B230216G23Rik	RIKEN cDNA B230216G23 gene	-1.14	0.847	-2.31	0.19	-1.28	0.016	1.21	0.575	-0.88
1444600_at	Nrbp	nuclear receptor binding protein	-1.95	0.07	-1.16	0.833	-1.4	0.542	1.09	0.738	-0.86
1441340_at	Cep68	centrosomal protein 68	-1.51	0.107	-4.16	0.075	1.18	0.75	-1.45	0.067	-1.48
1433876_at	Lrrc24	leucine rich repeat containing 24	-1.29	0.271	-1.63	0.407	-1.43	0.233	1.65	0.377	-0.68
1431654_at	1700112M01Rik	RIKEN cDNA 1700112M01 gene	-2.02	0.036	-1.12	0.79	-1.43	0.39	1.01	0.95	-0.89
1422060_at	Parvb /// LOC67602	parvin, beta /// similar to parvin, beta	-2.39	0.018	-1.2	0.468	-1.19	0.753	2.99	0.339	-0.45
1442504_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	1.13	0.693	-2.3	0.013	-1.91	0.028	-1.18	0.026	-1.06
1422320_x_at	Phxr5	per-hexamer repeat gene 5	-2.11	0.101	-1.22	0.227	-1.26	0.274	1.05	0.802	-0.88
1438345_at	---	---	-1.28	0.13	-1.52	0.151	-1.54	0.052	1.51	0.216	-0.71
1442954_at	---	Transcribed locus	-1.23	0.383	-1.75	0.226	-1.42	0.145	1.51	0.168	-0.72
1431735_at	4930469G21Rik	RIKEN cDNA 4930469G21 gene	-2.4	0.117	-1.05	0.949	-1.39	0.386	1.18	0.645	-0.92
1453765_at	A330106J01Rik	RIKEN cDNA A330106J01 gene	-1.01	0.994	-1.59	0.412	-2.15	0.077	3.39	0.038	-0.34
1440433_at	Nmt2	N-myristoyltransferase 2	-1.15	0.872	-1.69	0.318	-1.59	0.075	1.11	0.633	-0.83
1440553_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	-1.39	0.525	-2.73	0.067	1	0.984	-1.99	0.238	-1.28
1447225_at	Slc16a5	solute carrier family 16 (monocarboxylic acid transporters), member 5	-1.89	0.122	-2.45	0.056	1.15	0.409	-1.15	0.719	-1.09
1429946_at	2610301F02Rik	RIKEN cDNA 2610301F02 gene	-1.19	0.577	-1.28	0.435	-2.13	0.089	1.36	0.389	-0.81
1443491_at	Ptprk	Protein tyrosine phosphatase, receptor type, K	-1.45	0.258	-1.15	0.645	-1.89	0.007	1	0.988	-0.87
1457921_at	1810037C20Rik	RIKEN cDNA 1810037C20 gene	-1.36	0.107	-1.73	0.301	-1.29	0.526	1.13	0.366	-0.81
1458803_at	Slfn9 /// LOC67761	schlafen 9 /// similar to schlafen 9	-1.55	0.457	-1.47	0.271	-1.31	0.542	1.23	0.209	-0.77
1458553_at	Plat	plasminogen activator, tissue	-1.45	0.286	-1.78	0.076	-1.19	0.246	1.36	0.471	-0.77
1457251_x_at	Adcy1	Adenylate cyclase 1	1.05	0.939	-4.78	0	-1.21	0.712	-1.14	0.843	-1.52
1440713_at	4933407H18Rik	RIKEN cDNA 4933407H18 gene	-1.06	0.928	-1.74	0.337	-1.76	0.432	1.25	0.728	-0.82
1446327_at	---	---	-1.04	0.884	-1.25	0.429	-3.08	0.003	1.48	0.088	-0.97
1441134_at	6820424L24Rik	RIKEN cDNA 6820424L24 gene	-2.27	0.101	-1.4	0.612	-1.07	0.85	1.46	0.301	-0.82
1444578_at	Spop	Speckle-type POZ protein	-3.91	0.049	1.2	0.498	-1.57	0.371	-1.36	0.024	-1.41
1443611_at	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	-1.5	0.196	-2.02	0.077	-1.08	0.805	1.74	0.087	-0.72
1442777_at	---	Transcribed locus	-1.22	0.612	-2.18	0.139	-1.23	0.559	1.39	0.083	-0.81
1424260_at	Slc12a1	solute carrier family 12, member 1	-1.06	0.583	-5.43	0.185	-1.03	0.945	1.3	0.43	-1.56
1454586_at	1500002K03Rik	RIKEN cDNA 1500002K03 gene	-2.21	0.253	-1.94	0.126	1.12	0.777	-2.14	0.461	-1.29
1456974_at	Onecut1	one cut domain, family member 1	-1.19	0.734	-2.83	0.005	-1.11	0.888	1.62	0.452	-0.88
1441778_at	Adcyap1	adenylate cyclase activating polypeptide 1	-1.26	0.646	-1.68	0.159	-1.43	0.399	1.55	0.067	-0.7
1454397_at	4632418H02Rik	RIKEN cDNA 4632418H02 gene	1.01	0.901	-1.78	0.067	-1.94	0.015	-1.41	0.022	-1.03
1421505_at	Mixl1	Mix1 homeobox-like 1 (Xenopus laevis)	-2.95	0.001	-2.38	0.292	1.33	0.551	-3.54	0.19	-1.88
1416617_at	Acss1	acyl-CoA synthetase short-chain family member 1	-1.58	0.028	-2.02	0.324	-1.04	0.372	1.15	0.489	-0.87
1444771_at	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	1.06	0.819	-2.57	0.02	-1.56	0.289	-1.01	0.99	-1.02
1460461_at	4921521K07Rik	RIKEN cDNA 4921521K07 gene	-2.29	0.152	-2.6	0.016	1.27	0.642	-1.86	0.088	-1.37
1432046_at	4930404K06Rik	RIKEN cDNA 4930404K06 gene	1.24	0.404	-4.32	0.005	-1.61	0.353	-1.52	0.291	-1.55
1440635_at	Palld	palladin, cytoskeletal associated protein	-2.7	0.117	-1.32	0.54	-1.04	0.934	1.91	0.304	-0.79
1444697_at	4732490B19Rik	RIKEN cDNA 4732490B19 gene	-1.56	0.483	-1.29	0.636	-1.48	0.385	1.53	0.508	-0.7
1425959_x_at	Klra1 /// Klra12 /// K	killer cell lectin-like receptor, subfamily A, member 1 /// killer cell lectin-like recept	-1.36	0.193	-2.2	0.271	-1.11	0.847	1.23	0.776	-0.86
1442409_at	D9Wsu90e	DNA segment, Chr 9, Wayne State University 90, expressed	1	1	-1.78	0.531	-1.88	0.03	-2.53	0.014	-1.3
1458115_at	4930512H18Rik	RIKEN cDNA 4930512H18 gene	-1.42	0.542	-1.87	0.476	-1.17	0.564	1.16	0.789	-0.83
1449475_at	Atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	1.08	0.758	-1.88	0.295	-2.07	0.169	-2.21	0.282	-1.27
1442892_at	Mcc	Mutated in colorectal cancers	-1.91	0.351	-1.33	0.385	-1.22	0.45	1.2	0.766	-0.82
1446267_at	D17Ertd657e	DNA segment, Chr 17, ERATO Doi 657, expressed	1.05	0.961	-2.3	0.418	-1.63	0.083	-2.55	0.408	-1.36
1447461_at	---	---	-1.49	0.675	-1.43	0.541	-1.38	0.402	1.23	0.765	-0.77
1456923_at	Trpm3	transient receptor potential cation channel, subfamily M, member 3	-1.45	0.05	-1.66	0.161	-1.24	0.671	1.8	0.457	-0.64
1421596_s_at	H28	histocompatibility 28	-1.41	0.47	-1.22	0.427	-1.78	0.192	2.8	0.304	-0.4

1437823_at	2310040A07Rik	RIKEN cDNA 2310040A07 gene	-1.04	0.94	-2.63	0.198	-1.33	0.367	1.31	0.207	-0.92
1431435_at	---	---	-2.94	0.026	-1.65	0.228	1.15	0.649	-1.86	0.151	-1.32
1452905_at	Gtl2 /// Lphn1	GTL2, imprinted maternally expressed untranslated mRNA /// latrophilin 1	-1.15	0.521	-3.42	0.028	-1.07	0.657	1.39	0.239	-1.06
1439380_x_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.23	0.406	-2.19	0.15	-1.22	0.133	1.79	0.197	-0.71
1444469_at	1110059H15Rik	RIKEN cDNA 1110059H15 gene	-1.39	0.472	-2.04	0.073	-1.13	0.654	1.35	0.445	-0.8
1442735_at	Oaz2	Ornithine decarboxylase antizyme 2	-1.07	0.225	-1.42	0.699	-2.18	0.062	1.03	0.961	-0.91
1459068_at	Tmem109	Transmembrane protein 109	1.08	0.814	-2.21	0.168	-1.76	0.077	-1.44	0.459	-1.08
1449237_at	Aloxe3	arachidonate lipoxygenase 3	-1.55	0.281	-1.37	0.141	-1.38	0.219	1.02	0.893	-0.82
1439991_a_at	Pabpnl1	poly(A)binding protein nuclear-like 1	-1.73	0.188	1.05	0.828	-2.13	0.177	-2.45	0.076	-1.31
1442498_at	C78662	EST C78662	-1.64	0.141	-1.12	0.752	-1.68	0.194	1.18	0.366	-0.81
1419376_at	1110018M03Rik	RIKEN cDNA 1110018M03 gene	-1.25	0.113	-1.17	0.45	-2.23	0.016	1.04	0.942	-0.9
1433005_at	4833446E11Rik	RIKEN cDNA 4833446E11 gene	-1.85	0.116	-1.4	0.479	-1.18	0.534	1.89	0.144	-0.64
1443428_at	---	---	-1.21	0.667	-1.86	0.252	-1.37	0.621	1.04	0.951	-0.85
1439042_at	Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	-1.62	0.58	-1.59	0.278	-1.18	0.772	1.07	0.408	-0.83
1442824_at	8030497I03Rik	RIKEN cDNA 8030497I03 gene	-1.24	0.222	-1.24	0.335	-2.05	0.033	1.14	0.651	-0.85
1440350_at	---	---	-1.77	0.219	-1.4	0.475	-1.22	0.575	1.05	0.885	-0.83
1438775_at	Ppargc1b	Peroxisome proliferative activated receptor, gamma, coactivator 1 beta	-1.2	0.436	-2.01	0.152	-1.29	0.584	2.1	0.251	-0.6
1441377_at	Kif6	kinesin family member 6	-2.48	0.146	-1.21	0.533	-1.15	0.563	1.98	0.373	-0.71
1443803_x_at	Hoxa5	homeo box A5	-1.06	0.667	-2.1	0.145	-1.46	0.227	1.12	0.451	-0.88
1422310_at	Snn	stannin	-1.63	0.339	-1.62	0.242	-1.15	0.399	1.98	0.15	-0.61
1445780_at	---	---	1.23	0.29	-2.1	0.24	-2.52	0.178	-2.07	0.311	-1.36
1442689_at	D9Ertd278e	DNA segment, Chr 9, ERATO Doi 278, expressed	-1.58	0.239	-1.94	0.36	-1.05	0.839	1.4	0.125	-0.79
1441578_at	---	---	-1.78	0.081	-1.91	0.023	1.02	0.941	-1.21	0.539	-0.97
1438438_at	2900002H16Rik	RIKEN cDNA 2900002H16 gene	-1.65	0.123	-1.23	0.303	-1.46	0.047	1.09	0.684	-0.81
1424471_at	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	-1.12	0.594	-2.9	0.183	-1.16	0.521	1.01	0.974	-1.04
1446599_at	---	---	-1.17	0.484	-1.27	0.606	-2.15	0.029	2.99	0.012	-0.4
1457933_at	Gm1964	Gene model 1964, (NCBI)	-1.1	0.829	-2.16	0.126	-1.37	0.074	5.35	0.198	0.18
1421482_at	Bsnd	Bartter syndrome, infantile, with sensorineural deafness (Barttin)	-1.08	0.823	-1.58	0.406	-1.83	0.381	1.38	0.551	-0.78
1443035_at	---	---	-1.72	0.082	-1.15	0.731	-1.54	0.208	1.18	0.724	-0.81
1432468_at	Lcn9	lipocalin 9	-1.88	0.286	-1.81	0.39	1.02	0.975	-1.03	0.945	-0.93
1436432_at	B230343J05Rik	RIKEN cDNA B230343J05 gene	-1.5	0.574	-1.38	0.494	-1.41	0.144	1.03	0.974	-0.81
1445699_at	---	---	-1.38	0.093	-1.65	0.437	-1.29	0.481	1.44	0.353	-0.72
1428601_at	1700003E16Rik	RIKEN cDNA 1700003E16 gene	-2.27	0.232	-1.6	0.042	1.04	0.903	-1.95	0.333	-1.19
1458378_at	Grin3a	glutamate receptor ionotropic, NMDA3A	-2.22	0.124	-1.97	0.171	1.15	0.814	-2.12	0.343	-1.29
1444533_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.13	0.607	-3.96	0.182	-1.38	0.391	-1.15	0.867	-1.34
1451526_at	Arhgap12	Rho GTPase activating protein 12	-1.39	0.147	-1.37	0.204	-1.52	0.037	1.11	0.751	-0.79
1421548_at	Pcdhb2	protocadherin beta 2	-1.61	0.5	-2.74	0.056	1.12	0.806	-1.13	0.849	-1.09
1457637_at	Prickle1	Prickle like 1 (Drosophila)	-1.01	0.884	-1.63	0.239	-1.99	0.059	1.04	0.89	-0.89
1421470_at	Grpr	gastrin releasing peptide receptor	-2.53	0.401	-1.73	0.132	1.14	0.86	-1.16	0.782	-1.07
1442816_at	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	-1.51	0.239	-1.16	0.665	-1.72	0.397	1.42	0.481	-0.74
1442193_at	A430028G04Rik	RIKEN cDNA A430028G04 gene	-2.46	0.095	-1.42	0.538	-1	0.998	1.87	0.392	-0.75
1441236_at	Slc9a3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	-1.26	0.265	-2.1	0.082	-1.19	0.559	1.08	0.558	-0.87
1456418_at	---	PREDICTED: Mus musculus similar to Inward rectifier potassium channel 13 (Pot	-1.48	0.02	-1.34	0.527	-1.46	0.084	1.05	0.72	-0.81
1431679_at	2510042H12Rik	RIKEN cDNA 2510042H12 gene	-1.07	0.91	-3.17	0.13	-1.16	0.767	1.44	0.357	-0.99
1427528_a_at	Epha7	Eph receptor A7	-2.33	0.228	-1.48	0.438	1.01	0.979	-3.17	0.221	-1.5
1429938_at	A930009E05Rik	RIKEN cDNA A930009E05 gene	-1.49	0.033	-2.53	0.29	1.04	0.934	-1.3	0.551	-1.07
1457758_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	-1.14	0.876	-1.41	0.362	-1.9	0.084	1.06	0.758	-0.85
1424063_at	Abpa	androgen binding protein alpha	-2.33	0.028	-1.15	0.695	-1.24	0.333	1.2	0.464	-0.88
1427817_at	LOC641050	hypothetical protein LOC641050	-1.05	0.957	-1.88	0.295	-1.6	0.203	1.42	0.565	-0.78
1454737_at	Dusp9	dual specificity phosphatase 9	-1.27	0.503	-1.55	0.06	-1.47	0.016	1.05	0.703	-0.81
1450343_at	V1rd1	vomeronasal 1 receptor, D1	-2	0.301	-1.47	0.547	-1.07	0.846	1.19	0.812	-0.84
1447115_at	C78409	Expressed sequence C78409	-1.13	0.883	-2.41	0.071	-1.23	0.574	1.53	0.546	-0.81
1421573_at	4930533N22Rik	RIKEN cDNA 4930533N22 gene	-2	0.066	-1.33	0.722	-1.16	0.518	1.16	0.843	-0.83

1443726_at	Smyd1	SET and MYND domain containing 1	-1.86	0.14	-1.59	0.123	-1.06	0.918	1.43	0.061	-0.77
1421091_at	Serpina12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsi	-1.12	0.766	-2.08	0.422	-1.36	0.134	3	0.121	-0.39
1427775_at	Defb10	defensin beta 10	-1.42	0.193	-2.3	0.026	-1.03	0.907	1.36	0.079	-0.85
1449701_at	D6Ertd109e	DNA segment, Chr 6, ERATO Doi 109, expressed	-1.42	0.557	-1.17	0.708	-1.79	0.354	1.27	0.544	-0.78
1444005_at	---	---	-1.38	0.334	-1.44	0.468	-1.44	0.095	1.5	0.439	-0.69
1446323_at	---	---	-1.37	0.227	-1.6	0.191	-1.32	0.16	1.31	0.253	-0.74
1439379_x_at	Prm1	protamine 1	-2.62	0.459	-1.3	0.351	-1.04	0.694	1.95	0.076	-0.75
1417641_at	Galntl5	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.34	0.562	-3.4	0.235	1.07	0.817	-1.59	0.337	-1.31
1457294_at	Tmtc3	Transmembrane and tetratricopeptide repeat containing 3	-1.27	0.144	-1.37	0.128	-1.68	0.063	1.37	0.064	-0.74
1459443_at	Kcnq1	Potassium voltage-gated channel, subfamily Q, member 1	-1.3	0.21	-1.16	0.633	-2.07	0.06	3.37	0.006	-0.29
1430285_at	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	-1.27	0.604	-1.35	0.316	-1.71	0.099	2.28	0.224	-0.51
1441380_at	2810439F02Rik	RIKEN cDNA 2810439F02 gene	-1.17	0.567	-1.8	0.027	-1.42	0.184	2.14	0.395	-0.56
1448393_at	Cldn7	claudin 7	-1.2	0.099	-2.77	0.178	-1.08	0.481	1.84	0.088	-0.81
1447242_at	Parl	Presenilin associated, rhomboid-like	1	0.977	-1.62	0.167	-2.01	0.16	-1.83	0.334	-1.11
1439620_at	Car13	carbonic anhydrase 13	-2.08	0.295	-1.17	0.708	-1.28	0.528	1.74	0.118	-0.7
1424596_s_at	Lmcd1	LIM and cysteine-rich domains 1	1.1	0.726	-3.15	0.19	-1.42	0.02	-1.08	0.433	-1.14
1427436_at	Six2	sine oculis-related homeobox 2 homolog (Drosophila)	-1.87	0.277	-1.45	0.371	-1.12	0.636	1.04	0.913	-0.85
1435136_at	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	-1.24	0.468	-1.48	0.13	-1.58	0.011	1.93	0.227	-0.59
1438240_at	Ccin	calicin	-5	0.317	1.26	0.694	-1.52	0.259	-1.21	0.558	-1.62
1459287_at	Wdfy3	WD repeat and FYVE domain containing 3	-1.89	0.057	-1.91	0.188	1.07	0.91	-1.21	0.619	-0.99
1449892_at	Lyzl1	lysozyme-like 1	-1.17	0.048	-1.6	0.582	-1.57	0.406	3.66	0.242	-0.17
1452900_at	LOC671160	similar to Proline oxidase, mitochondrial precursor (Proline dehydrogenase)	-1.83	0.149	-1	0.996	-1.74	0.058	1.15	0.449	-0.85
1442259_at	---	---	-1.42	0.478	-1.27	0.701	-1.59	0.038	1.14	0.787	-0.79
1442780_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	1.13	0.854	-2.87	0.137	-1.56	0.417	-1.69	0.358	-1.25
1433630_at	Map6d1	MAP6 domain containing 1	1.2	0.844	-3.72	0.196	-1.53	0.164	-1.1	0.867	-1.29
1446832_at	---	---	1.04	0.864	-1.48	0.182	-2.46	0.052	-1.11	0.707	-1
1433289_at	9530078B04Rik	RIKEN cDNA 9530078B04 gene	-1.59	0.37	-1.06	0.906	-1.83	0.042	1.02	0.944	-0.86
1427356_at	2310031A18Rik	RIKEN cDNA 2310031A18 gene	-1.29	0.544	-1.62	0.156	-1.38	0.343	1.26	0.778	-0.76
1417569_at	Ncald	neurocalcin delta	-1.31	0.372	-1.36	0.093	-1.61	0.15	1.05	0.794	-0.81
1441626_at	---	---	-1.14	0.727	-2.24	0.261	-1.26	0.652	1.16	0.615	-0.87
1442244_at	Inadl	InaD-like (Drosophila)	1.34	0.241	-3.12	0.286	-2.17	0.007	-2.02	0.037	-1.49
1438877_at	Trpm6	transient receptor potential cation channel, subfamily M, member 6	-1.06	0.859	-2.12	0.006	-1.41	0.007	1.11	0.747	-0.87
1446643_at	5330409N07Rik	RIKEN cDNA 5330409N07 gene	-1.75	0.585	-2.56	0.01	1.16	0.827	-1.26	0.66	-1.1
1419997_at	---	---	-1.2	0.692	-2.72	0.069	-1.09	0.765	1.25	0.7	-0.94
1435700_at	Tln2	talin 2	-1.12	0.728	-1.74	0.075	-1.53	0.023	1.29	0.074	-0.78
1429906_at	A930035E12Rik	RIKEN cDNA A930035E12 gene	-1.18	0.716	-1.73	0.374	-1.43	0.19	1.22	0.513	-0.78
1456568_at	Gsn	Gelsolin	-2.07	0.384	-1.1	0.56	-1.38	0.581	1.54	0.535	-0.75
1451991_at	Epha7	Eph receptor A7	-1.85	0.357	-1.08	0.852	-1.52	0.455	1.28	0.73	-0.79
1425852_at	A230107C01Rik	RIKEN cDNA A230107C01 gene	-1.3	0.445	-2.14	0.517	-1.13	0.783	1.18	0.795	-0.85
1445470_at	LOC235580 /// LOC	similar to alpha 3 type VI collagen isoform 4 precursor /// similar to alpha 3 type V	-1.79	0.155	-1.31	0.083	-1.25	0.679	1.71	0.399	-0.66
1446644_at	Brd3	Bromodomain containing 3	-1.34	0.206	-1.3	0.44	-1.64	0.175	1.06	0.715	-0.81
1438906_at	---	---	-1.37	0.218	-1.29	0.074	-1.61	0.013	1.14	0.108	-0.78
1436369_at	2900076A07Rik	RIKEN cDNA 2900076A07 gene	-1.38	0.421	-2.61	0.23	1.02	0.973	-1.55	0.102	-1.13
1419230_at	Krt12	keratin 12	1.07	0.903	-2.36	0.193	-1.58	0.518	-1.88	0.452	-1.19
1441365_at	Foxp2	forkhead box P2	-2.15	0.055	-1.17	0.12	-1.24	0.649	1.19	0.618	-0.84
1442897_at	2610024E20Rik	RIKEN cDNA 2610024E20 gene	-1.3	0.694	-1.5	0.371	-1.45	0.324	1.4	0.412	-0.71
1446395_at	Robo2	Roundabout homolog 2 (Drosophila)	-1.21	0.467	-1.74	0.068	-1.39	0.354	1.28	0.701	-0.76
1427703_at	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	-1.03	0.915	-1.42	0.24	-2.22	0.026	1.24	0.425	-0.86
1431478_at	3110035G12Rik	RIKEN cDNA 3110035G12 gene	-1.07	0.918	-1.3	0.616	-2.37	0.057	1.52	0.402	-0.81
1459883_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230001K	1.01	0.948	-2.58	0.164	-1.37	0.379	-1.02	0.913	-0.99
1421856_at	S100a3	S100 calcium binding protein A3	1.36	0.6	-2.76	0.205	-2.48	0.036	-1.32	0.387	-1.3
1444873_at	Hip1	Huntingtin interacting protein 1	-2.9	0.065	-1.02	0.97	-1.25	0.637	1.16	0.449	-1
1428036_at	---	MRNA similar to phosphatidylinositol glycan, class S (cDNA clone MGC:41618 IM	-1.21	0.493	-1.44	0.512	-1.64	0.237	1.09	0.836	-0.8

1459293_at	C030038J10Rik	RIKEN cDNA C030038J10 gene	1.02	0.955	-1.35	0.027	-2.69	0.003	-1.27	0.66	-1.07
1446848_at	---	---	1.28	0.662	-2.6	0.023	-2.16	0.033	-2.28	0.095	-1.44
1443966_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630040	-1.44	0.151	-1.5	0.011	-1.3	0.154	1.01	0.941	-0.81
1430606_at	2310020F24Rik	RIKEN cDNA 2310020F24 gene	-1.62	0.374	-2.12	0.303	1.04	0.823	-1.03	0.914	-0.93
1450567_a_at	Col2a1	procollagen, type II, alpha 1	-1.16	0.219	-2.02	0.425	-1.29	0.146	1.48	0.453	-0.75
1431979_at	4930444M15Rik	RIKEN cDNA 4930444M15 gene	-1.61	0.679	-1.19	0.833	-1.51	0.36	2.17	0.21	-0.53
1449722_at	---	Transcribed locus	-1.22	0.19	-1.69	0.085	-1.4	0.145	1.79	0.011	-0.63
1459533_at	D19Ertd79e	DNA segment, Chr 19, ERATO Doi 79, expressed	-1.49	0.322	-1	0.999	-2.19	0.316	1.06	0.873	-0.9
1443018_at	Ncam1	Neural cell adhesion molecule 1	-1.42	0.601	-1.22	0.701	-1.66	0.05	1.01	0.971	-0.82
1443546_at	Hdlbp	High density lipoprotein (HDL) binding protein	-1.41	0.172	-1.3	0.3	-1.54	0.003	1.25	0.19	-0.75
1458603_at	---	---	-1.44	0.01	-1.29	0.191	-1.51	0.083	1.08	0.651	-0.79
1442560_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4933433O05 pr	-1.22	0.124	-1.9	0.104	-1.27	0.439	2.02	0.113	-0.59
1449601_x_at	---	Transcribed locus	-1.18	0.605	-1.62	0.434	-1.5	0.219	1.04	0.897	-0.82
1439816_at	LOC433270	Hypothetical gene supported by AK087915	-1.79	0.043	-1.74	0.101	-1	0.984	1.43	0.334	-0.78
1436099_at	AI836003	expressed sequence AI836003	-1.94	0.016	-1.5	0.018	-1.06	0.658	1.17	0.615	-0.83
1449167_at	Epb4.1l4a	erythrocyte protein band 4.1-like 4a	-1.38	0.199	-1.78	0.472	-1.19	0.251	2.09	0.08	-0.56
1455624_at	---	---	1.06	0.651	-2.18	0.09	-1.64	0.542	-1.71	0.331	-1.12
1419981_at	Riok3	RIO kinase 3 (yeast)	-1.38	0.605	-1.6	0.226	-1.28	0.21	1.11	0.569	-0.79
1444675_at	AL023051	expressed sequence AL023051	-1.09	0.626	-1.24	0.613	-2.46	0.047	1.52	0.273	-0.82
1420452_at	Krtap5-2	keratin associated protein 5-2	-2.37	0.067	-1.24	0.241	-1.11	0.609	2.22	0.039	-0.63
1458279_at	Foxo3a	Forkhead box O3a	-1.19	0.592	-1.44	0.191	-1.69	0.044	1.62	0.249	-0.67
1459816_x_at	---	---	-2.44	0.064	-1.14	0.71	-1.19	0.557	1.06	0.922	-0.93
1457843_at	Lypd6	LY6/PLAUR domain containing 6	-1.32	0.395	-1.3	0.592	-1.65	0.403	1.07	0.874	-0.8
1457881_at	Osbpl6	oxysterol binding protein-like 6	-1.1	0.313	-2.65	0.197	-1.18	0.252	1.01	0.956	-0.98
1422840_at	1700013N18Rik	RIKEN cDNA 1700013N18 gene	-2.66	0.415	-1.19	0.754	-1.09	0.845	1.49	0.539	-0.87
1422339_at	Gja3	gap junction membrane channel protein alpha 3	-1.28	0.634	-1.65	0.228	-1.34	0.592	1.84	0.122	-0.61
1442658_at	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	1.01	0.969	-1.78	0.056	-1.78	0.064	-1.23	0.435	-0.95
1457441_at	Ebf1	early B-cell factor 1	-2.53	0.095	1.11	0.738	-1.59	0.342	-2.3	0.012	-1.33
1450574_at	Cyp11b2	cytochrome P450, family 11, subfamily b, polypeptide 2	-1.42	0.583	-2.19	0.052	-1.03	0.953	1.09	0.824	-0.89
1457520_at	Grhl2	Grainyhead-like 2 (Drosophila)	-1.64	0.162	-1.32	0.385	-1.31	0.353	1.07	0.764	-0.8
1456601_x_at	Fxyd2	FXYD domain-containing ion transport regulator 2	-1.09	0.251	-7.07	0.163	1.08	0.857	-1.62	0.42	-2.18
1420236_at	---	Transcribed locus	-2.56	0.47	1.03	0.887	-1.4	0.609	-1	0.996	-0.98
1447937_a_at	4933409K07Rik ///	RIKEN cDNA 4933409K07 gene /// similar to 4933409K07Rik protein /// similar to	-2.04	0.271	-1.53	0.131	-1.01	0.967	2.25	0.075	-0.58
1425449_at	Ppap2a	phosphatidic acid phosphatase 2a	-2.78	0.178	-1.02	0.957	-1.26	0.54	1.2	0.586	-0.96
1445441_at	LOC380907	similar to RIKEN cDNA 1700129C05	-2.23	0.026	-1.29	0.583	-1.1	0.767	1.3	0.296	-0.83
1422358_at	Fpr-rs4	formyl peptide receptor, related sequence 4	-1.42	0.095	-1.03	0.88	-2.19	0.006	1.11	0.422	-0.88
1458251_at	AU022166	expressed sequence AU022166	-2.02	0.221	-1.57	0.073	1	0.999	-1.45	0.058	-1.01
1434013_at	Ablim3	actin binding LIM protein family, member 3	-1.65	0.344	-2.04	0.054	1.04	0.899	-1.47	0.409	-1.03
1428358_at	1810010M01Rik	RIKEN cDNA 1810010M01 gene	-1.13	0.184	-2.14	0.024	-1.27	0.453	1.91	0.074	-0.66
1457867_at	Sgpp2	sphingosine-1-phosphate phosphotase 2	-1.05	0.281	-2.18	0.111	-1.38	0.144	2.43	0.167	-0.54
1456344_at	Tnc	Tenascin C	-1.18	0.337	-1.06	0.867	-2.9	0.299	1.06	0.88	-1.02
1457412_at	Scn8a	sodium channel, voltage-gated, type VIII, alpha	1	0.996	-1.45	0.45	-2.25	0.094	-1.01	0.988	-0.93
1456491_at	AI606861	Expressed sequence AI606861	-1.98	0.101	-1.47	0.334	-1.05	0.304	1.1	0.757	-0.85
1458800_at	Tnrc6c	Trinucleotide repeat containing 6C	1.1	0.729	-1.89	0.15	-1.97	0.056	-1.06	0.896	-0.95
1453376_at	4921524J06Rik	RIKEN cDNA 4921524J06 gene	-1.45	0.572	-3.37	0	1.15	0.775	-1.86	0.473	-1.38
1441649_at	Sesn1	Sestrin 1	1.08	0.724	-1.75	0.035	-2.06	0.007	-1.21	0.386	-0.99
1442536_at	LOC619719	hypothetical protein LOC619719	-1.13	0.803	-2.04	0.044	-1.32	0.445	1.03	0.817	-0.86
1438248_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	-1.17	0.595	-1.45	0.233	-1.69	0.004	1.15	0.739	-0.79
1450618_a_at	Sprr2a	small proline-rich protein 2A	-1.86	0.321	-1.08	0.878	-1.48	0.081	1.09	0.74	-0.83
1435121_at	Dio3as	deiodinase, iodothyronine type III, antisense	-1.43	0.499	-1.18	0.699	-1.69	0.004	1.2	0.636	-0.77
1439757_s_at	Epha4	Eph receptor A4	-1.58	0.635	-2.02	0.379	1.01	0.981	-1.17	0.736	-0.94
1456130_at	LOC553091	hypothetical LOC553091	-1.58	0.3	-1.01	0.989	-1.95	0.031	1.01	0.974	-0.88
1449766_at	Syt6	synaptotagmin VI	-1.2	0.282	-1.85	0.252	-1.31	0.129	1.59	0.157	-0.69

1439870_at	A330008L17Rik	RIKEN cDNA A330008L17 gene	-3.23	0.021	1.33	0.676	-1.99	0.173	-1.04	0.948	-1.23
1457879_at	A230107O07Rik	RIKEN cDNA A230107O07 gene	-1.06	0.875	-2.06	0.002	-1.42	0.449	1.89	0.191	-0.66
1418979_at	Akr1c14	aldo-keto reductase family 1, member C14	-3.56	0.021	-1.45	0.149	1.17	0.602	-1.22	0.826	-1.27
1446225_at	Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	-1.62	0.013	-2.45	0.091	1.11	0.256	-1.31	0.172	-1.07
1457395_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	-1.49	0.101	-2.17	0.067	1	0.988	-1.01	0.989	-0.91
1429809_at	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	-1.27	0.522	-1.54	0.157	-1.42	0.186	1.23	0.616	-0.75
1427513_at	BC024137	cDNA sequence BC024137	-1.35	0.52	-1.93	0.025	-1.13	0.622	1	0.999	-0.85
1431729_at	Spata17	spermatogenesis associated 17	-1.69	0.015	-1.54	0.42	-1.12	0.678	1.07	0.897	-0.82
1442672_at	0610040F04Rik	RIKEN cDNA 0610040F04 gene	-1.7	0.329	-1.87	0.22	1.01	0.972	-1.42	0.49	-0.99
1438057_at	---	Transcribed locus	-2.68	0.096	-1.01	0.985	-1.29	0.291	1.08	0.848	-0.97
1447526_at	D5Ertd255e	DNA segment, Chr 5, ERATO Doi 255, expressed	-1.54	0.017	-1.2	0.377	-1.52	0.036	1.31	0.426	-0.74
1431241_at	Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	-1.63	0.088	-1.39	0.128	-1.24	0.154	1.16	0.676	-0.77
1449547_at	Asb14	ankyrin repeat and SOCS box-containing protein 14	-2.19	0.398	-1.4	0.527	-1.03	0.869	1.29	0.627	-0.83
1432966_at	4921507H08Rik	RIKEN cDNA 4921507H08 gene	-1.05	0.922	-1.11	0.879	-3.45	0.014	1.1	0.681	-1.13
1458034_at	1200016B10Rik	RIKEN cDNA 1200016B10 gene	-1.08	0.839	-1.69	0.379	-1.6	0.386	1.03	0.919	-0.84
1460098_at	---	---	-1.53	0.067	-1.26	0.315	-1.45	0.244	1.16	0.42	-0.77
1438284_at	Ocrl	oculocerebrorenal syndrome of Lowe	-1.38	0.158	-1.27	0.459	-1.59	0.021	1.34	0.001	-0.73
1421693_a_at	Gpr98	G protein-coupled receptor 98	-1.43	0.254	1.02	0.955	-2.38	0.164	-1.26	0.768	-1.01
1454140_at	Ncam1	Neural cell adhesion molecule 1	-1.59	0.088	-1.35	0.608	-1.3	0.636	1.06	0.893	-0.79
1432457_at	4930448F12Rik	RIKEN cDNA 4930448F12 gene	-1.79	0.549	-1.58	0.433	-1.05	0.233	1.08	0.863	-0.84
1447144_at	9130011E15Rik	RIKEN cDNA 9130011E15 gene	-1.11	0.389	-1.08	0.884	-3.2	0.022	1.45	0.143	-0.98
1454530_at	---	---	1.09	0.84	-2.77	0.156	-1.45	0.375	-1.15	0.664	-1.07
1437157_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-2.69	0.049	-2.02	0.141	1.28	0.665	-1.45	0.694	-1.22
1440747_at	Cpox	coproporphyrinogen oxidase	-1.52	0.386	-1.79	0.119	-1.08	0.709	5.48	0.153	0.27
1458729_at	Fkbp4	FK506 binding protein 4	1.06	0.191	-2.12	0.078	-1.64	0.127	-1.33	0.64	-1.01
1447911_at	Tead1	TEA domain family member 1	-1.37	0.482	-1.85	0.164	-1.15	0.669	1.79	0.046	-0.64
1419955_at	Zfand3	Zinc finger, AN1-type domain 3	-1.23	0.818	-2.25	0.428	-1.13	0.815	1.54	0.201	-0.77
1425583_at	---	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library,	-1.63	0.163	-1.84	0.069	-1.01	0.977	1.21	0.756	-0.82
1455934_at	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	-1	0.997	-2.55	0.025	-1.32	0.434	1.16	0.77	-0.93
1447094_at	---	---	-1.2	0.497	-1.25	0.203	-1.95	0.038	1.79	0.152	-0.65
1440094_at	BC030870	cDNA sequence BC030870	-2.53	0.304	1.07	0.795	-1.46	0.261	-1.62	0.227	-1.14
1447906_at	Ptprg	Protein tyrosine phosphatase, receptor type, G	1.12	0.819	-1.56	0.111	-2.57	0.11	-1.44	0.317	-1.11
1459436_at	Zranb3	Zinc finger, RAN-binding domain containing 3	-1.51	0.589	-1.05	0.946	-1.86	0.354	1.19	0.798	-0.81
1440129_at	Aurka	Aurora kinase A	-1.16	0.756	-2.07	0.16	-1.25	0.572	1.86	0.314	-0.65
1454564_at	4933401J01Rik	RIKEN cDNA 4933401J01 gene	-1.48	0.623	-1.32	0.637	-1.4	0.392	1.25	0.272	-0.74
1457727_at	LOC544864	hypothetical protein LOC544864	-1.33	0.133	-2.09	0.3	-1.09	0.757	1.39	0.27	-0.78
1431850_at	3200001D21Rik	RIKEN cDNA 3200001D21 gene	-1.67	0.359	1.07	0.857	-2.1	0.099	-1.99	0.064	-1.17
1454999_at	Phf21b	PHD finger protein 21B	-2.78	0	-2.55	0.393	1.4	0.505	-2.02	0.44	-1.49
1450467_at	Bsn	bassoon	-1.32	0.395	-1.37	0.262	-1.52	0.462	1.01	0.961	-0.8
1443334_at	D430042O09Rik	RIKEN cDNA D430042O09 gene	-1.55	0.366	-1.41	0.629	-1.27	0.598	1.06	0.921	-0.79
1444641_at	Adcy3	Adenylate cyclase 3	-1.32	0.045	-1.43	0.117	-1.45	0.183	1.15	0.614	-0.76
1432733_at	4933402E15Rik	RIKEN cDNA 4933402E15 gene	-3.44	0.071	-1.2	0.746	1.03	0.954	-1.08	0.785	-1.18
1446932_at	---	---	-1.17	0.739	-1.2	0.687	-2.17	0.036	1.9	0.146	-0.66
1440542_at	7420416P09Rik	RIKEN cDNA 7420416P09 gene	-2.19	0.012	-1.03	0.908	-1.39	0.478	1.49	0.201	-0.78
1419387_s_at	Muc13	mucin 13, epithelial transmembrane	-1.37	0.327	-1.51	0.128	-1.32	0.195	1.87	0.304	-0.58
1443511_at	Rora	RAR-related orphan receptor alpha	1.01	0.934	-1.41	0.571	-2.33	0.09	-1.02	0.946	-0.94
1446478_at	D130067I03Rik	RIKEN cDNA D130067I03 gene	1.03	0.952	-1.97	0.357	-1.63	0.494	-1.11	0.703	-0.92
1454404_at	2610011E03Rik	RIKEN cDNA 2610011E03 gene	1.05	0.818	-3.07	0.08	-1.29	0.397	-2.28	0.072	-1.4
1459697_at	Thada	Thyroid adenoma associated	-2.97	0.264	-1.22	0.757	-1.01	0.98	1.4	0.269	-0.95
1443142_at	Btrc	Beta-transducin repeat containing protein	-1.51	0.053	-1.54	0.148	-1.2	0.101	3.99	0.196	-0.06
1443241_at	Pus7	Pseudouridylate synthase 7 homolog (S. cerevisiae)	-1.22	0.79	-2.05	0.245	-1.19	0.367	1.14	0.405	-0.83
1441390_at	Spdya	speedy homolog A (Drosophila)	-2.28	0.156	-1.54	0.479	1.06	0.929	-1.1	0.709	-0.96
1430111_a_at	Bcat1	branched chain aminotransferase 1, cytosolic	-1.59	0.55	-1.88	0.08	-1.01	0.889	1.2	0.564	-0.82

1435094_at	Kcnj16	potassium inwardly-rectifying channel, subfamily J, member 16	1.15	0.073	-1.97	0.357	-2.03	0.255	-1.52	0.289	-1.09
1446473_at	---	---	-1.21	0.063	-1.42	0.441	-1.6	0.27	1.03	0.821	-0.8
1444422_at	Pcdh19	protocadherin 19	-1.77	0.169	-1.42	0.237	-1.13	0.671	1.55	0.37	-0.69
1458074_at	Rslcan24	Regulator of sex-limitation candidate 24	-1.42	0.251	-1.32	0.363	-1.45	0.418	1.15	0.809	-0.76
1441252_at	2010001A14Rik	RIKEN cDNA 2010001A14 gene	-1.17	0.72	-1.47	0.309	-1.61	0.071	1.15	0.574	-0.78
1436988_at	5430433G21Rik	RIKEN cDNA 5430433G21 gene	-1.07	0.782	-2.73	0.128	-1.18	0.616	1.09	0.81	-0.97
1420055_at	Slc35c2	solute carrier family 35, member C2	-1.11	0.526	-2.08	0.086	-1.29	0.159	1.6	0.229	-0.72
1455356_at	Camsap1	calmodulin regulated spectrin-associated protein 1	-1.41	0.042	-1.24	0.157	-1.58	0.07	1.02	0.931	-0.8
1450549_s_at	Elk4	ELK4, member of ETS oncogene family	-1.13	0.655	-2.7	0.078	-1.12	0.816	2	0.154	-0.74
1420009_at	Wwc1	WW, C2 and coiled-coil domain containing 1	-1.29	0.202	-1.95	0.292	-1.16	0.729	3.3	0.094	-0.27
1433387_at	2900022M07Rik	RIKEN cDNA 2900022M07 gene	-2.04	0.424	1.11	0.627	-1.81	0.06	-1.01	0.984	-0.94
1443006_at	Syn3	Synapsin III	-1.46	0.243	-1.53	0.034	-1.23	0.438	1.46	0.072	-0.69
1443983_at	Sorbs1	Sorbin and SH3 domain containing 1	-1.22	0.569	-1.18	0.601	-2.07	0.12	1.18	0.554	-0.82
1419965_at	C79445	expressed sequence C79445	-3.12	0.29	1.06	0.842	-1.3	0.662	-1.13	0.65	-1.12
1435962_at	Rps6 /// LOC21473	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	-1.28	0.696	-1.51	0.126	-1.41	0.238	1.12	0.745	-0.77
1448724_at	Cish	cytokine inducible SH2-containing protein	-1.39	0.028	-1.72	0.321	-1.18	0.213	2.31	0.254	-0.49
1457902_at	---	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hy	1.17	0.641	-1.73	0.439	-2.48	0.26	-1.19	0.461	-1.06
1430169_at	1700007K09Rik	RIKEN cDNA 1700007K09 gene	-1.45	0.495	-1.21	0.463	-1.57	0.176	2.28	0.16	-0.49
1446356_at	Ppp2r5e	Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-1.15	0.103	-1.47	0.151	-1.65	0.019	1.26	0.463	-0.75
1432677_at	Gbf1	Golgi-specific brefeldin A-resistance factor 1	-1.06	0.701	-1.17	0.664	-2.85	0.086	1.08	0.48	-1
1438782_at	Cntn4	contactin 4	1.01	0.986	-1.55	0.304	-2	0.095	-2.63	0.177	-1.29
1445676_at	Kcnn2	Potassium intermediate/small conductance calcium-activated channel, subfamily	-1.98	0.031	-1.11	0.699	-1.33	0.297	2.16	0.156	-0.57
1422906_at	Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	-1.22	0.03	-1.38	0.008	-1.63	0.204	3.99	0.179	-0.06
1432750_at	2810409C01Rik	RIKEN cDNA 2810409C01 gene	1.01	0.967	-1.52	0.424	-2.07	0.022	-1.63	0.299	-1.05
1443656_at	Fut8	fucosyltransferase 8	-1.2	0.798	-2.08	0.273	-1.19	0.589	1.67	0.367	-0.7
1447126_at	Cdyl2	Chromodomain protein, Y chromosome-like 2	-1.01	0.911	-1.89	0.114	-1.56	0.018	1.09	0.505	-0.84
1437797_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.54	0.056	-1.23	0.359	-1.44	0.186	1.03	0.798	-0.8
1444706_at	E430014L09Rik	RIKEN cDNA E430014L09 gene	-1.19	0.238	-1.3	0.404	-1.84	0.035	1.07	0.81	-0.81
1456969_at	9530092O11Rik	RIKEN cDNA 9530092O11 gene	-1.64	0.617	-1.01	0.975	-1.78	0.311	1.34	0.717	-0.77
1447659_x_at	Atp6v1h	ATPase, H+ transporting, lysosomal V1 subunit H	-3.54	0.033	1.28	0.535	-1.69	0.319	-1.78	0.512	-1.43
1431242_at	6330575P09Rik	RIKEN cDNA 6330575P09 gene	-1.55	0.084	-2.17	0.261	1.05	0.896	-2.07	0.187	-1.18
1458317_at	Eml1	Echinoderm microtubule associated protein like 1	-1.55	0.611	-1.26	0.559	-1.4	0.106	1.61	0.089	-0.65
1459392_at	Phf8	PHD finger protein 8	-1.02	0.937	-2.18	0.045	-1.39	0.193	1.05	0.803	-0.88
1449539_at	Ms4a11	membrane-spanning 4-domains, subfamily A, member 11	-1.25	0.606	-1.2	0.812	-1.91	0.222	1.88	0.358	-0.62
1458760_at	---	---	-1.1	0.812	-1.36	0.577	-1.95	0.271	1.62	0.204	-0.7
1432797_at	2900060N12Rik	RIKEN cDNA 2900060N12 gene	-1.94	0.185	-1.9	0.068	1.12	0.786	-1.15	0.087	-0.97
1449596_at	C78142	expressed sequence C78142	-1.02	0.974	-1.61	0.153	-1.79	0.091	2	0.226	-0.61
1458913_at	4831440E17Rik	RIKEN cDNA 4831440E17 gene	1.15	0.659	-2.41	0.116	-1.67	0.145	-1.82	0.065	-1.19
1458993_at	AU022882	expressed sequence AU022882	1.25	0.57	-4.2	0.009	-1.49	0.419	-4.76	0.19	-2.3
1457732_at	Pcmtd2	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	-1.09	0.238	-1.98	0.017	-1.36	0.017	1	0.997	-0.86
1449754_at	AA511261	expressed sequence AA511261	-1.59	0.239	-1.27	0.583	-1.34	0.427	1.39	0.612	-0.7
1422426_at	Cmar	cell matrix adhesion regulator	-1.46	0.261	-1.29	0.309	-1.43	0.214	1.22	0.413	-0.74
1444124_a_at	E330017L17Rik	RIKEN cDNA E330017L17 gene	-1.76	0.277	-1.04	0.947	-1.59	0.292	1.78	0.129	-0.65
1420561_at	Trpc7	transient receptor potential cation channel, subfamily C, member 7	-1.35	0.562	-1.17	0.593	-1.77	0.21	2.34	0.36	-0.49
1437548_at	Bicd1	bicaudal D homolog 1 (Drosophila)	-1.51	0.003	-1.48	0.524	-1.21	0.248	1.8	0.118	-0.6
1447220_at	1700125H20Rik	RIKEN cDNA 1700125H20 gene	1.27	0.79	-3.36	0.002	-1.7	0.264	-1.83	0.325	-1.4
1459363_at	Atxn2	Ataxin 2	-1.28	0.237	-1.04	0.871	-2.39	0.007	1.26	0.426	-0.86
1431603_at	4931407E12Rik	RIKEN cDNA 4931407E12 gene	-2.31	0.035	1.03	0.923	-1.43	0.338	-1.36	0.505	-1.02
1425923_at	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	-1.86	0.35	-1.25	0.375	-1.22	0.452	1.39	0.534	-0.73
1453901_at	Aldoa-ps2	aldolase 1, A isoform, pseudogene 2	-1.34	0.609	-1.11	0.809	-1.95	0.057	1.86	0.135	-0.63
1452516_at	LOC545814 /// 493	sperm motility kinase 2-like /// RIKEN cDNA 4931427P12 gene	-1.48	0.493	-2.39	0.034	1.07	0.899	-1.78	0.078	-1.15
1443720_s_at	Bmpr1b	bone morphogenetic protein receptor, type 1B	-2.47	0.039	1.03	0.966	-1.38	0.328	-1.16	0.818	-0.99
1459790_x_at	Alx3	aristaless 3	-1.17	0.438	-1.68	0.358	-1.41	0.522	1.58	0.599	-0.67

1418995_at	---	---	-1.52	0.126	-1.68	0.273	-1.1	0.556	1.04	0.385	-0.82
1432910_at	Btbd7	BTB (POZ) domain containing 7	-1.29	0.445	-1.3	0.229	-1.62	0.002	1.13	0.241	-0.77
1454720_at	Apba3 /// Hs3st5	amyloid beta (A4) precursor protein-binding, family A, member 3 /// heparan sulfa	-3.38	0.268	1.11	0.745	-1.32	0.55	-1.32	0.346	-1.23
1447927_at	Mpa2l /// LOC6265	macrophage activation 2 like /// similar to macrophage activation 2 like /// similar t	1.1	0.584	-2.05	0.01	-1.73	0.033	-1.3	0.325	-0.99
1427551_at	Usp29	ubiquitin specific peptidase 29	-1.67	0.344	-1.05	0.937	-1.64	0.308	2.59	0.058	-0.44
1457137_at	---	Transcribed locus	-2.28	0.167	-1.17	0.695	-1.15	0.722	1.45	0.595	-0.79
1455919_at	Gm879	Gene model 879, (NCBI)	-1.97	0.55	-1.41	0.343	-1.06	0.922	1.26	0.395	-0.79
1432669_at	9030420N05Rik	RIKEN cDNA 9030420N05 gene	-1.4	0.054	-1.06	0.832	-1.95	0.038	2.3	0.113	-0.53
1439284_at	E230025E14Rik	RIKEN cDNA E230025E14 gene	-1.22	0.48	-1.59	0.438	-1.4	0.151	1.08	0.813	-0.78
1439545_at	Nrf1	Nuclear respiratory factor 1	-1.28	0.02	-1.47	0.029	-1.42	0.05	1.34	0.139	-0.71
1435206_at	Slc24a4	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	-1.92	0.212	-2.24	0.005	1.2	0.227	-2.07	0.283	-1.26
1433322_at	4930529F21Rik	RIKEN cDNA 4930529F21 gene	-1.82	0.263	-1.35	0.66	-1.15	0.707	1.44	0.199	-0.72
1437472_at	Unc13a	unc-13 homolog A (C. elegans)	-1.09	0.778	-1.45	0.628	-1.8	0.356	2.24	0.077	-0.53
1433168_x_at	5830456J23Rik	RIKEN cDNA 5830456J23 gene	1.08	0.803	-2.46	0.039	-1.48	0.614	-1.62	0.217	-1.12
1432090_at	Ccdc83	coiled-coil domain containing 83	-2.76	0.02	-1.32	0.66	1.05	0.945	-2.09	0.447	-1.28
1428041_at	1600002H07Rik	RIKEN cDNA 1600002H07 gene	-3.2	0.097	1.04	0.925	-1.23	0.439	-1.13	0.899	-1.13
1459564_at	C87580	expressed sequence C87580	1	0.997	-2.55	0.057	-1.29	0.336	-1.68	0.176	-1.13
1419831_at	AA416453	expressed sequence AA416453	1.26	0.687	-2.18	0.108	-2.22	0.028	-1.28	0.482	-1.11
1440716_at	6430604M11Rik	RIKEN cDNA 6430604M11 gene	-2.26	0.341	-1.23	0.581	-1.1	0.638	1.39	0.362	-0.8
1422290_at	Htr1d	5-hydroxytryptamine (serotonin) receptor 1D	-1.34	0.467	-2.37	0.256	-1	0.999	1.41	0.231	-0.82
1445950_at	C87926	cDNA sequence, C87926	-1.82	0.397	-1.9	0.271	1.09	0.711	-1.53	0.108	-1.04
1448016_at	Sass6	spindle assembly 6 homolog (C. elegans)	-1.22	0.452	-1.88	0.133	-1.22	0.191	2.54	0.146	-0.45
1422606_at	C1qtnf3	C1q and tumor necrosis factor related protein 3	-1	0.986	-1.16	0.458	-3.25	0.004	1.89	0.262	-0.88
1431647_a_at	Ceacam13	CEA-related cell adhesion molecule 13	-3.3	0.105	1.1	0.828	-1.3	0.678	-2.13	0.464	-1.41
1456122_at	---	---	-1.15	0.565	-1.52	0.192	-1.56	0.182	1.01	0.971	-0.81
1439749_at	Zap70	zeta-chain (TCR) associated protein kinase	-1.18	0.156	-1.44	0.034	-1.59	0.22	1.74	0.511	-0.62
1421517_at	St6galnac1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	1.01	0.987	-1.21	0.366	-2.99	0.062	-1.43	0.379	-1.16
1449071_at	Myl7	myosin, light polypeptide 7, regulatory	-3.12	0.393	1.11	0.811	-1.36	0.267	-1.27	0.737	-1.16
1457175_at	Numb	Numb gene homolog (Drosophila)	-1.31	0.148	-1.52	0.1	-1.35	0.119	1.1	0.683	-0.77
1422298_at	5530401N06Rik	RIKEN cDNA 5530401N06 gene	-1.43	0.358	-1.14	0.795	-1.69	0.021	1.63	0.257	-0.66
1430352_at	8430417A20Rik	RIKEN cDNA 8430417A20 gene	1	0.997	-1.27	0.272	-2.64	0.194	-1.46	0.295	-1.09
1446303_at	Igf1r	insulin-like growth factor I receptor	-1.22	0.45	-1.45	0.107	-1.52	0.191	1.16	0.533	-0.76
1430073_at	2900016B01Rik	RIKEN cDNA 2900016B01 gene	-2.12	0.447	-1.34	0.621	-1.05	0.644	1.11	0.697	-0.85
1431351_at	Pvt1	plasmacytoma variant translocation 1	-1.62	0.124	-1.64	0.297	-1.06	0.83	1.54	0.217	-0.7
1442962_at	AU022052	expressed sequence AU022052	-1.59	0.173	-1.36	0.232	-1.24	0.633	2.21	0.135	-0.5
1421769_at	Lmx1b	LIM homeobox transcription factor 1 beta	-1.74	0.186	-1.95	0.206	1.08	0.77	-1.32	0.497	-0.98
1416626_at	Pla2g1b	phospholipase A2, group IB, pancreas	-1.25	0.607	-1.52	0.442	-1.4	0.24	1.11	0.883	-0.77
1447049_at	Iqwd1	IQ motif and WD repeats 1	-1.19	0.661	-1.74	0.047	-1.33	0.116	1.73	0.136	-0.63
1444711_at	Ankrd15	ankyrin repeat domain 15	-1.05	0.925	-1.77	0.317	-1.52	0.633	1.23	0.47	-0.78
1454131_at	4931413K12Rik	RIKEN cDNA 4931413K12 gene	-1.37	0.024	-1.77	0.273	-1.14	0.796	1.97	0.36	-0.58
1433157_at	6330562C20Rik	RIKEN cDNA 6330562C20 gene	-2.49	0.177	-1.34	0.494	1.02	0.958	-1.32	0.521	-1.03
1455446_x_at	Acadsb	acyl-Coenzyme A dehydrogenase, short/branched chain	-1.2	0.007	-1.35	0.014	-1.68	0.013	1.13	0.478	-0.78
1448991_a_at	Ina	internexin neuronal intermediate filament protein, alpha	1.02	0.966	-2.04	0.043	-1.5	0.166	-2.43	0.147	-1.24
1447091_at	Jmjd2c	Jumonji domain containing 2C	-1.07	0.915	-1.45	0.257	-1.82	0.04	1.39	0.416	-0.74
1427426_at	Kcnq5	potassium voltage-gated channel, subfamily Q, member 5	1.12	0.514	-3.42	0.05	-1.33	0.548	-1.22	0.557	-1.21
1451823_at	Clca4	chloride channel calcium activated 4	-4.13	0.095	1.55	0.324	-2.61	0.066	-1.39	0.469	-1.65
1447656_at	Zdhhc17	zinc finger, DHHC domain containing 17	-1.71	0.061	-1.44	0.349	-1.12	0.816	1.11	0.869	-0.79
1446935_at	9130011E15Rik	RIKEN cDNA 9130011E15 gene	-4.73	0.224	-1.63	0.37	1.35	0.013	-1.14	0.793	-1.54
1447299_at	---	---	1.14	0.884	-1.72	0.341	-2.2	0.025	-1.02	0.896	-0.95
1425208_at	Lbh	limb-bud and heart	-1.7	0.627	-2.03	0.342	1.09	0.889	-1.44	0.632	-1.02
1454528_at	A930011E06Rik	RIKEN cDNA A930011E06 gene	-1.84	0.222	-1.01	0.978	-1.56	0.316	1.04	0.961	-0.84
1432303_at	9330198I05Rik	RIKEN cDNA 9330198I05 gene	-1.46	0.047	-1.26	0.374	-1.44	0.323	1.52	0.403	-0.66
1444914_at	---	---	-1.61	0.301	-2.83	0.243	1.2	0.641	-1.64	0.275	-1.22

1445837_at	Ga17	Dendritic cell protein GA17	-1.28	0.579	1.05	0.705	-2.92	0.003	-1.91	0.067	-1.27
1447273_x_at	Atp10a	ATPase, class V, type 10A	-2.16	0.204	-1.25	0.721	-1.1	0.758	1.06	0.75	-0.86
1437574_at	Adamts18	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.53	0.194	-3.02	0.404	1.19	0.672	-1.47	0.618	-1.21
1449593_at	---	---	1.12	0.753	-1.53	0.482	-2.47	0.163	-1.52	0.306	-1.1
1443153_at	Trip11	Thyroid hormone receptor interactor 11	-1.52	0.323	1.01	0.957	-1.99	0.005	-1.79	0.04	-1.07
1457539_at	D10Ertd709e	DNA segment, Chr 10, ERATO Doi 709, expressed	-1.2	0.329	-1.58	0.169	-1.41	0.09	1.15	0.287	-0.76
1415846_a_at	Ldhc	lactate dehydrogenase C	-2.33	0.357	-1.89	0.182	1.22	0.719	-1.52	0.518	-1.13
1449381_a_at	Pacsin1	protein kinase C and casein kinase substrate in neurons 1	-2.29	0.47	1.02	0.868	-1.4	0.302	-2.92	0.059	-1.4
1430265_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.88	0.192	1.08	0.867	-1.78	0.067	-1.3	0.123	-0.97
1446965_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	-1.21	0.445	-1.3	0.167	-1.73	0.029	2.03	0.142	-0.55
1432789_at	8030476L19Rik	RIKEN cDNA 8030476L19 gene	-3.96	0.339	-1.16	0.775	1.06	0.87	-1.12	0.878	-1.29
1445518_at	Zfhx1b	Zinc finger homeobox 1b	-1.15	0.498	-1.32	0.264	-1.82	0.057	1.12	0.717	-0.79
1439669_at	6430571L13Rik	RIKEN cDNA 6430571L13 gene	-1.16	0.568	-1.25	0.73	-1.95	0.263	2.22	0.181	-0.53
1459133_at	Edem3	ER degradation enhancer, mannosidase alpha-like 3	1.07	0.825	-1.56	0.114	-2.16	0.02	-1.33	0.216	-0.99
1459365_at	4930429A22Rik	RIKEN cDNA 4930429A22 gene	-1.16	0.64	-1.19	0.449	-2.09	0.104	1.44	0.488	-0.75
1439915_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	-1.23	0.228	-1.6	0.289	-1.35	0.465	1.43	0.153	-0.69
1443062_at	Auts2	autism susceptibility candidate 2	1.04	0.967	-1.15	0.655	-3.69	0.065	-2.01	0.307	-1.45
1426561_a_at	Npnt	nephronectin	1.14	0.376	-1.63	0.54	-2.37	0.004	-1.73	0.133	-1.15
1445939_at	Mtus1	Mitochondrial tumor suppressor 1	-1.29	0.665	-1.12	0.883	-1.97	0.028	2.34	0.098	-0.51
1441330_at	Crb1	crumbs homolog 1 (Drosophila)	-1.52	0.294	-1.02	0.963	-1.84	0.009	2.48	0.28	-0.48
1444509_at	---	Transcribed locus	-1.14	0.741	-1.94	0.294	-1.28	0.434	1.79	0.135	-0.64
1422296_at	5730470L24Rik	RIKEN cDNA 5730470L24 gene	-1.67	0.063	-1.26	0.664	-1.28	0.422	1.34	0.691	-0.71
1421396_at	Pcsk1	proprotein convertase subtilisin/kexin type 1	-1.36	0.767	-1.67	0.429	-1.18	0.217	1.17	0.501	-0.76
1435537_at	Ptprd	protein tyrosine phosphatase, receptor type, D	-1.16	0.205	-1.34	0.051	-1.75	0.016	1.12	0.774	-0.79
1441376_at	Gabarapl2	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	-1.14	0.083	-1.56	0.012	-1.52	0.074	1.45	0.201	-0.69
1445381_at	---	---	-2.54	0.097	-1.27	0.475	-1.01	0.988	1.48	0.304	-0.83
1431541_at	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisia	-1.55	0.479	-1.92	0.394	1.01	0.967	-1.19	0.76	-0.91
1420260_at	Phf7	PHD finger protein 7	-1.36	0.256	-1.37	0.532	-1.4	0.495	1.07	0.803	-0.77
1446576_at	4931419K03Rik	RIKEN cDNA 4931419K03 gene	-1.68	0.512	-1.57	0.606	-1.06	0.93	3.3	0.337	-0.25
1454940_at	Psma5 /// LOC5456	proteasome (prosome, macropain) subunit, alpha type 5 /// similar to Proteasome	-1.11	0.645	-1.87	0.158	-1.34	0.258	1	0.994	-0.83
1425126_at	Ncam1	neural cell adhesion molecule 1	-1.7	0.58	1.2	0.632	-2.57	0.088	-2.73	0.029	-1.45
1425800_at	Rad9b	RAD9 homolog B (S. cerevisiae)	-1.17	0.541	-2.24	0.084	-1.14	0.522	1.66	0.269	-0.72
1445515_at	---	---	-1.93	0.363	-1.16	0.741	-1.25	0.163	1.3	0.474	-0.76
1442718_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.82	0.222	1.09	0.799	-1.86	0.307	-1.42	0.237	-1
1441754_at	---	---	1.07	0.848	-2.72	0.064	-1.34	0.403	-1	0.986	-1
1442633_at	---	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypoth	-1.03	0.82	-2.1	0.049	-1.36	0.083	1.44	0.589	-0.76
1451032_at	Fhl4	four and a half LIM domains 4	-3.26	0.05	-1.17	0.79	1.02	0.969	-2.81	0.165	-1.56
1432994_at	2900057E15Rik	RIKEN cDNA 2900057E15 gene	1.28	0.736	-2.95	0.312	-1.78	0.295	-1.01	0.971	-1.12
1445217_at	A730073F16Rik	RIKEN cDNA A730073F16 gene	1.04	0.948	-1.73	0.535	-1.78	0.469	-1.48	0.135	-0.99
1444472_at	Snf1lk2	SNF1-like kinase 2	-1.3	0.399	-1.32	0.324	-1.53	0.022	1.15	0.551	-0.75
1445327_at	Cyfip1	Cytoplasmic FMR1 interacting protein 1	-1.13	0.764	-1.83	0.128	-1.34	0.257	1.35	0.116	-0.74
1447531_x_at	---	---	-1.21	0.607	-1.4	0.379	-1.56	0.073	1.18	0.687	-0.75
1437827_s_at	Pfpl	Pore forming protein-like	-1.94	0.427	-1.07	0.866	-1.37	0.393	1.35	0.638	-0.76
1442921_at	Mmp24	Matrix metallopeptidase 24	-1.72	0.254	-2.22	0.066	1.15	0.689	-1.37	0.653	-1.04
1431851_at	4930534P07Rik	RIKEN cDNA 4930534P07 gene	-4.01	0.08	-2.17	0.152	1.47	0.17	-1.32	0.554	-1.51
1431260_at	4833417C18Rik	RIKEN cDNA 4833417C18 gene	-1.3	0.534	-1.78	0.059	-1.18	0.603	1.15	0.292	-0.78
1433160_at	1700008N17Rik	RIKEN cDNA 1700008N17 gene	-1.11	0.892	-1.78	0.022	-1.39	0.482	1.21	0.716	-0.77
1446114_at	Inpp5a	Inositol polyphosphate-5-phosphatase A	-2.3	0.269	1.14	0.835	-1.64	0.1	-2.8	0.225	-1.4
1425759_at	Nobox	NOBOX oogenesis homeobox	-1.07	0.927	-1.84	0.237	-1.43	0.478	1.82	0.449	-0.63
1436239_at	Slc5a5	solute carrier family 5 (sodium iodide symporter), member 5	-2.38	0.005	-1.82	0.023	1.21	0.501	-1.05	0.656	-1.01
1458367_at	Gm94	gene model 94, (NCBI)	-1.73	0.434	-3.4	0.025	1.31	0.422	-1.08	0.914	-1.22
1418213_at	Krt23	keratin 23	-5	0.004	1.23	0.852	-1.33	0.113	-1.81	0.284	-1.73
1439586_at	LOC548102	hypothetical LOC548102	-1.22	0.538	-1.46	0.003	-1.48	0.077	1.14	0.75	-0.75

1427865_at	---	---	-1.61	0.495	1.26	0.297	-3.35	0.025	-2.56	0.364	-1.56
1440345_at	AI450353	expressed sequence AI450353	-1.63	0.355	-1.18	0.162	-1.39	0.517	1.29	0.388	-0.73
1450277_at	Avpr2	arginine vasopressin receptor 2	1	0.961	-2.07	0.02	-1.44	0.602	-1.09	0.726	-0.9
1446526_at	9330199F22Rik	RIKEN cDNA 9330199F22 gene	-1.25	0.103	-1.97	0.283	-1.14	0.553	1.02	0.965	-0.84
1443613_x_at	Ascc2	Activating signal cointegrator 1 complex subunit 2	-1.46	0.717	-1.39	0.09	-1.28	0.263	1.03	0.966	-0.78
1440506_at	Slc7a2	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	-1.66	0.387	-1.87	0.144	1.05	0.828	-1.78	0.35	-1.07
1438747_at	A930006K02Rik	RIKEN cDNA A930006K02 gene	-1.33	0.472	-1.58	0.377	-1.25	0.63	2.09	0.261	-0.52
1440662_at	Rgl1	Ral guanine nucleotide dissociation stimulator,-like 1	-1.48	0.233	-1.09	0.851	-1.7	0.065	1.08	0.872	-0.8
1440436_at	A730030A06	hypothetical protein A730030A06	-1.41	0.174	-1.2	0.553	-1.56	0.084	1.81	0.291	-0.59
1458473_at	Pou6f2	POU domain, class 6, transcription factor 2	-1.48	0.433	-1.28	0.517	-1.37	0.114	1.02	0.886	-0.78
1421048_a_at	Ypel1	yippee-like 1 (Drosophila)	-1.29	0.402	-1.89	0.15	-1.14	0.333	1.03	0.692	-0.82
1454457_at	4930439G18Rik	RIKEN cDNA 4930439G18 gene	-1.56	0.324	-1.41	0.139	-1.2	0.519	1.11	0.78	-0.76
1449463_at	Klk1b8	kallikrein 1-related peptidase b8	-1.54	0.463	-1.28	0.731	-1.32	0.521	1.46	0.302	-0.67
1449881_a_at	Casr	calcium-sensing receptor	-1.13	0.314	-1.46	0.387	-1.62	0.094	1.57	0.577	-0.66
1446909_at	Amotl1	Angiomotin-like 1	-2.08	0.248	-1.01	0.987	-1.4	0.569	1.52	0.155	-0.74
1420585_a_at	Nxf2	nuclear RNA export factor 2	-1.39	0.227	-1.21	0.567	-1.55	0.024	1.24	0.477	-0.73
1455782_at	Samd7	sterile alpha motif domain containing 7	-2.61	0.048	1.13	0.695	-1.49	0.471	-1.23	0.687	-1.05
1448949_at	Car4	carbonic anhydrase 4	-1.13	0.394	-1.53	0.481	-1.53	0.006	1.87	0.113	-0.58
1437049_at	---	Transcribed locus	-1.26	0.07	-1.42	0.315	-1.46	0.109	1.57	0.102	-0.64
1458472_at	4932417H02Rik	RIKEN cDNA 4932417H02 gene	-1.2	0.538	-2.99	0.153	1.02	0.928	-1.3	0.307	-1.12
1458817_at	---	---	-1.23	0.829	-1.46	0.577	-1.45	0.459	1.61	0.292	-0.63
1444642_at	---	Transcribed locus	-1.15	0.533	-1.3	0.469	-1.82	0.118	1.21	0.355	-0.76
1450595_at	V1rc1	vomeronasal 1 receptor, C1	-1.54	0.183	-1.62	0.368	-1.08	0.729	1.62	0.205	-0.66
1457565_at	C130052G03Rik	RIKEN cDNA C130052G03 gene	-2.24	0.056	-1.19	0.715	-1.11	0.795	2.3	0.269	-0.56
1418171_at	Tceal8	transcription elongation factor A (SII)-like 8	-1.25	0.055	-1.29	0.138	-1.63	0.007	2.69	0.321	-0.37
1445757_at	Tbx3	T-box 3	1.22	0.648	-2.16	0.07	-1.98	0.007	-1.16	0.414	-1.02
1438743_at	Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	-1.54	0.563	-1.39	0.284	-1.22	0.335	1.25	0.322	-0.73
1459325_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.49	0.172	-1.36	0.177	-1.28	0.082	1.21	0.683	-0.73
1459248_at	Ptpn9	Protein tyrosine phosphatase, non-receptor type 9	-1.51	0.529	1.06	0.877	-2.13	0.145	-1.61	0.178	-1.05
1432957_at	5730407O05Rik	RIKEN cDNA 5730407O05 gene	-1.24	0.809	-1.1	0.9	-2.13	0.248	1.74	0.477	-0.68
1433394_at	Mast4	microtubule associated serine/threonine kinase family member 4	-1.24	0.422	-1.62	0.481	-1.31	0.093	1.01	0.966	-0.79
1440697_at	AI746446	expressed sequence AI746446	-1.24	0.415	-2.7	0.065	1.01	0.98	-1.07	0.883	-1
1427812_at	Ids	iduronate 2-sulfatase	-1.77	0.531	-1.38	0.548	-1.11	0.72	1.16	0.85	-0.77
1442862_at	---	---	1.04	0.63	-2.01	0.282	-1.53	0.003	-1.31	0.241	-0.95
1430096_at	2900017F05Rik	RIKEN cDNA 2900017F05 gene	-1.98	0.188	-1.38	0.359	-1.04	0.851	1.59	0.551	-0.7
1422634_a_at	Vsig2	V-set and immunoglobulin domain containing 2	-1	0.995	-1.78	0.144	-1.59	0.003	1.17	0.738	-0.8
1424296_at	Gclc	glutamate-cysteine ligase, catalytic subunit	-1.32	0.081	-1.52	0.065	-1.3	0.007	2.39	0.199	-0.44
1431412_at	2810455B08Rik	RIKEN cDNA 2810455B08 gene	1.04	0.866	-1.71	0.044	-1.76	0.027	-1.34	0.307	-0.94
1456104_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1.76	0.07	-1.54	0.207	-1.03	0.787	1.07	0.645	-0.81
1443557_at	---	---	-1.79	0.562	-1.93	0.225	1.12	0.596	-1.4	0.252	-1
1440969_at	BC030308	cDNA sequence BC030308	-1.21	0.212	-1.2	0.587	-1.89	0.006	1.08	0.581	-0.8
1435104_at	D130004H04Rik	RIKEN cDNA D130004H04 gene	-3.09	0.298	-1.27	0.642	1.08	0.874	-2.55	0.23	-1.46
1444530_at	---	Transcribed locus	-1.15	0.544	-1.64	0.013	-1.41	0.252	1.03	0.867	-0.79
1459822_at	Rae1	RAE1 RNA export 1 homolog (S. pombe)	-1.04	0.954	-1.33	0.719	-2.1	0.267	1.23	0.786	-0.81
1446651_at	---	---	-2.14	0.399	-1.26	0.688	-1.07	0.897	2.16	0.34	-0.58
1431770_at	Cherp	calcium homeostasis endoplasmic reticulum protein	-1.2	0.775	-1.48	0.321	-1.45	0.103	1.11	0.491	-0.76
1443981_at	---	---	-1.04	0.927	-2.17	0.003	-1.29	0.014	1.18	0.66	-0.83
1454235_a_at	Ing5	inhibitor of growth family, member 5	-1.48	0.487	-1.92	0.287	-1	0.995	1.02	0.957	-0.85
1450046_at	Tmem59	transmembrane protein 59	-1.48	0.107	-1.8	0.004	-1.04	0.745	1.39	0.38	-0.73
1459210_at	Tmem108	transmembrane protein 108	-2.25	0.125	1.19	0.576	-1.8	0.002	-1.69	0.195	-1.14
1453625_at	2210407P21Rik	RIKEN cDNA 2210407P21 gene	-1.52	0.372	-1.42	0.222	-1.2	0.642	1.65	0.438	-0.62
1428994_s_at	1110017I16Rik	RIKEN cDNA 1110017I16 gene	-1.02	0.976	-3.59	0.351	-1.07	0.892	1.11	0.848	-1.14
1453966_at	2610008G14Rik	RIKEN cDNA 2610008G14 gene	-1.25	0.529	-1.14	0.76	-1.95	0.329	1.22	0.783	-0.78

1460122_at	Tmem41b	transmembrane protein 41B	-1.28	0.018	-1.42	0.185	-1.42	0.035	1.36	0.184	-0.69
1453523_at	A030006P16Rik	RIKEN cDNA A030006P16 gene	1.01	0.92	-1.21	0.635	-2.84	0.022	-1.09	0.838	-1.03
1456459_x_at	Ccdc53	coiled-coil domain containing 53	1.13	0.922	-2.54	0.108	-1.49	0.466	-1.58	0.533	-1.12
1447532_at	1700025G04Rik	RIKEN cDNA 1700025G04 gene	-1.62	0.703	-1.62	0.424	-1.04	0.832	1.19	0.231	-0.77
1448044_a_at	---	Adult male kidney cDNA, RIKEN full-length enriched library, clone:F530012N16 p	-1.31	0.154	-1.72	0.055	-1.18	0.716	2	0.196	-0.55
1429052_at	Ptprd	protein tyrosine phosphatase, receptor type, D	-1.05	0.408	-1.29	0.294	-2.13	0.013	1.06	0.88	-0.85
1455619_at	BC062258	cDNA sequence BC062258	1	0.998	-1.93	0.207	-1.48	0.216	-1.54	0.012	-0.99
1445509_at	Atf7	Activating transcription factor 7	-1.57	0.431	-1.72	0.112	-1.02	0.93	1.26	0.072	-0.76
1437579_at	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	-1.24	0.186	-1.78	0.126	-1.2	0.283	1.47	0.37	-0.69
1432788_at	6720420G18Rik	RIKEN cDNA 6720420G18 gene	-1.95	0.475	-1.33	0.554	-1.07	0.801	1.53	0.229	-0.71
1447835_at	2610528K11Rik	RIKEN cDNA 2610528K11 gene	-1.58	0.408	-1.28	0.686	-1.28	0.545	1.92	0.131	-0.55
1420071_at	Serpinb6e	serine (or cysteine) peptidase inhibitor, clade B, member 6e	-1.4	0.722	-1.18	0.757	-1.57	0.246	1.73	0.233	-0.61
1433581_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	-1.28	0.288	-1.09	0.232	-2	0.084	1.31	0.37	-0.76
1441050_at	Strn3	Striatin, calmodulin binding protein 3	-1.04	0.87	-1.31	0.182	-2.11	0.047	1.03	0.858	-0.86
1441366_at	---	---	-1.5	0.008	-2.28	0.381	1.09	0.868	-1.08	0.587	-0.94
1445527_at	Kpna3	Karyopherin (importin) alpha 3	-1.57	0.515	-1.11	0.903	-1.51	0.128	1.08	0.479	-0.78
1434319_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	-1.53	0.604	-1.03	0.88	-1.73	0.193	1.18	0.472	-0.78
1457766_at	Wfdc6a	WAP four-disulfide core domain 6A	-1.26	0.61	-1.01	0.984	-2.38	0.039	1.45	0.271	-0.8
1421390_at	Slc12a1	solute carrier family 12, member 1	-1.54	0.327	-1.52	0.498	-1.13	0.694	1.63	0.574	-0.64
1458550_at	Myo1d	myosin ID	-1.15	0.597	-1.3	0.404	-1.78	0.025	2.38	0.239	-0.46
1419763_at	2610020O08Rik	RIKEN cDNA 2610020O08 gene	-1.56	0.042	-2.13	0.054	1.09	0.691	-1.08	0.844	-0.92
1430633_s_at	C430045I18Rik	RIKEN cDNA C430045I18 gene	-1.44	0.213	-1.44	0.294	-1.23	0.288	1.44	0.166	-0.67
1444046_at	D430041B17Rik	RIKEN cDNA D430041B17 gene	-1.76	0.115	-1.7	0.128	1.04	0.917	-1.01	0.969	-0.86
1430899_at	Muc5ac	mucin 5, subtypes A and C, tracheobronchial/gastric	-1.74	0.365	-1.09	0.855	-1.41	0.629	1.24	0.651	-0.75
1455145_at	---	14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:32224(	-1.14	0.47	-1.37	0.256	-1.68	0.034	2.09	0.076	-0.53
1443892_at	LOC435970 /// LOC	hypothetical LOC435970 /// similar to gonadotropin inducible ovarian transcriptior	-2.82	0.071	-1.26	0.592	1.05	0.933	-1.13	0.909	-1.04
1456834_at	Ibrdc2	IBR domain containing 2	-1.82	0.503	1.24	0.569	-2.45	0.081	-1.1	0.795	-1.03
1456102_a_at	Cul5	cullin 5	-1.11	0.486	-1.17	0.494	-2.25	0.018	1.05	0.884	-0.87
1452859_at	1200016B10Rik	RIKEN cDNA 1200016B10 gene	-1.28	0.03	-1.27	0.051	-1.57	0.037	1.21	0.475	-0.73
1442412_at	Dnahc9	dynein, axonemal, heavy chain 9	-1.28	0.466	-1.57	0.385	-1.28	0.317	1.49	0.569	-0.66
1447077_at	Add3	Adducin 3 (gamma)	1.2	0.838	-2.88	0.021	-1.53	0.137	-1.57	0.114	-1.2
1459129_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930548A09 pr(	-1.46	0.14	-1.24	0.385	-1.42	0.167	1.07	0.681	-0.76
1445767_at	Ptprd	protein tyrosine phosphatase, receptor type, D	1.04	0.965	-1.41	0.553	-2.18	0.215	-2.59	0.296	-1.29
1453213_at	Spata9	spermatogenesis associated 9	-2.26	0.167	-1.13	0.77	-1.14	0.392	1.1	0.879	-0.86
1449716_s_at	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	-1.85	0.037	-1.33	0.225	-1.1	0.423	1.13	0.62	-0.79
1437577_at	---	---	-1.27	0.146	-1.19	0.08	-1.75	0.002	1.1	0.393	-0.78
1443715_at	LOC380843 /// LOC	similar to RNA binding motif protein 24 /// similar to RNA binding motif protein 24	-1.2	0.661	-1.16	0.79	-1.96	0.171	1.39	0.524	-0.73
1419196_at	Hamp1	hepcidin antimicrobial peptide 1	-1.18	0.051	-1.78	0.273	-1.25	0.325	2.14	0.096	-0.52
1458314_at	Slc1a2	Solute carrier family 1 (glial high affinity glutamate transporter), member 2	-2.76	0.275	-1.27	0.255	1.06	0.754	-4.8	0.009	-1.94
1459349_at	A930011G23Rik	RIKEN cDNA A930011G23 gene	-1.12	0.731	-1.62	0.213	-1.45	0.382	1.29	0.526	-0.72
1439016_x_at	Sprr2a	small proline-rich protein 2A	-1.46	0.146	-1.88	0.02	-1.01	0.94	1.21	0.223	-0.79
1447241_at	H2afy2	H2A histone family, member Y2	-1.42	0.238	-1.43	0.341	-1.25	0.177	1.37	0.121	-0.68
1458428_at	Kcnt1	potassium channel, subfamily T, member 1	-1.58	0.013	-1	0.992	-1.74	0.142	1.15	0.502	-0.79
1432739_at	2900060K15Rik	RIKEN cDNA 2900060K15 gene	-2.46	0.112	1.05	0.947	-1.33	0.4	-2.57	0.252	-1.33
1443589_at	DXErtd242e	DNA segment, Chr X, ERATO Doi 242, expressed	1.23	0.633	-1.63	0.388	-2.82	0.083	-1.26	0.199	-1.12
1444067_at	Pde1c	phosphodiesterase 1C	-2.01	0.114	-1.22	0.647	-1.13	0.756	1.09	0.726	-0.82
1420435_at	1700011A15Rik	RIKEN cDNA 1700011A15 gene	-2.71	0.013	-1.07	0.862	-1.11	0.842	1.17	0.618	-0.93
1445788_at	Igf2bp1	Insulin-like growth factor 2, binding protein 1	-1.33	0.724	-1.32	0.659	-1.43	0.159	1.09	0.905	-0.75
1438912_at	Hdgfrp2	hepatoma-derived growth factor, related protein 2	-1.1	0.476	-2.17	0.028	-1.2	0.412	1.21	0.3	-0.82
1430489_at	5430416G10Rik	RIKEN cDNA 5430416G10 gene	-1.34	0.183	-1.1	0.748	-1.82	0.09	1.63	0.057	-0.66
1423606_at	Postn	periostin, osteoblast specific factor	-1.37	0.371	1.06	0.714	-2.41	0.014	-1.7	0.135	-1.11
1434297_at	E130304F04Rik	RIKEN cDNA E130304F04 gene	-1.95	0.207	-1.76	0.14	1.12	0.773	-2.72	0.261	-1.33
1446789_at	Zcrb1	Zinc finger CCHC-type and RNA binding motif 1	-1.85	0.237	-1.22	0.803	-1.18	0.115	1.32	0.492	-0.73

1429346_a_at	4933440J22Rik	RIKEN cDNA 4933440J22 gene	-1.27	0.215	-1.62	0.221	-1.25	0.481	1.52	0.375	-0.65
1436713_s_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.06	0.476	-1.48	0.345	-1.7	0.187	1.18	0.363	-0.76
1432658_at	2810403D21Rik	RIKEN cDNA 2810403D21 gene	-2.19	0.54	-2.39	0.297	1.33	0.515	-2.62	0.358	-1.47
1432040_at	Kcnq1ot1	KCNQ1 overlapping transcript 1	-1.61	0.023	-1.39	0.134	-1.16	0.393	1	0.995	-0.79
1419197_x_at	Hamp1	hepcidin antimicrobial peptide 1	-1.29	0.432	-1.77	0.284	-1.16	0.393	2.27	0.007	-0.49
1443587_at	AK129128	cDNA sequence AK129128	-1.48	0.711	-1.98	0.35	1.03	0.964	-2.2	0.222	-1.16
1447673_x_at	1700015C15Rik	RIKEN cDNA 1700015C15 gene	-1.2	0.301	-1.36	0.631	-1.56	0.301	1.59	0.015	-0.63
1429669_at	4930488L21Rik	RIKEN cDNA 4930488L21 gene	-1.5	0.139	-1.16	0.572	-1.48	0.341	1.03	0.948	-0.78
1453906_at	Thrap2	thyroid hormone receptor associated protein 2	-1.27	0.476	-1.38	0.514	-1.44	0.2	1.06	0.851	-0.76
1442730_at	---	---	1.15	0.508	-2.42	0.243	-1.56	0.461	-1.67	0.199	-1.13
1418683_at	Lin7b	lin-7 homolog B (C. elegans)	-1.44	0.746	1.04	0.89	-2.11	0.058	-2.95	0.107	-1.37
1447065_at	9630041C05	hypothetical protein 9630041C05	-2.37	0.414	-1.62	0.153	1.17	0.658	-2.82	0.015	-1.41
1441163_at	Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	-1.22	0.498	-3.43	0.159	1.1	0.829	-1.19	0.454	-1.19
1429725_at	Atbf1	AT motif binding factor 1	-1.18	0.677	-2.22	0.074	-1.1	0.44	1.16	0.626	-0.83
1459373_at	Epb4.1	Erythrocyte protein band 4.1	-1.12	0.712	-1.34	0.286	-1.75	0.184	3.04	0.239	-0.29
1431868_at	Akap4	A kinase (PRKA) anchor protein 4	-3.22	0.103	-1.4	0.394	1.19	0.559	-1.74	0.222	-1.29
1427587_at	Zfp28	zinc finger protein 28	-1.24	0.087	-2.67	0.075	1.03	0.913	-1.1	0.745	-0.99
1447340_at	---	Adult male kidney cDNA, RIKEN full-length enriched library, clone:F530214C21 p	-1.55	0.29	-1.18	0.319	-1.39	0.052	1.09	0.843	-0.76
1451647_at	Slc24a1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	-1.5	0.182	-1.13	0.816	-1.52	0.405	1.1	0.892	-0.76
1459144_at	Fndc3a	Fibronectin type III domain containing 3a	-1.21	0.357	-1.51	0.099	-1.38	0.028	1.15	0.712	-0.74
1455228_at	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	-1.44	0.096	-1.24	0.043	-1.41	0.005	1.34	0.385	-0.69
1446035_at	---	PREDICTED: Mus musculus similar to Protein CXorf22 (LOC629131), mRNA	-3.35	0.067	1.3	0.635	-1.63	0.214	-3.07	0.129	-1.69
1445427_at	Nlk	Nemo like kinase	1.18	0.709	-2.3	0.308	-1.67	0.271	-1.38	0.398	-1.04
1459230_at	D530025C14Rik	RIKEN cDNA B430319G15 gene	-1.17	0.233	-1.67	0.057	-1.32	0.14	1.85	0.257	-0.58
1421702_at	Rdh1	retinol dehydrogenase 1 (all trans)	-1.49	0.507	-1.72	0.248	-1.04	0.939	1.26	0.633	-0.75
1419802_at	Ccdc12	coiled-coil domain containing 12	-1.75	0.134	-1.03	0.924	-1.49	0.231	1.21	0.399	-0.76
1455764_at	B930007L02Rik	RIKEN cDNA B930007L02 gene	-1.69	0.209	-1.38	0.643	-1.12	0.358	1.15	0.65	-0.76
1442293_at	---	Transcribed locus	-1.41	0.108	-1.69	0.121	-1.1	0.585	1.33	0.414	-0.72
1433338_at	6720460K10Rik	RIKEN cDNA 6720460K10 gene	-1.16	0.541	-1.21	0.602	-1.89	0.085	1.2	0.491	-0.77
1418352_at	Hsd17b2	hydroxysteroid (17-beta) dehydrogenase 2	1.04	0.775	-1.65	0.033	-1.78	0.286	-2.23	0.222	-1.15
1451886_at	Speg	SPEG complex locus	-2.76	0.031	-1.11	0.862	-1.05	0.93	1.53	0.148	-0.85
1456345_at	A630057N01Rik	RIKEN cDNA A630057N01 gene	-1.43	0.455	-1.11	0.841	-1.64	0.305	1.47	0.25	-0.68
1437940_at	Apba1	amyloid beta (A4) precursor protein binding, family A, member 1	-1.46	0.306	-1.4	0.279	-1.23	0.15	1.31	0.35	-0.69
1427808_at	Nfya	nuclear transcription factor-Y alpha	-2.19	0.277	-1.08	0.881	-1.21	0.558	1.3	0.69	-0.79
1458957_at	LOC623548	Similar to pyridoxal (pyridoxine, vitamin B6) kinase	1.11	0.894	-2.17	0.157	-1.56	0.441	-1.13	0.778	-0.94
1449661_at	Suz12	Suppressor of zeste 12 homolog (Drosophila)	-1.21	0.425	-1.36	0.492	-1.53	0.237	1.73	0.157	-0.59
1420269_at	Npm1	Nucleophosmin 1	-1.86	0.207	-1.05	0.87	-1.37	0.51	2.17	0.143	-0.53
1431991_at	2410004P03Rik	RIKEN cDNA 2410004P03 gene	-1.92	0.123	-1.39	0.357	-1.02	0.94	1.1	0.845	-0.81
1436468_at	Zdhhc8	zinc finger, DHHC domain containing 8	-2.33	0.066	-1.61	0.258	1.17	0.226	-1.53	0.033	-1.08
1448381_at	Gfm1	G elongation factor, mitochondrial 1	-1.29	0.404	-1.35	0.072	-1.44	0.002	1.24	0.448	-0.71
1456960_at	Adk	Adenosine kinase	-1.23	0.351	-1.19	0.327	-1.77	0.009	1.38	0.322	-0.7
1453642_at	6530411M01Rik	RIKEN cDNA 6530411M01 gene	-1.96	0.512	-1.52	0.489	1.05	0.705	-1.68	0.276	-1.03
1439132_at	Phf8	PHD finger protein 8	-1.08	0.445	-1.51	0.345	-1.6	0.22	1.22	0.694	-0.74
1433357_at	5730422E09Rik	RIKEN cDNA 5730422E09 gene	1.16	0.028	-1.72	0.397	-2.11	0.066	-1.3	0.274	-0.99
1439691_at	D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579, expressed	-1.31	0.06	-1.36	0.217	-1.39	0.065	1.36	0.193	-0.67
1432210_at	4933401H06Rik	RIKEN cDNA 4933401H06 gene	-2.77	0.087	-1	0.994	-1.16	0.611	1.08	0.796	-0.96
1436089_at	Ints6	integrator complex subunit 6	-1.78	0.003	-1.17	0.141	-1.25	0.135	1.28	0.49	-0.73
1456921_at	A2bp1	Ataxin 2 binding protein 1	-1.09	0.904	-1.3	0.182	-1.88	0.269	1.12	0.855	-0.79
1452858_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	-1.38	0.101	-1.52	0.179	-1.2	0.188	1.5	0.374	-0.65
1447421_at	---	Transcribed locus	-1.53	0.002	1.03	0.908	-1.87	0.032	-1.23	0.364	-0.9
1434910_at	---	---	-1.37	0.035	-1.6	0.106	-1.16	0.004	1.03	0.689	-0.77
1455698_at	Tloc1	translocation protein 1	-1.13	0.606	-1.42	0.18	-1.6	0.141	1.15	0.625	-0.75
1439449_at	Satb1	special AT-rich sequence binding protein 1	-2.38	0.081	1.18	0.731	-1.61	0.262	-4.48	0.01	-1.82

1447732_x_at	Peg3	paternally expressed 3	-1.09	0.844	-2.77	0.047	-1.06	0.648	2.13	0.307	-0.7
1458880_at	---	---	1.14	0.779	-1.45	0.434	-2.55	0.025	-1.72	0.342	-1.15
1433090_at	---	---	-3.23	0.215	-1.27	0.637	1.12	0.769	-1.18	0.165	-1.14
1438796_at	---	---	-2.05	0.419	1.49	0.113	-4.11	0.059	-2.29	0.034	-1.74
1443637_at	2900084M01Rik	RIKEN cDNA 2900084M01 gene	-1.29	0.597	-2.21	0.177	-1.01	0.985	1.24	0.721	-0.82
1457925_at	C530049I24Rik	RIKEN cDNA C530049I24 gene	-1.04	0.762	-1.45	0.134	-1.75	0.408	1.03	0.969	-0.8
1444502_at	Pet112l	PET112-like (yeast)	-1.6	0.072	-1.03	0.926	-1.6	0.142	1.71	0.194	-0.63
1427363_at	Myo10	Myosin X	-1.11	0.129	-1.5	0.048	-1.54	0.065	1.23	0.002	-0.73
1436631_at	2010010M04Rik	RIKEN cDNA 2010010M04 gene	-1.06	0.457	-1.35	0.105	-1.89	0.009	1.12	0.258	-0.79
1446537_at	Ga17	Dendritic cell protein GA17	1.24	0.365	-1.71	0.123	-2.55	0.001	-1.53	0.232	-1.14
1426035_at	LOC574418	hypothetical LOC574418	-1.06	0.947	-1.37	0.492	-1.84	0.076	1.55	0.457	-0.68
1418547_at	Tfpi2	tissue factor pathway inhibitor 2	-1.38	0.203	1.02	0.846	-2.09	0.038	-1.35	0.284	-0.95
1450500_at	Uhmk1 /// LOC677	U2AF homology motif (UHM) kinase 1 /// similar to U2AF homology motif (UHM) k	-1.27	0.657	-1.84	0.159	-1.12	0.783	1.79	0.167	-0.61
1459878_a_at	A430107O13Rik	RIKEN cDNA A430107O13 gene	1.25	0.349	-2.14	0.025	-1.99	0.047	-1.1	0.628	-0.99
1425369_a_at	Sox10	SRY-box containing gene 10	1.13	0.489	-1.53	0.075	-2.29	0.291	-1.43	0.221	-1.03
1425839_at	Fkbp11	FK506 binding protein 11	-1.84	0.307	-1.32	0.65	-1.09	0.836	1.37	0.166	-0.72
1431925_at	4933433H22Rik	RIKEN cDNA 4933433H22 gene	-1.68	0.396	-1.27	0.642	-1.2	0.554	2.11	0.215	-0.51
1443029_at	Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	-1.27	0.256	-1.16	0.487	-1.76	0.034	1.24	0.336	-0.74
1428032_at	Acvr1c	activin A receptor, type IC	-1.2	0.438	-1.52	0.118	-1.37	0.161	1.11	0.718	-0.74
1436531_at	Metap2	methionine aminopeptidase 2	-1.47	0.124	-1.24	0.322	-1.37	0.035	2.68	0.249	-0.35
1439572_at	---	---	1.01	0.91	-1.8	0.002	-1.53	0.069	-1.05	0.829	-0.84
1437512_x_at	Ebna1bp2	EBNA1 binding protein 2	-1.97	0.2	-1.41	0.208	1	0.992	-1.19	0.438	-0.89
1449067_at	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	-1.12	0.438	-1.43	0.337	-1.6	0.246	1.16	0.867	-0.75
1453184_at	2310040C09Rik	RIKEN cDNA 2310040C09 gene	1.13	0.643	-3.31	0.22	-1.26	0.502	-2.2	0.427	-1.41
1431803_at	Cyp2d13	cytochrome P450, family 2, subfamily d, polypeptide 13	-1.25	0.442	-1.84	0	-1.14	0.724	1.02	0.964	-0.8
1453102_at	Flrt3	fibronectin leucine rich transmembrane protein 3	1.18	0.54	-2.2	0.363	-1.71	0.098	-2.15	0.127	-1.22
1433026_at	---	---	-1.29	0.379	-1.43	0.362	-1.33	0.361	1.28	0.558	-0.7
1433167_at	4930444E06Rik	RIKEN cDNA 4930444E06 gene	1	0.987	-2.47	0.114	-1.23	0.418	-1.26	0.294	-0.99
1460316_at	Acsl1	acyl-CoA synthetase long-chain family member 1	-1.31	0.057	-1.9	0.017	-1.07	0.729	1.55	0.108	-0.68
1447785_x_at	D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	-1.63	0.118	-1.36	0.39	-1.14	0.543	1.19	0.645	-0.74
1440311_at	Sorbs1	sorbin and SH3 domain containing 1	-1.23	0.65	-1.2	0.454	-1.74	0.208	1.63	0.232	-0.64
1457389_at	9830166K06Rik	RIKEN cDNA 9830166K06 gene	-1.39	0.665	-1.61	0.166	-1.13	0.623	1.15	0.622	-0.75
1436294_at	Ankrd29	ankyrin repeat domain 29	1	0.999	-1.69	0.278	-1.59	0.082	-1.51	0.081	-0.95
1460588_at	---	10 days lactation, adult female mammary gland cDNA, RIKEN full-length enriche	-1.33	0.483	-1.75	0.076	-1.11	0.631	1.01	0.972	-0.8
1427290_at	Krt81	keratin 81	-1.52	0.099	-1.28	0.177	-1.27	0.284	1.38	0.07	-0.67
1452677_at	Pnpt1 /// LOC6355	polyribonucleotide nucleotidyltransferase 1 /// similar to polyribonucleotide nucleo	-2.57	0.189	-1.4	0.39	1.12	0.773	-1.04	0.933	-0.97
1441055_at	Palm2	paralemmin 2	1.1	0.901	-1.92	0.175	-1.65	0.031	-1.18	0.718	-0.91
1438583_at	Ern1	Endoplasmic reticulum (ER) to nucleus signalling 1	-1.2	0.416	-1.31	0.072	-1.58	0.086	1.29	0.017	-0.7
1446454_at	---	---	-1.13	0.899	-2.33	0.275	-1.09	0.803	1.49	0.289	-0.77
1440157_at	Scml4	Sex comb on midleg-like 4 (Drosophila)	1.1	0.576	-2.03	0.105	-1.59	0.348	-3.35	0.061	-1.47
1436637_at	Wbscr1	Williams-Beuren syndrome chromosome region 1 homolog (human)	-1.94	0.135	-1.01	0.95	-1.38	0.334	1.15	0.429	-0.8
1416460_at	Miox	myo-inositol oxygenase	-1.15	0.22	-12.46	0.211	1.27	0.74	-3.06	0.351	-3.85
1458598_at	Peg13	paternally expressed 13	-2.39	0.223	-1.36	0.647	1.07	0.82	-1.02	0.82	-0.93
1431841_at	4930434E21Rik	RIKEN cDNA 4930434E21 gene	-1.53	0.246	-1.88	0.232	1.04	0.923	-1.36	0.451	-0.93
1446360_at	Rora	RAR-related orphan receptor alpha	1.05	0.93	-1.12	0.829	-3.47	0.041	-2.17	0.208	-1.43
1442034_at	Fastkd1	FAST kinase domains 1	-2.05	0.258	-1.74	0.289	1.17	0.698	-1.46	0.636	-1.02
1454001_at	---	---	-1.71	0.549	-1.62	0.558	1.02	0.958	-1.06	0.911	-0.84
1444594_at	Tbx3	T-box 3	-1.15	0.668	-1.3	0.331	-1.7	0.055	1.19	0.413	-0.74
1421788_x_at	Egfbp2	epidermal growth factor binding protein type B	-1.25	0.699	-2.2	0.02	-1.03	0.927	2.06	0.097	-0.61
1420385_at	Gna14	guanine nucleotide binding protein, alpha 14	-1.2	0.138	-1.35	0.091	-1.54	0.024	2.05	0.027	-0.51
1429928_at	1700030B21Rik	RIKEN cDNA 1700030B21 gene	-1.19	0.631	-3.6	0.105	1.11	0.578	-1.73	0.315	-1.35
1432437_at	4933413N12Rik	RIKEN cDNA 4933413N12 gene	-1.63	0.187	-1.45	0.338	-1.08	0.755	1.09	0.896	-0.77
1447046_at	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	-1.32	0.758	-1.24	0.321	-1.51	0.112	2.77	0.274	-0.33

1447604_at	BC053393	cDNA sequence BC053393	-1	0.986	-2.41	0.163	-1.23	0.423	1.06	0.872	-0.9
1430204_at	5033425G24Rik	RIKEN cDNA 5033425G24 gene	1.04	0.616	-1.36	0.311	-2.22	0.039	-1.17	0.589	-0.93
1446933_at	---	---	-1.3	0.443	-1.27	0.407	-1.48	0.076	1.02	0.921	-0.76
1458897_at	Ust	uronyl-2-sulfotransferase	-1.76	0.1	-1.15	0.377	-1.26	0.122	1.05	0.892	-0.78
1458323_at	4930444A19Rik	RIKEN cDNA 4930444A19 gene	-1.13	0.79	-1.19	0.604	-1.98	0.272	1.67	0.423	-0.66
1422173_at	Ipf1	insulin promoter factor 1, homeodomain transcription factor	-3.61	0.016	-1.04	0.915	-1.01	0.957	2.11	0.167	-0.89
1453965_at	4930432O09Rik	RIKEN cDNA 4930432O09 gene	-1.7	0.219	1	0.999	-1.56	0.232	-1.32	0.61	-0.9
1436304_at	C030003D03Rik	RIKEN cDNA C030003D03 gene	-1.17	0.825	-1.65	0.48	-1.31	0.45	2.7	0.109	-0.36
1444495_at	---	---	-1.37	0.205	-1.02	0.964	-1.92	0.066	1.3	0.753	-0.75
1431216_s_at	Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	1.15	0.468	-1.29	0.691	-3.25	0.221	-1.76	0.129	-1.29
1444856_at	Crebbp	CREB binding protein	1.03	0.885	-1.72	0.055	-1.6	0.03	-1.46	0.148	-0.94
1429812_at	2610002D18Rik	RIKEN cDNA 2610002D18 gene	-1.03	0.9	-1.67	0.369	-1.51	0.201	2.25	0.247	-0.49
1420676_at	Sprrl3	small proline rich-like 3	-1.49	0.425	-1.5	0.515	-1.12	0.799	2.47	0.366	-0.41
1458340_at	---	Transcribed locus	-1.54	0.492	-2.62	0.112	1.2	0.641	-1.77	0.218	-1.18
1446982_at	Pard3	Par-3 (partitioning defective 3) homolog (C. elegans)	-1.22	0.375	-1.09	0.729	-2.04	0.004	1.02	0.933	-0.83
1440008_at	2310043L19Rik	RIKEN cDNA 2310043L19 gene	-1.37	0.354	1	0.998	-2	0.129	-2.65	0.22	-1.26
1438344_at	4833424O15Rik	RIKEN cDNA 4833424O15 gene	-1.63	0.625	1.06	0.847	-1.79	0.215	-2.27	0.017	-1.16
1437655_at	D430020J02Rik	RIKEN cDNA D430020J02 gene	-1.12	0.815	-1.56	0.266	-1.43	0.544	1.01	0.987	-0.78
1443175_at	A830010M09Rik	RIKEN cDNA A830010M09 gene	-1.98	0.305	-1.63	0.435	1.11	0.807	-2.04	0.306	-1.13
1439684_at	4930570G19Rik	RIKEN cDNA 4930570G19 gene	-1.13	0.89	-2.31	0.027	-1.1	0.816	1.53	0.498	-0.75
1459812_x_at	Tspan7	tetraspanin 7	-1.6	0.309	-1.38	0.482	-1.13	0.766	1.37	0.544	-0.69
1455745_at	Cln8	ceroid-lipofuscinosis, neuronal 8	-1.43	0.444	-1.47	0.086	-1.18	0.311	2.78	0.109	-0.32
1459100_at	AU015253	expressed sequence AU015253	-1.68	0.28	-1.09	0.829	-1.39	0.113	1.05	0.913	-0.78
1430529_at	Csnk1a1	casein kinase 1, alpha 1	-1.17	0.34	-1.61	0.067	-1.32	0.178	1.1	0.501	-0.75
1435435_at	Cttnbp2	cortactin binding protein 2	-1.14	0.489	-1.06	0.92	-2.42	0.185	1.07	0.208	-0.89
1421674_at	---	---	-1.16	0.809	-1.25	0.443	-1.74	0.27	1.51	0.54	-0.66
1456082_x_at	Cct4	chaperonin subunit 4 (delta)	-1.3	0.303	-1.36	0.234	-1.37	0.21	1.12	0.524	-0.73
1457099_at	D030011O10Rik	RIKEN cDNA D030011O10 gene	-1.56	0.134	-2.08	0.072	1.11	0.502	-1.43	0.326	-0.99
1459493_at	Setbp1	SET binding protein 1	1.01	0.878	-1.56	0.55	-1.72	0.017	-1.22	0.062	-0.87
1446888_at	---	---	-1.42	0.765	-1.07	0.899	-1.68	0.25	1.83	0.277	-0.59
1442267_at	Stxbp4	syntaxin binding protein 4	-1.05	0.891	-1.15	0.664	-2.44	0.08	2.67	0.19	-0.49
1443056_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	1	0.991	-1.41	0.128	-1.91	0.099	-1.5	0.298	-0.96
1436837_at	Mael	maelstrom homolog (Drosophila)	-1.07	0.909	-1.74	0.341	-1.38	0.372	1.14	0.558	-0.76
1426712_at	Slc6a15	solute carrier family 6 (neurotransmitter transporter), member 15	-1.27	0.141	-1.85	0.314	-1.11	0.66	1.17	0.692	-0.76
1436692_at	---	12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000003N	-1.32	0.205	-1.12	0.602	-1.73	0.008	1.07	0.666	-0.77
1450045_at	Srrm1	serine/arginine repetitive matrix 1	-1.22	0.11	-1.4	0.01	-1.43	0.038	1.1	0.649	-0.74
1443663_at	Prkg1	Protein kinase, cGMP-dependent, type I	-1.34	0.469	1.04	0.823	-2.26	0.006	-1.69	0.456	-1.06
1424881_at	Trib1	tribbles homolog 1 (Drosophila)	-1.29	0.313	-1.62	0.107	-1.18	0.453	1.62	0.308	-0.62
1457947_at	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	-1.72	0.14	-1.48	0.65	-1.02	0.93	1.34	0.479	-0.72
1430438_at	8430439J12Rik	RIKEN cDNA 8430439J12 gene	-1.41	0.35	-1.3	0.152	-1.32	0.129	1.07	0.69	-0.74
1445452_at	Traf1	Tnf receptor-associated factor 1	1.14	0.566	-2.01	0.242	-1.66	0.043	-1.97	0.143	-1.13
1438690_at	Tyms	Thymidylate synthase	-1.31	0.119	-1.19	0.661	-1.59	0.262	4.17	0.186	0.02
1446503_at	---	---	-1.8	0.05	-1.76	0.183	1.11	0.724	-1.33	0.224	-0.94
1438495_at	Top1	topoisomerase (DNA) I	-1.32	0.036	-1.31	0.221	-1.39	0.174	1.79	0.139	-0.56
1421453_at	Jph2	junctophilin 2	-1.33	0.202	-1.51	0.606	-1.21	0.508	1.18	0.252	-0.72
1446361_at	Gprk5	G protein-coupled receptor kinase 5	-1.35	0.024	-1.22	0.719	-1.48	0.218	1.14	0.415	-0.73
1429844_at	2310043J07Rik	RIKEN cDNA 2310043J07 gene	-1.82	0.152	-2.41	0.056	1.27	0.631	-1.15	0.816	-1.03
1448397_at	Gjb6	gap junction membrane channel protein beta 6	-1.69	0.335	-1.32	0.46	-1.13	0.707	1.05	0.822	-0.77
1418689_at	Cts6	cathepsin 6	-1.95	0.433	-1.2	0.674	-1.12	0.696	1.45	0.292	-0.71
1459167_at	Cdc42bpb	Cdc42 binding protein kinase beta	-1.13	0.431	-1.55	0.19	-1.41	0.342	1.05	0.923	-0.76
1441871_at	1810044D09Rik	RIKEN cDNA 1810044D09 gene	-2.41	0.002	-1.18	0.414	-1.02	0.892	1.23	0.457	-0.85
1450192_at	Lhcgr	luteinizing hormone/choriogonadotropin receptor	1.02	0.966	-1.36	0.591	-2.09	0.278	-1.82	0.57	-1.06
1459192_at	---	Transcribed locus	-1.45	0.318	-1.72	0.365	-1.03	0.943	1.19	0.674	-0.75

1453918_at	4933426F18Rik	RIKEN cDNA 4933426F18 gene	1.03	0.95	-2.62	0.178	-1.2	0.735	-3.07	0.152	-1.47
1416682_at	Ube3a	ubiquitin protein ligase E3A	-1.48	0.147	-1.18	0.652	-1.41	0.141	1.06	0.629	-0.75
1442651_at	Wwox	WW domain-containing oxidoreductase	1.06	0.846	-1.88	0.074	-1.54	0.115	-1.29	0.555	-0.91
1421850_at	Mtap1b	microtubule-associated protein 1 B	-1.78	0.173	-1.33	0.423	-1.08	0.752	1.03	0.966	-0.79
1442625_at	Plekhc1	Pleckstrin homology domain containing, family C (with FERM domain) member 1	-1.01	0.986	-1.28	0.037	-2.16	0.037	1.01	0.986	-0.86
1440307_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	1.06	0.63	-1.77	0.02	-1.62	0.201	-1.51	0.05	-0.96
1440220_at	AI503564	expressed sequence AI503564	-1.13	0.378	-1.4	0.009	-1.57	0.009	1.52	0.015	-0.64
1450805_at	Sgcd	sarcoglycan, delta (dystrophin-associated glycoprotein)	-1.88	0.172	-1.13	0.83	-1.21	0.08	1.93	0.06	-0.57
1426595_at	Slc18a1	solute carrier family 18 (vesicular monoamine), member 1	-1.43	0.21	-1.14	0.434	-1.51	0.305	1.78	0.157	-0.57
1446956_at	BC004022	cDNA sequence BC004022	-1.25	0.344	1.02	0.875	-2.42	0.226	-1.11	0.771	-0.94
1453528_at	Lta4h	leukotriene A4 hydrolase	1.1	0.858	-2.59	0.196	-1.32	0.426	-1.61	0.114	-1.11
1446456_at	---	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130003J	-1.84	0.25	-2.92	0.117	1.35	0.304	-1.73	0.173	-1.28
1457682_at	9030420J04Rik	RIKEN cDNA 9030420J04 gene	1.02	0.91	-1.18	0.147	-2.64	0.009	-1.22	0.53	-1.01
1451662_x_at	Akap4	A kinase (PRKA) anchor protein 4	-1.68	0.332	-1.51	0.462	-1.02	0.947	1.97	0.254	-0.56
1442691_at	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030049N05	-1.32	0.266	-1.26	0.146	-1.45	0.148	1.03	0.904	-0.75
1435345_at	Ceecam1	cerebral endothelial cell adhesion molecule 1	-1.81	0.043	-1.28	0.371	-1.11	0.211	3.35	0.153	-0.21
1430107_at	9230116B18Rik	RIKEN cDNA 9230116B18 gene	-1.18	0.738	-1.41	0.244	-1.47	0.167	1.23	0.732	-0.71
1431884_at	1110019B22Rik	RIKEN cDNA 1110019B22 gene	1.03	0.969	-2.19	0.279	-1.34	0.59	-1.57	0.496	-1.01
1430894_at	5530401N12Rik	RIKEN cDNA 5530401N12 gene	-2.21	0.198	-1.58	0.284	1.15	0.659	-2.18	0.29	-1.2
1454279_at	Oaz3	ornithine decarboxylase antizyme 3	-1.66	0.631	-1.29	0.687	-1.16	0.768	1.73	0.4	-0.6
1451966_at	Mrap	melanocortin 2 receptor accessory protein	1.03	0.97	-1.87	0.044	-1.47	0.34	-2.5	0.299	-1.2
1427607_at	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	-1.39	0.045	-1.85	0.308	-1.02	0.97	1.48	0.583	-0.7
1443839_at	1700010H22Rik	RIKEN cDNA 1700010H22 gene	-1.19	0.622	-1.81	0.372	-1.17	0.171	1.15	0.527	-0.76
1440993_at	AW111846	Expressed sequence AW111846	-1.2	0.068	-1.32	0.213	-1.54	0.31	1.9	0.277	-0.54
1432700_at	2810047J09Rik	RIKEN cDNA 2810047J09 gene	-2.65	0	-1.05	0.919	-1.09	0.864	1.11	0.872	-0.92
1437062_s_at	Phyhipl	phytanoyl-CoA hydroxylase interacting protein-like	1.07	0.423	-2.23	0.22	-1.38	0.355	-2.43	0.043	-1.24
1438588_at	Plagl1	Pleiomorphic adenoma gene-like 1	-1.43	0.44	-1.41	0.332	-1.2	0.444	1.63	0.167	-0.6
1445938_at	5930427L02Rik	RIKEN cDNA 5930427L02 gene	1.15	0.7	-1.3	0.753	-3.12	0.011	-2.09	0.372	-1.34
1435851_at	Lgi1	leucine-rich repeat LGI family, member 1	-1.16	0.675	-1.94	0.341	-1.15	0.705	1.3	0.647	-0.74
1438676_at	Mpa2l /// LOC6265	macrophage activation 2 like /// similar to macrophage activation 2 like /// similar t	-1.31	0.309	-2.15	0.035	1.01	0.957	-1.39	0.003	-0.96
1456989_at	Oxgr1	oxoglutarate (alpha-ketoglutarate) receptor 1	-1.38	0.277	-1.48	0.307	-1.19	0.657	1.98	0.08	-0.52
1454470_at	4930404F17Rik	RIKEN cDNA 4930404F17 gene	-1.25	0.219	-1.38	0.645	-1.39	0.481	1.64	0.271	-0.6
1458980_at	---	---	1.05	0.897	-1.47	0.552	-1.95	0.083	-1.06	0.811	-0.86
1442743_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643053	-1.42	0.025	-1.41	0.016	-1.2	0.145	1.22	0.495	-0.7
1458552_at	D430050E20Rik	RIKEN cDNA D430050E20 gene	-1.52	0.007	-1.79	0.059	1.03	0.903	-1.5	0.174	-0.95
1443145_at	Apbb1ip	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting prote	-1.64	0.33	-1.43	0.075	-1.07	0.748	1.09	0.69	-0.76
1454025_at	Ddo	D-aspartate oxidase	-2.63	0.291	-1.63	0.369	1.25	0.065	-1	0.996	-1
1437393_at	AI875142	expressed sequence AI875142	-1.44	0.011	-1.22	0.156	-1.36	0.134	1.07	0.415	-0.74
1444554_at	Tnrc6b	Trinucleotide repeat containing 6b	-1.54	0.141	-1.42	0.558	-1.12	0.674	1.35	0.067	-0.68
1427018_at	Tsnaxip1	translin-associated factor X (Tsnax) interacting protein 1	-1.18	0.742	-1.59	0.628	-1.3	0.316	1.32	0.465	-0.69
1427286_at	D11Bwg0517e	DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed	-1.41	0.213	1.13	0.619	-2.45	0.143	-1.06	0.931	-0.95
1445495_at	---	---	-1.77	0.118	-1.51	0.351	1.02	0.938	-2.26	0.013	-1.13
1447809_x_at	---	---	-1.14	0.621	-1.67	0.154	-1.29	0.496	1.9	0.355	-0.55
1453730_at	Samd8	sterile alpha motif domain containing 8	-1.47	0.069	-1.35	0.544	-1.22	0.588	1.4	0.265	-0.66
1434200_at	BC010981	cDNA sequence BC010981	-1.29	0.453	-1.32	0.316	-1.4	0.038	1.17	0.545	-0.71
1453215_at	Rnase10	ribonuclease, RNase A family, 10 (non-active)	1.12	0.779	-1.47	0.107	-2.25	0.028	-1	0.997	-0.9
1440762_at	Syn2	synapsin II	-1.35	0.675	-1.33	0.669	-1.33	0.403	1.54	0.483	-0.62
1456972_at	C80256	expressed sequence C80256	-1.42	0.599	-1.12	0.822	-1.54	0.084	1.39	0.5	-0.67
1453563_at	Nmral1	NmrA-like family domain containing 1	1.05	0.946	-1.86	0.12	-1.51	0.148	-1.08	0.788	-0.85
1444667_at	Brdt	bromodomain, testis-specific	1.16	0.635	-2.88	0.009	-1.35	0.346	-1.13	0.847	-1.05
1450375_at	Pspn	persephin	-1.31	0.346	-1.26	0.538	-1.45	0.195	1.13	0.833	-0.72
1441852_x_at	Atg16l1	autophagy-related 16-like 1 (yeast)	-1.29	0.797	-2.11	0.012	-1	0.995	1.18	0.723	-0.8
1425658_at	Cd109	CD109 antigen	1.27	0.735	-1.76	0.108	-2.43	0.043	-1.48	0.577	-1.1

1446593_at	Trio	Triple functional domain (PTPRF interacting)	1.1	0.738	-1.44	0.043	-2.22	0.009	-1.17	0.667	-0.93
1427425_at	9130208E07Rik	RIKEN cDNA 9130208E07 gene	-1.13	0.457	-1.33	0.098	-1.63	0.012	3.02	0.234	-0.27
1428983_at	Scx	scleraxis	-1.4	0.612	-1.01	0.983	-1.84	0.038	1.01	0.974	-0.81
1459368_at	---	---	-1.25	0.586	-1.19	0.842	-1.65	0.321	1.2	0.602	-0.72
1448819_at	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	-1.12	0.129	-1.33	0.008	-1.65	0.077	1.3	0.259	-0.7
1459076_at	BC052040	CDNA sequence BC052040	1.12	0.609	-2.39	0.014	-1.4	0.206	-1.03	0.956	-0.93
1441001_at	AI225934	expressed sequence AI225934	1.37	0.158	-1.78	0.008	-3.1	0.028	-1.02	0.934	-1.13
1457800_at	2900019G14Rik	RIKEN cDNA 2900019G14 gene	-1.81	0.033	-1.07	0.611	-1.3	0.369	1.57	0.2	-0.65
1442265_at	Fancc	Fanconi anemia, complementation group C	-1.5	0.092	-1.53	0.383	-1.07	0.654	1.37	0.437	-0.69
1442603_at	Pb1	Polybromo 1	-1.09	0.743	-1.22	0.529	-1.94	0.087	1.3	0.321	-0.74
1459179_at	D8Ertd268e	DNA segment, Chr 8, ERATO Doi 268, expressed	-1.46	0.616	-1.21	0.722	-1.36	0.625	3.39	0.343	-0.16
1421539_at	Zic4	zinc finger protein of the cerebellum 4	-1.67	0.404	-1.02	0.898	-1.48	0.338	1.7	0.394	-0.62
1445277_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13000	1.03	0.854	-1.34	0.318	-2.11	0.024	-2.46	0.025	-1.22
1440079_at	3632454L22Rik	RIKEN cDNA 3632454L22 gene	-1.59	0.63	-1.11	0.817	-1.38	0.056	1.31	0.327	-0.69
1440474_at	---	---	-2.08	0.092	-1.54	0.266	1.12	0.826	-1.66	0.346	-1.04
1442641_at	Ankhd1	Ankyrin repeat and KH domain containing 1	-1.12	0.616	-1.5	0.111	-1.44	0.16	1.09	0.714	-0.74
1427328_a_at	Clasp2	CLIP associating protein 2	-1.77	0.16	-1.44	0.368	-1	0.992	1.79	0.533	-0.61
1459851_x_at	Riok1	RIO kinase 1 (yeast)	-1.22	0.151	-2.34	0.04	1.01	0.981	-1.07	0.858	-0.91
1420416_at	Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.04	0.811	-1.86	0.332	-1.48	0.025	-1.09	0.71	-0.85
1454414_at	Btbd7	BTB (POZ) domain containing 7	-1.11	0.734	-1.17	0.672	-2	0.154	1.22	0.178	-0.77
1436985_at	Zfp644	zinc finger protein 644	-1.02	0.964	-1.5	0.324	-1.67	0.018	1.28	0.454	-0.73
1424691_at	5930434B04Rik	RIKEN cDNA 5930434B04 gene	-2.02	0.208	1.18	0.408	-1.73	0.16	-1.52	0.523	-1.02
1446418_at	Atg7	Autophagy-related 7 (yeast)	-1.28	0.286	-1.34	0.169	-1.37	0.047	1.1	0.307	-0.72
1444372_at	Arcn1	Archain 1	1.03	0.936	-1.61	0.088	-1.65	0.09	-1.37	0.372	-0.9
1443195_at	---	---	-1.11	0.71	-1.22	0.655	-1.88	0.063	1.56	0.123	-0.66
1422238_at	Usmg1	upregulated during skeletal muscle growth 1	-1.44	0.446	-3.55	0.007	1.27	0.096	-1.07	0.641	-1.19
1427517_at	Boc	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) b	-1.07	0.889	-1.69	0.263	-1.38	0.249	2.57	0.067	-0.39
1439183_at	Asah3	N-acylsphingosine amidohydrolase (alkaline ceramidase) 3	-1.29	0.699	-1.46	0.637	-1.26	0.55	1.37	#DIV/0!	-0.66
1454311_at	---	---	1.02	0.904	-1.89	0.021	-1.42	0.037	-1.48	0.084	-0.94
1417577_at	Trpc3	transient receptor potential cation channel, subfamily C, member 3	-1.2	0.422	-1.51	0.354	-1.31	0.514	1.51	0.055	-0.63
1438066_at	Gtf2b	General transcription factor IIB	1.34	0.744	-4.49	0	-1.45	0.312	-1.89	0.228	-1.62
1444319_at	E2f8	E2F transcription factor 8	-1.17	0.585	-1.85	0.198	-1.16	0.6	2.55	0.388	-0.41
1430942_at	8430437O03Rik	RIKEN cDNA 8430437O03 gene	-1.21	0.195	-1.28	0.193	-1.55	0.095	1.35	0.282	-0.67
1430113_at	4933424C13Rik	RIKEN cDNA 4933424C13 gene	-1.14	0.864	-1.46	0.392	-1.45	0.564	1.06	0.928	-0.75
1433255_at	8430437B07Rik	RIKEN cDNA 8430437B07 gene	-1.28	0.438	-1.32	0.665	-1.4	0.063	1.27	0.118	-0.68
1446059_at	St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	-1.23	0.282	-1.5	0.105	-1.29	0.485	1.14	0.543	-0.72
1420186_at	---	---	1.01	0.974	-2.01	0.266	-1.33	0.191	-1.22	0.393	-0.89
1452967_at	1700006H03Rik	RIKEN cDNA 1700006H03 gene	-1.2	0.517	-2.08	0.033	-1.06	0.82	1.43	0.483	-0.73
1458792_at	D12Ertd208e	DNA segment, Chr 12, ERATO Doi 208, expressed	-1.39	0.658	-1.27	0.605	-1.34	0.517	1.99	0.352	-0.5
1447267_at	C85319	expressed sequence C85319	-1.05	0.874	-1.65	0.115	-1.43	0.255	1.06	0.864	-0.77
1446873_at	---	---	-2.3	0.372	1.11	0.855	-1.41	0.439	-2.12	0.355	-1.18
1447171_at	Nedd4l	Neural precursor cell expressed, developmentally down-regulated gene 4-like	-1.6	0.099	1	0.999	-1.59	0.271	-1.87	0.215	-1.01
1459990_at	Ddr1	discoidin domain receptor family, member 1	-1.33	0.293	-1.54	0.068	-1.17	0.648	1.17	0.606	-0.72
1447782_x_at	Tbl3	transducin (beta)-like 3	-1.19	0.415	-2	0.062	-1.09	0.813	1.8	0.283	-0.62
1423977_at	4930453N24Rik ///	RIKEN cDNA 4930453N24 gene /// similar to CG13876-PA /// similar to CG13876	-1.01	0.993	-2.34	0.147	-1.2	0.662	1.22	0.08	-0.83
1437660_at	Nktr	natural killer tumor recognition sequence	-1.15	0.528	-1.27	0.157	-1.66	0.016	1.06	0.501	-0.76
1420215_x_at	1810012K16Rik	RIKEN cDNA 1810012K16 gene	-1.98	0.223	1.14	0.729	-1.63	0.173	-1.62	0.08	-1.02
1457212_at	---	Transcribed locus	-2.19	0.395	-2.31	0.374	1.36	0.5	-1.21	0.818	-1.08
1430504_at	1700108E19Rik	RIKEN cDNA 1700108E19 gene	-1.7	0.414	-1.19	0.579	-1.21	0.501	1.26	0.58	-0.71
1418756_at	Trh	thyrotropin releasing hormone	-1.19	0.324	-1.09	0.891	-2.01	0.337	1.14	0.346	-0.79
1443846_x_at	Pank2	Pantothenate kinase 2 (Hallervorden-Spatz syndrome)	-1.26	0.559	-1.45	0.469	-1.29	0.104	1.32	0.303	-0.67
1445046_at	D8Ertd317e	DNA segment, Chr 8, ERATO Doi 317, expressed	-2.82	0.226	1	0.999	-1.11	0.793	-1.06	0.914	-1
1458797_at	---	---	-3.36	0.041	1.09	0.799	-1.15	0.782	-1.1	0.732	-1.13

1442966_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	-1.21	0.766	-2.82	0.184	1.08	0.831	-1.64	0.341	-1.15
1430919_at	4930525F21Rik	RIKEN cDNA 4930525F21 gene	-1.74	0.451	-1.25	0.686	-1.14	0.618	2.36	0.16	-0.44
1421531_at	Akap3	A kinase (PRKA) anchor protein 3	-3.37	0.022	-1.4	0.184	1.25	0.571	-2.03	0.306	-1.39
1447317_at	---	Transcribed locus	-1.8	0.085	-1.55	0.528	1.06	0.875	-1.16	0.799	-0.86
1421503_at	Pcdh15	protocadherin 15	-1.7	0.258	1.02	0.971	-1.54	0.406	-1.39	0.461	-0.9
1432712_at	4933425M03Rik	RIKEN cDNA 4933425M03 gene	-1.62	0.182	-1.4	0.5	-1.08	0.667	1.32	0.07	-0.69
1427509_at	Baiap3	BAI1-associated protein 3	-1.3	0.112	-1.59	0.175	-1.17	0.442	1.51	0.477	-0.64
1432972_at	4921518B13Rik	RIKEN cDNA 4921518B13 gene	-1.22	0.228	-1.99	0.02	-1.07	0.904	1.29	0.543	-0.75
1430457_at	Daf2	decay accelerating factor 2	-2.79	0.118	-1.08	0.904	-1.03	0.959	2.62	0.324	-0.57
1449457_at	Acot12	acyl-CoA thioesterase 12	-1.19	0.088	-1.67	0.004	-1.22	0.605	2.71	0.004	-0.34
1446094_at	Atbf1	AT motif binding factor 1	-1.05	0.748	-1.32	0.14	-1.84	0.006	1.08	0.733	-0.78
1429602_at	Cd164l2	D164 sialomucin-like 2	-1.26	0.49	-1.54	0.571	-1.23	0.347	1.31	0.16	-0.68
1428238_at	2700059D21Rik	RIKEN cDNA 2700059D21 gene	-1.59	0.591	-1.34	0.519	-1.14	0.699	1.5	0.178	-0.64
1430644_at	Wbscr25	Williams Beuren syndrome chromosome region 25 (human)	-2.83	0.323	1.05	0.87	-1.17	0.69	-1.78	0.414	-1.18
1452873_at	5830415F09Rik	RIKEN cDNA 5830415F09 gene	-1.42	0.351	-1.32	0.108	-1.26	0.396	1.85	0.316	-0.54
1420027_at	C80171	expressed sequence C80171	-1.83	0.507	-1.17	0.694	-1.16	0.766	1.85	0.28	-0.58
1450323_at	5730493B19Rik	RIKEN cDNA 5730493B19 gene	-1.2	0.346	-1.5	0.221	-1.32	0.049	1.38	0.122	-0.66
1421194_at	Itga4	integrin alpha 4	-2.85	0.153	1.09	0.83	-1.22	0.447	-1.04	0.803	-1.01
1446340_at	Ar	Androgen receptor	-1.01	0.984	-1.15	0.694	-2.47	0.193	1.56	0.504	-0.77
1444777_at	Rai14	Retinoic acid induced 14	1.02	0.881	-1.25	0.09	-2.31	0.003	-1.09	0.557	-0.9
1455053_a_at	Dcun1d1	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	-1.26	0.235	-1.23	0.22	-1.52	0.041	1.53	0.451	-0.62
1458768_at	Epb4.1l5	Erythrocyte protein band 4.1-like 5	-1.05	0.742	-1.55	0.065	-1.51	0.089	1.15	0.815	-0.74
1416872_at	Tspan6	tetraspanin 6	-1.19	0.159	-1.37	0.288	-1.45	0.034	1.26	0.186	-0.69
1443625_at	Nat11	N-acetyltransferase 11	-1.43	0.289	-1.57	0.071	-1.08	0.802	1.22	0.123	-0.72
1441629_at	Grip1	Glutamate receptor interacting protein 1	-1.19	0.16	-1.19	0.573	-1.73	0.007	1.61	0.42	-0.62
1447096_at	---	Transcribed locus	-1.5	0.011	1.14	0.602	-2.21	0.009	-1.36	0.153	-0.98
1432773_at	2610105M22Rik	RIKEN cDNA 2610105M22 gene	-1.26	0.413	-2.02	0.191	-1.03	0.951	3.26	0.002	-0.26
1431795_a_at	Sema3b	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	-1.55	0.316	-1.25	0.698	-1.23	0.376	1.6	0.286	-0.61
1442488_at	Gpc5	Glypican 5	1.18	0.779	-3.59	0.033	-1.24	0.643	-1.4	0.084	-1.26
1458509_at	Mre11a	Meiotic recombination 11 homolog A (S. cerevisiae)	-1.11	0.715	-2.14	0.032	-1.12	0.298	1.07	0.867	-0.82
1429783_at	Pdlim5	PDZ and LIM domain 5	-1.53	0.631	-1.84	0.082	1.06	0.822	-1.39	0.391	-0.92
1440114_x_at	Ankrd47	ankyrin repeat domain 47	1.07	0.232	-1.92	0.035	-1.49	0.019	-2	0.227	-1.08
1420768_a_at	D11Lgp2e	DNA segment, Chr 11, Lothar Hennighausen 2, expressed	-1.99	0.235	-1.39	0.512	1.04	0.96	-1.39	0.683	-0.93
1430701_a_at	5730528L13Rik	RIKEN cDNA 5730528L13 gene	-1.04	0.78	-1.41	0.434	-1.69	0.2	1.11	0.719	-0.76
1420284_at	Bat4	HLA-B associated transcript 4	-2.47	0.108	-1.74	0.004	1.28	0.46	-1.28	0.235	-1.05
1447955_at	LOC670127	similar to heterochromatin protein 1, binding protein 3	-1.28	0.322	-1.81	0.531	-1.08	0.427	1.39	0.269	-0.69
1450315_at	V1rd14	vomeronasal 1 receptor, D14	-1.55	0.475	1.04	0.878	-1.73	0.042	-1.05	0.916	-0.82
1450301_at	H28	histocompatibility 28	-1.84	0.513	1.08	0.923	-1.57	0.476	-1.99	0.375	-1.08
1442522_at	---	---	-1.16	0.534	-1.66	0.256	-1.25	0.501	1.38	0.334	-0.67
1420300_at	---	---	-1.99	0.567	-1.22	0.785	-1.06	0.889	1.2	0.725	-0.77
1443342_at	---	Transcribed locus	1.01	0.981	-2.11	0.257	-1.29	0.499	-1.08	0.76	-0.87
1418461_at	Sh3d19	SH3 domain protein D19	-1.38	0.098	-1.51	0.051	-1.14	0.312	1.26	0.533	-0.69
1443307_at	Psmc2	Proteasome (prosome, macropain) 26S subunit, ATPase 2	1	0.993	-1.46	0.237	-1.73	0.021	-1.03	0.877	-0.8
1457671_at	9330120H11Rik	RIKEN cDNA 9330120H11 gene	-1.3	0.639	-1.39	0.125	-1.29	0.367	1.56	0.16	-0.61
1454088_at	5330411O13Rik	RIKEN cDNA 5330411O13 gene	-2.37	0.279	-1.24	0.651	1.04	0.947	-1.09	0.679	-0.92
1435707_at	Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	-1.23	0.395	-1.68	0.119	-1.17	0.436	1.01	0.959	-0.77
1444555_at	Ches1	Checkpoint suppressor 1	-2.02	0.301	1.24	0.685	-1.89	0.133	-1.57	0.197	-1.06
1440416_at	Usp46	Ubiquitin specific peptidase 46	-1.13	0.643	-1.17	0.546	-1.91	0.059	1.84	0.248	-0.59
1453700_s_at	4933403O03Rik ///	RIKEN cDNA 4933403O03 gene /// similar to double homeobox, 4	-1.19	0.856	-1.9	0.162	-1.11	0.85	1.07	0.884	-0.78
1458368_at	Myh4	myosin, heavy polypeptide 4, skeletal muscle	-2.1	0.24	-1.4	0.662	1.08	0.624	-1.51	0.29	-0.98
1421535_a_at	Pde4a	phosphodiesterase 4A, cAMP specific	1.01	0.973	-2.73	0.011	-1.12	0.385	-1	0.985	-0.96
1430711_at	4933416E03Rik	RIKEN cDNA 4933416E03 gene	-1.49	0.603	-1.38	0.65	-1.15	0.792	1.56	0.312	-0.61
1457485_at	Fbxw11	F-box and WD-40 domain protein 11	-1.15	0.225	-1.27	0.37	-1.63	0.093	1.1	0.375	-0.74

1459152_at	C78515	expressed sequence C78515	-1.19	0.74	-1.42	0.272	-1.38	0.65	1.63	0.56	-0.59
1429150_at	Ccdc77	coiled-coil domain containing 77	-1.57	0.229	-1.28	0.025	-1.18	0.34	1.54	0.292	-0.62
1438703_at	Ankrd26	ankyrin repeat domain 26	-1.2	0.311	-1.5	0.118	-1.3	0.033	1.11	0.689	-0.72
1460022_at	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-1.13	0.795	-1.53	0.62	-1.37	0.477	1.63	0.148	-0.6
1458885_at	---	---	-2.14	0.173	-1.22	0.288	-1.02	0.899	1.16	0.739	-0.81
1424454_at	Tmem87a	transmembrane protein 87A	-1.35	0.736	-2.9	0.176	1.18	0.698	-2.02	0.362	-1.27
1450090_at	Zfp101	zinc finger protein 101	-1.22	0.27	-1.57	0.016	-1.24	0.267	1.51	0.255	-0.63
1446963_at	---	---	-1.06	0.671	-1.42	0.403	-1.62	0.166	2.61	0.085	-0.37
1443678_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-1.37	0.763	-1.13	0.856	-1.54	0.219	1.29	0.457	-0.69
1445431_at	Stk39	Serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	-1.47	0.03	-1.79	0.176	1.03	0.953	-1.38	0.221	-0.9
1431182_at	Hspa8 /// LOC6212	heat shock protein 8 /// similar to heat shock protein 8 /// similar to heat shock pro	-2.1	0.404	-1.35	0.463	1.05	0.911	-1.24	0.704	-0.91
1460540_at	Nrxn1	neurexin I	-2.29	0.032	-1.15	0.752	-1.04	0.903	1.12	0.63	-0.84
1438028_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	-1.27	0.042	-1.27	0.007	-1.46	0.02	1.04	0.568	-0.74
1458794_at	---	---	-1.22	0.464	-1.51	0.307	-1.28	0.653	2.44	0.043	-0.39
1437228_at	BC048651	cDNA sequence BC048651	-1.45	0.073	-1.22	0.473	-1.31	0.311	1.12	0.331	-0.72
1449081_at	Ces3	carboxylesterase 3	-1.45	0.228	-1.36	0.343	-1.18	0.067	2.62	0.039	-0.34
1459631_at	Rps12 /// LOC4328	ribosomal protein S12 /// similar to ribosomal protein S12 /// similar to ribosomal p	-3.03	0.193	-1.01	0.982	-1.05	0.824	1.16	0.775	-0.99
1427664_at	4930453N24Rik	RIKEN cDNA 4930453N24 gene	-2.21	0.296	1.17	0.723	-1.54	0.399	-1.03	0.968	-0.9
1442463_at	Rab10	RAB10, member RAS oncogene family	-1.52	0.303	-1.13	0.746	-1.38	0.297	1.17	0.777	-0.72
1457997_at	Leng4	leukocyte receptor cluster (LRC) member 4	-1.84	0.104	1	0.996	-1.38	0.099	-1.54	0.079	-0.94
1455095_at	Hist2h2be	histone 2, H2be	-1.4	0.236	-1.22	0.241	-1.36	0.082	1.52	0.375	-0.62
1424310_at	---	---	-1.04	0.843	-1.49	0.034	-1.58	0.042	1.01	0.466	-0.77
1458078_at	Chd9	chromodomain helicase DNA binding protein 9	1.07	0.882	-1.77	0.083	-1.58	0.072	-1.46	0.212	-0.93
1433329_at	4930573C08Rik	RIKEN cDNA 4930573C08 gene	-2.03	0.183	-1.76	0.277	1.21	0.362	-1.02	0.905	-0.9
1454302_at	5730410E19Rik	RIKEN cDNA 5730410E19 gene	-1.81	0.185	-1.22	0.7	-1.11	0.823	1.05	0.848	-0.77
1446855_at	Vps13d	vacuolar protein sorting 13 D (yeast)	-1.57	0.081	-1.34	0.297	-1.13	0.654	1.01	0.981	-0.76
1450692_at	Kif4	kinesin family member 4	-1.94	0.407	-1.16	0.855	-1.12	0.675	3.69	0.157	-0.13
1422269_at	Insm2	insulinoma-associated 2	1.13	0.171	-1.79	0.218	-1.72	0.317	-1.57	0.504	-0.99
1449604_at	Acp1 /// LOC61999	acid phosphatase 1, soluble /// similar to acid phosphatase 1, soluble /// similar to	-2.7	0.071	1.22	0.769	-1.48	0.329	-1.2	0.612	-1.04
1445418_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.17	0.652	-1.66	0.292	-1.23	0.65	1.01	0.97	-0.76
1422728_at	Inha	inhibin alpha	1.14	0.103	-2.11	0.058	-1.51	0.105	-1.31	0.597	-0.95
1431002_x_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	-1.24	0.279	-1.62	0.087	-1.18	0.307	1.17	0.249	-0.72
1431443_at	1810008B01Rik	RIKEN cDNA 1810008B01 gene	-1.8	0.113	-1.12	0.776	-1.21	0.308	1.18	0.221	-0.74
1430092_at	Serac1	serine active site containing 1	-1.05	0.736	-1.32	0.287	-1.78	0.128	1.08	0.843	-0.77
1453568_at	2310032F03Rik	RIKEN cDNA 2310032F03 gene	1.02	0.946	-1.47	0.439	-1.74	0.311	-3.18	0.098	-1.35
1447325_at	Ches1	Checkpoint suppressor 1	1.11	0.659	-1.38	0.582	-2.28	0.091	-2.03	0.078	-1.15
1421171_at	Adam12	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	-1.2	0.198	-1.19	0.792	-1.68	0.264	1.46	0.58	-0.65
1425955_at	Cav2	caveolin 2	-1.12	0.7	-1.17	0.582	-1.92	0.026	1.15	0.532	-0.76
1422169_a_at	Bdnf	brain derived neurotrophic factor	-1.24	0.489	-1.27	0.733	-1.48	0.13	1.49	0.505	-0.62
1430432_at	Trim42	tripartite motif-containing 42	-1.01	0.989	-1.2	0.757	-2.24	0.068	1.51	0.479	-0.73
1429051_s_at	Sox11	SRY-box containing gene 11	-1.03	0.905	-1.25	0.663	-2	0.081	1.46	0.561	-0.7
1438305_at	Rims1	regulating synaptic membrane exocytosis 1	-2.21	0.164	-1.15	0.824	-1.05	0.855	2.07	0.098	-0.59
1420270_at	---	---	-1.81	0.045	-1.27	0.589	-1.07	0.733	1.25	0.6	-0.72
1439895_at	AU021025	expressed sequence AU021025	-1.33	0.137	-1.09	0.627	-1.68	0.023	1.09	0.569	-0.75
1425075_at	Gatad2b	GATA zinc finger domain containing 2B	-1.39	0.22	-1.28	0.638	-1.3	0.305	1.36	0.251	-0.65
1442527_at	C87583	expressed sequence C87583	-2.26	0.367	-1.72	0.027	1.25	0.569	-2.45	0.202	-1.3
1457084_at	Nalp9b	NACHT, LRR and PYD containing protein 9b	-1.79	0.559	-1.47	0.348	1.03	0.945	-2.38	0.152	-1.15
1440797_at	Dlx6os2	Dlx6 opposite strand transcript 2	-1.45	0.504	-2.05	0.145	1.09	0.624	-1.02	0.954	-0.86
1431967_at	1700006A11Rik	RIKEN cDNA 1700006A11 gene	-1	0.993	-1.32	0.735	-1.94	0.38	1.26	0.655	-0.75
1455967_at	Sorbs1	sorbin and SH3 domain containing 1	-1.16	0.432	-1.39	0.236	-1.45	0.202	1.65	0.22	-0.59
1430674_at	1700016C15Rik	RIKEN cDNA 1700016C15 gene	1.11	0.78	-1.71	0.486	-1.73	0.345	-1.51	0.337	-0.96
1419734_at	Actb	actin, beta, cytoplasmic	-1.04	0.953	-1.07	0.854	-2.69	0.375	1.89	0.108	-0.73
1447822_x_at	2700038N03Rik	RIKEN cDNA 2700038N03 gene	-1.56	0.031	-1.37	0.223	-1.11	0.496	2.06	0.16	-0.5

1442852_at	---	---	-1.31	0.623	-1.33	0.312	-1.32	0.464	1.08	0.813	-0.72
1455730_at	Dlg7	discs, large homolog 7 (Drosophila)	-1.06	0.929	-1.9	0.208	-1.25	0.621	4.72	0.191	0.13
1443472_at	C77691	expressed sequence C77691	1.23	0.844	-2.18	0.033	-1.71	0.247	-1.41	0.299	-1.02
1451685_at	Mllt6 /// LOC63949(	myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog (Drosopl	-1.71	0.008	-1.18	0.763	-1.19	0.125	1.46	0.382	-0.65
1432392_at	Kif2c	kinesin family member 2C	-1.2	0.645	-1.54	0.089	-1.27	0.524	1.44	0.276	-0.64
1417682_a_at	Prss2	protease, serine, 2	-1.8	0.187	-1.78	0.2	1.16	0.693	-1.22	0.523	-0.91
1441651_at	4930414N06Rik	RIKEN cDNA 4930414N06 gene	-1.18	0.205	-1.15	0.598	-1.79	0.121	1.13	0.671	-0.75
1427339_at	Slc30a2	solute carrier family 30 (zinc transporter), member 2	-1.24	0.232	-1.62	0.371	-1.17	0.69	1.16	0.19	-0.72
1444981_at	Punc	Putative neuronal cell adhesion molecule	-1.49	0.144	-1.25	0.308	-1.25	0.29	1.02	0.716	-0.74
1426887_at	Nudt11	nudix (nucleoside diphosphate linked moiety X)-type motif 11	-1.44	0.261	-1.15	0.748	-1.41	0.111	1.19	0.246	-0.7
1424030_at	Grhl1	grainyhead-like 1 (Drosophila)	-1.61	0.25	-1.83	0.426	1.11	0.344	-1.18	0.759	-0.88
1445673_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	-2.28	0.33	-1.23	0.715	1.02	0.95	-1.73	0.136	-1.05
1456746_a_at	Cd99l2	Cd99 antigen-like 2	-1.13	0.571	-1.27	0.11	-1.66	0.114	1.35	0.145	-0.68
1427634_at	Kcnh7	potassium voltage-gated channel, subfamily H (eag-related), member 7	-1.67	0.002	-1.01	0.993	-1.47	0.305	1.94	0.013	-0.55
1433948_at	Pla2g1b	Phospholipase A2, group IB, pancreas	-2.85	0.211	-1.04	0.952	-1.04	0.945	1.16	0.677	-0.94
1449639_at	0610040J01Rik	RIKEN cDNA 0610040J01 gene	-1.29	0.436	-1.6	0.088	-1.15	0.397	1.1	0.835	-0.73
1426136_x_at	Klra21	killer cell lectin-like receptor subfamily A, member 21	-2.69	0.154	1.11	0.351	-1.27	0.305	-1.07	0.89	-0.98
1449854_at	Nr0b2	nuclear receptor subfamily 0, group B, member 2	-1.24	0.231	-1.61	0.039	-1.18	0.725	2.11	0.29	-0.48
1432133_at	2210022J03Rik	RIKEN cDNA 2210022J03 gene	-1.47	0.528	-1.79	0.183	1.04	0.924	-1.49	0.35	-0.93
1453084_s_at	Col22a1	collagen, type XXII, alpha 1	-1.66	0.007	-1.73	0.285	1.1	0.584	-1.18	0.841	-0.87
1436287_at	---	13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110033I2	1.06	0.738	-1.6	0.384	-1.68	0.228	-1.71	0.315	-0.98
1416444_at	Elovl2	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2	-1.22	0.098	-1.56	0.014	-1.23	0.669	1.45	0.429	-0.64
1419325_at	Nmu	neuromedin U	-1.01	0.662	-1.62	0.049	-1.48	0.171	1.35	0.172	-0.69
1459757_x_at	Cnot10	CCR4-NOT transcription complex, subunit 10	-1.53	0.285	-1.27	0.511	-1.2	0.325	1.02	0.92	-0.74
1450749_a_at	Nr4a2	nuclear receptor subfamily 4, group A, member 2	-1.03	0.662	-2.13	0.031	-1.19	0.409	1.32	0.545	-0.76
1452345_at	Lmod2	leiomodin 2 (cardiac)	-3.5	0.342	-1.02	0.964	1.01	0.921	-1.42	0.378	-1.23
1432563_at	1700116B05Rik	RIKEN cDNA 1700116B05 gene	-1.16	0.588	-2.58	0.212	1.02	0.87	-1.26	0.59	-0.99
1458852_at	---	---	-1.98	0.019	-1.68	0.055	1.18	0.445	-1.61	0.121	-1.03
1439734_at	Mmp15	Matrix metallopeptidase 15	-1.32	0.516	-1.92	0.15	-1	0.991	1.09	0.782	-0.79
1459308_at	Kcnn3	Potassium intermediate/small conductance calcium-activated channel, subfamily	-1.3	0.441	-1.48	0.283	-1.21	0.46	2	0.047	-0.49
1441450_s_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	-1.18	0.371	-1.4	0.22	-1.4	0.207	1.18	0.452	-0.7
1447295_at	Cutl1	Cut-like 1 (Drosophila)	-1.39	0.042	-1.17	0.293	-1.42	0.247	1.05	0.778	-0.73
1446610_at	Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	-3	0.179	1.35	0.432	-1.68	0.344	-1.84	0.282	-1.29
1430953_at	3200001G23Rik	RIKEN cDNA 3200001G23 gene	1	0.973	-1.05	0.792	-3.08	0.134	-1.45	0.02	-1.15
1424897_at	Gpr85	G protein-coupled receptor 85	-1.2	0.497	-2.28	0.025	1	0.988	-1.11	0.836	-0.9
1432626_at	5730507A11Rik	RIKEN cDNA 5730507A11 gene	-1.44	0.145	1.06	0.832	-1.92	0.024	-1.4	0.449	-0.92
1428965_at	Ccdc54	coiled-coil domain containing 54	-1.24	0.117	-1.31	0.683	-1.42	0.003	1.2	0.472	-0.69
1458035_at	Sgpp2	Sphingosine-1-phosphate phosphotase 2	-1.55	0.2	-1.15	0.853	-1.32	0.381	1.36	0.588	-0.66
1438269_at	Zbtb38	zinc finger and BTB domain containing 38	-1.83	0.22	-1.04	0.892	-1.31	0.452	1.26	0.345	-0.73
1440472_at	Spag17	sperm associated antigen 17	-1.24	0.67	-1.44	0.598	-1.28	0.431	1.08	0.867	-0.72
1447036_at	Chl1	cell adhesion molecule with homology to L1CAM	-1.31	0.334	-1.27	0.464	-1.38	0.47	1.33	0.442	-0.66
1440375_at	5730419I09Rik	RIKEN cDNA 5730419I09 gene	-1.04	0.891	-1.41	0.504	-1.63	0.098	1.22	0.37	-0.72
1422652_at	Cryga	crystallin, gamma A	-1.39	0.023	-1.09	0.843	-1.56	0.209	2.19	0.085	-0.46
1424699_at	4921511K06Rik	RIKEN cDNA 4921511K06 gene	1.14	0.721	-2.56	0.411	-1.33	0.316	-1.19	0.15	-0.99
1423360_at	Yme1l1	YME1-like 1 (S. cerevisiae)	-1.28	0.292	-1.21	0.164	-1.49	0.059	1.05	0.839	-0.73
1423849_a_at	Clk3	CDC-like kinase 3	-1.31	0.105	-1.28	0.033	-1.36	0.202	1.3	0.442	-0.66
1426622_a_at	Qpct /// LOC639942	glutaminyl-peptide cyclotransferase (glutaminyl cyclase) /// similar to Glutaminyl-p	1.1	0.848	-1.69	0.006	-1.69	0.052	-1.13	0.437	-0.85
1457714_at	2310005N03Rik	RIKEN cDNA 2310005N03 gene	-3.19	0.25	-1.09	0.907	1.05	0.876	-2.4	0.287	-1.41
1437424_at	Syde2 /// LOC6396	synapse defective 1, Rho GTPase, homolog 2 (C. elegans) /// similar to synapse	-1.28	0.219	-1.52	0.244	-1.2	0.339	1.27	0.447	-0.68
1435043_at	Plcb1	phospholipase C, beta 1	-1.11	0.343	-1.17	0.315	-1.89	0.067	1.24	0.415	-0.73
1420595_at	Dlx4	distal-less homeobox 4	-1.53	0.017	-1.46	0.047	-1.06	0.789	1.01	0.974	-0.76
1454223_at	4933423P22Rik	RIKEN cDNA 4933423P22 gene	-1.48	0.225	-1.37	0.086	-1.14	0.379	1.11	0.676	-0.72
1420848_at	Sufu	suppressor of fused homolog (Drosophila)	-1.83	0.131	-1.39	0.472	1.01	0.964	-1.11	0.293	-0.83

1453122_at	4921533L14Rik	RIKEN cDNA 4921533L14 gene	-1.17	0.094	-1.31	0.082	-1.52	0.031	1.16	0.639	-0.71
1417678_at	Mmp24	matrix metallopeptidase 24	-1.43	0.618	-1.32	0.472	-1.22	0.421	1.06	0.79	-0.73
1430494_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	-1.24	0.505	-1.52	0.002	-1.22	0.55	1	0.984	-0.75
1447854_s_at	Hist2h2be	histone 2, H2be	-1.33	0.177	-1.2	0.486	-1.43	0.008	1.33	0.426	-0.66
1420151_at	---	---	1.26	0.679	-1.56	0.433	-2.66	0.045	-1.18	0.608	-1.03
1425389_a_at	Runx2	runt related transcription factor 2	-1.54	0.443	-1.29	0.449	-1.17	0.318	1.43	0.435	-0.64
1419663_at	Ogn	osteoglycin	1.04	0.829	-2.12	0.015	-1.29	0.076	-1.6	0.383	-0.99
1426081_a_at	Dio2	deiodinase, iodothyronine, type II	-1.46	0.078	-1.06	0.878	-1.54	0.372	1.41	0.512	-0.66
1458884_at	---	---	1.08	0.85	-1.32	0.61	-2.26	0.001	-1.18	0.667	-0.92
1431536_at	4933432K03Rik	RIKEN cDNA 4933432K03 gene	-1.17	0.855	-1.41	0.524	-1.4	0.357	1.35	0.716	-0.66
1443234_at	BC088983	CDNA sequence BC088983	-1.07	0.749	-1.35	0.502	-1.65	0.011	1.1	0.75	-0.74
1446173_at	---	---	-2.01	0.039	-1.85	0.25	1.24	0.548	-1.85	0.372	-1.12
1445634_at	Mapt	Microtubule-associated protein tau	-1.38	0.14	-1.22	0.389	-1.36	0.427	1.09	0.728	-0.72
1435301_at	1110004E09Rik	RIKEN cDNA 1110004E09 gene	-1.12	0.39	-1.7	0.443	-1.24	0.248	1.28	0.371	-0.7
1420061_s_at	AA675344	expressed sequence AA675344	-1.05	0.9	-1.46	0.468	-1.55	0.302	1.33	0.406	-0.68
1430721_at	4931431C16Rik	RIKEN cDNA 4931431C16 gene	1.45	0.424	-2.43	0.185	-2.39	0.073	-1.04	0.951	-1.1
1439245_at	Tnrc6a	trinucleotide repeat containing 6a	-1.34	0.419	-1.31	0.275	-1.29	0.438	1.11	0.678	-0.71
1445804_at	9630020C08Rik	RIKEN cDNA 9630020C08 gene	-1.14	0.486	-1.67	0.532	-1.24	0.59	1.02	0.977	-0.76
1459568_at	Tmtc4	Transmembrane and tetratricopeptide repeat containing 4	1.23	0.303	-1.72	0.294	-2.09	0.021	-1.61	0.182	-1.05
1438166_x_at	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	-1.65	0.182	-1.26	0.033	-1.13	0.445	1.02	0.938	-0.76
1423496_a_at	Punc	putative neuronal cell adhesion molecule	-1.42	0.524	-1.09	0.807	-1.52	0.174	1.07	0.752	-0.74
1440788_at	Gas8	Growth arrest specific 8	-2.36	0.119	-2.67	0.192	1.49	0.272	-1.05	0.921	-1.15
1431111_at	Eno1 /// LOC23894	enolase 1, alpha non-neuron /// similar to enolase 1, alpha non-neuron /// similar t	1.01	0.96	-1.8	0.029	-1.38	0.494	-1.2	0.448	-0.84
1459328_at	4930429A22Rik	RIKEN cDNA 4930429A22 gene	-1.43	0.678	-1.53	0.462	-1.07	0.894	1.23	0.647	-0.7
1439535_at	---	---	-1.28	0.197	-1.06	0.872	-1.79	0.042	1.27	0.492	-0.72
1458672_at	Tcte2	T-complex-associated testis expressed 2	-1.99	0.327	-1.1	0.741	-1.15	0.456	1.09	0.778	-0.79
1438251_x_at	Htra1	HtrA serine peptidase 1	-1.17	0.093	-2.87	0.027	1.08	0.764	-1.71	0.218	-1.17
1456049_at	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	1.08	0.912	-1.6	0.481	-1.71	0.276	-1.9	0.315	-1.03
1426153_a_at	Dsg2	desmoglein 2	-1.42	0.503	-2.7	0.4	1.21	0.775	-1.36	0.033	-1.07
1455961_at	---	---	1.01	0.949	-2.14	0.099	-1.23	0.067	-1.43	0.158	-0.95
1437781_at	---	Transcribed locus	-1.3	0.183	1	0.996	-1.94	0.051	-2.16	0.533	-1.1
1442389_at	Oas1f	2'-5' oligoadenylate synthetase 1F	-1.62	0.267	-1.81	0.252	1.11	0.889	-1.56	0.323	-0.97
1444593_at	Phlppl	PH domain and leucine rich repeat protein phosphatase-like	-1.35	0.589	-1.08	0.867	-1.6	0.082	1.61	0.196	-0.61
1453727_at	2610101J03Rik	RIKEN cDNA 2610101J03 gene	-1.49	0.288	-1.36	0.193	-1.14	0.202	1.09	0.77	-0.72
1447670_at	Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	-1.34	0.531	-1.18	0.486	-1.44	0.105	1.04	0.907	-0.73
1446918_at	Lphn3	Latrophilin 3	-2.98	0.022	1.28	0.008	-1.49	0.269	-1.42	0.245	-1.15
1456315_a_at	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	-1.4	0.003	-1.16	0.126	-1.41	0.079	2.69	0.254	-0.32
1429274_at	2310010M24Rik	RIKEN cDNA 2310010M24 gene	1.13	0.625	-1.91	0.323	-1.59	0.24	-2.44	0.02	-1.2
1441030_at	Rai14	retinoic acid induced 14	-1.16	0.686	1.01	0.968	-2.43	0.006	-1.78	0.099	-1.09
1439652_at	---	---	1.01	0.962	-1.25	0.022	-2.08	0.03	-1.73	0.113	-1.01
1457534_at	Ubap2l	Ubiquitin associated protein 2-like	1.02	0.934	-1.44	0.214	-1.74	0.014	-1.02	0.946	-0.8
1449080_at	Hdac2	histone deacetylase 2	-1.24	0.287	-1.24	0.256	-1.48	0.043	1.01	0.957	-0.74
1442843_at	4933411D12Rik	RIKEN cDNA 4933411D12 gene	-1.34	0.029	-1.1	0.527	-1.6	0.02	2.42	0.24	-0.4
1441042_at	Fgf1	fibroblast growth factor 1	-1.1	0.498	-1.31	0.155	-1.63	0.022	1.03	0.963	-0.75
1436328_at	Rnmt	RNA (guanine-7-) methyltransferase	-1.12	0.41	-1.39	0.146	-1.47	0.05	1.02	0.848	-0.74
1440677_at	LOC245305	similar to hypothetical protein FLJ38281	-1.8	0.511	-1.6	0.305	1.11	0.784	-1.11	0.684	-0.85
1434915_s_at	Lrrc19	leucine rich repeat containing 19	-1.41	0.189	-1.38	0.622	-1.17	0.761	1.14	0.854	-0.71
1434772_at	Adora2b	adenosine A2b receptor	-1.67	0.35	-1.26	0.727	-1.12	0.589	1.32	0.703	-0.68
1449919_at	Krtap6-2	keratin associated protein 6-2	-1	0.998	-1.25	0.65	-2.04	0.245	1.5	0.442	-0.7
1448186_at	Pnliprp2	pancreatic lipase-related protein 2	-1.42	0.206	-1.39	0.393	-1.15	0.712	1.22	0.676	-0.69
1434197_at	Atrn	attractin	-1.46	0.038	-1.37	0.004	-1.14	0.438	1.22	0.531	-0.69
1421782_a_at	Smr2	submaxillary gland androgen regulated protein 2	-1.56	0.25	-1.21	0.628	-1.22	0.641	1.01	0.989	-0.74
1433270_at	9530004M16Rik	RIKEN cDNA 9530004M16 gene	-1.2	0.026	-1.43	0.054	-1.32	0.598	1.09	0.902	-0.71

1456831_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	1	0.985	-1.83	0.12	-1.36	0.281	-1.87	0.015	-1.01
1457131_at	Fry	furry homolog (Drosophila)	-2.44	0.084	-1.99	0.332	1.38	0.253	-1.06	0.848	-1.03
1450239_at	Glra3	glycine receptor, alpha 3 subunit	-3.08	0.451	1.13	0.682	-1.2	0.254	-1.37	0.638	-1.13
1441736_at	Itfg1	Integrin alpha FG-GAP repeat containing 1	-1.27	0.239	-1.24	0.506	-1.44	0.105	1.11	0.551	-0.71
1431427_at	5430427M07Rik	RIKEN cDNA 5430427M07 gene	-1.53	0.483	-1.22	0.679	-1.23	0.274	1.2	0.768	-0.69
1446878_at	Lonrf2	LON peptidase N-terminal domain and ring finger 2	1	0.997	-2.07	0.297	-1.25	0.496	-1.31	0.569	-0.91
1441883_at	0610010O12Rik	RIKEN cDNA 0610010O12 gene	-1.05	0.669	-1.92	0.014	-1.22	0.075	2.58	0.227	-0.4
1438139_at	Arhgap28	Rho GTPase activating protein 28	-1.68	0.476	-1.85	0.093	1.15	0.595	-1.67	0.491	-1.01
1453227_at	Rhobtb3	Rho-related BTB domain containing 3	-1.25	0.464	-1.43	0.263	-1.26	0.627	2.89	0.001	-0.26
1458423_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	1.14	0.859	-2.22	0.31	-1.42	0.105	-2.2	0.237	-1.18
1424228_at	Polr3h	polymerase (RNA) III (DNA directed) polypeptide H	-1.25	0.623	-1.52	0.273	-1.21	0.129	1.07	0.871	-0.73
1419429_at	Cntfr	ciliary neurotrophic factor receptor	-2.18	0.001	-1.76	0.113	1.26	0.627	-1.09	0.701	-0.94
1444434_at	Wdr33	WD repeat domain 33	-1.15	0.688	-2.08	0.262	-1.06	0.92	1.53	0.318	-0.69
1450263_at	Pcdhb5	protocadherin beta 5	-1.78	0.28	-1.27	0.498	-1.06	0.911	2.19	0.19	-0.48
1434030_at	BC034507	cDNA sequence BC034507	-1.16	0.136	-1.46	0.193	-1.35	0.024	1.03	0.862	-0.73
1459880_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	-1.08	0.864	-1.96	0.017	-1.17	0.619	1.59	0.124	-0.65
1454129_at	4933416M06Rik	RIKEN cDNA 4933416M06 gene	-1.08	0.172	-1.59	0.244	-1.36	0.593	1.09	0.887	-0.74
1442102_at	Aco2	Aconitase 2, mitochondrial	-1.16	0.544	-1.43	0.316	-1.36	0.062	1.09	0.692	-0.72
1441534_at	C86753	expressed sequence C86753	-2.41	0.051	1.06	0.754	-1.23	0.749	-1.08	0.857	-0.91
1449611_at	Cd82	CD82 antigen	-2.8	0.143	1.06	0.852	-1.14	0.726	-1.22	0.577	-1.03
1458953_at	D5Ertd215e	DNA segment, Chr 5, ERATO Doi 215, expressed	-1.36	0.424	-2.08	0.496	1.07	0.902	-1.11	0.665	-0.87
1435489_at	LOC552912	hypothetical LOC552912	-1.14	0.679	-1.96	0.139	-1.11	0.711	1.05	0.778	-0.79
1444896_at	---	---	-2.01	0.206	-1.27	0.601	1.01	0.99	-1.05	0.914	-0.83
1456286_at	Cog3	Component of oligomeric golgi complex 3	-1.37	0.015	-1.19	0.195	-1.39	0.126	1.03	0.898	-0.73
1429096_at	2810455D13Rik	RIKEN cDNA 2810455D13 gene	-1.32	0.315	-1.18	0.42	-1.45	0.202	1.21	0.519	-0.69
1420421_s_at	Klrb1b	killer cell lectin-like receptor subfamily B member 1B	-1.07	0.933	-1.02	0.864	-2.62	0.012	1.22	0.405	-0.87
1435282_at	Gm967	gene model 967, (NCBI)	-1.2	0.255	-1.6	0.016	-1.2	0.268	1.2	0.435	-0.7
1439315_at	LOC628919	Similar to shroom	-1.69	0.397	1.11	0.78	-1.69	0.374	-2.42	0.209	-1.17
1432785_at	A930028O11Rik	RIKEN cDNA A930028O11 gene	1.28	0.372	-2.73	0.277	-1.55	0.387	-1.36	0.201	-1.09
1460137_at	Fgf12	Fibroblast growth factor 12	-2.36	0.411	-1.09	0.851	-1.05	0.891	1.78	0.4	-0.68
1445970_at	AU022526	expressed sequence AU022526	-1.5	0.561	-1.62	0.329	1.01	0.988	-1.13	0.775	-0.81
1438752_at	A230058F20Rik	RIKEN cDNA A230058F20 gene	-1.4	0.004	1.18	0.744	-2.5	0.243	-1.23	0.511	-0.99
1438471_at	Wtap	Wilms' tumour 1-associating protein	1.01	0.977	-1.52	0.5	-1.6	0.039	-1.24	0.578	-0.84
1417838_at	Ssty2 /// LOC38213	spermiogenesis specific transcript on the Y 2 /// similar to RIKEN cDNA 1700029I	-1.37	0.714	-2.26	0.169	1.12	0.616	-1.25	0.64	-0.94
1455931_at	Chrna3	cholinergic receptor, nicotinic, alpha polypeptide 3	-2.13	0.498	-1.53	0.37	1.17	0.457	-1.09	0.666	-0.89
1446443_at	B230213L16Rik	RIKEN cDNA B230213L16 gene	-1.39	0.124	-1.35	0.102	-1.2	0.471	1.04	0.781	-0.73
1445185_at	Ttll10	tubulin tyrosine ligase-like family, member 10	-2.44	0.525	-1.92	0.301	1.36	0.313	-1.05	0.897	-1.01
1429109_at	Msl2l1	male-specific lethal 2-like 1 (Drosophila)	-1.73	0.536	-1.56	0.385	1.07	0.858	-1.22	0.747	-0.86
1436835_at	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	-1.15	0.844	-1.38	0.133	-1.44	0.286	1.25	0.091	-0.68
1450484_a_at	Tyki	thymidylate kinase family LPS-inducible member	-1.36	0.19	-1.48	0.137	-1.13	0.428	1.64	0.292	-0.58
1436653_at	4833401D15Rik	RIKEN cDNA 4833401D15 gene	-1.73	0.559	-1.59	0.204	1.09	0.661	-1.21	0.432	-0.86
1459180_at	---	Transcribed locus	-1.39	0.719	-2.39	0.071	1.16	0.704	-1.21	0.607	-0.96
1441379_at	AU045094	expressed sequence AU045094	1.44	0.373	-2.51	0.219	-2.18	0.323	-2.68	0.272	-1.48
1453046_at	LOC623215	similar to diacylglycerol kinase, eta isoform 2	-2.63	0.292	-1.03	0.918	-1.06	0.913	1.91	0.355	-0.7
1451677_at	Narf	nuclear prelamin A recognition factor	-1.11	0.704	-1.18	0.594	-1.83	0.374	3.93	0.287	-0.05
1418366_at	Hist2h3c1 /// Hist2h	histone 2, H3c1 /// histone 2, H2aa1 /// histone 1, H2ad /// histone 1, H2an /// hist	-1.37	0.295	-1.39	0.152	-1.19	0.319	1.34	0.518	-0.65
1440112_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	-1.32	0.765	-1.54	0.128	-1.13	0.813	2.09	0.029	-0.47
1424499_s_at	5730596K20Rik	RIKEN cDNA 5730596K20 gene	-1.12	0.271	-1.9	0.147	-1.14	0.185	1.37	0.381	-0.7
1456416_at	Cbfa2t2h	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 homolog (hur	-1.58	0.315	1.01	0.991	-1.53	0.1	-1.13	0.435	-0.81
1431658_at	Hist1h4j	histone 1, H4j	-1.46	0.576	-1.17	0.549	-1.33	0.499	2.26	0.232	-0.42
1451634_at	2810051F02Rik	RIKEN cDNA 2810051F02 gene	1.02	0.939	-1.6	0.12	-1.55	0.079	-1.07	0.668	-0.8
1449631_at	Eno3	Enolase 3, beta muscle	-1.56	0.216	-1.44	0.443	-1.04	0.84	1.32	0.228	-0.68
1451996_at	Tm2d1	TM2 domain containing 1	-1.38	0.092	-1.14	0.211	-1.44	0.043	1.01	0.902	-0.74

1432714_at	6430709C05Rik	RIKEN cDNA 6430709C05 gene	-2.22	0.292	1.29	0.703	-1.81	0.302	-3.05	0.111	-1.44
1430400_at	4930521A18Rik	RIKEN cDNA 4930521A18 gene	1.04	0.915	-1.28	0.616	-2.12	0.048	-1.59	0.497	-0.99
1416136_at	Mmp2	matrix metallopeptidase 2	-1.01	0.872	-1.22	0.137	-2.04	0.06	1.68	0.012	-0.65
1445263_at	Cst7	Cystatin F (leukocystatin)	-1.18	0.268	-1.34	0.009	-1.43	0.167	1.23	0.355	-0.68
1449844_at	Slco1a1	solute carrier organic anion transporter family, member 1a1	1.53	0.058	-58.47	0.077	-1.33	0.393	-1.04	0.946	-14.83
1443069_at	Prkca	Protein kinase C, alpha	-1.19	0.467	-1.41	0.108	-1.34	0.119	1.14	0.577	-0.7
1439064_at	BC030046	cDNA sequence BC030046	-1.82	0.524	-1.38	0.536	1.02	0.958	-1.52	0.524	-0.93
1443614_at	---	Transcribed locus	1.04	0.927	-1.54	0.507	-1.64	0.141	-1.21	0.808	-0.84
1440554_at	---	---	-1.31	0.331	-1.11	0.386	-1.59	0.019	1.28	0.377	-0.68
1433618_at	C330006A16Rik	RIKEN cDNA C330006A16 gene	-1.72	0.472	-1.51	0.384	1.05	0.874	-1.02	0.957	-0.8
1421100_a_at	Dab1	disabled homolog 1 (Drosophila)	-1.58	0.495	1.07	0.911	-1.69	0.228	-2.17	0.31	-1.09
1442427_at	9630026M06Rik	RIKEN cDNA 9630026M06 gene	-1.3	0.308	-1.14	0.386	-1.55	0.021	1.13	0.627	-0.71
1432609_at	---	---	-1.55	0.515	-1.99	0.237	1.15	0.346	-1.16	0.082	-0.89
1427538_at	Zfp369	zinc finger protein 369	-2.42	0.356	1.17	0.633	-1.39	0.469	-1.25	0.651	-0.98
1449270_at	Plxdc2	plexin domain containing 2	-1.14	0.715	-1.16	0.547	-1.8	0.035	1.58	0.116	-0.63
1439698_at	Zfp276	Zinc finger protein (C2H2 type) 276	-1.35	0.216	-2.46	0.161	1.15	0.79	-1.42	0.275	-1.02
1454251_at	1700034J04Rik	RIKEN cDNA 1700034J04 gene	-1.87	0.208	-1.18	0.274	-1.09	0.85	1.46	0.58	-0.67
1424969_s_at	---	---	-1.32	0.726	-1.21	0.667	-1.4	0.62	1.03	0.938	-0.73
1444119_at	B930006L02Rik	RIKEN cDNA B930006L02 gene	-1.14	0.548	-1.1	0.635	-1.93	0.012	1.31	0.289	-0.72
1433054_at	Itgb2l	integrin beta 2-like	-1.61	0.212	-1.22	0.813	-1.17	0.735	1.19	0.706	-0.7
1429702_at	2900072G11Rik	RIKEN cDNA 2900072G11 gene	-1.18	0.305	1.02	0.902	-2.34	0.025	-1.28	0.103	-0.94
1419425_at	Cnr1	cannabinoid receptor 1 (brain)	-1.32	0.643	-1.1	0.538	-1.58	0.001	1.48	0.122	-0.63
1453538_at	A330102K23Rik	RIKEN cDNA A330102K23 gene	-1.59	0.458	-1.01	0.988	-1.47	0.555	1.02	0.962	-0.76
1420570_x_at	Tcl1b3	T-cell leukemia/lymphoma 1B, 3	-1.69	0.265	-1.29	0.488	-1.07	0.829	1.37	0.598	-0.67
1439925_at	Tm4sf1	transmembrane 4 superfamily member 1	-1.05	0.813	-1.48	0.328	-1.5	0.03	1.04	0.89	-0.74
1416745_x_at	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	-1.05	0.766	-1.55	0.37	-1.42	0.139	2	0.185	-0.51
1425362_at	Hrbl	HIV-1 Rev binding protein-like	-1.44	0.329	-1.05	0.743	-1.54	0.009	1.91	0.357	-0.53
1447695_at	2610035D17Rik	RIKEN cDNA 2610035D17 gene	-1.2	0.356	-1.1	0.47	-1.79	0.113	1.36	0.649	-0.68
1440718_at	BC052328	cDNA sequence BC052328	1.31	0.471	-2.44	0.203	-1.72	0.298	-1.34	0.714	-1.05
1459948_at	Ghr	Growth hormone receptor	1.19	0.222	-1.87	0.09	-1.75	0.08	-1.09	0.687	-0.88
1447751_x_at	Dus2l	dihydrouridine synthase 2-like (SMM1, S. cerevisiae)	-3.64	0.098	-1.04	0.928	1.06	0.892	-3.76	0.019	-1.84
1453011_at	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	-1.14	0.438	-1.04	0.91	-2.17	0.133	1.05	0.955	-0.82
1440259_at	Man1a2	Mannosidase, alpha, class 1A, member 2	1	0.99	-1.41	0.206	-1.7	0.019	-1.24	0.137	-0.84
1445254_at	---	---	-1.02	0.944	-1.26	0.378	-1.9	0.159	3.01	0.24	-0.29
1429139_at	Otud7b	OTU domain containing 7B	-1.09	0.755	-1.57	0.074	-1.34	0.434	1.02	0.937	-0.75
1459738_x_at	---	---	-1.31	0.633	-1.29	0.542	-1.32	0.133	1.06	0.935	-0.71
1452017_at	Sox15	SRY-box containing gene 15	1.08	0.446	-2.24	0.267	-1.3	0.526	-1.78	0.273	-1.06
1432431_s_at	2900006F19Rik	RIKEN cDNA 2900006F19 gene	-1.22	0.064	-1.12	0.477	-1.71	0.019	1.45	0.476	-0.65
1449456_a_at	Cma1	chymase 1, mast cell	-1.47	0.239	-1.68	0.264	1.03	0.94	-1.04	0.891	-0.79
1442996_x_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630027M	1	0.992	-1.26	0.195	-2	0.005	-1.13	0.673	-0.84
1458939_at	Synj2bp	Synaptojanin 2 binding protein	-1.17	0.612	-1.55	0.33	-1.25	0.63	1.26	0.479	-0.68
1439461_x_at	2410003A14Rik	RIKEN cDNA 2410003A14 gene	-1.38	0.199	-1.21	0.244	-1.33	0.213	1.14	0.593	-0.7
1417708_at	Syt3	synaptotagmin III	-1.49	0.257	-1.14	0.767	-1.33	0.226	1.35	0.372	-0.65
1441822_at	1700008F19Rik	RIKEN cDNA 1700008F19 gene	-1.22	0.688	-2.29	0.048	1.04	0.801	-2.66	0.058	-1.28
1439533_at	1700125D06Rik	RIKEN cDNA 1700125D06 gene	-1.49	0.263	-1.1	0.724	-1.39	0.127	1.3	0.065	-0.67
1439201_at	Usp14	ubiquitin specific peptidase 14	-1.39	0.106	-1.49	0.046	-1.1	0.711	1.44	0.283	-0.64
1422162_at	Dcc	deleted in colorectal carcinoma	-1.16	0.617	1.04	0.905	-2.51	0.006	-1.57	0.262	-1.05
1458070_at	Vtcn1	V-set domain containing T cell activation inhibitor 1	-1.03	0.861	-2.77	0.126	-1.03	0.935	1.11	0.708	-0.93
1436513_at	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-1.18	0.607	-1.39	0.023	-1.36	0.216	1.09	0.672	-0.71
1444938_at	---	Transcribed locus	-1.51	0.405	-2.59	0.248	1.25	0.692	-1.37	0.586	-1.05
1443245_at	---	---	1.32	0.731	-2.15	0.19	-1.95	0.199	-1.02	0.928	-0.95
1439249_at	Wac	WW domain containing adaptor with coiled-coil	-1.49	0.377	-1.14	0.675	-1.32	0.23	1.29	0.387	-0.67
1439053_at	D10Bwg1070e	DNA segment, Chr 10, Brigham & Women's Genetics 1070 expressed	1.09	0.913	-2.13	0.033	-1.34	0.214	-1.41	0.116	-0.95

1435594_at	Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	-1.16	0.522	-1.25	0.305	-1.56	0.227	1.39	0.511	-0.65
1450854_at	Pa2g4	proliferation-associated 2G4	-1.56	0.188	-1.3	0.147	-1.12	0.304	1.78	0.183	-0.55
1447254_at	---	---	-1.28	0.589	-1.51	0.555	-1.16	0.405	1.5	0.113	-0.61
1458970_at	Rad50	RAD50 homolog (S. cerevisiae)	-3.62	0.002	-1.23	0.366	1.21	0.335	-1.03	0.903	-1.17
1444973_at	Kcnma1	Potassium large conductance calcium-activated channel, subfamily M, alpha mer	1.03	0.858	-1.81	0.233	-1.39	0.066	-1.26	0.03	-0.86
1457017_at	---	---	-1.52	0.415	1	0.988	-1.56	0.087	-1.54	0.273	-0.9
1421449_at	Csmd1	CUB and Sushi multiple domains 1	-1.12	0.874	-1.28	0.691	-1.59	0.452	1.19	0.696	-0.7
1457584_at	AI848100	expressed sequence AI848100	-1.37	0.263	-1.12	0.767	-1.46	0.293	1.06	0.808	-0.72
1432082_at	4933436I20Rik	RIKEN cDNA 4933436I20 gene	-3.09	0.301	1.08	0.838	-1.12	0.729	-2.01	0.255	-1.28
1440985_at	D130023J23Rik	RIKEN cDNA D130023J23 gene	-1.38	0.295	-1.11	0.835	-1.48	0.313	1.01	0.956	-0.74
1442908_at	Tm9sf1	Transmembrane 9 superfamily member 1	-1.38	0.099	-2.06	0.328	1.1	0.689	-1.08	0.756	-0.86
1456706_at	4833441D16Rik	RIKEN cDNA 4833441D16 gene	-1.2	0.297	-1.04	0.76	-1.96	0.008	1.01	0.977	-0.8
1429747_at	1700009N14Rik	RIKEN cDNA 1700009N14 gene	-1.5	0.065	-1.27	0.445	-1.17	0.72	2.51	0.006	-0.36
1426325_at	Kif1c	kinesin family member 1C	-1.45	0.508	-2.88	0.014	1.27	0.617	-1.22	0.694	-1.07
1436561_at	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	-1.85	0.349	-1.19	0.76	-1.08	0.85	6.55	0.097	0.61
1427690_a_at	Tpte	transmembrane phosphatase with tensin homology	1.1	0.767	-2.31	0.097	-1.3	0.435	-1.93	0.185	-1.11
1436933_at	Akap13	A kinase (PRKA) anchor protein 13	-1.23	0.167	-1.2	0.487	-1.52	0.011	1.16	0.492	-0.7
1446604_at	---	---	-1.5	0.316	-1.32	0.165	-1.13	0.535	1.07	0.875	-0.72
1431923_at	2810401C16Rik	RIKEN cDNA 2810401C16 gene	-1.22	0.504	-1.61	0.469	-1.16	0.766	1.13	0.114	-0.71
1454199_at	1700014N06Rik	RIKEN cDNA 1700014N06 gene	1.06	0.619	-2.26	0.104	-1.24	0.421	-1.49	0.611	-0.98
1438720_at	9330159F19Rik	RIKEN cDNA 9330159F19 gene	1.07	0.857	-1.46	0.301	-1.81	0.232	-2.45	0.11	-1.16
1429685_at	C030002O17Rik	RIKEN cDNA C030002O17 gene	-1.09	0.677	-1.43	0.572	-1.45	0.256	1.23	0.8	-0.69
1438592_at	Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	-1.19	0.161	-1.31	0.204	-1.42	0.01	1.1	0.769	-0.71
1435227_at	---	---	-1.49	0.03	-2.33	0.334	1.2	0.456	-2.3	0.153	-1.23
1432964_at	2410049M19Rik	RIKEN cDNA 2410049M19 gene	-1.49	0.003	1.06	0.941	-1.73	0.198	-1.91	0.375	-1.02
1455057_at	Gmps	guanine monphosphate synthetase	-1.12	0.565	-1.44	0.06	-1.39	0.048	1.01	0.959	-0.74
1452696_a_at	4933439C10Rik	RIKEN cDNA 4933439C10 gene	1.01	0.863	-1.97	0.154	-1.26	0.23	-1.73	0.16	-0.99
1435120_at	---	Transcribed locus	1.12	0.389	-1.51	0.039	-1.9	0.039	-1.13	0.58	-0.86
1441517_at	Spred1	Sprouty protein with EVH-1 domain 1, related sequence	-1.19	0.442	-1.42	0.391	-1.32	0.396	1.42	0.593	-0.63
1432292_at	4930504C09Rik	RIKEN cDNA 4930504C09 gene	-2.1	0.341	-1.51	0.439	1.17	0.724	-1.85	0.072	-1.07
1446913_at	---	---	-1.31	0.695	-1.04	0.954	-1.73	0.235	1.51	0.503	-0.64
1424558_a_at	Cabyr	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	-1.27	0.291	-1.17	0.589	-1.52	0.09	1.47	0.45	-0.62
1443470_at	A530058N18Rik	RIKEN cDNA A530058N18 gene	-1.62	0.607	-1.2	0.788	-1.17	0.587	2.77	0.357	-0.3
1458811_at	9430047L24Rik	RIKEN cDNA 9430047L24 gene	-1.05	0.943	-1.31	0.67	-1.68	0.241	2.04	0.207	-0.5
1429913_at	Kcnk16	potassium channel, subfamily K, member 16	-4.45	0.002	-2.85	0.056	1.73	0.364	-1.12	0.867	-1.67
1431432_at	Cfl2	cofilin 2, muscle	-1.09	0.836	-1.66	0.293	-1.27	0.057	1	0.998	-0.76
1451441_at	2210415F13Rik	RIKEN cDNA 2210415F13 gene	-1.67	0.186	-1.03	0.95	-1.36	0.322	1.82	0.474	-0.56
1449584_at	Dgkg	diacylglycerol kinase, gamma	-1.05	0.561	-2.48	0.008	-1.05	0.639	1.21	0.303	-0.84
1436274_at	---	Transcribed locus	-1.26	0.602	-2.32	0.232	1.09	0.867	-1.24	0.741	-0.94
1458309_at	---	Transcribed locus	-1.2	0.387	-1.1	0.524	-1.75	0.01	1.11	0.694	-0.74
1423485_at	Rad54l2	Rad54 like 2 (S. cerevisiae)	-2	0.58	-1.32	0.561	1.05	0.864	-1.52	0.373	-0.95
1454364_at	9530025L08Rik	RIKEN cDNA 9530025L08 gene	-1.47	0.238	-1.12	0.555	-1.36	0.592	1.54	0.161	-0.6
1447416_at	Gm239	gene model 239, (NCBI)	-1.45	0.211	-1.62	0.381	1	1	-1.17	0.708	-0.81
1453408_s_at	4930519G04Rik	RIKEN cDNA 4930519G04 gene	-1.03	0.897	-1.56	0.322	-1.43	0.24	1.05	0.882	-0.74
1420557_at	Epha5	Eph receptor A5	-1.58	0.156	-1.02	0.954	-1.45	0.064	1.43	0.113	-0.65
1431341_at	Ppp2cb	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	-1.29	0.336	-1.99	0.005	1.03	0.925	-1.14	0.041	-0.85
1429426_at	Rnf139	ring finger protein 139	-1	0.994	-1.35	0.298	-1.75	0.015	1.62	0.375	-0.62
1426959_at	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	-1.17	0.215	-1.99	0.047	-1.05	0.928	1.58	0.32	-0.66
1432475_at	1700014B07Rik	RIKEN cDNA 1700014B07 gene	1.06	0.942	-2.77	0.004	-1.12	0.727	-1.45	0.052	-1.07
1446836_at	---	---	-1.87	0.279	-1.44	0.582	1.08	0.9	-2.99	0.063	-1.31
1440958_at	---	---	1.12	0.603	-2.75	0.086	-1.2	0.659	-1.1	0.555	-0.98
1458413_at	Fbxw8	F-box and WD-40 domain protein 8	1.04	0.924	-1.5	0.406	-1.66	0.351	-1.15	0.789	-0.82
1435612_at	Opcml	opioid binding protein/cell adhesion molecule-like	1.17	0.448	-2.25	0.017	-1.44	0.386	-1.23	0.701	-0.94

1418589_a_at	Mlf1	myeloid leukemia factor 1	-1.91	0.23	-1.34	0.392	1.04	0.901	-1.12	0.622	-0.83
1439848_at	Bves	blood vessel epicardial substance	1.16	0.438	-2.09	0.354	-1.49	0.571	-2.81	0.085	-1.31
1446760_at	Trip13	thyroid hormone receptor interactor 13	-1.27	0.665	-1.29	0.452	-1.34	0.483	1.25	0.483	-0.66
1442062_at	7120426M23Rik	RIKEN cDNA 7120426M23 gene	-1.3	0.203	-1.17	0.193	-1.46	0.25	1.25	0.312	-0.67
1432337_at	Fancl	Fanconi anemia, complementation group L	-1.02	0.974	-1.48	0.435	-1.52	0.41	1.24	0.563	-0.7
1441565_at	---	---	-1.41	0.446	-1.91	0.01	1.08	0.187	-1.17	0.309	-0.85
1453187_at	Ociad2	OCIA domain containing 2	-1.24	0.056	-1.49	0.144	-1.2	0.318	1.84	0.132	-0.52
1435719_at	AI448984	expressed sequence AI448984	-1.28	0.011	-1.24	0.233	-1.39	0.099	1.06	0.834	-0.71
1457041_at	1700026B20Rik	RIKEN cDNA 1700026B20 gene	-3.34	0.137	-1.09	0.889	1.1	0.418	-1.99	0.154	-1.33
1440035_at	---	---	-1.07	0.705	-1.29	0.701	-1.65	0.005	1.06	0.828	-0.74
1439404_x_at	Zfa /// Zfx	zinc finger protein, autosomal /// zinc finger protein X-linked	-1.51	0.076	-1.06	0.833	-1.41	0.2	1.66	0.081	-0.58
1426720_at	Apbb2	amyloid beta (A4) precursor protein-binding, family B, member 2	1.02	0.94	-1.43	0.053	-1.67	0.018	-1.21	0.624	-0.83
1432745_at	9430092D12Rik	RIKEN cDNA 9430092D12 gene	-2.02	0.121	1.04	0.922	-1.28	0.548	-1.33	0.415	-0.9
1426732_at	Des	desmin	-1.72	0.12	-1.07	0.607	-1.25	0.387	1.28	0.636	-0.69
1418336_at	Afg3l1	AFG3(ATPase family gene 3)-like 1 (yeast)	-1.24	0.504	-2.17	0.056	1.05	0.813	-1.08	0.572	-0.86
1445379_at	Atp11c	Atpase, class VI, type 11C	-1.08	0.802	-1.23	0.156	-1.73	0.089	1.09	0.586	-0.74
1459802_at	---	---	-1.73	0.447	-2.39	0.03	1.32	0.449	-1.2	0.753	-1
1434413_at	---	---	-1.05	0.899	-1.27	0.022	-1.76	0.063	1.18	0.486	-0.72
1454309_at	2810002N01Rik	RIKEN cDNA 2810002N01 gene	-1.63	0.073	-1.01	0.993	-1.41	0.513	1.11	0.232	-0.73
1431180_at	1700123A16Rik ///	RIKEN cDNA 1700123A16 gene /// similar to zinc finger protein 709	-1.3	0.653	-1.6	0.025	-1.09	0.584	1.11	0.742	-0.72
1449691_at	Zfp644	Zinc finger protein 644	-1.12	0.801	-1.44	0.182	-1.39	0.287	1.19	0.417	-0.69
1445493_at	AU022255	expressed sequence AU022255	-1.48	0.522	1.04	0.945	-1.67	0.016	-1.08	0.864	-0.8
1459200_at	---	---	-1.29	0.735	-1.09	0.871	-1.61	0.227	1.37	0.55	-0.66
1442365_at	Rtn3	Reticulon 3	-1.16	0.641	-1.19	0.307	-1.63	0.001	1.1	0.7	-0.72
1427445_a_at	Ttn	titin	-2.44	0.141	-1.61	0.147	1.28	0.645	-1.04	0.936	-0.95
1446972_at	D15Wsu126e	DNA segment, Chr 15, Wayne State University 126, expressed	-1.02	0.898	-1.06	0.758	-2.55	0.007	1.41	0.208	-0.8
1445203_at	Pdzd2	PDZ domain containing 2	-1.17	0.69	-1.25	0.458	-1.51	0.014	1.35	0.082	-0.65
1445704_x_at	2900093B09Rik	RIKEN cDNA 2900093B09 gene	-1.18	0.694	-1.16	0.788	-1.65	0.234	1.19	0.75	-0.7
1451939_a_at	Srpx	sushi-repeat-containing protein	1.05	0.758	-1.32	0.318	-1.97	0.009	-1.65	0.347	-0.97
1445555_at	Trpm3	Transient receptor potential cation channel, subfamily M, member 3	-1.1	0.259	-1.34	0.433	-1.5	0.294	1.81	0.498	-0.53
1445624_at	D8Ertd587e	DNA segment, Chr 8, ERATO Doi 587, expressed	-1.4	0.094	-1.37	0.07	-1.15	0.134	2.52	0.096	-0.35
1447039_at	Ptch1	Patched homolog 1	1.21	0.491	-1.83	0.212	-1.79	0.098	-1.94	0.155	-1.09
1456559_at	Emx2os	empty spiracles homolog 2 (Drosophila) opposite strand	-1.09	0.491	-1.46	0.358	-1.39	0.452	1.5	0.303	-0.61
1430241_at	Fbxl17	F-box and leucine-rich repeat protein 17	-1.48	0.119	-1.28	0.406	-1.16	0.388	1.15	0.523	-0.69
1438790_x_at	Tmem41b	transmembrane protein 41B	-1.22	0.173	-1.33	0.032	-1.34	0.137	1.28	0.436	-0.65
1430564_at	Mobkl1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	1.08	0.806	-1.68	0.26	-1.57	0.012	-1.05	0.874	-0.8
1443295_at	---	Transcribed locus	-2.18	0.222	1.26	0.654	-1.65	0.263	-1.02	0.979	-0.9
1441397_at	Pard3	Par-3 (partitioning defective 3) homolog (C. elegans)	-1.06	0.762	-1.07	0.839	-2.28	0.02	1.22	0.365	-0.8
1453685_at	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-1.04	0.821	-1.7	0.1	-1.3	0.459	2.07	0.314	-0.49
1446755_at	Scg5	Secretogranin V	-2.71	0.053	1.05	0.747	-1.12	0.639	-1.18	0.536	-0.99
1435844_at	A330009N23Rik	RIKEN cDNA A330009N23 gene	-1.55	0.032	1.02	0.935	-1.54	0.031	-1.22	0.483	-0.82
1430851_at	Zfp444	zinc finger protein 444	-1.88	0.051	-1.21	0.661	-1.04	0.821	1	0.989	-0.78
1417436_at	Large	like-glycosyltransferase	-1.44	0.695	-2.75	0.203	1.26	0.637	-2.45	0.221	-1.34
1433425_at	1700101I19Rik	RIKEN cDNA 1700101I19 gene	-1.38	0.007	-1.13	0.603	-1.42	0.008	1.03	0.855	-0.72
1424673_at	Clec2h	C-type lectin domain family 2, member h	-1.15	0.56	-5.85	0.017	1.28	0.268	-1.03	0.967	-1.69
1445761_at	D4Ertd628e	DNA segment, Chr 4, ERATO Doi 628, expressed	-1.44	0.117	-1.27	0.5	-1.2	0.495	1.26	0.547	-0.66
1419426_s_at	Ccl21b /// Ccl21a ///	chemokine (C-C motif) ligand 21b /// chemokine (C-C motif) ligand 21a /// chemok	1.26	0.049	-2.81	0.109	-1.43	0.024	-2.83	0.06	-1.45
1457328_at	Adra2c	adrenergic receptor, alpha 2c	-1.48	0.294	-1.1	0.837	-1.36	0.572	1.11	0.895	-0.71
1436655_at	1300002A08Rik	RIKEN cDNA 1300002A08 gene	-1.17	0.712	-1.45	0.201	-1.29	0.552	1.01	0.931	-0.72
1454368_at	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	-2.52	0.144	1.18	0.714	-1.34	0.643	-1.19	0.598	-0.97
1430918_at	3-Mar	membrane-associated ring finger (C3HC4) 3	-1.28	0.37	-1.21	0.707	-1.4	0.294	3.49	0.256	-0.1
1425342_a_at	Kcnk3	potassium channel, subfamily K, member 3	-1.36	0.4	-1.22	0.331	-1.3	0.39	1.17	0.536	-0.68
1443097_at	Nf1	Neurofibromatosis 1	1.06	0.869	-1.78	0.06	-1.43	0.099	-1.71	0.304	-0.96

1430119_at	Fndc1	fibronectin type III domain containing 1	-1.23	0.394	-1.91	0.218	-1.02	0.949	1.33	0.214	-0.71
1460157_at	---	---	-3.44	0.091	1.32	0.333	-1.41	0.535	-1.07	0.752	-1.15
1442878_at	Prdx6	peroxiredoxin 6	-1.02	0.868	-1.32	0.467	-1.71	0.077	1.2	0.585	-0.71
1432904_at	3110037C07Rik	RIKEN cDNA 3110037C07 gene	1.18	0.458	-1.33	0.357	-2.57	0.086	-1.71	0.416	-1.11
1441891_x_at	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	-1.14	0.226	-2.09	0.093	-1.04	0.859	1.91	0.201	-0.59
1450492_at	Cngb3	cyclic nucleotide gated channel beta 3	-1.09	0.755	-1.65	0.218	-1.25	0.569	1.09	0.832	-0.73
1431723_at	1600022D10Rik	RIKEN cDNA 1600022D10 gene	-1.84	0.418	-1.08	0.898	-1.18	0.709	1.03	0.949	-0.77
1445588_at	Ankrd44	ankyrin repeat domain 44	-1.3	0.405	1.03	0.958	-1.9	0.019	-2.23	0.16	-1.1
1445927_at	D13Ertd212e	DNA segment, Chr 13, ERATO Doi 212, expressed	-1.48	0.433	-1.04	0.966	-1.47	0.257	1.23	0.728	-0.69
1429378_x_at	AY761184	cDNA sequence AY761184	-1.6	0.153	-1.15	0.558	-1.21	0.429	1.21	0.673	-0.69
1421335_a_at	Egfl7	EGF-like domain 7	-1.34	0.154	-1.13	0.499	-1.45	0.119	1.05	0.773	-0.72
1433311_at	D530031A16Rik	RIKEN cDNA D530031A16 gene	-1.65	0.438	-1.27	0.448	-1.08	0.853	1.21	0.743	-0.7
1436491_at	5830431A10Rik	RIKEN cDNA 5830431A10 gene	-1.39	0.664	-1.8	0.422	1.04	0.6	-4.39	0.032	-1.63
1420578_at	Optc	opticin	1	1	-1.7	0.411	-1.37	0.47	-2.11	0.095	-1.04
1434527_at	Nalp4b	NACHT, leucine rich repeat and PYD containing 4B	1.02	0.955	-1.06	0.935	-2.81	0.077	-1.54	0.379	-1.1
1435607_at	Grm2	G protein-coupled receptor, family C, group 1, member B	-1.39	0.2	-1.83	0.407	1.06	0.934	-1.01	0.958	-0.8
1458376_at	B930025B16Rik	RIKEN cDNA B930025B16 gene	-1.42	0.081	1.18	0.138	-2.29	0.003	-1.51	0.297	-1.01
1443406_at	Plscr4	phospholipid scramblase 4	-1.22	0.084	-1.26	0.449	-1.42	0.237	1.1	0.855	-0.7
1442879_at	---	---	-1.35	0.39	-1.65	0.487	-1.02	0.926	1.11	0.757	-0.73
1427772_at	Defb15	defensin beta 15	-2.38	0.166	-1.5	0.382	1.23	0.742	-2.38	0.547	-1.26
1447263_at	Metap2	Methionine aminopeptidase 2	-1.02	0.917	-1.56	0.039	-1.42	0.167	2.56	0.201	-0.36
1450296_at	Klrb1a	killer cell lectin-like receptor subfamily B member 1A	-2.53	0.306	1.39	0.674	-1.85	0.244	-1.64	0.162	-1.16
1419953_at	C80678	expressed sequence C80678	1.15	0.058	-1.23	0.575	-2.74	0.1	-1.75	0.579	-1.14
1425642_at	Cep290	centrosomal protein 290	-1.55	0.442	-1.19	0.197	-1.19	0.499	2.26	0.082	-0.42
1456793_at	Cyt1	cytokine like 1	1.1	0.784	-1.57	0.184	-1.72	0.251	-1.25	0.571	-0.86
1460604_at	Cybrd1	cytochrome b reductase 1	1.02	0.951	-1.25	0.769	-2	0.054	-2.07	0.151	-1.07
1458862_at	C78704	expressed sequence C78704	-1.27	0.445	-1.32	0.555	-1.29	0.555	1.29	0.197	-0.65
1422585_at	Odf1	outer dense fiber of sperm tails 1	-1.76	0.466	1.14	0.729	-1.62	0.383	-1.07	0.704	-0.83
1445446_at	---	Transcribed locus	-1.98	0.08	-1.07	0.863	-1.14	0.54	1.05	0.777	-0.78
1459027_at	---	Transcribed locus	-2.08	0.071	-1.79	0.321	1.28	0.492	-1.2	0.786	-0.95
1431389_at	Tbkbp1	TBK1 binding protein 1	-1.23	0.768	-1.36	0.509	-1.3	0.126	1.02	0.939	-0.71
1458663_at	Large	Like-glycosyltransferase	-1.16	0.27	1.03	0.939	-2.31	0.009	-1.18	0.541	-0.91
1430763_at	4930563E22Rik	RIKEN cDNA 4930563E22 gene	-1.78	0.035	-1.3	0.066	-1.01	0.972	1.1	0.388	-0.75
1428778_at	Sfi1	Sfi1 homolog, spindle assembly associated (yeast)	-1.39	0.234	-1.49	0.16	-1.07	0.769	1.22	0.502	-0.68
1425301_at	Ncam2	neural cell adhesion molecule 2	-1.28	0.664	-1.39	0.478	-1.21	0.627	1.92	0.187	-0.49
1449903_at	Crtam	cytotoxic and regulatory T cell molecule	1.14	0.652	-1.77	0.244	-1.62	0.274	-1.27	0.62	-0.88
1450909_at	Eif4e	eukaryotic translation initiation factor 4E	-1.55	0.014	-1.18	0.309	-1.21	0.422	1.39	0.154	-0.64
1445282_at	Mkln1	Muskelin 1, intracellular mediator containing kelch motifs	-1.3	0.062	-1.02	0.8	-1.74	0.034	1.07	0.757	-0.75
1448365_at	Exosc7	exosome component 7	-1.4	0.143	-1.28	0.024	-1.21	0.04	1.21	0.541	-0.67
1440465_at	Cutl1	Cut-like 1 (Drosophila)	-1.42	0.018	-1.17	0.442	-1.31	0.241	1.05	0.845	-0.71
1444749_at	Apod	Apolipoprotein D	-1.68	0.466	-1.84	0.486	1.19	0.639	-1.31	0.518	-0.91
1439286_at	Grik2	Glutamate receptor, ionotropic, kainate 2 (beta 2)	-1.51	0.531	-1.08	0.911	-1.36	0.414	1.16	0.734	-0.7
1430304_at	Wdr76	WD repeat domain 76	-1.36	0.126	-1.86	0.12	1.05	0.889	-1.04	0.829	-0.8
1418212_at	Omg	oligodendrocyte myelin glycoprotein	-1.55	0.011	1.08	0.684	-1.67	0.389	-2.16	0.179	-1.07
1442986_at	Elk3	ELK3, member of ETS oncogene family	1.25	0.687	-2.27	0.212	-1.59	0.086	-1.67	0.185	-1.07
1442551_at	---	---	-1.77	0.171	-1.37	0.548	1.03	0.936	-1.08	0.856	-0.8
1417565_at	Abhd5	abhydrolase domain containing 5	-1.24	0.377	-1.28	0.012	-1.35	0.054	1.96	0.325	-0.48
1453834_at	1500002C15Rik	RIKEN cDNA 1500002C15 gene	1.19	0.838	-1.4	0.416	-2.36	0.051	-1.44	0.581	-1
1439366_at	Grsf1	G-rich RNA sequence binding factor 1	-3.33	0.386	1.19	0.413	-1.2	0.641	-1.38	0.416	-1.18
1447256_at	---	17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920178F	-1.15	0.755	-1.32	0.569	-1.43	0.452	1.19	0.788	-0.68
1433316_at	4930477O15Rik	RIKEN cDNA 4930477O15 gene	-2.47	0.483	-1.28	0.604	1.14	0.779	-2.18	0.368	-1.2
1454141_at	5730416O20Rik	RIKEN cDNA 5730416O20 gene	-1.6	0.173	1.23	0.244	-2.13	0.05	-1.27	0.68	-0.94
1444657_at	B3bp	Bcl3 binding protein	-1.42	0.531	-1.47	0.347	-1.07	0.86	1.24	0.475	-0.68

1432056_at	Cpvl	carboxypeptidase, vitellogenic-like	-1.59	0.491	-1.09	0.727	-1.29	0.277	1.01	0.99	-0.74
1450619_x_at	Cmar	cell matrix adhesion regulator	-1.21	0.619	-1.71	0.039	-1.09	0.488	1.24	0.486	-0.69
1439897_at	Nebl	Nebulette	-4.53	0.065	-1.1	0.876	1.2	0.31	-1.81	0.092	-1.56
1457262_at	2610207I05Rik	RIKEN cDNA 2610207I05 gene	1.21	0.122	-1.92	0.353	-1.68	0.117	-2.28	0.108	-1.17
1454511_at	9430018C23Rik	RIKEN cDNA 9430018C23 gene	-1.15	0.855	1.05	0.919	-2.48	0.2	-1.18	0.747	-0.94
1431219_at	B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	1.12	0.746	-1.7	0.435	-1.61	0.123	-1.46	0.246	-0.92
1445797_at	Pam	Peptidylglycine alpha-amidating monooxygenase	-2.15	0.058	-1.18	0.744	1.01	0.977	-1.06	0.871	-0.84
1431662_at	4930555F03Rik	RIKEN cDNA 4930555F03 gene	1.07	0.921	-2.06	0.267	-1.3	0.637	-1.19	0.756	-0.87
1456317_at	Aldh3b2	aldehyde dehydrogenase 3 family, member B2	-1.27	0.088	-1.21	0.648	-1.4	0.096	1.9	0.045	-0.5
1448855_at	Rassf1	Ras association (RalGDS/AF-6) domain family 1	-1.43	0.018	-1.43	0.304	-1.08	0.751	1.17	0.501	-0.69
1440056_at	---	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C63000	-1.04	0.755	-2.86	0.023	1.01	0.968	-1.58	0.396	-1.12
1449279_at	Gpx2	glutathione peroxidase 2	-1.2	0.739	-1.57	0.204	-1.17	0.547	1.08	0.902	-0.71
1420718_at	Odz2 /// LOC66949	odd Oz/ten-m homolog 2 (Drosophila) /// similar to odd Oz/ten-m homolog 2	-1.67	0.111	-1.17	0.823	-1.14	0.738	1.22	0.607	-0.69
1439281_at	---	PREDICTED: Mus musculus similar to solute carrier family 26, member 8 isoform	-1.18	0.582	-1.11	0.858	-1.72	0.125	1.12	0.854	-0.72
1435685_x_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.37	0.083	-1.3	0.237	-1.21	0.614	1.27	0.341	-0.65
1456213_x_at	Qars	glutaminyl-tRNA synthetase	-1.46	0.278	-1.12	0.202	-1.34	0.325	1.02	0.787	-0.73
1430207_at	4933437N03Rik	RIKEN cDNA 4933437N03 gene	-1.51	0.354	-1.02	0.955	-1.46	0.583	1.26	0.584	-0.68
1450389_s_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	-1.56	0.314	-1.33	0.171	-1.07	0.558	6.86	0.225	0.72
1424217_at	Papola	poly (A) polymerase alpha	-1.21	0.101	-1.24	0.325	-1.45	0.164	1.23	0.111	-0.67
1443297_at	Tbc1d12	TBC1D12: TBC1 domain family, member 12	-1.07	0.898	-1.36	0.509	-1.52	0.342	2.84	0.09	-0.28
1443121_at	---	---	1.03	0.9	-1.96	0.003	-1.28	0.406	-1.14	0.25	-0.84
1459390_at	---	Transcribed locus	-2.01	0.195	-1.36	0.197	1.09	0.798	-1.67	0.123	-0.99
1448738_at	Calb1	calbindin-28K	-1.38	0.024	1.1	0.715	-1.99	0.032	-1.34	0.269	-0.9
1429822_at	4633401B06Rik	RIKEN cDNA 4633401B06 gene	1.1	0.653	-1.42	0.251	-1.92	0.004	-1.16	0.609	-0.85
1446431_at	Dnm3	Dynamin 3	-1.33	0.098	-1.45	0.335	-1.13	0.519	1.27	0.264	-0.66
1428160_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-1.19	0.272	-1.48	0.166	-1.23	0.155	1.08	0.732	-0.7
1444461_at	Zmynd11	Zinc finger, MYND domain containing 11	1.16	0.786	-1.55	0.148	-1.9	0.037	-3.08	0.034	-1.34
1417888_at	Trim13	tripartite motif protein 13	-1.11	0.548	-1.44	0.431	-1.36	0.189	1.29	0.252	-0.66
1443636_at	Abcb9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	-1.45	0.348	-1.34	0.106	-1.12	0.64	1.13	0.457	-0.7
1431995_at	Antxr1	anthrax toxin receptor 1	-1.11	0.697	-1.17	0.797	-1.74	0.019	1.25	0.168	-0.69
1431677_at	4631424J17Rik	RIKEN cDNA 4631424J17 gene	1.04	0.828	-1.43	0.084	-1.69	0.213	-1	0.986	-0.77
1452794_x_at	Speer1-ps1 /// LOC	spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1 /// simila	-2.08	0.329	-1.34	0.256	1.1	0.544	-1.35	0.638	-0.92
1460080_at	AI645535	expressed sequence AI645535	-1.53	0.186	-1.28	0.171	-1.12	0.417	1.16	0.663	-0.69
1451909_a_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	-1.33	0.026	-1.24	0.087	-1.29	0.286	1.13	0.157	-0.68
1441404_at	Pafah1b1	Platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	-1.22	0.167	-1.36	0.263	-1.29	0.514	1.1	0.567	-0.69
1435986_x_at	Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	-1.28	0.362	-1.26	0.223	-1.33	0.086	1.11	0.642	-0.69
1426026_at	Prpf6	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	-1.37	0.06	-2.15	0.267	1.13	0.761	-1.03	0.949	-0.85
1421279_at	Lamc2	laminin, gamma 2	-1.18	0.246	1.09	0.798	-2.58	0.135	-3.45	0.047	-1.53
1441791_at	Oprm1	Opioid receptor, mu 1	-1.31	0.298	-1.42	0.06	-1.15	0.487	1.53	0.369	-0.59
1442279_at	Epc1	Enhancer of polycomb homolog 1 (Drosophila)	-1.13	0.725	1.02	0.745	-2.35	0.033	-1	0.983	-0.87
1456446_at	4930523C07Rik	RIKEN cDNA 4930523C07 gene	1.08	0.774	-1.37	0.398	-1.95	0.011	-1.95	0.026	-1.04
1441406_at	---	---	-1.29	0.805	-2.22	0.253	1.11	0.81	-1.48	0.55	-0.97
1434422_at	---	---	-1.12	0.515	-1.36	0.026	-1.42	0.133	1	0.996	-0.73
1458390_at	Anapc10	anaphase promoting complex subunit 10	-1.41	0.147	-1.52	0.519	-1.04	0.842	1.32	0.077	-0.66
1419877_x_at	---	Transcribed locus	-1.93	0.476	1.12	0.731	-1.46	0.279	-1.44	0.298	-0.92
1432932_at	---	---	-2.66	0.238	1.03	0.952	-1.08	0.861	-3	0.044	-1.43
1455477_s_at	Pdzk1ip1	PDZK1 interacting protein 1	-1.13	0.065	-1.46	0.085	-1.31	0.238	4.23	0.168	0.08
1423465_at	Frrs1 /// LOC63599	ferric-chelate reductase 1 /// similar to stromal cell derived factor receptor 2	-1.21	0.146	-1.22	0.183	-1.47	0.057	1.59	0.2	-0.58
1430369_at	Epb4.1	erythrocyte protein band 4.1	-1.15	0.779	-1.76	0.115	-1.12	0.735	2.98	0.245	-0.26
1433760_a_at	Rhbdd3	rhomboid domain containing 3	-1.03	0.798	-1.02	0.952	-2.68	0.009	1.7	0.242	-0.76
1441802_at	Spred2	sprouty-related, EVH1 domain containing 2	1.21	0.357	-1.29	0.273	-2.92	0.038	-3.43	0.037	-1.61
1454440_at	4930421C12Rik	RIKEN cDNA 4930421C12 gene	1.3	0.525	-2	0.247	-1.87	0.141	-2.36	0.045	-1.23
1448261_at	Cdh1	cadherin 1	-1.04	0.738	-3.8	0.02	1.11	0.249	-1.38	0.041	-1.28

1441437_at	Rbms1	RNA binding motif, single stranded interacting protein 1	1.08	0.613	-1.12	0.662	-2.77	0.013	-1.75	0.012	-1.14
1416325_at	Crisp1	cysteine-rich secretory protein 1	-1.23	0.58	-1.35	0.577	-1.29	0.663	1.12	0.805	-0.69
1444180_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	1.02	0.954	-1.32	0.095	-1.79	0.009	-1.7	0.103	-0.95
1439923_at	Tubgcp5	tubulin, gamma complex associated protein 5	1.49	0.571	-2.61	0.198	-2.18	0.101	-1.07	0.904	-1.09
1430795_at	5830407F19Rik	RIKEN cDNA 5830407F19 gene	-1.3	0.06	-1.52	0.287	-1.11	0.637	1.22	0.26	-0.68
1444604_at	Ezh1	Enhancer of zeste homolog 1 (Drosophila)	-1.31	0.516	-1.45	0.046	-1.14	0.441	1.99	0.055	-0.48
1444301_at	Pcdh10	protocadherin 10	-1.96	0.135	-1.9	0.502	1.29	0.563	-1.62	0.435	-1.05
1444311_at	---	---	-1.96	0.134	-1.5	0.504	1.16	0.468	-1.08	0.809	-0.85
1443561_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	-1.6	0.344	1.06	0.922	-1.56	0.169	-3.48	0.042	-1.39
1438763_at	Dnahc2 /// Dnhd3	dynein, axonemal, heavy chain 2 /// dynein heavy chain domain 3	-1.55	0.354	-1.72	0.112	1.11	0.547	-1.04	0.93	-0.8
1447020_at	Zfpm2	Zinc finger protein, multitype 2	-1.7	0.135	1.17	0.629	-1.75	0.025	-1.13	0.826	-0.85
1440444_at	Fads1	fatty acid desaturase 1	-1.36	0.348	-1.44	0.408	-1.11	0.555	2.41	0.234	-0.37
1423576_a_at	Fhl4	four and a half LIM domains 4	-1.11	0.85	-1.04	0.963	-2.14	0.387	1.1	0.794	-0.8
1452567_at	Gcap8	granule cell antiserum positive 8	-3.11	0.054	-1.01	0.975	1.02	0.964	-1.13	0.55	-1.06
1442059_at	Fxr1h	fragile X mental retardation gene 1, autosomal homolog	-1.45	0.485	-1.05	0.818	-1.44	0.08	1.13	0.561	-0.7
1458213_at	Nfat5	Nuclear factor of activated T-cells 5	1.09	0.789	-1.73	0.087	-1.5	0.124	-1.56	0.117	-0.93
1443642_at	Taok2	TAO kinase 2	-2.04	0.253	-1.05	0.899	-1.12	0.719	3.7	0.078	-0.13
1444077_at	---	Transcribed locus	-1.32	0.286	1.14	0.811	-2.28	0.31	-1.02	0.947	-0.87
1458926_at	5830415L20Rik	RIKEN cDNA 5830415L20 gene	-1.03	0.939	-1.83	0.184	-1.22	0.165	1.77	0.052	-0.58
1445494_at	Aaas	Achalasia, adrenocortical insufficiency, alacrimia	-2.01	0.46	1.13	0.591	-1.41	0.353	-1.75	0.439	-1.01
1445536_at	AW061096	expressed sequence AW061096	-1.6	0.231	-1.08	0.763	-1.28	0.459	1.36	0.499	-0.65
1453028_at	4631424J17Rik	RIKEN cDNA 4631424J17 gene	-1.2	0.07	-1.24	0.339	-1.44	0.139	1.06	0.827	-0.71
1459543_at	AA407787	expressed sequence AA407787	-1.32	0.652	-1.31	0.702	-1.23	0.624	1.78	0.251	-0.52
1458409_at	C86595	expressed sequence C86595	-1.8	0.212	1.4	0.538	-2.65	0.073	-1.01	0.973	-1.01
1446185_at	Frap1	FK506 binding protein 12-rapamycin associated protein 1	-1.28	0.497	-1.33	0.599	-1.24	0.454	1.22	0.724	-0.66
1446109_at	Wdfy3	WD repeat and FYVE domain containing 3	1.48	0.003	-2.81	0.247	-1.99	0.267	-1.27	0.69	-1.15
1447631_at	Myst2	MYST histone acetyltransferase 2	-1.13	0.287	-1.33	0.295	-1.44	0.102	1.26	0.2	-0.66
1421362_a_at	Frk	fyn-related kinase	-1.12	0.406	-1.85	0.276	-1.11	0.758	1.83	0.353	-0.56
1434724_at	Usp31	ubiquitin specific peptidase 31	-1.12	0.417	-1.46	0.001	-1.32	0.404	1.29	0.454	-0.65
1460389_at	Cdk8	cyclin-dependent kinase 8	-1.11	0.714	-1.3	0.051	-1.51	0.081	1.04	0.811	-0.72
1432114_at	1110035E04Rik	RIKEN cDNA 1110035E04 gene	-1.19	0.607	-1.52	0.312	-1.19	0.433	1.08	0.752	-0.71
1458822_at	---	---	1.23	0.83	-1.31	0.409	-2.91	0.058	-1.58	0.481	-1.14
1453809_at	Lypd5	Ly6/Plaur domain containing 5	-3.22	0.005	-1.44	0.494	1.33	0.382	-1.53	0.014	-1.22
1445092_at	---	---	-1.25	0.433	-1.51	0.405	-1.14	0.591	1.11	0.792	-0.7
1439926_at	4632417D23Rik	RIKEN cDNA 4632417D23 gene	-1.54	0.312	1.13	0.759	-1.81	0.153	-1.67	0.225	-0.97
1445606_a_at	2900009J06Rik	RIKEN cDNA 2900009J06 gene	-1.15	0.781	-1.47	0.308	-1.27	0.333	1.53	0.323	-0.59
1432512_at	4931433A01Rik	RIKEN cDNA 4931433A01 gene	-1.83	0.412	-1.08	0.851	-1.16	0.628	1.34	0.293	-0.68
1448209_a_at	Slc22a17	solute carrier family 22 (organic cation transporter), member 17	-1.25	0.479	-1.62	0.014	-1.09	0.169	1.02	0.957	-0.74
1449073_at	Flnc	filamin C, gamma (actin binding protein 280)	1.03	0.952	-2.02	0.073	-1.23	0.549	-1.61	0.527	-0.96
1424214_at	9130213B05Rik	RIKEN cDNA 9130213B05 gene	-1.74	0.103	-1.31	0.268	1	0.985	-1.95	0.244	-1
1418669_at	Hspg2	perlecan (heparan sulfate proteoglycan 2)	-1.38	0.193	-1.45	0.222	-1.09	0.653	1.19	0.48	-0.68
1447308_at	Lass5	longevity assurance homolog 5 (S. cerevisiae)	-1.02	0.957	-1.78	0.276	-1.26	0.013	1.08	0.724	-0.75
1438039_at	Hectd1	HECT domain containing 1	-1.16	0.624	-1.45	0.023	-1.27	0.115	1.2	0.438	-0.67
1444651_at	LOC553089	hypothetical LOC553089	1.04	0.882	-1.2	0.434	-2.14	0.015	-1.11	0.736	-0.85
1452597_at	2310061C15Rik	RIKEN cDNA 2310061C15 gene	-1.17	0.086	-1.22	0.242	-1.52	0.002	2.03	0.177	-0.47
1450346_at	Gpr50	G-protein-coupled receptor 50	-1.29	0.174	-1.23	0.456	-1.35	0.364	1.11	0.657	-0.69
1446689_at	D230007K08Rik	RIKEN cDNA D230007K08 gene	-2.06	0.082	1.02	0.935	-1.2	0.453	-1.37	0.563	-0.9
1453332_at	2410002O22Rik	RIKEN cDNA 2410002O22 gene	-1.26	0.256	-1.72	0.016	-1.04	0.868	1.22	0.548	-0.7
1430081_at	Phf15	PHD finger protein 15	1.01	0.956	-1.28	0.55	-1.83	0.029	-1.84	0.012	-0.99
1419887_at	Nudcd1	NudC domain containing 1	-1.93	0.228	-1.39	0.478	1.1	0.827	-1.09	0.841	-0.83
1452723_at	Klf9	Kruppel-like factor 9	-1.07	0.673	-1.65	0.134	-1.25	0.547	1.14	0.782	-0.71
1421678_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	-1.37	0.592	-1.8	0.005	1.05	0.866	-1.55	0.107	-0.92
1459220_at	C78651	expressed sequence C78651	-1.08	0.853	-1.71	0.106	-1.21	0.541	1.43	0.443	-0.64

1456756_at	E430016P22Rik	RIKEN cDNA E430016P22 gene	-1.16	0.513	-1.83	0.256	-1.08	0.803	1.03	0.94	-0.76
1441153_at	Utrn	Utrophin	1.12	0.353	-1.41	0.014	-1.98	0.013	-1.66	0.304	-0.98
1446829_at	D12Ertd216e	DNA segment, Chr 12, ERATO Doi 216, expressed	-1.14	0.74	-2.77	0.314	1.1	0.886	-1.87	0.338	-1.17
1454537_at	4930556A12Rik	RIKEN cDNA 4930556A12 gene	-2.5	0.433	-3.18	0.014	1.62	0.303	-2.07	0.478	-1.53
1429986_at	Gpr173	G-protein coupled receptor 173	-3.39	0.094	-1.49	0.567	1.37	0.534	-1.5	0.494	-1.25
1445525_at	Kif14	kinesin family member 14	-1.28	0.244	-1.27	0.599	-1.3	0.569	1.51	0.47	-0.58
1460666_a_at	Ebf3	early B-cell factor 3	-1.05	0.883	-1.2	0.738	-1.82	0.078	1.7	0.342	-0.59
1455179_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-1.16	0.12	-1.23	0.37	-1.5	0.146	1.61	0.288	-0.57
1460002_at	Tlk1	tousled-like kinase 1	-1.13	0.51	-1.97	0.095	-1.06	0.671	1.17	0.581	-0.75
1449431_at	Trpc6	transient receptor potential cation channel, subfamily C, member 6	-1.11	0.894	-1.12	0.861	-1.86	0.039	1.4	0.582	-0.67
1455716_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.1	0.748	-1.42	0.629	-1.38	0.428	1.05	0.912	-0.71
1442242_at	C79127	expressed sequence C79127	-1.05	0.941	-1.57	0.422	-1.32	0.522	1.1	0.902	-0.71
1430946_at	2600014E21Rik	RIKEN cDNA 2600014E21 gene	1.35	0.555	-2.12	0.003	-1.92	0.067	-1.66	0.516	-1.09
1436624_at	Dnm3	dynamin 3	-1.31	0.018	-1.09	0.748	-1.51	0.04	1.65	0.035	-0.57
1440514_at	D3Ertd508e	DNA segment, Chr 3, ERATO Doi 508, expressed	1.01	0.99	-1.93	0.284	-1.23	0.596	-1.48	0.292	-0.91
1447373_at	1810015C04Rik	RIKEN cDNA 1810015C04 gene	-1.3	0.62	-1.33	0.575	-1.22	0.124	1.98	0.14	-0.47
1423085_at	Efnb3	ephrin B3	-1.22	0.819	-1.52	0.322	-1.16	0.578	1.41	0.131	-0.62
1446230_at	Gm944	Gene model 944, (NCBI)	-1.09	0.747	-1.16	0.433	-1.78	0.09	5.7	0.179	0.42
1436404_at	Tlcd1	TLC domain containing 1	-1.2	0.023	-1.19	0.262	-1.49	0.031	3.81	0.228	-0.02
1431596_at	---	---	1.31	0.668	-1.47	0.231	-2.84	0.015	-1.21	0.655	-1.05
1445312_at	C530043G21Rik	RIKEN cDNA C530043G21 gene	-1.42	0.536	-1.42	0.358	-1.08	0.767	1.03	0.876	-0.72
1426638_at	Six3	sine oculis-related homeobox 3 homolog (Drosophila)	-2.19	0.088	1.21	0.379	-1.5	0.077	-1.91	0.426	-1.09
1458865_at	---	---	-1.54	0.518	-1.09	0.875	-1.29	0.573	1.61	0.31	-0.58
1451942_x_at	Klra20	killer cell lectin-like receptor subfamily A, member 20	1.11	0.644	-1.36	0.436	-2.03	0.109	-1.32	0.688	-0.9
1440603_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030(	-2.75	0.39	-1.01	0.981	-1.01	0.954	1.01	0.989	-0.94
1459160_at	Gm879	Gene model 879, (NCBI)	-2.92	0.438	1.18	0.825	-1.22	0.606	-1.8	0.492	-1.19
1432087_at	4933406G16Rik	RIKEN cDNA 4933406G16 gene	-1.02	0.984	-1.05	0.895	-2.44	0.068	1.44	0.061	-0.77
1454031_at	2310029O18Rik	RIKEN cDNA 2310029O18 gene	-1.12	0.576	-1.1	0.823	-1.85	0.002	1.43	0.109	-0.66
1459094_at	Snap91	Synaptosomal-associated protein 91	-1.89	0.392	1.06	0.924	-1.33	0.355	-1.19	0.617	-0.84
1425868_at	Hist2h2bb	Histone 2, H2bb	1.15	0.478	-2.63	0.233	-1.24	0.44	-1.42	0.201	-1.03
1440195_at	Serbp1	Serpine1 mRNA binding protein 1	-1.18	0.281	-1.17	0.181	-1.56	0.283	1.12	0.61	-0.7
1439930_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.03	0.851	-1.39	0.168	-1.7	0.054	-1.52	0.152	-0.89
1458237_at	---	---	-2.95	0.411	-1.08	0.905	1.08	0.921	-1.15	0.879	-1.03
1419991_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	1.04	0.964	-1.32	0.351	-1.83	0.156	-2	0.459	-1.03
1418558_at	Rax	retina and anterior neural fold homeobox	-1.11	0.336	-1.17	0.715	-1.69	0.198	1.19	0.448	-0.7
1437482_at	Srd5a2l2	steroid 5 alpha-reductase 2-like 2	-1.38	0.623	-1.32	0.639	-1.17	0.679	1.97	0.184	-0.47
1445616_at	Eif4g3	Eukaryotic translation initiation factor 4 gamma, 3	-1.63	0.079	-1.07	0.844	-1.25	0.613	1.33	0.66	-0.66
1443651_at	Phc3	Polyhomeotic-like 3 (Drosophila)	1.09	0.926	-1.15	0.684	-2.6	0.051	-1.63	0.339	-1.07
1429516_at	Ubr2	ubiquitin protein ligase E3 component n-recognin 2	-1.55	0.44	-1.14	0.576	-1.22	0.512	1.24	0.303	-0.67
1423376_a_at	Dok4	docking protein 4	-1.02	0.929	-2.16	0.398	-1.11	0.639	1.28	0.454	-0.75
1437315_at	Gpr172b	G protein-coupled receptor 172B	-1.14	0.114	-1.08	0.777	-1.84	0.175	1.78	0.043	-0.57
1435286_at	AW125296	expressed sequence AW125296	-1.24	0.786	-3.09	0.182	1.21	0.728	-1.76	0.447	-1.22
1440529_at	---	Transcribed locus	-2.47	0.098	-1.46	0.335	1.25	0.667	-5.19	0.013	-1.97
1430346_at	5730507A09Rik	RIKEN cDNA 5730507A09 gene	-1.36	0.576	-1.15	0.726	-1.35	0.461	1.35	0.436	-0.63
1446177_at	---	---	-1.87	0.041	-2.04	0.051	1.32	0.538	-1.08	0.699	-0.92
1428896_at	Pdgfrl	platelet-derived growth factor receptor-like	-1.63	0.05	1.22	0.506	-1.96	0.004	-1.07	0.585	-0.86
1450542_s_at	Magea1 /// Magea2	melanoma antigen, family A, 1 /// melanoma antigen, family A, 2 /// melanoma ant	-1.46	0.03	-1.4	0.547	-1.06	0.899	1.38	0.38	-0.63
1424152_at	---	CDNA clone IMAGE:30031514	-1.06	0.899	1.08	0.87	-3.17	0.002	-1.34	0.509	-1.12
1458287_at	---	Transcribed locus	-1.86	0.1	-1.13	0.635	-1.09	0.875	1.49	0.582	-0.64
1446494_at	---	Non-coding RNA Kis2-T1 mRNA, complete sequence, alternatively spliced	1.07	0.827	-1.42	0.336	-1.77	0.176	-1.17	0.771	-0.82
1416771_at	Trappc3	trafficking protein particle complex 3	-1.83	0.352	-1.31	0.526	1.03	0.943	-2.3	0.211	-1.1
1442202_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	-1.41	0.43	-1.3	0.485	-1.15	0.664	1.43	0.346	-0.61
1424794_at	Rnf186	ring finger protein 186	-1.27	0.42	-1.4	0.303	-1.19	0.375	1.05	0.888	-0.7

1430428_at	2310066F23Rik	RIKEN cDNA 2310066F23 gene	-1.43	0.03	1.03	0.854	-1.63	0.062	-1.32	0.04	-0.84
1429976_at	Clasp2	CLIP associating protein 2	-1.3	0.799	-1.75	0.272	1.01	0.974	-1.17	0.661	-0.8
1421246_at	Pax9	paired box gene 9	-1.66	0.394	-1.61	0.297	1.12	0.85	-1.73	0.468	-0.97
1416697_at	Dpp4	dipeptidylpeptidase 4	1.01	0.945	-1.19	0.056	-2.03	0.088	-3.01	0.05	-1.3
1451376_at	5730596K20Rik	RIKEN cDNA 5730596K20 gene	-1.19	0.382	-1.31	0.071	-1.35	0.087	1.34	0.479	-0.63
1444094_at	---	---	1.02	0.904	-1.72	0.028	-1.35	0.36	-1.89	0.173	-0.98
1440908_at	D030063E12	hypothetical protein D030063E12	-1.21	0.145	-1.46	0.308	-1.2	0.46	1.19	0.372	-0.67
1423892_at	Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	-1.04	0.859	-2.39	0.005	-1.04	0.708	1.01	0.95	-0.86
1444808_at	Pawr	PRKC, apoptosis, WT1, regulator	-1.19	0.283	-1.14	0.526	-1.59	0.149	1.07	0.893	-0.71
1449790_at	---	---	1.2	0.571	-1.77	0.276	-1.71	0.037	-1.42	0.013	-0.93
1446391_at	Snca	Synuclein, alpha	-1.27	0.052	-1.21	0.654	-1.36	0.359	6.6	0.178	0.69
1446807_at	Usp8	ubiquitin specific peptidase 8	1.03	0.947	-1.18	0.298	-2.11	0.007	-1.11	0.54	-0.84
1439635_at	Rgs9	regulator of G-protein signaling 9	-2.91	0.002	1.11	0.821	-1.13	0.767	-2.12	0.307	-1.26
1456360_at	Dcun1d1	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	-1.47	0.369	-1.47	0.104	-1.01	0.972	1.97	0.265	-0.5
1432572_at	4931406H21Rik	RIKEN cDNA 4931406H21 gene	-1.75	0.259	1.02	0.775	-1.33	0.134	-1.02	0.913	-0.77
1444804_at	D17Ertd96e	DNA segment, Chr 17, ERATO Doi 96, expressed	1.3	0.712	-1.45	0.43	-2.81	0.016	-1.37	0.33	-1.08
1440149_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-2.25	0.456	1.02	0.982	-1.13	0.795	-2.62	0.204	-1.25
1450863_a_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	-1	0.967	-4.04	0.004	1.1	0.64	-1.58	0.221	-1.38
1421281_at	Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	-1.04	0.899	-1.34	0.596	-1.57	0.355	1.13	0.806	-0.7
1431887_at	Rbm31y	RNA binding motif 31, Y-linked	-2.03	0.529	-1.26	0.641	1.06	0.877	-2.47	0.415	-1.17
1443847_x_at	---	Transcribed locus	1.61	0.168	-2.22	0.105	-3.43	0.004	-1.12	0.814	-1.29
1457213_a_at	Dgkh	diacylglycerol kinase, eta	-1.35	0.168	-1.54	0.148	-1.04	0.759	1	0.991	-0.73
1444183_at	C030013C21Rik	RIKEN cDNA C030013C21 gene	-1.37	0.169	-1	0.984	-1.6	0.175	2.97	0.06	-0.25
1438414_at	Fkrp	fukutin related protein	-1.44	0.6	-1.87	0.279	1.12	0.751	-1.62	0.043	-0.95
1441214_at	Exph5	exophilin 5	1.12	0.517	-1.58	0.019	-1.7	0.028	-1.49	0.243	-0.91
1419043_a_at	Iigp1	interferon inducible GTPase 1	-1.07	0.804	-1.31	0.064	-1.54	0.126	1.1	0.66	-0.7
1430819_at	Asahl	N-acylsphingosine amidohydrolase (acid ceramidase)-like	-1.71	0.175	-1.13	0.839	-1.13	0.662	1.35	0.358	-0.66
1430983_at	Pdia6	protein disulfide isomerase associated 6	-1.06	0.83	-1.31	0.524	-1.57	0.065	1.24	0.63	-0.67
1453385_at	1110015C02Rik	RIKEN cDNA 1110015C02 gene	-1.63	0.149	-1.3	0.221	-1.03	0.91	1.07	0.777	-0.72
1420402_at	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	-1.2	0.361	1.01	0.952	-1.98	0.296	-1.21	0.381	-0.84
1432864_at	---	---	1.03	0.931	-1.42	0.157	-1.62	0.19	-1.36	0.393	-0.84
1456203_at	1110020A10Rik	RIKEN cDNA 1110020A10 gene	1.15	0.614	-1.59	0.276	-1.76	0.113	-1.39	0.493	-0.9
1437654_at	3110001K24Rik	RIKEN cDNA 3110001K24 gene	-1.31	0.231	-1.82	0.032	1.04	0.786	-1.42	0.274	-0.88
1429693_at	Dab2	disabled homolog 2 (Drosophila)	-1.38	0.09	1.05	0.894	-1.72	0.086	-1.2	0.643	-0.81
1420245_x_at	Tagln2 /// LOC6724	transgelin 2 /// similar to transgelin 2	-1	0.995	-1.79	0.222	-1.26	0.584	1.07	0.861	-0.75
1441505_at	---	---	-1.13	0.516	-1.03	0.926	-2.04	0.005	1.18	0.527	-0.76
1452552_at	Npn2	neoplastic progression 2	-1.83	0.432	1.47	0.33	-2.97	0.092	-1.31	0.607	-1.16
1418780_at	Cyp39a1	cytochrome P450, family 39, subfamily a, polypeptide 1	-2.05	0.3	-1.55	0.106	1.22	0.592	-3.18	0.09	-1.39
1427326_at	4732471D19Rik	RIKEN cDNA 4732471D19 gene	-1.43	0.015	-1.34	0.457	-1.1	0.636	1.07	0.782	-0.7
1431092_at	Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C	-1.43	0.362	-2.66	0.207	1.28	0.326	-1.11	0.812	-0.98
1425236_at	Col20a1	collagen, type XX, alpha 1	-1.2	0.772	-1.32	0.56	-1.31	0.667	1.28	0.35	-0.64
1456335_at	Gm106	gene model 106, (NCBI)	-1.07	0.767	-1.74	0.473	-1.19	0.515	2.28	0.024	-0.43
1431838_at	1700128E19Rik	RIKEN cDNA 1700128E19 gene	-1.81	0.086	-1.37	0.259	1.07	0.761	-1.38	0.07	-0.87
1425636_at	Hhat	hedgehog acyltransferase	1.06	0.673	-1.25	0.46	-2.04	0.091	-1.16	0.637	-0.85
1441435_at	Tbl1x	Transducin (beta)-like 1 X-linked	1.03	0.939	-1.31	0.168	-1.77	0.009	-1.43	0.048	-0.87
1420926_at	Arx	aristaless related homeobox gene (Drosophila)	-1.79	0.311	1.35	0.489	-2.28	0.053	-1.46	0.516	-1.04
1429505_at	2310076G13Rik	RIKEN cDNA 2310076G13 gene	1.02	0.934	-1.3	0.003	-1.78	0.018	-1.06	0.734	-0.78
1445126_at	Ldb2	LIM domain binding 2	-1.28	0.572	-1.09	0.867	-1.54	0.059	1.13	0.821	-0.69
1424308_at	Slc24a3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	-1.14	0.611	-1.9	0.034	-1.06	0.801	1.09	0.76	-0.75
1446198_at	Mier3	Mesoderm induction early response 1, family member 3	-1.73	0.251	1.08	0.732	-1.43	0.164	-1.31	0.111	-0.85
1416790_a_at	Tdg /// LOC545124	thymine DNA glycosylase /// similar to thymine DNA glycosylase isoform 2 /// simi	-1.22	0.074	-1.6	0.001	-1.1	0.268	1.32	0.264	-0.65
1442586_at	Socs2	suppressor of cytokine signaling 2	-1.13	0.019	-1.11	0.573	-1.78	0.068	1.11	0.459	-0.73
1418951_at	Txlnb	taxilin beta	-3.42	0.247	-2.44	0.213	1.65	0.27	-1.16	0.659	-1.34

1435931_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-1.29	0.129	-1.06	0.79	-1.58	0.051	1.28	0.354	-0.66
1422825_at	Cart	cocaine and amphetamine regulated transcript	-1.04	0.932	-3.53	0.099	1.11	0.81	-3.75	0.042	-1.8
1440371_at	---	2 days neonate sympathetic ganglion cDNA, RIKEN full-length enriched library, c	-1.26	0.574	-1.2	0.723	-1.38	0.087	1.58	0.304	-0.57
1446632_at	Cacnb2	Calcium channel, voltage-dependent, beta 2 subunit	-1.13	0.657	1.01	0.952	-2.18	0.04	-1.26	0.543	-0.89
1428622_at	Depdc6	DEP domain containing 6	-1.06	0.615	-1.33	0.018	-1.53	0.043	1.02	0.879	-0.72
1452455_at	Fer1l3	fer-1-like 3, myoferlin (C. elegans)	-1.51	0.643	-1.01	0.986	-1.43	0.514	1.85	0.155	-0.53
1443276_at	Htr5a	5-hydroxytryptamine (serotonin) receptor 5A	-1.35	0.576	-1.21	0.708	-1.28	0.326	1.53	0.385	-0.58
1420803_at	Tex18	testis expressed gene 18	-2.27	0.176	-1.2	0.626	1.08	0.855	-1.28	0.722	-0.92
1422076_at	Acot4	acyl-CoA thioesterase 4	1.03	0.932	-1.47	0.269	-1.55	0.442	-1.65	0.564	-0.91
1438811_at	Dlg7	discs, large homolog 7 (Drosophila)	-1.91	0.233	-1.02	0.98	-1.18	0.498	3.36	0.258	-0.19
1423638_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.05	0.89	-1.58	0.031	-1.5	0.038	-1.05	0.909	-0.77
1459218_at	D330001F17Rik	RIKEN cDNA D330001F17 gene	-1.02	0.98	-1.25	0.529	-1.75	0.083	1.03	0.959	-0.75
1426544_a_at	Ttc14	tetratricopeptide repeat domain 14	1.08	0.623	-1.51	0.229	-1.63	0.092	-1.42	0.389	-0.87
1430611_at	Zdhhc25	zinc finger, DHHC domain containing 25	-5.04	0.017	1.48	0.545	-1.49	0.307	-1.01	0.987	-1.51
1428289_at	Klf9	Kruppel-like factor 9	-1.23	0.538	-1.31	0.301	-1.29	0.369	1.03	0.962	-0.7
1459010_at	5430437P03Rik	RIKEN cDNA 5430437P03 gene	1.09	0.847	-1.56	0.105	-1.6	0.113	-1.01	0.94	-0.77
1434160_at	Zfp592	zinc finger protein 592	-1.36	0.403	-1.42	0.055	-1.1	0.608	1.07	0.691	-0.7
1455591_at	---	---	-1.33	0.154	1.04	0.93	-1.78	0.054	-1.13	0.628	-0.8
1420462_at	Il1rapl2	interleukin 1 receptor accessory protein-like 2	1.25	0.417	-2.15	0.19	-1.56	0.286	-1.89	0.513	-1.09
1453117_at	Surf2	surfeit gene 2	-1.35	0.396	-1.22	0.568	-1.26	0.629	1.52	0.492	-0.58
1422550_a_at	Mtap6	microtubule-associated protein 6	-1.38	0.41	-1.61	0.45	1.01	0.966	-1.08	0.832	-0.77
1457166_at	AA536749	Expressed sequence AA536749	-1.25	0.278	1.1	0.828	-2.17	0.016	-1.24	0.474	-0.89
1429377_at	2410004A20Rik	RIKEN cDNA 2410004A20 gene	-1.06	0.818	-2.44	0.045	-1	0.995	1.15	0.205	-0.84
1440420_at	Stk24	Serine/threonine kinase 24 (STE20 homolog, yeast)	-2.04	0.039	-1	0.999	-1.15	0.791	1.73	0.244	-0.62
1431908_at	4933408J17Rik	RIKEN cDNA 4933408J17 gene	-1.6	0.562	-1.12	0.836	-1.19	0.729	1.52	0.611	-0.6
1456862_at	Six4	sine oculis-related homeobox 4 homolog (Drosophila)	-1.46	0.178	-2.24	0.3	1.23	0.26	-2.86	0.412	-1.33
1444430_at	Armc8	Armadillo repeat containing 8	-1.15	0.563	-1.09	0.734	-1.77	0.07	1.13	0.178	-0.72
1433814_at	Wnt5b	Wingless-related MMTV integration site 5B	-1	0.991	-1.31	0.509	-1.68	0.257	1.33	0.194	-0.67
1444425_at	Zfp53	Zinc finger protein 53	1.04	0.895	-1.74	0.185	-1.36	0.148	-1.1	0.776	-0.79
1439610_at	Rab27b	RAB27b, member RAS oncogene family	-1.05	0.633	-1.19	0.647	-1.78	0.006	2.56	0.332	-0.37
1433312_at	2700057C20Rik	RIKEN cDNA 2700057C20 gene	-1.95	0.295	-1.25	0.75	1.04	0.944	-2.53	0.15	-1.17
1457988_at	Sec63	SEC63-like (S. cerevisiae)	1.06	0.746	-1.48	0.147	-1.62	0.008	-1.2	0.549	-0.81
1446260_at	Six6os1	Six6 opposite strand transcript 1	-1.88	0.365	-1.26	0.646	1.03	0.948	-1.31	0.215	-0.85
1426250_s_at	9130404D08Rik	RIKEN cDNA 9130404D08 gene	1.02	0.935	-2.58	0.036	-1.05	0.815	-1.02	0.899	-0.91
1450993_at	Pask	PAS domain containing serine/threonine kinase	-1.03	0.967	-1.27	0.61	-1.67	0.094	2.09	0.279	-0.47
1457477_at	Mbnl2	Muscleblind-like 2	-1.34	0.395	1.18	0.287	-2.32	0.006	-1.23	0.469	-0.93
1460086_at	---	---	1.02	0.939	-1.49	0.374	-1.51	0.262	-1.05	0.813	-0.76
1445074_at	---	16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830036I	-1.25	0.719	-2.06	0.258	1.07	0.902	-1.43	0.486	-0.92
1454910_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330008M	-1.83	0.326	-1.6	0.149	1.18	0.543	-1.39	0.074	-0.91
1457760_at	A930004J17Rik	RIKEN cDNA A930004J17 gene	-1.02	0.871	-1.24	0.225	-1.74	0.137	1.41	0.143	-0.65
1426122_a_at	Coro6	coronin, actin binding protein 6	-1.37	0.624	-2.24	0.093	1.18	0.264	-1.17	0.432	-0.9
1441486_at	C430014M02Rik	RIKEN cDNA C430014M02 gene	-1.3	0.656	-1.32	0.416	-1.21	0.304	1	0.993	-0.71
1458273_at	---	Transcribed locus	-1.61	0.071	-1.2	0.751	-1.11	0.738	1.33	0.199	-0.65
1442234_at	LOC667085	hypothetical protein LOC667085	-1.68	0.36	-1.27	0.563	-1.03	0.916	1.73	0.049	-0.56
1420185_at	Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	-1.64	0.593	-1.16	0.575	-1.13	0.342	1.77	0.151	-0.54
1450783_at	---	---	1.13	0.757	-1.46	0.239	-1.85	0.092	-1.17	0.457	-0.84
1429814_at	Pank1	pantothenate kinase 1	-1.08	0.866	-1.5	0.197	-1.31	0.671	1.22	0.763	-0.67
1446444_at	Mnab	membrane associated DNA binding protein	1.09	0.809	-1.4	0.467	-1.82	0.104	-1.5	0.114	-0.91
1421000_at	Cnot4	CCR4-NOT transcription complex, subunit 4	1.05	0.79	-1.3	0.049	-1.87	0.016	-1.39	0.089	-0.88
1445913_at	A730090H04Rik	RIKEN cDNA A730090H04 gene	-1.39	0.19	1.25	0.726	-2.6	0.344	-1.24	0.761	-0.99
1418903_at	Aqp2	aquaporin 2	1.29	0.385	-1.63	0.54	-2.18	0.033	-1.1	0.807	-0.9
1416733_at	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	-1.47	0.068	-1.06	0.645	-1.35	0.034	1.24	0.186	-0.66
1433161_at	1700008N17Rik	RIKEN cDNA 1700008N17 gene	-1.04	0.963	-1.62	0.065	-1.29	0.387	1.08	0.797	-0.72

1459576_at	---	---	-1.52	0.205	1.15	0.758	-1.81	0.362	-1.21	0.591	-0.85
1421555_at	Adrb3	adrenergic receptor, beta 3	-2.27	0.136	-1.58	0.408	1.28	0.473	-1.19	0.807	-0.94
1436428_at	Chrnb2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	-1.37	0.251	-1.5	0.219	-1.04	0.816	1.11	0.746	-0.7
1437920_at	Epha5	Eph receptor A5	-2.18	0.3	1.25	0.747	-1.54	0.522	-1.8	0.478	-1.07
1445400_at	Hbxip	Hepatitis B virus x interacting protein	-1.05	0.777	-1.38	0.545	-1.46	0.077	1.43	0.324	-0.62
1458262_at	Exdl1	Vexonuclease 3'-5' domain-like 1	-1.19	0.758	-1.55	0.069	-1.15	0.8	1.05	0.935	-0.71
1455811_at	Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	-2.25	0.099	-1.53	0.444	1.26	0.329	-1.25	0.673	-0.94
1450221_at	4933417A18Rik	RIKEN cDNA 4933417A18 gene	1.23	0.707	-1.33	0.56	-2.62	0.225	-1.82	0.199	-1.14
1423032_at	Rpl39	ribosomal protein L39	-1.71	0.036	-1.3	0.427	1.01	0.973	-1.07	0.898	-0.77
1459467_at	AA986715	expressed sequence AA986715	-1.32	0.22	-1.03	0.937	-1.58	0.122	1.54	0.476	-0.6
1433135_at	Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	1.15	0.75	-2.62	0.35	-1.21	0.513	-1.38	0.496	-1.01
1435846_x_at	---	---	-1.67	0.2	-1.19	0.47	-1.09	0.531	1.25	0.169	-0.67
1417067_s_at	Cabc1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	1.02	0.947	-1.47	0.164	-1.51	0.155	-1.79	0.226	-0.94
1420723_at	Vnn3	vanin 3	-1.38	0.619	-1.56	0.097	-1.01	0.959	1.51	0.172	-0.61
1419131_at	F13b	coagulation factor XIII, beta subunit	-1.21	0.381	-1.09	0.179	-1.62	0.284	1.33	0.594	-0.65
1433170_at	2900034C19Rik	RIKEN cDNA 2900034C19 gene	-1.1	0.866	-1.12	0.646	-1.8	0.327	1.36	0.526	-0.66
1422826_at	Igfals	insulin-like growth factor binding protein, acid labile subunit	1.02	0.93	-1.26	0.252	-1.84	0.182	-1.6	0.329	-0.92
1457958_at	Ankrd26	Ankyrin repeat domain 26	-1.23	0.592	-1.76	0.065	-1.02	0.958	1.07	0.78	-0.73
1438830_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420422E1	1.32	0.669	-1.91	0.127	-1.94	0.288	-1.58	0.339	-1.03
1444250_at	---	---	-1.48	0.19	-1.29	0.242	-1.1	0.544	1.97	0.224	-0.47
1443100_at	Thrb	Thyroid hormone receptor beta	1.08	0.473	-1.37	0.132	-1.8	0.017	-1.14	0.448	-0.81
1424451_at	Acaa1b	acetyl-Coenzyme A acyltransferase 1B	-1.15	0.406	-1.68	0.339	-1.12	0.722	2.08	0.328	-0.47
1435530_at	Camsap1	calmodulin regulated spectrin-associated protein 1	-1.03	0.831	-1.27	0.384	-1.67	0.062	1.27	0.432	-0.67
1444671_at	Rasal2	RAS protein activator like 2	1.21	0.621	-1.55	0.352	-1.99	0.04	-1.35	0.327	-0.92
1444790_at	1810005K13Rik	RIKEN cDNA 1810005K13 gene	1.21	0.495	-2.1	0.048	-1.48	0.023	-1.7	0.504	-1.02
1444002_at	Foxl2	forkhead box L2	1.59	0.396	-1.88	0.276	-4.23	0.009	-1.24	0.542	-1.44
1415927_at	Actc1	actin, alpha, cardiac	-1.55	0.527	-1.57	0.353	1.08	0.809	-1.13	0.711	-0.79
1432161_a_at	Ptar1	protein prenyltransferase alpha subunit repeat containing 1	-1.18	0.813	-1.16	0.672	-1.55	0.199	1.26	0.518	-0.65
1420564_at	Insrr	insulin receptor-related receptor	-1.93	0.061	1.12	0.314	-1.38	0.456	-1.48	0.474	-0.92
1437890_at	1500005I02Rik	RIKEN cDNA 1500005I02 gene	-1.59	0.285	-1.41	0.288	1.02	0.913	-1.16	0.546	-0.78
1425353_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-1.33	0.512	-1.03	0.948	-1.57	0.517	1.48	0.419	-0.61
1445921_at	D2Ertd397e	DNA segment, Chr 2, ERATO Doi 397, expressed	1.22	0.371	-1.64	0.358	-1.89	0.366	-2.25	0.409	-1.14
1442874_at	Ascc1	Activating signal cointegrator 1 complex subunit 1	1.09	0.659	-1.47	0.244	-1.7	0.057	-2.05	0.033	-1.03
1442320_at	LOC553096	hypothetical LOC553096	1.09	0.733	-1.2	0.18	-2.26	0.002	-1.49	0.229	-0.97
1459370_at	Cacng5	Calcium channel, voltage-dependent, gamma subunit 5	-1.01	0.777	-1.04	0.908	-2.44	0.071	1.92	0.226	-0.64
1432619_at	---	---	-1.72	0.484	-1.28	0.547	-1	0.997	1.01	0.972	-0.75
1428740_a_at	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	-2.32	0.344	-1.64	0.512	1.32	0.411	-3.63	0.152	-1.57
1443996_at	Fgfr2	Fibroblast growth factor receptor 2	-1.14	0.479	-1.05	0.933	-1.87	0.077	1.39	0.413	-0.67
1441031_at	Padi1	peptidyl arginine deiminase, type I	-1.36	0.528	-1.65	0.289	1.02	0.956	-3.6	0.003	-1.4
1449178_at	Pdlim3	PDZ and LIM domain 3	-1.45	0.179	-1.69	0.197	1.08	0.611	-1.7	0.133	-0.94
1439314_at	Clock	circadian locomoter output cycles kaput	-1.15	0.488	1.01	0.97	-2.09	0.041	-1.55	0.265	-0.94
1442885_at	Scap	SREBP cleavage activating protein	1.03	0.925	-1.65	0.212	-1.38	0.173	-1.74	0.047	-0.93
1447074_at	Zbtb24	zinc finger and BTB domain containing 24	1.05	0.92	-1.74	0.037	-1.36	0.283	-1.01	0.985	-0.76
1417588_at	Galnt3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.22	0.282	-1.27	0.605	-1.32	0.115	1.11	0.705	-0.68
1454050_at	4921521D15Rik	RIKEN cDNA 4921521D15 gene	-1.14	0.593	-1.82	0.315	-1.07	0.661	1.14	0.46	-0.72
1441488_at	---	Transcribed locus	1.06	0.918	-1.77	0.378	-1.34	0.423	-1.09	0.909	-0.79
1439743_at	AW048948	expressed sequence AW048948	-1.31	0.61	-1.25	0.434	-1.24	0.414	1.32	0.327	-0.62
1432243_a_at	4933433G15Rik	RIKEN cDNA 4933433G15 gene	-1.16	0.772	-1.54	0.282	-1.17	0.709	1.9	0.049	-0.49
1434291_a_at	Serf1	small EDRK-rich factor 1	-1.47	0.396	-1.01	0.967	-1.44	0.004	1.03	0.909	-0.72
1454188_at	4921508D12Rik	RIKEN cDNA 4921508D12 gene	-1.11	0.706	-1.67	0.22	-1.15	0.688	1.1	0.723	-0.71
1432709_at	4930505O19Rik	RIKEN cDNA 4930505O19 gene	-1.52	0.34	1.17	0.856	-1.88	0.278	-2.37	0.266	-1.15
1454867_at	Mn1	meningioma 1	1.04	0.896	-1.95	0.086	-1.24	0.458	-1.5	0.199	-0.91
1425983_x_at	Hipk2	homeodomain interacting protein kinase 2	-1.17	0.17	-1.39	0.145	-1.26	0.288	1.8	0.226	-0.51

1457730_at	Fancm	Fanconi anemia, complementation group M	-1.85	0.087	-1.13	0.549	-1.06	0.596	1.26	0.364	-0.7
1444314_at	4921506I22Rik	RIKEN cDNA 4921506I22 gene	-1.28	0.091	-1.36	0.234	-1.18	0.473	1.03	0.924	-0.7
1458089_at	Fkbp5	FK506 binding protein 5	1.08	0.912	-1.4	0.552	-1.77	0.285	-1.42	0.036	-0.87
1430066_at	4930589M24Rik	RIKEN cDNA 4930589M24 gene	-1.2	0.183	-1.21	0.666	-1.42	0.375	2.19	0.075	-0.41
1457607_at	AW046457	expressed sequence AW046457	-4.01	0.012	1.67	0.09	-2.22	0.016	-1.45	0.508	-1.5
1432624_at	5830487K18Rik	RIKEN cDNA 5830487K18 gene	-1.49	0.547	1.17	0.409	-1.9	0.136	-1.81	0.226	-1.01
1446822_at	---	---	-1.73	0.123	-1.3	0.16	1.02	0.909	-1.3	0.649	-0.83
1451266_at	Mrpl50	mitochondrial ribosomal protein L50	-1.32	0.147	-1.11	0.192	-1.41	0.205	1.04	0.864	-0.7
1417057_a_at	Ppid /// Lamp3 /// L(	peptidylprolyl isomerase D (cyclophilin D) /// lysosomal-associated membrane prc	-1.14	0.424	-1.23	0.019	-1.48	0.058	1.13	0.627	-0.68
1427873_at	Defcr15	defensin related cryptdin 15	-1.35	0.481	1.11	0.721	-1.95	0.033	-2.41	0.14	-1.15
1449657_at	MGC107702	similar to proteasome (prosome, macropain) subunit, beta type 7	-1.17	0.293	-1.38	0.328	-1.27	0.123	1.03	0.874	-0.7
1460312_at	Olfr157	olfactory receptor 157	-2.18	0.387	-1.15	0.499	1.04	0.873	-1.13	0.802	-0.86
1439307_at	Cdh2	Cadherin 2	-1.46	0.27	-1.62	0.014	1.06	0.495	-1.06	0.597	-0.77
1445613_at	Nr2c2	Nuclear receptor subfamily 2, group C, member 2	1.03	0.785	-1.3	0.23	-1.76	0.101	-1.49	0.118	-0.88
1438764_at	Anxa7	annexin A7	-1.17	0.042	-1.17	0.586	-1.52	0.122	1.11	0.476	-0.69
1439400_x_at	5430433E21Rik	RIKEN cDNA 5430433E21 gene	-2.39	0.027	-1.25	0.028	1.15	0.705	-1.31	0.494	-0.95
1440059_at	Map4k5	Mitogen-activated protein kinase kinase kinase kinase 5	-1.74	0.118	-1.17	0.396	-1.07	0.837	1.14	0.239	-0.71
1441734_at	Camk2a	Calcium/calmodulin-dependent protein kinase II alpha	-2.46	0.198	1.05	0.921	-1.1	0.791	-2.19	0.384	-1.17
1445082_at	Kif16b	Kinesin family member 16B	-1.29	0.251	-1.24	0.49	-1.27	0.078	1.05	0.918	-0.69
1422420_at	Mb	myoglobin	-1.37	0.598	-2.71	0.341	1.27	0.204	-1.41	0.03	-1.05
1447445_at	---	Transcribed locus	-1.6	0.549	1.1	0.847	-1.55	0.099	-2.42	0.058	-1.12
1430305_at	2500004C02Rik	RIKEN cDNA 2500004C02 gene	-1.56	0.178	-1.26	0.594	-1.07	0.777	1.1	0.564	-0.7
1451531_at	Cbwd1	COBW domain containing 1	-1.19	0.183	-1.49	0.037	-1.17	0.46	1.05	0.892	-0.7
1454710_at	Spink2	serine peptidase inhibitor, Kazal type 2	-1.88	0.186	-1.49	0.506	1.17	0.58	-1.02	0.98	-0.81
1425244_a_at	Theg	testicular haploid expressed gene	1.02	0.98	-1.15	0.557	-2.08	0.345	-1.04	0.947	-0.81
1449602_at	Klhl5	Kelch-like 5 (Drosophila)	-1.66	0.333	1.16	0.74	-1.64	0.193	-1.47	0.414	-0.9
1427099_at	Maz	MYC-associated zinc finger protein (purine-binding transcription factor)	-1.21	0.364	-1.42	0.085	-1.2	0.459	1.37	0.234	-0.61
1444970_at	C79870	expressed sequence C79870	-2.01	0.213	-1.07	0.863	-1.07	0.85	1.09	0.636	-0.76
1443629_at	Nav1	neuron navigator 1	-1.11	0.837	-1.88	0.064	-1.07	0.866	1.09	0.799	-0.74
1439796_at	AI747448	expressed sequence AI747448	1.1	0.919	-1.59	0.532	-1.56	0.138	-1.24	0.535	-0.82
1441034_at	Itsn1	Intersectin 1 (SH3 domain protein 1A)	-1.34	0.773	-1.1	0.817	-1.41	0.462	4.39	0.197	0.14
1438337_x_at	9930032O22Rik	RIKEN cDNA 9930032O22 gene	-1.15	0.707	-1.18	0.725	-1.54	0.19	1.12	0.816	-0.69
1444445_at	C77648	expressed sequence C77648	1.02	0.924	-1.17	0.189	-2.02	0.009	-1.33	0.24	-0.88
1431336_at	Scara5	scavenger receptor class A, member 5 (putative)	1.26	0.732	-2.36	0.171	-1.47	0.245	-1.18	0.789	-0.94
1442146_at	Mta3	Metastasis associated 3	-1.28	0.754	-2.28	0.054	1.15	0.298	-1.01	0.914	-0.86
1418876_at	Foxd1	forkhead box D1	-1.23	0.333	-1.42	0.585	-1.17	0.802	1.68	0.274	-0.54
1441877_x_at	Tssc1	tumor suppressing subtransferable candidate 1	-1.1	0.882	-2.07	0.066	-1.02	0.96	1.33	0.137	-0.72
1433194_at	4930433M22Rik	RIKEN cDNA 4930433M22 gene	1.03	0.816	-1.33	0.378	-1.69	0.401	-1.28	0.724	-0.82
1459960_at	---	Transcribed locus	-1	0.97	-3.78	0.016	1.11	0.857	-1.06	0.916	-1.18
1443265_at	Cd44	CD44 antigen	-1.22	0.154	-1.67	0.5	-1.05	0.866	1.16	0.676	-0.69
1427111_s_at	Raver1	ribonucleoprotein, PTB-binding 1	-1.18	0.724	-1.84	0.135	-1.02	0.86	1.15	0.692	-0.72
1446102_at	D9Ertd292e	DNA segment, Chr 9, ERATO Doi 292, expressed	-1.56	0.316	-1.13	0.789	-1.18	0.199	1.12	0.759	-0.69
1453339_at	1700008I05Rik	RIKEN cDNA 1700008I05 gene	-1.62	0.572	1.12	0.823	-1.59	0.545	-1.75	0.142	-0.96
1454453_at	2610011I18Rik	RIKEN cDNA 2610011I18 gene	-1.83	0.444	1.02	0.963	-1.24	0.195	-1.5	0.064	-0.89
1429694_at	4930402H24Rik	RIKEN cDNA 4930402H24 gene	-1.15	0.54	-1.46	0.183	-1.23	0.215	1.13	0.552	-0.68
1447366_at	---	---	-1.89	0.384	-1.29	0.313	1.07	0.863	-2.65	0.029	-1.19
1460695_a_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	-1.2	0.096	-1.25	0.375	-1.36	0.002	1.02	0.859	-0.7
1441545_at	9230115F04Rik	RIKEN cDNA 9230115F04 gene	1.01	0.803	-1.23	0.363	-1.82	0.025	-2.26	0.086	-1.08
1435655_at	Snora65	small nucleolar RNA, H/ACA box 65	-1.4	0.07	-1.76	0.018	1.09	0.673	-1.77	0.025	-0.96
1460226_at	Trap1a	tumor rejection antigen P1A	-1.21	0.635	-1.41	0.486	-1.2	0.107	1.46	0.462	-0.59
1447518_at	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	-1.4	0.162	-1.4	0.354	-1.06	0.62	1.11	0.495	-0.69
1442085_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	-1.71	0.293	-1.53	0.136	1.13	0.685	-1.16	0.513	-0.82
1457949_at	---	Transcribed locus	-1.27	0.056	-1.22	0.142	-1.31	0.11	1.1	0.734	-0.67

1459188_at	Ryk	Receptor-like tyrosine kinase	-1.22	0.798	1.21	0.801	-2.9	0.309	-1.6	0.67	-1.13
1429256_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.61	0.205	-1.15	0.664	-1.14	0.757	1.09	0.862	-0.7
1446178_at	Bicc1	Bicaudal C homolog 1 (Drosophila)	1.04	0.796	-1.07	0.919	-2.51	0.044	-2.82	0.013	-1.34
1444247_at	C81557	expressed sequence C81557	-1.04	0.898	-1.29	0.571	-1.58	0.13	1.49	0.174	-0.6
1446090_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930002E	-1.03	0.946	-1.34	0.078	-1.53	0.022	1.75	0.054	-0.54
1455959_s_at	---	---	-1.37	0.028	-1.38	0.036	-1.09	0.289	2.58	0.206	-0.31
1439813_at	Sppl3	Signal peptide peptidase 3	-1.07	0.72	-1.1	0.04	-1.9	0.016	1.21	0.38	-0.71
1443696_s_at	Habp2	hyaluronic acid binding protein 2	1.02	0.973	-1.02	0.96	-2.69	0.037	-1.62	0.237	-1.08
1431763_a_at	Ctrl	chymotrypsin-like	1.18	0.558	-2.97	0.13	-1.16	0.429	-1.49	0.209	-1.11
1440297_at	4931406I20Rik	RIKEN cDNA 4931406I20 gene	1.12	0.814	-1.43	0.599	-1.79	0.214	-1.57	0.017	-0.92
1422816_a_at	Mutyh	mutY homolog (E. coli)	-1.08	0.724	-3.03	0.043	1.12	0.366	-1.53	0.07	-1.13
1454243_at	Ick	intestinal cell kinase	-1.02	0.928	-1.22	0.319	-1.77	0.037	1.18	0.149	-0.7
1424846_at	Cep68	centrosomal protein 68	-1.38	0.353	-1.24	0.082	-1.18	0.342	1.08	0.611	-0.68
1448841_at	Pfpl	pore forming protein-like	-1.05	0.821	1.02	0.919	-2.5	0.043	-1.16	0.791	-0.92
1443278_at	Dcc	Deleted in colorectal carcinoma	-1.56	0.05	-1.14	0.801	-1.17	0.825	1.2	0.354	-0.67
1433182_at	4930431N21Rik	RIKEN cDNA 4930431N21 gene	1.13	0.235	-1.63	0.464	-1.58	0.269	-1.1	0.154	-0.79
1458551_at	Mef2c	Myocyte enhancer factor 2C	1.23	0.566	-1.77	0.371	-1.71	0.191	-1.84	0.176	-1.02
1458142_at	Zdhhc9	zinc finger, DHHC domain containing 9	-1.56	0.256	1.02	0.95	-1.4	0.215	-1.06	0.811	-0.75
1439638_at	Erbb2ip	Erbb2 interacting protein	-1.23	0.442	1.04	0.878	-1.9	0.073	-1.65	0.092	-0.94
1441237_at	D5Ertd163e	DNA segment, Chr 5, ERATO Doi 163, expressed	-1.05	0.941	-1.25	0.619	-1.6	0.376	2.48	0.107	-0.36
1438923_at	Fibp	Fibroblast growth factor (acidic) intracellular binding protein	-1.13	0.865	-1.74	0.041	-1.1	0.9	3.84	0.324	-0.03
1421619_at	Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	-1.39	0.19	-1.54	0.289	1	0.995	-1.03	0.87	-0.74
1440391_at	LOC638038	hypothetical protein LOC638038	-1.34	0.027	-1.38	0.226	-1.1	0.499	1.02	0.914	-0.7
1429793_at	1600014K23Rik	RIKEN cDNA 1600014K23 gene	-1.06	0.821	-1.12	0.753	-1.84	0.16	2.68	0.046	-0.34
1421726_at	Ap4b1	adaptor-related protein complex AP-4, beta 1	-1.39	0.085	-1.42	0.183	-1.05	0.726	1.16	0.425	-0.67
1434597_at	Larp5	La ribonucleoprotein domain family, member 5	-1.12	0.223	-1.33	0.046	-1.36	0.007	1.27	0.195	-0.64
1433273_at	2610200G18Rik	RIKEN cDNA 2610200G18 gene	-1.64	0.174	-1.2	0.74	-1.07	0.592	1.38	0.49	-0.63
1456252_x_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	-1.42	0.247	-1.05	0.92	-1.39	0.388	1.61	0.559	-0.56
1441143_at	E130309D14Rik	RIKEN cDNA E130309D14 gene	-1.87	0.231	-1.99	0.393	1.34	0.131	-1.12	0.531	-0.91
1451515_s_at	Glyat	glycine-N-acyltransferase	-1.36	0.052	-1.18	0.095	-1.26	0.251	1.49	0.238	-0.58
1430651_s_at	Zfp191	zinc finger protein 191	1.06	0.734	-1.34	0.514	-1.76	0.103	-1.2	0.337	-0.81
1444109_at	C130009A20Rik	RIKEN cDNA C130009A20 gene	1.06	0.892	-1.5	0.277	-1.54	0.106	-1.1	0.498	-0.77
1424992_at	Tprkb	Tp53rk binding protein	-1.11	0.729	-1.19	0.344	-1.57	0.328	1.27	0.189	-0.65
1438823_at	---	Transcribed locus	-1.68	0.062	1.1	0.836	-1.47	0.457	-2.18	0.177	-1.06
1433379_at	9430019H13Rik	RIKEN cDNA 9430019H13 gene	-1.13	0.28	-1.47	0.304	-1.23	0.054	1.3	0.516	-0.63
1430178_at	2810408A11Rik	RIKEN cDNA 2810408A11 gene	-1.45	0.245	-1.55	0.382	1.04	0.714	-1.26	0.627	-0.8
1435523_s_at	2700089E24Rik	RIKEN cDNA 2700089E24 gene	-1.62	0.106	-1.32	0.467	1	0.983	-1.16	0.388	-0.78
1436228_at	---	---	-1.14	0.633	-1.22	0.401	-1.47	0.054	1.06	0.706	-0.69
1435445_at	Ccnt2	cyclin T2	-1.08	0.813	-1.2	0.36	-1.62	0.091	1.01	0.972	-0.72
1443722_at	6030419C18Rik	RIKEN cDNA 6030419C18 gene	-1.3	0.1	-1.04	0.857	-1.55	0.07	1.08	0.827	-0.7
1434840_at	Hrb	HIV-1 Rev binding protein	-1.11	0.477	-1.3	0.014	-1.42	0.045	1.13	0.611	-0.67
1417952_at	Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	-2.01	0.038	1.06	0.699	-1.23	0.377	-1.06	0.835	-0.81
1416305_at	Sh3bp4	SH3-domain binding protein 4	-1.11	0.432	-2.45	0.142	1.06	0.111	-1.47	0.127	-0.99
1458857_at	---	Transcribed locus	-1.31	0.595	1.03	0.915	-1.71	0.056	-1.1	0.813	-0.77
1459376_at	Hivep2	Human immunodeficiency virus type I enhancer binding protein 2	1.03	0.912	-1.19	0.325	-1.97	0.012	-1.71	0.167	-0.96
1420136_a_at	---	---	-1.1	0.579	-1.22	0.064	-1.54	0.176	2.37	0.244	-0.37
1446902_at	AU022538	expressed sequence AU022538	-1.16	0.524	-1.55	0.317	-1.15	0.647	2.43	0.071	-0.36
1458500_at	AU021034	expressed sequence AU021034	-2.26	0.308	-1.13	0.829	1.05	0.831	-1.13	0.771	-0.87
1444330_at	D2Ertd173e	DNA segment, Chr 2, ERATO Doi 173, expressed	-1.8	0.537	-1.86	0.384	1.28	0.736	-1.11	0.801	-0.87
1450683_at	Tagln3	transgelin 3	-1.19	0.69	1.16	0.671	-2.68	0.023	-1.25	0.731	-0.99
1445415_at	B230303A05	Hypothetical protein B230303A05	-2.57	0.396	-1.34	0.319	1.24	0.359	-1.51	0.233	-1.05
1443402_at	Phka2	Phosphorylase kinase alpha 2	-1.53	0.365	1.07	0.811	-1.53	0.163	-1.25	0.252	-0.81
1435765_at	E130114P18Rik	RIKEN cDNA E130114P18 gene	-1.57	0.58	-1.06	0.837	-1.25	0.196	2.31	0.022	-0.39

1454833_at	Rpl35	ribosomal protein L35	-1.5	0.031	-1.13	0.662	-1.21	0.602	1.09	0.778	-0.69
1436440_at	B230107K20Rik	RIKEN cDNA B230107K20 gene	-1.24	0.404	-1.48	0.342	-1.12	0.618	1.04	0.725	-0.7
1447691_x_at	Bicc1	Bicaudal C homolog 1 (Drosophila)	-1.17	0.502	-1.22	0.621	-1.42	0.059	1.1	0.598	-0.68
1439420_x_at	Ggtla1	gamma-glutamyltransferase-like activity 1	-1.22	0.636	-1.11	0.786	-1.52	0.028	1.2	0.757	-0.66
1445215_at	2600003E23Rik	RIKEN cDNA 2600003E23 gene	-1.19	0.632	1.03	0.926	-1.96	0.155	-1	0.995	-0.78
1423173_at	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	-1.43	0.005	1.2	0.395	-2.09	0.066	-1.03	0.848	-0.84
1459411_at	Sdccag10	Serologically defined colon cancer antigen 10	-1.31	0.078	1.05	0.834	-1.78	0.114	-1.21	0.506	-0.81
1432723_at	4933408K01Rik	RIKEN cDNA 4933408K01 gene	-1.22	0.591	-1.05	0.915	-1.64	0.399	1.4	0.314	-0.63
1443778_at	LOC672274	similar to Transcription factor SOX-4	-1.54	0.519	1.19	0.167	-1.85	0.236	-1.23	0.75	-0.86
1421689_at	Krtap8-2	keratin associated protein 8-2	-3.33	0.167	-1.07	0.81	1.14	0.808	-1.14	0.722	-1.1
1447286_at	Emb	Embigin	-1.71	0.601	1.09	0.882	-1.43	0.239	-4.2	0.035	-1.56
1439298_at	---	---	-1.09	0.535	-1.28	0.009	-1.47	0.23	1.01	0.95	-0.71
1458757_at	Ptbp2	Polypyrimidine tract binding protein 2	-2.38	0.273	-1.12	0.872	1.07	0.832	-1.32	0.664	-0.94
1457080_at	---	Transcribed locus	1.06	0.854	-2.3	0.157	-1.13	0.72	-1.45	0.314	-0.96
1425010_at	Zfp119	zinc finger protein 119	-1.88	0.028	1.11	0.621	-1.36	0.495	-1.04	0.908	-0.79
1440565_at	Zbtb20	Zinc finger and BTB domain containing 20	-1.54	0.083	-1.13	0.488	-1.18	0.407	1.39	0.233	-0.62
1434595_at	Trim9	tripartite motif protein 9	-1.25	0.707	-1.21	0.532	-1.32	0.136	1.32	0.323	-0.62
1457970_at	---	---	1.19	0.261	-1.69	0.222	-1.67	0.125	-1.18	0.119	-0.84
1451404_at	ORF19	open reading frame 19	-1.09	0.703	-1.63	0.095	-1.18	0.399	1.03	0.912	-0.72
1435064_a_at	Tmem27	transmembrane protein 27	-1.11	0.367	-14.72	0.127	1.41	0.502	-1.27	0.235	-3.92
1456701_at	B230208H17Rik	RIKEN cDNA B230208H17 gene	1.05	0.924	-1.43	0.413	-1.57	0.105	-1.97	0.178	-0.98
1455536_at	A630023A22Rik	RIKEN cDNA A630023A22 gene	-1.12	0.823	1.05	0.901	-2.32	0.022	-2.11	0.353	-1.12
1439150_x_at	Grtp1	GH regulated TBC protein 1	-1.11	0.571	-1.15	0.518	-1.64	0.415	3.06	0.073	-0.21
1456496_at	Dapk3	Death-associated kinase 3	-2.63	0.086	-1.17	0.655	1.15	0.748	-1.03	0.929	-0.92
1435260_at	---	---	1.16	0.254	-1.59	0.068	-1.69	0.011	-1.8	0.017	-0.98
1435726_at	Lima1	LIM domain and actin binding 1	-1.42	0.497	-1.4	0.14	-1.04	0.938	2.95	0.049	-0.23
1458477_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630098	-1.38	0.442	-1.58	0.466	1.02	0.963	-1.2	0.495	-0.78
1442126_at	5830417C01Rik	RIKEN cDNA 5830417C01 gene	1.12	0.715	-1.25	0.234	-2.17	0.051	-2.35	0.061	-1.16
1459845_at	Cbx5	Chromobox homolog 5 (Drosophila HP1a)	-1.41	0.093	-1.13	0.805	-1.27	0.546	1.55	0.255	-0.57
1435384_at	Ube2n	ubiquitin-conjugating enzyme E2N	-1.18	0.499	-1.21	0.263	-1.41	0.039	1.2	0.226	-0.65
1456299_at	E330012B07Rik	RIKEN cDNA E330012B07 gene	1.46	0.685	-3.67	0.029	-1.53	0.201	-1.34	0.235	-1.27
1432679_at	Itgav	integrin alpha V	-1.52	0.127	1.08	0.869	-1.55	0.058	-1.52	0.423	-0.88
1449480_at	Sap18	Sin3-associated polypeptide 18	1.01	0.966	-1.46	0.053	-1.44	0.015	-1.35	0.032	-0.81
1435000_at	Gspt1	G1 to S phase transition 1	-1.21	0.063	-1.28	0.021	-1.29	0.001	1.03	0.887	-0.69
1424097_at	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	-1.03	0.758	-1.32	0.583	-1.52	0.11	1.74	0.114	-0.53
1445088_at	Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	-2.15	0.506	1.2	0.148	-1.39	0.489	-1.24	0.498	-0.89
1432567_at	A430105D02Rik	RIKEN cDNA A430105D02 gene	-1.28	0.552	-2.01	0.243	1.1	0.863	-1.16	0.684	-0.84
1415712_at	Zranb1	zinc finger, RAN-binding domain containing 1	1.06	0.222	-1.27	0.196	-1.87	0.003	-1	0.983	-0.77
1430416_at	4931431B13Rik	RIKEN cDNA 4931431B13 gene	-3.01	0.005	1.25	0.509	-1.26	0.633	-1.06	0.884	-1.02
1440404_at	---	---	-1.13	0.552	1.09	0.816	-2.44	0.03	-1.32	0.412	-0.95
1422332_at	Ifna11	interferon alpha 11	-1.86	0.186	-1.88	0.142	1.32	0.47	-1.13	0.421	-0.89
1442958_at	---	Lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730002L0	-2.57	0.056	1.55	0.451	-2.25	0.121	-1.33	0.227	-1.15
1424132_at	Hras1	Harvey rat sarcoma virus oncogene 1	-1.13	0.701	-1.34	0.399	-1.33	0.111	1.38	0.344	-0.6
1444286_at	---	Transcribed locus, weakly similar to XP_530798.1 PREDICTED: hypothetical pro	-1.44	0.498	-1.08	0.841	-1.31	0.529	1.04	0.908	-0.7
1433147_at	Cald1	caldesmon 1	-1.05	0.924	1.05	0.82	-2.63	0.06	-1.7	0.125	-1.08
1459551_at	---	---	1.27	0.694	-2.39	0.103	-1.43	0.368	-2.52	0.296	-1.27
1446618_at	LOC432971	hypothetical gene supported by AK038224	-1.24	0.108	-1.08	0.546	-1.53	0.123	1.13	0.369	-0.68
1459663_at	---	---	-1.56	0.381	1.22	0.648	-1.91	0.076	-1.62	0.041	-0.97
1453388_at	4933416M07Rik	RIKEN cDNA 4933416M07 gene	1.06	0.869	-1.53	0.44	-1.49	0.147	-1.83	0.433	-0.95
1459461_at	---	---	-1.21	0.359	-1.19	0.629	-1.39	0.028	1.11	0.678	-0.67
1432484_at	2310061C15Rik	RIKEN cDNA 2310061C15 gene	-1.09	0.789	-2.08	0.148	-1.02	0.926	1.53	0.177	-0.66
1438249_at	Usp7	Ubiquitin specific peptidase 7	-1.1	0.155	-1.34	0.001	-1.37	0.297	1.28	0.456	-0.63
1425175_at	C1ql3	C1q-like 3	-1.54	0.324	-1.52	0.122	1.08	0.866	-1.02	0.941	-0.75

1458984_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-1.05	0.685	-1.4	0.22	-1.39	0.009	1.37	0.28	-0.62
1457177_at	Rora	RAR-related orphan receptor alpha	-1.11	0.678	-1.02	0.903	-1.99	0.044	1.14	0.694	-0.74
1447336_at	---	Adult male kidney cDNA, RIKEN full-length enriched library, clone:F530012N16 p	-1.18	0.817	-1.64	0.117	-1.08	0.894	1.79	0.361	-0.53
1459622_at	Gm22	gene model 22, (NCBI)	-1.58	0.191	-1.09	0.762	-1.21	0.362	1.07	0.815	-0.7
1456535_at	Vps13c	vacuolar protein sorting 13C (yeast)	-1.53	0.049	-1.28	0.56	-1.05	0.904	1.21	0.71	-0.66
1451150_at	Zfp410	zinc finger protein 410	-1.27	0.264	-1.28	0.063	-1.23	0.403	1.38	0.373	-0.6
1450265_at	Smad9	MAD homolog 9 (Drosophila)	-2.23	0.105	1.08	0.902	-1.17	0.694	-1.07	0.908	-0.85
1460510_a_at	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	-1.27	0.506	-1.29	0.462	-1.22	0.273	1.44	0.381	-0.58
1433098_at	---	---	-1.93	0.057	1.18	0.768	-1.45	0.305	-2.06	0.069	-1.07
1454939_at	Phf20l1	PHD finger protein 20-like 1	-1.33	0.422	-1.31	0.368	-1.15	0.408	1.23	0.235	-0.64
1454239_at	4930578G10Rik	RIKEN cDNA 4930578G10 gene	-1.42	0.409	1.02	0.983	-1.5	0.312	-1.17	0.717	-0.77
1456276_at	---	---	-1.3	0.557	-1.2	0.69	-1.28	0.677	1.25	0.571	-0.63
1445067_at	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	-1.12	0.11	-1.23	0.281	-1.47	0.058	1.17	0.218	-0.66
1429169_at	Rbm3	RNA binding motif protein 3	-1.17	0.583	-1.33	0.234	-1.29	0.41	1.26	0.353	-0.63
1439983_a_at	Accn3	amiloride-sensitive cation channel 3	-1.09	0.664	-2.31	0.229	1.03	0.842	-2.22	0.418	-1.15
1440660_at	Nfia	Nuclear factor I/A	-1.27	0.072	-1.06	0.737	-1.52	0.087	1.49	0.052	-0.59
1442990_at	---	---	-1.66	0.618	-1.34	0.621	1.03	0.944	-1.11	0.774	-0.77
1420162_at	AA409749	expressed sequence AA409749	-2.13	0.195	-3.27	0.059	1.61	0.214	-1.63	0.473	-1.35
1451539_at	Baiap2l1	BAI1-associated protein 2-like 1	-1.01	0.958	-1.43	0.344	-1.44	0.005	1.44	0.556	-0.61
1459882_at	---	---	-1.3	0.198	-1.43	0.052	-1.09	0.706	1.49	0.07	-0.58
1459360_at	Sp3	Trans-acting transcription factor 3	-1.32	0.21	1.08	0.629	-1.82	0.04	-1.3	0.211	-0.84
1431199_at	0610031G08Rik	RIKEN cDNA 0610031G08 gene	-1.51	0.096	-1.42	0.046	1.02	0.965	-1.41	0.482	-0.83
1453137_at	Fbxo30	F-box protein 30	-1.14	0.455	-1.31	0.202	-1.34	0.002	5.13	0.204	0.34
1456804_at	Av381130	hypothetical protein LOC627821	-3.8	0.007	-1.25	0.463	1.32	0.586	-1.68	0.532	-1.35
1453337_at	1700013E18Rik	RIKEN cDNA 1700013E18 gene	-1.39	0.309	1.02	0.942	-1.55	0.427	-1.3	0.725	-0.8
1437853_x_at	Ndn	necdin	1.13	0.682	-1.68	0.161	-1.51	0.222	-1.54	0.274	-0.9
1429064_at	Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	-1.24	0.031	-1.09	0.434	-1.51	0.088	1.21	0.403	-0.66
1456242_at	Esgp	embryonic stem cell- and germ cell-specific protein	1.02	0.949	-1.94	0.413	-1.17	0.822	-1.27	0.726	-0.84
1442943_at	Usp20	Ubiquitin specific peptidase 20	1.01	0.994	-1.43	0.586	-1.46	0.414	-1.13	0.751	-0.75
1416489_at	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	-1.26	0.25	-1.15	0.4	-1.38	0.044	3.81	0.179	0
1428486_at	1700123L14Rik	RIKEN cDNA 1700123L14 gene	-1.05	0.927	1.02	0.978	-2.38	0.024	-2.16	0.173	-1.14
1451447_at	Cuedc1	CUE domain containing 1	-1.66	0.077	-1.49	0.36	1.11	0.617	-1.68	0.195	-0.93
1441104_at	Myo5b	myosin Vb	1.12	0.783	-1.31	0.652	-2	0.171	-1.04	0.914	-0.81
1427573_at	Chic1	cysteine-rich hydrophobic domain 1	-1.24	0.212	-1.41	0.272	-1.15	0.341	1.17	0.257	-0.66
1427620_at	Parc	p53-associated parkin-like cytoplasmic protein	-1.56	0.058	-1.77	0.052	1.18	0.087	-1.47	0.326	-0.9
1443066_at	---	---	-1.79	0.059	-1.17	0.394	-1.03	0.955	1.38	0.5	-0.65
1459339_at	1700049G17Rik	RIKEN cDNA 1700049G17 gene	-1.24	0.376	-1.41	0.092	-1.14	0.529	1.05	0.671	-0.69
1451502_at	Pla2g10	phospholipase A2, group X	-2.69	0.208	-1.07	0.69	1.08	0.839	-1.03	0.923	-0.93
1443811_at	Prkg1	Protein kinase, cGMP-dependent, type I	-1.27	0.713	-1.03	0.938	-1.58	0.122	1.21	0.764	-0.67
1452530_a_at	Runx1	runt related transcription factor 1	-1.58	0.215	-1.07	0.919	-1.21	0.575	1.25	0.738	-0.65
1433319_at	5430437A18Rik	RIKEN cDNA 5430437A18 gene	-1.9	0.473	-1.04	0.962	-1.11	0.849	1.48	0.395	-0.64
1447675_x_at	Myod1	myogenic differentiation 1	1.09	0.898	-1.3	0.664	-1.87	0.08	-2.22	0.288	-1.08
1427151_at	Qser1	glutamine and serine rich 1	-1.28	0.301	-1.18	0.505	-1.31	0.11	1.05	0.582	-0.68
1423343_at	Slco1c1	solute carrier organic anion transporter family, member 1c1	-1.86	0.23	-2.27	0.285	1.41	0.338	-1.22	0.617	-0.98
1425685_at	2310005E10Rik	RIKEN cDNA 2310005E10 gene	1.07	0.452	-1.8	0.383	-1.31	0.482	-1.05	0.91	-0.77
1453926_at	Rad54l	RAD54 like (S. cerevisiae)	-1.05	0.846	-1.35	0.631	-1.43	0.61	2.3	0.321	-0.38
1415917_at	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahy	-1.2	0.077	-1.12	0.476	-1.5	0.043	2.19	0.174	-0.41
1440824_at	Fbxo45	F-box protein 45	1.27	0.68	-2.37	0.108	-1.44	0.263	-1.11	0.289	-0.91
1457461_at	A630039O03Rik	RIKEN cDNA A630039O03 gene	1.38	0.17	-2.06	0.15	-1.91	0.328	-1.08	0.509	-0.92
1427550_at	Peg10	paternally expressed 10	-1.15	0.848	-1.16	0.713	-1.51	0.057	1.19	0.767	-0.66
1459727_at	AW125646	expressed sequence AW125646	-1.93	0.472	1.19	0.747	-1.46	0.511	-1.32	0.228	-0.88
1416670_at	Setdb1	SET domain, bifurcated 1	-1.11	0.618	-1.65	0.445	-1.13	0.833	1.18	0.816	-0.68
1426155_a_at	Osr2	odd-skipped related 2 (Drosophila)	-1.32	0.498	-1.11	0.136	-1.36	0.629	1.24	0.77	-0.64

1446684_at	Garnl1	GTPase activating RANGAP domain-like 1	1.18	0.462	-1.42	0.506	-1.95	0.037	-1.5	0.241	-0.92
1458697_at	---	Transcribed locus	-1.03	0.942	-2.06	0.393	-1.07	0.477	1.28	0.667	-0.72
1440785_at	Rxfp1	relaxin/insulin-like family peptide receptor 1	-1.46	0.018	1.05	0.884	-1.51	0.151	-1.41	0.606	-0.84
1442805_at	A130086G11Rik	RIKEN cDNA A130086G11 gene	-1.24	0.106	-1.55	0.304	-1.07	0.706	1.28	0.421	-0.64
1431964_at	4921518J05Rik	RIKEN cDNA 4921518J05 gene	-1.05	0.95	-1.4	0.339	-1.37	0.469	1.21	0.606	-0.66
1442041_at	LOC552876	hypothetical LOC552876	1.1	0.735	-1.25	0.547	-2.04	0.037	-1.79	0.197	-0.99
1444781_at	Xab1	XPA binding protein 1	1.35	0.41	-1.95	0.055	-1.91	0.174	-1.51	0.469	-1
1459997_s_at	Tmem17	transmembrane protein 17	1.18	0.376	-2.09	0.442	-1.37	0.149	-1.49	0.475	-0.94
1434097_at	---	Transcribed locus	-1.18	0.333	-1.44	0.036	-1.18	0.038	1.04	0.806	-0.69
1436057_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.05	0.92	-1.62	0.454	-1.22	0.546	1.07	0.829	-0.71
1460050_x_at	5630401D24Rik	RIKEN cDNA 5630401D24 gene	-1.23	0.71	-1.38	0.152	-1.17	0.389	1.12	0.283	-0.66
1455754_at	Lmo3	LIM domain only 3	-1.17	0.631	-1.33	0.383	-1.28	0.609	1.06	0.833	-0.68
1459556_at	BC013481	CDNA sequence BC013481	1.22	0.356	-1.55	0.25	-1.89	0.002	-1.22	0.714	-0.86
1454304_at	Epn2	epsin 2	-1.26	0.445	-1.05	0.922	-1.56	0.092	1.43	0.523	-0.61
1444926_at	---	---	-1.72	0.133	1.1	0.902	-1.41	0.628	-1.64	0.171	-0.92
1435731_x_at	Stag1	Stromal antigen 1	-1.64	0.082	-1.14	0.046	-1.1	0.29	1.42	0.096	-0.62
1456753_at	---	---	-1.19	0.223	-1.16	0.547	-1.44	0.03	1.99	0.166	-0.45
1432503_a_at	Pdcl2	phosducin-like 2	-2.38	0.1	-1.22	0.781	1.15	0.78	-1.23	0.746	-0.92
1445036_at	D11Ertd518e	DNA segment, Chr 11, ERATO Doi 518, expressed	-1.01	0.971	-1.67	0.295	-1.24	0.758	1.74	0.448	-0.55
1441372_at	5930405F01Rik	RIKEN cDNA 5930405F01 gene	1	0.989	-1.21	0.642	-1.78	0.166	-1.68	0.26	-0.92
1429942_at	Gmeb1	glucocorticoid modulatory element binding protein 1	-1.35	0.2	-1.26	0.256	-1.17	0.411	1.15	0.424	-0.66
1419126_at	Hoxd9	homeo box D9	-1.1	0.07	-1.53	0.358	-1.21	0.802	2.25	0.205	-0.4
1417933_at	Igfbp6	insulin-like growth factor binding protein 6	-1.4	0.335	-1.26	0.451	-1.13	0.636	2.05	0.086	-0.43
1446937_at	Falz	fetal Alzheimer antigen	-1.59	0.117	-1.05	0.9	-1.23	0.054	1.01	0.96	-0.72
1420007_at	---	---	-1.14	0.741	-1.49	0.02	-1.18	0.559	1.45	0.189	-0.59
1451270_at	Dusp18	dual specificity phosphatase 18	-1.24	0.634	-1.83	0.173	1.04	0.826	-2.98	0.062	-1.25
1445982_at	Gpc6	Glypican 6	1.25	0.765	-1.41	0.113	-2.29	0.262	-2.82	0.257	-1.32
1449597_at	LOC236874	similar to odorant binding protein Ia	-1.07	0.86	-1.23	0.788	-1.55	0.588	2.99	0.194	-0.21
1443401_at	Astn2	Astrotactin 2	-2.27	0.272	-1.09	0.855	1.04	0.883	-1.04	0.949	-0.84
1417713_at	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	-1.11	0.32	-1.23	0.022	-1.47	0.073	1.18	0.416	-0.66
1444478_at	2900057D21Rik	RIKEN cDNA 2900057D21 gene	-1.55	0.161	-1.48	0.129	1.07	0.743	-1.55	0.072	-0.88
1426335_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	-1.27	0.443	-2.07	0.32	1.13	0.497	-1.74	0.376	-0.99
1422161_at	Siglec1	sialic acid binding Ig-like lectin 1, sialoadhesin	-1.66	0.517	1.06	0.859	-1.37	0.353	-1.73	0.332	-0.92
1437430_at	Slc45a2	solute carrier family 45, member 2	-1.2	0.673	1.12	0.754	-2.28	0.012	-1.82	0.607	-1.04
1427726_at	LOC633417	similar to histocompatibility 2, T region locus 3	-1.28	0.645	-1.52	0.34	-1.05	0.903	1.01	0.973	-0.71
1435336_at	Celsr2	cadherin EGF LAG seven-pass G-type receptor 2	-1.17	0.051	-2.29	0.127	1.1	0.602	-1.1	0.596	-0.86
1455328_at	Accn2	amiloride-sensitive cation channel 2, neuronal	-2.68	0.208	-1.97	0.071	1.51	0.025	-1.31	0.437	-1.11
1422195_s_at	Tbx15	T-box 15	1.31	0.422	-2.33	0.37	-1.52	0.482	-1.11	0.826	-0.91
1453098_at	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	-1.84	0.078	-1.08	0.817	-1.08	0.804	1.16	0.303	-0.71
1443026_at	Grip1	Glutamate receptor interacting protein 1	-1.16	0.559	-1.24	0.754	-1.38	0.011	1.07	0.903	-0.68
1439549_at	Prrg3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	-1.07	0.681	-1.24	0.394	-1.53	0.058	1.18	0.12	-0.67
1439762_x_at	Adra2c	adrenergic receptor, alpha 2c	-1.89	0.294	-1.33	0.549	1.12	0.875	-2.7	0.321	-1.2
1449786_at	Zdhhc7	zinc finger, DHHC domain containing 7	1.19	0.813	-1.94	0.277	-1.44	0.253	-1.5	0.254	-0.92
1450274_at	1700108E19Rik	RIKEN cDNA 1700108E19 gene	-2.49	0.057	-1.25	0.77	1.19	0.694	-1.69	0.422	-1.06
1429930_at	Ccdc19	coiled-coil domain containing 19	-1.45	0.203	-1.26	0.371	-1.1	0.57	1.18	0.642	-0.66
1418657_at	Znhit4	zinc finger, HIT type 4	-1.6	0.201	-1.35	0.384	1.03	0.883	-1.77	0.103	-0.92
1441953_at	Stox2	Storkhead box 2	-1.41	0.137	-1.1	0.769	-1.28	0.355	1.42	0.329	-0.59
1420795_at	Fgf9	fibroblast growth factor 9	-1.37	0.264	-1.1	0.679	-1.32	0.238	1.22	0.379	-0.64
1420931_at	Mapk8	mitogen activated protein kinase 8	-2.5	0.064	-1.41	0.427	1.29	0.498	-1.82	0.011	-1.11
1456685_at	Nsg2	neuron specific gene family member 2	-1.56	0.474	-1.59	0.305	1.13	0.853	-1.95	0.194	-0.99
1441702_at	Rfx3	Regulatory factor X, 3 (influences HLA class II expression)	-2.11	0.25	-1.61	0.397	1.3	0.153	-1.34	0.084	-0.94
1457233_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	1.1	0.485	-1.46	0.229	-1.64	0.028	-1.66	0.174	-0.91
1457630_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	-2.31	0.339	-1.45	0.54	1.27	0.728	-2.73	0.207	-1.3

1435667_at	Rims1	regulating synaptic membrane exocytosis 1	-1.51	0.187	-1.49	0.373	1.06	0.881	-3.41	0.018	-1.34
1457469_at	---	---	-1.19	0.591	-1.18	0.775	-1.4	0.24	1.54	0.252	-0.56
1430211_at	4930415O20Rik	RIKEN cDNA 4930415O20 gene	-1.16	0.662	-1.24	0.471	-1.37	0.481	1.55	0.211	-0.56
1454273_at	1700025H01Rik	RIKEN cDNA 1700025H01 gene	1.16	0.544	-1.16	0.789	-2.63	0.204	-1.17	0.4	-0.95
1422338_at	Gpr63	G protein-coupled receptor 63	1.05	0.862	-1.06	0.826	-2.48	0.06	-1.73	0.537	-1.05
1458858_at	---	---	-1.24	0.317	-1.64	0.576	-1.02	0.966	1.8	0.184	-0.52
1423406_at	Sv2a	synaptic vesicle glycoprotein 2 a	-1.5	0.109	1.09	0.859	-1.56	0.315	-1.29	0.62	-0.81
1427502_at	Adam4	a disintegrin and metallopeptidase domain 4	-1.24	0.467	-1.02	0.94	-1.64	0.137	1.64	0.175	-0.56
1459930_at	Ube2h	Ubiquitin-conjugating enzyme E2H	-1.32	0.575	-1.23	0.79	-1.21	0.587	1.3	0.176	-0.62
1429044_at	Camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	-1.06	0.483	-1.18	0.269	-1.64	0.006	2.01	0.135	-0.47
1435390_at	Exod1	exonuclease domain containing 1	-1.39	0.271	-1.21	0.248	-1.18	0.451	1.64	0.194	-0.53
1446206_at	B230209C24Rik	RIKEN cDNA B230209C24 gene	-2.35	0.525	1.44	0.396	-1.88	0.296	-1.42	0.361	-1.05
1433944_at	Hectd2	HECT domain containing 2	1.02	0.956	-2.03	0.078	-1.14	0.681	-1.4	0.396	-0.89
1456689_at	Rnf10	Ring finger protein 10	-1.03	0.941	-1.64	0.009	-1.22	0.414	2.12	0.17	-0.44
1447511_at	---	Transcribed locus	1.36	0.052	-1.71	0.362	-2.22	0.135	-4.4	0.024	-1.74
1418968_at	Rb1cc1	RB1-inducible coiled-coil 1	-1.11	0.507	-1.18	0.138	-1.54	0.074	1.11	0.629	-0.68
1429401_at	Stox2	storkhead box 2	-1.32	0.245	-1.13	0.532	-1.32	0.013	1.25	0.442	-0.63
1445940_at	D4Ertd298e	DNA segment, Chr 4, ERATO Doi 298, expressed	-1.3	0.328	-1.24	0.421	-1.22	0.614	1.22	0.336	-0.63
1438255_at	Ches1	checkpoint suppressor 1	1.03	0.206	-1.43	0.026	-1.5	0.061	-1.34	0.536	-0.81
1450685_at	Arpp19	cAMP-regulated phosphoprotein 19	-1.21	0.072	-1.15	0.038	-1.43	0.026	1.08	0.595	-0.68
1416744_at	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	-1.53	0.341	-1.29	0.351	-1.03	0.934	1.3	0.386	-0.64
1449760_at	---	Transcribed locus	-1.47	0.175	-1.01	0.912	-1.37	0.184	1.4	0.253	-0.61
1458256_at	5830446M03Rik	RIKEN cDNA 5830446M03 gene	-1.82	0.102	1.02	0.961	-1.2	0.352	-1.2	0.498	-0.8
1427249_x_at	Mup3	major urinary protein 3	1.68	0.235	-4.66	0.007	-1.97	0.129	-1.05	0.743	-1.5
1445306_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.1	0.887	-2.11	0.056	-1.21	0.326	-2.13	0.081	-1.09
1430033_at	5330431K02Rik	RIKEN cDNA 5330431K02 gene	1.2	0.287	-2.05	0.07	-1.41	0.089	-1.54	0.162	-0.95
1427883_a_at	Col3a1	procollagen, type III, alpha 1	-1.13	0.218	1.13	0.29	-2.57	0.055	-1.07	0.792	-0.91
1453437_at	2810407D09Rik	RIKEN cDNA 2810407D09 gene	-1.31	0.34	-1.13	0.467	-1.33	0.078	1.15	0.439	-0.65
1420063_at	---	Transcribed locus	-1.96	0.535	-2.06	0.122	1.41	0.566	-1.41	0.512	-1.01
1422696_at	Ttyh1	tweety homolog 1 (Drosophila)	-1.32	0.695	-1.1	0.885	-1.37	0.558	1.13	0.783	-0.66
1446440_at	---	CDNA clone IMAGE:40051559	1.08	0.362	-1.15	0.8	-2.23	0.007	-1.29	0.454	-0.9
1452529_a_at	Creb1	cAMP responsive element binding protein 1	-1.42	0.452	-1.45	0.235	1.01	0.982	-1.08	0.627	-0.74
1427963_s_at	Rdh9	retinol dehydrogenase 9	-1	0.83	-2.12	0.001	-1.07	0.621	1.1	0.769	-0.77
1451867_x_at	Arhgap6	Rho GTPase activating protein 6	-1.42	0.015	-1.2	0.387	-1.15	0.383	1.02	0.909	-0.69
1442402_at	Sh3rf1	SH3 domain containing ring finger 1	1.15	0.7	-1.36	0.094	-1.94	0.021	-1.13	0.407	-0.82
1458873_at	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	-1.47	0.145	-1.25	0.462	-1.09	0.749	1.17	0.36	-0.66
1443109_at	5830417C01Rik	RIKEN cDNA 5830417C01 gene	-1.4	0.255	1.01	0.977	-1.46	0.017	-1.93	0.144	-0.95
1452808_at	Snupn	snurportin 1	-1.33	0.225	-1.36	0.477	-1.09	0.438	1.01	0.964	-0.69
1457281_at	4930461P20Rik	RIKEN cDNA 4930461P20 gene	-1.07	0.821	-1.38	0.117	-1.35	0.47	1.47	0.215	-0.58
1437382_at	Acvr2a	Activin receptor IIA	-1.03	0.455	-1.04	0.694	-2.11	0.014	1.08	0.778	-0.78
1444446_at	---	---	1	0.99	-1.16	0.62	-1.86	0.033	-1.1	0.727	-0.78
1436161_at	Aprin	androgen-induced proliferation inhibitor	-1.09	0.372	-1.22	0.136	-1.5	0.087	1.06	0.562	-0.69
1438081_at	Mcc	mutated in colorectal cancers	-1.32	0.37	-1.19	0.359	-1.25	0.46	1.93	0.057	-0.45
1420735_at	Gabrr2	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	-1.12	0.816	-1.04	0.928	-1.83	0.309	1.08	0.866	-0.73
1427371_at	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a	1.24	0.42	-2.17	0.016	-1.43	0.225	-1.14	0.709	-0.87
1439880_at	D630023F18Rik	RIKEN cDNA D630023F18 gene	-1.61	0.098	-1.05	0.896	-1.21	0.617	1.28	0.329	-0.65
1439844_at	8430426J06Rik	RIKEN cDNA 8430426J06 gene	-1.37	0.387	-1.05	0.845	-1.39	0.156	1.06	0.896	-0.69
1446390_at	Elk1	ELK1, member of ETS oncogene family	-1.04	0.864	-1.85	0.402	-1.11	0.478	1.31	0.679	-0.67
1451913_a_at	Hyou1	hypoxia up-regulated 1	-1.63	0.386	-1.63	0.351	1.18	0.632	-1.39	0.224	-0.87
1434627_at	Nrf1	Nuclear respiratory factor 1	-1.26	0.248	-1.04	0.478	-1.55	0.037	1.02	0.801	-0.71
1431424_at	2810055G20Rik	RIKEN cDNA 2810055G20 gene	1.17	0.384	-1.46	0.023	-1.84	0.005	-1.37	0.227	-0.87
1446758_at	Bre	brain and reproductive organ-expressed protein	-1.22	0.524	-1.09	0.617	-1.5	0.221	1.02	0.926	-0.7
1440448_at	---	Transcribed locus	-1.05	0.732	-1.12	0.739	-1.79	0.062	1.11	0.491	-0.71

1432250_at	Utp14a	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	-1.16	0.7	-1.51	0.223	-1.14	0.398	1.04	0.563	-0.69
1454581_at	5330425B07Rik	RIKEN cDNA 5330425B07 gene	-1.11	0.72	-1.05	0.917	-1.81	0.079	1.35	0.078	-0.66
1422610_s_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	-1.09	0.901	-2.05	0.244	1	0.999	-3.89	0.046	-1.51
1440930_a_at	Scrt2	scratch homolog 2, zinc finger protein (Drosophila)	1.3	0.71	-1.64	0.194	-2.03	0.209	-2.42	0.288	-1.2
1432396_at	3110018I06Rik	RIKEN cDNA 3110018I06 gene	1.32	0.63	-2.18	0.011	-1.61	0.096	-1.09	0.653	-0.89
1429517_at	Zfyve20	zinc finger, FYVE domain containing 20	-1.76	0.17	-2.17	0.101	1.38	0.494	-1.45	0.386	-1
1437015_x_at	Pla2g1b	phospholipase A2, group IB, pancreas	-1.15	0.835	1.12	0.873	-2.39	0.011	-1.93	0.395	-1.09
1456842_at	---	PREDICTED: Mus musculus hypothetical protein LOC628013 (LOC628013), mR	1.1	0.846	-2.2	0.207	-1.17	0.788	-2.15	0.453	-1.11
1432556_a_at	3100002J23Rik	RIKEN cDNA 3100002J23 gene	-1.06	0.905	-2.26	0.355	1.02	0.942	-1.64	0.612	-0.99
1431173_at	A930008G19Rik	RIKEN cDNA A930008G19 gene	-1.28	0.31	-1.05	0.808	-1.49	0.08	1.42	0.342	-0.6
1454854_at	Ostb	organic solute transporter beta	1.01	0.9	-1.45	0.418	-1.42	0.373	-1.6	0.208	-0.86
1420929_at	Ctnnal1	catenin (cadherin associated protein), alpha-like 1	1.04	0.875	-1.83	0.016	-1.22	0.371	-1.34	0.409	-0.84
1446352_at	2410016O06Rik	RIKEN cDNA 2410016O06 gene	-1.72	0.511	-1.08	0.895	-1.11	0.76	2.59	0.113	-0.33
1447515_at	---	Transcribed locus	1.23	0.688	-1.6	0.092	-1.82	0.16	-1.11	0.711	-0.82
1437605_at	Nphs2	nephrosis 2 homolog, podocin (human)	1.31	0.291	-1.81	0.145	-1.85	0.022	-2.37	0.096	-1.18
1442471_at	Ephb2	Eph receptor B2	-1.33	0.048	-1.27	0.414	-1.16	0.521	1.08	0.415	-0.67
1425421_at	Rbbp6	Retinoblastoma binding protein 6	1.05	0.659	-1.23	0.207	-1.86	0.02	-1.36	0.214	-0.85
1442914_at	---	Transcribed locus, weakly similar to XP_858458.1 PREDICTED: hypothetical pro	-1.24	0.151	1.06	0.838	-1.87	0.277	-2.47	0.036	-1.13
1453136_at	Fbxo30	F-box protein 30	-1.37	0.18	-1.14	0.592	-1.25	0.184	4.86	0.189	0.27
1447490_at	---	Transcribed locus	-1.27	0.775	-1.08	0.749	-1.44	0.512	1.3	0.616	-0.62
1431882_at	Als2cr12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (hum	-3.29	0.053	-1.49	0.016	1.43	0.29	-1.45	0.188	-1.2
1421635_at	Cnnm4	cyclin M4	-1.85	0.443	1.1	0.72	-1.3	0.591	-1.34	0.707	-0.85
1435370_a_at	Ces3	carboxylesterase 3	-1.35	0.391	-1.26	0.393	-1.15	0.008	4.84	0.057	0.27
1440454_at	A530088I07Rik	RIKEN cDNA A530088I07 gene	-1.43	0.238	-1.13	0.433	-1.21	0.542	1.11	0.672	-0.67
1441270_at	Akap2	A kinase (PRKA) anchor protein 2	1.24	0.746	-4.55	0.088	-1.06	0.837	-1.27	0.105	-1.41
1421472_at	2900083I11Rik	RIKEN cDNA 2900083I11 gene	-1.47	0.079	-1.43	0.588	1.03	0.763	-1.02	0.901	-0.72
1453280_at	Mageb5 /// LOC629	melanoma antigen, family B, 5 /// similar to Melanoma-associated antigen B3 (MA	-1.15	0.872	-1.01	0.989	-1.85	0.385	1.03	0.855	-0.74
1452836_at	Lpin2	lipin 2	-1.19	0.279	-1.3	0.439	-1.25	0.392	1.84	0.147	-0.48
1440904_at	Senp5	SUMO/sentrin specific peptidase 5	-1.29	0.282	-2.22	0.029	1.18	0.397	-1.28	0.149	-0.9
1433205_at	2810436B12Rik	RIKEN cDNA 2810436B12 gene	1.3	0.432	-1.79	0.309	-1.81	0.091	-1.63	0.287	-0.99
1436577_at	Arhgef9	Cdc42 guanine nucleotide exchange factor (GEF) 9	1.13	0.839	-2.06	0.091	-1.27	0.479	-1.33	0.593	-0.88
1442532_at	---	---	-1.29	0.385	1.04	0.896	-1.68	0.068	-1.54	0.004	-0.87
1427641_at	Dlx4	Distal-less homeobox 4	-1.32	0.741	-2.48	0.078	1.25	0.498	-2.28	0.012	-1.21
1432640_at	4633401L03Rik	RIKEN cDNA 4633401L03 gene	1.22	0.065	-1.31	0.686	-2.37	0.115	-1.34	0.551	-0.95
1439472_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	-2.21	0.186	-1.06	0.912	1.01	0.979	-3.08	0	-1.33
1440979_at	Igf2r	Insulin-like growth factor 2 receptor	1.18	0.245	-1.74	0.247	-1.53	0.056	-1.89	0.183	-0.99
1435891_x_at	2610021A01Rik ///	RIKEN cDNA 2610021A01 gene /// similar to zinc finger protein 347	-1.24	0.426	-1.14	0.541	-1.38	0.121	1.11	0.583	-0.66
1441680_at	Rbms3	RNA binding motif, single stranded interacting protein	-1.5	0.167	1.26	0.496	-2.08	0.015	-1.64	0.204	-0.99
1456705_at	Zfp532	Zinc finger protein 532	-2.07	0.015	1.23	0.579	-1.44	0.137	-1.15	0.651	-0.86
1440037_at	Pbx1	pre B-cell leukemia transcription factor 1	-1.12	0.744	1.03	0.841	-2.07	0.005	-1.12	0.671	-0.82
1420458_at	Tac4	tachykinin 4	-1.53	0.322	-1.04	0.84	-1.26	0.591	1.08	0.823	-0.69
1424949_at	Huwe1	HECT, UBA and WWE domain containing 1	-1.12	0.209	-1.25	0.02	-1.4	0.054	1	1	-0.69
1458711_at	---	---	-1.2	0.793	-1.54	0.405	-1.08	0.907	1.57	0.042	-0.56
1451144_at	Bxdc2	brix domain containing 2	-1.22	0.107	-1.33	0.038	-1.2	0.013	1.05	0.714	-0.67
1419929_at	D15Ertd55e	DNA segment, Chr 15, ERATO Doi 55, expressed	-1.66	0.454	1.21	0.393	-1.68	0.045	-1.03	0.96	-0.79
1445928_at	6-Mar	membrane-associated ring finger (C3HC4) 6	1.11	0.794	-1.36	0.367	-1.76	0.072	-1	0.996	-0.75
1418445_at	---	---	-1.21	0.357	-1.31	0.095	-1.23	0.385	1.32	0.4	-0.6
1427118_at	krt86	keratin 86	-2.06	0.264	1.01	0.984	-1.09	0.874	-3.31	0.101	-1.36
1441021_at	Letmd1	LETM1 domain containing 1	-1.67	0.574	-3.49	0.004	1.52	0.185	-1.82	0.091	-1.36
1442071_at	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	-1.34	0.161	-1.56	0.172	1.02	0.954	-1.33	0.2	-0.8
1437024_at	Smpd4	sphingomyelin phosphodiesterase 4	-1.03	0.886	-1.62	0.163	-1.23	0.439	2.24	0.28	-0.41
1441902_x_at	---	---	-1.74	0.013	-1.32	0.355	1.08	0.738	-1.24	0.13	-0.81
1453409_at	Cgrrf1	cell growth regulator with ring finger domain 1	-1.53	0.286	-1.06	0.776	-1.24	0.482	1.48	0.301	-0.59

1450586_at	Bdkrb1	bradykinin receptor, beta 1	1.03	0.93	-1.32	0.3	-1.61	0.064	-1.23	0.515	-0.78
1442396_at	A730020M07Rik	RIKEN cDNA A730020M07 gene	-1.59	0.017	-1.33	0.515	1.03	0.907	-1.61	0.315	-0.88
1459938_at	C330024D21Rik	RIKEN cDNA C330024D21 gene	-3.03	0.007	-1.42	0.479	1.38	0.155	-1.55	0.458	-1.16
1452096_s_at	D230025D16Rik	RIKEN cDNA D230025D16 gene	-1.08	0.372	-1.49	0.033	-1.23	0.187	1	0.993	-0.7
1420024_s_at	Etf1	eukaryotic translation termination factor 1	-1.27	0.413	-1.09	0.653	-1.42	0.045	1.26	0.431	-0.63
1439445_x_at	Acly	ATP citrate lyase	-1.73	0.384	1.18	0.506	-1.52	0.167	-1.06	0.532	-0.79
1454759_at	Git1	G protein-coupled receptor kinase-interactor 1	-1.22	0.139	-1.87	0.094	1.05	0.671	-1.18	0.69	-0.8
1460654_at	Slc30a3	solute carrier family 30 (zinc transporter), member 3	-2.14	0.253	1.03	0.942	-1.1	0.824	-1.29	0.203	-0.87
1427732_s_at	Abcg4	ATP-binding cassette, sub-family G (WHITE), member 4	-1.49	0.35	-1.08	0.899	-1.23	0.469	3.84	0.225	0.01
1447218_at	1110003F02Rik	RIKEN cDNA 1110003F02 gene	-1.71	0.478	-1.11	0.82	-1.08	0.594	2.31	0.187	-0.4
1434264_at	Ank2	ankyrin 2, brain	1.04	0.906	-1.56	0.197	-1.38	0.445	-1.53	0.419	-0.86
1443313_at	A530058N18Rik	RIKEN cDNA A530058N18 gene	-1.28	0.364	-1.3	0.471	-1.16	0.552	1.47	0.308	-0.57
1428698_at	2310004I03Rik	RIKEN cDNA 2310004I03 gene	1.04	0.76	-1.19	0.379	-1.88	0.001	-1.08	0.75	-0.78
1437141_x_at	Dym	dymeclin	-1.35	0.241	-1.41	0.101	-1.04	0.718	1.42	0.159	-0.59
1443436_at	Map2k2	Mitogen activated protein kinase kinase 2	-1.31	0.246	-1.15	0.505	-1.29	0.205	1.06	0.647	-0.67
1453815_at	Spbc25	spindle pole body component 25 homolog (S. cerevisiae)	-1.51	0.153	-1.15	0.583	-1.14	0.648	3.23	0.149	-0.14
1444597_at	---	Transcribed locus	-1.52	0.293	-1.49	0.341	1.08	0.865	-1.47	0.594	-0.85
1429838_at	Spag16	sperm associated antigen 16	1.02	0.962	-1.17	0.558	-1.86	0.228	-1.15	0.738	-0.79
1434488_at	Arfrp1	ADP-ribosylation factor related protein 1	-1.52	0.12	-1.45	0.054	1.06	0.67	-1.34	0.057	-0.81
1427766_at	Tcra-V8	T-cell receptor alpha, variable 8	-1.83	0.534	1.04	0.918	-1.21	0.642	-1.08	0.878	-0.77
1425127_at	Hsd3b2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	-1.67	0.136	-3.15	0.022	1.5	0.458	-1.95	0.18	-1.32
1425595_at	Gabbr1	gamma-aminobutyric acid (GABA-B) receptor, 1	-1.33	0.631	1.03	0.944	-1.6	0.274	-1.16	0.725	-0.76
1440740_at	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	1.08	0.696	-1.46	0.022	-1.55	0.024	-1.08	0.396	-0.75
1431163_at	2700046G09Rik	RIKEN cDNA 2700046G09 gene	-1.22	0.109	-1.06	0.58	-1.54	0.171	1.02	0.922	-0.7
1439963_x_at	1700129I04Rik	RIKEN cDNA 1700129I04 gene	1.17	0.635	-2.76	0.14	-1.14	0.85	-1.55	0.585	-1.07
1426060_at	---	---	-1.71	0.404	1.02	0.901	-1.24	0.276	-1.62	0.155	-0.89
1434916_at	Vkorc1l1	vitamin K epoxide reductase complex, subunit 1-like 1	-1.39	0.153	-1.15	0.254	-1.22	0.126	1.8	0.226	-0.49
1441017_at	Zcchc14	zinc finger, CCHC domain containing 14	1	0.996	-1.42	0.204	-1.41	0.093	-1.35	0.662	-0.8
1453781_at	---	---	-1.29	0.025	-1.64	0.054	1.03	0.895	-1.05	0.851	-0.74
1418846_at	Ap4m1	adaptor-related protein complex AP-4, mu 1	1.01	0.975	-1.81	0.111	-1.18	0.433	-1.16	0.243	-0.78
1451869_at	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	-1.35	0.203	-1.02	0.955	-1.46	0.2	1.64	0.004	-0.54
1420946_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-1.02	0.952	-1.22	0.481	-1.63	0.237	1.05	0.838	-0.7
1429572_at	Nsun7	NOL1/NOP2/Sun domain family, member 7	-2.05	0.411	-1.18	0.571	1.08	0.884	-1.59	0.498	-0.94
1446975_at	Casz1	Castor homolog 1, zinc finger (Drosophila)	-3.14	0.036	-1.03	0.927	1.13	0.804	-1.17	0.266	-1.05
1427961_s_at	Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	-1.12	0.106	-1.24	0.038	-1.4	0.329	1.88	0.099	-0.47
1458338_x_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	-1.17	0.643	-1.03	0.946	-1.72	0.085	1.58	0.349	-0.58
1433352_at	C430049A07Rik	RIKEN cDNA C430049A07 gene	-2.52	0.007	-1.34	0.599	1.27	0.374	-1.4	0.286	-1
1445932_at	Celsr1	Cadherin EGF LAG seven-pass G-type receptor 1	1.29	0.802	-1.46	0.352	-2.31	0.227	-1.55	0.583	-1.01
1432214_at	1700017D01Rik	RIKEN cDNA 1700017D01 gene	1.12	0.903	-2.56	0.202	-1.1	0.879	-1.09	0.796	-0.91
1444616_x_at	---	Transcribed locus	-1.18	0.716	-1.04	0.822	-1.64	0.063	1.46	0.562	-0.6
1433663_s_at	AU014645	expressed sequence AU014645	-1.25	0.128	-1.12	0.417	-1.39	0.146	1.02	0.919	-0.69
1423277_at	Ptprk	protein tyrosine phosphatase, receptor type, K	-1.15	0.027	-1.37	0.081	-1.23	0.213	1.18	0.421	-0.64
1436460_at	BC030440	cDNA sequence BC030440	-1.54	0.227	-1.15	0.665	-1.12	0.057	2.18	0.169	-0.41
1421494_at	1110033F04Rik	RIKEN cDNA 1110033F04 gene	-1.1	0.878	-1.7	0.443	-1.09	0.803	1.72	0.349	-0.54
1427196_at	Wnk4	WNK lysine deficient protein kinase 4	-1.02	0.938	-1.91	0.018	-1.1	0.086	2.09	0.101	-0.48
1435912_at	Ubxd7	UBX domain containing 7	-1.05	0.177	-1.36	0.137	-1.37	0	1.2	0.16	-0.65
1445176_at	---	---	-1.35	0.674	-1.22	0.676	-1.18	0.803	1	0.975	-0.68
1429486_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-1.31	0.302	-1.03	0.898	-1.47	0.072	1.49	0.293	-0.58
1426395_s_at	Eif3s1	eukaryotic translation initiation factor 3, subunit 1 alpha	-1.28	0.202	-1.4	0.008	-1.09	0.496	1.4	0.411	-0.59
1417199_at	1300007B12Rik	RIKEN cDNA 1300007B12 gene	-1.09	0.578	-1.25	0.036	-1.43	0.036	1.14	0.588	-0.66
1437759_at	Pfkp	Phosphofructokinase, platelet	-1.04	0.856	-2.65	0.036	1.08	0.81	-1.13	0.654	-0.93
1428203_at	C030002O17Rik	RIKEN cDNA C030002O17 gene	-1.79	0.293	-3.02	0.042	1.52	0.366	-1.02	0.897	-1.07
1441668_at	E130107B13Rik	RIKEN cDNA E130107B13 gene	-1.54	0.209	-1.32	0.196	1.01	0.939	-1.4	0.076	-0.81

1457434_s_at	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a	-1.19	0.381	-1.04	0.747	-1.63	0.011	2.83	0.262	-0.26
1457216_at	Rc3h1	RING CCCH (C3H) domains 1	1.05	0.852	-1.43	0.211	-1.51	0.039	-1.01	0.949	-0.72
1431800_at	1300010F03Rik	RIKEN cDNA 1300010F03 gene	1.01	0.846	-1.4	0.242	-1.44	0.136	-1.65	0.345	-0.87
1459313_at	---	Transcribed locus	1.34	0.719	-1.84	0.405	-1.87	0.014	-2.5	0.291	-1.22
1427237_at	2410015M20Rik	RIKEN cDNA 2410015M20 gene	1.03	0.968	-2.39	0.26	-1.03	0.932	-2.27	0.372	-1.17
1422921_at	Vpreb3	pre-B lymphocyte gene 3	-1.31	0.177	-1.91	0.338	1.13	0.751	-2.9	0.044	-1.25
1459440_at	Nav3	Neuron navigator 3	-1.47	0.39	1.01	0.985	-1.38	0.519	-1.42	0.098	-0.82
1416167_at	Prdx4	peroxiredoxin 4	-1.11	0.351	-1.34	0.006	-1.3	0.012	1.7	0.009	-0.51
1428324_at	---	---	1.11	0.647	-1.67	0.087	-1.41	0.035	-1.39	0.111	-0.84
1456922_at	4933437K13Rik	RIKEN cDNA 4933437K13 gene	-1.71	0.103	1.13	0.829	-1.42	0.175	-2.13	0.017	-1.03
1439540_at	2-Mar	membrane-associated ring finger (C3HC4) 2	-1.06	0.894	-2	0.128	-1.03	0.884	3.15	0.242	-0.24
1420944_at	Zfp185	zinc finger protein 185	-1.25	0.568	-1.38	0.293	-1.12	0.755	1.22	0.727	-0.63
1436701_at	Trim61	tripartite motif-containing 61	1.08	0.926	-1.65	0.506	-1.38	0.295	-1.34	0.591	-0.82
1457580_at	Chd8	chromodomain helicase DNA binding protein 8	1	0.992	-1.17	0.613	-1.79	0.162	-1.43	0.241	-0.85
1454016_at	---	---	-1.06	0.9	-3.43	0.02	1.18	0.715	-1.54	0.466	-1.21
1456577_x_at	Pitrm1	pitrilysin metallepetidase 1	-1.18	0.58	-1.26	0.434	-1.28	0.154	1.91	0.303	-0.45
1439344_at	---	Transcribed locus	-1.14	0.588	-1.14	0.505	-1.51	0.051	1.08	0.631	-0.68
1449828_at	Ptgfr	prostaglandin F receptor	-1.29	0.682	-1.61	0.492	1.02	0.957	-1.39	0.053	-0.82
1423307_s_at	Tgoln1 /// Tgoln2	trans-golgi network protein /// trans-golgi network protein 2	-1.1	0.25	-1.43	0.001	-1.24	0.245	1.04	0.868	-0.68
1416042_s_at	Nasp	nuclear autoantigenic sperm protein (histone-binding)	-1.32	0.13	-1.32	0.026	-1.11	0.458	1.69	0.202	-0.51
1451186_at	Isg20l1	interferon stimulated exonuclease gene 20-like 1	-1.02	0.969	-1.35	0.656	-1.43	0.1	1.42	0.261	-0.6
1437564_at	Polg	polymerase (DNA directed), gamma	1.02	0.965	-1.25	0.784	-1.68	0.249	-1.28	0.116	-0.8
1442277_at	Chka	choline kinase alpha	-1.08	0.752	1.05	0.894	-2.26	0.006	-1.38	0.185	-0.92
1443867_at	Ankrd12	ankyrin repeat domain 12	-1.34	0.272	1.02	0.923	-1.53	0.205	-1.22	0.604	-0.77
1434766_at	---	Mus musculus, clone IMAGE:1512359, mRNA	-1.09	0.339	-1.32	0.052	-1.35	0.008	1.4	0.425	-0.59
1455094_s_at	Ube2g1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	-1.17	0.313	-1.17	0.183	-1.42	0.203	1.2	0.092	-0.64
1420741_x_at	2310069N01Rik	RIKEN cDNA 2310069N01 gene	-1.6	0.132	-1.96	0.125	1.28	0.534	-1.2	0.734	-0.87
1455748_at	Gpr178	G protein-coupled receptor 178	-1.96	0.198	1.15	0.531	-1.32	0.289	-1.78	0.386	-0.98
1445705_x_at	Dpp8	dipeptidylpeptidase 8	1.37	0.327	-1.6	0.495	-2.36	0.353	-1.46	0.594	-1.01
1450610_at	Ucn	urocortin	-1.37	0.388	-1.74	0.332	1.11	0.758	-2.95	0.178	-1.24
1427861_at	Arl6ip3	ADP-ribosylation factor-like 6 interacting protein 3	-1.18	0.587	-1.49	0.466	-1.11	0.519	1.08	0.714	-0.67
1454866_s_at	Clic6	chloride intracellular channel 6	-3.79	0.005	-1.45	0.381	1.47	0.148	-1.26	0.784	-1.26
1452138_a_at	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	-1.15	0.471	-2.54	0.049	1.15	0.621	-1.47	0.562	-1
1439294_at	D530008I22	hypothetical protein D530008I22	-1.11	0.628	-1.61	0.418	-1.12	0.55	1.1	0.671	-0.68
1439203_at	Satb1	Special AT-rich sequence binding protein 1	1.01	0.958	-1.29	0.417	-1.59	0.013	-2.29	0.344	-1.04
1435065_x_at	Vav2	Vav2 oncogene	-1.29	0.367	-2.86	0.05	1.29	0.287	-1.26	0.515	-1.03
1457586_at	Rasa2	RAS p21 protein activator 2	-1.19	0.403	1.12	0.757	-2.21	0.001	-1.65	0.142	-0.98
1446120_at	Uhmk1	U2AF homology motif (UHM) kinase 1	-1.24	0.225	1.13	0.663	-2.05	0.186	-1.04	0.95	-0.8
1449443_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	-1.02	0.894	-1.84	0.127	-1.11	0.603	1.24	0.085	-0.68
1438516_at	Rif1	Rap1 interacting factor 1 homolog (yeast)	-1.04	0.693	-1.4	0.215	-1.35	0.064	1.03	0.87	-0.69
1456390_at	---	---	-1.08	0.608	-1.19	0.061	-1.53	0.011	1.09	0.483	-0.68
1456384_at	Nlgn3	neuroligin 3	-1.17	0.826	1.18	0.78	-2.62	0.09	-1.54	0.643	-1.04
1418802_at	R74862	expressed sequence R74862	-1.07	0.828	-1.76	0.353	-1.09	0.755	1.18	0.031	-0.69
1456231_at	Pla2g3	phospholipase A2, group III	-1.12	0.101	-1.92	0.284	1.01	0.959	-1.13	0.429	-0.79
1446051_at	Gm1140	gene model 1140, (NCBI)	-1.55	0.573	-1.55	0.405	1.13	0.817	-1.21	0.742	-0.8
1418694_at	Kcmf1	potassium channel modulatory factor 1	-1.02	0.848	-1.38	0.057	-1.39	0.026	1.11	0.518	-0.67
1418496_at	Foxa1	forkhead box A1	-1.21	0.254	-2.44	0.014	1.18	0.235	-1.2	0.754	-0.92
1457515_at	Hipk1	Homeodomain interacting protein kinase 1	-1.16	0.5	-1.43	0.325	-1.16	0.435	1.81	0.232	-0.49
1418537_at	0610042E07Rik	RIKEN cDNA 0610042E07 gene	-1.56	0.116	-1.3	0.041	1.01	0.937	-1.39	0.165	-0.81
1453004_at	3110004L20Rik	RIKEN cDNA 3110004L20 gene	-1.23	0.297	-1.19	0.053	-1.31	0.166	3.98	0.162	0.06
1429431_at	Zfpn1a5	zinc finger protein, subfamily 1A, 5	-1.06	0.011	-1.24	0.165	-1.5	0.029	1.58	0.214	-0.55
1454410_at	9130414P19Rik	RIKEN cDNA 9130414P19 gene	-2.19	0.257	-1.07	0.938	1.03	0.868	-2.02	0.283	-1.06
1419918_at	Tmed7	transmembrane emp24 protein transport domain containing 7	-1.07	0.783	-1.09	0.492	-1.75	0.043	1.19	0.158	-0.68

1437589_x_at	Lime1	Lck interacting transmembrane adaptor 1	-1.77	0.003	-1.22	0.167	1.03	0.755	-1.42	0.334	-0.84
1440901_at	Dgkb	diacylglycerol kinase, beta	-1.21	0.064	-1.29	0.556	-1.22	0.483	1.11	0.827	-0.65
1453976_at	4432414F05Rik	RIKEN cDNA 4432414F05 gene	-1.2	0.447	-1.14	0.756	-1.41	0.332	1.22	0.462	-0.63
1451485_at	3300001P08Rik	RIKEN cDNA 3300001P08 gene	-1.03	0.834	-1.32	0.26	-1.44	0.215	1.02	0.93	-0.69
1446253_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	-1.56	0.038	-1.38	0.198	1.05	0.217	-1.19	0.674	-0.77
1439330_at	D230040J21Rik	RIKEN cDNA D230040J21 gene	-1.44	0.01	1.12	0.712	-1.66	0.085	-1.27	0.076	-0.81
1430538_at	2210013O21Rik	RIKEN cDNA 2210013O21 gene	-1.05	0.607	-1.23	0.047	-1.52	0	1.05	0.744	-0.69
1424405_at	Mbip	MAP3K12 binding inhibitory protein 1	-1.35	0.18	1.05	0.6	-1.59	0.002	-1.2	0.158	-0.77
1422099_a_at	Oprl1	opioid receptor-like 1	1.21	0.836	-1.6	0.289	-1.71	0.317	-1.21	0.743	-0.83
1455808_at	4922502D21Rik	RIKEN cDNA 4922502D21 gene	-1.16	0.473	-1	1	-1.78	0.374	1.25	0.384	-0.67
1427061_at	Rbbp8	retinoblastoma binding protein 8	-1.39	0.17	-1.03	0.819	-1.37	0.048	1.7	0.14	-0.52
1459304_at	A730054J21Rik	RIKEN cDNA A730054J21 gene	-1.55	0.475	-1.24	0.187	-1.03	0.909	2.08	0.273	-0.43
1460126_at	Usp34	Ubiquitin specific peptidase 34	1.21	0.184	-1.63	0.019	-1.66	0.027	-1.14	0.651	-0.81
1443681_at	AI595406	Expressed sequence AI595406	-1.29	0.483	-1.2	0.565	-1.24	0.383	1.24	0.431	-0.62
1421617_at	Trpm8	transient receptor potential cation channel, subfamily M, member 8	-2.36	0.431	1.43	0.232	-1.76	0.266	-2.33	0.079	-1.25
1428401_at	Zcchc3	zinc finger, CCHC domain containing 3	-1.16	0.242	-1.4	0.158	-1.18	0.031	1.26	0.329	-0.62
1430790_at	4930485G23Rik	RIKEN cDNA 4930485G23 gene	-2.1	0.403	1.14	0.623	-1.24	0.67	-1.94	0.351	-1.03
1418517_at	Irx3	Iroquois related homeobox 3 (Drosophila)	-1.28	0.573	-3.28	0.019	1.34	0.215	-1.53	0.254	-1.19
1445896_at	2810433D01Rik	RIKEN cDNA 2810433D01 gene	1.07	0.505	-1.25	0.73	-1.8	0.047	-4.05	0.008	-1.51
1457447_at	Rb1	Retinoblastoma 1	-1.11	0.409	-1.16	0.236	-1.52	0.109	1.29	0.269	-0.62
1456809_at	---	Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830435O18	-1.41	0.015	-1.52	0.145	1.06	0.873	-1.03	0.878	-0.73
1459887_at	---	Transcribed locus	1.13	0.738	-1.68	0.003	-1.44	0.139	-1.19	0.456	-0.79
1425492_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	-1.07	0.663	-1.24	0.011	-1.46	0.016	1.11	0.557	-0.67
1445512_at	---	---	1.07	0.753	-1.36	0.335	-1.63	0.123	-1.09	0.712	-0.75
1434053_x_at	Atp5k	ATP synthase, H+ transporting, mitochondrial F1F0 complex, subunit e	-1.19	0.003	-1.3	0.069	-1.23	0.082	1.06	0.257	-0.67
1432473_a_at	Abca14	ATP-binding cassette, sub-family A (ABC1), member 14	-2.35	0.063	1.15	0.546	-1.18	0.653	-1.3	0.658	-0.92
1444759_at	Prickle1	prickle like 1 (Drosophila)	-1.84	0.154	-1.51	0.481	1.22	0.826	-1.43	0.543	-0.89
1447174_at	Dach1	Dachshund 1 (Drosophila)	-1.26	0.319	-1.02	0.982	-1.55	0.13	1.48	0.482	-0.59
1456408_x_at	4933439C10Rik	RIKEN cDNA 4933439C10 gene	-1.66	0.022	1.05	0.922	-1.29	0.224	-1.7	0.232	-0.9
1453667_at	1700065D16Rik	RIKEN cDNA 1700065D16 gene	1.37	0.589	-2.19	0.269	-1.67	0.242	-1.17	0.726	-0.91
1425314_at	Gpr98	G protein-coupled receptor 98	-1.58	0.418	1.07	0.786	-1.38	0.088	-1.17	0.806	-0.77
1448042_s_at	Rnf2	ring finger protein 2	-1.59	0.05	1.06	0.904	-1.35	0.537	-1.87	0.547	-0.94
1455807_at	Tspyl5	testis-specific protein, Y-encoded-like 5	-1.17	0.374	-1.56	0.228	-1.08	0.554	1.92	0.137	-0.47
1447156_at	Chm	Choroidermia	1.05	0.768	-1.43	0.006	-1.47	0.028	-1.5	0.264	-0.84
1440392_at	Akap13	A kinase (PRKA) anchor protein 13	-1.2	0.27	-1.13	0.526	-1.43	0.185	1.74	0.168	-0.5
1459245_s_at	Grid2	glutamate receptor, ionotropic, delta 2	-2.24	0.295	-1.01	0.965	-1.01	0.746	1.73	0.345	-0.63
1456717_at	Tead1	TEA domain family member 1	-1.04	0.961	1.12	0.84	-2.98	0.209	-1.32	0.129	-1.05
1440264_at	---	---	1.05	0.879	-1.83	0.129	-1.22	0.295	-2.29	0.069	-1.07
1443972_at	AI465300	expressed sequence AI465300	-1.55	0.426	1.03	0.969	-1.33	0.489	-2.47	0.017	-1.08
1447606_x_at	Aqp11	aquaporin 11	-1.75	0.206	-1.01	0.926	-1.16	0.57	1.3	0.216	-0.65
1454966_at	Itga8	integrin alpha 8	-1.13	0.505	-1.16	0.26	-1.48	0.045	1.11	0.78	-0.66
1433109_at	Mif	macrophage migration inhibitory factor	-1.92	0.113	-1.01	0.986	-1.1	0.791	1.07	0.847	-0.74
1454063_at	4933412E24Rik	RIKEN cDNA 4933412E24 gene	-1.48	0.609	-1.75	0.322	1.18	0.796	-1.44	0.263	-0.87
1420118_s_at	---	---	-1.54	0.648	1.14	0.842	-1.56	0.142	-1.01	0.964	-0.74
1421363_at	Cyp2c39	cytochrome P450, family 2, subfamily c, polypeptide 39	-1.39	0.677	1.09	0.564	-1.62	0.44	-1.11	0.861	-0.76
1438553_x_at	4930453N24Rik	RIKEN cDNA 4930453N24 gene	-1.07	0.75	-1.21	0.266	-1.49	0.032	1.16	0.455	-0.66
1424944_at	Pcp2	Purkinje cell protein 2 (L7)	-1.14	0.832	1.08	0.903	-2.15	0.251	-1.23	0.525	-0.86
1445815_at	Fzd8	frizzled homolog 8 (Drosophila)	1.39	0.211	-1.97	0.128	-1.9	0.055	-1.58	0.351	-1.02
1442352_at	9430091N11Rik	RIKEN cDNA 9430091N11 gene	-1.49	0.568	1.42	0.515	-3.01	0.074	-1.34	0.492	-1.1
1450750_a_at	Nr4a2	nuclear receptor subfamily 4, group A, member 2	-1.69	0.144	-1.02	0.966	-1.18	0.439	1.07	0.699	-0.7
1453771_at	Gulp1	GULP, engulfment adaptor PTB domain containing 1	1.12	0.701	-1.82	0.105	-1.32	0.133	-1.3	0.204	-0.83
1453656_a_at	4933431G14Rik	RIKEN cDNA 4933431G14 gene	-1.01	0.961	-1.98	0.06	-1.07	0.886	1.16	0.661	-0.73
1441707_at	---	---	-1.13	0.543	1.01	0.957	-1.87	0.03	-1.33	0.456	-0.83

1447122_at	---	---	-1.06	0.44	-1.24	0.064	-1.47	0.06	1.14	0.393	-0.66
1453716_at	4930480K23Rik	RIKEN cDNA 4930480K23 gene	-1.24	0.522	-1.94	0.087	1.1	0.67	-1.19	0.003	-0.82
1432593_at	4933428P19Rik	RIKEN cDNA 4933428P19 gene	-1.34	0.116	-1.22	0.497	-1.16	0.422	2.17	0.243	-0.39
1424717_at	Mis12	MIS12 homolog (yeast)	-1.46	0.282	-1.14	0.373	-1.15	0.302	1.7	0.248	-0.51
1460401_at	Edem3	ER degradation enhancer, mannosidase alpha-like 3	-1.13	0.229	-1.21	0.235	-1.39	0.059	1.05	0.272	-0.67
1449030_at	Syn2	synapsin II	-1.42	0.333	-1.16	0.664	-1.17	0.718	1.85	0.26	-0.47
1431346_at	6330405D24Rik	RIKEN cDNA 6330405D24 gene	-1.17	0.809	-1.54	0.346	-1.09	0.833	1.34	0.216	-0.61
1440272_at	Eif2s1	Eukaryotic translation initiation factor 2, subunit 1 alpha	-1.49	0.132	1.11	0.541	-1.56	0.097	-1.14	0.723	-0.77
1439763_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	-1	0.999	-1.17	0.738	-1.74	0.239	1.41	0.353	-0.63
1441473_at	LOC666775 /// LOC	hypothetical protein LOC666775 /// hypothetical protein LOC671556	-1.07	0.892	-1.93	0.265	-1.03	0.81	1.02	0.945	-0.75
1420930_s_at	Ctnnal1	catenin (cadherin associated protein), alpha-like 1	-1.14	0.196	-1.23	0.393	-1.35	0.052	1.03	0.881	-0.67
1445079_at	D15Ertd320e	DNA segment, Chr 15, ERATO Doi 320, expressed	-1.29	0.337	-1.62	0.401	1.04	0.913	-1.48	0.387	-0.84
1443716_at	---	---	-1.05	0.86	-1.39	0.651	-1.33	0.207	1.15	0.48	-0.65
1439177_at	---	Transcribed locus	-1.22	0.435	-1.18	0.681	-1.31	0.24	1.13	0.864	-0.65
1422349_at	Ccr1l1	chemokine (C-C motif) receptor 1-like 1	-1.52	0.022	-1.41	0.452	1.06	0.896	-1.08	0.886	-0.74
1424087_at	1810042K04Rik	RIKEN cDNA 1810042K04 gene	-1.41	0.277	1.03	0.878	-1.46	0.297	-1.08	0.575	-0.73
1444308_at	---	---	-1.03	0.885	-1.6	0.194	-1.2	0.455	1.64	0.282	-0.55
1447121_at	0610038K03Rik	RIKEN cDNA 0610038K03 gene	1	0.993	-1.6	0.032	-1.25	0.255	-1.33	0.374	-0.79
1425117_at	0610012D14Rik	RIKEN cDNA 0610012D14 gene	-1.21	0.295	-1.21	0.057	-1.3	0.529	1.44	0.501	-0.57
1423498_at	Aldoa-ps1	aldolase 1, A isoform, pseudogene 1	1.14	0.508	-2.06	0.29	-1.25	0.616	-1.08	0.709	-0.81
1438300_at	4921511I16Rik	RIKEN cDNA 4921511I16 gene	-1.33	0.431	-1.05	0.879	-1.39	0.08	1.14	0.059	-0.66
1445974_at	---	Transcribed locus	-1.13	0.749	-1.19	0.796	-1.43	0.601	1.07	0.834	-0.67
1455454_at	Akr1c19	aldo-keto reductase family 1, member C19	-1.15	0.273	-1.45	0.325	-1.15	0.478	1	0.984	-0.69
1457913_at	5730601F06Rik	RIKEN cDNA 5730601F06 gene	1.12	0.176	-1.13	0.264	-2.37	0.01	-1.62	0.215	-1
1441760_at	LOC243302 /// LOC	similar to 40S ribosomal protein S25 /// similar to 40S ribosomal protein S25 /// hy	1.33	0.554	-3.01	0.312	-1.3	0.093	-1.16	0.506	-1.04
1448002_x_at	2610001J05Rik	RIKEN cDNA 2610001J05 gene	-1.19	0.694	-1.9	0.358	1.06	0.872	-1.54	0.381	-0.89
1453548_at	---	---	-1.43	0.007	-1.62	0.359	1.11	0.757	-1.33	0.602	-0.82
1419620_at	Pttg1	pituitary tumor-transforming 1	-1.3	0.27	-1.57	0.021	1.02	0.879	-1.2	0.435	-0.76
1440885_at	Evl	Ena-vasodilator stimulated phosphoprotein	-1.54	0.025	1	0.99	-1.29	0.219	-1.95	0.113	-0.94
1455508_at	A530082C11Rik	RIKEN cDNA A530082C11 gene	-1.15	0.311	-1.38	0.093	-1.2	0.179	1.2	0.194	-0.63
1440800_at	LOC665193	hypothetical protein LOC665193	-1.06	0.864	-1.29	0.491	-1.42	0.302	1.21	0.526	-0.64
1438581_at	4932439K10Rik	RIKEN cDNA 4932439K10 gene	-1.64	0.391	1.33	0.645	-2.06	0.038	-1.27	0.682	-0.91
1457374_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	-1.15	0.303	1.09	0.649	-2.15	0.016	-1.43	0.198	-0.91
1453987_at	Btbd5	BTB (POZ) domain containing 5	1.17	0.852	-2.13	0.067	-1.28	0.173	-1.66	0.011	-0.97
1459020_at	Amigo1	adhesion molecule with Ig like domain 1	-1.5	0.145	-1.04	0.923	-1.25	0.221	1.37	0.511	-0.61
1453779_at	1700020L24Rik	RIKEN cDNA 1700020L24 gene	-1.26	0.624	-4.99	0.012	1.43	0.361	-1.45	0.366	-1.56
1425768_at	Diablo	diablo homolog (Drosophila)	-2.14	0.149	-1.12	0.73	1.07	0.672	-1.05	0.868	-0.81
1446413_at	4930555G07Rik	RIKEN cDNA 4930555G07 gene	-1.08	0.836	-1.28	0.448	-1.39	0.52	1.84	0.284	-0.48
1428561_at	2610002J23Rik	RIKEN cDNA 2610002J23 gene	-1.21	0.017	-1.23	0.157	-1.27	0.055	1.02	0.842	-0.67
1419694_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	1.11	0.725	-2.71	0.029	-1.05	0.929	-1.36	0.051	-1
1457067_at	Vps4b	Vacuolar protein sorting 4b (yeast)	-1.1	0.495	-1.39	0.395	-1.25	0.14	1.1	0.57	-0.66
1422605_at	Ppp1r1a	protein phosphatase 1, regulatory (inhibitor) subunit 1A	1	0.987	-2.1	0.127	-1.05	0.881	-1.89	0.282	-1.01
1419453_at	Uchl5	ubiquitin carboxyl-terminal esterase L5	-1.22	0.542	-1.2	0.558	-1.29	0.075	1.06	0.809	-0.66
1459168_at	Zfp521	Zinc finger protein 521	-1.35	0.392	-1.1	0.778	-1.29	0.17	1.34	0.437	-0.6
1440586_at	B430203I24Rik	RIKEN cDNA B430203I24 gene	-1.16	0.015	1.11	0.744	-2.18	0.022	-1.12	0.553	-0.84
1432817_x_at	4930413G21Rik	RIKEN cDNA 4930413G21 gene	1.2	0.644	-1.57	0.086	-1.7	0.277	-1.19	0.78	-0.81
1432110_at	4930402F06Rik	RIKEN cDNA 4930402F06 gene	1.14	0.895	-1.34	0.394	-1.84	0.143	-1.15	0.432	-0.8
1434905_at	BC064011	cDNA sequence BC064011	-1.01	0.976	-1.13	0.769	-1.8	0.073	2.2	0.027	-0.43
1436253_at	Pex16	peroxisome biogenesis factor 16	1.37	0.473	-1.39	0.104	-2.91	0.132	-1.13	0.688	-1.02
1422288_at	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	-1.01	0.952	-1.51	0.076	-1.29	0.355	1.11	0.636	-0.67
1446218_at	Ppfia2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	-1.88	0.24	-1.23	0.397	1.09	0.816	-1.26	0.524	-0.82
1445662_x_at	---	Transcribed locus	-1.74	0.142	1.04	0.852	-1.23	0.333	-1.47	0.104	-0.85
1458682_at	D130059P03Rik	RIKEN cDNA D130059P03 gene	1.68	0.382	-4.53	0.051	-1.89	0.184	-1.01	0.989	-1.44

1444767_at	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	1.24	0.726	-1.59	0.289	-1.78	0.097	-1.43	0.334	-0.89
1421423_at	Prlpo	prolactin-like protein O	-2.09	0.343	-1.65	0.147	1.35	0.396	-1.32	0.577	-0.93
1442722_at	---	Transcribed locus	-2.32	0.315	-1.56	0.164	1.36	0.634	-1.3	0.73	-0.95
1439263_at	Fin15	fibroblast growth factor inducible 15	-1.13	0.481	-1.27	0.059	-1.32	0.376	1.16	0.504	-0.64
1454010_a_at	1700025E21Rik	RIKEN cDNA 1700025E21 gene	-1.31	0.22	1.08	0.884	-1.69	0.214	-2.2	0.059	-1.03
1420554_a_at	Rac3	RAS-related C3 botulinum substrate 3	-1.27	0.267	-2.01	0.058	1.14	0.709	-1.14	0.539	-0.82
1438927_x_at	LOC227054 /// Rpl2	similar to 60S ribosomal protein L23a /// ribosomal protein L23a /// hypothetical ge	-1.88	0.44	-1.65	0.48	1.29	0.461	-2.21	0.1	-1.11
1441556_at	Baz2b	Bromodomain adjacent to zinc finger domain, 2B	1.07	0.37	-1.36	0.083	-1.59	0.021	-1.72	0.015	-0.9
1439840_at	A430088C08Rik	RIKEN cDNA A430088C08 gene	1.01	0.955	-1.28	0.286	-1.56	0.088	-1.77	0.304	-0.9
1437347_at	Ednrb	endothelin receptor type B	1.06	0.632	-1.06	0.797	-2.36	0.005	-2.63	0.008	-1.24
1433115_at	5730552O08Rik	RIKEN cDNA 5730552O08 gene	-1.13	0.823	-1.11	0.523	-1.55	0.361	1.64	0.468	-0.54
1456810_at	Vps54	vacuolar protein sorting 54 (yeast)	-1.4	0.105	1.14	0.595	-1.74	0.075	-1.11	0.701	-0.78
1431519_at	4933406L23Rik	RIKEN cDNA 4933406L23 gene	1.14	0.763	-1.75	0.282	-1.4	0.199	-1.49	0.424	-0.87
1447718_at	Pde4b	phosphodiesterase 4B, cAMP specific	-1.18	0.829	-1.85	0.287	1.04	0.933	-3.45	0.387	-1.36
1437821_at	Diap1	Diaphanous homolog 1 (Drosophila)	1.08	0.493	-1.31	0.313	-1.71	0.007	-1.33	0.316	-0.82
1430622_at	4833423F13Rik	RIKEN cDNA 4833423F13 gene	-1.11	0.729	1.07	0.836	-2.15	0.033	-2.67	0.053	-1.22
1416324_s_at	Kctd20	potassium channel tetramerisation domain containing 20	-1.25	0.372	-1.14	0.236	-1.33	0.023	1.03	0.842	-0.67
1445164_at	2210418O10Rik	RIKEN cDNA 2210418O10 gene	-1.23	0.684	-1.02	0.978	-1.57	0.303	1.52	0.54	-0.57
1446626_at	D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	-1.12	0.746	-1.15	0.613	-1.51	0.11	1.93	0.111	-0.46
1425606_at	Slc5a8	solute carrier family 5 (iodide transporter), member 8	-1.31	0.473	-1.31	0.558	-1.1	0.775	2.14	0.415	-0.4
1436396_at	D430033N04Rik	RIKEN cDNA D430033N04 gene	-1.23	0.436	-1.51	0.392	-1.05	0.823	2.86	0.092	-0.23
1445505_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	-1.37	0.587	1.03	0.962	-1.5	0.469	-1.63	0.324	-0.87
1443604_at	---	---	-2.17	0.467	-1.64	0.282	1.36	0.405	-1.79	0.156	-1.06
1431674_at	2610303G11Rik	RIKEN cDNA 2610303G11 gene	-1.27	0.558	-1.64	0.022	1.04	0.866	-1.74	0.443	-0.9
1455002_at	Ptp4a1	protein tyrosine phosphatase 4a1	-1.15	0.326	-1.21	0.304	-1.36	0.099	1.31	0.278	-0.6
1459518_at	Gm489	Gene model 489, (NCBI)	-1.96	0.237	-1.1	0.725	1.01	0.948	-1.37	0.48	-0.86
1446305_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.63	0.516	1.05	0.943	-1.3	0.596	-1.59	0.217	-0.87
1441178_at	Dtwd2	DTW domain containing 2	-1.35	0.477	-1.16	0.423	-1.21	0.55	1.09	0.701	-0.66
1441617_at	Pcqap	positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated protein	-1.28	0.044	1.01	0.924	-1.55	0.092	-1.26	0.013	-0.77
1418176_at	Vdr	vitamin D receptor	-1.19	0.031	-1.53	0.397	-1.07	0.521	1.3	0.283	-0.62
1453104_at	Mapk1	mitogen activated protein kinase 1	-1.24	0.166	-1.21	0.048	-1.25	0.029	1.03	0.767	-0.67
1438213_at	A830018L16Rik	RIKEN cDNA A830018L16 gene	-1.44	0.582	-2.26	0.197	1.3	0.281	-1.35	0.622	-0.94
1429483_at	Ndp52	nuclear domain 10 protein 52	-1.45	0.564	-1.49	0.509	1.07	0.85	-1.32	0.479	-0.8
1454653_at	Cpne9	copine family member IX	-1.8	0.109	-1.23	0.534	1.07	0.48	-1.3	0.186	-0.82
1458360_at	Spock2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	-1.7	0.244	-1.4	0.387	1.13	0.767	-1.27	0.663	-0.81
1455037_at	Plxna2	plexin A2	-1.23	0.342	-1.19	0.31	-1.28	0.351	1.24	0.567	-0.62
1456986_at	Zbtb16	Zinc finger and BTB domain containing 16	1.02	0.98	-1.19	0.751	-1.74	0.286	-2.07	0.147	-0.99
1446346_at	---	---	-1.23	0.608	1.01	0.983	-1.61	0.361	-1.42	0.423	-0.81
1418668_at	Acsm1	acyl-CoA synthetase medium-chain family member 1	-1.19	0.527	-1.1	0.19	-1.46	0.218	1.75	0.201	-0.5
1446161_at	Taf11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.3	0.575	-1.52	0.335	1.01	0.982	-1.04	0.953	-0.71
1428519_at	2610528E23Rik	RIKEN cDNA 2610528E23 gene	-1.08	0.755	-1.46	0.144	-1.22	0.167	1.26	0.373	-0.62
1440213_a_at	2010001M06Rik	RIKEN cDNA 2010001M06 gene	-1.1	0.693	-1.26	0.465	-1.38	0.151	1	0.99	-0.68
1440703_at	2810429I04Rik	RIKEN cDNA 2810429I04 gene	-1.83	0.219	1.21	0.546	-1.47	0.306	-1.79	0.215	-0.97
1442426_at	Wapal	wings apart-like homolog (Drosophila)	-1.25	0.039	-1.28	0.184	-1.17	0.212	1.62	0.277	-0.52
1433271_at	9530004M16Rik	RIKEN cDNA 9530004M16 gene	1.04	0.934	-1.36	0.028	-1.51	0.371	-1.12	0.697	-0.74
1421325_at	Pla2g2f	phospholipase A2, group IIF	-1.11	0.855	-1.51	0.313	-1.15	0.818	1.34	0.587	-0.61
1431410_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	1.03	0.964	-1.72	0.404	-1.21	0.404	-1.84	0.398	-0.93
1442464_at	Fbxl20	F-box and leucine-rich repeat protein 20	-1.51	0.232	-1.22	0.075	-1.05	0.761	1.01	0.957	-0.69
1444825_at	---	---	-3.35	0.094	-1.35	0.315	1.4	0.29	-1.02	0.963	-1.08
1435510_at	Ppm1h	protein phosphatase 1H (PP2C domain containing)	-1.27	0.292	-1.55	0.046	1	0.989	-1.62	0.159	-0.86
1441966_at	Trpm3	transient receptor potential cation channel, subfamily M, member 3	-1.45	0.411	-1.13	0.759	-1.16	0.213	1.33	0.101	-0.6
1431788_at	1700008G05Rik	RIKEN cDNA 1700008G05 gene	-1.58	0.111	-1.07	0.78	-1.15	0.208	1.08	0.853	-0.68
1459982_a_at	---	---	-1.31	0.122	-1.41	0.641	-1.04	0.883	1.12	0.775	-0.66

1449161_at	Edn2	endothelin 2	-1.38	0.588	-1.03	0.941	-1.35	0.323	1.45	0.2	-0.58
1432735_at	1700017H01Rik	RIKEN cDNA 1700017H01 gene	-1.12	0.721	-2.07	0.319	1.06	0.725	-1.25	0.203	-0.84
1441863_x_at	---	---	-1.5	0.332	-1.27	0.589	-1.02	0.972	1.89	0.32	-0.47
1427738_at	D0Kist2	DNA segment, KIST 2	-1.52	0.495	1.14	0.802	-1.56	0.296	-1.78	0.351	-0.93
1457811_at	---	---	1.17	0.036	-1.51	0.008	-1.67	0.102	-1.24	0.326	-0.81
1416490_at	Tmed6	transmembrane emp24 protein transport domain containing 6	-1.29	0.345	1.04	0.949	-1.6	0.201	-1.38	0.186	-0.81
1444186_at	2900006B13Rik	RIKEN cDNA 2900006B13 gene	-1.52	0.555	-1.41	0.287	1.07	0.89	-1.25	0.56	-0.78
1443789_x_at	Cox8c	cytochrome c oxidase, subunit VIIIc	-1.55	0.477	-2.08	0.302	1.31	0.382	-1.32	0.647	-0.91
1429904_at	4930507A01Rik	RIKEN cDNA 4930507A01 gene	1.08	0.898	-1.99	0.333	-1.17	0.382	-1.25	0.285	-0.83
1425172_at	Rho	rhodopsin	-1.14	0.703	-1.47	0.55	-1.13	0.788	1.35	0.515	-0.6
1452315_at	Kif11	kinesin family member 11	-1.14	0.755	-1.39	0.466	-1.18	0.079	2.79	0.284	-0.23
1420734_at	Ppp1r3f	protein phosphatase 1, regulatory (inhibitor) subunit 3F	-1.19	0.131	-1.94	0.29	1.08	0.672	-1.09	0.763	-0.78
1453371_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	1.11	0.568	-1.06	0.689	-2.63	0.006	-1.85	0.05	-1.11
1427584_at	Amot	angiomotin	-1.61	0.132	-1.39	0.489	1.1	0.751	-1.27	0.452	-0.79
1425246_at	0610008F07Rik	RIKEN cDNA 0610008F07 gene	-1.22	0.433	-1.36	0.134	-1.13	0.652	1.14	0.491	-0.64
1442080_at	Creb3l2	CAMP responsive element binding protein 3-like 2	-1.19	0.307	-1.12	0.472	-1.42	0.146	1.41	0.004	-0.58
1420881_at	Nsd1	nuclear receptor-binding SET-domain protein 1	-1.18	0.85	-2.08	0.287	1.11	0.793	-1.87	0.191	-1
1460714_at	Tcfcp2l1	Transcription factor CP2-like 1	-1.38	0.065	-1.81	0.094	1.16	0.718	-1.44	0.562	-0.87
1426362_at	Tmem144	transmembrane protein 144	-1.28	0.073	-1.48	0.018	-1.02	0.927	1.47	0.322	-0.58
1436155_at	Nmnat2	nicotinamide nucleotide adenylyltransferase 2	-1.08	0.891	-1.27	0.243	-1.38	0.081	1.33	0.31	-0.6
1456682_at	Lonrf2	LON peptidase N-terminal domain and ring finger 2	1.04	0.961	-1.33	0.547	-1.54	0.106	-2.68	0.197	-1.13
1430162_at	3830417A13Rik	RIKEN cDNA 3830417A13 gene	-1.47	0.624	-1.14	0.807	-1.13	0.688	1.16	0.842	-0.65
1450485_at	Sox3	SRY-box containing gene 3	-1.19	0.767	-4.35	0.097	1.37	0.541	-1.13	0.705	-1.32
1434670_at	Kif5a	kinesin family member 5A	-1.06	0.923	1.05	0.906	-2.24	0.175	-1.43	0.185	-0.92
1445184_at	9130019O22Rik	RIKEN cDNA 9130019O22 gene	-1.09	0.708	-1.91	0.345	-1	0.997	1.2	0.771	-0.7
1434020_at	Pdap1	PDGFA associated protein 1	-1.04	0.793	-1.44	0.017	-1.28	0.226	1.46	0.252	-0.57
1460484_at	Ttl	tubulin tyrosine ligase	-1.16	0.214	-1.59	0.505	-1.05	0.806	1.07	0.867	-0.69
1451739_at	Klf5	Kruppel-like factor 5	-1.09	0.524	-1.44	0.085	-1.21	0.185	1.52	0.489	-0.56
1436082_at	Myef2	Myelin basic protein expression factor 2, repressor	-1.34	0.477	-1.03	0.934	-1.38	0.256	1.71	0.369	-0.51
1442509_at	Evi5	Ecotropic viral integration site 5	-1.19	0.013	-1.07	0.71	-1.5	0.014	3.03	0.232	-0.18
1438548_x_at	Rhbdd3	rhomboid domain containing 3	-1.14	0.504	-1.15	0.246	-1.44	0.088	1.18	0.628	-0.64
1421893_a_at	Tpp2	tripeptidyl peptidase II	-1.34	0.304	-1.86	0	1.15	0.52	-1.11	0.612	-0.79
1442192_at	Tyms	thymidylate synthase	-1.07	0.811	-1.08	0.818	-1.72	0.028	1.9	0.315	-0.49
1453447_at	1700109H08Rik	RIKEN cDNA 1700109H08 gene	-1.95	0.168	1.03	0.947	-1.12	0.816	-2.31	0.052	-1.09
1424306_at	Elovl4	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	-1.12	0.845	1.1	0.804	-2.2	0.135	-1.03	0.876	-0.81
1431409_at	C030015A19Rik	RIKEN cDNA C030015A19 gene	-1.23	0.546	-1.24	0.428	-1.21	0.258	1.03	0.896	-0.66
1452310_at	Tada2l	transcriptional adaptor 2 (ADA2 homolog, yeast)-like	-1.17	0.043	-1.24	0.141	-1.28	0.205	1.39	0.102	-0.58
1434804_at	Sec15l2	SEC15-like 2 (S. cerevisiae)	-1.11	0.51	-1.05	0.509	-1.71	0.001	1.03	0.81	-0.71
1417347_at	Pycard	PYD and CARD domain containing	-1.44	0.173	1.05	0.884	-1.44	0.054	-2.4	0.245	-1.06
1447481_at	Setd5	SET domain containing 5	1.09	0.757	-1.68	0.185	-1.32	0.256	-1.05	0.778	-0.74
1422252_a_at	Cdc25c	cell division cycle 25 homolog C (S. cerevisiae)	-1.48	0.174	-1	0.989	-1.3	0.654	2.85	0.127	-0.23
1446409_at	Gtdc1	glycosyltransferase-like domain containing 1	-2.18	0.21	-1.37	0.379	1.25	0.554	-1.01	0.978	-0.83
1417508_at	Rnf19	ring finger protein (C3HC4 type) 19	-1.22	0.027	-1.19	0.082	-1.28	0.016	1.66	0.284	-0.51
1424219_at	Mrm1	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	-1.21	0.286	-1.6	0.269	-1.01	0.956	2.14	0.133	-0.42
1435564_at	C230078M08Rik	RIKEN cDNA C230078M08 gene	-2.15	0.277	1.14	0.812	-1.19	0.621	-2.66	0.197	-1.21
1442452_at	Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (huma	-1.19	0.525	-1.5	0.321	-1.07	0.636	2.91	0.186	-0.21
1442481_at	LOC675578	hypothetical protein LOC675578	1.25	0.515	-3.05	0.03	-1.16	0.251	-1.12	0.4	-1.02
1459106_at	---	PREDICTED: Mus musculus hypothetical protein LOC622817 (LOC622817), mR	-1.6	0.559	1.09	0.911	-1.38	0.461	-1.14	0.418	-0.76
1429955_at	5031434O11Rik	RIKEN cDNA 5031434O11 gene	-1.23	0.705	-1.63	0.407	1.02	0.931	-1.08	0.742	-0.73
1459385_at	Camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	-1.17	0.772	-2.49	0.187	1.18	0.684	-1.11	0.803	-0.9
1457093_at	Gapvd1	GTPase activating protein and VPS9 domains 1	-1.3	0.152	-1.28	0.191	-1.12	0.373	1.1	0.394	-0.65
1427042_at	Mal2	mal, T-cell differentiation protein 2	-1.19	0.305	-1.21	0.282	-1.3	0.037	1.58	0.622	-0.53
1454272_at	9630015K15Rik	RIKEN cDNA 9630015K15 gene	-3.62	0.279	1.29	0.633	-1.14	0.808	-1.88	0.024	-1.34

1444541_at	Myo9a	Myosin IXa	-1.47	0.009	-1.01	0.945	-1.29	0.028	1.17	0.15	-0.65
1441704_at	Plekha5	Pleckstrin homology domain containing, family A member 5	-1.2	0.664	1.11	0.818	-2	0.019	-1.58	0.323	-0.92
1447468_at	---	Transcribed locus	-1.35	0.638	1.3	0.545	-2.51	0.19	-1.43	0.657	-1
1454262_at	1700124P09Rik	RIKEN cDNA 1700124P09 gene	-1.62	0.186	-1.13	0.752	-1.06	0.739	1.1	0.637	-0.68
1431184_a_at	4930503B20Rik	RIKEN cDNA 4930503B20 gene	-1.24	0.681	-1.62	0.133	1.02	0.976	-1.54	0.415	-0.85
1429647_at	1700027L20Rik	RIKEN cDNA 1700027L20 gene	1.46	0.611	-1.79	0.272	-2.37	0.044	-1.71	0.373	-1.1
1438788_at	D5Wsu152e	DNA segment, Chr 5, Wayne State University 152, expressed	1.02	0.747	-1.36	0.087	-1.47	0.043	-1.32	0.197	-0.78
1432221_at	5330417H12Rik	RIKEN cDNA 5330417H12 gene	-1.5	0.421	-1.09	0.799	-1.16	0.665	1.75	0.241	-0.5
1441149_at	---	---	1.3	0.052	-1.38	0.42	-2.41	0.023	-1.41	0.682	-0.97
1441035_at	Kcne1	potassium voltage-gated channel, Isk-related subfamily, member 1	-2.12	0.04	1.26	0.673	-1.4	0.134	-1.22	0.138	-0.87
1458239_at	---	---	-1.24	0.543	-1.29	0.592	-1.16	0.379	1.35	0.281	-0.59
1453539_at	Alkbh8	alkB, alkylation repair homolog 8 (E. coli)	-1.09	0.562	-1.72	0.31	-1.06	0.723	1.35	0.59	-0.63
1416970_a_at	Cox7a2	cytochrome c oxidase, subunit VIIa 2	-1.14	0.004	-1.26	0.081	-1.29	0	1.03	0.728	-0.66
1447760_x_at	Ehf	ets homologous factor	1.02	0.968	-1.22	0.149	-1.64	0.376	-1.82	0.164	-0.92
1458470_at	---	---	1.04	0.945	-1.59	0.398	-1.29	0.114	-1.28	0.357	-0.78
1442681_at	Tsen2	TRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	-1.26	0.351	-1.22	0.616	-1.2	0.384	1.35	0.245	-0.58
1431809_at	4932442L08Rik	RIKEN cDNA 4932442L08 gene	-1.01	0.979	-1.27	0.667	-1.5	0.409	1.6	0.242	-0.55
1420968_at	Btbd14b	BTB (POZ) domain containing 14B	-1.12	0.884	-1.73	0.005	-1.03	0.943	1.45	0.451	-0.61
1459656_at	---	PREDICTED: Mus musculus similar to potassium voltage-gated channel, subfam	1.39	0.689	-2.14	0.191	-1.71	0.264	-2.27	0.135	-1.18
1445530_at	5330401P04Rik	RIKEN cDNA 5330401P04 gene	-1.32	0.541	1.2	0.242	-2.03	0.292	-1.4	0.413	-0.89
1445910_at	C79999	expressed sequence C79999	-1.17	0.591	-1.33	0.507	-1.2	0.547	1.08	0.734	-0.65
1440101_at	---	---	-1.3	0.02	-1.19	0.723	-1.2	0.698	2.01	0.164	-0.42
1427276_at	Smc4	structural maintenance of chromosomes 4	-1.23	0.167	-1.14	0.506	-1.32	0.126	1.72	0.353	-0.49
1456138_at	Lypd6	LY6/PLAUR domain containing 6	-1.02	0.821	-1.74	0.312	-1.13	0.552	1.14	0.537	-0.69
1426408_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	-1.1	0.123	-1.3	0.104	-1.3	0.134	1.2	0.461	-0.63
1443185_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	-1.33	0.071	1.07	0.863	-1.61	0.102	-2.19	0.145	-1.02
1459683_at	LOC218695	similar to spermatogenic cell-specific gene 2	-2.26	0.174	1.26	0.587	-1.35	0.364	-1.1	0.814	-0.86
1437801_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// similar to	-1.04	0.806	-1.27	0.224	-1.43	0.319	1.02	0.856	-0.68
1442949_at	Nfkb1	Nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	-1.41	0.366	-1.39	0.419	1.02	0.948	-1.96	0.466	-0.94
1450365_at	Myoz3	myozenin 3	-1.19	0.724	-1.63	0.438	-1.01	0.989	1.6	0.123	-0.56
1444110_at	Tcn2	transcobalamin 2	-1.58	0.183	1.16	0.339	-1.54	0.188	-1.36	0.092	-0.83
1420405_at	Slco1a4	solute carrier organic anion transporter family, member 1a4	-1.04	0.9	-1.85	0.126	-1.06	0.796	1.54	0.143	-0.6
1434962_x_at	Ccl27	chemokine (C-C motif) ligand 27	-1.18	0.035	-1.2	0.497	-1.31	0.031	1.09	0.529	-0.65
1426270_at	Smc5	structural maintenance of chromosomes 5	-1.55	0.111	-1.06	0.661	-1.17	0.397	1.23	0.283	-0.64
1443953_at	Tex2	testis expressed gene 2	-1.25	0.473	-1.19	0.16	-1.24	0.014	1.13	0.329	-0.64
1449637_at	Cdh4	cadherin 4	-1.7	0.557	1.32	0.692	-1.87	0.345	-1.39	0.287	-0.91
1446735_at	Itsn2	intersectin 2	1.08	0.223	-1.25	0.301	-1.76	0.01	-1.81	0.074	-0.94
1438492_at	Socs7	Suppressor of cytokine signaling 7	-1.72	0.432	-1.12	0.8	-1.03	0.945	2.32	0.054	-0.39
1430109_at	4833412E19Rik	RIKEN cDNA 4833412E19 gene	-1.18	0.369	-1.06	0.764	-1.51	0.11	1.82	0.154	-0.48
1439093_at	---	---	-1.46	0.049	-1.05	0.751	-1.23	0.224	2.1	0.301	-0.41
1454835_at	Epm2aip1	EPM2A (laforin) interacting protein 1	-1.23	0.077	-1.17	0.287	-1.28	0.224	1.01	0.973	-0.67
1425540_at	Otc	ornithine transcarbamylase	-1.18	0.706	-1.33	0.144	-1.18	0.702	1.9	0.434	-0.45
1439917_at	Pdzd8	PDZ domain containing 8	1.08	0.597	-1.39	0.091	-1.54	0.048	-1.29	0.113	-0.78
1432726_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1.02	0.975	-3.69	0.015	1.19	0.682	-1.54	0.446	-1.26
1453411_at	2010110K16Rik	RIKEN cDNA 2010110K16 gene	-1.29	0.078	1.26	0.531	-2.42	0.13	-1.26	0.472	-0.93
1452109_at	Il17re	interleukin 17 receptor E	-1.13	0.635	-2.1	0.069	1.08	0.616	-1.03	0.885	-0.79
1447593_x_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	-1.43	0.637	1.03	0.938	-1.39	0.224	-1.66	0.349	-0.86
1445157_at	---	---	-1.29	0.745	-1.2	0.273	-1.2	0.59	1.02	0.948	-0.67
1443157_at	Glis3	GLIS family zinc finger 3	-1.55	0.271	1.25	0.486	-1.81	0.008	-1.08	0.538	-0.8
1458613_at	Arrdc1	arrestin domain containing 1	1.06	0.525	-1.26	0.489	-1.69	0.176	-1.28	0.552	-0.79
1450496_a_at	2810433K01Rik	RIKEN cDNA 2810433K01 gene	-1.07	0.931	-1.95	0.452	-1	0.999	4.53	0.209	0.13
1424364_a_at	1110020P15Rik	RIKEN cDNA 1110020P15 gene	-1.18	0.011	-1.29	0.074	-1.21	0.234	1.33	0.119	-0.59
1416265_at	Capn10	calpain 10	-1.22	0.271	-1.38	0.295	-1.11	0.414	1.01	0.919	-0.67

1451934_at	H2-D1	histocompatibility 2, D region locus 1	-1.21	0.637	-1.16	0.772	-1.31	0.13	1.31	0.698	-0.59
1443249_at	3-Mar	Membrane-associated ring finger (C3HC4) 3	-1.08	0.747	-1.08	0.85	-1.67	0.018	3.85	0.224	0
1439696_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	-1.43	0.419	1.15	0.724	-1.65	0.041	-1.44	0.475	-0.85
1456258_at	Emx2	empty spiracles homolog 2 (Drosophila)	-1.12	0.428	1.09	0.872	-2.13	0.072	-1.56	0.408	-0.93
1450109_s_at	Abcc2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	-1.28	0.09	-1.15	0.388	-1.25	0.691	2.16	0.056	-0.38
1460215_at	Rpo1-4	RNA polymerase 1-4	-1.06	0.24	-1.31	0.753	-1.35	0.355	1.05	0.836	-0.67
1440460_at	4930504O13Rik	RIKEN cDNA 4930504O13 gene	-1.97	0.022	-1.1	0.599	1.03	0.856	-1.15	0.296	-0.8
1455982_at	Jmjd4	jumonji domain containing 4	-1.37	0.351	-1.4	0.296	1.01	0.954	-1.09	0.736	-0.72
1443457_at	A230055J12Rik	RIKEN cDNA A230055J12 gene	1.04	0.931	-1.23	0.704	-1.68	0.144	-1.11	0.722	-0.75
1422401_at	Sprr3	small proline-rich protein 3	-2.47	0.068	-2.01	0.201	1.55	0.384	-1.09	0.818	-1.01
1458951_at	Vrk1	vaccinia related kinase 1	-1.63	0.155	1.04	0.869	-1.27	0.016	-1.02	0.845	-0.72
1430034_at	Cct4	chaperonin subunit 4 (delta)	-1.04	0.791	-1.44	0.126	-1.26	0.117	1.45	0.212	-0.57
1426113_x_at	Tcra /// A430107P0	T-cell receptor alpha chain /// RIKEN cDNA A430107P09 gene	-1.26	0.145	-1.65	0.118	1.05	0.778	-2.23	0.102	-1.02
1459090_at	Ubxd4	UBX domain containing 4	-1.2	0.617	-1.3	0.536	-1.18	0.37	1.03	0.609	-0.66
1425773_s_at	Nmnat1	nicotinamide nucleotide adenylyltransferase 1	-1.19	0.296	-1.79	0.021	1.05	0.694	-1.41	0.306	-0.84
1444659_at	Trip11	Thyroid hormone receptor interactor 11	-1.49	0.413	1.15	0.678	-1.59	0.244	-1.55	0.137	-0.87
1453424_at	Fyco1	FYVE and coiled-coil domain containing 1	1.03	0.791	-1.34	0.017	-1.47	0.109	-1.49	0.077	-0.82
1437491_at	Bicd2	bicaudal D homolog 2 (Drosophila)	-1.07	0.887	-1.05	0.885	-1.78	0.337	1.67	0.236	-0.56
1438254_at	1110007A13Rik	RIKEN cDNA 1110007A13 gene	-1.45	0.059	1.09	0.383	-1.48	0.013	-1.31	0.087	-0.79
1454270_at	Grifin	galectin-related inter-fiber protein	-2.26	0.018	-1.03	0.951	1.04	0.921	-1.55	0.067	-0.95
1431527_at	Cd164	CD164 antigen	-2.65	0.163	1.1	0.912	-1.02	0.939	-1.46	0.51	-1.01
1440943_at	B230208H17Rik	RIKEN cDNA B230208H17 gene	-1.04	0.907	-1.13	0.644	-1.66	0.09	1.05	0.831	-0.7
1454393_at	2310047C04Rik	RIKEN cDNA 2310047C04 gene	-1.21	0.466	1.2	0.696	-2.35	0.064	-1.26	0.141	-0.9
1449726_at	Txnl2 /// LOC62001	thioredoxin-like 2 /// similar to thioredoxin-like 2	-1.1	0.913	-1.07	0.851	-1.64	0.081	1.13	0.605	-0.67
1446240_at	Kns2	Kinesin 2	1.09	0.648	-1.61	0.384	-1.35	0.204	-1.37	0.484	-0.81
1432369_at	3010027C24Rik	RIKEN cDNA 3010027C24 gene	-1.31	0.483	-1.39	0.361	-1.04	0.947	1.02	0.94	-0.68
1439238_at	Unc84b	unc-84 homolog B (C. elegans)	1.11	0.437	-1.68	0.17	-1.33	0.148	-1.1	0.491	-0.75
1437594_x_at	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	-1.27	0.649	-1.58	0.174	1.03	0.732	-1.23	0.532	-0.76
1423512_at	AW209491	expressed sequence AW209491	-1.14	0.241	-1.2	0.045	-1.35	0.096	1.12	0.6	-0.64
1441301_at	Jakmip1	Janus kinase and microtubule interacting protein 1	-2.46	0.427	-1.21	0.637	1.22	0.615	-1.68	0.072	-1.03
1430016_at	4930584F24Rik	RIKEN cDNA 4930584F24 gene	-2.61	0.332	1.23	0.555	-1.2	0.655	-1.61	0.458	-1.05
1458661_at	Morf4l1	Mortality factor 4 like 1	-1.08	0.584	1.06	0.697	-2.13	0.017	-1.1	0.631	-0.81
1437604_x_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	-1.51	0.209	-1.07	0.88	-1.17	0.164	1.01	0.968	-0.69
1430502_at	9130206N08Rik	RIKEN cDNA 9130206N08 gene	1.18	0.753	-1.64	0.404	-1.52	0.406	-1.54	0.443	-0.88
1437474_at	Gatad2b	GATA zinc finger domain containing 2B	-1.17	0.139	-1.19	0.207	-1.32	0.187	1.05	0.758	-0.66
1444448_at	1300007F04Rik	RIKEN cDNA 1300007F04 gene	-4.47	0.017	1.53	0.509	-1.43	0.478	-2.17	0.109	-1.64
1417233_at	Chchd4	coiled-coil-helix-coiled-coil-helix domain containing 4	-1.31	0.14	-1.19	0.209	-1.18	0.337	1.21	0.543	-0.62
1431246_at	Iqce	IQ motif containing E	-1.31	0.04	-1.27	0.568	-1.11	0.73	1.12	0.194	-0.64
1440294_at	Setd2	SET domain containing 2	1.13	0.613	-1.33	0.576	-1.75	0.075	-1.14	0.603	-0.77
1433865_at	E330016L19Rik ///	RIKEN cDNA E330016L19 gene /// RIKEN cDNA E330010L02 gene	1.2	0.83	-2.09	0.098	-1.3	0.531	-1.4	0.489	-0.9
1437373_at	Isg20l1	interferon stimulated exonuclease gene 20-like 1	-1.12	0.734	-1.74	0.19	-1.02	0.874	1.26	0.183	-0.66
1435798_a_at	Sfrs14	splicing factor, arginine/serine-rich 14	-1.44	0.4	-1.42	0.071	1.05	0.186	-1.13	0.047	-0.73
1442802_x_at	Bat2	HLA-B associated transcript 2	-1.31	0.501	-1.03	0.926	-1.4	0.044	1.03	0.729	-0.68
1445688_at	Hcfc1	host cell factor C1	1.24	0.425	-1.65	0.433	-1.64	0.415	-2.04	0.254	-1.02
1432748_at	4933403J19Rik	RIKEN cDNA 4933403J19 gene	-2.3	0.122	1.2	0.583	-1.22	0.651	-1.43	0.232	-0.94
1432903_at	---	---	1.08	0.677	-1.15	0.626	-1.96	0.372	-1.91	0.452	-0.99
1458849_at	Asah2	N-acylsphingosine amidohydrolase 2	-1.45	0.132	-1.1	0.623	-1.17	0.377	1.28	0.292	-0.61
1425692_a_at	Dnahc8	dynein, axonemal, heavy chain 8	-1.05	0.945	-1.32	0.693	-1.34	0.334	1.23	0.445	-0.62
1434341_x_at	1110020P15Rik ///	RIKEN cDNA 1110020P15 gene /// similar to ubiquinol-cytochrome c reductase c	-1.15	0.071	-1.38	0.024	-1.16	0.416	1.06	0.712	-0.66
1439020_at	AW146020	expressed sequence AW146020	-1.34	0.476	-1.21	0.465	-1.14	0.573	1.22	0.407	-0.62
1429325_at	Wdr51b	WD repeat domain 51B	-1.39	0.141	-1.42	0.483	1.03	0.853	-1.22	0.413	-0.75
1455191_x_at	Pip5k1b	Phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-1.91	0.341	-1.65	0.11	1.32	0.571	-1.55	0.446	-0.95
1460476_s_at	1200015N20Rik	RIKEN cDNA 1200015N20 gene	-1.19	0.841	-1.91	0.222	1.09	0.796	-1.44	0.524	-0.86

1452731_x_at	LOC544988 /// B93	hypothetical protein LOC544988 /// RIKEN cDNA B930046C15 gene /// hypotheti	-1.03	0.943	-2.31	0.252	1.05	0.713	-1.08	0.856	-0.84
1426063_a_at	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	-1.88	0.503	1.24	0.539	-1.46	0.41	-1.34	0.225	-0.86
1438834_at	Mospd2	motile sperm domain containing 2	1.09	0.561	-1.35	0.4	-1.61	0.005	-1.18	0.564	-0.76
1448080_at	E2f8	E2F transcription factor 8	-1.14	0.882	-1.6	0.062	-1.05	0.892	1.3	0.736	-0.62
1424347_at	Ppp6c	protein phosphatase 6, catalytic subunit	-1.12	0.254	-1.1	0.127	-1.53	0.009	1.14	0.183	-0.65
1444764_at	A130022J21Rik	RIKEN cDNA A130022J21 gene	-1.14	0.612	1.02	0.945	-1.79	0.15	-1.05	0.887	-0.74
1444353_at	C030040A22Rik	RIKEN cDNA C030040A22 gene	-1.25	0.671	-1.27	0.67	-1.15	0.664	1.04	0.953	-0.66
1443014_at	4833403I15Rik	RIKEN cDNA 4833403I15 gene	1	0.99	-1.13	0.737	-1.76	0.282	-1.44	0.44	-0.83
1421564_at	Serpina3c	serine (or cysteine) peptidase inhibitor, clade A, member 3C	1.14	0.831	-1.97	0.222	-1.24	0.411	-1.47	0.317	-0.89
1431989_at	4930433E13Rik	RIKEN cDNA 4930433E13 gene	-1.04	0.69	-1.34	0.464	-1.34	0.123	1.07	0.842	-0.66
1441724_at	---	---	-1.14	0.525	-1.01	0.973	-1.71	0.073	1.1	0.16	-0.69
1433207_at	5033430J17Rik	RIKEN cDNA 5033430J17 gene	-1.85	0.116	1.46	0.581	-2.19	0.09	-1.31	0.237	-0.97
1431863_at	4931430N09Rik	RIKEN cDNA 4931430N09 gene	-1.7	0.503	-1.01	0.982	-1.14	0.724	1.84	0.33	-0.5
1446983_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	1.02	0.938	-1.35	0.574	-1.45	0.081	-1.26	0.716	-0.76
1436101_at	Rnf24	ring finger protein 24	-1.69	0.004	1.01	0.979	-1.17	0.345	-1.07	0.755	-0.73
1449756_at	Dnajc17	DnaJ (Hsp40) homolog, subfamily C, member 17	-2.18	0.185	1.01	0.994	-1.01	0.985	-1.15	0.656	-0.83
1447384_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	1.16	0.591	-1.21	0.72	-2.13	0.183	-1.03	0.96	-0.8
1439715_at	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	1.18	0.483	-1.48	0.384	-1.67	0.407	-2.47	0.103	-1.11
1445478_at	---	---	-1.22	0.525	-1.22	0.519	-1.23	0.276	1.06	0.792	-0.65
1422373_at	Olfr71	olfactory receptor 71	-1.02	0.96	-1.34	0.35	-1.38	0.142	2.2	0.084	-0.38
1455136_at	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	-2.75	0.089	-1.15	0.795	1.22	0.619	-1.07	0.93	-0.94
1442929_at	St8sia5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	-1.57	0.369	1.06	0.827	-1.31	0.618	-1.04	0.941	-0.72
1457153_at	LOC552882	hypothetical LOC552882	1.03	0.932	-1.9	0.125	-1.11	0.729	-1.03	0.906	-0.75
1432083_a_at	Lrrc23	leucine rich repeat containing 23	-1.84	0.436	-1.2	0.821	1.08	0.81	-1.64	0.11	-0.9
1434817_s_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	-1.28	0.101	-1.46	0.029	-1.01	0.943	1.33	0.259	-0.6
1435588_at	Wdfy1	WD repeat and FYVE domain containing 1	-1.4	0.39	-1.27	0.36	-1.05	0.823	1.04	0.892	-0.67
1442809_at	Scn9a /// LOC6718	sodium channel, voltage-gated, type IX, alpha /// similar to sodium channel 25	1.05	0.936	-1.05	0.945	-2.24	0.233	-1.16	0.794	-0.85
1438818_at	Nmd3	NMD3 homolog (S. cerevisiae)	-1.47	0.558	1.08	0.79	-1.44	0.033	-1.48	0.404	-0.83
1416225_at	Adh1	alcohol dehydrogenase 1 (class I)	-1.03	0.676	-1.22	0.376	-1.5	0.126	1.36	0.632	-0.6
1438292_x_at	Adk	adenosine kinase	-1.04	0.235	-1.1	0.548	-1.71	0.008	1.89	0.083	-0.49
1443005_at	Zfhx1a	zinc finger homeobox 1a	-1.37	0.193	-1.16	0.49	-1.15	0.371	1.06	0.788	-0.66
1457120_at	Itk	IL2-inducible T-cell kinase	-2.05	0.528	1.12	0.85	-1.17	0.568	-2.42	0.116	-1.13
1442045_at	---	---	-1.73	0.589	1.11	0.877	-1.29	0.448	-1.3	0.159	-0.8
1418303_at	1700113O17Rik	RIKEN cDNA 1700113O17 gene	-1.84	0.386	-1.05	0.913	-1.04	0.818	2.72	0.034	-0.3
1457954_at	---	---	1.07	0.801	-2.08	0.184	-1.1	0.748	-1.22	0.416	-0.83
1460354_a_at	Mrpl13	mitochondrial ribosomal protein L13	-1.15	0.264	-1.12	0.348	-1.45	0.072	1.02	0.921	-0.67
1451699_at	LOC668468 /// LOC	similar to putative retrovirus-related gag protein /// hypothetical protein LOC66863	-1.67	0.29	-1.1	0.771	-1.05	0.835	1.9	0.098	-0.48
1441431_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	-1.44	0.458	-1.17	0.682	-1.1	0.711	1.02	0.94	-0.67
1442394_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430024H	1.37	0.496	-2.08	0.049	-1.65	0.147	-1.87	0.253	-1.06
1441043_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930579G14 pr	1.16	0.551	-2.51	0.051	-1.12	0.802	-1.24	0.624	-0.93
1415916_a_at	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahy	-1.23	0.037	-1.13	0.366	-1.32	0.043	2.36	0.15	-0.33
1417996_at	Ngb	neuroglobin	1.03	0.971	-1.48	0.35	-1.32	0.296	-1.95	0.041	-0.93
1421132_at	Pvrl3	poliovirus receptor-related 3	1.04	0.848	-1.37	0.352	-1.45	0.1	-2.46	0.222	-1.06
1431849_at	4933432B09Rik	RIKEN cDNA 4933432B09 gene	1.1	0.893	-2.45	0.204	-1.05	0.619	-2.16	0.357	-1.14
1424968_at	2210023G05Rik	RIKEN cDNA 2210023G05 gene	-1.14	0.734	-1.15	0.319	-1.41	0.061	4.3	0.18	0.15
1433365_at	4930563N14Rik	RIKEN cDNA 4930563N14 gene	1.19	0.228	-1.46	0.672	-1.71	0.352	-1.02	0.98	-0.75
1420154_at	---	---	-1.13	0.579	-1.09	0.869	-1.54	0.477	1.09	0.722	-0.67
1418739_at	Sgk2	serum/glucocorticoid regulated kinase 2	-1.15	0.315	-1.52	0.189	-1.07	0.827	1.12	0.225	-0.66
1435091_at	Zfp568	zinc finger protein 568	-1.35	0.132	-1.17	0.106	-1.16	0.203	1.25	0.34	-0.61
1429581_at	Acad9	acyl-Coenzyme A dehydrogenase family, member 9	-1.38	0.233	-1.54	0.071	1.08	0.686	-1.3	0.244	-0.78
1443081_at	Gata6	GATA binding protein 6	1.07	0.916	-1.14	0.832	-1.95	0.026	-1.39	0.156	-0.85
1441273_at	Lrch2	Leucine-rich repeats and calponin homology (CH) domain containing 2	-2.75	0.365	-2.61	0.191	1.71	0.121	-1.97	0.078	-1.4
1420348_at	Lhx5	LIM homeobox protein 5	-1.12	0.783	-2.45	0.099	1.16	0.717	-1.44	0.313	-0.96

1446801_at	---	---	-1.7	0.241	1.34	0.363	-1.89	0.185	-1.52	0.61	-0.94
1444598_at	Etv6	Ets variant gene 6 (TEL oncogene)	1.02	0.939	-1.23	0.357	-1.6	0.062	-1.65	0.257	-0.86
1441873_at	Prlpe	prolactin-like protein E	1.31	0.585	-1.39	0.637	-2.35	0.358	-2.08	0.477	-1.13
1431094_at	1110006E14Rik	RIKEN cDNA 1110006E14 gene	-1.1	0.877	-1.01	0.986	-1.79	0.005	1.74	0.217	-0.54
1417848_at	Zfp704	zinc finger protein 704	-1.18	0.262	-1.06	0.761	-1.5	0.021	1.13	0.418	-0.65
1439088_at	Pdzd8	PDZ domain containing 8	-1.15	0.607	-1.19	0.497	-1.34	0.055	1.09	0.744	-0.65
1436731_at	Zfp533	zinc finger protein 533	-1.09	0.721	-1.24	0.327	-1.36	0.407	1.07	0.881	-0.66
1442421_at	---	---	-1.51	0.195	-1.07	0.844	-1.15	0.687	1.19	0.604	-0.64
1420044_at	---	---	-1.35	0.317	-1.46	0.015	1.03	0.854	-1.41	0.157	-0.8
1439659_at	Trfp /// Usp49	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila) //	-1.06	0.808	-1.54	0.028	-1.15	0.389	1.69	0.142	-0.52
1455864_at	Trim75	tripartite motif-containing 75	-1.23	0.703	1.26	0.753	-2.59	0.129	-1.23	0.664	-0.95
1429540_at	Cnfn	cornifelin	-1.11	0.661	-1.23	0.615	-1.35	0.123	1.18	0.584	-0.63
1432186_at	1700028J19Rik	RIKEN cDNA 1700028J19 gene	1.4	0.253	-1.98	0.214	-1.81	0.251	-1.16	0.853	-0.89
1445957_at	Evl	Ena-vasodilator stimulated phosphoprotein	-1.03	0.906	-1.65	0.236	-1.14	0.557	1.25	0.631	-0.64
1457053_at	BC016423	CDNA sequence BC016423	1.01	0.91	-1.32	0.31	-1.45	0.318	-1.25	0.308	-0.75
1455866_x_at	Txnl1	thioredoxin-like 1	-1.61	0.039	-1.71	0.061	1.25	0.646	-2.18	0.185	-1.06
1431211_s_at	Them5	thioesterase superfamily member 5	-2.51	0.054	1.08	0.936	-1.02	0.972	-1.74	0.453	-1.05
1454502_at	2900022B07Rik	RIKEN cDNA 2900022B07 gene	-1.86	0.048	-1.01	0.98	-1.07	0.765	1.62	0.291	-0.58
1450139_at	Ern2	endoplasmic reticulum (ER) to nucleus signalling 2	-1.78	0.358	1.54	0.329	-2.79	0.015	-1.63	0.433	-1.17
1439333_at	Kcnv1	potassium channel, subfamily V, member 1	-2.58	0.281	1.67	0.46	-2.49	0.022	-1.9	0.117	-1.33
1421050_at	Vps25	vacuolar protein sorting 25 (yeast)	-1.1	0.55	-1.38	0.338	-1.21	0.359	1.13	0.546	-0.64
1423753_at	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	-1.2	0.207	1.07	0.653	-1.8	0.002	-1.46	0.031	-0.85
1435961_at	BC047219	cDNA sequence BC047219	-1.07	0.858	-1.93	0.162	1	0.974	-1.82	0.044	-0.95
1453620_at	3010022N24Rik	RIKEN cDNA 3010022N24 gene	-2.22	0.111	-1.46	0.419	1.32	0.497	-1.01	0.989	-0.84
1456202_at	BC094219	cDNA sequence BC094219	-2.73	0.495	1.29	0.58	-1.25	0.721	-5.27	0.05	-1.99
1442155_at	4632427E13Rik	RIKEN cDNA 4632427E13 gene	1.12	0.622	-1.11	0.581	-2.26	0.002	-1.25	0.164	-0.87
1442887_at	AI853363	expressed sequence AI853363	-1.17	0.746	-1.29	0.39	-1.21	0.74	1.67	0.48	-0.5
1440019_at	Gpr22	G protein-coupled receptor 22	-1.44	0.695	1.26	0.438	-1.97	0.072	-1.41	0.586	-0.89
1453652_at	4933400F21Rik	RIKEN cDNA 4933400F21 gene	-1.33	0.66	-2.07	0.29	1.22	0.582	-1.74	0.128	-0.98
1416014_at	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	-1.16	0.516	-1.25	0.178	-1.25	0.118	1.17	0.406	-0.62
1435006_s_at	Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-1.32	0.013	-1.18	0.106	-1.17	0.226	1.47	0.095	-0.55
1428411_at	1700020I14Rik	RIKEN cDNA 1700020I14 gene	-1.14	0.009	-1.11	0.388	-1.46	0.054	1.08	0.553	-0.66
1454466_at	4933407I18Rik	RIKEN cDNA 4933407I18 gene	1.09	0.924	-2.34	0.424	-1.06	0.886	-1.13	0.832	-0.86
1446922_at	---	---	-2.01	0.124	-1.13	0.439	1.08	0.847	-1.33	0.434	-0.85
1419894_at	MGC107702	Similar to proteasome (prosome, macropain) subunit, beta type 7	1.19	0.793	-1.66	0.175	-1.5	0.086	-1.06	0.717	-0.76
1450800_at	Syt8	synaptotagmin VIII	-1.86	0.582	1.04	0.928	-1.13	0.86	-1.89	0.335	-0.96
1450415_at	Pde6a	phosphodiesterase 6A, cGMP-specific, rod, alpha	1.01	0.981	-1.62	0.311	-1.21	0.7	-1.16	0.845	-0.74
1452751_at	Ebf3	early B-cell factor 3	-1.04	0.466	-1.39	0.635	-1.29	0.609	1.33	0.378	-0.6
1420103_at	---	---	-1.78	0.114	-1.11	0.761	-1	0.983	1.5	0.13	-0.6
1447022_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930402K03 pr	1.04	0.888	-1.76	0.501	-1.17	0.355	-1.42	0.105	-0.83
1444493_at	Tbc1d2b	TBC1 domain family, member 2B	-1.09	0.753	-1.73	0.056	-1.03	0.857	1.01	0.958	-0.71
1459136_at	Bach2	BTB and CNC homology 2	1.05	0.879	-1.38	0.528	-1.47	0.271	-2.93	0.217	-1.18
1420031_at	Chek1	checkpoint kinase 1 homolog (S. pombe)	1.26	0.723	-1.25	0.738	-2.46	0.067	-1.9	0.359	-1.09
1419937_at	AA536749	expressed sequence AA536749	1.25	0.66	-1.76	0.156	-1.56	0.302	-1.66	0.051	-0.93
1445526_at	AY512915	cDNA sequence AY512915	-2.14	0.253	1.13	0.797	-1.16	0.123	-1.26	0.411	-0.86
1454126_at	0710001A04Rik	RIKEN cDNA 0710001A04 gene	-1.2	0.637	-1.38	0.171	-1.1	0.866	1.9	0.155	-0.45
1428266_at	Myl3	myosin, light polypeptide 3	-1.67	0.318	-1.76	0.131	1.3	0.527	-1.12	0.619	-0.81
1453551_at	Polq	polymerase (DNA directed), theta	-1.65	0.032	-1.04	0.918	-1.12	0.763	1.24	0.601	-0.64
1439805_at	Nfat5	Nuclear factor of activated T-cells 5	1.11	0.122	-1.36	0.313	-1.61	0.007	-1.45	0.105	-0.83
1447124_at	---	Transcribed locus	-1.26	0.145	-1.27	0.105	-1.13	0.528	1.08	0.867	-0.65
1419924_at	A730024A03Rik	RIKEN cDNA A730024A03 gene	-1.25	0.747	-1.95	0.071	1.15	0.59	-1.24	0.26	-0.82
1423511_at	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	-1.26	0.064	-1.13	0.343	-1.28	0.022	1.59	0.269	-0.52
1433300_at	2900005I04Rik	RIKEN cDNA 2900005I04 gene	-1.52	0.21	-3.34	0.127	1.5	0.632	-1.71	0.255	-1.27

1436871_at	Sfrs7	splicing factor, arginine/serine-rich 7	-1.63	0.261	-1.22	0.301	1.03	0.78	-1.23	0.597	-0.76
1418953_at	Fbxo16	F-box protein 16	-1.4	0.142	-1.62	0.074	1.13	0.473	-1.05	0.872	-0.74
1419478_at	Sectm1	secreted and transmembrane 1	1.08	0.664	-1.79	0.191	-1.21	0.558	-2.58	0.236	-1.13
1419067_a_at	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	-1.14	0.305	-1.35	0.159	-1.19	0.124	1.6	0.164	-0.52
1444947_at	Lasp1	LIM and SH3 protein 1	-1.25	0.383	-1.57	0.149	1.03	0.902	-1.26	0.381	-0.76
1424417_at	---	---	-1.41	0.146	-1.19	0.542	-1.09	0.748	1.02	0.856	-0.67
1443392_at	Trpv1	Transient receptor potential cation channel, subfamily V, member 1	-1.46	0.354	-1.19	0.637	-1.07	0.763	1.35	0.621	-0.59
1458222_at	---	Transcribed locus	-1.44	0.105	-1.15	0.485	-1.11	0.373	1.03	0.903	-0.67
1419628_at	Chx10	C. elegans ceh-10 homeo domain containing homolog	-1.35	0.186	-1.67	0.223	1.13	0.705	-1.01	0.963	-0.73
1455992_at	Vgll4	vestigial like 4 (Drosophila)	-1.45	0.082	-1.65	0.07	1.17	0.573	-1.32	0.088	-0.81
1440672_at	LOC638394 /// LOC	similar to zinc finger protein 541 /// similar to zinc finger protein 541 /// similar to z	-1.34	0.564	-1.47	0.669	1.04	0.811	-1.05	0.954	-0.71
1457029_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	-1.13	0.405	-1.9	0.142	1.06	0.865	-1.08	0.864	-0.77
1422986_at	Esrrb	estrogen related receptor, beta	-1.11	0.811	-1.59	0.205	-1.07	0.738	1.4	0.125	-0.59
1436755_at	Itih5	inter-alpha (globulin) inhibitor H5	1.17	0.659	-1.81	0.078	-1.34	0.449	-1.73	0.324	-0.93
1456917_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibite	1.07	0.446	-1.28	0.317	-1.63	0.006	-1.85	0.081	-0.92
1439173_at	Hook1	hook homolog 1 (Drosophila)	1.02	0.958	-1.19	0.434	-1.65	0.06	-1.97	0.066	-0.95
1436347_a_at	5530601H04Rik	RIKEN cDNA 5530601H04 gene	-1.06	0.781	-1.48	0.234	-1.19	0.292	1.03	0.767	-0.67
1455627_at	Col8a1	procollagen, type VIII, alpha 1	-1.43	0.35	-1.12	0.642	-1.14	0.612	1.28	0.108	-0.6
1415719_s_at	Armc1	armadillo repeat containing 1	-1.17	0.306	-1.1	0.117	-1.42	0.103	1.33	0.226	-0.59
1446048_at	---	---	1.01	0.976	-1.4	0.08	-1.35	0.139	-1.91	0.048	-0.91
1428779_at	Zbtb41	zinc finger and BTB domain containing 41 homolog	-1.16	0.311	-1.26	0.007	-1.24	0.085	1.06	0.792	-0.65
1446619_at	A130038J17Rik	RIKEN cDNA A130038J17 gene	-1.33	0.232	-1.3	0.578	-1.07	0.847	1.25	0.559	-0.61
1442880_at	---	---	1.47	0.454	-1.76	0.07	-2.31	0.118	-1.41	0.235	-1
1427116_at	Setd1a	SET domain containing 1A	-1.54	0.184	-1.2	0.125	-1.02	0.925	1.13	0.535	-0.66
1443042_at	Robo1	Roundabout homolog 1 (Drosophila)	-1.05	0.928	-1.03	0.925	-1.83	0.133	1.73	0.028	-0.55
1454090_at	Pdss1	prenyl (solanesyl) diphosphate synthase, subunit 1	-1.65	0.199	1.32	0.288	-1.84	0.296	-1.08	0.747	-0.81
1458294_at	---	Transcribed locus	-1.21	0.632	-1.04	0.93	-1.48	0.221	1.81	0.168	-0.48
1457465_at	Shroom4	shroom family member 4	-1.01	0.942	-1.39	0.381	-1.34	0.277	1.03	0.844	-0.67
1429832_at	Ppih /// LOC43306	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomerase H /// hypothetica	1.12	0.491	-2.08	0.059	-1.15	0.248	-1.01	0.987	-0.78
1449091_at	Cldn8	claudin 8	-1.23	0.216	-1.35	0.135	-1.1	0.793	1.88	0.35	-0.45
1456059_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1.45	0.146	-1.21	0.064	-1.05	0.733	1.32	0.286	-0.6
1450996_at	Fshb	follicle stimulating hormone beta	-1.51	0.338	1.14	0.131	-1.51	0.633	-1.44	0.484	-0.83
1439765_x_at	Krt42	keratin 42	-1.4	0.163	-1.12	0.557	-1.17	0.405	1.09	0.789	-0.65
1443489_at	C330002D13Rik	RIKEN cDNA C330002D13 gene	-1.14	0.536	-1.15	0.338	-1.39	0.156	1.18	0.015	-0.62
1440457_at	Cltc	Clathrin, heavy polypeptide (Hc)	-1.22	0.445	-1.19	0.247	-1.24	0.254	1.4	0.22	-0.56
1419553_a_at	Rabggtb	RAB geranylgeranyl transferase, b subunit	-1.4	0.053	-1.26	0.058	-1.05	0.717	1.38	0.408	-0.58
1435443_at	Eya3	eyes absent 3 homolog (Drosophila)	-1.05	0.724	-1.21	0.27	-1.45	0.144	1.11	0.552	-0.65
1453418_at	Col24a1	procollagen, type XXIV, alpha 1	1.36	0.251	-1.19	0.54	-3.8	0.002	-2.34	0.304	-1.49
1459379_at	---	---	1.03	0.792	-1.59	0.191	-1.24	0.311	-1.2	0.183	-0.75
1460499_at	9230110I02Rik	RIKEN cDNA 9230110I02 gene	-1.44	0.076	1.06	0.835	-1.4	0.005	-1.82	0.213	-0.9
1451047_at	Itm2a	integral membrane protein 2A	-1.41	0.083	1.2	0.17	-1.81	0.021	-2.61	0.051	-1.16
1433849_at	Cdc27	cell division cycle 27 homolog (S. cerevisiae)	-1	0.993	-1.42	0.14	-1.31	0.265	1.84	0.301	-0.47
1428638_at	Efhc2	EF-hand domain (C-terminal) containing 2	1.16	0.109	-3.05	0.29	-1.02	0.921	-1.16	0.81	-1.02
1453859_at	2410003P15Rik	RIKEN cDNA 2410003P15 gene	-2.14	0.164	-1.53	0.397	1.35	0.634	-1.06	0.95	-0.85
1431238_at	Pqlc1	PQ loop repeat containing 1	-1.5	0.276	-1.99	0.262	1.3	0.2	-1.48	0.501	-0.92
1460583_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	-1.16	0.364	-1.39	0.53	-1.12	0.497	1.18	0.588	-0.63
1437443_at	---	PREDICTED: Mus musculus hypothetical protein LOC620382 (LOC620382), mR	-1.17	0.489	-1.24	0.049	-1.24	0.326	1.03	0.853	-0.66
1443485_at	Epha7	Eph receptor A7	-1.04	0.948	1.03	0.905	-2.11	0.022	-1.55	0.331	-0.92
1442033_at	C1qtnf9	C1q and tumor necrosis factor related protein 9	-1.35	0.141	-1.31	0.493	-1.03	0.919	1.71	0.136	-0.5
1457641_at	Crebbp	CREB binding protein	-1.38	0.294	1.15	0.471	-1.68	0.06	-1.5	0.007	-0.85
1457535_at	4932438A13Rik	RIKEN cDNA 4932438A13 gene	1.04	0.589	-1.44	0.134	-1.35	0.097	-1.19	0.261	-0.74
1440025_at	Kptn	kaptin	-1.8	0.211	-1.14	0.685	1.03	0.86	-1.29	0.287	-0.8
1440972_at	Nsd1	nuclear receptor-binding SET-domain protein 1	1.03	0.54	-1.33	0.004	-1.45	0.111	-1.24	0.414	-0.75

1430040_at	Hspa12a	heat shock protein 12A	-4.17	0.014	-1.22	0.57	1.41	0.607	-1.02	0.96	-1.25
1438824_at	Slc20a1	solute carrier family 20, member 1	-1.17	0.545	-1.01	0.978	-1.6	0.089	1.81	0.254	-0.49
1457462_at	---	---	1.11	0.672	-1.44	0.023	-1.51	0.136	-1.05	0.808	-0.72
1460116_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1.09	0.592	-1.22	0.269	-1.79	0.018	-1.08	0.738	-0.75
1454930_at	Lrrc35	leucine rich repeat containing 35	-1.14	0.376	-1.36	0.263	-1.16	0.053	2.24	0.207	-0.36
1419938_s_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	-1.31	0.137	-1.65	0.075	1.1	0.805	-1.55	0.093	-0.85
1440516_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330017K	-2.1	0.108	-1.01	0.985	1.01	0.987	-1.08	0.731	-0.8
1418910_at	Bmp7	bone morphogenetic protein 7	1.12	0.158	-1.94	0.021	-1.19	0.266	-1.21	0.608	-0.81
1424221_at	Susd4	sushi domain containing 4	1.22	0.435	-2.24	0.051	-1.25	0.073	-1.09	0.803	-0.84
1450801_at	Adam21	a disintegrin and metallopeptidase domain 21	1.11	0.715	-1.64	0.233	-1.33	0.517	-1.44	0.555	-0.83
1425000_s_at	5430407P10Rik	RIKEN cDNA 5430407P10 gene	-1.8	0.137	-1.03	0.921	-1.06	0.82	1.02	0.963	-0.72
1421361_at	Grk1	G protein-coupled receptor kinase 1	-1.03	0.888	1.1	0.74	-2.53	0.315	-1.06	0.795	-0.88
1425004_s_at	Mocs1	molybdenum cofactor synthesis 1	-1.24	0.428	-1.19	0.339	-1.21	0.193	2.12	0.079	-0.38
1426713_s_at	Eprs /// LOC633677	glutamyl-prolyl-tRNA synthetase /// similar to Bifunctional aminoacyl-tRNA synthe	-1.19	0.104	-1.16	0.021	-1.31	0.118	1.2	0.468	-0.61
1422727_at	Nme5	expressed in non-metastatic cells 5	-1.46	0.157	-1.12	0.599	-1.12	0.663	1.28	0.522	-0.6
1446258_at	Sntb1	Syntrophin, basic 1	1.16	0.127	-1.72	0.107	-1.37	0.125	-1.45	0.279	-0.85
1419150_at	Myf6	myogenic factor 6	-1.74	0.028	-1.3	0.735	1.13	0.654	-1.64	0.02	-0.89
1424589_s_at	Rnpc3	RNA-binding region (RNP1, RRM) containing 3	-1.22	0.53	-1.1	0.393	-1.35	0.117	1.26	0.509	-0.6
1443380_at	Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	-1.44	0.758	1.08	0.848	-1.43	0.523	-1.3	0.618	-0.77
1454208_at	4930483O08Rik	RIKEN cDNA 4930483O08 gene	1.03	0.834	-2.05	0.174	-1.05	0.903	-1.1	0.597	-0.79
1442920_at	Klf3	Kruppel-like factor 3 (basic)	-1.16	0.349	-1.31	0.06	-1.18	0.284	1.33	0.374	-0.58
1448925_at	Twist2	twist homolog 2 (Drosophila)	-1.44	0.218	-1.17	0.659	-1.08	0.821	1.13	0.744	-0.64
1435073_a_at	Armc9	armadillo repeat containing 9	-1.02	0.898	-1.71	0.219	-1.1	0.587	1.21	0.528	-0.66
1451689_a_at	Sox10	SRY-box containing gene 10	-2.14	0.38	1.06	0.845	-1.06	0.916	-2.34	0.309	-1.12
1443180_at	Ergic2	ERGIC and golgi 2	-1.33	0.179	-1.18	0.446	-1.15	0.416	1.19	0.381	-0.62
1450837_at	Prh1	proline rich protein HaeIII subfamily 1	-1.15	0.473	-1.1	0.658	-1.43	0.574	1.36	0.089	-0.58
1433044_at	Cspg2	chondroitin sulfate proteoglycan 2	1.13	0.623	-1.82	0.045	-1.27	0.321	-2	0.03	-0.99
1418119_at	Rbm8a	RNA binding motif protein 8a	-1.06	0.653	-1.29	0.064	-1.33	0.023	1.08	0.589	-0.65
1442577_at	KIAA0415	KIAA0415 protein	-1.78	0.344	-1.06	0.801	-1.03	0.9	2.86	0.135	-0.25
1458690_at	7-Mar	membrane-associated ring finger (C3HC4) 7	-1.07	0.738	1.01	0.97	-1.9	0.003	-1.78	0.085	-0.94
1442973_at	C80865	expressed sequence C80865	1.18	0.779	-1.62	0.453	-1.48	0.596	-1.14	0.863	-0.77
1449487_at	Ccdc70	coiled-coil domain containing 70	-1.08	0.229	-2.51	0.121	1.15	0.35	-1.28	0.7	-0.93
1431156_at	9430040K09Rik	RIKEN cDNA 9430040K09 gene	-1	0.98	-1.1	0.698	-1.79	0.04	1.12	0.815	-0.69
1448694_at	Jun	Jun oncogene	-1.63	0.117	-1.07	0.753	-1.09	0.415	1.51	0.076	-0.57
1419087_s_at	Sf3a1	splicing factor 3a, subunit 1	-1.18	0.382	-1.36	0.349	-1.13	0.287	1.66	0.237	-0.5
1450680_at	Rag1	recombination activating gene 1	-1.11	0.262	-1.04	0.937	-1.64	0.593	1.44	0.346	-0.59
1421542_at	Dzip1	DAZ interacting protein 1	-1.22	0.515	-1.64	0.337	1.04	0.935	-1.56	0.515	-0.84
1441918_x_at	RP23-262J21.5	similar to NK13	-1.36	0.325	1.35	0.521	-2.58	0.047	-5.13	0.086	-1.93
1443178_at	Rnf13	ring finger protein 13	-1.83	0.068	-1.69	0.371	1.33	0.604	-1.92	0.137	-1.03
1421563_at	Atp7b	ATPase, Cu++ transporting, beta polypeptide	-1.34	0.335	-1.3	0.328	-1.05	0.762	1.43	0.12	-0.56
1444073_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	-1.28	0.423	-1.08	0.66	-1.3	0.463	1.21	0.699	-0.62
1428639_at	Lin9	lin-9 homolog (C. elegans)	-1.26	0.424	-1.11	0.642	-1.29	0.38	1.4	0.54	-0.56
1433362_at	4930527F18Rik	RIKEN cDNA 4930527F18 gene	-1.26	0.228	-1.2	0.416	-1.18	0.391	1.33	0.654	-0.58
1444687_at	C1ql2	complement component 1, q subcomponent-like 2	-1.04	0.877	-1.2	0.325	-1.48	0.182	1.36	0.527	-0.59
1453923_at	Ccdc83	coiled-coil domain containing 83	-1.38	0.439	-1.12	0.813	-1.18	0.52	1.31	0.436	-0.59
1435398_at	Stxbp5	syntaxin binding protein 5 (tomosyn)	-1.15	0.284	-1.36	0.121	-1.15	0.597	1.42	0.254	-0.56
1435320_at	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	-1.05	0.63	-1.3	0.096	-1.33	0.295	1.36	0.321	-0.58
1442248_at	Trio	Triple functional domain (PTPRF interacting)	-1.37	0.267	1.08	0.714	-1.51	0.095	-1.6	0.156	-0.85
1427169_at	Als2cr19	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (hum	-1.02	0.839	-1.22	0.451	-1.5	0.032	1.34	0.291	-0.6
1440417_at	D19Ertd409e	DNA segment, Chr 19, ERATO Doi 409, expressed	1.02	0.771	-1.14	0.237	-1.74	0.046	-1.41	0.222	-0.82
1433898_at	AV025504	Expressed sequence AV025504	-1.03	0.543	-2.48	0.008	1.1	0.463	-1.21	0.264	-0.91
1454792_s_at	Sephs1	selenophosphate synthetase 1	-1.04	0.094	-1.27	0.049	-1.38	0.007	1.32	0.234	-0.59
1449640_at	Tlr7	toll-like receptor 7	-2.37	0.426	1.29	0.648	-1.31	0.471	-1.42	0.305	-0.95

1450209_at	Hoxd4	homeo box D4	-2.2	0.498	-1.07	0.9	1.08	0.8	-1.32	0.497	-0.87
1440418_at	---	---	-1.79	0.445	-1.37	0.711	1.18	0.754	-1.49	0.63	-0.87
1439007_at	Alg6	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase	-1.14	0.17	-1.28	0.099	-1.23	0.196	1.38	0.142	-0.57
1457812_at	Trp53bp1	transformation related protein 53 binding protein 1	-1.06	0.859	-1.15	0.42	-1.51	0.083	1.09	0.675	-0.66
1420562_at	Slurp1	secreted Ly6/Plaur domain containing 1	-1.03	0.961	-1.62	0.454	-1.13	0.816	1.02	0.968	-0.69
1440524_at	Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	-1.42	0.654	1.08	0.768	-1.44	0.089	-1.64	0.428	-0.86
1439401_x_at	Ppp2r5e	Protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-1.4	0.345	-1.23	0.385	-1.06	0.713	1.16	0.014	-0.63
1460455_at	1110059H15Rik	RIKEN cDNA 1110059H15 gene	-1.23	0.153	-1.11	0.201	-1.32	0.17	1.27	0.141	-0.6
1456912_at	Zfp691	zinc finger protein 691	-1.16	0.535	-1.19	0.623	-1.3	0.597	1.05	0.872	-0.65
1419042_at	Iigp1	interferon inducible GTPase 1	-1.05	0.647	-1.18	0.121	-1.5	0.184	1.11	0.594	-0.65
1455621_at	BC066107	cDNA sequence BC066107	-1.44	0.372	1.16	0.554	-1.63	0.036	-1.64	0.269	-0.89
1451669_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	-1.16	0.531	-1.21	0.042	-1.26	0.14	1.24	0.16	-0.6
1431114_at	Dock4	dedicator of cytokinesis 4	1.02	0.965	-1.01	0.965	-2.15	0.037	-1.37	0.169	-0.88
1442561_at	Mamdc1	MAM domain containing 1	-1.6	0.567	1.16	0.857	-1.46	0.345	-1.7	0.488	-0.9
1422149_at	Mllt7	myeloid/lymphoid or mixed lineage-leukemia translocation to 7 homolog (Drosopl	-2.01	0.573	-1.1	0.545	1.06	0.67	-1.86	0.444	-0.97
1423623_at	2810021B07Rik	RIKEN cDNA 2810021B07 gene	-1.31	0.06	-1.5	0.053	1.05	0.769	-1.12	0.588	-0.72
1453857_at	Rnf180	ring finger protein 180	-1.3	0.435	-1.18	0.722	-1.16	0.482	1.13	0.741	-0.63
1458961_at	Eya3	eyes absent 3 homolog (Drosophila)	1.08	0.829	-1.32	0.293	-1.58	0.296	-1.44	0.162	-0.81
1423397_at	Ugt2b38	UDP glucuronosyltransferase 2 family, polypeptide B38	-2.36	0.003	-5.41	0.031	1.87	0.106	-1.58	0.459	-1.87
1420293_at	Aytl2	acyltransferase like 2	-1.26	0.578	-1.94	0.296	1.17	0.594	-1.3	0.587	-0.83
1433530_at	2210411K19Rik	RIKEN cDNA 2210411K19 gene	-1.22	0.047	-1.15	0.526	-1.28	0.249	1.02	0.951	-0.66
1444285_at	Morf4l1	Mortality factor 4 like 1	-1.69	0.016	1.36	0.526	-1.93	0.008	-1.48	0.04	-0.93
1444744_at	Dido1	Death inducer-obliterator 1	-1.47	0.321	-1.33	0.127	1.04	0.591	-1.02	0.885	-0.69
1423337_at	Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	-1.03	0.807	-1.32	0.06	-1.34	0.139	1.02	0.926	-0.67
1458169_at	Gm700 /// LOC668	gene model 700, (NCBI) /// similar to Motilin receptor (G-protein coupled receptor	-1.39	0.318	1.11	0.715	-1.54	0.179	-1.29	0.459	-0.78
1423193_at	Pspc1	paraspeckle protein 1	-1.42	0.212	-1.31	0.252	1.01	0.962	-1.08	0.511	-0.7
1433375_at	D530037P16Rik	RIKEN cDNA D530037P16 gene	1.02	0.883	-1.03	0.916	-2.08	0.354	-1.08	0.887	-0.79
1458829_at	---	---	1.03	0.932	-1.15	0.693	-1.73	0.175	-1.51	0.298	-0.84
1460144_at	BC052040	CDNA sequence BC052040	-1.02	0.977	-1.1	0.762	-1.72	0.26	1.08	0.796	-0.69
1420201_at	---	---	-1.25	0.811	-2.57	0.16	1.28	0.19	-1.11	0.811	-0.91
1419828_at	Usp31	ubiquitin specific peptidase 31	-1.28	0.203	-1.19	0.541	-1.17	0.405	3.39	0.236	-0.06
1440096_at	Ecm2	extracellular matrix protein 2, female organ and adipocyte specific	-1	0.993	1.06	0.829	-2.37	0.008	-1.82	0.553	-1.03
1449234_at	Car15	carbonic anhydrase 15	1.14	0.414	-2.27	0.104	-1.12	0.631	-1.26	0.234	-0.88
1428458_at	Pop1	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae)	-1.32	0.264	-1.32	0.409	-1.04	0.893	1.28	0.438	-0.6
1447186_at	Slc6a16 /// LOC672	solute carrier family 6, member 16 /// similar to Orphan sodium- and chloride-dep	-1.33	0.313	-1.32	0.566	-1.04	0.922	1.25	0.557	-0.61
1444574_at	Elf2	E74-like factor 2	1.09	0.863	-1.35	0.095	-1.56	0.011	-1.07	0.83	-0.72
1459850_x_at	Glrb	glycine receptor, beta subunit	-2.05	0.514	1.22	0.31	-1.3	0.24	-1.38	0.064	-0.88
1458554_at	9330169B04Rik	RIKEN cDNA 9330169B04 gene	-1.86	0.2	1.23	0.598	-1.41	0.366	-1.48	0.345	-0.88
1432317_at	9430078K24Rik	RIKEN cDNA 9430078K24 gene	1.07	0.741	-2.28	0.018	-1.03	0.896	-2.36	0.273	-1.15
1455216_at	Paqr6	progestin and adipoQ receptor family member VI	-2.23	0.057	1.21	0.767	-1.22	0.401	-1.25	0.512	-0.87
1439371_x_at	Timm44	translocase of inner mitochondrial membrane 44	-1.21	0.196	-1.48	0.102	-1.02	0.943	1.13	0.372	-0.65
1423936_at	Kctd5	potassium channel tetramerisation domain containing 5	-1.12	0.389	-1.56	0.049	-1.06	0.643	1.09	0.175	-0.66
1425424_at	MGC7817	hypothetical protein LOC620031	-1.36	0.058	1.13	0.556	-1.65	0.093	-1.46	0.171	-0.83
1416272_at	Map2k1ip1	mitogen-activated protein kinase kinase 1 interacting protein 1	-1.24	0.182	-1.08	0.391	-1.34	0.175	1.05	0.561	-0.65
1459268_at	5330439C02Rik	RIKEN cDNA 5330439C02 gene	-1.16	0.707	-1.21	0.374	-1.27	0.629	1.85	0.322	-0.45
1430138_at	Cd3eap	CD3E antigen, epsilon polypeptide associated protein	-1.54	0.31	1.17	0.64	-1.52	0.134	-1.32	0.126	-0.8
1437175_at	Pdik1l	PDLIM1 interacting kinase 1 like	-1.02	0.784	-1.26	0.118	-1.42	0.005	1.28	0.37	-0.61
1457189_at	Itpr1	Inositol 1,4,5-triphosphate receptor 1	-1.11	0.716	1.05	0.887	-1.89	0.025	-1.66	0.18	-0.9
1442103_at	Nipbl	Nipped-B homolog (Drosophila)	-1.13	0.473	1.03	0.93	-1.78	0.021	-1.13	0.421	-0.75
1425254_at	Foxn4	forkhead box N4	-2.23	0.103	1.25	0.708	-1.28	0.675	-1.14	0.835	-0.85
1458342_at	Tmem90a	transmembrane protein 90a	-1.22	0.621	1.21	0.622	-2.21	0.012	-1.49	0.401	-0.93
1458799_at	A330033J07Rik	RIKEN cDNA A330033J07 gene	-1.53	0.111	1.19	0.691	-1.58	0.432	-1.69	0.371	-0.9
1447795_at	Bspry	B-box and SPRY domain containing	1.04	0.731	-2.02	0.491	-1.07	0.427	-2.11	0.106	-1.04

1451202_at	C330007P06Rik	RIKEN cDNA C330007P06 gene	-1.13	0.208	-1.19	0.056	-1.33	0.002	1.2	0.06	-0.61
1433521_at	Ankrd13c	ankyrin repeat domain 13c	-1.2	0.038	-1.24	0.003	-1.2	0.141	1.05	0.47	-0.65
1456396_at	---	---	-1.62	0.251	-1.3	0.095	1.09	0.661	-1.15	0.653	-0.74
1450222_x_at	Klk1b4	kallikrein 1-related pepidase b4	-1.3	0.365	-1.07	0.85	-1.29	0.544	1.41	0.552	-0.56
1458111_at	C530043G21Rik	RIKEN cDNA C530043G21 gene	1.14	0.711	-1.31	0.572	-1.73	0.032	-1.43	0.149	-0.83
1419785_at	AA516738	expressed sequence AA516738	-1.29	0.398	-1.7	0.427	1.12	0.848	-1.31	0.667	-0.8
1457491_at	---	---	1.09	0.456	-1.22	0.427	-1.75	0.004	-1.54	0.05	-0.86
1437720_at	Lgtn	Ligatin	-1.29	0.403	-1.32	0.359	-1.06	0.771	1.22	0.576	-0.61
1457470_at	D3Ertd452e	DNA segment, Chr 3, ERATO Doi 452, expressed	-1.82	0.007	1.27	0.597	-1.52	0.195	-1.21	0.638	-0.82
1430061_at	1700105P06Rik	RIKEN cDNA 1700105P06 gene	-1.01	0.958	1.01	0.959	-2.09	0.354	-1.35	0.375	-0.86
1450875_at	Gpr37	G protein-coupled receptor 37	1.13	0.862	-1.39	0.554	-1.6	0.138	-1.5	0.385	-0.84
1460443_at	Brms1l	breast cancer metastasis-suppressor 1-like	-1.32	0.203	-1.16	0.287	-1.17	0.199	1.21	0.342	-0.61
1445078_at	D7Ertd526e	DNA segment, Chr 7, ERATO Doi 526, expressed	-2.29	0.053	-1.49	0.472	1.37	0.576	-1.66	0.394	-1.02
1447240_at	---	---	1.1	0.695	-1.09	0.596	-2.16	0.017	-1.36	0.345	-0.88
1439488_at	---	7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430	-1.28	0.066	-1.17	0.498	-1.19	0.339	1.53	0.03	-0.53
1434977_at	4933403F05Rik	RIKEN cDNA 4933403F05 gene	-1.17	0.441	-1.12	0.38	-1.37	0.086	1.21	0.494	-0.61
1435399_at	2310068J10Rik	RIKEN cDNA 2310068J10 gene	1.02	0.94	-1.25	0.617	-1.52	0.076	-1.93	0.066	-0.92
1419844_a_at	LOC545086	hypothetical protein LOC545086	1.05	0.912	-1.1	0.887	-1.94	0.056	-1.57	0.282	-0.89
1458321_at	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	-1.03	0.781	-1.51	0.394	-1.18	0.48	1.74	0.304	-0.5
1430662_at	9430091E24Rik	RIKEN cDNA 9430091E24 gene	-1.5	0.19	-1.24	0.639	1.01	0.979	-1.41	0.006	-0.79
1460016_at	Tmem164	transmembrane protein 164	-1.24	0.05	1.11	0.776	-1.78	0.067	-1.19	0.211	-0.77
1441013_at	C81521	expressed sequence C81521	-1.12	0.606	1.22	0.457	-2.76	0.008	-1.29	0.462	-0.99
1457851_at	D10Ertd276e	DNA segment, Chr 10, ERATO Doi 276, expressed	-1.06	0.893	-1.28	0.132	-1.33	0.02	5.57	0.14	0.48
1428756_at	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-1.18	0.02	-1.2	0.096	-1.26	0.036	1.12	0.587	-0.63
1430989_a_at	1700020I14Rik	RIKEN cDNA 1700020I14 gene	-1.09	0.665	-1.04	0.631	-1.67	0.018	1.24	0.35	-0.64
1447106_at	Lrrk2	Leucine-rich repeat kinase 2	-1.9	0.468	-1.08	0.614	1.03	0.956	-1.5	0.699	-0.86
1445464_at	---	---	-1.84	0.562	1.41	0.547	-1.89	0.207	-1.49	0.319	-0.95
1434233_at	2610030H06Rik	RIKEN cDNA 2610030H06 gene	-1.46	0.155	-1.4	0.026	1.08	0.719	-1.13	0.584	-0.73
1440373_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.01	0.966	-1.09	0.636	-1.83	0.014	-1.05	0.744	-0.74
1440691_at	Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	-1.33	0.17	-1.08	0.64	-1.24	0.329	1.08	0.616	-0.64
1438569_at	Ccdc38	coiled-coil domain containing 38	-1.21	0.788	-1.14	0.708	-1.29	0.62	1.71	0.373	-0.48
1432402_at	4930402F11Rik	RIKEN cDNA 4930402F11 gene	-1.78	0.188	1.32	0.533	-1.67	0.176	-1.03	0.931	-0.79
1440929_at	---	---	-1.44	0.396	-1.15	0.697	-1.09	0.637	1.24	0.174	-0.61
1457180_at	Dip2c	DIP2 disco-interacting protein 2 homolog C (Drosophila)	-1.01	0.969	-1.11	0.702	-1.7	0.119	1.73	0.312	-0.52
1451319_at	Senp1	SUMO1/sentrin specific peptidase 1	-1.23	0.532	-1.36	0.522	-1.08	0.735	1.23	0.282	-0.61
1443184_at	Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	1.09	0.746	-1.7	0.188	-1.24	0.321	-1.27	0.178	-0.78
1444207_at	Cml3	Camello-like 3	-1.07	0.78	-1.61	0.038	-1.08	0.753	1.61	0.203	-0.54
1427147_at	F730047E07Rik	RIKEN cDNA F730047E07 gene	-1.23	0.529	-1.37	0.195	-1.07	0.688	2.21	0.186	-0.37
1453415_at	Zc3h6	zinc finger CCCH type containing 6	-1.08	0.84	-1.3	0.328	-1.27	0.547	1.02	0.98	-0.66
1452879_at	Synpo2	synaptopodin 2	1.29	0.109	-3.74	0.003	-1.09	0.751	-1.14	0.585	-1.17
1435562_at	Pdzd8	PDZ domain containing 8	-1.09	0.405	-1.48	0.115	-1.13	0.415	1.23	0.475	-0.62
1444356_at	Rab6ip2	Rab6 interacting protein 2	1.03	0.913	-1.48	0.39	-1.29	0.654	-1.38	0.614	-0.78
1423979_a_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), mem	-1.25	0.352	-1.75	0.127	1.11	0.586	-1.16	0.627	-0.76
1432115_a_at	Pign	phosphatidylinositol glycan anchor biosynthesis, class N	-2.74	0.342	1.23	0.671	-1.13	0.858	-1.34	0.609	-0.99
1443628_at	---	---	-1.12	0.693	-1.07	0.763	-1.53	0.21	1.16	0.469	-0.64
1420298_at	---	---	-2.54	0.373	-2.46	0.432	1.68	0.245	-1.08	0.901	-1.1
1425475_at	Col4a5	procollagen, type IV, alpha 5	-1.53	0.005	-1.47	0.041	1.15	0.608	-1.21	0.41	-0.77
1424199_at	Seh1l	SEH1-like (S. cerevisiae	-1.26	0.025	-1.25	0.03	-1.13	0.321	1.45	0.196	-0.55
1429106_at	4921509J17Rik	RIKEN cDNA 4921509J17 gene	-1.37	0.053	-1.17	0.492	-1.12	0.518	2.01	0.255	-0.41
1442417_at	Med8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	-1.22	0.185	-1.18	0.144	-1.23	0.249	1.12	0.249	-0.63
1420174_s_at	---	---	-1.28	0.49	-1.13	0.449	-1.22	0.178	1.02	0.898	-0.65
1443838_x_at	Fads2	fatty acid desaturase 2	-1.21	0.214	-1.36	0.451	-1.09	0.841	1.12	0.847	-0.63
1435167_at	Ranbp6	RAN binding protein 6	-1.15	0.549	-1.17	0.291	-1.32	0.051	1.17	0.448	-0.62

1435162_at	Prkg2	protein kinase, cGMP-dependent, type II	-1.05	0.828	-1.41	0.12	-1.22	0.066	1.14	0.831	-0.64
1440221_at	AA408650	expressed sequence AA408650	-1.2	0.497	-1.31	0.144	-1.12	0.181	1.18	0.591	-0.61
1447048_at	6720458F09Rik	RIKEN cDNA 6720458F09 gene	-1.85	0.417	-1.52	0.228	1.28	0.621	-1.11	0.328	-0.8
1432391_at	Ccdc21	coiled-coil domain containing 21	-1.01	0.949	-1.09	0.673	-1.73	0.207	1.06	0.504	-0.69
1430500_s_at	Mtx2	metaxin 2	-1.3	0.005	-1.31	0.008	-1.06	0.327	1.04	0.825	-0.66
1442844_at	A830052D11Rik	RIKEN cDNA A830052D11 gene	1.1	0.801	-1.38	0.405	-1.53	0.461	-1.12	0.616	-0.73
1445428_at	---	---	1.1	0.703	-1.31	0.443	-1.62	0.068	-1.4	0.256	-0.81
1444775_at	9930033D15Rik	RIKEN cDNA 9930033D15 gene	1.41	0.172	-2.73	0.199	-1.41	0.185	-1.12	0.735	-0.96
1451856_at	Tnrc15	trinucleotide repeat containing 15	-1.58	0.231	-1.17	0.787	-1.01	0.981	1.1	0.641	-0.66
1450600_at	Olfr1508	olfactory receptor 1508	-1.09	0.608	-1.3	0.391	-1.26	0.172	1.4	0.013	-0.56
1440567_at	D030051N19Rik	RIKEN cDNA D030051N19 gene	1.12	0.428	-1.37	0.299	-1.56	0.192	-1.24	0.267	-0.77
1443008_at	Msi2	Musashi homolog 2 (Drosophila)	-1.43	0.254	-1.04	0.86	-1.21	0.678	1.17	0.582	-0.63
1457975_at	Gtpbp3	GTP binding protein 3	-1.87	0.213	-1.07	0.828	1.01	0.983	-1.2	0.477	-0.78
1458007_at	Myo1b	myosin IB	-1	0.997	-1.02	0.931	-1.97	0.002	1.32	0.512	-0.67
1446580_at	9430083G14Rik	RIKEN cDNA 9430083G14 gene	1.07	0.766	-1.21	0.767	-1.69	0.128	-1.72	0.282	-0.89
1418938_at	Dio2	deiodinase, iodothyronine, type II	-1.18	0.36	-1.56	0.355	-1	0.998	1.14	0.758	-0.65
1427848_at	Tcrb-V13	T-cell receptor beta, variable 13	-4.95	0.08	-1.97	0	1.77	0.13	-1.65	0.423	-1.7
1439487_at	Lig4	ligase IV, DNA, ATP-dependent	1.19	0.48	-1.68	0.051	-1.44	0.008	-1.29	0.301	-0.8
1441466_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	-1.27	0.141	-1.17	0.58	-1.19	0.615	1.39	0.236	-0.56
1444145_at	Mettl6	Methyltransferase like 6	-1.31	0.432	-1.02	0.946	-1.35	0.1	1.04	0.903	-0.66
1449140_at	Nudcd2	NudC domain containing 2	-1.45	0.17	-1.03	0.811	-1.22	0.403	1.69	0.234	-0.5
1421055_at	Lats2 /// Xpo4	large tumor suppressor 2 /// exportin 4	-1.15	0.457	-1.12	0.547	-1.37	0.029	1.33	0.273	-0.58
1430183_at	Pbx1	Pre B-cell leukemia transcription factor 1	-1.01	0.982	1.08	0.798	-2.41	0.018	-1.39	0.124	-0.93
1447874_x_at	Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	-1.41	0.339	-1.01	0.942	-1.28	0.248	1.29	0.088	-0.6
1458925_at	Zfp82	zinc finger protein 82	-1.41	0.659	-1.05	0.888	-1.22	0.512	1.08	0.87	-0.65
1454354_at	8030476L19Rik	RIKEN cDNA 8030476L19 gene	-1.02	0.813	-1.4	0.073	-1.26	0.298	1.37	0.073	-0.58
1457802_at	B930012P20Rik	RIKEN cDNA B930012P20 gene	-1.19	0.307	1.16	0.459	-2.06	0.032	-1.26	0.588	-0.84
1444438_at	Cib3	calcium and integrin binding family member 3	1.55	0.425	-2.39	0.051	-1.96	0.15	-1.56	0.395	-1.09
1458280_at	Ascc2	Activating signal cointegrator 1 complex subunit 2	-1.34	0.626	-1.4	0.472	1.02	0.891	-1.44	0.099	-0.79
1460614_at	Mier3	mesoderm induction early response 1, family member 3	-1.19	0.053	-1.05	0.367	-1.46	0.005	2.05	0.243	-0.41
1444746_at	Ptbp2	Polypyrimidine tract binding protein 2	1.07	0.602	-1.17	0.167	-1.79	0.002	-1.3	0.142	-0.8
1433750_at	Slc31a1	solute carrier family 31, member 1	-1.14	0.161	-1.03	0.612	-1.57	0.045	1.33	0.444	-0.6
1443505_at	Prok1	Prokineticin 1	1.33	0.16	-3.26	0.013	-1.19	0.657	-1.11	0.372	-1.06
1449090_a_at	Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-1.27	0.398	-1.04	0.795	-1.35	0.042	1.02	0.804	-0.66
1430738_at	4833419K08Rik	RIKEN cDNA 4833419K08 gene	-2.27	0.44	-1.23	0.522	1.23	0.534	-3.01	0.179	-1.32
1438313_at	---	Transcribed locus	1.02	0.9	-1.94	0.183	-1.06	0.884	-1.8	0.072	-0.94
1441531_at	Plcb4	phospholipase C, beta 4	-1.05	0.712	1.11	0.682	-2.36	0.001	-1.58	0.049	-0.97
1436728_s_at	Rtel1	regulator of telomere elongation helicase 1	-1.47	0.017	-1.18	0.199	-1.05	0.892	1.21	0.492	-0.62
1435950_at	Hr	hairless	-1.68	0.05	1.11	0.757	-1.29	0.353	-1.75	0.08	-0.9
1453377_at	Sh2d4a	SH2 domain containing 4A	-1.23	0.036	-1.07	0.599	-1.36	0.102	1.51	0.298	-0.54
1424029_at	Tspyl4	TSPY-like 4	-1.11	0.423	-1.95	0.107	1.07	0.386	-1.69	0.089	-0.92
1420208_at	---	---	-1.27	0.723	-1.48	0.639	1.02	0.923	-1.66	0.531	-0.85
1443741_x_at	Whsc1 /// LOC6223	Wolf-Hirschhorn syndrome candidate 1 (human) /// similar to Wolf-Hirschhorn syn	-1.13	0.686	-1.16	0.484	-1.35	0.299	1.06	0.796	-0.65
1434733_at	Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	-1.89	0.025	-1.19	0.557	1.12	0.528	-1.14	0.753	-0.78
1429305_at	Ankrd10	ankyrin repeat domain 10	-1.12	0.222	-1.43	0.096	-1.13	0.27	1.87	0.345	-0.45
1433088_at	5330430C04Rik	RIKEN cDNA 5330430C04 gene	-1.79	0.077	-1.11	0.564	1.02	0.938	-1.23	0.418	-0.78
1417957_a_at	Tspan1	tetraspanin 1	-1.04	0.708	-1.64	0.121	-1.1	0.705	1.34	0.162	-0.61
1457385_at	---	---	-1.35	0.257	-1.02	0.956	-1.3	0.284	1.19	0.484	-0.62
1449733_s_at	Siah1a	seven in absentia 1A	-1.18	0.334	-1.1	0.101	-1.38	0.042	1.1	0.611	-0.64
1436744_x_at	Fbxw14 /// LOC668	F-box and WD-40 domain protein 14 /// similar to F-box and WD-40 domain prote	-1.68	0.213	-1.62	0.427	1.27	0.448	-1.02	0.969	-0.76
1436700_a_at	Ddx48	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	1.29	0.644	-1.98	0.056	-1.45	0.303	-1.39	0.665	-0.88
1458361_at	Dclre1c	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)	-1.49	0.281	-1.23	0.629	1	0.992	-1.21	0.431	-0.73
1425286_at	Crygn	crystallin, gamma N	-1.38	0.077	-1.24	0.705	-1.05	0.928	1.42	0.585	-0.56

1441211_at	Kcns2	K+ voltage-gated channel, subfamily S, 2	-1.41	0.496	-1.3	0.664	1	0.989	-1.54	0.363	-0.81
1455100_at	Akr1d1	aldo-keto reductase family 1, member D1	-1.7	0.256	-1.07	0.362	-1.04	0.916	1.72	0.366	-0.52
1442876_at	Mapk1	Mitogen activated protein kinase 1	-1.99	0.419	1.61	0.191	-2.66	0.035	-1.21	0.682	-1.06
1417645_at	Sspn	sarcospan	-1.07	0.925	-2.8	0.01	1.19	0.245	-1.25	0.582	-0.98
1429545_at	Ube2i /// F830028C	ubiquitin-conjugating enzyme E2I /// RIKEN cDNA F830028O17 gene /// similar to	-1.33	0.028	-1.15	0.729	-1.15	0.094	1.02	0.898	-0.65
1431570_at	4930588G17Rik	RIKEN cDNA 4930588G17 gene	-1.57	0.435	1.1	0.834	-1.33	0.538	-1.01	0.977	-0.7
1428221_at	Klhdc8b	kelch domain containing 8B	1.08	0.852	-1.37	0.437	-1.49	0.033	-1.2	0.76	-0.74
1439882_at	Sec23ip	Sec23 interacting protein	-1.01	0.974	-1.28	0.506	-1.4	0.218	1.24	0.145	-0.61
1424037_at	Itpka	inositol 1,4,5-trisphosphate 3-kinase A	-2.31	0.068	-1.42	0.556	1.35	0.202	-1.69	0.199	-1.02
1421242_at	Rnf144	ring finger protein 144	-3.37	0.041	-1.34	0.218	1.45	0.473	-1.14	0.789	-1.1
1422589_at	Rab3a	RAB3A, member RAS oncogene family	-1.12	0.7	-2.38	0.361	1.18	0.372	-1.12	0.787	-0.86
1427754_a_at	Dnm1	dynamin 1	1.1	0.654	-1.69	0.341	-1.26	0.231	-1.23	0.352	-0.77
1458908_at	Dtna	Dystrobrevin alpha	-1.03	0.954	1.08	0.811	-2.31	0.118	-2.27	0.165	-1.13
1460006_at	Atbf1	AT motif binding factor 1	-1.01	0.959	-1.08	0.684	-1.74	0.035	1.12	0.666	-0.68
1443952_at	Thra	thyroid hormone receptor alpha	-1.13	0.575	-1.01	0.917	-1.62	0.086	1.37	0.111	-0.6
1436730_at	Clcc1	chloride channel CLIC-like 1	-1.23	0.04	1.09	0.789	-1.71	0.093	-1.08	0.706	-0.73
1423220_at	Eif4e /// LOC63052	eukaryotic translation initiation factor 4E /// hypothetical LOC630527	-1.12	0.343	-1.08	0.633	-1.51	0.001	1.62	0.31	-0.52
1429161_at	Arv1	ARV1 homolog (yeast)	-1.36	0.138	-1.4	0.16	1.04	0.851	-1.45	0.086	-0.79
1455675_a_at	Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	-1.24	0.247	-1.16	0.288	-1.22	0.202	1.26	0.256	-0.59
1460533_at	4933440K10Rik	RIKEN cDNA 4933440K10 gene	-1.77	0.532	-1.77	0.419	1.36	0.486	-2.33	0.303	-1.13
1427320_at	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2	-1.16	0.63	1.15	0.315	-2.1	0.001	-1.37	0.341	-0.87
1440847_at	Mtss1	metastasis suppressor 1	-1.8	0.005	-1.18	0.043	1.09	0.818	-1.9	0.124	-0.95
1431387_at	Anxa11	Annexin A11	-2.7	0.464	-1.65	0.431	1.51	0.357	-1.25	0.412	-1.02
1439597_at	4932417H02Rik	RIKEN cDNA 4932417H02 gene	-1.41	0.149	-1.06	0.838	-1.2	0.436	1	0.984	-0.67
1453845_at	4733401D01Rik	RIKEN cDNA 4733401D01 gene	-1.8	0.37	1.1	0.874	-1.2	0.716	-1.39	0.629	-0.82
1448426_at	Sardh	sarcosine dehydrogenase	-1.22	0.228	-1.24	0.285	-1.16	0.709	1.59	0.445	-0.51
1455475_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	-1.09	0.563	-1.27	0.294	-1.28	0.31	1.03	0.884	-0.65
1446475_at	Mbnl2	Muscleblind-like 2	-1.34	0.382	1.25	0.34	-2.03	0.033	-1.54	0.146	-0.91
1422241_a_at	Ndufa1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	-1.24	0.009	-1.17	0.081	-1.21	0.003	1.07	0.531	-0.64
1437321_at	---	---	-2.77	0.108	-1.26	0.446	1.34	0.579	-1.2	0.845	-0.97
1449771_at	---	---	-1.51	0.494	1.11	0.794	-1.4	0.415	-1.09	0.842	-0.72
1444974_at	AU023617	expressed sequence AU023617	-1.34	0.691	1.06	0.715	-1.46	0.103	-1.34	0.581	-0.77
1443777_at	---	---	-1.64	0.472	-1.24	0.526	1.07	0.808	-1.72	0.349	-0.88
1460005_at	AF013969 /// LOC6	expressed sequence AF013969 /// similar to CG5514-PB, isoform B /// region cor	-1.1	0.726	-1.53	0.134	-1.08	0.693	1.18	0.473	-0.63
1446126_at	---	Transcribed locus	-1.87	0.041	1.08	0.52	-1.15	0.568	-1.15	0.473	-0.77
1428588_a_at	Mrpl41	mitochondrial ribosomal protein L41	-1.01	0.903	-1.13	0.416	-1.61	0.025	1.19	0.262	-0.64
1422979_at	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	-1.14	0.805	-1.18	0.763	-1.31	0.523	3.91	0.238	0.07
1431844_at	Kcnmb2	potassium large conductance calcium-activated channel, subfamily M, beta meml	-1.61	0.021	-1.6	0.574	1.25	0.221	-1.75	0.218	-0.93
1433437_at	Dock8	dedicator of cytokinesis 8	-1.97	0.087	-1.54	0.108	1.33	0.666	-2.25	0.385	-1.11
1443819_x_at	Fis1	fission 1 (mitochondrial outer membrane) homolog (yeast)	1.03	0.85	-1.13	0.403	-1.73	0.053	-1.24	0.436	-0.77
1457178_at	Rabgap1l	RAB GTPase activating protein 1-like	-1.33	0.345	-1.12	0.522	-1.18	0.485	1.2	0.159	-0.61
1427540_at	Zwint	ZW10 interactor	-1.14	0.176	-1.26	0.418	-1.21	0.252	1.33	0.47	-0.57
1449676_at	Rab2	RAB2, member RAS oncogene family	1.11	0.682	-1.15	0.552	-1.97	0.045	-1.9	0.172	-0.98
1460668_at	Gal	galanin	-1.26	0.514	1.11	0.809	-1.71	0.13	-1.14	0.771	-0.75
1426718_at	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	-1.12	0.597	-1.25	0.013	-1.25	0.06	1	0.98	-0.65
1453396_at	1700123D08Rik	RIKEN cDNA 1700123D08 gene	-1.68	0.278	-1.3	0.447	1.13	0.861	-1.43	0.534	-0.82
1458460_at	Stim1	Stromal interaction molecule 1	-1.15	0.723	1	0.983	-1.62	0.032	-1.35	0.156	-0.78
1420053_at	Psmb1	Proteasome (prosome, macropain) subunit, beta type 1	-1.15	0.663	-1.13	0.548	-1.35	0.342	1.04	0.883	-0.65
1460577_at	AA591059	Expressed sequence AA591059	-1.19	0.048	-1.13	0.367	-1.31	0.097	1.4	0.263	-0.56
1456866_x_at	1700027D21Rik	RIKEN cDNA 1700027D21 gene	1.19	0.585	-1.76	0.133	-1.37	0.591	-1.19	0.646	-0.78
1448532_at	Prlpc2	prolactin-like protein C 2	-2.25	0.271	1.55	0.249	-2.01	0.252	-1.31	0.618	-1
1435160_at	1110064P04Rik	RIKEN cDNA 1110064P04 gene	-1.05	0.847	-1.07	0.697	-1.64	0.023	1.08	0.52	-0.67
1427053_at	Abi3bp	ABI gene family, member 3 (NESH) binding protein	1.28	0.501	-1.7	0.021	-1.61	0.243	-1.62	0.22	-0.91

1457890_at	D6Ertd234e	DNA segment, Chr 6, ERATO Doi 234, expressed	-1.15	0.807	-1.08	0.638	-1.43	0.44	2.11	0.261	-0.39
1444338_at	---	---	-3.87	0.009	1.26	0.763	-1.02	0.951	-1.23	0.696	-1.22
1428761_a_at	Snapc3	small nuclear RNA activating complex, polypeptide 3	1.22	0.446	-1.6	0.07	-1.54	0.011	-1.41	0.431	-0.83
1447748_x_at	Slc29a2	solute carrier family 29 (nucleoside transporters), member 2	1.06	0.756	-1.57	0.282	-1.25	0.607	-1.12	0.824	-0.72
1417005_at	Kns2	kinesin 2	-1.05	0.856	-1.46	0.034	-1.17	0.526	1.08	0.661	-0.65
1437362_at	A930028L21Rik	RIKEN cDNA A930028L21 gene	-1.16	0.504	-1.6	0.22	1.01	0.981	-1.4	0.163	-0.79
1445646_at	Btbd1	BTB (POZ) domain containing 1	1.12	0.426	-1.22	0.259	-1.81	0.022	-1.69	0.228	-0.9
1455510_at	Spop	Speckle-type POZ protein	-1.1	0.305	-1.11	0.104	-1.46	0.093	1.08	0.737	-0.65
1424853_s_at	Cyp4a10 /// BC013	cytochrome P450, family 4, subfamily a, polypeptide 10 /// cDNA sequence BC01	-1	0.836	-1.97	0.151	-1.01	0.92	1.55	0.533	-0.61
1445134_at	Mkl2	MKL/myocardin-like 2	1.37	0.627	-1.94	0.31	-1.65	0.203	-1.76	0.473	-0.99
1434800_at	Sv2b	synaptic vesicle glycoprotein 2 b	-2.09	0.033	1.18	0.717	-1.2	0.528	-1.36	0.194	-0.87
1432814_at	2900064F13Rik	RIKEN cDNA 2900064F13 gene	1	0.996	-1.92	0.409	-1.03	0.869	-2.5	0.252	-1.11
1460730_at	Eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha)	-1.32	0.2	-1.23	0.035	-1.09	0.505	1.34	0.341	-0.57
1453284_at	4930405M20Rik	RIKEN cDNA 4930405M20 gene	-1.2	0.221	-1.42	0.011	-1.05	0.51	1.06	0.734	-0.65
1431019_at	Lrrc28	leucine rich repeat containing 28	-1.25	0.384	-1.22	0.442	-1.15	0.688	1.29	0.687	-0.58
1420183_at	Lor	Loricrin	-1.3	0.333	-1.16	0.722	-1.16	0.706	1.01	0.982	-0.65
1443012_at	Tcf12	Transcription factor 12	-1.33	0.215	1.21	0.367	-1.89	0.016	-1.65	0.211	-0.91
1443247_at	Gfod1	Glucose-fructose oxidoreductase domain containing 1	-1.79	0.281	1.28	0.411	-1.53	0.369	-1.44	0.19	-0.87
1458494_at	---	Transcribed locus	1.25	0.679	-2.23	0.259	-1.25	0.629	-1.37	0.597	-0.9
1422668_at	Serpinb9b	serine (or cysteine) peptidase inhibitor, clade B, member 9b	-1.47	0.299	-1.18	0.581	-1.03	0.938	1.29	0.142	-0.6
1434135_at	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	-1.34	0.124	-1.06	0.593	-1.25	0.192	1.01	0.95	-0.66
1452837_at	Lpin2	lipin 2	-1.16	0.305	-1.28	0.472	-1.18	0.208	1.95	0.104	-0.42
1422307_at	---	---	-1.03	0.838	-1.22	0.235	-1.41	0.154	1.52	0.154	-0.54
1442264_at	Rasgrp2	RAS, guanyl releasing protein 2	1.03	0.558	-1.14	0.46	-1.7	0.006	-1.74	0.094	-0.89
1433912_at	Tiprl	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	-1.19	0.591	-1.21	0.255	-1.21	0.115	1.04	0.86	-0.64
1447596_at	---	Transcribed locus	-1.18	0.662	-1.45	0.473	-1.04	0.299	1.2	0.281	-0.62
1447224_at	---	Transcribed locus	-1.82	0.563	1.14	0.778	-1.25	0.664	-1.33	0.615	-0.81
1454957_at	Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	-1.03	0.887	-1.47	0.034	-1.2	0.402	1.12	0.658	-0.64
1430414_at	5730406G12Rik	RIKEN cDNA 5730406G12 gene	-1.21	0.317	-1.38	0.252	-1.06	0.819	1.28	0.339	-0.59
1441574_at	Pitpnc1	Phosphatidylinositol transfer protein, cytoplasmic 1	-1.35	0.074	1.05	0.862	-1.44	0.237	-1.34	0.238	-0.77
1431731_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	1.12	#DIV/0!	-1.09	0.365	-2.19	0.301	-1.05	0.907	-0.8
1437329_at	Ptplb	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	-1.16	0.324	-1.05	0.132	-1.47	0.084	1.15	0.656	-0.63
1424801_at	Enah	enabled homolog (Drosophila)	1.07	0.377	-1.61	0.343	-1.25	0.207	-1.4	0.107	-0.8
1451545_at	Tdrd3	tudor domain containing 3	-1.11	0.396	-1.14	0.493	-1.4	0.024	1.27	0.385	-0.59
1439647_at	LOC545611	hypothetical LOC545611	-1.39	0.394	-1.26	0.116	-1.02	0.899	1.06	0.534	-0.65
1452157_at	Eprs /// LOC63367	glutamyl-prolyl-tRNA synthetase /// similar to Bifunctional aminoacyl-tRNA synthe	-1.25	0.215	-1.11	0.479	-1.26	0.117	1.33	0.255	-0.57
1444391_at	---	Transcribed locus	1.13	0.473	-2.04	0.25	-1.14	0.535	-1.39	0.336	-0.86
1444912_at	---	---	1.25	0.56	-1.54	0.242	-1.69	0.107	-1.45	0.22	-0.86
1453975_a_at	1700029M20Rik	RIKEN cDNA 1700029M20 gene	1.14	0.77	-1.18	0.818	-1.97	0.272	-1.21	0.17	-0.81
1450475_at	Dlx3	distal-less homeobox 3	-2.99	0.215	-1.23	0.631	1.35	0.52	-1.76	0.132	-1.16
1417182_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	-1.24	0.076	-1.18	0.244	-1.19	0.368	1.04	0.891	-0.64
1450193_at	Hcn1	hyperpolarization-activated, cyclic nucleotide-gated K+ 1	-2.72	0.026	1.55	0.477	-1.73	0.082	-1.2	0.626	-1.03
1453869_at	LOC328277	hypothetical protein LOC328277	-1.26	0.578	-1.18	0.525	-1.16	0.187	1.13	0.723	-0.62
1444956_at	Gabarapl2	Gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	-1.22	0.482	-1.32	0.612	-1.09	0.458	2.07	0.179	-0.39
1430758_x_at	Bcas1	breast carcinoma amplified sequence 1	-1.65	0.445	-1.38	0.516	1.16	0.777	-1.81	0.657	-0.92
1457971_at	Cspp1	Centrosome and spindle pole associated protein 1	1.27	0.555	-1.74	0.113	-1.53	0.074	-2.02	0.032	-1.01
1432645_at	Atrn	Attractin	1	0.996	-1.19	0.62	-1.54	0.115	-1.14	0.812	-0.71
1432316_at	4933439N14Rik	RIKEN cDNA 4933439N14 gene	1.03	0.719	-1.83	0.063	-1.08	0.903	-1.04	0.963	-0.73
1449999_a_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	-2.3	0.065	1.43	0.587	-1.58	0.014	-1.13	0.832	-0.89
1428008_at	Dnm1l	dynamin 1-like	1.35	0.598	-2.01	0.357	-1.54	0.135	-1.09	0.893	-0.82
1424098_at	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	-1.01	0.853	-1.47	0.324	-1.21	0.332	2.3	0.015	-0.35
1420181_at	1700011M02Rik ///	RIKEN cDNA 1700011M02 gene /// hypothetical protein LOC668339	-1.34	0.427	1.03	0.937	-1.39	0.587	-1.91	0.479	-0.9
1451690_a_at	Pvrl4	poliovirus receptor-related 4	-1.06	0.923	-1.41	0.456	-1.19	0.54	2	0.403	-0.41

1436977_at	Eps8	Epidermal growth factor receptor pathway substrate 8	-1.19	0.215	1.17	0.665	-2.07	0.035	-1.12	0.316	-0.8
1458605_at	Arl15	ADP-ribosylation factor-like 15	-1.2	0.65	1.15	0.453	-1.96	0.034	-1.14	0.719	-0.79
1446248_at	Slc18a1	solute carrier family 18 (vesicular monoamine), member 1	-1.07	0.845	-1.46	0.196	-1.14	0.261	1.42	0.012	-0.56
1416681_at	Ube3a	ubiquitin protein ligase E3A	-1.04	0.782	-1.24	0.111	-1.37	0.183	1.15	0.679	-0.63
1455055_at	4930562D19Rik	RIKEN cDNA 4930562D19 gene	-1.26	0.221	-1.72	0.004	1.12	0.511	-1.11	0.022	-0.74
1434598_at	Larp5	La ribonucleoprotein domain family, member 5	-1.27	0.159	-1.18	0.03	-1.16	0.142	1.14	0.5	-0.62
1422159_at	Ppef2	protein phosphatase, EF hand calcium-binding domain 2	-1.23	0.376	-1.53	0.447	1.03	0.881	-1.21	0.202	-0.74
1453161_at	Thrap1	thyroid hormone receptor associated protein 1	-1	1	-2.29	0.062	1.06	0.863	-2.14	0.103	-1.09
1436895_at	Centd1	centaurin, delta 1	1.17	0.694	-1.28	0.236	-1.82	0.044	-1.56	0.362	-0.87
1460292_a_at	Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.14	0.787	-1.2	0.738	-1.88	0.074	-1.17	0.724	-0.78
1431104_at	4930522H14Rik	RIKEN cDNA 4930522H14 gene	-2.2	0.446	1.06	0.815	-1.02	0.904	-2.59	0.006	-1.19
1447331_at	Fbxo42	F-box protein 42	-1.41	0.5	-1.2	0.773	-1.05	0.925	1.72	0.411	-0.49
1419409_at	Sprrl5	small proline rich-like 5	1.02	0.969	-1.31	0.658	-1.41	0.269	-1.05	0.946	-0.69
1454599_at	4930425F17Rik	RIKEN cDNA 4930425F17 gene	-1.08	0.801	-1.47	0.109	-1.12	0.502	1.3	0.283	-0.59
1432409_at	Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	1.14	0.411	-1.84	0.322	-1.23	0.673	-1.04	0.932	-0.74
1441467_at	Tspan5	Tetraspanin 5	-1.09	0.744	1.21	0.629	-2.68	0.117	-1.61	0.126	-1.04
1427049_s_at	Smo	smoothened homolog (Drosophila)	-1.07	0.538	-1.1	0.66	-1.53	0.223	1.05	0.79	-0.66
1454014_a_at	Mkks	McKusick-Kaufman syndrome protein	-1.11	0.502	-1.18	0.135	-1.34	0.027	1.01	0.949	-0.65
1420522_at	Ccdc50	coiled-coil domain containing 50	-1.47	0.143	-1.57	0.004	1.18	0.3	-1.21	0.501	-0.77
1438403_s_at	---	---	1.19	0.811	-1.27	0.17	-1.91	0.212	-1.16	0.695	-0.79
1460149_at	Atp13a5	ATPase type 13A5	-1.16	0.586	-1.01	0.977	-1.56	0.449	2.39	0.308	-0.33
1422297_at	Pfdn5	prefoldin 5	-1.71	0.208	-1.28	0.652	1.13	0.85	-1.58	0.283	-0.86
1458044_at	Cml1	camello-like 1	-1.68	0.437	-1.09	0.857	-1.02	0.956	1.15	0.742	-0.66
1421096_at	Trpc1	transient receptor potential cation channel, subfamily C, member 1	-1.17	0.624	-1.06	0.878	-1.44	0.199	1.02	0.855	-0.66
1424371_at	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	-1.17	0.631	-1.3	0.335	-1.14	0.392	1.98	0.159	-0.41
1444526_at	Ssr1	signal sequence receptor, alpha	1.05	0.94	-1.58	0.342	-1.23	0.525	-1.16	0.698	-0.73
1454489_at	4930513L20Rik	RIKEN cDNA 4930513L20 gene	-1.31	0.63	-1.1	0.848	-1.22	0.622	1.57	0.47	-0.51
1444993_at	LOC664949 /// LOC	similar to mortality factor 4 like 1 (predicted) /// similar to mortality factor 4 like 1 (p	-1.08	0.855	-2.22	0.376	1.13	0.54	-3.18	0.12	-1.34
1436277_at	D330010C22Rik	RIKEN cDNA 330010C22 gene	-1.53	0.152	-1.76	0.09	1.28	0.68	-2.08	0.006	-1.02
1434037_s_at	Pcaf	p300/CBP-associated factor	-1.08	0.579	-1.3	0.011	-1.25	0.102	1.18	0.132	-0.61
1420259_at	Pkp2	Plakophilin 2	-1.84	0.236	1.35	0.138	-1.67	0.156	-1.15	0.67	-0.83
1420037_at	Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform	1.05	0.856	-1.09	0.358	-1.87	0.054	-1.24	0.586	-0.79
1455590_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	-1.15	0.159	-1.16	0.565	-1.31	0.04	1.02	0.617	-0.65
1433089_at	---	---	-1.76	0.535	1.39	0.296	-1.86	0.336	-2.27	0.366	-1.12
1444376_at	Sesn1	Sestrin 1	-1.08	0.457	1.1	0.756	-2.09	0.049	-1.71	0.081	-0.94
1439415_x_at	LOC622373	similar to 40S ribosomal protein S21	-1.47	0.116	1.04	0.767	-1.29	0.102	-1.69	0.147	-0.85
1419517_at	Cnih3	cornichon homolog 3 (Drosophila)	1.02	0.973	-1.72	0.107	-1.11	0.823	-1.98	0.37	-0.95
1419944_at	Ccnb1	cyclin B1	-1.15	0.836	-1.34	0.318	-1.13	0.823	2.59	0.107	-0.26
1424672_at	Dmxl1	Dmx-like 1	-1.39	0.18	1.02	0.906	-1.33	0.168	-1.27	0.098	-0.74
1419034_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	-1.08	0.836	-1.39	0.193	-1.18	0.524	1.36	0.187	-0.57
1451030_at	Akr1c21	aldo-keto reductase family 1, member C21	-1.22	0.206	-2.55	0.198	1.28	0.457	-1.45	0.077	-0.98
1452617_at	Ssbp1	single-stranded DNA binding protein 1	-1.45	0.408	-1.24	0.149	1	0.994	-1.56	0.291	-0.81
1452582_at	Galm	galactose mutarotase	-1.14	0.102	-1.27	0.277	-1.19	0.537	1.36	0.367	-0.56
1459619_at	Epb4.1l2	erythrocyte protein band 4.1-like 2	1.19	0.37	-1.23	0.56	-2.02	0.007	-1.63	0.116	-0.92
1449084_s_at	Sh3d19	SH3 domain protein D19	-1.42	0.311	-1.23	0.253	-1.02	0.931	1.34	0.234	-0.58
1452344_at	Synj2	synaptojanin 2	-1.66	0.4	-1.16	0.794	1.03	0.854	-1.75	0.157	-0.88
1451827_a_at	Nox4	NADPH oxidase 4	-1.14	0.299	-1.4	0.189	-1.11	0.706	1.72	0.267	-0.48
1441275_at	Kbtbd8	kelch repeat and BTB (POZ) domain containing 8	-1.03	0.963	-1.38	0.546	-1.25	0.641	1.21	0.512	-0.61
1427054_s_at	Abi3bp	ABI gene family, member 3 (NESH) binding protein	1.22	0.18	-1.51	0.096	-1.63	0.111	-1.52	0.286	-0.86
1443711_at	Chd8	Chromodomain helicase DNA binding protein 8	1.04	0.945	-1.53	0.184	-1.25	0.44	-1.19	0.708	-0.73
1453594_at	4930451G09Rik	RIKEN cDNA 4930451G09 gene	-1.02	0.858	-1.68	0.172	-1.08	0.837	1.02	0.895	-0.69
1457363_at	LOC654469	hypothetical protein LOC654469	-1.55	0.021	-1.36	0.161	1.12	0.508	-1.32	0.75	-0.78
1454322_at	4933404M09Rik	RIKEN cDNA 4933404M09 gene	1.14	0.854	-1.25	0.18	-1.79	0.364	-1.68	0.247	-0.89

1422040_at	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaph	-2.54	0.292	-1.68	0.367	1.51	0.464	-2.29	0.256	-1.25
1446805_at	Gabra2	Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	-2.2	0.022	-1	0.997	1.05	0.88	-2.66	0.206	-1.2
1447109_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.05	0.612	-1.16	0.594	-1.71	0.061	-1.18	0.311	-0.75
1424390_at	Nupl1	Nucleoporin like 1	-1.27	0.11	-1.22	0.261	-1.12	0.551	1.61	0.242	-0.5
1427955_a_at	Deb1	differentially expressed in B16F10 1	-1.19	0.018	-1.07	0.292	-1.37	0.077	1.19	0.324	-0.61
1428523_at	Lphn3	latrophilin 3	-2.05	0.454	1.12	0.855	-1.12	0.508	-1.69	0.083	-0.93
1438719_at	AI585793	expressed sequence AI585793	1.04	0.947	-1.31	0.216	-1.44	0.251	-1.09	0.793	-0.7
1452975_at	Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	-1.09	0.758	-2.08	0.036	1.1	0.571	-1.45	0.178	-0.88
1451262_a_at	Jtv1	JTV1 gene	-1.38	0.143	-1.09	0.55	-1.17	0.045	1.04	0.849	-0.65
1433400_at	5033405D04Rik	RIKEN cDNA 5033405D04 gene	-1.4	0.165	-1.08	0.712	-1.16	0.394	1.06	0.894	-0.65
1425372_at	Dnajc19	DnaJ (Hsp40) homolog, subfamily C, member 19	-1.36	0.489	-1.42	0.155	1.06	0.761	-1.16	0.5	-0.72
1458030_at	---	---	-1.95	0.088	1.11	0.604	-1.14	0.425	-1.51	0.043	-0.87
1440320_at	---	---	-1.25	0.225	1.1	0.692	-1.68	0.282	-1.22	0.31	-0.76
1453087_at	6330403L08Rik	RIKEN cDNA 6330403L08 gene	-1.12	0.223	-2.03	0.123	1.11	0.715	-1.27	0.417	-0.82
1447565_at	1700082C02Rik	RIKEN cDNA 1700082C02 gene	-1.06	0.852	-1.39	0.511	-1.2	0.781	1.03	0.974	-0.65
1458950_at	---	Transcribed locus	1.19	0.438	-1.57	0.544	-1.49	0.334	-1.2	0.724	-0.77
1425243_at	Cd207	CD 207 antigen	-2.59	0.337	1.76	0	-2.82	0.249	-1.61	0.168	-1.32
1460711_at	4930461P20Rik	RIKEN cDNA 4930461P20 gene	-1.15	0.173	-1.31	0.011	-1.15	0.206	1.17	0.267	-0.61
1437289_at	Impad1	inositol monophosphatase domain containing 1	-1.05	0.496	-1.01	0.89	-1.77	0.059	1.02	0.745	-0.7
1454113_at	4930472D12Rik	RIKEN cDNA 4930472D12 gene	-2.63	0.17	-1.09	0.624	1.2	0.756	-1.36	0.29	-0.97
1453715_at	Sv2c	synaptic vesicle glycoprotein 2c	-1.36	0.046	-1.04	0.911	-1.25	0.553	1.22	0.516	-0.61
1458493_a_at	---	---	-1.04	0.853	-1.19	0.688	-1.43	0.335	1.56	0.34	-0.52
1437273_at	Htra4	HtrA serine peptidase 4	-1.27	0.012	-1.4	0.23	1	0.996	-1.04	0.898	-0.68
1429282_at	Thap1	THAP domain containing, apoptosis associated protein 1	-1.4	0.232	-1.2	0.337	-1.05	0.863	1.24	0.206	-0.6
1454135_at	4930458K08Rik	RIKEN cDNA 4930458K08 gene	-1.55	0.34	-1.16	0.523	-1	0.992	1.02	0.952	-0.67
1444216_at	Emx1	empty spiracles homolog 1 (Drosophila)	1.03	0.957	-2.08	0.069	-1.01	0.968	-1.14	0.874	-0.8
1451472_at	3230401I01Rik	RIKEN cDNA 3230401I01 gene	1.1	0.79	-1.51	0.628	-1.36	0.691	-1.64	0.369	-0.85
1435360_at	Zfp651	zinc finger protein 651	-1.18	0.256	-1.41	0.051	-1.06	0.789	1.42	0.286	-0.56
1431540_at	4930511E03Rik	RIKEN cDNA 4930511E03 gene	-1.33	0.624	-1.01	0.979	-1.31	0.401	1.12	0.749	-0.63
1433421_at	4930527J03Rik	RIKEN cDNA 4930527J03 gene	-1.82	0.199	-1.01	0.976	-1.04	0.931	1.31	0.102	-0.64
1416838_at	Mut	methylmalonyl-Coenzyme A mutase	-1.21	0.091	-1.18	0.183	-1.21	0.238	1.03	0.878	-0.64
1457110_at	Pank1	pantothenate kinase 1	1.21	0.647	-1.52	0.059	-1.57	0.06	-1.21	0.394	-0.77
1458135_at	G630014P10Rik	RIKEN cDNA G630014P10 gene	1.35	0.566	-1.74	0.526	-1.73	0.115	-1.26	0.371	-0.85
1424849_at	Wdr62	WD repeat domain 62	-1.19	0.259	-1.26	0.786	-1.15	0.862	2.18	0.195	-0.35
1424353_at	Lrpprc	leucine-rich PPR-motif containing	-1.35	0.117	-1.26	0.074	-1.04	0.782	1.25	0.276	-0.6
1433370_at	4930474A20Rik	RIKEN cDNA 4930474A20 gene	-1.29	0.659	-1.65	0.22	1.12	0.428	-1.46	0.285	-0.82
1442123_at	2010012P19Rik	RIKEN cDNA 2010012P19 gene	-1.45	0.405	-1.09	0.829	-1.11	0.652	1.88	0.134	-0.44
1453734_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-1.59	0.012	1.06	0.739	-1.22	0.484	-1.13	0.491	-0.72
1440003_at	---	Transcribed locus	-1.21	0.215	-1.72	0.024	1.1	0.012	-1.16	0.571	-0.75
1430322_at	Arl13b	ADP-ribosylation factor-like 13B	-1.59	0.503	-1.15	0.745	1	0.994	-1.17	0.812	-0.73
1440900_at	Gpr174	G protein-coupled receptor 174	-1.34	0.551	-1.43	0.433	1.06	0.798	-2.05	0.147	-0.94
1448691_at	Ubqln4	ubiquilin 4	-1.23	0.196	-1.14	0.535	-1.23	0.449	1.12	0.282	-0.62
1454899_at	Lpp	LIM domain containing preferred translocation partner in lipoma	-1.07	0.533	1.01	0.88	-1.77	0.011	-1.36	0.298	-0.8
1460024_at	Tnrc6b	trinucleotide repeat containing 6b	-1.23	0.437	-1.09	0.038	-1.29	0.307	1.27	0.485	-0.59
1443017_at	Cpeb2	cytoplasmic polyadenylation element binding protein 2	-1.07	0.795	-1.59	0.107	-1.07	0.846	1.03	0.883	-0.67
1445449_at	Pde4b	Phosphodiesterase 4B, cAMP specific	1.41	0.279	-2.51	0.141	-1.43	0.329	-1.26	0.654	-0.95
1452419_at	Heatr1	HEAT repeat containing 1	-1.79	0.279	-1.7	0.298	1.36	0.724	-1.35	0.468	-0.87
1420140_at	Bcdin3	bin3, bicoid-interacting 3, homolog (Drosophila)	-1.15	0.487	-1.15	0.644	-1.31	0.047	1.01	0.954	-0.65
1435633_at	4631424J17Rik	RIKEN cDNA 4631424J17 gene	-1.18	0.577	-1.15	0.637	-1.27	0.374	1.16	0.547	-0.61
1435299_at	C230069N13	hypothetical protein C230069N13	-1.13	0.359	-1.22	0.235	-1.25	0.213	1.01	0.982	-0.65
1444812_at	Prdm10	PR domain containing 10	1.07	0.576	-1.37	0.587	-1.42	0.139	-1.1	0.745	-0.71
1452466_a_at	Rbm6	RNA binding motif protein 6	-1.23	0.416	-1.1	0.236	-1.28	0.267	1.26	0.196	-0.59
1454654_at	Dirc2	disrupted in renal carcinoma 2 (human)	-1.04	0.595	-1.35	0.206	-1.25	0.087	1.01	0.974	-0.66

1458491_at	4930422I07Rik	RIKEN cDNA 4930422I07 gene	-1.23	0.071	-1.18	0.514	-1.19	0.415	1.32	0.373	-0.57
1426550_at	Sidt1	SID1 transmembrane family, member 1	1.05	0.901	-1.62	0.155	-1.19	0.523	-1.9	0.264	-0.92
1436387_at	C330006P03Rik	RIKEN cDNA C330006P03 gene	-1.19	0.555	-1.03	0.873	-1.43	0.074	1.14	0.736	-0.63
1429594_at	Slc38a2	solute carrier family 38, member 2	-1.25	0.028	-1.45	0.047	1.01	0.95	-1.77	0.023	-0.86
1450058_at	Asph	aspartate-beta-hydroxylase	-1.09	0.637	-1.17	0.198	-1.38	0.179	1.61	0.392	-0.5
1430804_at	Slc13a1	solute carrier family 13 (sodium/sulphate symporters), member 1	-1.11	0.806	-1.13	0.809	-1.4	0.511	1.36	0.554	-0.57
1425909_at	---	CDNA clone MGC:11898 IMAGE:3598523	1.01	0.985	-1.28	0.548	-1.4	0.089	-1.3	0.278	-0.74
1443581_at	St6gal1	Beta galactoside alpha 2,6 sialyltransferase 1	-1.5	0.396	1.05	0.912	-1.26	0.322	-1.63	0.156	-0.84
1458290_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	1.12	0.399	-1.71	0.021	-1.24	0.006	-1.1	0.616	-0.73
1420770_at	Klk1b24	kallikrein 1-related peptidase b24	-1.96	0.008	1.35	0.32	-1.54	0.17	-1.65	0.131	-0.95
1447527_at	Irf2	Interferon regulatory factor 2	1.24	0.135	-1.26	0.042	-2.15	0.008	-1.73	0.201	-0.97
1447975_a_at	LOC545261	hypothetical protein LOC545261	-1.5	0.477	1.22	0.339	-1.61	0.039	-1.1	0.766	-0.75
1459932_at	D8Ertd28e	DNA segment, Chr 8, ERATO Doi 28, expressed	-1.38	0.359	1.15	0.862	-1.59	0.152	-2.26	0.117	-1.02
1429086_at	Grhl2	grainyhead-like 2 (Drosophila)	-1.06	0.619	-1.61	0.215	-1.07	0.777	1.01	0.973	-0.68
1428429_at	Rgmb	RGM domain family, member B	-1.36	0.116	-1.52	0.069	1.11	0.678	-1.2	0.65	-0.74
1444393_at	Rims1	Regulating synaptic membrane exocytosis 1	1.03	0.633	-1.99	0.039	-1.03	0.942	-1.11	0.91	-0.77
1433799_at	Rdh13	retinol dehydrogenase 13 (all-trans and 9-cis)	-1.39	0.173	-1.02	0.891	-1.23	0.075	1.02	0.86	-0.66
1444483_at	4931428D14Rik	RIKEN cDNA 4931428D14 gene	-1.26	0.013	1.05	0.949	-1.51	0.015	-1	0.986	-0.68
1434267_at	Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	-1.24	0.166	-1.25	0.137	-1.11	0.335	1.72	0.21	-0.47
1442369_at	4832406H04Rik	RIKEN cDNA 4832406H04 gene	-1.67	0.451	-1.99	0.238	1.41	0.066	-1.91	0.348	-1.04
1436114_at	Gm96	gene model 96, (NCBI)	-1.59	0.602	-1.36	0.633	1.14	0.752	-1.15	0.731	-0.74
1418173_at	Krt25	keratin 25	-1.46	0.461	1.07	0.834	-1.33	0.477	-1.6	0.313	-0.83
1456071_a_at	Cycs /// LOC67071	cytochrome c, somatic /// similar to Cytochrome c, somatic /// similar to Cytochron	-1.28	0.015	-1.28	0.01	-1.06	0.408	1.23	0.345	-0.6
1427011_a_at	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	-1.37	0.09	-1.34	0.009	1.03	0.859	-1.44	0.039	-0.78
1428359_s_at	1810010M01Rik	RIKEN cDNA 1810010M01 gene	-1.28	0.693	-1.35	0.554	-1.02	0.968	3.21	0.013	-0.11
1446119_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	1.12	0.64	-1.68	0.288	-1.26	0.559	-1.34	0.24	-0.79
1455810_a_at	E130112L23Rik ///	RIKEN cDNA E130112L23 gene /// similar to quattro	-1.08	0.751	-1.31	0.68	-1.23	0.351	1.73	0.28	-0.47
1420736_at	Sim1	single-minded homolog 1 (Drosophila)	-1.54	0.09	-1.16	0.823	-1	0.991	1.07	0.864	-0.66
1453029_s_at	1110059H15Rik	RIKEN cDNA 1110059H15 gene	-1.12	0.426	-1.3	0.035	-1.19	0.107	1.09	0.602	-0.63
1448461_a_at	Thoc7	THO complex 7 homolog (Drosophila)	-1.16	0.215	-1.15	0.238	-1.29	0.011	1.23	0.303	-0.59
1435976_at	---	---	-1.66	0.2	-1.18	0.305	1.06	0.76	-1.48	0.195	-0.81
1430972_x_at	Aqr	aquarius	-1.72	0.538	1.05	0.939	-1.14	0.673	-1.59	0.086	-0.85
1445923_at	1700055N04Rik	RIKEN cDNA 1700055N04 gene	-2.45	0.304	1.26	0.325	-1.18	0.14	-1.34	0.173	-0.93
1457856_at	---	---	-1.48	0.333	1.13	0.811	-1.42	0.146	-1.25	0.292	-0.76
1441465_at	Cnot3	CCR4-NOT transcription complex, subunit 3	-1.29	0.045	-1.22	0.158	-1.1	0.66	1.1	0.575	-0.63
1455384_x_at	D030056L22Rik	RIKEN cDNA D030056L22 gene	-1.06	0.492	-1.5	0.023	-1.11	0.275	1.64	0.233	-0.51
1457422_at	9030205A07Rik	RIKEN cDNA 9030205A07 Gene	-2.03	0.465	1.3	0.561	-1.39	0.639	-1.31	0.032	-0.86
1459922_at	AI646383	expressed sequence AI646383	1.1	0.713	-2.24	0.01	-1.04	0.907	-1.3	0.15	-0.87
1440573_at	Erbb2ip	Erbb2 interacting protein	1.04	0.849	-1.36	0.018	-1.36	0.056	-1.41	0.281	-0.77
1452254_at	Mtmr9	myotubularin related protein 9	-1.31	0.083	-1.22	0.125	-1.08	0.503	1.42	0.285	-0.55
1423766_at	Pak1ip1	PAK1 interacting protein 1	-1.28	0.027	-1.23	0.106	-1.1	0.056	1.13	0.445	-0.62
1432228_at	4933406B15Rik	RIKEN cDNA 4933406B15 gene	-1.88	0.048	1.13	0.803	-1.18	0.738	-2.21	0.184	-1.03
1442617_at	Cbfb	Core binding factor beta	1.02	0.951	-1.05	0.909	-1.9	0.011	-1.52	0.195	-0.86
1429056_at	Narg1l	NMDA receptor regulated 1-like	-1.06	0.685	-1.15	0.152	-1.43	0.019	1.28	0.438	-0.59
1440850_at	Rnf12	ring finger protein 12	1.2	0.237	-1.49	0.277	-1.57	0.036	-1.01	0.938	-0.72
1452219_at	Tmem63b	transmembrane protein 63b	-1.07	0.456	-1.33	0.044	-1.22	0.383	1.01	0.938	-0.65
1427595_at	Acaca /// LOC6722	acetyl-Coenzyme A carboxylase alpha /// similar to acetyl-coenzyme A carboxyla	-3.12	0.076	-1	0.998	1.19	0.634	-1.38	0.366	-1.08
1457716_at	Otud7b	OTU domain containing 7B	1.02	0.878	-1.25	0.31	-1.46	0.161	-1.24	0.067	-0.73
1459430_at	Gpr158	G protein-coupled receptor 158	-1.09	0.867	-1.2	0.16	-1.31	0.646	1.12	0.78	-0.62
1446914_at	C80425	expressed sequence C80425	-1.49	0.304	-1.21	0.683	1.01	0.968	-1.08	0.869	-0.69
1430411_at	6330525I24Rik	RIKEN cDNA 6330525I24 gene	-1.65	0.392	-1.39	0.273	1.18	0.701	-1.32	0.569	-0.79
1459272_at	Peli1	Pellino 1	-1.41	0.246	-1.22	0.517	-1.02	0.906	1.04	0.9	-0.65
1460318_at	Csrp3	cysteine and glycine-rich protein 3	-1.07	0.691	-1.12	0.255	-1.46	0.185	1.02	0.856	-0.66

1459219_at	---	---	-1.08	0.408	1.12	0.759	-2.18	0.011	-1.97	0.006	-1.02
1453483_at	1700023E05Rik	RIKEN cDNA 1700023E05 gene	-1.49	0.115	-1.18	0.061	-1.01	0.953	1.19	0.189	-0.62
1416337_at	Uqcrb	ubiquinol-cytochrome c reductase binding protein	-1.3	0.03	-1.19	0.12	-1.11	0.139	1.03	0.799	-0.64
1441016_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.85	0.159	-1.47	0.129	1.29	0.451	-1.5	0.223	-0.88
1455585_at	Rnf168	ring fnger protein 168	-1.02	0.612	-1.24	0.156	-1.38	0.033	1.59	0.169	-0.51
1448944_at	Nrp1	neuropilin 1	-1.02	0.865	-1.07	0.662	-1.68	0.023	1.02	0.93	-0.69
1427804_at	---	---	1.26	0.585	-1.11	0.878	-2.87	0.038	-1.16	0.605	-0.97
1416578_at	Rbx1	ring-box 1	-1.13	0.462	-1.18	0.575	-1.29	0.011	1.1	0.546	-0.62
1417202_s_at	Ube1c	ubiquitin-activating enzyme E1C	-1.18	0.042	-1.12	0.297	-1.3	0.047	1.01	0.92	-0.65
1439798_at	Hoxc10	homeo box C10	-1.2	0.262	-1.5	0.345	1.01	0.975	-1.67	0.453	-0.84
1432191_at	---	---	-2.88	0.124	1.23	0.747	-1.07	0.888	-1.9	0.419	-1.16
1434133_s_at	Wdr42a	WD repeat domain 42A	-1.16	0.52	-1.2	0.408	-1.22	0.253	1.15	0.533	-0.61
1432833_at	4933435G04Rik	RIKEN cDNA 4933435G04 gene	-1.08	0.148	-1.45	0.586	-1.11	0.577	1.22	0.064	-0.61
1423590_at	Napsa	napsin A aspartic peptidase	1.04	0.433	-2.02	0.209	-1.03	0.853	-1.85	0.201	-0.96
1458868_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	1.38	0.623	-2.16	0.024	-1.5	0.196	-1.75	0.165	-1.01
1442547_at	---	Transcribed locus	1.15	0.343	-1.55	0.555	-1.39	0.021	-1.26	0.417	-0.76
1441240_at	Rpa1	Replication protein A1	-1.66	0.61	1.14	0.735	-1.29	0.441	-1.17	0.472	-0.75
1445915_at	H2-K1	Histocompatibility 2, K1, K region	-1.26	0.167	-1.11	0.23	-1.23	0.128	1.1	0.46	-0.62
1454692_x_at	Hnrpk	Heterogeneous nuclear ribonucleoprotein K	-1.39	0.334	1.14	0.154	-1.54	0.105	-1.1	0.099	-0.72
1446991_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	1.18	0.447	-2.47	0.216	-1.08	0.878	-1.38	0.148	-0.94
1443877_a_at	Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	-1.7	0.059	1.17	0.682	-1.32	0.263	-1.21	0.652	-0.77
1448646_at	Wdr12	WD repeat domain 12	-1.18	0.267	-1.29	0.052	-1.13	0.47	1.29	0.43	-0.58
1445644_at	A830091I15Rik	RIKEN cDNA A830091I15 gene	-2.07	0.349	1.03	0.953	-1	0.996	-2.06	0.359	-1.03
1443818_at	---	---	1.21	0.487	-1.72	0.459	-1.39	0.589	-1.01	0.979	-0.73
1427353_at	Clasp1	CLIP associating protein 1	1.01	0.947	-1.68	0.029	-1.1	0.521	-1.54	0.074	-0.83
1435179_at	C130071C03Rik	RIKEN cDNA C130071C03 gene	-1.06	0.829	1.28	0.601	-3.58	0.021	-3.09	0.165	-1.61
1424909_at	Lrrc46	leucine rich repeat containing 46	-2.86	0.019	-1.04	0.831	1.2	0.489	-1.93	0.171	-1.16
1444060_at	2610027K06Rik	RIKEN cDNA 2610027K06 gene	-1.34	0.445	-2.33	0.207	1.33	0.447	-1.41	0.722	-0.93
1444166_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	1.02	0.908	-1.37	0.656	-1.33	0.553	-1.15	0.844	-0.7
1420264_at	---	---	-2.51	0.18	-1.23	0.654	1.3	0.524	-1.26	0.534	-0.92
1438079_at	BC050078	cDNA sequence BC050078	-1.03	0.925	-1.59	0.102	-1.1	0.516	1.05	0.678	-0.67
1442818_at	LOC671796 /// LOC	hypothetical protein LOC671796 /// hypothetical protein LOC675117	-1.47	0.476	-1.81	0.522	1.28	0.523	-1.24	0.083	-0.81
1441014_at	Atrx	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	1.1	0.882	-1.01	0.983	-2.37	0.018	-2.98	0.087	-1.31
1457440_at	Sstr4	somatostatin receptor 4	-1.12	0.771	-1.98	0.02	1.11	0.61	-2.09	0.049	-1.02
1450708_at	Scg2	secretogranin II	-3.58	0.01	2.01	0.134	-4.57	0.023	-1.3	0.722	-1.86
1458594_at	Shprh	SNF2 histone linker PHD RING helicase	-1.19	0.734	-2.1	0.252	1.19	0.674	-1.44	0.63	-0.88
1452193_a_at	Wasl	Wiskott-Aldrich syndrome-like (human)	-1.1	0.584	-1.21	0.059	-1.29	0.13	1.02	0.953	-0.65
1444454_at	Rb1	Retinoblastoma 1	-1.2	0.537	-1.05	0.893	-1.37	0.178	1.17	0.583	-0.61
1455541_a_at	4430402I18Rik	RIKEN cDNA 4430402I18 gene	-1.34	0.069	-1.39	0.452	1.05	0.833	-2.36	0.222	-1.01
1431646_a_at	Stx6	syntaxin 6	-1.01	0.984	-1.77	0.154	-1.05	0.85	1.06	0.369	-0.69
1421612_a_at	H2afy3 /// H2afy2	H2A histone family, member Y3 /// H2A histone family, member Y2	-1.19	0.149	-1.11	0.826	-1.29	0.147	1.38	0.318	-0.56
1424442_a_at	Pja2	praja 2, RING-H2 motif containing	-1.03	0.88	-1.23	0.076	-1.38	0.018	1.16	0.109	-0.62
1460629_at	Trim16	tripartite motif protein 16	-1.03	0.699	-1.41	0.386	-1.21	0.426	1.74	0.115	-0.48
1443226_at	5730470L24Rik	RIKEN cDNA 5730470L24 gene	1.03	0.881	-1.28	0.474	-1.43	0.067	-1.63	0.247	-0.83
1440849_at	6330417G04Rik	RIKEN cDNA 6330417G04 gene	-1.16	0.225	-1.14	0.658	-1.29	0.162	1	0.994	-0.65
1448989_a_at	Myo1b	myosin IB	-1.02	0.965	-1.21	0.142	-1.41	0.173	1.05	0.91	-0.65
1453860_s_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	-1.53	0.484	-1.24	0.401	1.05	0.768	-1.01	0.985	-0.68
1427152_at	Qser1	glutamine and serine rich 1	-1.29	0.159	-1.05	0.828	-1.27	0.112	1.01	0.959	-0.65
1451638_s_at	Armc1 /// LOC6343	armadillo repeat containing 1 /// similar to armadillo repeat-containing protein	-1.13	0.316	-1.16	0.015	-1.3	0.107	1.35	0.256	-0.56
1424530_at	Sec14l2	SEC14-like 2 (S. cerevisiae)	-1.01	0.953	-1.43	0.051	-1.22	0.303	4.28	0.173	0.16
1436061_at	---	---	1.03	0.789	-1.57	0.174	-1.17	0.434	-1.96	0.286	-0.92
1443196_at	---	---	1.07	0.76	-1.6	0.127	-1.23	0.469	-1.42	0.389	-0.79
1453287_at	5730557B15Rik	RIKEN cDNA 5730557B15 gene	1.18	0.291	-1.61	0.075	-1.41	0.076	-1.4	0.018	-0.81

1422611_s_at	Igf2bp3	insulin-like growth factor 2 mRNA binding protein 3	-1.31	0.606	-1.85	0.174	1.21	0.726	-1.18	0.788	-0.78
1454263_at	Gscl	goosecoid-like	-1.8	0.411	1.07	0.837	-1.13	0.626	-1.44	0.508	-0.82
1437774_at	1700020I14Rik	RIKEN cDNA 1700020I14 gene	-1.04	0.559	-1.1	0.639	-1.54	0.09	1.71	0.106	-0.5
1448059_at	Mipol1	mirror-image polydactyly gene 1 homolog (human)	-2.21	0.428	1.46	0.475	-1.65	0.159	-1.04	0.961	-0.86
1438369_x_at	Tmem85	transmembrane protein 85	1	0.996	-1.24	0.081	-1.42	0.163	-1.54	0.411	-0.8
1445592_at	---	---	-1.09	0.905	-1.25	0.297	-1.25	0.672	1.27	0.765	-0.58
1457999_at	2410005O16Rik	RIKEN cDNA 2410005O16 gene	1.04	0.862	-1.22	0.204	-1.54	0.079	-1.15	0.666	-0.71
1423137_at	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	1.02	0.797	-1.28	0.051	-1.41	0.036	-1.86	0.101	-0.88
1424584_a_at	Ranbp10	RAN binding protein 10	-1.24	0.139	-1.22	0.018	-1.12	0.265	3.17	0.117	-0.1
1447530_at	F8a	Factor 8-associated gene A	1.09	0.909	-1.21	0.755	-1.68	0.297	-1.54	0.58	-0.83
1452885_at	Sfrs2ip	splicing factor, arginine/serine-rich 2, interacting protein	-1.17	0.452	-1.3	0.076	-1.12	0.745	1.29	0.224	-0.58
1437156_at	Efcbp1	EF hand calcium binding protein 1	-1.02	0.97	-1.21	0.22	-1.41	0.234	2.24	0.021	-0.35
1433420_at	4930527J03Rik	RIKEN cDNA 4930527J03 gene	-1.11	0.679	-1.01	0.961	-1.59	0.013	1.33	0.263	-0.59
1439337_at	Tom1l1	target of myb1-like 1 (chicken)	-1.67	0.114	-1.11	0.704	1.02	0.694	-1.47	0.207	-0.81
1460056_at	1700109F18Rik	RIKEN cDNA 1700109F18 gene	1.13	0.16	-2.25	0.461	-1.06	0.861	-1.48	0.295	-0.92
1455551_at	Uevld	UEV and lactate/malate dehyrogenase domains	-1.35	0.059	-1.11	0.084	-1.15	0.133	1.15	0.503	-0.61
1429355_at	3300001K11Rik	RIKEN cDNA 3300001K11 gene	-1.1	0.853	1.15	0.436	-2.22	0.105	-1.17	0.885	-0.83
1415714_a_at	2610209M04Rik	RIKEN cDNA 2610209M04 gene	-1.13	0.176	-1.31	0.014	-1.15	0.058	1.17	0.304	-0.61
1457466_at	AA409368	expressed sequence AA409368	1.14	0.429	-1.03	0.944	-2.49	0.025	-1.26	0.616	-0.91
1429555_at	Cldnd1	claudin domain containing 1	-1.17	0.244	-1.08	0.229	-1.36	0.174	1.12	0.367	-0.62
1439450_x_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	1.02	0.927	-1.24	0.133	-1.45	0.011	-2.17	0.131	-0.96
1454403_at	4930466I24Rik	RIKEN cDNA 4930466I24 gene	-1.74	0.225	1.38	0.393	-1.79	0.167	-1.17	0.559	-0.83
1457932_at	Hivep2	Human immunodeficiency virus type I enhancer binding protein 2	1.07	0.654	-2.19	0.306	-1.01	0.982	-2.93	0.253	-1.27
1422234_at	Tacr2	tachykinin receptor 2	-1.39	0.296	-1.23	0.49	-1.02	0.969	1.04	0.931	-0.65
1441635_at	Olfml2a	Olfactomedin-like 2A	-1.4	0.094	1.01	0.949	-1.26	0.203	-1.27	0.075	-0.73
1440015_at	---	Transcribed locus	-1.21	0.164	1.12	0.744	-1.77	0.043	-2	0.004	-0.96
1441497_at	AA388235	expressed sequence AA388235	-1.76	0.015	-1.06	0.863	-1	0.991	1.19	0.547	-0.65
1432089_at	4930550C17Rik	RIKEN cDNA 4930550C17 gene	1.06	0.941	-1.17	0.712	-1.67	0.349	-1.61	0.368	-0.85
1447280_at	Dtna	Dystrobrevin alpha	-1.46	0.04	1.09	0.88	-1.34	0.455	-1.07	0.905	-0.7
1441995_at	Ncam1	Neural cell adhesion molecule 1	-1.03	0.967	-1.58	0.329	-1.1	0.775	1.03	0.863	-0.67
1444012_at	Yipf3	Yip1 domain family, member 3	-1.35	0.405	-1.36	0.214	1.04	0.833	-2.05	0.051	-0.93
1429031_at	4833408D11Rik	RIKEN cDNA 4833408D11 gene	1.1	0.684	-1.57	0.117	-1.29	0.121	-1.7	0.019	-0.86
1446572_at	Usp53	Ubiquitin specific peptidase 53	1.12	0.445	-1.31	0.453	-1.58	0.217	-2.03	0.495	-0.95
1449987_at	Alk	anaplastic lymphoma kinase	1.07	0.505	-1.44	0.492	-1.33	0.115	-1.34	0.34	-0.76
1425806_a_at	Surb7	SRB7 (suppressor of RNA polymerase B) homolog (S. cerevisiae)	-1.26	0.076	-1.09	0.531	-1.24	0.126	1.08	0.708	-0.63
1445623_at	---	---	1.6	0.342	-1.97	0.277	-2.47	0.004	-1.03	0.849	-0.97
1457990_at	Anks1b /// LOC544	ankyrin repeat and sterile alpha motif domain containing 1B /// similar to AIDA-1b	1.07	0.832	-1.88	0.193	-1.09	0.779	-2.25	0.233	-1.04
1429966_at	3110057O12Rik	RIKEN cDNA 3110057O12 gene	-1.27	0.454	-1.23	0.426	-1.09	0.794	1.08	0.618	-0.63
1433986_at	BC024659	cDNA sequence BC024659	-1.03	0.82	-1.08	0.193	-1.61	0.003	1.27	0.086	-0.61
1439081_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	1.13	0.531	-1.36	0.336	-1.54	0.106	-1.52	0.05	-0.82
1426773_at	Mfn1	mitofusin 1	-1.07	0.488	-1.42	0.033	-1.13	0.572	1.39	0.024	-0.56
1435434_at	Braf	Braf transforming gene	-1.18	0.335	-1.01	0.909	-1.46	0.035	1.01	0.963	-0.66
1435589_at	Ccdc85b	coiled-coil domain containing 85B	1.08	0.741	-1.57	0.074	-1.25	0.351	-1.55	0.156	-0.82
1457220_at	---	---	1	0.999	-1.28	0.395	-1.36	0.075	-1.16	0.6	-0.7
1444105_at	Acta2	actin, alpha 2, smooth muscle, aorta	-1.46	0.148	1.05	0.822	-1.29	0.543	-4.08	0.22	-1.44
1419613_at	Col7a1	procollagen, type VII, alpha 1	-1.18	0.298	-1.1	0.615	-1.31	0.502	1.12	0.522	-0.62
1448362_at	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	-1.98	0.467	-1.74	0.201	1.44	0.187	-2.49	0.201	-1.19
1446472_at	Ahctf1	AT hook containing transcription factor 1	-1.07	0.621	-1.26	0.235	-1.26	0.223	1.54	0.018	-0.51
1416544_at	Ezh2	enhancer of zeste homolog 2 (Drosophila)	-1.23	0.03	-1.18	0.16	-1.17	0.472	2.01	0.235	-0.39
1460612_at	Ranbp3	RAN binding protein 3	1.08	0.824	-1.54	0.187	-1.27	0.393	-1.12	0.145	-0.71
1423362_at	Sort1	sortilin 1	-1.14	0.411	-1.51	0.112	-1.02	0.929	1.35	0.236	-0.58
1458043_at	Btbd9	BTB (POZ) domain containing 9	-1.31	0.397	1.05	0.713	-1.42	0.054	-1.04	0.838	-0.68
1435987_x_at	1110059G02Rik	RIKEN cDNA 1110059G02 gene	-1.64	0.076	1.08	0.718	-1.21	0.219	-1.1	0.477	-0.72

1438260_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	-1.08	0.477	-1.19	0.628	-1.34	0.225	2.31	0.246	-0.32
1442761_at	Tpd52l2	Tumor protein D52-like 2	-2.18	0.061	1.14	0.679	-1.09	0.608	-1.24	0.523	-0.84
1434211_at	Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	-1.28	0.112	-1.2	0.374	-1.1	0.635	1.04	0.661	-0.64
1422579_at	Hspe1 /// LOC6284	heat shock protein 1 (chaperonin 10) /// similar to 10 kDa heat shock protein, mitc	-1.36	0.156	-1.34	0.039	1.04	0.865	-1.39	0.117	-0.76
1420810_at	1500003O03Rik	RIKEN cDNA 1500003O03 gene	-1.07	0.513	-1.48	0.076	-1.1	0.619	1.09	0.649	-0.64
1447411_at	Ugdh	UDP-glucose dehydrogenase	-1.33	0.422	1.08	0.647	-1.46	0.177	-1.51	0.01	-0.8
1429691_at	5430405N12Rik	RIKEN cDNA 5430405N12 gene	1.07	0.672	-1.29	0.265	-1.49	0.071	-1.08	0.87	-0.7
1457483_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	1.44	0.504	-1.36	0.184	-2.92	0.018	-1.68	0.036	-1.13
1459735_at	C430014M02Rik	RIKEN cDNA C430014M02 gene	-1.18	0.439	1.04	0.899	-1.56	0.027	-1.67	0.031	-0.85
1424257_at	Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	-1.19	0.094	-1.28	0.379	-1.11	0.524	1.11	0.547	-0.62
1435892_at	Asxl3	additional sex combs like 3 (Drosophila)	-1.41	0.329	-1.69	0.432	1.22	0.625	-2.68	0.315	-1.14
1454145_at	Pla2r1	phospholipase A2 receptor 1	1.67	0.362	-2.67	0.163	-2.09	0.177	-1.12	0.64	-1.05
1454639_x_at	Rpl41 /// 2210411K	ribosomal protein L41 /// RIKEN cDNA 2210411K19 gene	-1.36	0.069	1.11	0.589	-1.48	0.143	-1.13	0.671	-0.72
1454286_at	1110004M10Rik	RIKEN cDNA 1110004M10 gene	-1.22	0.295	1.01	0.949	-1.45	0.127	-2.1	0.044	-0.94
1454519_at	4930429L21Rik	RIKEN cDNA 4930429L21 gene	-2.37	0.085	1.2	0.834	-1.11	0.796	-1.05	0.8	-0.83
1454201_a_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	1.14	0.765	-1.45	0.169	-1.45	0.251	-1.52	0.615	-0.82
1427759_a_at	Art5	ADP-ribosyltransferase 5	1.26	0.658	-1.26	0.706	-2.12	0.28	-1.09	0.81	-0.8
1458807_at	Epb4.1	erythrocyte protein band 4.1	-1.01	0.983	-1.05	0.746	-1.74	0.135	2.9	0.199	-0.22
1445607_at	4833418A01Rik	RIKEN cDNA 4833418A01 gene	-1.38	0.185	1.13	0.566	-1.49	0.055	-1.29	0.383	-0.76
1441083_at	Clptm1	cleft lip and palate associated transmembrane protein 1	-2.72	0.059	1.2	0.432	-1.04	0.858	-1.05	0.801	-0.91
1418367_x_at	Hist2h3c1 /// Hist2h	histone 2, H3c1 /// histone 2, H2aa1 /// histone 1, H2ad /// histone 1, H2an /// hist	-1.15	0.228	-1.37	0.027	-1.08	0.517	1	0.985	-0.65
1419600_at	Defb4	defensin beta 4	-1.42	0.464	-1.26	0.582	1.02	0.964	-1.14	0.82	-0.7
1452052_s_at	Eif3s1	eukaryotic translation initiation factor 3, subunit 1 alpha	-1.15	0.279	-1.23	0.009	-1.19	0.019	1.31	0.327	-0.57
1416705_at	Rpe	ribulose-5-phosphate-3-epimerase	-1.08	0.329	-1.34	0.045	-1.18	0.164	1.04	0.844	-0.64
1446530_at	---	---	-1.38	0.53	-1.46	0.434	1.11	0.791	-1.52	0.062	-0.81
1445885_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	1.11	0.79	-1.17	0.611	-1.8	0.025	-1.01	0.972	-0.72
1455447_at	D430019H16Rik	RIKEN cDNA D430019H16 gene	1.08	0.76	-1.2	0.58	-1.63	0.259	-1.71	0.048	-0.87
1458067_at	A430041B07Rik	RIKEN cDNA A430041B07 gene	-1.4	0.06	-1.36	0.483	1.08	0.639	-2.18	0.008	-0.97
1424346_at	Ppp6c	protein phosphatase 6, catalytic subunit	-1.15	0.286	-1.13	0.07	-1.3	0.063	1.15	0.409	-0.61
1455045_at	Srr	serine racemase	-1.14	0.204	-1.15	0.202	-1.29	0.133	1.19	0.04	-0.6
1451785_at	Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	-1.61	0.253	-1.32	0.44	1.14	0.351	-1.58	0.278	-0.84
1443507_at	Slc4a1ap	Solute carrier family 4 (anion exchanger), member 1, adaptor protein	1.37	0.589	-1.45	0.223	-2.15	0.044	-1.34	0.438	-0.89
1420312_s_at	---	---	1.14	0.555	-1.17	0.466	-1.91	0.02	-1.38	0.351	-0.83
1445922_at	Xrcc4	X-ray repair complementing defective repair in Chinese hamster cells 4	-1.23	0.031	1	0.999	-1.42	0	-1.69	0.061	-0.83
1447184_at	AU021760	expressed sequence AU021760	1.04	0.393	-1.22	0.446	-1.52	0.13	-1.29	0.32	-0.75
1432363_at	2410018E23Rik	RIKEN cDNA 2410018E23 gene	-1.39	0.468	1.05	0.944	-1.33	0.531	-1.04	0.925	-0.68
1449576_at	Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	-1.04	0.886	-1.22	0.208	-1.36	0.089	1.52	0.2	-0.52
1434524_at	Eif2b3	eukaryotic translation initiation factor 2B, subunit 3	-1.26	0.034	-1.19	0.171	-1.12	0.32	1.65	0.319	-0.48
1447556_x_at	1700094D03Rik	RIKEN cDNA 1700094D03 gene	-1.53	0.274	-1.21	0.69	1.04	0.911	-1.46	0.315	-0.79
1454160_at	4930483C13Rik	RIKEN cDNA 4930483C13 gene	-1.41	0.533	-1.16	0.613	-1.05	0.92	1.05	0.882	-0.64
1443267_at	Tanc2	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-1.14	0.656	-1.17	0.685	-1.27	0.186	1.24	0.505	-0.58
1424183_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	-1.22	0.073	-1.47	0.044	1.03	0.796	-1.03	0.685	-0.68
1439075_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	-1.05	0.721	-1.22	0.314	-1.33	0.284	1.09	0.77	-0.63
1455011_at	Stard4	StAR-related lipid transfer (START) domain containing 4	-1.06	0.632	-1.07	0.643	-1.55	0.007	1.01	0.985	-0.67
1455287_at	Cdk6	cyclin-dependent kinase 6	-1.15	0.208	-1.02	0.744	-1.49	0.117	1.26	0.348	-0.6
1457516_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	-3.51	0.169	-1.15	0.753	1.37	0.117	-1.69	0.364	-1.25
1458219_at	Bcas2	breast carcinoma amplified sequence 2	1.07	0.864	-1.59	0.218	-1.22	0.297	-1.1	0.729	-0.71
1437039_at	Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	-1.14	0.235	-1.12	0.212	-1.33	0.028	1.42	0.308	-0.54
1441133_at	Stx6	Syntaxin 6	1.08	0.859	-1.79	0.105	-1.13	0.721	-1.46	0.075	-0.82
1455521_at	Klf12	Kruppel-like factor 12	1.03	0.703	-1.15	0.126	-1.61	0.023	-1.54	0.191	-0.82
1429897_a_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	-1.19	0.773	-1.56	0.122	1.05	0.8	-1.08	0.591	-0.7
1458631_at	4921533L14Rik	RIKEN cDNA 4921533L14 gene	-3.43	0.027	1.73	0.32	-1.99	0.13	-2.35	0.257	-1.51
1419341_at	Epha8	Eph receptor A8	-2.52	0.207	-1.46	0.46	1.44	0.358	-1.05	0.921	-0.9

1439868_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330108B	-1.13	0.381	-1.31	0.167	-1.14	0.451	1.33	0.456	-0.56
1457560_at	Ssbp3	Single-stranded DNA binding protein 3	-1.05	0.85	-1.15	0.721	-1.43	0.041	1.38	0.465	-0.56
1417511_at	Lyar	Ly1 antibody reactive clone	-1.15	0.168	-1.16	0.011	-1.26	0.081	1.15	0.55	-0.61
1454346_at	4930540E01Rik	RIKEN cDNA 4930540E01 gene	-1.17	0.724	-1.2	0.424	-1.2	0.171	1.25	0.515	-0.58
1422927_at	Yipf7	Yip1 domain family, member 7	-1.54	0.02	-1.62	0.497	1.26	0.144	-1.01	0.975	-0.73
1417770_s_at	---	---	-1.2	0.207	-1.11	0.363	-1.26	0.187	1.39	0.374	-0.55
1440152_x_at	Edf1 /// LOC665181	endothelial differentiation-related factor 1 /// similar to Endothelial differentiation-r	-1.52	0.354	-1.4	0.095	1.15	0.288	-1.37	0.302	-0.79
1442100_at	Inpp5f	inositol polyphosphate-5-phosphatase F	-1.25	0.177	1.09	0.666	-1.58	0.136	-1.81	0.109	-0.89
1419028_at	Arpp21	cyclic AMP-regulated phosphoprotein, 21	-1.32	0.486	-1.26	0.735	-1.03	0.9	1.01	0.96	-0.65
1441806_at	Chd1l	Chromodomain helicase DNA binding protein 1-like	-1.37	0.482	-1.24	0.486	-1.01	0.988	1.22	0.14	-0.6
1423749_s_at	Rangap1	RAN GTPase activating protein 1	-1.3	0.369	-1.31	0.192	-1.01	0.94	1.5	0.15	-0.53
1446145_at	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	-1.86	0.258	1.2	0.51	-1.27	0.246	-1.04	0.899	-0.74
1417486_at	Shd	src homology 2 domain-containing transforming protein D	1.19	0.258	-2.35	0.286	-1.1	0.786	-1.44	0.616	-0.93
1421114_a_at	Dspg3	dermatan sulphate proteoglycan 3	-2.67	0.042	-1.45	0.359	1.46	0.063	-1.25	0.617	-0.98
1459635_at	Dlgh1	Discs, large homolog 1 (Drosophila)	1.04	0.871	-1.05	0.832	-1.91	0.021	-1.26	0.252	-0.79
1438496_a_at	6330505F04Rik	RIKEN cDNA 6330505F04 gene	-1.2	0.498	-1.02	0.954	-1.41	0.034	1.4	0.284	-0.56
1418800_at	Bhlhb8	basic helix-loop-helix domain containing, class B, 8	-1.09	0.869	-1.12	0.808	-1.4	0.235	1.55	0.195	-0.51
1443554_at	Ssbp3	Single-stranded DNA binding protein 3	-1.17	0.278	-1.17	0.706	-1.22	0.47	1.7	0.267	-0.47
1443820_x_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	1.12	0.586	-1.3	0.298	-1.56	0.014	-1.58	0.286	-0.83
1420094_at	Hnrpdl	Heterogeneous nuclear ribonucleoprotein D-like	-2.94	0.122	-1.26	0.69	1.39	0.261	-1.43	0.122	-1.06
1417774_at	Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	-1.02	0.941	-1.27	0.357	-1.32	0.171	1.25	0.29	-0.59
1420360_at	Dkk1	dickkopf homolog 1 (Xenopus laevis)	-1.55	0.159	1.28	0.566	-1.67	0.224	-1.47	0.345	-0.85
1452475_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	-1.36	0.153	1.02	0.897	-1.29	0.205	-1.37	0.125	-0.75
1436431_at	1700025G04Rik	RIKEN cDNA 1700025G04 gene	-1.01	0.876	-1.36	0.502	-1.25	0.443	1.16	0.711	-0.61
1441652_at	Bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	1.04	0.927	-1.29	0.701	-1.4	0.087	-1.1	0.879	-0.69
1447456_x_at	LOC671351	similar to common salivary protein 1	-1.19	0.703	-1.66	0.218	1.08	0.599	-1.56	0.151	-0.83
1455707_at	C130037N17Rik	RIKEN cDNA C130037N17 gene	1.08	0.373	-2.02	0.16	-1.06	0.747	-1.56	0.062	-0.89
1438973_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.55	0.202	1.01	0.923	-1.15	0.741	-1.2	0.235	-0.72
1444900_at	D18Ertd289e	DNA segment, Chr 18, ERATO Doi 289, expressed	1.12	0.74	-1.32	0.423	-1.55	0.275	-1.06	0.855	-0.7
1424182_at	Acat1	acetyl-Coenzyme A acetyltransferase 1	-1.25	0.125	-1.51	0.204	1.07	0.663	-1.13	0.657	-0.71
1430214_a_at	2610020H08Rik	RIKEN cDNA 2610020H08 gene	-1.09	0.697	-1.22	0.421	-1.27	0.4	1.09	0.674	-0.62
1446964_at	---	---	1.31	0.729	-1.25	0.685	-2.37	0.187	-1.29	0.715	-0.9
1429318_a_at	Qk	quaking	-1.12	0.514	-1.11	0.396	-1.37	0.05	1.27	0.096	-0.58
1439338_at	LOC620417	hypothetical protein LOC620416	1.14	0.868	-1.45	0.586	-1.43	0.405	-1.2	0.787	-0.73
1453141_at	0610009L18Rik	RIKEN cDNA 0610009L18 gene	-1.13	0.414	-1.64	0.026	1.03	0.573	-1.61	0.23	-0.84
1416678_at	Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	-1.14	0.094	-1.17	0.028	-1.26	0.183	1.06	0.7	-0.63
1432003_a_at	Rnf41	ring finger protein 41	-1.57	0.016	-1.23	0.065	1.08	0.577	-1.46	0.012	-0.8
1444087_at	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	1.12	0.815	-1.48	0.33	-1.37	0.073	-1.06	0.771	-0.7
1416539_at	Siae	sialic acid acetylesterase	-1.22	0.282	-1.21	0.095	-1.13	0.243	1.02	0.866	-0.64
1439365_at	Myt1	Myelin transcription factor 1	-1.47	0.465	-2.69	0.043	1.47	0.542	-1.14	0.846	-0.96
1444916_at	---	PREDICTED: Mus musculus similar to Kinesin-Like Protein family member (klp-6	-1.29	0.726	-1.89	0.225	1.23	0.718	-1.34	0.33	-0.83
1447984_at	D1Ertd75e	DNA segment, Chr 1, ERATO Doi 75, expressed	1.07	0.739	-1.23	0.225	-1.55	0.13	-1.29	0.423	-0.75
1454745_at	Arhgap29	Rho GTPase activating protein 29	1.02	0.803	-1.15	0.441	-1.56	0.022	-1.34	0.021	-0.76
1459788_at	AI790205	expressed sequence AI790205	-1.65	0.221	-1.06	0.752	-1.03	0.846	1.12	0.543	-0.65
1418974_at	Blzf1	basic leucine zipper nuclear factor 1	-1.53	0.111	-1.28	0.464	1.09	0.816	-1	0.994	-0.68
1437789_at	Birc6	baculoviral IAP repeat-containing 6	1.15	0.411	-1.35	0.073	-1.57	0.039	-1.48	0.229	-0.81
1459495_at	Tmem16a	Transmembrane protein 16A	-1.16	0.773	-1.12	0.625	-1.3	0.023	1.01	0.971	-0.64
1448910_at	Pecr	peroxisomal trans-2-enoyl-CoA reductase	-1.42	0.094	-1.35	0.027	1.08	0.699	-1.08	0.451	-0.69
1422299_a_at	Styxl1	serine/threonine/tyrosine interacting-like 1	-1.32	0.005	-1.27	0.189	-1.02	0.946	1.23	0.029	-0.59
1458293_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	-1.49	0.251	-1.2	0.589	1.02	0.911	-1.07	0.752	-0.68
1446628_at	Zbtb24	zinc finger and BTB domain containing 24	1.11	0.788	-1.1	0.85	-1.99	0.024	-1.2	0.619	-0.79
1433611_s_at	Bud31	BUD31 homolog (yeast)	-1.09	0.186	-1.12	0.204	-1.41	0.054	1.12	0.57	-0.62
1453823_a_at	A930028L21Rik	RIKEN cDNA A930028L21 gene	-1.02	0.975	-2.18	0.112	1.08	0.678	-1.25	0.656	-0.84

1419725_at	Slc26a4	solute carrier family 26, member 4	-1.79	0.003	-1.54	0.503	1.32	0.269	-1.2	0.447	-0.8
1451542_at	Ssbp2	single-stranded DNA binding protein 2	-1.27	0.596	-1.02	0.936	-1.32	0.023	1.19	0.486	-0.6
1417778_at	Zfp35	zinc finger protein 35	-1.14	0.654	-1.05	0.64	-1.43	0.012	1.05	0.788	-0.64
1451177_at	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	-1.06	0.834	-1.19	0.176	-1.35	0.13	2.39	0.23	-0.3
1446272_at	Pctk2	PCTAIRE-motif protein kinase 2	-1.49	0.077	1.18	0.585	-1.48	0.04	-1.63	0.169	-0.86
1455584_at	Sdf4	stromal cell derived factor 4	1.05	0.77	-1.14	0.452	-1.66	0.012	-1.07	0.69	-0.71
1418534_at	---	---	1.17	0.652	-1.75	0.338	-1.27	0.348	-1.08	0.829	-0.73
1426727_s_at	Ppp1r10	protein phosphatase 1, regulatory subunit 10	-1.08	0.812	-1.45	0.34	-1.09	0.426	1.21	0.326	-0.6
1442275_at	4933402J07Rik	RIKEN cDNA 4933402J07 gene	-1.06	0.241	-1.18	0.204	-1.36	0.386	1.26	0.46	-0.58
1422264_s_at	Klf9	Kruppel-like factor 9	-1.09	0.747	-1.1	0.673	-1.42	0.011	1.25	0.329	-0.59
1437077_at	AW495713	expressed sequence AW495713	-1.18	0.107	-1.4	0.021	-1.03	0.857	1	0.98	-0.65
1421234_at	Tcf1	transcription factor 1	-2.12	0.391	1.47	0.002	-1.71	0.138	-2.77	0.003	-1.28
1432734_at	4933402E15Rik	RIKEN cDNA 4933402E15 gene	-1.34	0.403	1.12	0.675	-1.51	0.355	-1.41	0.262	-0.78
1426610_a_at	Ttf1	transcription termination factor 1	-1.24	0.535	-1.12	0.371	-1.2	0.259	1.14	0.354	-0.61
1442513_at	BC016423 /// LOC6	cDNA sequence BC016423 /// similar to cDNA sequence BC016423	1.06	0.934	-1.27	0.219	-1.46	0.233	-1.19	0.726	-0.72
1452888_at	1110034G24Rik	RIKEN cDNA 1110034G24 gene	-1.08	0.539	-1.04	0.787	-1.54	0.085	1	0.956	-0.67
1443293_at	---	---	1.17	0.658	-1.37	0.426	-1.6	0.071	-1.61	0.187	-0.85
1419203_at	Gtlf3a	gene trap locus F3a	-1.06	0.86	-1.14	0.531	-1.41	0.095	2.05	0.239	-0.39
1418111_at	1810008K16Rik	RIKEN cDNA 1810008K16 gene	-1.28	0.693	-1.57	0.226	1.11	0.844	-1.25	0.765	-0.75
1442284_at	---	---	-1.29	0.136	-1.61	0.059	1.13	0.518	-1.44	0.12	-0.8
1454497_at	5230401M06Rik	RIKEN cDNA 5230401M06 gene	-1.42	0.262	-1.34	0.244	1.08	0.846	-2.56	0.101	-1.06
1454751_at	G430022H21Rik	RIKEN cDNA G430022H21 gene	-1.19	0.028	-1.16	0.464	-1.21	0.282	1.03	0.747	-0.63
1448681_at	Il15ra	interleukin 15 receptor, alpha chain	-1.38	0.187	-1.33	0.32	1.05	0.819	-1.24	0.489	-0.72
1429093_at	Ddi2	DNA-damage inducible protein 2	-1.27	0.113	-1.05	0.447	-1.26	0.138	1.53	0.123	-0.51
1439124_at	9530020G05Rik	RIKEN cDNA 9530020G05 gene	-1.26	0.316	-1.15	0.509	-1.15	0.572	1.31	0.241	-0.56
1429219_at	1200009F10Rik	RIKEN cDNA 1200009F10 gene	-1.1	0.054	-1.04	0.85	-1.51	0.003	1.29	0.167	-0.59
1445357_at	AI851613	expressed sequence AI851613	-1.53	0.502	1.23	0.288	-1.54	0.317	-1.14	0.782	-0.75
1434426_at	B130055D15Rik	RIKEN cDNA B130055D15 gene	-1.15	0.424	-1.19	0.593	-1.22	0.362	1.97	0.174	-0.4
1429065_at	1200009F10Rik	RIKEN cDNA 1200009F10 gene	-1.11	0.357	1.09	0.618	-1.85	0.022	-1.3	0.156	-0.79
1416269_at	Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	-1.14	0.193	-1.28	0.063	-1.15	0.33	1.12	0.417	-0.61
1440632_at	Pcdhb4	protocadherin beta 4	1.16	0.693	-1.51	0.525	-1.4	0.338	-1.37	0.652	-0.78
1440160_x_at	2010321M09Rik	RIKEN cDNA 2010321M09 gene	-1.28	0.001	-1.3	0.448	-1.02	0.936	1.07	0.41	-0.63
1416680_at	Ube3a	ubiquitin protein ligase E3A	1.02	0.878	-1.18	0.237	-1.51	0.021	-1.63	0.045	-0.82
1423679_at	2810432L12Rik	RIKEN cDNA 2810432L12 gene	-1.08	0.582	-1.42	0.092	-1.11	0.106	1.5	0.286	-0.53
1431455_at	4933401B01Rik	RIKEN cDNA 4933401B01 gene	-1.01	0.978	-1.51	0.34	-1.14	0.773	1.21	0.542	-0.61
1430736_at	9030411M15Rik ///	RIKEN cDNA 9030411M15 gene /// similar to CG8486-PA, isoform A /// similar to	-2.1	0.252	1.47	0.632	-1.72	0.289	-1.02	0.956	-0.84
1417175_at	Csnk1e	casein kinase 1, epsilon	-1.17	0.652	-1.18	0.553	-1.21	0.215	1.15	0.701	-0.6
1434923_at	2810437L13Rik	RIKEN cDNA 2810437L13 gene	-1.2	0.283	-1.13	0.161	-1.24	0.136	1.24	0.348	-0.58
1436914_at	Ctdspl2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	-1	0.92	-1.13	0.264	-1.53	0.002	1.23	0.353	-0.61
1458469_at	Cblb	Casitas B-lineage lymphoma b	1.04	0.88	-1.1	0.432	-1.72	0.034	-1.94	0.086	-0.93
1435664_at	Zfp397	zinc finger protein 397	1.01	0.952	-1.12	0.525	-1.59	0.049	-1.28	0.092	-0.75
1429798_s_at	Cmtm5	CKLF-like MARVEL transmembrane domain containing 5	-1.29	0.032	-1.05	0.804	-1.24	0.511	1.22	0.578	-0.59
1421903_at	Ixl	intersex-like (Drosophila)	-1.03	0.792	-1.12	0.181	-1.49	0.109	1.02	0.942	-0.66
1442944_at	C76555	expressed sequence C76555	1.26	0.64	-1.42	0.247	-1.76	0.178	-1.15	0.362	-0.77
1445781_at	Sh3d19	SH3 domain protein D19	1.07	0.52	-1.06	0.746	-1.94	0.022	-3.56	0.181	-1.37
1448279_at	Arpc3	actin related protein 2/3 complex, subunit 3	-1.57	0.291	-1.26	0.457	1.1	0.811	-2.19	0.18	-0.98
1442499_at	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	1.06	0.418	-1.3	0.278	-1.42	0.065	-1.25	0.516	-0.73
1418349_at	Hbegf	heparin-binding EGF-like growth factor	-1.56	0.133	1.14	0.678	-1.33	0.421	-1.02	0.956	-0.69
1457547_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330081M	-1.24	0.536	1.04	0.931	-1.46	0.282	-1.1	0.815	-0.69
1435277_x_at	Nme1	expressed in non-metastatic cells 1, protein	-1.12	0.769	1.15	0.15	-2.05	0.058	-1.87	0.155	-0.97
1429091_at	1600002K03Rik	RIKEN cDNA 1600002K03 gene	1.01	0.973	-1.46	0.025	-1.19	0.292	-1.19	0.403	-0.71
1443379_at	A430033K04Rik	RIKEN cDNA A430033K04 gene	1.15	0.694	-1.75	0.076	-1.23	0.145	-1.2	0.057	-0.76
1421558_at	T2	brachyury 2	-1.7	0.128	-1.37	0.677	1.21	0.147	-2.74	0.243	-1.15

1435809_at	Ankrd34	ankyrin repeat domain 34	-2.12	0.239	-1.04	0.932	1.09	0.835	-1.12	0.848	-0.79
1460589_at	Zfp597	zinc finger protein 597	-1.4	0.004	1	0.989	-1.23	0.448	-1.68	0.029	-0.83
1442056_at	Zfp608	Zinc finger protein 608	1.12	0.097	-1.06	0.848	-2.17	0.076	-2.28	0.068	-1.1
1436331_at	Vps13d	vacuolar protein sorting 13 D (yeast)	-1.49	0.018	-1.05	0.797	-1.1	0.541	1.15	0.452	-0.62
1426579_at	Gnl2	guanine nucleotide binding protein-like 2 (nucleolar)	-1.22	0.128	-1.08	0.631	-1.27	0.028	1.14	0.563	-0.61
1444663_at	Vezf1	Vascular endothelial zinc finger 1	1.23	0.539	-1.91	0.104	-1.28	0.359	-1.29	0.372	-0.81
1417107_at	Tpd52l2	tumor protein D52-like 2	-1.11	0.136	-1.13	0.284	-1.34	0.025	1.22	0.338	-0.59
1446737_a_at	Hook3	hook homolog 3 (Drosophila)	-1.2	0.288	-1.28	0.002	-1.09	0.576	1.69	0.131	-0.47
1438964_x_at	Tfpt	TCF3 (E2A) fusion partner	-1.36	0.421	1.06	0.878	-1.36	0.142	-1.12	0.44	-0.69
1431313_at	5730442P18Rik	RIKEN cDNA 5730442P18 gene	-1.26	0.581	-1.38	0.583	1.02	0.959	-1.13	0.825	-0.69
1437330_at	Lrrk1	leucine-rich repeat kinase 1	-2.31	0.081	-1.08	0.852	1.17	0.482	-1.25	0.692	-0.87
1433851_at	Ppp4r2	protein phosphatase 4, regulatory subunit 2	-1.13	0.491	-1.17	0.335	-1.26	0.147	1.04	0.761	-0.63
1416227_at	Arpc1b /// LOC4347	actin related protein 2/3 complex, subunit 1B /// similar to Actin-related protein 2/3	-1.31	0.111	1.13	0.619	-1.55	0.388	-1.18	0.553	-0.73
1441712_at	Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	-1.11	0.737	-1.04	0.916	-1.49	0.053	1.04	0.94	-0.65
1438229_at	Pggt1b	protein geranylgeranyltransferase type I, beta subunit	-1.19	0.086	-1.08	0.139	-1.3	0.092	1.12	0.305	-0.61
1454071_at	Ly6k	lymphocyte antigen 6 complex, locus K	-2.07	0.347	-1.95	0.209	1.54	0.192	-1.35	0.638	-0.96
1446329_at	---	---	-1.59	0.202	1.41	0.444	-2	0.077	-1.65	0.452	-0.96
1456808_at	4933426M11Rik	RIKEN cDNA 4933426M11 gene	-1.04	0.894	1.07	0.768	-1.96	0.007	-1.4	0.016	-0.84
1432199_at	4930568D16Rik	RIKEN cDNA 4930568D16 gene	1.15	0.407	-1.25	0.386	-1.73	0.178	-1.71	0.439	-0.88
1448269_a_at	Klhl13	kelch-like 13 (Drosophila)	-1.19	0.419	-1.08	0.624	-1.3	0.231	1.11	0.616	-0.61
1440440_at	---	---	1.36	0.374	-1.35	0.386	-2.29	0.044	-2.81	0.237	-1.27
1449719_at	4930453N24Rik	RIKEN cDNA 4930453N24 gene	-1.12	0.83	-1.42	0.342	-1.07	0.822	1.49	0.334	-0.53
1446953_at	Tcf4	Transcription factor 4	-1.16	0.115	1.05	0.447	-1.61	0.085	-1.33	0.275	-0.76
1416098_at	Syngr3	synaptogyrin 3	-1.68	0.299	1.16	0.698	-1.28	0.187	-1	0.999	-0.7
1441411_at	Lims1	LIM and senescent cell antigen-like domains 1	-1.03	0.875	1.03	0.919	-1.86	0.004	-1.18	0.222	-0.76
1432736_at	4933430H06Rik	RIKEN cDNA 4933430H06 gene	-1.06	0.682	-1.43	0.288	-1.12	0.539	1.52	0.311	-0.52
1427119_at	Spink4	serine peptidase inhibitor, Kazal type 4	1.31	0.57	-1.81	0.091	-1.49	0.146	-1.74	0.315	-0.93
1458108_at	Ptcd2	Pentatricopeptide repeat domain 2	1.12	0.558	-1.57	0.245	-1.29	0.017	-1.81	0.034	-0.89
1422372_at	Olfr15	olfactory receptor 15	-1.72	0.063	-1.6	0.484	1.33	0.327	-1.32	0.368	-0.83
1434565_at	Cgrrf1	cell growth regulator with ring finger domain 1	-1.16	0.354	-1.07	0.362	-1.35	0.084	1.34	0.244	-0.56
1442905_at	Arf4	ADP-ribosylation factor 4	1.02	0.927	-1.33	0.301	-1.32	0.237	-1.21	0.525	-0.71
1421422_at	AF397014	cDNA sequence AF397014	-1.12	0.601	-1.73	0.052	1.06	0.847	-2.08	0.215	-0.97
1432410_a_at	Bmp7	bone morphogenetic protein 7	1.24	0.427	-1.42	0.497	-1.69	0.092	-1.78	0.408	-0.91
1431243_at	1700120J03Rik	RIKEN cDNA 1700120J03 gene	1.04	0.536	-1.57	0.42	-1.17	0.616	-2.32	0.15	-1
1438122_at	2900006K08Rik	RIKEN cDNA 2900006K08 gene	-1.38	0.334	-1.37	0.492	1.09	0.746	-1.06	0.566	-0.68
1455566_s_at	2810022L02Rik	RIKEN cDNA 2810022L02 gene	1.13	0.525	-1.11	0.598	-1.98	0.031	-1.15	0.38	-0.78
1438882_at	Arhgap18	Rho GTPase activating protein 18	-1.26	0.019	1.07	0.788	-1.48	0.06	-1.36	0.226	-0.76
1437497_a_at	Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1	-1.2	0.29	-1.2	0.464	-1.15	0.517	1.29	0.389	-0.57
1422790_at	Nppc	natriuretic peptide precursor type C	-1.08	0.865	-1	0.997	-1.64	0.4	1.2	0.689	-0.63
1442972_at	Coro1c	Coronin, actin binding protein 1C	-1.33	0.36	1.23	0.651	-1.8	0.138	-1	0.996	-0.73
1427272_at	Btbd15	BTB (POZ) domain containing 15	-1.29	0.3	-2.48	0.005	1.36	0.573	-1.16	0.741	-0.89
1430156_at	4930520O04Rik	RIKEN cDNA 4930520O04 gene	-1.23	0.799	-1.16	0.728	-1.16	0.79	2.67	0.202	-0.22
1445712_at	---	Transcribed locus	1.32	0.037	-1.09	0.869	-3.38	0.18	-1.03	0.949	-1.04
1424264_at	Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	-1.15	0.564	-1.04	0.769	-1.42	0.042	1.34	0.039	-0.57
1429009_at	Snrp70	U1 small nuclear ribonucleoprotein polypeptide A	-1.17	0.249	-1.07	0.692	-1.34	0.139	1.01	0.97	-0.64
1453514_at	Gpm6b	glycoprotein m6b	-1.27	0.731	1.28	0.562	-2.15	0.112	-1.4	0.371	-0.88
1430710_at	---	---	-1.14	0.455	-1.65	0.212	1.05	0.662	-1.09	0.828	-0.71
1446676_at	A130033P14	hypothetical protein A130033P14	-2.19	0.142	1.2	0.731	-1.14	0.321	-1.14	0.694	-0.82
1441986_at	Zcchc6	zinc finger, CCHC domain containing 6	-1.22	0.27	-1.25	0.374	-1.09	0.526	2.26	0.172	-0.33
1441321_at	LOC552911	hypothetical LOC552911	-1.12	0.143	1.25	0.413	-2.54	0	-1.13	0.649	-0.88
1433272_at	A430110A21Rik	RIKEN cDNA A430110A21 gene	-1.78	0.312	1.06	0.915	-1.09	0.859	-1.26	0.443	-0.77
1446317_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-2.48	0.077	-1.13	0.808	1.25	0.644	-1.11	0.795	-0.87
1416293_at	Nfib	nuclear factor I/B	-1.08	0.844	-2.14	0.101	1.15	0.257	-2.37	0.399	-1.11

1440372_at	Arl15	ADP-ribosylation factor-like 15	-1.01	0.902	1.08	0.517	-2.1	0.05	-1.09	0.702	-0.78
1442254_at	Dgkd	Diacylglycerol kinase, delta	1.14	0.021	-1.25	0.431	-1.68	0.123	-2.09	0.164	-0.97
1434102_at	Nfib	nuclear factor I/B	1.05	0.861	-1.16	0.463	-1.58	0.162	-1.03	0.944	-0.68
1419104_at	Abhd6	abhydrolase domain containing 6	1	0.984	-1.59	0.289	-1.11	0.402	-1.67	0.071	-0.84
1448455_at	Cln8	ceroid-lipofuscinosis, neuronal 8	-1.4	0.205	-1.09	0.641	-1.1	0.601	2.68	0.17	-0.23
1429240_at	Stard4	StAR-related lipid transfer (START) domain containing 4	-1.12	0.719	-1.04	0.742	-1.47	0.002	1.23	0.627	-0.6
1443544_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	-1.2	0.096	1.11	0.698	-1.68	0.03	-1.58	0.213	-0.84
1431929_a_at	Stx17	syntaxin 17	-1.18	0.611	-1.2	0.175	-1.16	0.072	1.13	0.636	-0.6
1438607_at	Zdhhc19	zinc finger, DHHC domain containing 19	1.46	0.584	-2.04	0.049	-1.71	0.022	-1.28	0.35	-0.89
1445322_x_at	E430025E21Rik	RIKEN cDNA E430025E21 gene	-1.08	0.824	-1.05	0.586	-1.51	0.07	1.1	0.804	-0.64
1458442_at	AI132709	expressed sequence AI132709	-1.17	0.677	-1.6	0.175	1.06	0.901	-1.17	0.443	-0.72
1427928_s_at	Cdc91l1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	-1.36	0.196	-1.31	0.019	1.04	0.769	-1.04	0.832	-0.67
1459321_at	---	---	1.22	0.664	-2.25	0.035	-1.14	0.033	-1.75	0.032	-0.98
1432882_at	4932431P20Rik	RIKEN cDNA 4932431P20 gene	-1.28	0.435	-1.06	0.584	-1.23	0.38	1.01	0.964	-0.64
1442104_at	Usp25	Ubiquitin specific peptidase 25	-1.03	0.948	-1.56	0.195	-1.08	0.804	2.41	0.115	-0.32
1438713_at	Rassf8	Ras association (RalGDS/AF-6) domain family 8	-1.18	0.623	-1.33	0.67	-1.06	0.817	1.53	0.135	-0.51
1418670_s_at	Hspg2	perlecan (heparan sulfate proteoglycan 2)	-1.07	0.856	1.05	0.91	-1.81	0.144	-1.86	0.203	-0.92
1436110_at	---	10 days neonate medulla oblongata cDNA, RIKEN full-length enriched library, clo	1.01	0.982	-1.35	0.222	-1.27	0.704	-3.94	0.4	-1.39
1450959_at	D930014E17Rik	RIKEN cDNA D930014E17 gene	-1.15	0.263	-1.33	0.157	-1.1	0.598	1.55	0.278	-0.5
1421074_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	-1.12	0.626	-1.57	0.098	1	0.968	-1.45	0.186	-0.78
1453645_at	2700046A07Rik	RIKEN cDNA 2700046A07 gene	-1.76	0.494	-2.65	0.205	1.59	0.175	-1.17	0.766	-1
1444027_at	Slc30a8	solute carrier family 30 (zinc transporter), member 8	-2.33	0.508	1.59	0.165	-1.94	0.139	-1.14	0.876	-0.95
1459571_at	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	1.18	0.197	-1.33	0.046	-1.64	0.013	-1.04	0.808	-0.71
1458629_at	---	---	1.07	0.918	-1.45	0.614	-1.29	0.349	-2.46	0.169	-1.03
1438865_at	H13	histocompatibility 13	-1.34	0.366	-2.51	0.018	1.39	0.206	-1.94	0.064	-1.1
1443521_at	Ggnbp2	Gametogenetin binding protein 2	-1.11	0.466	-1.09	0.521	-1.38	0.249	1.12	0.448	-0.62
1416755_at	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	-1.06	0.484	-1.23	0.144	-1.28	0.399	1.28	0.647	-0.57
1419345_at	Pth	parathyroid hormone	-1.28	0.796	-1.08	0.858	-1.2	0.796	1.34	0.278	-0.56
1447898_s_at	Sfrs6	splicing factor, arginine/serine-rich 6	-1.52	0.014	1.08	0.67	-1.25	0.028	-1.06	0.671	-0.69
1446064_at	---	---	-1.65	0.31	-1.18	0.702	1.08	0.834	-1.79	0.171	-0.88
1435369_at	Fastkd5	FAST kinase domains 5	-1.02	0.843	-1.35	0.006	-1.22	0.038	1.02	0.941	-0.64
1451290_at	Map1lc3a	microtubule-associated protein 1 light chain 3 alpha	-1.16	0.621	-1.53	0.063	1.02	0.951	-1.29	0.321	-0.74
1442304_at	---	16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830044I	1.09	0.84	-2.03	0.404	-1.04	0.889	-2.42	0.435	-1.1
1444015_at	Papola	Poly (A) polymerase alpha	-1.15	0.402	-1.08	0.697	-1.35	0.204	1.36	0.126	-0.55
1429969_at	4833403J16Rik	RIKEN cDNA 4833403J16 gene	-1.62	0.225	1.26	0.727	-1.52	0.06	-1.85	0.148	-0.93
1439159_at	---	---	-1.22	0.567	1.1	0.513	-1.61	0.078	-1.46	0.164	-0.8
1438259_at	---	---	-1.31	0.44	1.07	0.745	-1.41	0.048	-1.48	0.043	-0.78
1446236_at	C230072F16Rik	RIKEN cDNA C230072F16 gene	-1.06	0.838	-1.32	0.383	-1.18	0.49	1.14	0.781	-0.61
1418333_at	Mtf1	metal response element binding transcription factor 1	-1.34	0.006	-1.03	0.873	-1.22	0.023	1.17	0.505	-0.6
1416725_at	Tcf4	transcription factor 4	-2.46	0.364	-1.45	0.33	1.44	0.055	-1.49	0.1	-0.99
1428617_at	Hcfc2	host cell factor C2	-1.07	0.638	-1.32	0.104	-1.18	0.26	1.08	0.726	-0.62
1434300_at	2610101N10Rik	RIKEN cDNA 2610101N10 gene	-1.1	0.588	-1.19	0.144	-1.26	0.192	1.16	0.562	-0.6
1420526_at	Dcbld2	discoidin, CUB and LCCL domain containing 2	1.24	0.544	-2.91	0.013	-1.05	0.858	-1.19	0.611	-0.98
1438006_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	-1.14	0.1	-1.19	0.251	-1.21	0.202	1.15	0.191	-0.6
1447817_at	Hif1an	hypoxia-inducible factor 1, alpha subunit inhibitor	1.11	0.895	-2.08	0.225	-1.06	0.862	-1.25	0.639	-0.82
1436891_at	Usp15	ubiquitin specific peptidase 15	-1.3	0.133	-1.12	0.538	-1.15	0.57	1.52	0.261	-0.51
1420409_at	Krt35	keratin 35	1.12	0.636	-2.15	0.12	-1.05	0.901	-2.41	0.222	-1.12
1429810_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	1.01	0.97	-1.24	0.097	-1.38	0.279	-1.03	0.903	-0.66
1444996_at	Depdc5	DEP domain containing 5	1.19	0.814	-1.28	0.378	-1.76	0.241	-1.36	0.613	-0.8
1444092_at	9430025M13Rik	RIKEN cDNA 9430025M13 gene	-1.51	0.023	-1.09	0.647	-1.04	0.831	1	0.981	-0.66
1422336_at	Hoxa13	homeo box A13	-1.17	0.495	-1.25	0.665	-1.13	0.599	1.62	0.241	-0.48
1419847_at	Pskh1	Protein serine kinase H1	-1.37	0.267	1.02	0.972	-1.27	0.344	-1.09	0.759	-0.68
1420206_at	---	---	1.12	0.908	-1.81	0.435	-1.15	0.805	-1.42	0.46	-0.81

1452795_at	1110008B24Rik	RIKEN cDNA 1110008B24 gene	-1.14	0.157	-1.3	0.046	-1.12	0.203	1.02	0.885	-0.63
1418250_at	Arfl4	ADP-ribosylation factor 4-like	-1.27	0.167	-1.16	0.595	-1.13	0.533	1.28	0.425	-0.57
1458049_at	---	---	-1.28	0.107	-1.2	0.365	-1.08	0.83	2.31	0.353	-0.31
1441444_at	Nbeal1	Neurobeachin like 1	1.01	0.943	-1.05	0.791	-1.73	0.014	-1.43	0.086	-0.8
1451038_at	Apln	apelin	-1.03	0.719	-1.12	0.609	-1.47	0.148	1.18	0.603	-0.61
1425090_s_at	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	-1.07	0.336	-1.11	0.594	-1.41	0.433	1.08	0.219	-0.63
1455910_at	Klhdc3	kelch domain containing 3	-1.5	0.509	-1.07	0.903	-1.07	0.841	1.1	0.574	-0.63
1417552_at	Fap	fibroblast activation protein	-1.26	0.549	-1.18	0.674	-1.11	0.528	1.23	0.44	-0.58
1452809_at	9030607L17Rik	RIKEN cDNA 9030607L17 gene	-1.52	0.052	-1.14	0.643	1.01	0.952	-1.27	0.455	-0.73
1439136_at	Ssbp3	Single-stranded DNA binding protein 3	-1.21	0.169	-1.15	0.487	-1.19	0.664	1.63	0.307	-0.48
1427069_at	Fbxo28	F-box protein 28	-1.13	0.46	-1.13	0.431	-1.29	0.092	1.14	0.336	-0.6
1458385_at	Hspa4l	heat shock protein 4 like	-1.19	0.61	-1.27	0.337	-1.09	0.84	2.36	0.259	-0.3
1428672_at	Snrpf	small nuclear ribonucleoprotein polypeptide F	-1.33	0.402	1.11	0.224	-1.48	0.031	-1.62	0.372	-0.83
1420732_at	2510027J23Rik	RIKEN cDNA 2510027J23 gene	-1.27	0.805	1.36	0.599	-2.53	0.157	-1.42	0.284	-0.97
1424712_at	Ahctf1	AT hook containing transcription factor 1	-1.05	0.77	-1.56	0.01	-1.05	0.391	1.2	0.168	-0.61
1437650_at	C730026J16	hypothetical protein C730026J16	-1.16	0.007	-1.23	0.101	-1.16	0.347	1.01	0.926	-0.63
1429714_at	Sumf2	sulfatase modifying factor 2	-1.28	0.354	-1.14	0.669	-1.13	0.35	1.46	0.038	-0.52
1442332_at	Tgfbr3	Transforming growth factor, beta receptor III	1.09	0.782	-1.28	0.502	-1.5	0.031	-1.41	0.181	-0.77
1439367_x_at	Arf4	ADP-ribosylation factor 4	-1.49	0.158	-1.1	0.421	-1.04	0.841	1.27	0.286	-0.59
1447608_x_at	Btbd14a	BTB (POZ) domain containing 14A	-1.33	0.521	-1.58	0.314	1.16	0.107	-1.19	0.485	-0.73
1447132_at	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	-1.44	0.458	-1.26	0.561	1.05	0.407	-1.12	0.851	-0.69
1457513_at	6330569M22Rik	RIKEN cDNA 6330569M22 gene	1.07	0.141	-1.19	0.705	-1.58	0.013	-1.45	0.052	-0.79
1443883_at	2610042O14Rik	RIKEN cDNA 2610042O14 gene	-1.3	0.449	-1.35	0.484	1.03	0.895	-1.63	0.11	-0.81
1426993_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	-1.17	0.742	-1.35	0.364	-1.06	0.921	1.36	0.568	-0.55
1435391_at	3200001K10Rik	RIKEN cDNA 3200001K10 gene	-1.24	0.315	1.01	0.95	-1.37	0.286	-1.31	0.486	-0.73
1455579_at	Csn1s2a	casein alpha s2-like A	-1.17	0.574	-1.63	0.148	1.08	0.867	-2.07	0.255	-0.95
1427964_at	Cmtm8	CKLF-like MARVEL transmembrane domain containing 8	-1.12	0.116	-1.12	0.592	-1.33	0.233	1.19	0.013	-0.59
1420888_at	Bcl2l1	Bcl2-like 1	-1.2	0.256	-1.2	0.298	-1.14	0.555	2.4	0.206	-0.29
1454698_at	Ptplad1	protein tyrosine phosphatase-like A domain containing 1	-1.15	0.309	-1.07	0.607	-1.35	0.025	1.23	0.099	-0.59
1428146_s_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiol	-1.11	0.052	-1.34	0.133	-1.11	0.44	1.01	0.91	-0.64
1424956_at	Ahdc1	AT hook, DNA binding motif, containing 1	1.05	0.838	-1.33	0.341	-1.35	0.174	-1.19	0.572	-0.7
1437241_at	Tieg3	TGFB inducible early growth response 3	-1.2	0.531	-1.34	0.305	-1.03	0.911	1.87	0.102	-0.43
1455903_at	Tbc1d4	TBC1 domain family, member 4	1.12	0.774	-1.66	0.465	-1.22	0.397	-1.21	0.415	-0.74
1439601_at	2700008B19Rik	RIKEN cDNA 2700008B19 gene	-1.38	0.321	-1.43	0.059	1.12	0.418	-1.52	0.119	-0.8
1437126_at	Immt	Inner membrane protein, mitochondrial	1.19	0.01	-1.13	0.284	-2.15	0.007	-1.6	0.19	-0.92
1417513_at	Evi5	ecotropic viral integration site 5	-1.05	0.721	-1.28	0	-1.24	0.051	2.44	0.146	-0.28
1447858_x_at	Il4ra	interleukin 4 receptor, alpha	-1.29	0.41	1.04	0.905	-1.37	0.459	-1.34	0.45	-0.74
1447028_at	4930563E22Rik	RIKEN cDNA 4930563E22 gene	-1.45	0.107	-1.24	0.579	1.05	0.765	-1.64	0.147	-0.82
1450540_x_at	Krtap5-1	keratin associated protein 5-1	-1.26	0.193	-1.12	0.595	-1.16	0.71	2.24	0.326	-0.33
1443407_at	Rnf13	ring finger protein 13	1.05	0.884	-1.3	0.464	-1.38	0.242	-1.19	0.665	-0.7
1453522_at	6530401N04Rik	RIKEN cDNA 6530401N04 gene	-1.19	0.526	-1.12	0.385	-1.23	0.586	1.07	0.736	-0.62
1429615_at	Zfp91	zinc finger protein 91	-1.15	0.127	-1.14	0.118	-1.25	0.061	1.16	0.518	-0.6
1454117_at	5330439B14Rik	RIKEN cDNA 5330439B14 gene	1.03	0.965	-1.35	0.422	-1.3	0.61	-1.29	0.519	-0.73
1446428_at	D530005L17Rik	RIKEN cDNA D530005L17 gene	-1.21	0.673	-1.05	0.923	-1.3	0.209	1.31	0.107	-0.56
1422244_at	Pkdrej	polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea	-1.65	0.321	1.17	0.73	-1.3	0.195	-1.42	0.376	-0.8
1424237_at	Zfp639	zinc finger protein 639	-1.23	0.352	-1.13	0.149	-1.18	0.288	1.11	0.313	-0.61
1426279_at	5830415L20Rik	RIKEN cDNA 5830415L20 gene	-1.12	0.55	-1.1	0.437	-1.35	0.01	1.13	0.283	-0.61
1442009_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	1.61	0.505	-3.1	0.332	-1.63	0.188	-3.16	0.287	-1.57
1420034_at	Ppp2r2d	Protein phosphatase 2, regulatory subunit B, delta isoform	-1.06	0.853	-1.18	0.58	-1.33	0.066	1.1	0.85	-0.62
1439453_x_at	1500026D16Rik	RIKEN cDNA 1500026D16 gene	-1.06	0.626	-1.21	0.164	-1.29	0.06	1.31	0.372	-0.56
1439707_at	C230034O21Rik	RIKEN cDNA C230034O21 gene	-1.09	0.728	-1.08	0.719	-1.42	0.164	1.65	0.258	-0.49
1438919_x_at	Fdft1 /// LOC62771	farnesyl diphosphate farnesyl transferase 1 /// similar to farnesyl diphosphate farr	-1.45	0.266	-1.49	0.221	1.18	0.687	-1.27	0.463	-0.76
1424476_at	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-1.08	0.94	-1.18	0.548	-1.3	0.561	1.53	0.097	-0.51

1421662_a_at	Tusc3	tumor suppressor candidate 3	-1	0.978	-1.39	0.035	-1.21	0.131	1.12	0.677	-0.62
1421343_at	Bach2	BTB and CNC homology 2	-1.47	0.4	-1.43	0.496	1.16	0.768	-1.07	0.907	-0.7
1435134_at	Aadacl1	arylacetamide deacetylase-like 1	-1.05	0.262	-1.7	0.05	1	0.989	-1.43	0.078	-0.79
1441024_at	Stim2	stromal interaction molecule 2	-1.26	0.35	1.02	0.859	-1.38	0.056	-1.05	0.885	-0.67
1444815_at	C85328	expressed sequence C85328	1.04	0.865	-1.23	0.625	-1.45	0.458	-1.74	0.174	-0.84
1443558_s_at	C630002B14Rik	RIKEN cDNA C630002B14 gene	-1.57	0.074	-1.34	0.057	1.16	0.116	-1.16	0.332	-0.73
1436463_at	Jakmip2	Janus kinase and microtubule interacting protein 2	-2.5	0.45	-2.75	0.219	1.78	0.208	-1.32	0.319	-1.2
1426668_at	Slc30a9	solute carrier family 30 (zinc transporter), member 9	-1.11	0.548	-1.2	0.056	-1.23	0.118	1.99	0.22	-0.39
1439061_at	Ccdc84	coiled-coil domain containing 84	1.01	0.976	-1.46	0.041	-1.18	0.121	-1.24	0.231	-0.72
1417737_at	Mrps31	mitochondrial ribosomal protein S31	-1.08	0.423	-1.28	0.004	-1.19	0.152	1.09	0.675	-0.62
1419146_a_at	Gck	glucokinase	-1.42	0.01	-1.5	0.478	1.17	0.769	-1.67	0.465	-0.85
1451459_at	Ahctf1	AT hook containing transcription factor 1	-1.01	0.907	-1.35	0.016	-1.22	0.117	1.04	0.757	-0.64
1453078_at	8430408J07Rik	RIKEN cDNA 8430408J07 gene	-1.19	0.133	-1.03	0.771	-1.37	0.01	1.1	0.493	-0.62
1452247_at	Fxr1h	fragile X mental retardation gene 1, autosomal homolog	-1.11	0.528	-1.07	0.371	-1.41	0.034	1.03	0.834	-0.64
1449797_x_at	Prph1	Peripherin 1	-1.54	0.396	1.19	0.784	-1.42	0.407	-1.01	0.982	-0.69
1435130_at	LOC383103	similar to RIKEN cDNA 1810036I24	-1.43	0.357	-1.31	0.585	1.08	0.841	-1.08	0.769	-0.68
1434785_at	Cacng5	calcium channel, voltage-dependent, gamma subunit 5	1.12	0.771	-2.08	0.001	-1.06	0.793	-1.67	0.113	-0.92
1446653_at	---	---	1.17	0.594	-1.35	0.186	-1.58	0.091	-1.49	0.014	-0.81
1416267_at	Scoc	short coiled-coil protein	-1.29	0.184	-1	0.963	-1.3	0.077	2.98	0.217	-0.15
1421934_at	Cbx5	chromobox homolog 5 (Drosophila HP1a)	-1.1	0.195	-1.47	0.101	-1.05	0.813	2.06	0.136	-0.39
1420488_at	Mrps14	mitochondrial ribosomal protein S14	-1.45	0.091	-1.02	0.647	-1.14	0.658	1.05	0.622	-0.64
1431012_a_at	Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	-1.06	0.764	-1.52	0.069	-1.06	0.577	1.03	0.747	-0.65
1416823_a_at	Osbpl1a	oxysterol binding protein-like 1A	-1.17	0.43	-1.23	0.208	-1.14	0.414	1.68	0.053	-0.46
1440580_at	C030014M07Rik ///	RIKEN cDNA C030014M07 gene /// similar to RIKEN cDNA C920006C10	1.29	0.59	-2.59	0.017	-1.14	0.768	-3.37	0.107	-1.45
1454712_at	Mcart1	mitochondrial carrier triple repeat 1	-1.19	0.125	-1.12	0.306	-1.23	0.02	2.76	0.223	-0.2
1443886_at	Prkcz2	protein kinase C, zeta 2	-1.09	0.702	1.1	0.833	-1.9	0.275	-1.21	0.406	-0.77
1416672_s_at	Mcoln1	mucolipin 1	-1.44	0.335	-1.39	0.154	1.13	0.615	-1.59	0.018	-0.82
1454444_at	5730406E14Rik	RIKEN cDNA 5730406E14 gene	-2.4	0.446	-1.49	0.219	1.46	0.436	-1.02	0.972	-0.86
1426917_s_at	Scrn3	secernin 3	-1.14	0.547	-1.18	0.287	-1.22	0.283	3.52	0.22	0
1456110_at	Ankrd11	ankyrin repeat domain 11	1.01	0.958	-1.52	0.21	-1.14	0.571	-1.22	0.256	-0.72
1453068_at	Prdm2	PR domain containing 2, with ZNF domain	1.08	0.784	-1.44	0.094	-1.3	0.355	-1.08	0.639	-0.69
1417769_at	---	---	-1.28	0.292	-1.08	0.749	-1.19	0.374	1.35	0.409	-0.55
1422306_at	Lcn3	lipocalin 3	-1.34	0.478	1.02	0.963	-1.28	0.205	-3.5	0.012	-1.28
1421565_at	Robo3	roundabout homolog 3 (Drosophila)	1.04	0.91	-1.29	0.543	-1.37	0.039	-1.87	0.141	-0.87
1440441_at	Fbxl7	F-box and leucine-rich repeat protein 7	-1.1	0.561	1.16	0.75	-2.08	0	-1.4	0.38	-0.85
1455797_x_at	Lgtn	ligatin	-1.27	0.222	-1.16	0.245	-1.11	0.544	1.27	0.653	-0.57
1457327_at	Shprh	SNF2 histone linker PHD RING helicase	1.06	0.844	-1.43	0.35	-1.26	0.306	-1.57	0.423	-0.8
1417001_a_at	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	-1.21	0.133	1.07	0.702	-1.52	0.048	-1.75	0.049	-0.85
1443527_at	Terf1	telomeric repeat binding factor 1	-1.23	0.483	1.05	0.894	-1.46	0.087	-1.01	0.971	-0.66
1429306_at	Lzic	leucine zipper and CTNNBIP1 domain containing	-1.23	0.183	1.03	0.917	-1.42	0.143	-1.39	0.184	-0.75
1431861_a_at	Odf2l	outer dense fiber of sperm tails 2-like	-1.19	0.609	-1.41	0.12	-1	0.996	1.09	0.737	-0.63
1429746_at	1700007I06Rik	RIKEN cDNA 1700007I06 gene	-1.2	0.726	1.1	0.908	-1.62	0.445	-1.75	0.444	-0.87
1457912_at	E130317F20Rik	RIKEN cDNA E130317F20 gene	-1.36	0.692	1.06	0.906	-1.32	0.515	-3.3	0.216	-1.23
1460706_s_at	Rer1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	-1.24	0.325	-1.05	0.737	-1.27	0.181	1.05	0.76	-0.63
1439643_at	Acvr2a	Activin receptor IIA	1.21	0.138	-1.22	0.168	-1.93	0.001	-1.03	0.939	-0.74
1447624_s_at	Stox2	storkhead box 2	-1.34	0.173	-1.41	0.214	1.09	0.474	-1.1	0.641	-0.69
1444264_at	Tnfsf5ip1	Tumor necrosis factor superfamily, member 5-induced protein 1	-1.15	0.755	-1.06	0.829	-1.36	0.48	1.65	0.272	-0.48
1425765_at	LOC622757 /// LOC	LOC622757 gene /// similar to transcription elongation factor B (SIII), polypeptide	-1.07	0.879	-1.26	0.582	-1.21	0.586	1.17	0.365	-0.59
1420302_at	AA414903	expressed sequence AA414903	-2.64	0.302	1.57	0.517	-1.66	0.206	-2.95	0.036	-1.42
1452299_at	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	-1.07	0.623	-1.12	0.09	-1.39	0.035	1.34	0.401	-0.56
1447878_s_at	Fgfrl1	fibroblast growth factor receptor-like 1	-1.25	0.263	-1.07	0.788	-1.22	0.196	1.88	0.189	-0.42
1424750_at	Zbtb1	zinc finger and BTB domain containing 1	-1.1	0.226	-1.22	0.202	-1.23	0.282	1.08	0.509	-0.61
1432835_at	Cpb2	carboxypeptidase B2 (plasma)	-1.04	0.768	-1.67	0.157	-1.01	0.883	1.02	0.795	-0.67

1437267_x_at	Hnrph1	Heterogeneous nuclear ribonucleoprotein H1	-1.5	0.172	1.03	0.827	-1.18	0.133	-1.13	0.511	-0.69
1456733_x_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	-1.24	0.377	1.24	0.067	-1.97	0.19	-1.98	0.182	-0.99
1435042_at	9130004C02Rik	RIKEN cDNA 9130004C02 gene	1.06	0.867	-1.47	0.242	-1.24	0.046	-1.15	0.087	-0.7
1455869_at	Camk2b	Calcium/calmodulin-dependent protein kinase II, beta	1.2	0.499	-1.75	0.375	-1.28	0.372	-1.94	0.098	-0.94
1442216_at	Atp6v0d1	ATPase, H+ transporting, lysosomal V0 subunit D1	-1.17	0.543	-1.22	0.195	-1.14	0.569	1.04	0.714	-0.62
1421997_s_at	Itga3	integrin alpha 3	1.43	0.336	-2.23	0.233	-1.5	0.226	-1.28	0.048	-0.89
1459195_at	---	---	-1.64	0.225	-1.42	0.538	1.24	0.662	-1.73	0.365	-0.89
1455432_at	Taok1	TAO kinase 1	-1.06	0.367	-1.21	0.134	-1.27	0.012	1.1	0.35	-0.61
1458056_at	Sfrs12	splicing factor, arginine/serine-rich 12	-1.18	0.41	-1.23	0.233	-1.13	0.516	1.1	0.659	-0.61
1421730_at	Nr5a1	nuclear receptor subfamily 5, group A, member 1	1.65	0.433	-2.31	0.229	-2.16	0.053	-1	0.99	-0.95
1438026_at	Zfp560	zinc finger protein 560	-1.24	0.024	1.03	0.811	-1.4	0.008	-1.01	0.917	-0.66
1435823_x_at	Egfl7	EGF-like domain 7	-1.19	0.216	-1.14	0.125	-1.2	0.279	1.15	0.314	-0.6
1447089_at	Arl1	ADP-ribosylation factor-like 1	-1.59	0.413	-1.15	0.81	1.05	0.807	-2.89	0.216	-1.14
1454274_at	4930571C24Rik	RIKEN cDNA 4930571C24 gene	-1.28	0.277	-1.45	0.013	1.08	0.864	-1.15	0.363	-0.7
1426417_at	Yipf4	Yip1 domain family, member 4	-1.19	0.441	-1.09	0.587	-1.27	0.328	1.42	0.289	-0.53
1433567_at	Gmps	guanine monphosphate synthetase	-1.18	0.235	-1.31	0.028	-1.06	0.576	1.31	0.255	-0.56
1430338_at	4122401K19Rik	RIKEN cDNA 4122401K19 gene	-2.06	0.05	-1.26	0.642	1.27	0.574	-1.82	0.309	-0.97
1450940_at	Gdap1	ganglioside-induced differentiation-associated-protein 1	-1.12	0.878	-1.82	0.437	1.11	0.548	-2.04	0.065	-0.97
1455394_at	Pias4	protein inhibitor of activated STAT 4	-1.13	0.027	-1.51	0.359	1.01	0.981	-1.04	0.226	-0.67
1420788_at	Klrg1	killer cell lectin-like receptor subfamily G, member 1	1.14	0.584	-1.51	0.312	-1.35	0.249	-1.26	0.214	-0.74
1418152_at	Nsbp1	nucleosome binding protein 1	-1.08	0.585	-1.19	0.001	-1.28	0.014	1.29	0.112	-0.56
1456420_at	Arid4a	AT rich interactive domain 4A (Rbp1 like)	-1.51	0.183	-1.17	0.604	1.03	0.871	-1.25	0.245	-0.72
1448293_at	---	---	1.07	0.153	-1.54	0.342	-1.21	0.509	-2.8	0.066	-1.12
1457626_at	D3Wsu106e	DNA segment, Chr 3, Wayne State University 106, expressed	-1.24	0.278	1.12	0.575	-1.61	0.096	-1.38	0.086	-0.78
1419797_at	AA672641	expressed sequence AA672641	-1.14	0.892	-1.93	0.094	1.15	0.809	-1.31	0.716	-0.81
1429728_at	4930429M06Rik	RIKEN cDNA 4930429M06Rik	-1.14	0.624	-1.39	0.313	-1.05	0.854	1.08	0.706	-0.62
1451786_at	Muc20	mucin 20	-1.16	0.404	-1.04	0.952	-1.37	0.141	1.76	0.149	-0.45
1447463_at	---	---	-2.74	0.451	-1.82	0.248	1.64	0.447	-3.46	0.227	-1.6
1419858_at	Ifi203	Interferon activated gene 203	-1.29	0.422	-1.3	0.49	1.01	0.961	-1.91	0.269	-0.87
1440387_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	-1.69	0.067	-1.18	0.258	1.11	0.581	-1.08	0.511	-0.71
1429308_at	Prdm16	PR domain containing 16	-1.27	0.247	-1.51	0.641	1.1	0.393	-1.38	0.617	-0.77
1418414_at	Kcnh1	potassium voltage-gated channel, subfamily H (eag-related), member 1	-1.7	0.385	-1.09	0.87	1.04	0.87	-1.18	0.514	-0.73
1426647_at	9130011J15Rik	RIKEN cDNA 9130011J15 gene	-1.05	0.837	-1.27	0.129	-1.23	0.074	1.19	0.509	-0.59
1455766_at	Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	1.16	0.8	-1.41	0.4	-1.47	0.194	-1.44	0.641	-0.79
1437636_at	LOC623121	Similar to Interferon-activatable protein 203 (Ifi-203) (Interferon-inducible protein p	-1.18	0.608	1.05	0.929	-1.53	0.081	-2.37	0.083	-1.01
1425468_at	Plp1	proteolipid protein (myelin) 1	-1.37	0.586	-1.38	0.343	1.1	0.726	-1.91	0.296	-0.89
1460496_at	LOC433492	similar to RIKEN cDNA 5430413K10	-1.23	0.737	-1.85	0.013	1.19	0.637	-1.79	0.165	-0.92
1443765_at	1810058N05Rik	RIKEN cDNA 1810058N05 gene	-3.07	0.03	1.67	0.138	-1.81	0.105	-1.73	0.339	-1.23
1445236_at	LOC626410	Hypothetical protein LOC626410	-2.45	0.054	1.34	0.697	-1.25	0.188	-1.63	0.341	-1
1431429_a_at	Arl4a	ADP-ribosylation factor-like 4A	-1.21	0.312	-1.19	0.285	-1.13	0.499	2.67	0.209	-0.21
1441019_at	Fbxo3	F-box only protein 3	-1.37	0.265	-1.09	0.582	-1.1	0.352	1.69	0.083	-0.47
1434460_at	Bbs4	Bardet-Biedl syndrome 4 homolog (human)	-1.4	0.199	-1.39	0.172	1.12	0.545	-1.78	0.381	-0.86
1426823_s_at	Psme4	proteasome (prosome, macropain) activator subunit 4	-1.12	0.341	-1.2	0.037	-1.21	0.139	1.32	0.125	-0.55
1457181_at	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed	-1.34	0.283	-1.02	0.868	-1.21	0.491	1.08	0.352	-0.62
1435242_at	Aprin	androgen-induced proliferation inhibitor	-1.23	0.159	-1.22	0.185	-1.09	0.469	1.11	0.574	-0.61
1417499_at	Timm10	translocase of inner mitochondrial membrane 10 homolog (yeast)	-1.26	0.01	-1.26	0.019	-1.04	0.821	1.41	0.188	-0.54
1446372_at	Cd8b1	CD8 antigen, beta chain 1	-1.42	0.073	-1.27	0.234	1.06	0.43	-1.52	0.102	-0.79
1447635_at	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	-1.15	0.77	-1.4	0.298	-1.03	0.905	1.15	0.807	-0.61
1439266_a_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	-1.38	0.291	1.03	0.85	-1.25	0.351	-1.62	0.498	-0.8
1456191_x_at	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	-1.24	0.27	-1.23	0.113	-1.08	0.708	1.6	0.055	-0.49
1431305_at	Mcoln1	mucolipin 1	-1.52	0.357	-1.24	0.545	1.08	0.667	-1.76	0.314	-0.86
1443888_at	AU023762	Expressed sequence AU023762	-1.05	0.554	-1.07	0.667	-1.5	0.041	1.13	0.245	-0.62
1445434_at	Snupn	snurportin 1	-1.09	0.864	-1.38	0.249	-1.1	0.566	1.09	0.849	-0.62

1432426_a_at	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	-1.46	0.217	-1.07	0.551	-1.07	0.672	1.3	0.461	-0.57
1448134_at	X99384	cDNA sequence X99384	1.02	0.912	-1.19	0.058	-1.45	0.024	-1.01	0.969	-0.66
1456919_at	A930013B10Rik	RIKEN cDNA A930013B10 gene	-1.44	0.161	-1.31	0.46	1.09	0.75	-1.79	0.094	-0.86
1459701_x_at	---	---	1.28	0.192	-1.48	0.275	-1.66	0.029	-1.11	0.682	-0.75
1455351_at	AU023006	expressed sequence AU023006	-1.11	0.583	-1.03	0.736	-1.46	0.019	1.13	0.6	-0.62
1434434_s_at	Tcerg1	transcription elongation regulator 1 (CA150)	-1.2	0.119	-1.27	0.109	-1.07	0.208	1.2	0.454	-0.59
1443166_at	BC021395	CDNA sequence BC021395	1.01	0.974	-1.1	0.753	-1.57	0.196	-1.89	0.119	-0.89
1420116_s_at	Golph3	golgi phosphoprotein 3	-1.14	0.489	-1.13	0.39	-1.27	0.083	1.22	0.164	-0.58
1432230_at	Hip1	huntingtin interacting protein 1	-1.53	0.157	1.09	0.516	-1.24	0.125	-1.3	0.142	-0.74
1427561_a_at	Afm	afamin	-1.4	0.033	-1.25	0.244	1.04	0.755	-2.16	0.388	-0.94
1458971_at	---	---	-1.36	0.369	-1.31	0.428	1.06	0.781	-1.54	0.589	-0.79
1457392_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930031I16 product:	-1.08	0.608	-1.27	0.163	-1.18	0.484	1.08	0.664	-0.62
1428982_at	D530031C13Rik	RIKEN cDNA D530031C13 gene	-1.2	0.258	-1.15	0.129	-1.18	0.265	1.21	0.397	-0.58
1441480_at	Srp54	Signal recognition particle 54	-1.01	0.762	1.01	0.957	-1.82	0.005	-1.47	0.061	-0.82
1447823_x_at	Mapk12	mitogen-activated protein kinase 12	1.17	0.073	-2.16	0.171	-1.09	0.531	-1.15	0.51	-0.81
1453140_at	9030612M13Rik	RIKEN cDNA 9030612M13 gene	1.08	0.581	-1.23	0.097	-1.53	0.007	-1.05	0.826	-0.68
1444715_at	---	Transcribed locus	-1.21	0.839	1.39	0.6	-3	0.014	-1.71	0.426	-1.13
1426351_at	Hspd1	heat shock protein 1 (chaperonin)	-1.21	0.215	-1.28	0.071	-1.05	0.677	1.18	0.395	-0.59
1458161_at	Kcnq1ot1	KCNQ1 overlapping transcript 1	-1.06	0.554	1.07	0.708	-1.84	0.028	-1.04	0.826	-0.72
1459151_x_at	Ifi35	interferon-induced protein 35	-1.15	0.193	-1.14	0.404	-1.24	0.257	1.4	0.334	-0.53
1436844_at	6330403M23Rik	RIKEN cDNA 6330403M23 gene	-1.12	0.402	1.05	0.717	-1.62	0.005	-1.44	0.176	-0.78
1436770_x_at	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	-1.26	0.651	-1.24	0.119	-1.05	0.74	1.18	0.352	-0.59
1453042_at	Anks4b	ankyrin repeat and sterile alpha motif domain containing 4B	-1.38	0.063	-1.19	0.467	-1.02	0.959	1.57	0.347	-0.5
1444421_at	Etohd2	ethanol decreased 2	-1.21	0.559	-1.21	0.377	-1.1	0.252	1.64	0.223	-0.47
1417318_at	Dbc1	deleted in bladder cancer 1 (human)	1.19	0.809	-2.12	0.422	-1.12	0.738	-1.08	0.891	-0.78
1457514_at	Ylpm1	YLP motif containing 1	-1.23	0.502	-1.22	0.247	-1.08	0.878	1.4	0.305	-0.53
1458710_at	Polr2a	Polymerase (RNA) II (DNA directed) polypeptide A	-1.04	0.858	-1.24	0.555	-1.28	0.354	1	0.997	-0.64
1449789_x_at	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	-1.55	0.295	-1.2	0.299	1.08	0.796	-1.24	0.405	-0.73
1445999_at	D19Ertd132e	DNA segment, Chr 19, ERATO Doi 132, expressed	-1.1	0.757	1.01	0.974	-1.57	0.008	-1.29	0.169	-0.74
1433484_at	D6Ertd527e	DNA segment, Chr 6, ERATO Doi 527, expressed	-1.99	0.396	-1.06	0.931	1.11	0.823	-1.08	0.844	-0.76
1424649_a_at	Tspan8	tetraspanin 8	-1.04	0.789	-1.21	0.458	-1.31	0.128	5.4	0.229	0.46
1429143_at	Tekt3	tektin 3	-1.14	0.859	-2.14	0.416	1.21	0.06	-1.7	0.324	-0.94
1440999_at	Zfp697	zinc finger protein 697	-1.13	0.466	-1.69	0.006	1.07	0.722	-1.02	0.922	-0.69
1442751_at	Trio	Triple functional domain (PTPRF interacting)	-1.36	0.007	-1.15	0.714	-1.05	0.824	1.04	0.834	-0.63
1424250_a_at	Arhgef3	Rho guanine nucleotide exchange factor (GEF) 3	-1.31	0.02	1.14	0.565	-1.54	0.079	-1.89	0.109	-0.9
1421019_at	1700021F05Rik	RIKEN cDNA 1700021F05 gene	-1.14	0.146	-1.27	0.037	-1.12	0.091	1.25	0.279	-0.57
1445760_at	Rya3	antimicrobial peptide RYA3	-1.22	0.792	1.21	0.535	-1.92	0.205	-1.2	0.855	-0.78
1422510_at	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	1.15	0.308	-1.33	0.147	-1.52	0.145	-1.32	0.513	-0.76
1421568_at	Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	1.04	0.904	-1.64	0.097	-1.11	0.722	-1.18	0.584	-0.72
1444240_at	Shank1	SH3/ankyrin domain gene 1	1.1	0.782	-1.77	0.168	-1.13	0.556	-1.15	0.53	-0.73
1456593_at	Sytl2	Synaptotagmin-like 2	1.22	0.479	-1.31	0.455	-1.76	0.017	-1.39	0.398	-0.81
1452785_at	1700034H14Rik	RIKEN cDNA 1700034H14 gene	-1.28	0.042	-1.16	0.026	-1.09	0.378	1.05	0.627	-0.62
1438989_s_at	B130021B11Rik	RIKEN cDNA B130021B11 gene	1.3	0.236	-1.27	0.172	-2.13	0.03	-3.93	0.076	-1.51
1448133_at	Nmd3	NMD3 homolog (S. cerevisiae)	-1.18	0.666	-1.47	0.027	1.03	0.825	-1.21	0.204	-0.71
1426016_a_at	Tro	trophinin	1.13	0.857	-1.42	0.44	-1.38	0.24	-1.28	0.619	-0.74
1425614_x_at	H2-D1	histocompatibility 2, D region locus 1	-1.33	0.711	-1.44	0.198	1.11	0.536	-1.28	0.597	-0.73
1445147_at	Psme4	proteasome (prosome, macropain) activator subunit 4	-1.19	0.677	1.15	0.284	-1.78	0.02	-1.11	0.552	-0.73
1440733_at	1200009O22Rik	RIKEN cDNA 1200009O22 gene	-2.7	0.131	1.32	0.306	-1.15	0.354	-1.12	0.706	-0.91
1458439_a_at	2310047C04Rik	RIKEN cDNA 2310047C04 gene	1.07	0.564	-1.1	0.717	-1.75	0.01	-1.08	0.667	-0.71
1415764_at	Zc3h11a	zinc finger CCCH type containing 11A	1.02	0.854	-1.13	0.079	-1.53	0.025	-1.31	0.106	-0.74
1449734_s_at	Bbs4	Bardet-Biedl syndrome 4 homolog (human)	1.15	0.518	-1.47	0.051	-1.38	0.062	-1.74	0.055	-0.86
1442609_at	Prkce	Protein kinase C, epsilon	1.02	0.927	-1.1	0.525	-1.6	0.169	-2.84	0.112	-1.13
1458537_at	---	---	-1.32	0.086	-1.07	0.798	-1.16	0.259	1.12	0.746	-0.61

1417200_at	1300007B12Rik	RIKEN cDNA 1300007B12 gene	-1.09	0.144	-1.4	0.024	-1.08	0.702	1.35	0.344	-0.55
1439619_at	Tcf12	transcription factor 12	-1.17	0.623	1.17	0.517	-1.87	0.002	-1.24	0.423	-0.78
1432853_at	2900057C01Rik	RIKEN cDNA 2900057C01 gene	-1.19	0.763	-1.51	0.145	1.05	0.695	-1.11	0.669	-0.69
1420339_at	0610016J10Rik	RIKEN cDNA 0610016J10 gene	-1.06	0.475	-1.54	0.011	-1.03	0.844	3.06	0.2	-0.15
1460699_at	Rps27	ribosomal protein S27	-1.05	0.921	-1.17	0.792	-1.33	0.645	1.22	0.516	-0.58
1442859_at	Spred1	Sprouty protein with EVH-1 domain 1, related sequence	1.49	0.581	-3.02	0.239	-1.37	0.66	-1.56	0.34	-1.11
1450219_at	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	-1.42	0.059	-1.49	0.417	1.18	0.78	-1.48	0.607	-0.8
1447452_at	---	---	1.09	0.883	-1.21	0.128	-1.57	0.088	-1.08	0.821	-0.69
1446592_at	---	---	1.13	0.613	-1.34	0.036	-1.48	0.068	-1.34	0.232	-0.76
1440791_x_at	Tcea2	transcription elongation factor A (SII), 2	-1.82	0.09	-1.02	0.942	1.02	0.891	-1.17	0.515	-0.75
1422484_at	Cycs	cytochrome c, somatic	-1.24	0.175	-1.19	0.03	-1.1	0.511	1.09	0.603	-0.61
1456386_at	Rnpc2	RNA-binding region (RNP1, RRM) containing 2	-1.53	0.439	-1.19	0.594	1.06	0.793	-1.91	0.18	-0.89
1447219_at	---	Transcribed locus	1.24	0.422	-1.62	0.189	-1.44	0.132	-1.19	0.638	-0.75
1426031_a_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-1.21	0.203	-1.35	0.482	-1.01	0.964	1.53	0.405	-0.51
1437518_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:653(	-1.02	0.822	-2.25	0.341	1.13	0.767	-2.39	0.15	-1.13
1421892_at	---	---	-1.07	0.681	-1.2	0.765	-1.26	0.333	3.27	0.16	-0.07
1432782_at	4933435C09Rik	RIKEN cDNA 4933435C09 gene	-1.05	0.951	-1.28	0.674	-1.22	0.73	1.64	0.361	-0.48
1438733_at	Zfp689	zinc finger protein 689	1.31	0.434	-1.76	0.381	-1.48	0.364	-1.16	0.776	-0.77
1416361_a_at	Dync1i1	dynein cytoplasmic 1 intermediate chain 1	-1.07	0.779	1.05	0.879	-1.74	0.121	-1.34	0.476	-0.78
1451734_a_at	Dbn1	drebrin 1	1.02	0.897	-1.49	0.612	-1.16	0.763	-2.51	0.093	-1.03
1424527_at	Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform	-1.05	0.684	-1.17	0.107	-1.33	0.119	1.34	0.049	-0.55
1436070_at	Glo1	glyoxalase 1	-1.03	0.79	-1.23	0.018	-1.29	0.014	1.64	0.2	-0.48
1450998_at	Zfp110	zinc finger protein 110	1.02	0.891	-1.31	0.238	-1.29	0.11	-1.57	0.078	-0.79
1454170_at	E130101E03Rik	RIKEN cDNA E130101E03 gene	-2.62	0.297	-1.59	0.252	1.55	0.123	-2.11	0.151	-1.19
1454990_at	Arid2	AT rich interactive domain 2 (Arid-rfx like)	-1.09	0.384	-1.1	0.25	-1.37	0.015	1.1	0.714	-0.61
1437530_at	Pdcd10	Programmed cell death 10	-1.14	0.904	-1.1	0.799	-1.29	0.3	1.15	0.836	-0.6
1431118_at	6720427H10Rik	RIKEN cDNA 6720427H10 gene	1.07	0.7	-1.01	0.969	-1.99	0.014	-1.12	0.336	-0.76
1427374_at	Muc3 /// LOC66633	mucin 3, intestinal /// similar to mucin 17 /// similar to mucin 17	1.75	0.524	-2.79	0.072	-2.23	0.007	-1.13	0.536	-1.1
1444861_at	D13Ertd297e	DNA segment, Chr 13, ERATO Doi 297, expressed	-1.34	0.662	-1.09	0.871	-1.12	0.818	1.49	0.408	-0.52
1438526_at	Gpr158	G protein-coupled receptor 158	-1.97	0.101	-1.73	0.356	1.47	0.48	-1.71	0.637	-0.98
1439869_at	2900054J07Rik	RIKEN cDNA 2900054J07 gene	-1.73	0.16	-1.31	0.217	1.22	0.462	-1.39	0.129	-0.8
1431942_at	Wwox	WW domain-containing oxidoreductase	1.17	0.767	-1.3	0.52	-1.61	0.134	-1.47	0.235	-0.8
1454038_at	4833403I15Rik	RIKEN cDNA 4833403I15 gene	-1.68	0.289	1	0.999	-1.04	0.804	-1.34	0.127	-0.77
1435092_at	Arl4a	ADP-ribosylation factor-like 4A	-1.08	0.808	-1.27	0.4	-1.18	0.35	2.29	0.252	-0.31
1440354_at	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	-1.13	0.285	-1.45	0.516	-1.01	0.947	2.82	0.103	-0.2
1437718_x_at	Fmod	fibromodulin	-1.37	0.422	-2.29	0.226	1.39	0.473	-1.27	0.37	-0.89
1456780_at	Btrc	Beta-transducin repeat containing protein	-1.14	0.691	-1.1	0.753	-1.29	0.405	1.8	0.084	-0.43
1428646_at	LOC676870	region containing RIKEN cDNA 2310056B04 gene; pre B-cell leukemia transcripti	-1.08	0.487	-1.24	0.214	-1.21	0.294	1.02	0.931	-0.63
1434531_at	Mgat5b	mannoside acetylglucosaminyltransferase 5, isoenzyme B	1.21	0.778	-2.1	0.139	-1.14	0.75	-1.78	0.118	-0.95
1428006_at	Scfd1	sec1 family domain containing 1	-1.67	0.24	-1.34	0.131	1.21	0.7	-1.01	0.964	-0.7
1434173_s_at	D19Bwg1357e /// S	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed /// SWI/SN	1.09	0.188	-1.48	0.046	-1.26	0.075	-1.14	0.135	-0.7
1444349_at	---	---	1.2	0.157	-1.16	0.105	-2.02	0.003	-1.17	0.595	-0.79
1430820_a_at	Bbx	bobby sox homolog (Drosophila)	1.04	0.889	-1.36	0.268	-1.28	0.489	-1.09	0.612	-0.67
1450799_at	Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	-1.71	0.13	-1.12	0.559	1.08	0.815	-1.35	0.46	-0.77
1445260_at	Dcun1d1	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	-1.18	0.573	-1.11	0.393	-1.23	0.349	1.03	0.781	-0.62
1446057_at	Rlf	rearranged L-myc fusion sequence	-1.14	0.773	-1.02	0.909	-1.42	0.031	1.02	0.701	-0.64
1440368_at	Jmjd2b	Jumonji domain containing 2B	-1.22	0.428	-1.37	0.543	1.01	0.972	-1.39	0.37	-0.74
1432019_at	Trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	1.08	0.899	-2.06	0.151	-1	0.994	-2.6	0.291	-1.15
1447064_at	---	---	1.09	0.563	-1.08	0.523	-1.85	0.04	-1.13	0.694	-0.74
1442881_at	---	---	-1.09	0.409	-1.57	0.118	1	0.967	-1.76	0.312	-0.85
1441247_at	Pla2g3	Phospholipase A2, group III	-1.45	0.118	1.12	0.851	-1.33	0.278	-1.71	0.239	-0.84
1444762_at	Ppp1r12a	Protein phosphatase 1, regulatory (inhibitor) subunit 12A	1.02	0.882	-1.14	0.642	-1.51	0.011	-1.5	0.006	-0.78
1443471_at	Zbtb20	zinc finger and BTB domain containing 20	-1.18	0.238	-1	0.993	-1.4	0.1	1.23	0.444	-0.59

1431678_at	4930556N08Rik	RIKEN cDNA 4930556N08 gene	-1.5	0.087	-1.16	0.714	1.03	0.804	-1.19	0.689	-0.71
1438570_at	---	Transcribed locus	-1.74	0.294	1.17	0.575	-1.23	0.604	-3.13	0.081	-1.23
1431862_x_at	Odf2l	outer dense fiber of sperm tails 2-like	-1.38	0.147	-1.07	0.695	-1.11	0.76	1.16	0.757	-0.6
1441058_at	Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	-1.26	0.149	1.1	0.8	-1.5	0.222	-2.05	0.122	-0.93
1444819_at	C86090	expressed sequence C86090	-1.79	0.021	-1.01	0.981	1.01	0.96	-1.08	0.748	-0.72
1440174_at	E130307A14Rik	RIKEN cDNA E130307A14 gene	1.19	0.628	-1.12	0.849	-2.1	0.104	-1.08	0.866	-0.78
1439511_at	Cdk7	Cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	1	0.99	-1.02	0.868	-1.72	0.101	-1.21	0.503	-0.74
1457549_at	Ccnd3	Cyclin D3	1.2	0.412	-1.3	0.455	-1.69	0.198	-2.1	0.183	-0.97
1448462_at	Tdg /// LOC545124	thymine DNA glycosylase /// similar to thymine DNA glycosylase isoform 2 /// simi	-1.11	0.581	-1.21	0.021	-1.19	0.186	1.35	0.225	-0.54
1436221_at	D1Ertd471e	DNA segment, Chr 1, ERATO Doi 471, expressed	-1.2	0.55	-1.04	0.91	-1.31	0.624	1.41	0.39	-0.53
1451236_at	Rerg	RAS-like, estrogen-regulated, growth-inhibitor	-1.03	0.929	1.07	0.758	-1.92	0.015	-1.26	0.753	-0.79
1442003_at	---	Mus musculus, clone IMAGE:4219318, mRNA	-1.03	0.063	-1.29	0.198	-1.23	0.133	1.05	0.859	-0.62
1433565_at	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	-1.1	0.46	-1.11	0.59	-1.33	0.054	1.06	0.417	-0.62
1441196_at	C230076A16Rik	RIKEN cDNA C230076A16 gene	1.08	0.642	-1.49	0.132	-1.23	0.163	-1.19	0.355	-0.71
1432350_at	Sync	syncoilin	-1.48	0.482	-1.71	0.169	1.3	0.408	-1.24	0.474	-0.78
1419290_at	Mettl6	methyltransferase like 6	-1.07	0.637	-1.23	0.02	-1.23	0.031	1.02	0.926	-0.63
1447270_at	---	---	1.06	0.678	-1.06	0.553	-1.81	0.103	-1.06	0.707	-0.72
1458724_at	E230008O15Rik	RIKEN cDNA E230008O15 gene	-1.11	0.525	-1.14	0.599	-1.28	0.302	1.56	0.244	-0.49
1459977_x_at	Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransf	-1.26	0.582	-1.08	0.879	-1.19	0.673	1.13	0.732	-0.6
1429212_a_at	Lrrc51	leucine rich repeat containing 51	1.1	0.776	-1.89	0.006	-1.07	0.815	-2.33	0.045	-1.05
1418044_at	A630042L21Rik	RIKEN cDNA A630042L21 gene	-1.23	0.079	-1.03	0.779	-1.29	0.221	1.18	0.47	-0.59
1441045_at	---	---	-1.5	0.327	1.15	0.65	-1.35	0.075	-1.18	0.712	-0.72
1458393_at	Srr	serine racemase	-1.26	0.044	-1.22	0.25	-1.06	0.648	1.05	0.755	-0.62
1427105_at	2610510J17Rik	RIKEN cDNA 2610510J17 gene	-1.26	0.327	-1.27	0.426	-1.02	0.901	3.06	0.207	-0.12
1444928_at	Slc35f1	Solute carrier family 35, member F1	-1.07	0.914	-1.28	0.238	-1.18	0.469	1.34	0.239	-0.55
1449948_at	Ero1lb	ERO1-like beta (S. cerevisiae)	-1.23	0.404	-1.88	0.071	1.22	0.73	-1.94	0.251	-0.96
1449944_a_at	Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	-1.21	0.087	-1.18	0.086	-1.13	0.692	1.29	0.387	-0.56
1445459_at	Sstr5	somatostatin receptor 5	-1.14	0.788	-1.8	0.077	1.13	0.688	-1.77	0.238	-0.9
1451789_a_at	Ryk	receptor-like tyrosine kinase	-1.23	0.326	-1.22	0.434	-1.07	0.593	1.68	0.086	-0.46
1426625_at	Zfp623	zinc finger protein 623	1	0.959	-1.21	0.026	-1.37	0.042	-1.12	0.295	-0.67
1457923_at	C130045F17Rik	RIKEN cDNA C130045F17 gene	-1.48	0.025	-1.58	0.292	1.25	0.339	-1.11	0.736	-0.73
1420033_s_at	Ppp2r2d	protein phosphatase 2, regulatory subunit B, delta isoform	-1.05	0.704	-1.16	0.162	-1.35	0.104	1.15	0.306	-0.6
1427809_at	Lphn3	Latrophilin 3	-1.31	0.591	1.32	0.632	-2.06	0.104	-1.71	0.356	-0.94
1421299_a_at	Lef1	lymphoid enhancer binding factor 1	-1.47	0.16	1.01	0.983	-1.14	0.23	-1.98	0.108	-0.9
1423242_at	Mrps36	mitochondrial ribosomal protein S36	-1.27	0.413	-1.27	0.008	-1.02	0.903	1.42	0.331	-0.53
1431628_at	4930435H24Rik	RIKEN cDNA 4930435H24 gene	1.04	0.906	-1.47	0.356	-1.19	0.378	-1.22	0.435	-0.71
1430429_at	Pgs1	phosphatidylglycerophosphate synthase 1	-1.39	0.102	1.09	0.778	-1.31	0.058	-1.67	0.042	-0.82
1457336_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	1.02	0.933	-1.12	0.819	-1.54	0.33	-1.02	0.976	-0.66
1441526_at	Mbtd1	Mbt domain containing 1	1.04	0.251	-1.23	0.55	-1.4	0.27	-1.48	0.201	-0.77
1437164_x_at	Atp5o /// LOC43267	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit /// similar to	-1.04	0.573	-1.11	0.368	-1.42	0.027	1.13	0.361	-0.61
1440103_at	---	Transcribed locus	1.1	0.813	-1.11	0.782	-1.78	0.016	-1.47	0.506	-0.81
1434174_at	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	-1.14	0.36	-1.01	0.901	-1.43	0.017	1.11	0.518	-0.62
1435796_at	C530024P05Rik	RIKEN cDNA C530024P05 gene	-1.44	0.325	-1.48	0.286	1.19	0.579	-1.43	0.602	-0.79
1459539_at	---	---	-1.21	0.606	1.26	0.683	-2.09	0.056	-2.02	0.168	-1.02
1434479_at	Col5a1	Procollagen, type V, alpha 1	-1.03	0.836	-1.03	0.816	-1.62	0.012	2.35	0.291	-0.33
1450607_s_at	Ucn2	urocortin 2	-2.11	0.311	-2.6	0.146	1.7	0.253	-2	0.042	-1.25
1440707_at	Dmrt3	doublesex and mab-3 related transcription factor 3	-1.88	0.243	1.15	0.721	-1.13	0.794	-1.49	0.233	-0.84
1441152_at	---	---	1.13	0.141	-1.27	0.235	-1.54	0.017	-1.37	0.086	-0.76
1432982_at	4930456J16Rik	RIKEN cDNA 4930456J16 gene	-1.64	0.149	1.25	0.539	-1.42	0.358	-1.05	0.822	-0.71
1425901_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-1.35	0.21	-1.25	0.269	1.02	0.858	-1.79	0.056	-0.84
1436951_x_at	Txndc9	thioredoxin domain containing 9	-1.27	0.133	-1.09	0.195	-1.16	0.232	1.06	0.535	-0.62
1425921_a_at	1810055G02Rik	RIKEN cDNA 1810055G02 gene	-1.02	0.932	-1.36	0.492	-1.18	0.427	2.09	0.213	-0.37
1459254_at	Cdca2	cell division cycle associated 2	-1.12	0.84	-1.16	0.783	-1.23	0.496	1.81	0.302	-0.43

1431067_at	6330404A07Rik	RIKEN cDNA 6330404A07 gene	1.22	0.577	-1.54	0.227	-1.45	0.124	-1.57	0.218	-0.83
1416934_at	Mtm1	X-linked myotubular myopathy gene 1	-1.36	0.265	-1.2	0.316	-1	0.997	1.16	0.644	-0.6
1431405_a_at	4930413O22Rik	RIKEN cDNA 4930413O22 gene	-1.02	0.941	-1.08	0.685	-1.53	0.176	1.03	0.906	-0.65
1430650_at	Zfp191	zinc finger protein 191	1.02	0.903	-1.35	0.215	-1.25	0.461	-1.11	0.161	-0.67
1440278_at	---	---	-1.29	0.196	-1.06	0.941	-1.19	0.295	1.03	0.888	-0.62
1434073_at	Gprasp2	G protein-coupled receptor associated sorting protein 2	-1.12	0.759	-2	0.096	1.17	0.517	-1.05	0.889	-0.75
1447865_x_at	Pdzd11	PDZ domain containing 11	-1.24	0.127	-1.21	0.221	-1.08	0.648	1.59	0.412	-0.48
1460198_a_at	Psmb3 /// LOC2402	proteasome (prosome, macropain) subunit, beta type 3 /// similar to proteasome b	1.13	0.262	-1.11	0.322	-1.89	0.007	-1.43	0.327	-0.82
1433919_at	Asb4	ankyrin repeat and SOCS box-containing protein 4	1.14	0.866	-1.11	0.694	-1.92	0.163	-1.08	0.905	-0.74
1448594_at	Wisp1	WNT1 inducible signaling pathway protein 1	-1.15	0.541	1.3	0.453	-2.51	0.229	-1.03	0.95	-0.85
1458366_at	Asxl2	Additional sex combs like 2 (Drosophila)	-1.76	0.233	-1.18	0.521	1.15	0.529	-1.28	0.22	-0.77
1423039_a_at	---	---	-1.18	0.188	1.02	0.855	-1.43	0.014	-1.57	0.015	-0.79
1426992_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	-1.08	0.393	-1.08	0.519	-1.4	0.013	1.01	0.97	-0.64
1428811_at	Wfikkn2	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	1.14	0.854	-1.97	0.29	-1.09	0.797	-2.68	0.161	-1.15
1448807_at	Hrh3	histamine receptor H 3	1.08	0.331	-1.8	0.035	-1.08	0.826	-1.67	0.225	-0.87
1434123_at	Fut11	fucosyltransferase 11	1.1	0.537	-1.5	0.125	-1.25	0.366	-1.31	0.189	-0.74
1441525_at	Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	-1.23	0.729	1.09	0.629	-1.51	0.395	-1.65	0.572	-0.83
1445540_at	Dnm3	Dynamin 3	-1.63	0.126	-1.04	0.961	-1.01	0.934	1.35	0.252	-0.58
1440187_at	Taf3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.16	0.595	-1.54	0.238	-1.32	0.148	-1.13	0.481	-0.71
1421311_at	Pcdh10	protocadherin 10	-1.13	0.692	-2.13	0.215	1.21	0.367	-1.97	0.331	-1.01
1425891_a_at	Grtp1	GH regulated TBC protein 1	-1.16	0.525	-1.21	0.055	-1.14	0.351	2.02	0.336	-0.37
1437069_at	Osbpl8	oxysterol binding protein-like 8	-1	0.964	-1.19	0.095	-1.38	0.018	1.3	0.222	-0.57
1441816_at	2900056M20Rik	RIKEN cDNA 2900056M20 gene	-1.2	0.629	1.22	0.706	-1.95	0.057	-1.9	0.099	-0.96
1454935_at	D930001I22Rik	RIKEN cDNA D930001I22 gene	-1.15	0.273	-1.51	0.129	1.03	0.688	-1.06	0.534	-0.67
1445183_s_at	D7Ertd523e	DNA segment, Chr 7, ERATO Doi 523, expressed	-1.29	0.552	-2.11	0.061	1.31	0.28	-1.06	0.82	-0.79
1456149_at	D11Bwg0517e	DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed	-1.35	0.623	-1.07	0.91	-1.13	0.557	1.05	0.832	-0.62
1453190_at	Usp19	ubiquitin specific peptidase 19	-1.05	0.876	1.15	0.755	-2.18	0.037	-1.16	0.621	-0.81
1454055_at	1600029O15Rik	RIKEN cDNA 1600029O15 gene	1.15	0.825	-1.28	0.54	-1.58	0.219	-1.51	0.393	-0.81
1423459_at	Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	-1.07	0.605	-1.31	0.002	-1.16	0.378	1.12	0.581	-0.6
1456839_at	Gramd1b	GRAM domain containing 1B	1.56	0.439	-1.58	0.313	-2.66	0.009	-1.18	0.585	-0.96
1432872_at	4932702M13Rik	RIKEN cDNA 4932702M13 gene	-1.13	0.867	-1.57	0.513	1.04	0.903	-1.38	0.52	-0.76
1432021_at	Cpne3	copine III	-1.13	0.495	-1.31	0.495	-1.09	0.701	1.26	0.316	-0.57
1458351_s_at	Klhl2	kelch-like 2, Mayven (Drosophila)	1.01	0.961	-1.2	0.286	-1.38	0.169	-1.25	0.422	-0.71
1419348_at	Psp	parotid secretory protein	-1.25	0.784	-1.22	0.634	-1.05	0.86	1.27	0.461	-0.56
1440781_at	B830007D08Rik	RIKEN cDNA B830007D08 gene	-1.15	0.356	1.18	0.625	-1.94	0.067	-1.63	0.256	-0.88
1437767_s_at	Fts	fused toes	-1.18	0.195	1.05	0.886	-1.49	0.041	-1.19	0.642	-0.7
1456688_at	Top2b	Topoisomerase (DNA) II beta	-1.31	0.178	1.13	0.757	-1.48	0	-1.85	0.063	-0.88
1438539_at	Ascc1	Activating signal cointegrator 1 complex subunit 1	-1.36	0.253	1.06	0.828	-1.31	0.193	-1.25	0.141	-0.71
1441355_at	E030047P09Rik	RIKEN cDNA E030047P09 gene	1.21	0.771	-1.53	0.545	-1.42	0.014	-1.16	0.7	-0.73
1442998_at	Ctps2	Cytidine 5'-triphosphate synthase 2	1.06	0.823	-1.35	0.186	-1.31	0.25	-2.31	0.249	-0.98
1443002_at	Zfr	zinc finger RNA binding protein	-1.07	0.841	1.05	0.433	-1.74	0.084	-1.19	0.638	-0.73
1459818_x_at	Zmym3	zinc finger, MYM-type 3	-1.32	0.139	1.03	0.943	-1.28	0.339	-1.02	0.959	-0.65
1443918_at	2700050L05Rik	RIKEN cDNA 2700050L05 gene	-1.16	0.607	-1.07	0.429	-1.3	0.078	1.15	0.625	-0.6
1460712_s_at	Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	-1.41	0.188	-1.17	0.245	1	0.984	-1.21	0.055	-0.7
1435514_at	Lztfl1	leucine zipper transcription factor-like 1	-1.3	0.226	-1.29	0.386	1.03	0.924	-1.18	0.327	-0.69
1444170_at	6030446N20Rik	RIKEN cDNA 6030446N20 gene	-1.79	0.321	-1.56	0.327	1.37	0.311	-2.03	0.286	-1
1443624_at	BC013481	CDNA sequence BC013481	-1.1	0.158	-1.09	0.369	-1.35	0.128	1.29	0.205	-0.56
1452196_a_at	Nckap1	NCK-associated protein 1	-1.05	0.685	-1.09	0.132	-1.44	0.088	1.35	0.153	-0.56
1440060_at	LOC331480	hypothetical LOC331480	-1.36	0.034	1.13	0.45	-1.42	0.138	-1.26	0.241	-0.73
1458850_at	Myh6	Myosin, heavy polypeptide 6, cardiac muscle, alpha	-1.34	0.201	-1.66	0.172	1.21	0.287	-1.74	0.195	-0.88
1425410_at	Tprkb	Tp53rk binding protein	-1.09	0.102	-1.39	0.023	-1.08	0.745	1.02	0.926	-0.63
1443168_at	---	Adult male colon cDNA, RIKEN full-length enriched library, clone:9030003C19 pr	-1.05	0.947	-1.75	0.102	1.04	0.912	-1.4	0.001	-0.79
1432810_at	Ttc32	tetratricopeptide repeat domain 32	1.43	0.574	-4.1	0.214	-1.12	0.683	-1.02	0.867	-1.2

1423823_at	2610012O22Rik	RIKEN cDNA 2610012O22 gene	-1.32	0.059	-1.21	0.027	-1.01	0.949	1.31	0.344	-0.56
1432836_at	4833410I11Rik	RIKEN cDNA 4833410I11 gene	-1.75	0.309	1.53	0.44	-2.16	0.169	-2.09	0.182	-1.12
1453921_at	4930429F11Rik	RIKEN cDNA 4930429F11 gene	1.47	0.487	-2.67	0.065	-1.39	0.47	-1.45	0.628	-1.01
1459884_at	Cox7c	cytochrome c oxidase, subunit VIIc	-1.24	0.494	-1.53	0.193	1.11	0.542	-1.2	0.302	-0.72
1448445_at	Acp6	acid phosphatase 6, lysophosphatidic	-1.15	0.393	-1.46	0.051	1.02	0.93	-3.48	0.028	-1.27
1443559_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	1.37	0.445	-2.02	0.144	-1.43	0.547	-2.02	0.303	-1.02
1440626_at	Hoxd13	Homeo box D13	-1.4	0.642	-1.73	0.052	1.28	0.492	-1.27	0.486	-0.78
1456686_at	Zfhx1a	Zinc finger homeobox 1a	1.14	0.612	-1.43	0.081	-1.37	0.081	-1.39	0.1	-0.76
1428881_at	Kns2	kinesin 2	-1.25	0.15	-1.31	0.185	1.01	0.977	-1.14	0.262	-0.67
1440995_at	6430531B16Rik	RIKEN cDNA 6430531B16 gene	1.62	0.599	-1.9	0.242	-2.35	0.056	-1.27	0.618	-0.98
1433997_at	2410127E18Rik	RIKEN cDNA 2410127E18 gene	-1.13	0.356	-1.25	0.057	-1.13	0.341	1.37	0.321	-0.54
1429458_at	2410127L17Rik /// I	RIKEN cDNA 2410127L17 gene /// similar to RIKEN cDNA 2410127L17 /// similai	-1.25	0.063	-1.28	0.099	-1.01	0.923	1.45	0.283	-0.52
1456521_at	---	Transcribed locus	-2.25	0.072	-1.06	0.354	1.18	0.643	-1.17	0.796	-0.82
1418774_a_at	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	-1.17	0.326	1.16	0.412	-1.8	0	-1.22	0.631	-0.76
1419096_at	Apom	apolipoprotein M	-1.24	0.405	-1.01	0.904	-1.3	0.508	1.17	0.676	-0.59
1436305_at	Ibrdc1	IBR domain containing 1	-1.22	0.286	-1.17	0.113	-1.12	0.504	1.24	0.14	-0.57
1450028_a_at	Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	-1.22	0.063	-1.14	0.053	-1.15	0.179	2.06	0.208	-0.36
1458229_at	Robo2	roundabout homolog 2 (Drosophila)	-1.14	0.47	1.15	0.635	-1.85	0.003	-1.63	0.392	-0.87
1457602_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13004	-3.33	0.089	1.52	0.169	-1.34	0.292	-2.14	0.023	-1.32
1444976_at	---	---	1.15	0.834	-1.49	0.483	-1.35	0.281	-1.51	0.571	-0.8
1452411_at	Lrrc1	leucine rich repeat containing 1	1.18	0.193	-1.8	0.06	-1.2	0.093	-1.09	0.564	-0.73
1457133_at	---	Transcribed locus	-1.66	0.355	1.26	0.699	-1.43	0.451	-1	0.98	-0.71
1448122_at	Tcp1	t-complex protein 1	-1.07	0.331	-1.24	0.089	-1.21	0.139	1.11	0.153	-0.6
1446036_at	---	---	-1.52	0.654	1.2	0.543	-1.41	0.14	-3.26	0.21	-1.25
1454638_a_at	Pah	phenylalanine hydroxylase	-1.24	0.009	-1.31	0.312	-1	0.992	2.93	0.337	-0.15
1433913_at	C80913	expressed sequence C80913	-1.05	0.592	-1.17	0.188	-1.31	0.027	1.03	0.885	-0.63
1441092_at	9330159M07Rik	RIKEN cDNA 9330159M07 gene	-1.25	0.326	-1.13	0.477	-1.13	0.659	1.15	0.701	-0.59
1423919_at	BC023882	cDNA sequence BC023882	-1.12	0.631	-1.11	0.202	-1.29	0.219	1.07	0.657	-0.61
1417962_s_at	Ghr	growth hormone receptor	1.1	0.032	-1.47	0.019	-1.27	0.4	-1.15	0.605	-0.7
1456817_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930002A02 product	-1.6	0.432	-1.49	0.508	1.27	0.187	-1.81	0.299	-0.91
1441018_at	Usp24	ubiquitin specific peptidase 24	1.39	0.495	-1.35	0.343	-2.3	0.013	-1.33	0.456	-0.9
1438378_at	1700013G23Rik	RIKEN cDNA 1700013G23 gene	-1.23	0.589	-1.3	0.661	-1.01	0.978	3.01	0.107	-0.13
1442406_at	9230104K21Rik	RIKEN cDNA 9230104K21 gene	-1.02	0.842	-1.02	0.912	-1.62	0.039	2.98	0.207	-0.17
1459326_at	D9Ertd256e	DNA segment, Chr 9, ERATO Doi 256, expressed	-1.42	0.245	1.35	0.581	-1.94	0.057	-1.72	0.275	-0.93
1456017_x_at	LOC666466	similar to oocyte specific homeobox 2	1.32	0.252	-1.87	0.244	-1.4	0.664	-1.89	0.321	-0.96
1446193_at	---	---	-1.07	0.87	-1.09	0.847	-1.4	0.336	2.01	0.126	-0.39
1430896_s_at	Nudt7	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-1.05	0.699	-2.26	0.115	1.18	0.407	-1.49	0.061	-0.91
1430847_a_at	Crem	cAMP responsive element modulator	1	0.994	-1.42	0.401	-1.16	0.596	-2.6	0.086	-1.04
1425590_s_at	Aipl1	aryl hydrocarbon receptor-interacting protein-like 1	1.09	0.687	-1.54	0.453	-1.2	0.482	-1.51	0.587	-0.79
1420949_at	Znrf1	zinc and ring finger 1	-1.43	0.416	-1.24	0.417	1.07	0.604	-1.11	0.142	-0.68
1459439_at	Mrps5	mitochondrial ribosomal protein S5	1.21	0.574	-2.16	0.023	-1.11	0.726	-1.22	0.611	-0.82
1451027_at	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	-1.16	0.522	1.02	0.947	-1.45	0.053	-1.01	0.964	-0.65
1429753_at	Nxph4	neurexophilin 4	1.07	0.926	-1.35	0.276	-1.32	0.532	-1.06	0.916	-0.67
1448003_at	---	---	-1.16	0.553	1.05	0.628	-1.52	0.089	-1.63	0.124	-0.82
1453149_at	Slc25a32	solute carrier family 25, member 32	-1.2	0.486	-1.25	0.277	-1.07	0.444	1.11	0.474	-0.6
1447040_at	Alcam	Activated leukocyte cell adhesion molecule	1.08	0.859	-1.08	0.762	-1.77	0.003	-1.3	0.396	-0.77
1456669_at	---	Transcribed locus	-1.28	0.445	-1.51	0.475	1.13	0.808	-1.3	0.71	-0.74
1434513_at	Atp13a3	ATPase type 13A3	-1.07	0.551	-1.2	0.233	-1.24	0.123	1.2	0.342	-0.58
1416918_at	Dlgh3	discs, large homolog 3 (Drosophila)	-1.05	0.349	-1.17	0.148	-1.31	0.13	1.12	0.35	-0.6
1446005_at	D2Ertd337e	DNA segment, Chr 2, ERATO Doi 337, expressed	-1.3	0.171	-1.78	0.195	1.24	0.57	-2.44	0.029	-1.07
1418076_at	St14	suppression of tumorigenicity 14 (colon carcinoma)	-1.01	0.978	-1.83	0.38	1.03	0.882	-1.72	0.327	-0.88
1421496_at	Asah3l	N-acylsphingosine amidohydrolase 3-like	-1.07	0.919	-1.88	0.198	1.1	0.836	-1.97	0.04	-0.95
1423266_at	2810405K02Rik	RIKEN cDNA 2810405K02 gene	1.01	0.673	-1.32	0.003	-1.25	0.048	-1.21	0.44	-0.69

1433982_at	Usp28	ubiquitin specific peptidase 28	-1.51	0.304	1.01	0.952	-1.11	0.606	-2.31	0.051	-0.98
1446307_at	Papolg	Poly(A) polymerase gamma	-1.54	0.302	1.04	0.931	-1.13	0.532	-1.32	0.246	-0.74
1456716_s_at	3110002H16Rik	RIKEN cDNA 3110002H16 gene	-1.13	0.456	-1.35	0.033	-1.06	0.179	1.59	0.28	-0.49
1440479_at	Cbx4	Chromobox homolog 4 (Drosophila Pc class) /// 10 days lactation, adult female m	-1.53	0.586	-1.68	0.435	1.32	0.02	-1.35	0.452	-0.81
1434356_a_at	Psma5	proteasome (prosome, macropain) subunit, alpha type 5	-1.11	0.095	-1.15	0.029	-1.25	0.051	1.15	0.365	-0.59
1446883_at	4933427D06Rik	RIKEN cDNA 4933427D06 gene	-1.11	0.87	-1.98	0.209	1.17	0.756	-1.56	0.291	-0.87
1443135_at	Cog4	component of oligomeric golgi complex 4	1	0.987	-1.25	0.282	-1.3	0.169	-1.17	0.564	-0.68
1439244_a_at	Tnrc6a	trinucleotide repeat containing 6a	1.03	0.896	-1.24	0.041	-1.36	0.062	-1.52	0.196	-0.77
1430010_at	2810465G24Rik	RIKEN cDNA 2810465G24 gene	-1.16	0.81	-1.4	0.178	-1	0.994	3.29	0.163	-0.07
1420780_at	Ascl3	achaete-scute complex homolog-like 3 (Drosophila)	-1.55	0.018	-1.17	0.327	1.07	0.595	-1.69	0.281	-0.83
1444194_at	---	---	1.3	0.088	-1.19	0.558	-2.29	0.01	-1.2	0.417	-0.85
1427383_at	Irx6	Iroquois related homeobox 6 (Drosophila)	-2.52	0.141	-1.37	0.32	1.44	0.288	-1.13	0.838	-0.89
1439232_at	1500016L03Rik	RIKEN cDNA 1500016L03 gene	-1.06	0.776	-1.49	0.596	-1.04	0.901	2.14	0.341	-0.36
1455817_x_at	LOC668166	similar to Zinc finger X-linked protein ZXDB	-1.55	0.296	1.01	0.978	-1.09	0.635	-1.4	0.484	-0.76
1459044_at	AU015558	expressed sequence AU015558	-1.23	0.624	-1.43	0.584	1.06	0.863	-1.19	0.607	-0.7
1439790_at	Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	1.01	0.952	-1.03	0.721	-1.69	0.003	-1.19	0.127	-0.72
1418441_at	Col8a1	procollagen, type VIII, alpha 1	-2.07	0.492	-1.19	0.681	1.25	0.492	-1.01	0.971	-0.76
1454352_at	A930028O11Rik	RIKEN cDNA A930028O11 gene	-1.61	0.534	1.33	0.516	-1.6	0.223	-1.36	0.462	-0.81
1449021_at	Rpp21	ribonuclease P 21 subunit (human)	1	0.977	-1.4	0.084	-1.17	0.335	-1.13	0.056	-0.67
1425777_at	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	-1.39	0.565	-1.8	0.048	1.3	0.301	-1.2	0.724	-0.77
1456419_at	5730455P16Rik	RIKEN cDNA 5730455P16 gene	1.14	0.594	-1.35	0.195	-1.45	0.072	-1.08	0.636	-0.68
1430664_at	Zfp169	zinc finger protein 169	1.26	0.702	-1.73	0.229	-1.36	0.025	-2.84	0.211	-1.17
1427863_at	Hist1h3d	histone1, H3d	1	0.999	-1.34	0.518	-1.21	0.479	-1.19	0.304	-0.68
1450507_at	Pou2f3	POU domain, class 2, transcription factor 3	-2.33	0.137	-1.21	0.659	1.32	0.176	-1.06	0.849	-0.82
1451708_at	Gpr33	G protein-coupled receptor 33	-1.25	0.385	-1.28	0.216	-1.01	0.988	1.09	0.661	-0.61
1436320_at	---	CDNA clone IMAGE:1328649	1.01	0.935	-1.74	0.031	-1.02	0.935	-1.05	0.855	-0.7
1447359_at	Zfp575	zinc finger protein 575	-1.32	0.229	1.28	0.481	-1.87	0.215	-1.15	0.457	-0.76
1459811_at	Mtf2	metal response element binding transcription factor 2	-1.96	0.304	1.22	0.697	-1.18	0.785	-1.31	0.27	-0.81
1423585_at	Igfbp7 /// LOC6215	insulin-like growth factor binding protein 7 /// similar to O-acyltransferase (membra	1.01	0.913	-1.1	0.668	-1.53	0.145	-1.6	0.013	-0.8
1428153_at	Mrps10	mitochondrial ribosomal protein S10	-1.11	0.268	-1.25	0.236	-1.15	0.112	1.01	0.925	-0.62
1444488_at	Cadps	Ca<2+>dependent activator protein for secretion	1.51	0.253	-3.42	0.108	-1.3	0.091	-3.11	0.251	-1.58
1439920_at	---	Transcribed locus	1.53	0.075	-2.22	0.333	-1.69	0.229	-1.14	0.718	-0.88
1448963_at	Nfyc	nuclear transcription factor-Y gamma	-1.03	0.798	-1.18	0.278	-1.32	0.053	1.09	0.602	-0.61
1418928_a_at	2310038H17Rik	RIKEN cDNA 2310038H17 gene	-1.49	0.036	-1.21	0.072	1.08	0.615	-1.19	0.495	-0.7
1435708_at	Gls	Glutaminase	-1.22	0.315	1.04	0.943	-1.41	0.163	-1.45	0.338	-0.76
1436129_at	4930523C11Rik ///	RIKEN cDNA 4930523C11 gene /// a disintegrin and metallopeptidase domain 6	-1.16	0.797	1.1	0.702	-1.61	0.413	-1.51	0.139	-0.8
1448983_at	Cdrt4	CMT1A duplicated region transcript 4	-1.1	0.261	-1.2	0.172	-1.2	0.297	1.02	0.957	-0.62
1452739_at	Fbxo7	F-box only protein 7	-1.26	0.003	-1.24	0.026	-1.03	0.844	2.17	0.211	-0.34
1449629_s_at	Snrpd3	Small nuclear ribonucleoprotein D3	-1.09	0.475	-1.31	0.07	-1.13	0.31	1.11	0.664	-0.6
1425211_at	2010003O18Rik	RIKEN cDNA 2010003O18 gene	-1.11	0.338	-1.08	0.399	-1.34	0.005	1.32	0.178	-0.55
1424735_at	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	-1.29	0.468	-1.17	0.681	-1.06	0.879	1.18	0.479	-0.58
1441319_at	Rbm5	RNA binding motif protein 5	-1.29	0.165	1.3	0.308	-2	0.006	-1.26	0.029	-0.81
1440971_x_at	G630024C07Rik	RIKEN cDNA G630024C07 gene	-1.4	0.444	-1.18	0.365	1.01	0.881	-1.1	0.709	-0.67
1454943_a_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	-1.3	0.08	-1.16	0.571	-1.06	0.746	1.64	0.304	-0.47
1458981_at	---	Transcribed locus	1.12	0.831	-1.52	0.196	-1.26	0.326	-1.32	0.419	-0.74
1444437_at	Usp34	ubiquitin specific peptidase 34	-1.22	0.612	1.15	0.715	-1.65	0.069	-1.16	0.548	-0.72
1449142_a_at	Yipf5	Yip1 domain family, member 5	-1.14	0.631	-1.24	0.232	-1.12	0.476	1.02	0.867	-0.62
1442699_at	---	---	-1.62	0.378	1.18	0.361	-1.29	0.05	-1.17	0.169	-0.72
1443750_s_at	Rpp40	ribonuclease P 40 subunit (human)	-1.47	0.128	-1.26	0.003	1.1	0.621	-1.2	0.477	-0.71
1434234_at	Zfp341	zinc finger protein 341	1.08	0.785	-1.3	0.53	-1.39	0.358	-1.03	0.85	-0.66
1419736_a_at	Eif1ay	eukaryotic translation initiation factor 1A, Y-linked	-1.12	0.026	-1.07	0.474	-1.34	0.008	1.21	0.245	-0.58
1441737_s_at	Rassf1	Ras association (RalGDS/AF-6) domain family 1	-1.25	0.065	1.01	0.858	-1.32	0.087	-1.12	0.259	-0.67
1451059_at	Zfp474	zinc finger protein 474	-1.5	0.051	-1.08	0.928	-1.02	0.932	1.39	0.209	-0.55

1419024_at	Ptp4a1	protein tyrosine phosphatase 4a1	-1.23	0.234	-1.1	0.616	-1.18	0.366	1.84	0.173	-0.41
1420227_at	---	Transcribed locus	1.32	0.173	-1.35	0.328	-1.95	0.074	-1.1	0.865	-0.77
1444824_at	C76793	expressed sequence C76793	-1.29	0.538	-1.26	0.559	1.01	0.956	-1.97	0.369	-0.88
1416282_at	Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	-1.03	0.388	-1.16	0.009	-1.35	0.07	1.1	0.602	-0.61
1447724_x_at	Opa3	Optic atrophy 3 (human)	-1.02	0.918	-1.17	0.556	-1.36	0.163	1.26	0.434	-0.57
1423106_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	-1.22	0.102	-1.08	0.154	-1.2	0.16	1.03	0.772	-0.62
1420912_at	Aff4	AF4/FMR2 family, member 4	1.11	0.6	-1.27	0.216	-1.46	0.024	-1.85	0.044	-0.87
1437462_x_at	Mmp15	matrix metallopeptidase 15	1.06	0.504	-1.58	0.192	-1.13	0.374	-1.25	0.653	-0.73
1438222_at	D2Ertd612e	DNA segment, Chr 2, ERATO Doi 612, expressed	1.02	0.894	-1.18	0.247	-1.42	0.02	-1.07	0.723	-0.66
1448514_at	Cox5b	cytochrome c oxidase, subunit Vb	-1.16	0.231	-1.18	0.773	-1.15	0.743	1.11	0.834	-0.6
1432480_a_at	Cntd1	cyclin N-terminal domain containing 1	-1.35	0.477	-1.15	0.829	-1.03	0.883	1.95	0.088	-0.4
1434190_at	Sms	spermine synthase	-1.1	0.52	-1.08	0.7	-1.34	0.175	1.39	0.03	-0.54
1440706_at	Bmp8b	bone morphogenetic protein 8b	-1.77	0.282	1.25	0.661	-1.32	0.39	-1.28	0.112	-0.78
1425660_at	Btbd3	BTB (POZ) domain containing 3	-1.21	0.566	-1.25	0.105	-1.05	0.794	1.09	0.814	-0.61
1442117_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930003C13 product	1.12	0.889	-1.05	0.869	-1.97	0.176	-1.37	0.262	-0.82
1420659_at	Slamf6	SLAM family member 6	-1.55	0.345	-1.18	0.344	1.08	0.706	-2.02	0.136	-0.92
1419864_x_at	---	Transcribed locus	1.43	0.144	-1.47	0.002	-2.15	0.084	-1.64	0.362	-0.96
1440957_at	Defb29	defensin beta 29	1.15	0.034	-1.34	0.487	-1.47	0.283	-1.28	0.427	-0.74
1437965_at	Heatr1	HEAT repeat containing 1	1.05	0.917	-1.06	0.875	-1.72	0.05	-1.52	0.39	-0.81
1440463_at	Ngly1	N-glycanase 1	1.14	0.328	-1.11	0.806	-1.88	0.054	-1.08	0.837	-0.73
1455620_at	---	PREDICTED: Mus musculus similar to heparan sulfate D-glucosaminyl 3-O-sulfot	-1.25	0.727	-1.85	0.106	1.24	0.59	-1.13	0.717	-0.75
1445618_at	---	---	-1.21	0.205	-1.45	0.554	1.06	0.854	-1.28	0.505	-0.72
1429978_at	5830467E07Rik	RIKEN cDNA 5830467E07 gene	1.12	0.778	-1.13	0.541	-1.76	0.171	-1.4	0.542	-0.79
1433075_at	4931412I15Rik	RIKEN cDNA 4931412I15 gene	-1.26	0.632	-2.98	0.039	1.45	0.455	-1.42	0.59	-1.05
1425240_at	BC011426	cDNA sequence BC011426	1.06	0.5	-1.84	0.066	-1.02	0.903	-1.27	0.334	-0.77
1440427_at	BB124205	expressed sequence BB124205	-1.56	0.101	-1.11	0.514	1.03	0.832	-1.93	0.088	-0.89
1426884_at	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	-1.19	0.059	-1.19	0.229	-1.12	0.394	1.17	0.378	-0.58
1417132_at	Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)	-1.07	0.668	-1.45	0.197	-1.05	0.757	1.92	0.283	-0.41
1429304_at	Ankrd10	ankyrin repeat domain 10	-1.26	0.167	1.04	0.878	-1.35	0.139	-1.68	0.071	-0.81
1447650_at	Nmd3	NMD3 homolog (S. cerevisiae)	-1.07	0.051	-1.48	0.253	-1.03	0.782	1.09	0.338	-0.62
1440745_at	Prdm16	PR domain containing 16	-1.02	0.9	-1.14	0.562	-1.39	0.44	1.35	0.207	-0.55
1419268_at	Agr2	anterior gradient 2 (Xenopus laevis)	-1.22	0.741	-1.25	0.53	-1.04	0.912	1.75	0.4	-0.44
1415875_at	3010003L21Rik	RIKEN cDNA 3010003L21 gene	-1.52	0.499	-1.28	0.411	1.14	0.734	-1.19	0.812	-0.71
1459695_at	---	---	1.27	0.394	-1.14	0.528	-2.3	0	-1.42	0.346	-0.9
1429759_at	Rps6ka6	ribosomal protein S6 kinase polypeptide 6	1.03	0.912	-1.44	0.416	-1.17	0.322	-1.2	0.817	-0.7
1427741_x_at	Nkx2-3	NK2 transcription factor related, locus 3 (Drosophila)	1.29	0.671	-2.23	0.269	-1.18	0.736	-1.18	0.728	-0.83
1428164_at	Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	-1.27	0.294	-1.11	0.524	-1.13	0.182	1.46	0.223	-0.51
1418526_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	-1.06	0.524	-1.26	0.006	-1.19	0.216	1.51	0.295	-0.5
1445550_at	---	---	-1.16	0.362	-1.17	0.654	-1.16	0.278	1.12	0.727	-0.59
1451123_at	C330016O10Rik	RIKEN cDNA C330016O10 gene	1.01	0.958	-1.59	0.392	-1.06	0.68	-1.4	0.086	-0.76
1456892_at	D030036P13Rik	RIKEN cDNA D030036P13 gene	1.1	0.418	-1.82	0.045	-1.07	0.522	-1.07	0.813	-0.72
1415716_a_at	Rps27	ribosomal protein S27	1.03	0.523	-1.24	0.3	-1.34	0.034	-1.42	0.056	-0.74
1432978_at	9030607L02Rik	RIKEN cDNA 9030607L02 gene	-1.27	0.725	-1.26	0.684	1	0.998	-2.44	0.068	-0.99
1424771_at	H2afj /// LOC63240	H2A histone family, member J /// similar to H2A histone family, member J isoform	-1.3	0.404	-1.04	0.827	-1.18	0.124	1.24	0.003	-0.57
1453338_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.14	0.731	-1.7	0.177	-1.18	0.403	-1.75	0.118	-0.87
1418519_at	Aadat	aminoadipate aminotransferase	1.07	0.256	-1.37	0.133	-1.29	0.398	-1.64	0.18	-0.81
1426029_a_at	Nfat5	nuclear factor of activated T-cells 5	-1.57	0.354	-1.21	0.601	1.11	0.87	-1.4	0.212	-0.76
1438725_at	Thrap1	thyroid hormone receptor associated protein 1	-1.45	0.292	-1.45	0.06	1.2	0.106	-1.21	0.227	-0.73
1422446_x_at	Ins2	insulin II	-2.24	0.422	-1.05	0.635	1.18	0.728	-1.28	0.45	-0.85
1455102_at	D330037H05Rik ///	RIKEN cDNA D330037H05 gene /// similar to La-related protein 4 (La ribonucleop	-1.13	0.377	-1.18	0.288	-1.18	0.344	1.04	0.834	-0.61
1416570_s_at	Gfm1	G elongation factor, mitochondrial 1	-1.27	0.066	-1.27	0.049	-1	0.99	1.13	0.489	-0.6
1432325_at	4930502M04Rik	RIKEN cDNA 4930502M04 gene	-1.02	0.969	1	0.995	-1.66	0.219	-1.03	0.959	-0.68
1455289_at	Ankrd13b	ankyrin repeat domain 13b	-1.07	0.715	-1.37	0.46	-1.09	0.366	1.43	0.232	-0.53

1434182_at	Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	-1.19	0.576	-1.46	0.026	1.06	0.782	-1.21	0.452	-0.7
1433613_at	---	---	1.04	0.493	-1.12	0.471	-1.54	0.042	-1.32	0.064	-0.74
1451333_a_at	Acrbp	proacrosin binding protein	-1.42	0.238	-1.22	0.56	1.06	0.831	-1.54	0.33	-0.78
1427901_at	Mrps18c	mitochondrial ribosomal protein S18C	-1.09	0.433	-1.09	0.387	-1.35	0.041	1.1	0.407	-0.61
1453156_s_at	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	-1.15	0.381	-1.13	0.57	-1.2	0.127	1.14	0.622	-0.59
1442070_at	Mllt10	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosop	1.01	0.967	-1.41	0.313	-1.16	0.445	-1.12	0.74	-0.67
1452634_at	Obox3	oocyte specific homeobox 3	-1.86	0.033	1.62	0.391	-2.36	0.013	-1.34	0.343	-0.99
1421159_at	Cgnl1 /// LOC6774	cingulin-like 1 /// similar to cingulin-like 1 isoform 1	1.29	0.796	-2.19	0.092	-1.2	0.8	-1.73	0.272	-0.96
1416366_at	LOC675851	similar to NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2	-1.26	0.003	-1.15	0.057	-1.09	0.298	1.02	0.82	-0.62
1417920_at	Amn	amnionless	-1.02	0.8	-2.08	0.225	1.12	0.754	-1.48	0.202	-0.86
1432061_at	4933406B17Rik	RIKEN cDNA 4933406B17 gene	-1.53	0.518	1.01	0.967	-1.09	0.847	-1.41	0.14	-0.75
1445410_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-1.51	0.417	1.18	0.644	-1.36	0.074	-1.13	0.56	-0.71
1446022_at	Msi2	Musashi homolog 2 (Drosophila)	-1.24	0.181	1	0.993	-1.29	0.197	-1.07	0.821	-0.65
1454696_at	Gnb1	guanine nucleotide binding protein, beta 1	-1.26	0.509	1.04	0.812	-1.35	0.34	-1.05	0.854	-0.65
1436301_at	Ripk5	receptor interacting protein kinase 5	-1.06	0.536	-1.14	0.284	-1.31	0.088	1.14	0.292	-0.59
1416501_at	Pdpk1	3-phosphoinositide dependent protein kinase-1	-1.02	0.906	-1.19	0.032	-1.32	0.312	1.36	0.208	-0.54
1459153_at	Ston2	stonin 2	-1.09	0.667	-2.28	0.091	1.22	0.488	-2.45	0.265	-1.15
1415860_at	Kpna2 /// LOC6705	karyopherin (importin) alpha 2 /// similar to Importin alpha-2 subunit (Karyopherin	-1.09	0.689	-1.18	0.15	-1.23	0.214	1.78	0.193	-0.43
1433372_at	5330425B07Rik	RIKEN cDNA 5330425B07 gene	-1.23	0.802	-1.25	0.733	-1.03	0.935	1.83	0.427	-0.42
1458739_at	---	---	-1.54	0.44	1.59	0.125	-2.93	0.148	-1.41	0.009	-1.07
1416133_at	C920006C10Rik	RIKEN cDNA C920006C10 gene	-1.12	0.036	-1.13	0.123	-1.24	0.16	1.07	0.774	-0.61
1426902_at	Coq6	coenzyme Q6 homolog (yeast)	-1.11	0.6	-1.2	0.49	-1.19	0.093	1.04	0.811	-0.61
1456799_at	E130110O22Rik	RIKEN cDNA E130110O22 gene	1.2	0.091	-1.35	0.171	-1.56	0.211	-3.12	0.039	-1.21
1444615_x_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1.12	0.549	-1.29	0.371	-1.46	0.051	-1.27	0.319	-0.72
1430957_at	Arhgap26	Rho GTPase activating protein 26	-2.15	0.452	-1.25	0.538	1.31	0.381	-1.47	0.134	-0.89
1416432_at	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.19	0.024	-1.67	0.408	1.14	0.73	-1.72	0.15	-0.86
1455806_x_at	Ndufa12 /// LOC66	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 /// similar to 13kDa c	-1.14	0.365	-1.26	0.038	-1.1	0.133	1.23	0.066	-0.57
1425199_a_at	Epb4.1l5	erythrocyte protein band 4.1-like 5	-1.3	0.068	-1.12	0.297	-1.09	0.625	1.06	0.865	-0.61
1458825_at	Mier3	Mesoderm induction early response 1, family member 3	-1.27	0.428	1.02	0.946	-1.28	0.437	-1.19	0.542	-0.68
1446688_at	Gnaq	Guanine nucleotide binding protein, alpha q polypeptide	1.22	0.513	-1.28	0.365	-1.73	0.032	-1.33	0.33	-0.78
1424465_at	Ccdc58	coiled-coil domain containing 58	-1.31	0.009	-1.22	0.004	-1	0.994	1.13	0.708	-0.6
1433001_at	1700019L13Rik	RIKEN cDNA 1700019L13 gene	1.3	0.733	-2.3	0.167	-1.18	0.717	-1.41	0.576	-0.9
1429126_at	2600001M11Rik	RIKEN cDNA 2600001M11 gene	-1.21	0.068	-1.19	0.214	-1.09	0.652	1.54	0.16	-0.49
1426953_at	Hmgb2l1	high mobility group box 2-like 1	-1.07	0.237	-1.11	0.496	-1.34	0.101	1.2	0.48	-0.58
1448494_at	Gas1	growth arrest specific 1	-1.29	0.108	-1.39	0.415	1.08	0.829	-1.57	0.378	-0.79
1416848_at	Ubl5	ubiquitin-like 5	-1.37	0.014	-1.08	0.523	-1.08	0.514	1.04	0.563	-0.62
1429879_at	0610037L13Rik	RIKEN cDNA 0610037L13 gene	-2.2	0.008	1.52	0.134	-1.65	0.028	-1.37	0.323	-0.92
1437312_at	Bmpr1b	bone morphogenetic protein receptor, type 1B	-1.34	0.323	1.23	0.745	-1.66	0.087	-1.04	0.953	-0.7
1425141_at	Lactb2	lactamase, beta 2	-1.1	0.042	-1.26	0.014	-1.14	0.017	1.15	0.631	-0.59
1442946_at	Atxn7	Ataxin 7	-1	0.993	1.02	0.921	-1.77	0.004	-1.31	0.043	-0.76
1429453_a_at	Mrpl55	mitochondrial ribosomal protein L55	-1.07	0.596	-1.28	0.001	-1.15	0.165	1.47	0.081	-0.51
1417675_a_at	Mdn1	midasin homolog (yeast)	-1.49	0.036	1.06	0.756	-1.18	0.295	-1.65	0.097	-0.81
1445166_at	Pcgf3	Polycomb group ring finger 3	1.06	0.939	-1.4	0.12	-1.24	0.404	-1.9	0.242	-0.87
1426685_a_at	Cnot6	CCR4-NOT transcription complex, subunit 6	-1.02	0.935	-1.07	0.338	-1.5	0.004	1.03	0.874	-0.64
1445168_at	---	---	-1.2	0.766	-1.31	0.477	-1.01	0.95	1.15	0.75	-0.59
1460410_at	2310079F23Rik	RIKEN cDNA 2310079F23 gene	-1.11	0.829	-1.29	0.473	-1.1	0.72	1.13	0.682	-0.59
1435539_at	Hdh	Huntington disease gene homolog	1.01	0.975	-1.39	0.076	-1.18	0.355	-1.17	0.309	-0.68
1422910_s_at	Smc6	structural maintenance of chromosomes 6	-1.05	0.749	-1.16	0.53	-1.3	0.369	1.01	0.972	-0.63
1433237_at	3830422I06Rik	RIKEN cDNA 3830422I06 gene	-1.78	0.407	1.03	0.955	-1.01	0.979	-1.02	0.782	-0.7
1444405_at	E430029J22Rik	RIKEN cDNA E430029J22 gene	-3.04	0.276	1.46	0.083	-1.27	0.377	-3.24	0.034	-1.52
1451165_at	Lmbr1l	limb region 1 like	-1.79	0.363	-1	0.994	1.03	0.939	-1.87	0.373	-0.91
1424170_at	Phf5a	PHD finger protein 5A	-1.22	0.231	-1.18	0.052	-1.1	0.468	1.47	0.319	-0.51
1448793_a_at	Sdc4	syndecan 4	1.13	0.525	-1.16	0.476	-1.68	0.078	-1.61	0.072	-0.83

1424959_at	Anxa13	annexin A13	-1.19	0.553	-1.66	0.008	1.14	0.487	-1.72	0.31	-0.86
1449238_at	Psg16	pregnancy specific glycoprotein 16	-1.09	0.741	-1.31	0.593	-1.11	0.417	1.14	0.723	-0.59
1458257_at	---	---	-1.48	0.073	1.13	0.446	-1.28	0.089	-1.13	0.524	-0.69
1426105_a_at	Ubxd5	UBX domain containing 5	-1.59	0.198	-1.65	0.523	1.35	0.064	-1.4	0.009	-0.82
1444524_at	---	Activated spleen cDNA, RIKEN full-length enriched library, clone:F830206P12 pr	-1.73	0.263	1.33	0.627	-1.48	0.093	-1.01	0.909	-0.72
1448578_at	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	-1.54	0.141	-1.16	0.435	1.07	0.762	-1.4	0.327	-0.76
1455218_at	6330503K22Rik	RIKEN cDNA 6330503K22 gene	-1.05	0.522	-1.24	0.521	-1.21	0.221	2.98	0.165	-0.13
1436290_at	---	---	1.03	0.89	-1.33	0.521	-1.24	0.322	-1.01	0.978	-0.64
1440105_at	Jmjd2d	jumonji domain containing 2D	1.01	0.982	-1.04	0.913	-1.63	0.452	-1.16	0.622	-0.71
1429441_at	Fbxo30	F-box protein 30	-1.23	0.288	-1.21	0.235	-1.06	0.163	3.26	0.218	-0.06
1434669_at	Ralgps1	Ral GEF with PH domain and SH3 binding motif 1	-1.2	0.142	-1.46	0.358	1.07	0.72	-1.39	0.432	-0.75
1449201_at	Star	steroidogenic acute regulatory protein	-1.24	0.298	-3.16	0.288	1.46	0.484	-1.32	0.388	-1.07
1418179_at	Atg3	autophagy-related 3 (yeast)	-1.17	0.565	-1.15	0.656	-1.16	0.523	1.31	0.01	-0.54
1432438_at	4930597L12Rik	RIKEN cDNA 4930597L12 gene	-1.11	0.438	-1.31	0.322	-1.09	0.849	1.25	0.194	-0.56
1417624_at	Nab1	Ngfi-A binding protein 1	1.03	0.876	-1.07	0.707	-1.62	0	-1.32	0.264	-0.74
1440226_at	Zfp760	zinc finger protein 760	-1.22	0.182	1.07	0.708	-1.44	0.18	-1.57	0.011	-0.79
1440776_at	3732412D22Rik	RIKEN cDNA 3732412D22 gene	1.28	0.67	-1.41	0.621	-1.68	0.091	-1.81	0.463	-0.91
1437634_at	Thoc2	THO complex 2	-2.13	0.211	-1.51	0.106	1.45	0.258	-1.05	0.876	-0.81
1425327_at	BC008163	cDNA sequence BC008163	-1.08	0.771	-1.22	0.182	-1.2	0.407	1.62	0.226	-0.47
1425104_at	Kctd1	potassium channel tetramerisation domain containing 1	-1.36	0.098	-1.2	0.299	1.02	0.932	-1.04	0.655	-0.65
1415941_s_at	Zfand2a	zinc finger, AN1-type domain 2A	-1.41	0.161	1.1	0.661	-1.28	0.154	-1.32	0.225	-0.73
1429331_at	4632427E13Rik	RIKEN cDNA 4632427E13 gene	1.09	0.603	-1.22	0.177	-1.47	0.002	-1.41	0.306	-0.75
1438976_x_at	Mat2a	methionine adenosyltransferase II, alpha	-1.25	0.52	1.01	0.946	-1.3	0.108	-1.14	0.466	-0.67
1429195_at	---	---	-1.63	0.647	-1.04	0.947	1.01	0.99	-1.44	0.206	-0.77
1443256_at	Clca6	Chloride channel calcium activated 6	-1.31	0.501	-1.06	0.937	-1.14	0.742	1.14	0.812	-0.59
1451596_a_at	Sphk1	sphingosine kinase 1	-1.01	0.969	-1.55	0.226	-1.05	0.829	3.68	0.123	0.02
1429466_s_at	Aph1c /// Aph1b	anterior pharynx defective 1c homolog (C. elegans) /// anterior pharynx defective	-1.33	0.057	-1.33	0.599	1.08	0.759	-1.36	0.344	-0.73
1436156_at	Ccar1	cell division cycle and apoptosis regulator 1	-1.13	0.534	-1.17	0.23	-1.18	0.286	1.19	0.213	-0.57
1452729_at	Dpm3	dolichyl-phosphate mannosyltransferase polypeptide 3	-1.51	0.04	1.06	0.888	-1.17	0.691	-1.11	0.818	-0.68
1451084_at	Etfdh	electron transferring flavoprotein, dehydrogenase	-1.18	0.194	-1.31	0.099	-1.02	0.888	1.22	0.203	-0.58
1447056_at	Slit2	Slit homolog 2 (Drosophila)	-1.24	0.459	-1.03	0.913	-1.24	0.334	1.7	0.092	-0.45
1423953_at	Cdkal1	CDK5 regulatory subunit associated protein 1-like 1	1.07	0.617	-1.31	0.069	-1.33	0.118	-1.48	0.041	-0.76
1434339_at	Fnbp1l	formin binding protein 1-like	-1.28	0.224	1.02	0.855	-1.28	0.137	-1.43	0.045	-0.74
1438451_at	Grit	Rho GTPase-activating protein	-1.19	0.353	-1.39	0.054	1.02	0.912	-1.62	0.247	-0.79
1460055_at	Evi2a	Ecotropic viral integration site 2a	-1.66	0.076	1.08	0.768	-1.11	0.712	-1.4	0.382	-0.77
1456617_a_at	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	-1.22	0.002	-1.01	0.922	-1.3	0.113	1.05	0.79	-0.62
1440287_at	1110014D18Rik	RIKEN cDNA 1110014D18 gene	1.01	0.933	-1.18	0.359	-1.38	0.184	-1.45	0.035	-0.75
1421208_at	Ikbkg	inhibitor of kappaB kinase gamma	-1.31	0.301	-1.49	0.15	1.15	0.671	-1.14	0.65	-0.7
1418859_at	Rfxap	regulatory factor X-associated protein	-1.09	0.456	-1.45	0.064	-1.02	0.759	1.15	0.524	-0.6
1455246_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.12	0.756	-1.12	0.716	-1.25	0.503	1.16	0.552	-0.58
1430108_at	9030622M22Rik	RIKEN cDNA 9030622M22 gene	-1.17	0.61	-1.04	0.848	-1.3	0.502	1.63	0.062	-0.47
1426314_at	Ednrb	endothelin receptor type B	1.08	0.76	-1.11	0.731	-1.65	0.039	-1.53	0.054	-0.8
1424206_at	Smarca5 /// 923011	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.25	0.261	-1.13	0.392	-1.1	0.058	1.23	0.396	-0.56
1456898_at	Pura	purine rich element binding protein A	1.09	0.758	-1.27	0.047	-1.41	0.007	-1.2	0.276	-0.7
1440891_at	Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	1.79	0.041	-2.15	0.055	-3.06	0.013	-1.54	0.578	-1.24
1446095_at	Air	antisense Igf2r RNA	-1.2	0.792	1.38	0.616	-2.64	0.015	-1.05	0.869	-0.88
1431031_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-1.5	0.185	-1.11	0.712	1.02	0.925	-1.25	0.061	-0.71
1455267_at	Esrrg	estrogen-related receptor gamma	-1.19	0.158	-1.64	0.374	1.14	0.092	-2.9	0.107	-1.15
1453678_at	Mbd1	methyl-CpG binding domain protein 1	1.19	0.384	-1.64	0.31	-1.27	0.15	-1.27	0.276	-0.75
1434506_at	Arid2	AT rich interactive domain 2 (Arid-rfx like)	-1.15	0.576	-1.09	0.623	-1.26	0.213	1.47	0.186	-0.51
1437282_at	Dock2	Dedicator of cyto-kinesis 2	-1.8	0.309	-1.2	0.468	1.19	0.588	-2.01	0.086	-0.95
1420340_at	4930413O22Rik	RIKEN cDNA 4930413O22 gene	-1.42	0.255	-1.06	0.919	-1.06	0.794	1.03	0.893	-0.63
1418355_at	Nucb2	nucleobindin 2	1.02	0.865	-1.25	0.217	-1.3	0.043	-1.55	0.078	-0.77

1423146_at	Hes5	hairy and enhancer of split 5 (Drosophila)	-1.14	0.653	1.13	0.732	-1.71	0.22	-1.86	0.034	-0.9
1453576_at	Nipbl	Nipped-B homolog (Drosophila)	1.01	0.966	-1.1	0.045	-1.5	0.129	-1.34	0.301	-0.73
1426892_at	Utrn	utrophin	-1.15	0.501	1.13	0.685	-1.7	0.165	-1.81	0.23	-0.88
1444463_at	Arhgap12	Rho GTPase activating protein 12	1.49	0.264	-1.4	0.556	-2.59	0.033	-3.21	0.013	-1.43
1435246_at	Paqr8	progestin and adipoQ receptor family member VIII	-1.67	0.586	1.08	0.807	-1.1	0.524	-2	0.27	-0.92
1447217_at	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	-1.08	0.596	1	0.982	-1.53	0.114	-1.15	0.566	-0.69
1425143_a_at	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	-1.17	0.084	-1.29	0.051	-1.04	0.772	1.05	0.781	-0.61
1446380_at	9430076C15Rik	RIKEN cDNA 9430076C15 gene	-1.17	0.87	1.11	0.887	-1.62	0.253	-1.47	0.651	-0.79
1458960_at	Ryk	Receptor-like tyrosine kinase	-1	0.995	1.09	0.894	-1.99	0.209	-4.96	0.021	-1.72
1423364_a_at	Fts	fused toes	1.04	0.584	-1.2	0.017	-1.4	0.013	-1.4	0.058	-0.74
1426664_x_at	Slc45a3	solute carrier family 45, member 3	-1.29	0.22	-1.02	0.927	-1.2	0.17	1.22	0.34	-0.57
1430576_at	Tpp2	tripeptidyl peptidase II	1.36	0.45	-1.55	0.067	-1.71	0.06	-2.15	0.064	-1.01
1451390_s_at	Zfand2b	zinc finger, AN1 type domain 2B	-1.24	0.035	-1.03	0.791	-1.23	0.314	1.19	0.495	-0.58
1423250_a_at	Tgfb2	transforming growth factor, beta 2	-1.55	0.013	1.25	0.625	-1.45	0.323	-1.41	0.669	-0.79
1446827_at	Ncoa2	nuclear receptor coactivator 2	-1.26	0.422	1	0.995	-1.26	0.039	-1.16	0.24	-0.67
1441783_at	2410022M11Rik	RIKEN cDNA 2410022M11 gene	1.15	0.575	-2.13	0.048	-1.03	0.869	-1.11	0.856	-0.78
1445611_at	1810044A24Rik	RIKEN cDNA 1810044A24 gene	1.16	0.482	-1.85	0.079	-1.13	0.716	-1.69	0.164	-0.88
1441468_at	---	PREDICTED: Mus musculus similar to dachsous 2 isoform 2 (LOC627094), mRN	-1.06	0.718	-1.22	0.425	-1.21	0.513	1.55	0.323	-0.49
1420516_at	a	nonagouti	1.03	0.935	-1.08	0.678	-1.59	0.132	-1.01	0.965	-0.66
1454978_at	Ttyh3	tweety homolog 3 (Drosophila)	-1.09	0.563	-1.5	0.412	1.01	0.978	-1.12	0.6	-0.68
1432798_at	9530023I19Rik	RIKEN cDNA 9530023I19 gene	-1.3	0.565	1.05	0.81	-1.3	0.311	-1.2	0.173	-0.69
1449158_at	Kcnk2	potassium channel, subfamily K, member 2	-1.06	0.706	-1.25	0.67	-1.19	0.477	1.61	0.256	-0.47
1428423_at	Pcgf3	polycomb group ring finger 3	-1.12	0.116	-1.06	0.615	-1.33	0.067	1.55	0.2	-0.49
1446948_at	Denr	Density-regulated protein	1.19	0.481	-1.37	0.328	-1.51	0.328	-1.35	0.614	-0.76
1428933_at	Hdac8	histone deacetylase 8	-1.39	0.198	-1.37	0.203	1.14	0.562	-1.31	0.12	-0.73
1450417_a_at	Rps20 /// LOC2456	ribosomal protein S20 /// similar to 40S ribosomal protein S20 /// similar to 40S rib	-1.12	0.754	-1.15	0.507	-1.21	0.46	1.27	0.468	-0.55
1421686_at	Rfrp	RFamide-related peptide	-1.55	0.242	1.21	0.545	-1.37	0.127	-1.27	0.28	-0.74
1450401_at	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	1.04	0.899	-1.16	0.273	-1.45	0.073	-1.06	0.854	-0.66
1417286_at	Ndufa5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	-1.13	0.11	-1.17	0.263	-1.18	0.064	1.12	0.631	-0.59
1446529_at	1200003I07Rik	RIKEN cDNA 1200003I07 gene	-1.02	0.797	1.26	0.744	-2.81	0.019	-1.67	0.155	-1.06
1438335_at	6030413G23Rik	RIKEN cDNA 6030413G23 gene	-1.23	0.339	-1.44	0.33	1.08	0.832	-1.3	0.74	-0.72
1437506_at	---	---	-1.49	0.575	-1.47	0.557	1.24	0.483	-2.61	0.132	-1.08
1448102_a_at	Wdr61	WD repeat domain 61	-1.15	0.43	-1.12	0.004	-1.2	0.046	1.09	0.549	-0.6
1426172_a_at	Cd209a	CD209a antigen	1.16	0.8	-1.13	0.835	-1.82	0.141	-2.73	0.027	-1.13
1456789_at	Zfp462	Zinc finger protein 462	-1.18	0.253	1.14	0.714	-1.66	0.177	-1.21	0.378	-0.73
1419036_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	-1.07	0.629	-1.11	0.135	-1.32	0.047	1.15	0.262	-0.59
1419155_a_at	Sox4 /// LOC67227	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	1.16	0.449	-1.33	0.326	-1.47	0.273	-1.34	0.166	-0.75
1457487_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730014I(	-1.86	0.204	1.09	0.731	-1.04	0.905	-2.61	0.03	-1.1
1444838_at	C630010N09	hypothetical protein C630010N09	-1.61	0.012	-1	0.996	-1.03	0.925	1.34	0.057	-0.57
1436864_at	A430090L17Rik	RIKEN cDNA A430090L17 gene	-1.13	0.576	1.01	0.98	-1.43	0.205	-1.06	0.606	-0.65
1456611_at	D430015B01Rik	RIKEN cDNA D430015B01 gene	-1.62	0.143	-1.84	0.037	1.43	0.253	-1.62	0.145	-0.91
1431079_at	C1qtnf2	C1q and tumor necrosis factor related protein 2	1.03	0.934	-1.1	0.785	-1.53	0.125	-1.12	0.693	-0.68
1416793_at	Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	-1.17	0.078	-1.16	0.2	-1.15	0.019	1.47	0.268	-0.5
1452608_at	Mycbp	c-myc binding protein	-1.15	0.487	-1.32	0.162	-1.04	0.774	1.09	0.645	-0.61
1432307_at	1700086D15Rik	RIKEN cDNA 1700086D15 gene	-1.84	0.445	-1.79	0.352	1.49	0.371	-2.4	0.369	-1.14
1436108_at	Txndc9	thioredoxin domain containing 9	-1.01	0.951	-1.43	0.135	-1.11	0.448	1.44	0.168	-0.53
1440172_s_at	1700113H08Rik	RIKEN cDNA 1700113H08 gene	1.05	0.964	-1.16	0.815	-1.46	0.542	-2.22	0.336	-0.95
1419952_at	Stx5a	Syntaxin 5A	1.05	0.949	-1.44	0.211	-1.18	0.489	-1.1	0.823	-0.67
1436446_at	2310007O11Rik	RIKEN cDNA 2310007O11 gene	-1.18	0.423	-1.01	0.972	-1.34	0.006	1.8	0.076	-0.43
1450728_at	Fjx1	four jointed box 1 (Drosophila)	1.34	0.7	-2.12	0.134	-1.28	0.277	-1.07	0.828	-0.78
1431479_at	4921524L21Rik	RIKEN cDNA 4921524L21 gene	-1.41	0.532	-1.02	0.971	-1.11	0.87	1.19	0.79	-0.59
1444528_at	---	---	-1.41	0.164	-1.61	0.195	1.26	0.574	-2.31	0.085	-1.02
1459987_s_at	Cct3	chaperonin subunit 3 (gamma)	-1.3	0.023	-1.15	0.287	-1.05	0.793	1.14	0.591	-0.59

1443626_at	Chn2	Chimerin (chimaerin) 2	1.31	0.161	-1.3	0.505	-1.94	0.032	-1.33	0.144	-0.82
1417362_at	Rhcg	Rhesus blood group-associated C glycoprotein	-1.35	0.242	-1.47	0.37	1.17	0.456	-1.43	0.065	-0.77
1427243_at	AA536743	expressed sequence AA536743	-1.02	0.6	-1.05	0.688	-1.52	0.014	1.58	0.138	-0.5
1454275_at	---	---	-1.1	0.862	-1.29	0.619	-1.1	0.751	1.06	0.879	-0.61
1418034_at	Mrps9	mitochondrial ribosomal protein S9	1.02	0.906	-1.33	0.066	-1.22	0.326	-1.34	0.252	-0.72
1418399_at	Kctd9	potassium channel tetramerisation domain containing 9	-1.19	0.24	-1.15	0.373	-1.13	0.209	2.1	0.263	-0.34
1426798_a_at	---	---	-1.32	0.402	-1.24	0.222	1.02	0.938	-1.08	0.682	-0.65
1431201_at	Slc25a27	solute carrier family 25, member 27	-1.4	0.577	-1.16	0.781	1.01	0.968	-1.32	0.442	-0.71
1431531_at	1700025D03Rik	RIKEN cDNA 1700025D03 gene	-1	0.994	-1.15	0.756	-1.39	0.027	1.06	0.725	-0.62
1434000_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	-1.07	0.073	-1.13	0.29	-1.29	0.074	1.39	0.072	-0.53
1441300_at	Kcnf1	potassium voltage-gated channel, subfamily F, member 1	-1.14	0.543	-1.12	0.811	-1.21	0.51	1.91	0.414	-0.39
1429061_at	1810063B05Rik	RIKEN cDNA 1810063B05 gene	-1.34	0.149	-1.16	0.444	-1.01	0.922	1.28	0.386	-0.56
1440998_at	2310021P13Rik	RIKEN cDNA 2310021P13 gene	1.04	0.763	-1.32	0.096	-1.26	0.547	-1.46	0.056	-0.75
1425347_a_at	Zfp318	zinc finger protein 318	-1.06	0.723	-1.72	0.121	1.06	0.74	-2.62	0.035	-1.08
1429899_at	5730414N17Rik	RIKEN cDNA 5730414N17 gene	1.03	0.877	-1.44	0.091	-1.15	0.385	-1.53	0.242	-0.77
1449098_a_at	Poli	polymerase (DNA directed), iota	-1.28	0.238	-1.48	0.002	1.13	0.553	-1.24	0.512	-0.72
1448563_at	Phb	prohibitin	-1.21	0.176	-1.35	0.039	1.03	0.697	-1.22	0.329	-0.69
1446421_at	Schip1	Schwannomin interacting protein 1	-1.05	0.913	1.17	0.767	-2.15	0.026	-1.29	0.421	-0.83
1447815_x_at	6430527G18Rik	RIKEN cDNA 6430527G18 gene	-1.26	0.708	-1.51	0.437	1.13	0.566	-3.53	0.033	-1.29
1437177_at	D330037H05Rik ///	RIKEN cDNA D330037H05 gene /// similar to La-related protein 4 (La ribonucleop	-1.04	0.923	-1.21	0.519	-1.24	0.429	1.15	0.7	-0.59
1439981_at	A430001F24Rik	RIKEN cDNA A430001F24 gene	-2.25	0.089	-1.19	0.684	1.31	0.626	-1.87	0.178	-1
1417187_at	Hip2	huntingtin interacting protein 2	-1.45	0.271	-1.05	0.891	-1.05	0.943	3.2	0.017	-0.09
1423184_at	Itsn2	intersectin 2	1.2	0.681	-1.55	0.301	-1.33	0.401	-1.33	0.533	-0.75
1437818_at	9430016H08Rik	RIKEN cDNA 9430016H08 gene	-1.23	0.27	-1.21	0.074	-1.05	0.724	1.31	0.465	-0.55
1421778_at	V1rb2	vomeronasal 1, receptor B2	-1.43	0.121	-1.35	0.319	1.15	0.392	-2.29	0.321	-0.98
1447141_at	AW107722	expressed sequence AW107722	1.12	0.375	-1	0.99	-2.12	0.005	-1.87	0.031	-0.97
1420193_at	Krt17	keratin 17	-1.72	0.35	1.04	0.942	-1.03	0.961	-1.21	0.203	-0.73
1430237_at	Cldn22	claudin 22	-1.55	0.116	-1.27	0.355	1.16	0.51	-1.14	0.028	-0.7
1444395_at	Dixdc1	DIX domain containing 1	-1.55	0.358	-1.15	0.52	1.08	0.827	-1.27	0.665	-0.72
1446912_at	Tmem28	Transmembrane protein 28	-2.32	0.457	1.4	0.443	-1.31	0.498	-1.2	0.203	-0.86
1450361_at	Prop1	paired like homeodomain factor 1	-2.74	0.111	1.63	0.06	-1.67	0.11	-1.3	0.011	-1.02
1446971_at	D10Wsu159e	DNA segment, Chr 10, Wayne State University 159, expressed	-1.31	0.306	-1.01	0.984	-1.19	0.438	1.04	0.666	-0.62
1417400_at	Rai14	retinoic acid induced 14	-1.09	0.626	1.02	0.883	-1.54	0.032	-1.6	0.111	-0.8
1422369_at	V1ra6	vomeronasal 1 receptor, A6	-1.32	0.537	-2.33	0.009	1.4	0.44	-2.64	0.07	-1.22
1440082_at	Ptk2	PTK2 protein tyrosine kinase 2	1.22	0.55	-1.3	0.668	-1.66	0.073	-1.04	0.905	-0.69
1418997_at	---	---	-1.23	0.326	-1	1	-1.28	0.304	1.1	0.454	-0.6
1431378_at	---	---	-2.48	0.246	1.26	0.368	-1.08	0.898	-1.68	0.045	-0.99
1448543_at	2310042G06Rik	RIKEN cDNA 2310042G06 gene	-1.12	0.332	-1.07	0.502	-1.31	0.008	1.63	0.152	-0.47
1447569_at	1700081L11Rik	RIKEN cDNA 1700081L11 gene	-1.8	0.012	1.21	0.392	-1.22	0.709	-4.72	0.227	-1.63
1441576_at	2410002O22Rik	RIKEN cDNA 2410002O22 gene	-1.12	0.536	-1.08	0.66	-1.28	0.311	1.09	0.841	-0.6
1424884_at	Fbxw2	F-box and WD-40 domain protein 2	-1.21	0.128	-1.21	0.303	-1.06	0.534	1.08	0.806	-0.6
1424516_at	B230354K17Rik	RIKEN cDNA B230354K17 gene	-1.01	0.925	-1.18	0.054	-1.32	0.06	1.21	0.275	-0.58
1426786_s_at	Dhx38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	-1.36	0.085	-1.19	0.276	1.02	0.962	-1.12	0.613	-0.66
1453009_at	Cpm	carboxypeptidase M	-1.29	0.309	1.27	0.638	-1.81	0.03	-4.64	0.042	-1.62
1426958_at	Rps9 /// LOC27269	ribosomal protein S9 /// similar to ribosomal protein S9	-1.25	0.323	-1.64	0.183	1.18	0.334	-1.22	0.369	-0.73
1418574_a_at	Shfm1	split hand/foot malformation (ectrodactyly) type 1	-1.12	0.539	1.02	0.868	-1.47	0.007	-1.32	0.18	-0.72
1445085_at	Clstn1	Calsyntenin 1	-1.17	0.823	1.04	0.864	-1.44	0.4	-1.37	0.603	-0.73
1454918_at	Agps	alkylglycerone phosphate synthase	-1.37	0.266	1.12	0.629	-1.34	0.112	-1.25	0.335	-0.71
1455512_at	Gm879	gene model 879, (NCBI)	-2.32	0.052	1.29	0.496	-1.15	0.712	-1.66	0.136	-0.96
1418286_a_at	Efnb1	ephrin B1	-1.11	0.219	-1.15	0.32	-1.21	0.237	1.01	0.955	-0.62
1434612_s_at	Sbno1	sno, strawberry notch homolog 1 (Drosophila)	-1.15	0.179	-1.1	0.359	-1.23	0.188	1	0.999	-0.62
1443605_at	C81272	expressed sequence C81272	1.24	0.532	-1.25	0.747	-1.8	0.157	-1.4	0.312	-0.8
1439671_at	4930466K18Rik	RIKEN cDNA 4930466K18 gene	-1.14	0.318	-1.06	0.785	-1.29	0.4	1.18	0.412	-0.58

1456987_at	4932418E24Rik	RIKEN cDNA 4932418E24 gene	-1.13	0.787	-1.8	0.261	1.16	0.793	-1.2	0.686	-0.74
1439729_at	A930038B10Rik	RIKEN cDNA A930038B10 gene	-1.01	0.98	-1.86	0.356	1.07	0.872	-3.22	0.082	-1.25
1448609_at	Tst	thiosulfate sulfurtransferase, mitochondrial	-1.19	0.353	-1.14	0.249	-1.15	0.545	1.63	0.205	-0.46
1431416_a_at	Jam2	junction adhesion molecule 2	-1.47	0.369	-1.29	0.75	1.14	0.579	-1.38	0.692	-0.75
1441733_s_at	Nup153	nucleoporin 153	1.05	0.867	-1.14	0.578	-1.49	0.037	-1.22	0.135	-0.7
1452304_a_at	Arhgef5	Rho guanine nucleotide exchange factor (GEF) 5	-1.22	0.137	-1.06	0.551	-1.2	0.122	1.44	0.38	-0.51
1449274_at	2310038H17Rik	RIKEN cDNA 2310038H17 gene	-1.38	0.084	-1.16	0.253	1.01	0.956	-1.41	0.353	-0.74
1419905_s_at	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	1.14	0.152	-1.6	0.072	-1.21	0.144	-1.29	0.447	-0.74
1431945_at	Arl13a	ADP-ribosylation factor-like 13A	-1.12	0.859	-2.32	0.358	1.27	0.53	-1.86	0.365	-1.01
1436585_at	BB182297	expressed sequence BB182297	-1.01	0.95	-1.11	0.511	-1.42	0.003	1.08	0.7	-0.61
1438944_at	1700007J24Rik	RIKEN cDNA 1700007J24 gene	1.26	0.063	-2.39	0.012	-1.09	0.767	-1.37	0.573	-0.9
1443922_at	Rcor3	REST corepressor 3	-1.16	0.681	-1.1	0.7	-1.22	0.413	2.39	0.031	-0.27
1460536_at	2310079F09Rik	RIKEN cDNA 2310079F09 gene	-1.32	0.129	1.03	0.784	-1.24	0.445	-1.57	0.109	-0.78
1452821_at	Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	-1.06	0.706	-1.04	0.729	-1.45	0.177	1	0.987	-0.64
1417771_a_at	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	-1.1	0.409	-1.17	0.013	-1.21	0.122	1.17	0.521	-0.58
1420711_a_at	Pxmp3	peroxisomal membrane protein 3	-1.27	0.091	-1.09	0.139	-1.13	0.368	1.03	0.832	-0.61
1440065_at	Polr2j	Polymerase (RNA) II (DNA directed) polypeptide J	1.13	0.831	-1.77	0.128	-1.11	0.811	-1.38	0.454	-0.78
1454652_at	Zranb2	zinc finger, RAN-binding domain containing 2	-1.1	0.283	-1.09	0.383	-1.3	0.041	1.06	0.719	-0.61
1439755_at	---	---	-1.19	0.188	-1.55	0.207	1.11	0.767	-1.53	0.457	-0.79
1430309_at	Nipbl	Nipped-B homolog (Drosophila)	1.02	0.433	-1.15	0.04	-1.41	0.073	-1.15	0.476	-0.67
1441740_at	---	---	1.04	0.868	-1.04	0.818	-1.69	0.006	-1.26	0.091	-0.74
1439483_at	AI506816	expressed sequence AI506816	-1.25	0.61	-1.02	0.973	-1.23	0.585	1.88	0.244	-0.4
1436341_at	Hmbox1	homeobox containing 1	1.01	0.96	-1.19	0.192	-1.34	0.254	-1.06	0.751	-0.64
1443905_at	Sfrs8	Splicing factor, arginine/serine-rich 8	1.17	0.799	-1.32	0.654	-1.49	0.239	-1.29	0.359	-0.73
1427839_at	Igh-VJ558	Immunoglobulin heavy chain (J558 family)	1.32	0.551	-2.42	0.214	-1.17	0.765	-1.26	0.655	-0.88
1455020_at	Snx25	sorting nexin 25	-1.18	0.418	-1.09	0.27	-1.21	0.282	1.08	0.806	-0.6
1452275_at	Zfand3	zinc finger, AN1-type domain 3	1.08	0.524	-1.92	0.352	-1.01	0.945	-1.13	0.35	-0.74
1448033_at	Tatdn1	TatD DNase domain containing 1	-1.14	0.217	-1.16	0.042	-1.17	0.546	1.5	0.39	-0.49
1452712_at	Hnrpa3	heterogeneous nuclear ribonucleoprotein A3	-1.09	0.179	-1.11	0.229	-1.28	0.075	1.03	0.579	-0.61
1432165_at	8430422H06Rik	RIKEN cDNA 8430422H06 gene	-1.4	0.305	-1.59	0.375	1.26	0.454	-1.72	0.003	-0.86
1423800_at	Dars	aspartyl-tRNA synthetase	-1.17	0.105	-1.23	0.041	-1.08	0.295	1.04	0.759	-0.61
1418538_at	Kdelr3	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	1.24	0.083	-1.18	0.751	-1.96	0.002	-1.23	0.562	-0.78
1449313_at	Klk1b5	kallikrein 1-related peptidase b5	-1.68	0.164	1.07	0.906	-1.07	0.748	-2.08	0.326	-0.94
1445881_at	2310035P21Rik	RIKEN cDNA 2310035P21 gene	1.01	0.982	-1.15	0.673	-1.4	0.467	-1.54	0.133	-0.77
1441696_at	Sec22a	SEC22 vesicle trafficking protein-like A (S. cerevisiae)	1.09	0.375	-1.2	0.208	-1.48	0.017	-1.44	0.2	-0.76
1421661_at	Fprl1	formyl peptide receptor-like 1	-3.12	0.421	1.43	0.491	-1.18	0.177	-1.29	0.518	-1.04
1441056_at	Usp3	ubiquitin specific peptidase 3	1.23	0.501	-1.49	0.008	-1.43	0.006	-1.43	0.015	-0.78
1428812_at	1700040L02Rik	RIKEN cDNA 1700040L02 gene	-1.15	0.138	-1.66	0.285	1.13	0.615	-1.68	0.522	-0.84
1441784_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.45	0.483	1.07	0.774	-1.2	0.41	-1.33	0.384	-0.73
1445037_at	6430510B20Rik	RIKEN cDNA 6430510B20 gene	1.08	0.387	-1.27	0.342	-1.38	0.277	-1.44	0.079	-0.75
1437875_at	Bicd2	bicaudal D homolog 2 (Drosophila)	-1.19	0.18	-1.12	0.525	-1.15	0.184	1.16	0.321	-0.58
1457873_at	---	11 days embryo gonad cDNA, RIKEN full-length enriched library, clone:7030407I	1.2	0.828	-2.2	0.17	-1.06	0.844	-1.33	0.637	-0.85
1444127_at	Asb1	ankyrin repeat and SOCS box-containing protein 1	-1.13	0.881	-1.46	0.273	1.03	0.951	-1.03	0.941	-0.65
1416397_at	Mesdc1	mesoderm development candidate 1	-1.45	0.235	-1.1	0.619	-1	0.952	1.8	0.123	-0.44
1456421_at	4930578M01Rik	RIKEN cDNA 4930578M01 gene	1.21	0.463	-1.14	0.569	-1.97	0.352	-1.13	0.632	-0.76
1458167_at	---	---	-1.19	0.834	1.11	0.824	-1.55	0.21	-2.66	0.282	-1.07
1447027_s_at	Lias	lipoic acid synthetase	-1.13	0.037	-1.14	0.013	-1.2	0.064	1.1	0.647	-0.59
1436213_a_at	1110028C15Rik	RIKEN cDNA 1110028C15 gene	-1.43	0.358	1.13	0.667	-1.3	0.336	-1.03	0.865	-0.66
1434115_at	---	---	-1.23	0.361	1.08	0.714	-1.42	0.162	-1.3	0.492	-0.72
1460199_a_at	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	-1.12	0.528	-1.1	0.27	-1.26	0.033	1.28	0.408	-0.55
1438808_at	Trp53	transformation related protein 53	1.63	0.295	-2.04	0.128	-2.1	0.017	-1.41	0.065	-0.98
1418604_at	Avpr1a	arginine vasopressin receptor 1A	-1.59	0.229	-1.14	0.655	1.09	0.759	-1.5	0.014	-0.78
1423375_at	1700023B02Rik	RIKEN cDNA 1700023B02 gene	-1.45	0.116	-1.04	0.713	-1.06	0.723	1.59	0.283	-0.49

1443556_at	1110007F12Rik	RIKEN cDNA 1110007F12 gene	-1.26	0.562	-2.03	0.153	1.31	0.41	-1.21	0.816	-0.8
1434242_at	Usp37	ubiquitin specific peptidase 37	-1.05	0.77	-1.15	0.489	-1.29	0.491	1.42	0.208	-0.52
1434261_at	Sipa1l2	signal-induced proliferation-associated 1 like 2	1.03	0.602	-1.51	0.269	-1.11	0.593	-1.06	0.767	-0.66
1451264_at	Frmd6	FERM domain containing 6	1.09	0.252	-1.3	0.165	-1.36	0.125	-1.67	0.13	-0.81
1459979_x_at	Zfp68	zinc finger protein 68	-1.63	0.286	1.2	0.683	-1.28	0.151	-1.34	0.38	-0.76
1446813_s_at	D5Ertd560e	DNA segment, Chr 5, ERATO Doi 560, expressed	-2.17	0.322	-1.03	0.93	1.17	0.726	-1.21	0.349	-0.81
1432483_at	1700124K17Rik	RIKEN cDNA 1700124K17 gene	-4.75	0.346	-1.02	0.949	1.41	0.502	-1.95	0.331	-1.58
1435176_a_at	Id2	inhibitor of DNA binding 2	-1.43	0.197	1.13	0.549	-1.31	0.048	-1.55	0.171	-0.79
1446566_at	Ap2b1	Adaptor-related protein complex 2, beta 1 subunit	1.16	0.382	-1.03	0.868	-2.13	0.045	-1.28	0.384	-0.82
1444085_at	Pdss2	prenyl (solanesyl) diphosphate synthase, subunit 2	-1.19	0.439	-1.1	0.516	-1.17	0.535	1.3	0.237	-0.54
1424802_a_at	3300001P08Rik	RIKEN cDNA 3300001P08 gene	-1.11	0.276	1.01	0.921	-1.45	0.045	-1.35	0.012	-0.73
1457977_at	2310005N01Rik	RIKEN cDNA 2310005N01 gene	-1.47	0.185	-1.14	0.6	1.04	0.87	-1.2	0.005	-0.69
1435103_x_at	Farslb	phenylalanine-tRNA synthetase-like, beta subunit	-1.11	0.172	-1.2	0.006	-1.16	0.395	1.08	0.663	-0.6
1447312_at	Ankib1	Ankyrin repeat and IBR domain containing 1	1.01	0.961	-1.29	0.285	-1.23	0.367	-1.02	0.894	-0.63
1431330_at	3110002H16Rik	RIKEN cDNA 3110002H16 gene	-1.02	0.94	-1.42	0.373	-1.09	0.67	1.42	0.394	-0.53
1428353_at	Foxk2	forkhead box K2	-1.02	0.912	-1.16	0.198	-1.32	0.089	1.35	0.21	-0.54
1436495_s_at	Zfp260	zinc finger protein 260	1.03	0.598	-1.12	0.12	-1.48	0.021	-1.52	0.235	-0.77
1423309_at	Tgoln1	trans-golgi network protein	1.02	0.746	-1.16	0.161	-1.39	0.024	-1.26	0.487	-0.7
1419786_at	Ltbp1	latent transforming growth factor beta binding protein 1	1.24	0.107	-1.12	0.677	-2.15	0.011	-1.13	0.8	-0.79
1446043_at	C81086	expressed sequence C81086	-1.18	0.663	-1.03	0.947	-1.28	0.508	1.61	0.382	-0.47
1457978_at	Centg2	Centaurin, gamma 2	-2.4	0.11	-1.45	0.456	1.5	0.431	-2.59	0.154	-1.24
1453312_at	Iqwd1	IQ motif and WD repeats 1	-1.02	0.838	-1.21	0.407	-1.26	0.236	1.84	0.164	-0.41
1432239_at	1700102J08Rik	RIKEN cDNA 1700102J08 gene	1.4	0.525	-1.93	0.3	-1.47	0.548	-1.9	0.149	-0.97
1442553_at	Mapre2	microtubule-associated protein, RP/EB family, member 2	-1.29	0.586	-1.07	0.794	-1.12	0.454	1.47	0.231	-0.5
1452955_at	Gtf2h5	general transcription factor IIH, polypeptide 5	-1.21	0.403	-1.18	0.575	-1.08	0.271	1.01	0.945	-0.61
1421589_at	Krt31	keratin 31	-1.01	0.978	1.1	0.848	-1.99	0.15	-1.29	0.529	-0.8
1430661_at	Myl6b	myosin, light polypeptide 6B	1.32	0.313	-1.59	0.39	-1.55	0.257	-1.59	0.025	-0.85
1433730_at	Elmod2	ELMO domain containing 2	-1.21	0.194	-1.19	0.064	-1.06	0.62	1.13	0.514	-0.59
1418088_a_at	Stx8	syntaxin 8	-1.06	0.454	-1.25	0.046	-1.17	0.103	1.03	0.811	-0.61
1446374_at	Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	-1.05	0.884	1.07	0.901	-1.74	0.065	-1.65	0.267	-0.84
1416743_at	Uap1 /// LOC64050	UDP-N-acetylglucosamine pyrophosphorylase 1 /// similar to UDP-N-acetylhexos	-1.21	0.556	1.06	0.693	-1.4	0.165	-1.03	0.807	-0.64
1445245_at	B130065D12Rik	RIKEN cDNA B130065D12 gene	1.43	0.551	-1.44	0.418	-2.1	0.047	-1.21	0.505	-0.83
1437211_x_at	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	1.14	0.154	-1.34	0.148	-1.4	0.061	-1.37	0.293	-0.74
1443738_at	Ptdss2	Phosphatidylserine synthase 2	-1.67	0.318	-2.08	0.036	1.52	0.261	-1.25	0.7	-0.87
1440777_x_at	---	---	1.14	0.765	-1.21	0.636	-1.58	0.194	-1.48	0.302	-0.78
1447391_at	Rufy1	RUN and FYVE domain containing 1	-1.06	0.88	-1.74	0.114	1.08	0.794	-1.01	0.922	-0.68
1423275_at	Ints6	integrator complex subunit 6	1.02	0.824	-1.15	0.378	-1.41	0.115	-1.09	0.678	-0.66
1428866_at	2810037O22Rik	RIKEN cDNA 2810037O22 gene	-2.19	0.41	-1.02	0.93	1.17	0.543	-3.99	0.018	-1.51
1456296_at	5830418K08Rik	RIKEN cDNA 5830418K08 gene	1.09	0.626	-1.26	0.46	-1.39	0.271	-1.07	0.476	-0.66
1452939_a_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.05	0.848	1.03	0.919	-1.62	0.048	-1.5	0.091	-0.78
1460541_at	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-1.12	0.711	-1.48	0.507	1.03	0.75	-1.78	0.002	-0.84
1433968_a_at	---	---	-1.17	0.558	-1.02	0.927	-1.31	0.17	1.74	0.421	-0.44
1434184_s_at	9430080K19Rik	RIKEN cDNA 9430080K19 gene	1.02	0.906	-1.21	0.544	-1.32	0.232	-2.49	0.039	-1
1441561_at	Fbxl3	F-box and leucine-rich repeat protein 3	1.42	0.354	-2.02	0.151	-1.45	0.001	-1.03	0.852	-0.77
1450560_a_at	Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform	-1.07	0.532	-1.28	0.119	-1.14	0.324	1	0.979	-0.62
1416119_at	Txn1	thioredoxin 1	-1.15	0.022	-1.13	0.104	-1.18	0.015	1.02	0.903	-0.61
1420021_s_at	Suz12	suppressor of zeste 12 homolog (Drosophila)	-1.06	0.55	-1.08	0.148	-1.37	0.062	1.49	0.146	-0.5
1432506_at	Tmem86b	transmembrane protein 86B	-1.64	0.365	1.15	0.733	-1.19	0.526	-2.55	0.061	-1.06
1419961_s_at	C330003B14Rik	RIKEN cDNA C330003B14 gene	-2.22	0.016	1.25	0.385	-1.11	0.447	-1.29	0.265	-0.84
1429341_at	Oaz3	ornithine decarboxylase antizyme 3	-1.42	0.596	-1.34	0.537	1.15	0.812	-1.23	0.557	-0.71
1427191_at	Npr2	natriuretic peptide receptor 2	1.01	0.943	-1.6	0.028	-1.03	0.908	-1.38	0.213	-0.75
1437415_at	4933427D06Rik	RIKEN cDNA 4933427D06 gene	-1.25	0.388	-1.16	0.496	-1.07	0.71	1.43	0.123	-0.51
1445871_at	AI315376	expressed sequence AI315376	-2.1	0.242	-1.32	0.659	1.37	0.462	-1.89	0.111	-0.99

1439481_at	Ipo9	importin 9	-1.12	0.444	-1.02	0.837	-1.36	0.063	1.1	0.393	-0.6
1460611_at	C87499	expressed sequence C87499	-1.3	0.355	1.09	0.477	-1.35	0.615	-1.28	0.506	-0.71
1453817_at	Abca6	ATP-binding cassette, sub-family A (ABC1), member 6	-1.45	0.71	-1.01	0.966	-1.08	0.72	1.24	0.617	-0.58
1456606_a_at	Chst11 /// Phactr1	carbohydrate sulfotransferase 11 /// phosphatase and actin regulator 1	-1.18	0.493	-1.38	0.056	1.03	0.885	-1.42	0.074	-0.74
1456863_at	Epha4	Eph receptor A4	1.06	0.903	-1.65	0.494	-1.07	0.611	-1.25	0.657	-0.73
1432365_a_at	4930556L07Rik	RIKEN cDNA 4930556L07 gene	-1.38	0.507	1.04	0.911	-1.19	0.481	-1.17	0.54	-0.68
1436948_a_at	6430550H21Rik	RIKEN cDNA 6430550H21 gene	-1.17	0.657	-1.72	0.513	1.16	0.688	-1.35	0.322	-0.77
1421122_at	Cbll1	Casitas B-lineage lymphoma-like 1	-1.21	0.098	-1.23	0.044	-1.04	0.853	1.02	0.842	-0.61
1436220_at	Zfp287	zinc finger protein 287	1.16	0.044	-1.19	0.688	-1.64	0.115	-1.28	0.538	-0.74
1434088_at	Zfp496	zinc finger protein 496	-1.15	0.105	-1.21	0.293	-1.11	0.443	1.04	0.902	-0.61
1417830_at	Smc1a	structural maintenance of chromosomes 1A	-1.12	0.321	-1.12	0.078	-1.22	0.115	1.24	0.186	-0.56
1457882_at	5730466H23Rik	RIKEN cDNA 5730466H23 gene	-1.28	0.607	-1.14	0.48	-1.06	0.762	1.21	0.21	-0.57
1426448_at	Pja1	praja1, RING-H2 motif containing	-1.13	0.368	1.01	0.953	-1.4	0.081	-1.51	0.285	-0.76
1441184_at	Trpc4ap	Transient receptor potential cation channel, subfamily C, member 4 associated pr	-1.1	0.725	-1.44	0.543	-1	0.994	1.83	0.367	-0.43
1429487_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	-1.02	0.845	-1.04	0.759	-1.52	0.009	1.19	0.136	-0.6
1416834_x_at	Ndufb2	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2	-1.18	0.149	-1.11	0.24	-1.17	0.318	1.02	0.941	-0.61
1432802_at	9230106L01Rik	RIKEN cDNA 9230106L01 gene	-1.81	0.396	1.46	0.483	-1.71	0.207	-1.12	0.798	-0.79
1450943_at	2010012C16Rik	RIKEN cDNA 2010012C16 gene	-1.2	0.503	-1.17	0.403	-1.09	0.447	1.29	0.308	-0.54
1460077_at	Ttc3	tetratricopeptide repeat domain 3	-1.24	0.482	1.29	0.65	-1.97	0.022	-1.92	0.167	-0.96
1436560_at	AW124694	expressed sequence AW124694	-1.05	0.687	-1.09	0.814	-1.37	0.059	2.33	0.111	-0.29
1435459_at	Fmo2	flavin containing monooxygenase 2	-1.22	0.231	-1.22	0.357	-1.03	0.754	2.47	0.012	-0.25
1435921_at	D8Ertd587e	DNA segment, Chr 8, ERATO Doi 587, expressed	1.06	0.745	-1.31	0.028	-1.29	0.365	-1.58	0.078	-0.78
1426009_a_at	Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-2.39	0.584	-2.28	0.323	1.75	0.551	-4.7	0.395	-1.9
1444014_at	LOC670853	hypothetical protein LOC670853	1.36	0.31	-1.21	0.625	-2.38	0.014	-1.2	0.29	-0.86
1455129_at	Mtdh	Metadherin	-1.11	0.199	-1.23	0.025	-1.12	0.452	1	0.993	-0.62
1453688_at	Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	-1.12	0.073	1.06	0.778	-1.53	0.092	-1.45	0.134	-0.76
1427999_at	Snapc5	small nuclear RNA activating complex, polypeptide 5	1.27	0.053	-1.45	0.292	-1.55	0.345	-1.46	0.057	-0.8
1418880_at	Gfra3	glial cell line derived neurotrophic factor family receptor alpha 3	-1.49	0.006	-1.28	0.676	1.15	0.634	-1.08	0.858	-0.67
1451439_at	BC027231	cDNA sequence BC027231	-1.19	0.558	-1.45	0.187	1.07	0.266	-1.16	0.265	-0.68
1456537_at	A930033H14Rik	RIKEN cDNA A930033H14 gene	-1.07	0.604	-1.37	0.541	-1.06	0.859	1.4	0.192	-0.53
1449684_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	1.58	0.555	-2.08	0.348	-1.85	0.303	-1.03	0.943	-0.85
1425639_at	Centa2	centaurin, alpha 2	-1.02	0.691	-1.04	0.466	-1.5	0.169	1.23	0.606	-0.58
1435521_at	Msi2	Musashi homolog 2 (Drosophila)	1.2	0.517	-1.03	0.94	-2.34	0.047	-1.27	0.56	-0.86
1441814_s_at	Rpain	RPA interacting protein	-1.33	0.333	-1.03	0.792	-1.14	0.372	1.35	0.2	-0.54
1459984_at	Mia3	melanoma inhibitory activity 3	1.08	0.832	-1.5	0.194	-1.17	0.679	-1.16	0.219	-0.69
1418024_at	Narg1	NMDA receptor-regulated gene 1	1.01	0.944	-1.23	0.16	-1.29	0.065	-1.06	0.779	-0.64
1460435_at	1500002O20Rik	RIKEN cDNA 1500002O20 gene	-1.63	0.167	-1.14	0.356	1.11	0.225	-1.09	0.527	-0.69
1441666_at	---	Visual cortex cDNA, RIKEN full-length enriched library, clone:K530010N24 produ	-1.25	0.589	-1.06	0.922	-1.16	0.727	1.51	0.528	-0.49
1442169_at	Vldlr	very low density lipoprotein receptor	-1.26	0.332	1.19	0.83	-1.6	0.103	-1.14	0.812	-0.7
1420002_at	D7Ertd1e	DNA segment, Chr 7, ERATO Doi 1, expressed	1.21	0.511	-2.51	0.166	-1.01	0.972	-1.09	0.906	-0.85
1420128_s_at	Pigb	phosphatidylinositol glycan anchor biosynthesis, class B	1.36	0.723	-1.89	0.232	-1.4	0.525	-1.69	0.027	-0.91
1418543_s_at	Ccdc43	coiled-coil domain containing 43	-1.04	0.121	1.03	0.829	-1.65	0.067	-1.31	0.039	-0.74
1446774_at	Syvn1	synovial apoptosis inhibitor 1, synoviolin	-1.85	0.162	-1.33	0.444	1.31	0.292	-1.09	0.802	-0.74
1436028_at	Tmem33	transmembrane protein 33	-1.12	0.412	-1.14	0.142	-1.19	0.157	1.38	0.137	-0.52
1443171_at	---	---	-1.4	0.517	-1.1	0.704	-1.02	0.935	1.65	0.367	-0.47
1425382_a_at	Aqp4	aquaporin 4	-1.03	0.933	-1.32	0.62	-1.15	0.672	1.33	0.321	-0.54
1429301_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	-1.16	0.385	-1.12	0.303	-1.18	0.028	1.08	0.526	-0.59
1445340_at	Phr1	pam, highwire, rpm 1	1.01	0.985	-1.08	0.67	-1.5	0.06	-1.98	0.043	-0.89
1441323_at	---	Transcribed locus	-1.11	0.327	-1.26	0.43	-1.1	0.155	1.23	0.51	-0.56
1450568_at	Galr1	galanin receptor 1	-1.29	0.661	-1.03	0.85	-1.16	0.83	1.17	0.855	-0.58
1438477_a_at	Mcee	methylmalonyl CoA epimerase	-1.31	0.011	-1.24	0.185	1.03	0.852	-1.12	0.191	-0.66
1435319_at	Ihpk2	inositol hexaphosphate kinase 2	-1.24	0.386	1.09	0.736	-1.41	0.246	-1.22	0.237	-0.7
1447917_x_at	Ntan1	N-terminal Asn amidase	1.05	0.396	-1.15	0.399	-1.45	0.018	-1.26	0.187	-0.7

1453595_at	2900064B18Rik	RIKEN cDNA 2900064B18 gene	1.14	0.765	-1.14	0.7	-1.68	0.118	-2.16	0.043	-0.96
1430012_at	1110050K14Rik	RIKEN cDNA 1110050K14 gene	-1.15	0.691	-1.04	0.876	-1.3	0.514	1.5	0.369	-0.5
1417693_a_at	Gab1	growth factor receptor bound protein 2-associated protein 1	-1.07	0.646	-1.1	0.408	-1.32	0.223	2	0.14	-0.37
1440390_at	BC025575	cDNA sequence BC025575	1.02	0.912	-1.24	0.526	-1.28	0.441	-1.17	0.688	-0.67
1445828_at	---	---	-1.54	0.562	-2.89	0.091	1.61	0.409	-2.06	0.27	-1.22
1458424_at	Fa2h	Fatty acid 2-hydroxylase	-2.97	0.091	1.34	0.59	-1.08	0.823	-1.37	0.249	-1.02
1431293_a_at	Cldnd1	claudin domain containing 1	1.01	0.96	-1.11	0.394	-1.43	0.139	-1.18	0.552	-0.68
1427499_at	Zfp81	zinc finger protein 81	-1.06	0.884	-1.19	0.742	-1.22	0.34	1.1	0.751	-0.59
1443077_at	1700081L11Rik	RIKEN cDNA 1700081L11 gene	1.13	0.7	-1.15	0.738	-1.66	0.025	-1.19	0.304	-0.72
1441335_at	4930474N05Rik	RIKEN cDNA 4930474N05 gene	-1.51	0.498	-1.12	0.596	1.05	0.654	-1.01	0.981	-0.65
1429083_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	-1.19	0.387	-1.16	0.527	-1.11	0.728	1.42	0.042	-0.51
1444017_at	Peli1	Pellino 1	-1.25	0.391	1.16	0.412	-1.57	0.076	-1.78	0.19	-0.86
1434265_s_at	Ank2	ankyrin 2, brain	1.2	0.383	-1.25	0.645	-1.64	0.304	-1.55	0.019	-0.81
1435808_at	A230051G13Rik	RIKEN cDNA A230051G13 gene	-1.24	0.151	-1.15	0.565	-1.08	0.503	2.04	0.283	-0.36
1437286_x_at	---	---	-1.3	0.31	-1.17	0.331	-1.02	0.922	2.44	0.242	-0.26
1426256_at	Timm17a	translocase of inner mitochondrial membrane 17a	-1.07	0.293	-1.19	0.203	-1.21	0.035	1.12	0.529	-0.59
1422891_at	H2-Ea	histocompatibility 2, class II antigen E alpha	-1.49	0.382	-1.1	0.812	1.02	0.938	-1.12	0.546	-0.67
1434257_s_at	Pitpnb	phosphatidylinositol transfer protein, beta	-1.12	0.414	-1.32	0.008	-1.04	0.756	1.05	0.723	-0.61
1442971_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B	-1.1	0.817	1.22	0.56	-2.12	0.019	-1.78	0.085	-0.94
1450371_at	Tshb	thyroid stimulating hormone, beta subunit	-1.24	0.618	-1.61	0.442	1.17	0.598	-1.2	0.666	-0.72
1434033_at	Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	-1.08	0.653	-1.49	0.011	1.01	0.89	-1.25	0.103	-0.7
1440536_at	Slc22a5	Solute carrier family 22 (organic cation transporter), member 5	1.03	0.277	-1.03	0.877	-1.64	0.313	-1.08	0.856	-0.68
1433989_at	Slc6a11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	1.03	0.974	-1.17	0.752	-1.38	0.524	-2.96	0.218	-1.12
1424786_s_at	Wdr45	WD repeat domain 45	-1	0.979	-1.18	0.171	-1.31	0.003	1.01	0.926	-0.62
1456624_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	-1.11	0.222	-1.07	0.843	-1.29	0.183	1.99	0.13	-0.37
1458083_at	4932438A13Rik	RIKEN cDNA 4932438A13 gene	1.12	0.681	-1.17	0.414	-1.58	0.109	-1.28	0.227	-0.73
1419399_at	Mttp	microsomal triglyceride transfer protein	-1.15	0.417	-1.2	0.071	-1.1	0.732	1.28	0.679	-0.55
1445394_at	4933409K07Rik	RIKEN cDNA 4933409K07 gene	-1.5	0.325	-1.09	0.824	1.02	0.95	-1.4	0.126	-0.74
1437442_at	---	---	-1.35	0.39	1.06	0.841	-1.24	0.063	-1.17	0.42	-0.67
1429537_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	1.09	0.645	-1.1	0.462	-1.64	0.084	-1.01	0.978	-0.66
1447663_at	Akap13	A kinase (PRKA) anchor protein 13	-1.28	0.012	1.3	0.339	-1.89	0.026	-1.09	0.874	-0.74
1436639_at	Bola2	bolA-like 2 (E. coli)	-1.49	0.261	-1.08	0.835	1.01	0.961	-1.06	0.536	-0.66
1429188_at	Cox11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	-1.16	0.217	-1.32	0.055	-1.01	0.951	1.75	0.284	-0.44
1430424_at	4933433C11Rik	RIKEN cDNA 4933433C11 gene	-1.14	0.284	1.04	0.954	-1.46	0.405	-1.96	0.019	-0.88
1444609_at	Exoc4	Exocyst complex component 4	-1.1	0.594	-1.05	0.856	-1.33	0.312	1.08	0.407	-0.6
1430599_at	Myt1l	myelin transcription factor 1-like	-1.35	0.76	-1.32	0.675	1.11	0.803	-1.14	0.42	-0.68
1430372_at	D730045B01Rik	RIKEN cDNA D730045B01 gene	-1.54	0.499	1.08	0.865	-1.13	0.659	-1.19	0.605	-0.7
1441131_at	---	---	-1.03	0.674	1	0.999	-1.57	0.056	-1.31	0.01	-0.73
1449010_at	Hspa4l	heat shock protein 4 like	-1.2	0.098	-1.18	0.504	-1.08	0.764	2.28	0.271	-0.29
1433269_at	4930553M12Rik	RIKEN cDNA 4930553M12 gene	-1.11	0.8	-1.29	0.038	-1.07	0.647	1.06	0.448	-0.6
1454256_s_at	1700113I22Rik	RIKEN cDNA 1700113I22 gene	-1.07	0.641	-1.86	0.066	1.14	0.622	-1.46	0.45	-0.81
1427066_a_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	-1.18	0.585	-1.24	0.036	-1.05	0.787	1.11	0.633	-0.59
1442657_at	D1Ertd273e	DNA segment, Chr 1, ERATO Doi 273, expressed	-1.48	0.611	-1.48	0.427	1.26	0.631	-1.03	0.951	-0.68
1420015_s_at	Ppt1	palmitoyl-protein thioesterase 1	-1.13	0.261	-1.52	0.025	1.07	0.77	-1.27	0.569	-0.71
1436382_at	Zbtb12	zinc finger and BTB domain containing 12	-1.25	0.058	-2.49	0.042	1.41	0.154	-1.92	0.169	-1.06
1442490_at	C130090I23Rik	RIKEN cDNA C130090I23 gene	1.32	0.492	-1.21	0.614	-2.17	0.369	-1.37	0.706	-0.86
1446037_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	-1.24	0.059	-1.26	0.684	1.01	0.96	-2.02	0.013	-0.88
1430273_at	2410087M07Rik	RIKEN cDNA 2410087M07 gene	-1.03	0.936	-1.48	0.233	-1.04	0.825	1.89	0.064	-0.42
1428057_a_at	Ahnak	AHNAK nucleoprotein (desmoyokin)	1.12	0.575	-1.24	0.242	-1.46	0.244	-1.04	0.906	-0.66
1440845_at	E030031F02Rik	RIKEN cDNA E030031F02 gene	1.1	0.823	-1.38	0.573	-1.27	0.241	-2.69	0.043	-1.06
1419867_a_at	Ankhd1	ankyrin repeat and KH domain containing 1	1.07	0.508	-1.1	0.302	-1.59	0	-1.36	0.359	-0.75
1427606_at	Usp27x	ubiquitin specific peptidase 27, X chromosome	-1.09	0.902	-1.87	0.284	1.16	0.717	-1.21	0.798	-0.75
1429740_at	Ttc7	tetratricopeptide repeat domain 7	-1.04	0.857	-1.33	0.417	-1.12	0.407	1.37	0.32	-0.53

1439532_s_at	Kif13a	kinesin family member 13A	-1.01	0.987	-1.45	0.578	-1.08	0.352	1.02	0.953	-0.63
1419273_at	C80913	expressed sequence C80913	1.02	0.447	-1.22	0.08	-1.3	0.009	-1.27	0.147	-0.69
1447210_at	---	Transcribed locus	-1.29	0.482	-2.29	0.119	1.4	0.272	-1.16	0.477	-0.84
1454982_at	Arfgef2 /// LOC670	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibite	-1.17	0.435	-1.51	0.033	1.1	0.722	-1.06	0.415	-0.66
1421905_at	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	-1.04	0.949	-1.09	0.82	-1.37	0.305	1.26	0.287	-0.56
1420787_at	4933436I01Rik	RIKEN cDNA 4933436I01 gene	-1.02	0.958	-1.64	0.364	1.02	0.952	-1.3	0.029	-0.74
1454119_at	Mknk1	MAP kinase-interacting serine/threonine kinase 1	-2.72	0.368	1.28	0.672	-1.04	0.939	-1.68	0.246	-1.04
1447538_at	Crtc1	CREB regulated transcription coactivator 1	-1.21	0.686	-1.2	0.485	-1.05	0.88	1.04	0.524	-0.61
1439623_at	Otud1	OTU domain containing 1	1.15	0.545	-1.76	0.101	-1.12	0.509	-1.72	0.163	-0.86
1434447_at	AI838057	expressed sequence AI838057	-1.08	0.534	1.12	0.269	-1.78	0.003	-1.42	0.271	-0.79
1445097_at	Pik3r3	Phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	-1.41	0.456	1.21	0.414	-1.44	0.483	-1.39	0.165	-0.76
1458947_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	-1.12	0.443	1.18	0.177	-1.86	0.028	-1.06	0.746	-0.72
1428624_at	2810482I07Rik	RIKEN cDNA 2810482I07 gene	-1.14	0.339	-1.14	0.019	-1.17	0.197	1.18	0.186	-0.57
1455254_at	4833420G11Rik	RIKEN cDNA 4833420G11 gene	-1.14	0.044	-1.13	0.328	-1.18	0.09	1.99	0.204	-0.37
1418585_at	Ccnh	cyclin H	-1.04	0.583	-1.15	0.259	-1.29	0.039	1.07	0.816	-0.6
1440996_at	Nedd8	Neural precursor cell expressed, developmentally down-regulated gene 8	-1.07	0.632	-1.66	0.041	1.07	0.618	-1.34	0.25	-0.75
1422116_at	Aff2	AF4/FMR2 family, member 2	-1.63	0.607	1.05	0.937	-1.05	0.873	-1.67	0.071	-0.83
1432204_at	4930570B17Rik	RIKEN cDNA 4930570B17 gene	1.29	0.492	-1.8	0.328	-1.32	0.383	-2.01	0.175	-0.96
1426796_at	Kpna6	karyopherin (importin) alpha 6	-1.31	0.216	-1.12	0.579	-1.05	0.844	1.07	0.784	-0.6
1428570_at	Ccnc	cyclin C	-1.28	0.224	-1.13	0.558	-1.05	0.774	1.16	0.325	-0.58
1454320_at	5830420C07Rik	RIKEN cDNA 5830420C07 gene	-1.35	0.582	-1.28	0.587	1.09	0.839	-1.01	0.975	-0.64
1424091_at	AI449175	expressed sequence AI449175	-1.11	0.199	-1.44	0.03	1.01	0.923	-1.13	0.036	-0.67
1441445_at	Per3	period homolog 3 (Drosophila)	1.08	0.866	-1.1	0.903	-1.62	0.345	-1.09	0.766	-0.68
1429558_a_at	Larp7	La ribonucleoprotein domain family, member 7	-1.19	0.292	-1.15	0.166	-1.11	0.079	1.01	0.956	-0.61
1455182_at	Kif1b	kinesin family member 1B	1.04	0.866	-1.13	0.608	-1.45	0.266	-1.5	0.18	-0.76
1423206_s_at	2310003F16Rik	RIKEN cDNA 2310003F16 gene	-1.2	0.068	-1.09	0.232	-1.16	0.306	1.02	0.888	-0.61
1426977_at	Usp47	ubiquitin specific peptidase 47	-1.15	0.074	-1.13	0.073	-1.16	0.06	1.02	0.844	-0.61
1458119_at	Slc25a27	solute carrier family 25, member 27	1.07	0.891	-1.18	0.806	-1.45	0.289	-1.18	0.754	-0.68
1443673_x_at	---	---	-1.02	0.149	-1.05	0.779	-1.47	0.093	5.08	0.197	0.38
1442977_at	Col3a1	Procollagen, type III, alpha 1	-1.24	0.213	1.23	0.568	-1.74	0.085	-1.35	0.083	-0.77
1451124_at	Sod1	superoxide dismutase 1, soluble	-1.09	0.495	-1.11	0.564	-1.26	0.096	1.02	0.819	-0.61
1442337_at	Adcyap1r1	Adenylate cyclase activating polypeptide 1 receptor 1	-1.94	0.42	-2.32	0.421	1.66	0.251	-1.34	0.669	-0.98
1416031_s_at	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	-1.21	0.354	-1.21	0.011	-1.05	0.714	2.19	0.204	-0.32
1416965_at	Pcsk1n	proprotein convertase subtilisin/kexin type 1 inhibitor	1.48	0.616	-2.13	0.046	-1.5	0.322	-1.02	0.977	-0.79
1435613_x_at	Cox5b	cytochrome c oxidase, subunit Vb	-1.11	0.078	-1.34	0.106	-1.04	0.588	1.27	0.132	-0.55
1457628_at	Ccdc53	coiled-coil domain containing 53	-1.11	0.62	1.07	0.745	-1.55	0.086	-1.61	0.07	-0.8
1442298_at	Bicc1	Bicaudal C homolog 1 (Drosophila)	-1.38	0.101	1.28	0.139	-1.64	0.063	-1.04	0.647	-0.7
1445983_at	Nkrf	NF-kappaB repressing factor	-1.67	0.45	-1.24	0.752	1.21	0.604	-2.05	0.455	-0.94
1425687_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.23	0.509	-1.32	0.169	-1.61	0.063	-1.42	0.209	-0.78
1446994_at	Exosc2	Exosome component 2	-2.55	0.061	1.6	0.34	-1.61	0.538	-1.63	0.508	-1.05
1426181_a_at	Il24	interleukin 24	-4.25	0.109	1.83	0.215	-1.82	0.338	-1.28	0.346	-1.38
1454533_at	9430085L16Rik	RIKEN cDNA 9430085L16 gene	1.66	0.008	-2.28	0.106	-1.95	0.014	-2.85	0.406	-1.36
1438442_at	AI450236	expressed sequence AI450236	-1.36	0.252	1.22	0.377	-1.52	0.056	-1.86	0.273	-0.88
1443560_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930506M03 pr	-1.08	0.547	-1.26	0.274	-1.12	0.54	1.21	0.397	-0.56
1445856_at	6030443O07Rik	RIKEN cDNA 6030443O07 gene	-1.37	0.498	1.02	0.964	-1.16	0.506	-1.29	0.476	-0.7
1444531_at	Sod2	Superoxide dismutase 2, mitochondrial	-1.08	0.756	-1.05	0.762	-1.35	0.116	1.16	0.555	-0.58
1428157_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	1.08	0.658	-1.24	0.526	-1.39	0.125	-1.23	0.6	-0.69
1422590_at	Cdk5	cyclin-dependent kinase 5	-1.33	0.119	-1.38	0.168	1.14	0.563	-1.35	0.507	-0.73
1432314_at	4930554C24Rik	RIKEN cDNA 4930554C24 gene	-1.07	0.8	1.14	0.237	-1.86	0.205	-1.15	0.532	-0.73
1445724_at	Iqgap1	IQ motif containing GTPase activating protein 1	1.15	0.442	-1.13	0.78	-1.72	0.122	-2.26	0.083	-0.99
1418144_a_at	Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-1.09	0.484	-1.15	0.308	-1.21	0.385	1.17	0.323	-0.57
1415891_at	Suclg1	succinate-CoA ligase, GDP-forming, alpha subunit	-1.2	0.044	-1.33	0.08	1.03	0.77	-1.34	0.221	-0.71
1446655_at	Scyl3	SCY1-like 3 (S. cerevisiae)	-3.79	0.313	1.39	0.545	-1.04	0.938	-2.99	0.021	-1.61

1430468_at	2810449G22Rik	RIKEN cDNA 2810449G22 gene	-1.02	0.979	-1.02	0.984	-1.55	0.346	1.12	0.801	-0.62
1458637_x_at	Ube3c	Ubiquitin protein ligase E3C	1.03	0.908	-1.04	0.897	-1.62	0.082	-1.1	0.554	-0.68
1429908_at	6530403A03Rik	RIKEN cDNA 6530403A03 gene	-1.29	0.188	-1.42	0.089	1.13	0.229	-1.1	0.706	-0.67
1424647_at	Gabrp	gamma-aminobutyric acid (GABA-A) receptor, pi	-1.63	0.233	-1.05	0.896	1.04	0.909	-1.42	0.108	-0.76
1429926_at	6720473G16Rik	RIKEN cDNA 6720473G16 gene	1.03	0.919	-1.5	0.056	-1.09	0.342	-1.06	0.665	-0.66
1430163_at	1810048P08Rik	RIKEN cDNA 1810048P08 gene	-1.33	0.538	-1.04	0.887	-1.11	0.672	1.03	0.89	-0.61
1445045_at	Maml1	Mastermind like 1 (Drosophila)	-2.56	0.346	1.29	0.67	-1.07	0.898	-1.25	0.747	-0.9
1418681_at	Glt28d1	glycosyltransferase 28 domain containing 1	-1.18	0.027	-1.2	0.322	-1.07	0.402	1.18	0.429	-0.57
1437988_x_at	1700003E24Rik	RIKEN cDNA 1700003E24 gene	1.1	0.822	-1.85	0.209	-1.03	0.947	-1.54	0.461	-0.83
1438463_x_at	Zdhhc6	zinc finger, DHHC domain containing 6	-1.12	0.162	-1.1	0.158	-1.23	0.093	1.43	0.198	-0.51
1419237_at	Usp29	ubiquitin specific peptidase 29	1.4	0.592	-2.3	0.139	-1.28	0.639	-2	0.235	-1.04
1446670_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	-1.02	0.942	1.12	0.708	-1.95	0.108	-1.9	0.242	-0.94
1415986_at	Clcn4-2	chloride channel 4-2	-1.23	0.151	1.03	0.836	-1.3	0.188	-1.11	0.739	-0.65
1425235_s_at	Col20a1	collagen, type XX, alpha 1	-1.59	0.541	1.05	0.949	-1.07	0.92	-4.32	0.144	-1.48
1418616_at	Mafk	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	-1.27	0.247	-1.03	0.861	-1.17	0.448	1.86	0.215	-0.4
1437085_at	D630039A03Rik	RIKEN cDNA D630039A03 gene	-1.29	0.452	-1.57	0.063	1.2	0.27	-1.46	0.475	-0.78
1423024_at	Sh2d1b1	SH2 domain protein 1B1	-1.03	0.888	-1.37	0.597	-1.1	0.725	1.44	0.306	-0.51
1454424_at	2610040L17Rik	RIKEN cDNA 2610040L17 gene	-2.05	0.319	-1.07	0.855	1.19	0.766	-1.23	0.329	-0.79
1426110_a_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-1.36	0.047	-1.34	0.532	1.14	0.559	-1.58	0.205	-0.79
1427246_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-2.06	0.262	1.24	0.419	-1.12	0.715	-2.06	0.234	-1
1446544_at	Arntl	Aryl hydrocarbon receptor nuclear translocator-like	-1.41	0.146	-1.66	0.359	1.3	0.394	-4	0.048	-1.44
1429253_at	Zmym4	zinc finger, MYM-type 4	1.06	0.653	-1.12	0.581	-1.53	0.009	-1.17	0.313	-0.69
1450337_a_at	Nek8	NIMA (never in mitosis gene a)-related expressed kinase 8	-1.16	0.46	-1.19	0.419	-1.1	0.531	1.43	0.393	-0.5
1428989_at	0710001D07Rik	RIKEN cDNA 0710001D07 gene	-1.32	0.087	-1.21	0.34	1.03	0.799	-1.15	0.355	-0.66
1454727_at	AI173486	expressed sequence AI173486	-1.14	0.389	1.03	0.889	-1.41	0.09	-1.51	0.072	-0.76
1424868_at	Glyat	glycine-N-acyltransferase	-1.27	0.272	-1.48	0.042	1.15	0.577	-1.24	0.579	-0.71
1428229_at	Prkcn	protein kinase C, nu	1.1	0.167	-1.15	0.199	-1.55	0.002	-1.61	0.003	-0.8
1425388_a_at	Tpk1	thiamine pyrophosphokinase	-1.18	0.189	-1.18	0.002	-1.09	0.265	1.12	0.126	-0.58
1419906_at	Hpgd	Hydroxyprostaglandin dehydrogenase 15 (NAD)	1.37	0.302	-1.81	0.148	-1.44	0.237	-1.52	0.223	-0.85
1436438_s_at	---	---	-1.38	0.256	-1.24	0.236	1.08	0.739	-1.34	0.206	-0.72
1447338_at	---	Transcribed locus	-1.64	0.342	-1.01	0.964	1.01	0.97	-1.12	0.658	-0.69
1435797_at	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	-1.01	0.93	-1.37	0.089	-1.12	0.418	1.13	0.58	-0.59
1459712_at	Zfp182	zinc finger protein 182	-1.15	0.015	-1.04	0.867	-1.28	0.247	1.03	0.961	-0.61
1454862_at	Phldb2	pleckstrin homology-like domain, family B, member 2	-1.04	0.705	1.01	0.955	-1.54	0.011	-1.31	0.361	-0.72
1426135_a_at	Park2	parkin	-1.57	0.262	-1.45	0.33	1.29	0.593	-1.85	0.126	-0.9
1459968_at	Rbms1	RNA binding motif, single stranded interacting protein 1	1.2	0.636	-1.46	0.509	-1.37	0.161	-1.61	0.319	-0.81
1424103_at	Atg4b	autophagy-related 4B (yeast)	-1.25	0.16	-1.12	0.343	-1.08	0.76	1.14	0.686	-0.58
1445438_at	Ddhd1	DDHD domain containing 1	1.07	0.615	-1.07	0.843	-1.65	0.089	-1.15	0.472	-0.7
1433503_at	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	-1.17	0.099	-1.12	0.32	-1.16	0.219	1.16	0.24	-0.57
1435105_at	1110061N23Rik	RIKEN cDNA 1110061N23 gene	-1.43	0.377	-1.23	0.708	1.1	0.641	-1.18	0.507	-0.69
1437576_at	2810427A07Rik	RIKEN cDNA 2810427A07 gene	1.17	0.561	-1.14	0.354	-1.77	0.084	-1.23	0.242	-0.74
1436241_s_at	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	-2.05	0.012	-1.33	0.451	1.38	0.009	-1.02	0.946	-0.76
1456218_at	Snx22	sorting nexin 22	-1.15	0.421	-1.16	0.564	-1.14	0.141	1.99	0.243	-0.36
1451178_at	Mrpl53	mitochondrial ribosomal protein L53	-1.18	0.136	-1.13	0.141	-1.13	0.143	1.36	0.374	-0.52
1453169_a_at	Gtf2h1	general transcription factor II H, polypeptide 1	-1	0.996	-1.19	0.021	-1.29	0.011	1.02	0.919	-0.62
1440464_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.03	0.878	-1.24	0.482	-1.28	0.447	-1.68	0.14	-0.79
1451412_a_at	Ift20	intraflagellar transport 20 homolog (Chlamydomonas)	-1.18	0.052	-1.1	0.114	-1.17	0.277	1.03	0.796	-0.6
1437735_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	-1.21	0.314	1.05	0.65	-1.35	0.013	-1.42	0.133	-0.73
1429430_at	---	---	-1.35	0.083	-1.18	0.358	1.02	0.908	-1.63	0.166	-0.78
1427101_at	Metrn	meteorin, glial cell differentiation regulator	1.32	0.37	-2.16	0.413	-1.2	0.667	-1.17	0.702	-0.8
1431947_at	Ldlr	low density lipoprotein receptor	1.06	0.946	-1.12	0.684	-1.52	0.202	-1.85	0.058	-0.86
1443751_at	Cacnb4	Calcium channel, voltage-dependent, beta 4 subunit	-1.09	0.665	-1.12	0.413	-1.24	0.675	2.22	0.281	-0.31
1423969_at	Nup37	nucleoporin 37	-1.24	0.379	-1.11	0.44	-1.11	0.357	1.28	0.408	-0.54

1451393_at	Pex26	peroxisome biogenesis factor 26	-1.16	0.033	-1.34	0.065	1.01	0.934	-1.08	0.604	-0.64
1435420_at	C330016K18Rik	RIKEN cDNA C330016K18 gene	-1.26	0.63	-1.69	0.23	1.23	0.378	-1.2	0.552	-0.73
1419876_at	2810449G22Rik	RIKEN cDNA 2810449G22 gene	-1.47	0.441	1.06	0.668	-1.15	0.363	-1.54	0.556	-0.77
1427384_at	Chd6	chromodomain helicase DNA binding protein 6	1.02	0.886	-1.38	0.192	-1.14	0.361	-1.73	0.074	-0.81
1458809_at	---	---	1.18	0.771	-1.19	0.798	-1.67	0.039	-1.05	0.825	-0.68
1436073_at	A630007B06Rik ///	RIKEN cDNA A630007B06 gene /// similar to oocyte-testis gene 1	1.08	0.64	-1.25	0.148	-1.36	0.248	-1.12	0.409	-0.66
1440302_at	Slc25a3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	-1.12	0.628	-1.41	0.065	1.02	0.941	-1.67	0.254	-0.8
1455119_at	Ppapdc1a	phosphatidic acid phosphatase type 2 domain containing 1A	-1.3	0.697	-2.55	0.167	1.45	0.216	-2.65	0.324	-1.26
1441607_at	AU015603	expressed sequence AU015603	-1.27	0.581	-1.23	0.059	1.02	0.905	-1.26	0.322	-0.69
1456200_at	Ipmk	inositol polyphosphate multikinase	-1.04	0.767	-1.08	0.505	-1.36	0.062	1.39	0.298	-0.52
1451536_at	Mtfr1	mitochondrial fission regulator 1	-1.11	0.536	-1.16	0.003	-1.17	0.148	3.1	0.177	-0.09
1415723_at	Eif5	eukaryotic translation initiation factor 5	-1.07	0.777	-1.19	0.209	-1.2	0.254	1.34	0.219	-0.53
1448150_at	Nup62	nucleoporin 62	1.05	0.943	-1.17	0.821	-1.41	0.471	-1.22	0.06	-0.69
1416090_at	Pdhb	pyruvate dehydrogenase (lipoamide) beta	-1.31	0.043	-1.23	0.044	1.04	0.739	-1.06	0.696	-0.64
1453640_at	2210019G11Rik	RIKEN cDNA 2210019G11 gene	1.05	0.907	-1.16	0.805	-1.42	0.409	-1.91	0.168	-0.86
1432183_at	Tmem116	transmembrane protein 116	-1.49	0.218	-1.02	0.911	-1.04	0.792	1.29	0.446	-0.56
1427765_a_at	Tcrb-V13 /// LOC38	T-cell receptor beta, variable 13 /// similar to T-cell receptor beta chain V region C	1.05	0.907	-1.42	0.532	-1.15	0.783	-2.83	0.321	-1.09
1426932_at	Smarca2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.04	0.565	-1.09	0.435	-1.36	0.091	1.11	0.534	-0.59
1451272_a_at	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	-1.13	0.167	-1.11	0.414	-1.2	0.123	1.21	0.27	-0.56
1451865_at	Cxadr	coxsackievirus and adenovirus receptor	-1.08	0.913	-1.42	0.047	-1.02	0.961	1.58	0.264	-0.48
1429921_at	9530068E07Rik	RIKEN cDNA 9530068E07 gene	1.08	0.82	-1.29	0.663	-1.32	0.129	-1.6	0.271	-0.78
1438915_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	1.09	0.664	-1.08	0.723	-1.65	0.032	-1.49	0.343	-0.78
1418294_at	Epb4.1l4b	erythrocyte protein band 4.1-like 4b	1.05	0.188	-1.56	0.023	-1.08	0.528	-1.13	0.815	-0.68
1428738_a_at	D14Ertd449e	DNA segment, Chr 14, ERATO Doi 449, expressed	-1.33	0.062	-1.16	0.07	1.01	0.979	-1.11	0.531	-0.65
1428179_at	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	-1.14	0.081	-1.19	0.005	-1.11	0.15	1.05	0.513	-0.6
1458655_at	Wwtr1	WW domain containing transcription regulator 1	-1.19	0.724	1.26	0.628	-1.93	0.026	-1.05	0.717	-0.73
1427945_at	Dpyd	dihydropyrimidine dehydrogenase	-1.21	0.516	1.04	0.592	-1.34	0.185	-1.91	0.002	-0.85
1456934_at	---	---	-1.47	0.059	1.41	0.615	-1.89	0.069	-1.11	0.876	-0.76
1423819_s_at	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1	-1.07	0.51	-1.26	0.184	-1.12	0.548	1.32	0.301	-0.53
1458638_at	Mtdh	Metadherin	-1.83	0.481	1.65	0.235	-2.35	0.163	-1.14	0.808	-0.92
1430303_at	4921537D05Rik	RIKEN cDNA 4921537D05 gene	-1.21	0.324	-1.21	0.206	-1.03	0.913	1.4	0.332	-0.51
1459335_at	---	---	-1.16	0.501	1.17	0.737	-1.71	0.108	-1.2	0.169	-0.73
1437082_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	1.1	0.348	-1.22	0.323	-1.43	0.12	-1.27	0.564	-0.71
1438354_x_at	Cnn3	Calponin 3, acidic	1.05	0.819	-1.06	0.796	-1.61	0.063	-2.29	0.105	-0.98
1441477_at	Calu	calumenin	1.06	0.825	-1.06	0.88	-1.62	0.046	-1.27	0.452	-0.72
1420225_at	---	---	-1.03	#DIV/0!	1	0.995	-1.53	0.347	-3.79	0.189	-1.34
1434528_at	Aard	alanine and arginine rich domain containing protein	1.25	0.555	-1.13	0.466	-2.04	0	-2.2	0.267	-1.03
1424042_at	Tmem5	transmembrane protein 5	-1.04	0.569	-1.24	0.008	-1.18	0.231	1.05	0.714	-0.6
1458801_at	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	-1.01	0.976	-1	0.995	-1.58	0.094	1.63	0.481	-0.49
1435112_a_at	Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	-1.03	0.328	-1.21	0.135	-1.21	0.015	1.14	0.045	-0.58
1451041_at	Rock2	Rho-associated coiled-coil containing protein kinase 2	-1.17	0.157	1.03	0.847	-1.37	0.004	-1.03	0.858	-0.63
1444860_at	Lama3	Laminin, alpha 3	1.16	0.697	-1.05	0.931	-1.96	0.338	-1.71	0.458	-0.89
1449349_at	Nudt1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	-1.08	0.509	-1.24	0.02	-1.12	0.348	1.46	0.108	-0.5
1420495_a_at	Vps26a	vacuolar protein sorting 26 homolog A (yeast)	-1.15	0.299	-1.15	0.262	-1.14	0.255	1.07	0.27	-0.59
1426183_a_at	Cd209d	CD209d antigen	-1.64	0.369	-1.61	0.222	1.39	0.456	-2.19	0.042	-1.01
1455197_at	Rnd1	Rho family GTPase 1	-1.13	0.734	-1.48	0.123	1.06	0.817	-1.71	0.139	-0.82
1459975_at	---	Transcribed locus	-1.43	0.042	-1.03	0.813	-1.05	0.807	1.01	0.935	-0.63
1442733_at	---	---	-1.26	0.319	-1.21	0.337	-1.01	0.957	1.08	0.763	-0.6
1433743_at	Dach1	dachshund 1 (Drosophila)	-1.49	0.315	-1.05	0.891	-1.01	0.957	1.75	0.41	-0.45
1434660_at	Alkbh1	alkB, alkylation repair homolog 1 (E. coli)	-1.19	0.275	-1.28	0.164	1	0.994	-1.19	0.063	-0.67
1428906_at	Gtf2h5	general transcription factor IIH, polypeptide 5	-1.16	0.22	-1.08	0.062	-1.21	0.168	1.13	0.406	-0.58
1458824_at	Unc45a	unc-45 homolog A (C. elegans)	-1.19	0.325	1.04	0.963	-1.35	0.625	-1.91	0.114	-0.85
1440200_at	9630031F12Rik	RIKEN cDNA 9630031F12 gene	1.06	0.811	-1.69	0.382	-1.03	0.848	-1.35	0.195	-0.75

1446683_at	Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	-1.08	0.63	-1.11	0.774	-1.25	0.314	1.01	0.929	-0.61
1438992_x_at	Atf4	activating transcription factor 4	-1.23	0.477	-1.02	0.861	-1.21	0.139	1.06	0.714	-0.6
1452197_at	Smc4	structural maintenance of chromosomes 4	-1.1	0.64	-1.06	0.276	-1.3	0.052	1.29	0.388	-0.54
1452895_at	Fbxo45	F-box protein 45	-1.05	0.657	-1.27	0.146	-1.13	0.45	1.37	0.276	-0.52
1428791_at	Ube2h	ubiquitin-conjugating enzyme E2H	-1.2	0.058	-1.26	0.199	-1	0.987	1.27	0.147	-0.55
1423845_at	Csdc2	cold shock domain containing C2, RNA binding	1.37	0.422	-2.25	0.047	-1.24	0.618	-2.14	0.118	-1.06
1452005_at	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase	-1.21	0.286	-1.33	0.231	1.04	0.87	-1.01	0.947	-0.63
1434778_at	---	Transcribed locus	-1.1	0.484	-1.05	0.574	-1.33	0.014	1.33	0.342	-0.53
1441630_at	Ep400	E1A binding protein p400	-1.06	0.856	-1.28	0.471	-1.11	0.72	1.07	0.383	-0.6
1447342_at	---	---	-2.06	0.492	1.6	0.403	-1.89	0.335	-2.45	0.224	-1.2
1420985_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	1.04	0.823	-1.09	0.463	-1.5	0.032	-1.15	0.484	-0.68
1426640_s_at	Trib2	tribbles homolog 2 (Drosophila)	-1.47	0.045	1.16	0.481	-1.27	0.013	-2.01	0.06	-0.9
1446894_at	Arnt2	Aryl hydrocarbon receptor nuclear translocator 2	-1.17	0.816	-1.24	0.71	-1.04	0.923	1.22	0.756	-0.56
1458333_x_at	Utf1	undifferentiated embryonic cell transcription factor 1	1.07	0.792	-1.24	0.743	-1.35	0.627	-2.35	0.256	-0.97
1422094_a_at	Zfp329	zinc finger protein 329	-1.06	0.75	1.1	0.432	-1.73	0.012	-1.83	0.015	-0.88
1446144_at	Pex2	peroxin 2	-1.64	0.065	1.07	0.821	-1.06	0.829	-1.25	0.581	-0.72
1453208_at	2700089E24Rik	RIKEN cDNA 2700089E24 gene	1.04	0.626	-1.47	0.043	-1.11	0.422	-1.04	0.862	-0.65
1441392_at	---	Transcribed locus	-1.85	0.306	1.36	0.262	-1.4	0.241	-1.2	0.69	-0.77
1460670_at	Riok3	RIO kinase 3 (yeast)	-1.14	0.058	-1.1	0.25	-1.19	0.21	1.06	0.53	-0.59
1419458_at	Rgnef	Rho-guanine nucleotide exchange factor	-1.17	0.511	-1.01	0.911	-1.28	0.103	1.92	0.218	-0.39
1458208_s_at	---	---	1.03	0.805	-1.15	0.385	-1.39	0.404	-1.7	0.235	-0.8
1450422_a_at	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	-1.01	0.914	-1.15	0.307	-1.31	0.247	1.16	0.393	-0.58
1437668_at	Ccrl1	Chemokine (C-C motif) receptor-like 1	1.24	0.463	-1.41	0.218	-1.49	0.039	-1.57	0.227	-0.81
1429251_at	Prdm2	PR domain containing 2, with ZNF domain	-1.2	0.562	-1.5	0.021	1.12	0.386	-1.24	0.248	-0.7
1435768_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	-1.12	0.358	1.01	0.965	-1.38	0.112	-1.32	0.359	-0.7
1424079_x_at	2900073H19Rik	RIKEN cDNA 2900073H19 gene	1.05	0.612	-1.27	0.313	-1.27	0.076	-1.36	0.088	-0.71
1444676_at	---	---	-2.13	0.16	1.27	0.422	-1.14	0.67	-1.26	0.579	-0.81
1428872_at	4121402D02Rik	RIKEN cDNA 4121402D02 gene	-1.84	0.306	-1.5	0.239	1.42	0.483	-1.96	0.104	-0.97
1458200_at	Btbd14b	BTB (POZ) domain containing 14B	-1.19	0.543	-1.19	0.713	-1.06	0.654	1.25	0.376	-0.55
1417857_at	Mmaa	methylmalonic aciduria (cobalamin deficiency) type A	-1.33	0.306	-1.18	0.021	1.02	0.915	-1.26	0.251	-0.69
1433545_s_at	Acad11	acyl-Coenzyme A dehydrogenase family, member 11	-1.05	0.695	-1.49	0.061	1	1	-1.32	0.281	-0.72
1444685_at	---	---	-1.23	0.375	-1.42	0.083	1.1	0.686	-1.15	0.583	-0.67
1428454_at	Bcas3	breast carcinoma amplified sequence 3	-1.38	0.41	-1.04	0.843	-1.08	0.831	1.07	0.824	-0.6
1438836_at	Eftud2	Elongation factor Tu GTP binding domain containing 2	-1.81	0.27	-1.58	0.505	1.44	0.418	-2.25	0.136	-1.05
1443885_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-3.44	0.042	-1.19	0.803	1.49	0.417	-1.57	0.428	-1.18
1449094_at	Gja7	gap junction membrane channel protein alpha 7	1.1	0.561	-1.27	0.484	-1.37	0.025	-1.79	0.242	-0.83
1440956_at	Ccdc94	coiled-coil domain containing 94	-1.15	0.391	-1.31	0.122	-1.01	0.945	1.03	0.872	-0.61
1416850_s_at	Zcd1	zinc finger, CDGSH-type domain 1	-1.13	0.004	-1.25	0.217	-1.06	0.607	1.19	0.41	-0.56
1429488_at	Zdhhc21	zinc finger, DHHC domain containing 21	-1.09	0.68	1.01	0.875	-1.45	0.141	-1.23	0.487	-0.69
1458830_at	Fgf14	Fibroblast growth factor 14	-1.17	0.444	1.08	0.901	-1.45	0.555	-1.92	0.238	-0.86
1437120_at	Snx30	sorting nexin family member 30	1.02	0.648	-1.21	0.371	-1.29	0.262	-1.51	0.247	-0.75
1438769_a_at	Thyn1	thymocyte nuclear protein 1	-1.29	0.302	-1.09	0.46	-1.07	0.676	1.01	0.936	-0.61
1431746_a_at	Ube1c	ubiquitin-activating enzyme E1C	-1.18	0.34	-1.29	0.229	-1	1	1.12	0.709	-0.59
1427491_at	Nsun6	NOL1/NOP2/Sun domain family 6	1.02	0.937	-1.17	0.361	-1.33	0.33	-1.29	0.233	-0.69
1457301_at	AI931714	expressed sequence AI931714	1.26	0.644	-1.37	0.531	-1.56	0.117	-1.59	0.374	-0.82
1429800_at	9130221H12Rik	RIKEN cDNA 9130221H12 gene	-1.24	0.199	-1.23	0.262	1	0.981	-1.06	0.376	-0.63
1459973_x_at	Dpp4	dipeptidylpeptidase 4	1.14	0.455	-1.1	0.703	-1.74	0.013	-3.18	0.026	-1.22
1432678_at	Itgav	integrin alpha V	-1.19	0.831	-1.07	0.903	-1.18	0.74	1.14	0.612	-0.57
1433853_at	Mib1	mindbomb homolog 1 (Drosophila)	-1.33	0.633	-1.39	0.344	1.15	0.543	-1.51	0.133	-0.77
1418820_s_at	Zcchc10	zinc finger, CCHC domain containing 10	-1.16	0.56	-1.15	0.362	-1.11	0.511	1	0.994	-0.61
1420152_at	---	---	-1.15	0.74	-1.31	0.644	-1.01	0.978	1.24	0.158	-0.56
1435947_at	2810455D13Rik	RIKEN cDNA 2810455D13 gene	-1.04	0.709	-1.01	0.98	-1.49	0.015	1.26	0.524	-0.57
1450744_at	Ell2	elongation factor RNA polymerase II 2	-1.27	0.402	-1.11	0.564	-1.06	0.603	1.82	0.033	-0.41

1452159_at	2310001A20Rik	RIKEN cDNA 2310001A20 gene	-1.16	0.068	-1.07	0.444	-1.22	0.098	1.13	0.518	-0.58
1444691_at	Prkcn	protein kinase C, nu	-1.05	0.903	-1.54	0.047	1.02	0.961	-1.35	0.599	-0.73
1448236_at	Rdx	radixin	-1.06	0.639	-1.1	0.491	-1.3	0.211	1.15	0.239	-0.58
1435643_x_at	Ubb /// Gm1821	ubiquitin B /// gene model 1821, (NCBI)	1.01	0.878	-1.19	0.347	-1.29	0.025	-1.14	0.034	-0.65
1424253_at	1810073G14Rik	RIKEN cDNA 1810073G14 gene	-1.19	0.469	1.06	0.583	-1.38	0.121	-1.09	0.725	-0.65
1424074_at	Btf3l4	basic transcription factor 3-like 4	-1.17	0.11	-1.03	0.863	-1.25	0.173	1.23	0.367	-0.56
1426738_at	Dgkz	diacylglycerol kinase zeta	-1.25	0.383	-1.33	0.291	1.08	0.797	-2.09	0.06	-0.9
1421953_at	Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.2	0.661	-1.92	0.445	1.27	0.724	-1.51	0.402	-0.84
1441220_at	---	---	-1.29	0.177	1.05	0.938	-1.25	0.296	-1.27	0.613	-0.69
1458555_at	---	---	1.06	0.917	-1.52	0.532	-1.1	0.814	-2.22	0.398	-0.95
1429454_at	Gapvd1	GTPase activating protein and VPS9 domains 1	-1.1	0.31	-1.23	0.005	-1.11	0.257	1.36	0.227	-0.52
1449917_at	Pitx3	paired-like homeodomain transcription factor 3	-1.69	0.39	-1.39	0.5	1.31	0.574	-1.68	0.42	-0.86
1455616_at	AI586002	expressed sequence AI586002	-1.11	0.496	1.1	0.497	-1.62	0.094	-1.16	0.492	-0.7
1457634_at	4930488E11Rik ///	RIKEN cDNA 4930488E11 gene /// similar to thymosin beta-like protein /// similar	-1.3	0.584	1.08	0.864	-1.29	0.574	-1.25	0.613	-0.69
1419960_at	C330003B14Rik	RIKEN cDNA C330003B14 gene	-1.51	0.648	1.28	0.558	-1.48	0.421	-1.03	0.96	-0.68
1427539_a_at	Zwint	ZW10 interactor	-1.05	0.808	-1.05	0.664	-1.4	0.048	1.44	0.349	-0.51
1460359_at	Armcx3	armadillo repeat containing, X-linked 3	-1.05	0.69	1.01	0.953	-1.53	0.054	-1.31	0.197	-0.72
1433265_at	2810416A17Rik	RIKEN cDNA 2810416A17 gene	1.41	0.541	-1.3	0.723	-2.25	0.288	-1.95	0.254	-1.02
1449403_at	Pde9a	phosphodiesterase 9A	-1.1	0.109	-1.26	0.053	-1.08	0.66	1.1	0.652	-0.58
1429885_at	4930431P19Rik	RIKEN cDNA 4930431P19 gene	-2.04	0.325	1.25	0.162	-1.12	0.762	-1.26	0.045	-0.79
1447676_x_at	S100a16	S100 calcium binding protein A16	-1.05	0.136	1.06	0.57	-1.65	0.01	-1.21	0.503	-0.71
1419975_at	---	---	-1.14	0.542	1.08	0.7	-1.51	0.195	-1.29	0.349	-0.71
1424549_at	Degs2	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	-1.12	0.474	-2.11	0.328	1.26	0.045	-2.08	0.227	-1.01
1429491_s_at	Rif1 /// LOC671598	Rap1 interacting factor 1 homolog (yeast) /// similar to Telomere-associated prote	-1.08	0.246	-1.07	0.7	-1.31	0.079	1.39	0.153	-0.52
1450938_at	---	---	-1.21	0.169	1.02	0.914	-1.28	0.086	-1.11	0.633	-0.64
1450714_at	Azin1	antizyme inhibitor 1	-1.13	0.595	-1.13	0.508	-1.17	0.002	2.57	0.127	-0.22
1435262_at	---	Transcribed locus	-1.27	0.458	-1.12	0.22	-1.05	0.696	1.12	0.465	-0.58
1420158_s_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	-1.39	0.238	-1.28	0.602	1.12	0.628	-1.64	0.098	-0.8
1432042_a_at	Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	-1.11	0.43	-1.41	0.09	1.01	0.952	-1.25	0.335	-0.69
1418792_at	Sh3gl2	SH3-domain GRB2-like 2	1.07	0.641	-1.37	0.713	-1.21	0.467	-1.08	0.909	-0.65
1448288_at	Nfib	nuclear factor I/B	1.15	0.43	-1.13	0.481	-1.69	0.022	-1.1	0.828	-0.69
1441266_at	Strn3	Striatin, calmodulin binding protein 3	1.08	0.131	-1.09	0.372	-1.59	0.001	-1.06	0.535	-0.67
1455652_at	AW124694	expressed sequence AW124694	-1.1	0.571	-1.26	0.707	-1.08	0.332	1.08	0.702	-0.59
1459678_at	LOC497255	hypothetical LOC497255	1.07	0.626	-1.29	0.162	-1.29	0.012	-1.23	0.377	-0.68
1425998_at	Sytl4	synaptotagmin-like 4	1.73	0.33	-2.33	0.323	-2.13	0.239	-1.57	0.588	-1.08
1426969_at	Trim23	tripartite motif protein 23	-1.14	0.592	-1.1	0.199	-1.19	0.33	1.27	0.292	-0.54
1460299_at	Hlxb9	homeobox gene HB9	-2.04	0.046	-1.07	0.893	1.2	0.739	-1.99	0.196	-0.97
1448322_a_at	Cox4i1	cytochrome c oxidase subunit IV isoform 1	-1.16	0.098	-1.33	0.047	1.01	0.797	-1.07	0.394	-0.64
1435471_at	Zfp708	zinc finger protein 708	-1.41	0.124	1.04	0.832	-1.14	0.454	-2	0.066	-0.88
1424166_at	Msh3	mutS homolog 3 (E. coli)	-1.21	0.473	-1.11	0.66	-1.11	0.633	1.08	0.579	-0.59
1445234_at	C130030K03Rik	RIKEN cDNA C130030K03 gene	-1.34	0.096	-1.99	0.348	1.38	0.389	-2.06	0.263	-1
1455744_at	Gpr178	G protein-coupled receptor 178	-1.16	0.025	-1.11	0.708	-1.17	0.582	1.11	0.63	-0.58
1420950_at	Znrf1	zinc and ring finger 1	1.1	0.539	-1.44	0.116	-1.21	0.137	-1.36	0.344	-0.72
1420471_at	Hcrt	hypocretin	-1.34	0.319	-1.24	0.711	1.07	0.69	-1.26	0.673	-0.69
1444903_at	6-Mar	Membrane-associated ring finger (C3HC4) 6	1.16	0.629	-1.4	0.249	-1.32	0.329	-1.34	0.444	-0.73
1444793_at	---	---	-2.22	0.532	1.35	0.497	-1.21	0.637	-1.25	0.696	-0.83
1455300_at	E130014J05Rik	RIKEN cDNA E130014J05 gene	-1.09	0.737	1	0.934	-1.41	0.021	-1.3	0.473	-0.7
1447790_at	---	---	-1.57	0.449	1	0.999	-1.01	0.985	-1.62	0.17	-0.8
1455181_at	Rasa2	RAS p21 protein activator 2	1.02	0.887	-1.06	0.581	-1.51	0	-1.81	0.101	-0.84
1437184_at	Guf1	GUF1 GTPase homolog (S. cerevisiae)	-1.35	0.088	1.07	0.82	-1.23	0.474	-1.08	0.848	-0.65
1438908_at	Map3k12	mitogen activated protein kinase kinase kinase 12	-1.27	0.607	1.14	0.633	-1.43	0.32	-1.1	0.788	-0.66
1442539_at	Wwc2	WW, C2 and coiled-coil domain containing 2	1.14	0.255	-1.35	0.494	-1.34	0.373	-1.34	0.684	-0.72
1428348_at	Zfp336	zinc finger protein 336	-1.31	0.111	-1.02	0.636	-1.13	0.234	1.13	0.358	-0.58

1453212_at	Zfp383	zinc finger protein 383	-1.16	0.197	1.03	0.864	-1.36	0.095	-1.81	0.105	-0.82
1453131_at	Cd300lg	CD300 antigen like family member G	1.03	0.914	-1.25	0.142	-1.25	0.497	-1.67	0.33	-0.78
1425512_at	Map2k7	mitogen activated protein kinase kinase 7	-1.01	0.927	-1.19	0.118	-1.26	0.364	1.1	0.703	-0.59
1422447_at	Ins1	insulin I	-1.33	0.44	-1.28	0.23	1.09	0.785	-1.06	0.88	-0.64
1446396_at	Angptl1	Angiopoietin-like 1	-1.7	0.523	-1.23	0.566	1.23	0.672	-2	0.218	-0.93
1442898_at	LOC671579	hypothetical protein LOC671579	-1.02	0.953	-1.46	0.127	-1.04	0.913	1.12	0.865	-0.6
1444722_at	---	---	-1.03	0.701	-1.01	0.962	-1.48	0.041	1.15	0.211	-0.6
1421659_at	Adra1a	adrenergic receptor, alpha 1a	-1.25	0.028	-1.4	0.452	1.11	0.79	-1.76	0.434	-0.82
1438995_at	6330500D04Rik	RIKEN cDNA 6330500D04 gene	-1.27	0.82	-1.19	0.688	1.01	0.984	-2.3	0.074	-0.94
1443619_at	Tmem30a	transmembrane protein 30A	1.16	0.387	-1.15	0.472	-1.66	0.026	-1.36	0.221	-0.75
1440138_at	Ahdc1	AT hook, DNA binding motif, containing 1	-1.8	0.501	-1.91	0.103	1.55	0.384	-2	0.137	-1.04
1441075_at	Nostrin	nitric oxide synthase trafficker	-1.07	0.677	1.1	0.63	-1.69	0.005	-1.69	0.177	-0.84
1417535_at	Fbxo25	F-box only protein 25	1	0.977	-1.09	0.488	-1.41	0.011	-1.1	0.151	-0.65
1441410_at	D2Ertd112e	DNA segment, Chr 2, ERATO Doi 112, expressed	1.01	0.985	-1.4	0.162	-1.11	0.47	-1.51	0.067	-0.75
1452449_at	Hmbox1	homeobox containing 1	-1.45	0.333	-1.28	0.074	1.16	0.337	-1.09	0.426	-0.67
1448147_at	Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	-1.17	0.278	-1.02	0.97	-1.25	0.318	1.33	0.416	-0.53
1444291_at	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4	1.14	0.027	-1.57	0.33	-1.17	0.799	-1.14	0.79	-0.68
1423885_at	Lamc1	laminin, gamma 1	1.02	0.957	-1.08	0.76	-1.46	0.091	-1.07	0.636	-0.65
1437469_at	Zfp750	zinc finger protein 750	-1.06	0.888	-1.55	0.288	1.04	0.824	-2.78	0.301	-1.09
1441219_at	---	11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriche	-2.09	0.156	-1.97	0.257	1.64	0.354	-1.02	0.937	-0.86
1431535_at	Plb1	phospholipase B1	1.07	0.893	-1.16	0.677	-1.43	0.113	-1.5	0.168	-0.76
1421982_a_at	Unc50	unc-50 homolog (C. elegans)	-1.13	0.149	-1.15	0.058	-1.15	0.213	1.03	0.693	-0.6
1419462_s_at	Gtl3	gene trap locus 3	-1.19	0.222	-1.27	0.109	-1	0.981	1.39	0.083	-0.52
1446925_at	Btrc	beta-transducin repeat containing protein	-1.73	0.414	1.06	0.756	-1.01	0.984	-1.44	0.198	-0.78
1448931_at	F2rl1	coagulation factor II (thrombin) receptor-like 1	1.02	0.887	-1.29	0.694	-1.19	0.289	-1.59	0.278	-0.76
1432762_at	9530025H10Rik	RIKEN cDNA 9530025H10 gene	-1.04	0.96	-1.16	0.524	-1.25	0.464	1.35	0.422	-0.52
1417479_at	4930511A21Rik	RIKEN cDNA 4930511A21 gene	-1.21	0.33	-1.19	0.515	-1.04	0.807	1.13	0.541	-0.58
1452211_at	Psme4	proteasome (prosome, macropain) activator subunit 4	-1.2	0.163	-1.16	0.002	-1.08	0.208	1.32	0.444	-0.53
1437854_at	Lrrc18	Leucine rich repeat containing 18	-1.24	0.54	1.12	0.685	-1.43	0.619	-1.97	0.216	-0.88
1453805_at	Fuca1	Fucosidase, alpha-L- 1, tissue	-1.08	0.908	1.19	0.497	-1.96	0.281	-1.4	0.349	-0.81
1437995_x_at	7-Sep	septin 7	-1.47	0.117	1.02	0.894	-1.08	0.686	-1.18	0.583	-0.68
1456599_at	Nxt2	nuclear transport factor 2-like export factor 2	-1.18	0.582	-1.23	0.04	-1.03	0.871	1.52	0.412	-0.48
1439751_at	Zfp708	zinc finger protein 708	1.09	0.632	-1.31	0.418	-1.29	0.64	-1.28	0.468	-0.7
1452360_a_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	-1.04	0.872	-1.05	0.827	-1.4	0.312	1.11	0.468	-0.59
1433489_s_at	Fgfr2	fibroblast growth factor receptor 2	-1.06	0.805	1.01	0.936	-1.48	0.037	-1.38	0.213	-0.73
1450638_at	Pdcd5	programmed cell death 5	1.01	0.934	-1.27	0.003	-1.2	0.087	-1.23	0.137	-0.67
1460018_at	D11Ertd759e	DNA segment, Chr 11, ERATO Doi 759, expressed	-1.11	0.683	-1.14	0.699	-1.18	0.517	1.14	0.322	-0.57
1433758_at	Nisch	nischarin	-1.07	0.586	1.05	0.506	-1.55	0.084	-1.25	0.282	-0.7
1437207_at	Rnf170	ring finger protein 170	1.02	0.905	-1.2	0.699	-1.29	0.196	-1.02	0.907	-0.62
1451920_a_at	Recc1	replication factor C 1	-1.08	0.024	-1.09	0.352	-1.26	0.21	1.14	0.539	-0.57
1443947_at	Lims1	LIM and senescent cell antigen-like domains 1	1.1	0.748	-1.1	0.858	-1.62	0.108	-1.19	0.245	-0.7
1456362_at	Cyp11b1	cytochrome P450, family 11, subfamily b, polypeptide 1	-1.32	0.308	1.12	0.874	-1.33	0.21	-1.28	0.585	-0.7
1433017_at	8430420C20Rik	RIKEN cDNA 8430420C20 gene	-1.87	0.333	-1.19	0.672	1.26	0.704	-2.28	0.337	-1.02
1436024_at	A930025D01Rik	RIKEN cDNA A930025D01 gene	-1.17	0.56	-1.7	0.208	1.19	0.743	-1.01	0.974	-0.67
1415897_a_at	Mgst1	microsomal glutathione S-transferase 1	-1.01	0.939	-1.16	0.524	-1.29	0.003	1.06	0.636	-0.6
1450448_at	Stc1	stanniocalcin 1	-1.21	0.362	-1.17	0.807	-1.05	0.653	1.33	0.447	-0.53
1434134_at	Wdr42a	WD repeat domain 42A	-1.08	0.312	-1.29	0.164	-1.08	0.375	1	0.991	-0.61
1456543_at	Prokr1	prokineticin receptor 1	-1.02	0.982	-1.39	0.708	-1.08	0.838	4.63	0.226	0.29
1440941_at	LOC552912	hypothetical LOC552912	-1.31	0.347	-1.13	0.55	-1.02	0.934	1.13	0.714	-0.58
1429423_at	4930518I15Rik	RIKEN cDNA 4930518I15 gene	1.01	0.958	-1.23	0.326	-1.24	0.229	-1.32	0.237	-0.69
1449069_at	Zfp148	zinc finger protein 148	1.11	0.702	-1.21	0.247	-1.43	0.063	-1.4	0.129	-0.73
1424204_at	Mrpl13	mitochondrial ribosomal protein L13	-1.17	0.003	-1.16	0.072	-1.09	0.121	1.01	0.906	-0.6
1451892_at	Kl	klotho	-1.43	0.18	1.22	0.138	-1.4	0.517	-1.61	0.196	-0.81

1432617_at	4933424C09Rik	RIKEN cDNA 4933424C09 gene	-1.25	0.674	-1.07	0.918	-1.12	0.75	1.43	0.461	-0.5
1432201_a_at	Zswim2	zinc finger, SWIM domain containing 2	-1.19	0.369	-1.07	0.758	-1.17	0.574	1.08	0.844	-0.59
1426388_s_at	Ryk	receptor-like tyrosine kinase	-1.08	0.632	-1.24	0.037	-1.11	0.479	1.97	0.274	-0.36
1442215_at	Smo	smoothened homolog (Drosophila)	-1.36	0.573	1.43	0.22	-2.15	0.336	-1.17	0.657	-0.81
1453639_s_at	0610037D15Rik	RIKEN cDNA 0610037D15 gene	-1.15	0.801	1.05	0.677	-1.39	0.338	-1.54	0.31	-0.76
1459877_x_at	Rnf185	Ring finger protein 185	-1.3	0.173	1.02	0.813	-1.19	0.074	-1.17	0.497	-0.66
1454156_at	A230104H11Rik	RIKEN cDNA A230104H11 gene	-1.35	0.525	1.16	0.601	-1.37	0.356	-1.13	0.374	-0.67
1442640_at	Slfn5	Schlafen 5	1.21	0.723	-1.32	0.499	-1.52	0.168	-1.64	0.266	-0.81
1434764_at	Akap11	A kinase (PRKA) anchor protein 11	-1.17	0.276	-1.01	0.801	-1.27	0.012	1.01	0.922	-0.61
1437479_x_at	Tbx3	T-box 3	-1.3	0.423	1	0.997	-1.16	0.658	-1.35	0.56	-0.7
1447025_at	Ube2e2	Ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	1.34	0.5	-1.81	0.068	-1.35	0.282	-1.61	0.072	-0.86
1422397_a_at	Il15ra	interleukin 15 receptor, alpha chain	-1.47	0.015	-1.39	0.099	1.23	0.31	-1.14	0.329	-0.69
1447101_at	Rnf122	ring finger protein 122	-1.45	0.094	1.18	0.818	-1.3	0.477	-1.99	0.234	-0.89
1440289_at	Gabpb2	GA repeat binding protein, beta 2	-1.22	0.838	-1.33	0.299	1.06	0.844	-1.16	0.368	-0.66
1445853_at	---	---	-1.49	0.497	-2.39	0.326	1.54	0.202	-1.92	0.238	-1.06
1436705_at	Tmem32	transmembrane protein 32	-1.07	0.068	-1.06	0.611	-1.33	0.027	1.14	0.164	-0.58
1438454_at	B430203M17Rik	RIKEN cDNA B430203M17 gene	1.02	0.934	-1.04	0.821	-1.53	0.004	-1.77	0.1	-0.83
1459019_at	Sprn	shadow of prion protein	-1.18	0.707	-1.26	0.507	-1.01	0.945	1	0.998	-0.61
1440841_at	Ywhae	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eps	1.01	0.971	-1.14	0.087	-1.35	0.104	-1.1	0.811	-0.65
1435497_at	5730590G19Rik	RIKEN cDNA 5730590G19 gene	-1.26	0.037	-1.03	0.885	-1.15	0.695	3.82	0.187	0.1
1418191_at	Usp18	ubiquitin specific peptidase 18	-1.23	0.546	-1.45	0.093	1.13	0.612	-1.42	0.103	-0.74
1454061_at	Thumpd3	THUMP domain containing 3	1.17	0.437	-1.5	0.283	-1.25	0.146	-1.22	0.022	-0.7
1460392_a_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	-1.16	0.044	-1.03	0.583	-1.25	0.004	1.35	0.262	-0.52
1423339_s_at	Ccdc16	coiled-coil domain containing 16	1.05	0.653	-1.14	0.79	-1.43	0.091	-1	0.993	-0.63
1445397_at	---	---	-1.08	0.577	-1.29	0.652	-1.07	0.836	1.08	0.825	-0.59
1457467_at	Pknox1	Pbx/knotted 1 homeobox	-1.48	0.039	-1.09	0.64	1.04	0.843	-1.04	0.828	-0.64
1448809_at	Cse1l	chromosome segregation 1-like (S. cerevisiae)	-1.13	0.054	-1.07	0.363	-1.24	0.042	1.01	0.944	-0.61
1453277_at	3021401N23Rik	RIKEN cDNA 3021401N23 gene	1.1	0.707	-1.45	0.294	-1.18	0.753	-1.34	0.411	-0.72
1443465_at	---	---	-1.01	0.92	1.08	0.843	-1.77	0.149	-1.14	0.507	-0.71
1453728_a_at	Mrps17	mitochondrial ribosomal protein S17	-1.16	0.165	-1.12	0.075	-1.13	0.312	1	0.971	-0.6
1430837_a_at	Mbd1	methyl-CpG binding domain protein 1	-1.49	0.104	-1.1	0.852	1.06	0.851	-1.56	0.104	-0.78
1416987_at	Elp4	elongation protein 4 homolog (S. cerevisiae)	-1.01	0.953	-1.5	0.063	-1.03	0.935	1.24	0.627	-0.57
1451748_a_at	Setd3	SET domain containing 3	-1.29	0.179	-1.15	0.071	-1.01	0.928	1.31	0.294	-0.53
1457268_at	Dot1l	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	-1.13	0.637	-1.22	0.108	-1.08	0.705	1.1	0.722	-0.58
1424402_at	Rufy3	RUN and FYVE domain containing 3	-1.11	0.62	1.04	0.84	-1.45	0.087	-1.11	0.454	-0.66
1421127_at	Tmem42	transmembrane protein 42	1.04	0.884	-1.17	0.042	-1.36	0.01	-1.87	0.063	-0.84
1451791_at	Tfpi	tissue factor pathway inhibitor	-1.29	0.018	1.2	0.323	-1.52	0.006	-1.31	0.504	-0.73
1428822_a_at	Snx24	sorting nexing 24	-1.26	0.26	1.11	0.235	-1.36	0.003	-1.06	0.753	-0.65
1459530_at	Hsd17b12	Hydroxysteroid (17-beta) dehydrogenase 12	1.36	0.693	-1.5	0.091	-1.64	0.265	-1.72	0.102	-0.88
1422154_at	Gpr27	G protein-coupled receptor 27	-1.09	0.874	-1.92	0.372	1.19	0.409	-1.13	0.59	-0.74
1428607_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	-1.1	0.492	-1.4	0.174	1.01	0.925	-1.29	0.013	-0.69
1458263_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.04	0.946	-1.16	0.694	-1.37	0.164	-2.34	0.041	-0.96
1452474_a_at	Art3	ADP-ribosyltransferase 3	-1.02	0.844	-1.19	0.52	-1.23	0.513	2.18	0.004	-0.31
1444855_at	Bcl9l	B-cell CLL/lymphoma 9-like	-1.21	0.31	1.08	0.752	-1.37	0.339	-1.3	0.362	-0.7
1445800_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	-1.28	0.514	-1.31	0.675	1.09	0.802	-2.37	0.078	-0.97
1437358_at	Wdfy1	WD repeat and FYVE domain containing 1	-1.05	0.2	-1.13	0.515	-1.26	0.071	1.14	0.513	-0.57
1442072_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	-1.03	0.95	-1.4	0.464	-1.05	0.875	1.27	0.594	-0.55
1422250_at	Map3k2	mitogen activated protein kinase kinase kinase 2	-1.65	0.464	-1.22	0.619	1.21	0.467	-1.16	0.836	-0.71
1437695_at	Prokr2	prokineticin receptor 2	-1.79	0.245	1.15	0.753	-1.08	0.837	-1.62	0.3	-0.84
1457764_at	A530058O07Rik	RIKEN cDNA A530058O07 gene	-1.12	0.705	1.09	0.81	-1.53	0.223	-1.46	0.597	-0.75
1428073_a_at	Nup88	nucleoporin 88	-1.12	0.073	-1.22	0.001	-1.08	0.124	1.1	0.553	-0.58
1448212_at	Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1	-1.07	0.556	-1.15	0.167	-1.2	0.162	1.25	0.25	-0.54
1426293_at	6330581L23Rik	RIKEN cDNA 6330581L23 gene	1.15	0.412	-1.15	0.413	-1.63	0.011	-1.77	0.077	-0.85

1420661_a_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	-1.32	0.398	-1.24	0.054	1.07	0.139	-1.03	0.875	-0.63
1459271_at	---	Transcribed locus	-1.28	0.22	-1.6	0.296	1.23	0.409	-1.74	0.251	-0.85
1444940_at	C76411	expressed sequence C76411	-1.75	0.135	-2.98	0.137	1.73	0.212	-1.72	0.297	-1.18
1447279_at	---	Transcribed locus	-1.24	0.402	-1.05	0.919	-1.14	0.794	1.07	0.716	-0.59
1433616_a_at	2310028O11Rik	RIKEN cDNA 2310028O11 gene	-1.1	0.133	-1.24	0.032	-1.08	0.406	1.19	0.279	-0.56
1446549_at	Kbtbd11	Kelch repeat and BTB (POZ) domain containing 11	-1.31	0.311	-2.47	0.053	1.47	0.262	-1.26	0.578	-0.89
1418748_at	Casp14	caspase 14	1	0.986	-1.21	0.098	-1.24	0.489	-1.41	0.418	-0.71
1418351_a_at	Dnmt3b	DNA methyltransferase 3B	-1.03	0.888	-1.12	0.733	-1.29	0.245	1.42	0.224	-0.51
1428308_at	Pdrg1	p53 and DNA damage regulated 1	-1.29	0.074	-1.18	0.376	1.01	0.951	-1.42	0.282	-0.72
1449776_at	---	---	-1.46	0.276	1.01	0.985	-1.07	0.742	-1.79	0.267	-0.83
1442158_at	Mast4	microtubule associated serine/threonine kinase family member 4	-2.49	0.004	1.78	0.384	-2.18	0.257	-1.4	0.566	-1.07
1425300_at	Dak	dihydroxyacetone kinase 2 homolog (yeast)	-1.12	0.756	-1.24	0.316	-1.06	0.8	1.64	0.379	-0.45
1440489_at	Btbd4	BTB (POZ) domain containing 4	-1.18	0.307	-1.06	0.842	-1.19	0.048	1.09	0.674	-0.58
1434293_at	Hectd3	HECT domain containing 3	1.08	0.686	-1.28	0.118	-1.28	0.197	-1.3	0.052	-0.7
1427636_at	Tspy-ps	testis specific protein-Y encoded, pseudogene	-1.24	0.438	1.06	0.823	-1.31	0.559	-1	0.991	-0.62
1440090_at	Slc25a27	Solute carrier family 25, member 27	-1.05	0.354	1.07	0.526	-1.62	0.031	-1.51	0.136	-0.78
1453147_at	Polr3e	polymerase (RNA) III (DNA directed) polypeptide E	1.1	0.687	-1.37	0.254	-1.24	0.127	-1.11	0.57	-0.65
1416155_at	Hmgb3	high mobility group box 3	-1.06	0.614	-1.35	0.121	-1.05	0.818	4.09	0.158	0.16
1454504_at	Kcnip1	Kv channel-interacting protein 1	-1.1	0.771	-2.56	0.023	1.34	0.463	-1.3	0.449	-0.91
1446533_at	Crtc1	CREB regulated transcription coactivator 1	-1.61	0.203	-1.1	0.836	1.11	0.58	-1.1	0.722	-0.68
1435303_at	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.06	0.418	-1.19	0.545	-1.35	0.047	-1.36	0.041	-0.71
1424210_at	Spfh1	SPFH domain family, member 1	-1.2	0.309	1.05	0.394	-1.33	0.09	-1.09	0.351	-0.64
1457163_at	D730035F11Rik	RIKEN cDNA D730035F11 gene	-1.23	0.456	1.14	0.689	-1.46	0.12	-1.85	0.259	-0.85
1417657_s_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	1.03	0.538	-1.28	0.182	-1.21	0.228	-1.15	0.075	-0.65
1428323_at	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	-1.3	0.437	-1.37	0.3	1.14	0.622	-1.11	0.237	-0.66
1435080_x_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	-1.17	0.14	1.01	0.919	-1.29	0.101	-1.33	0.362	-0.69
1444450_at	9530096D07Rik	RIKEN cDNA 9530096D07 gene	-1.28	0.356	-1.35	0.281	1.11	0.215	-1.31	0.416	-0.71
1438299_at	3100002L24Rik /// 9	RIKEN cDNA 3100002L24 gene /// RIKEN cDNA 9230108I15 gene /// similar to g	1.04	0.85	-1.09	0.401	-1.47	0.218	-1.12	0.037	-0.66
1420390_s_at	Zfp354a	zinc finger protein 354A	-1.14	0.665	1.06	0.72	-1.44	0.026	-1.19	0.669	-0.68
1420851_at	Pard6g	par-6 partitioning defective 6 homolog gamma (C. elegans)	1.03	0.636	-1.29	0.512	-1.2	0.189	-1.12	0.701	-0.65
1433691_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	1.13	0.85	-1.62	0.005	-1.12	0.593	-1.05	0.904	-0.67
1429782_at	Grcc10	gene rich cluster, C10 gene	1.04	0.912	-1.18	0.661	-1.33	0.146	-1.99	0.148	-0.86
1460678_at	Klhdc2	kelch domain containing 2	-1.24	0.214	-1.1	0.343	-1.08	0.586	1.72	0.234	-0.43
1442623_at	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4	1.07	0.858	-1.14	0.539	-1.45	0.219	-1.4	0.299	-0.73
1455261_at	---	PREDICTED: Mus musculus similar to Hemoglobin alpha subunit (Hemoglobin al	1.09	0.453	-1.26	0.24	-1.32	0.149	-1.26	0.195	-0.69
1456976_at	Wnt5a	wingless-related MMTV integration site 5A	1.24	0.431	-1.68	0.227	-1.25	0.318	-1.15	0.698	-0.71
1427899_at	Rnf6	ring finger protein (C3H2C3 type) 6	-1.26	0.433	1.01	0.932	-1.19	0.172	-1.29	0.45	-0.68
1418610_at	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), m	1.2	0.498	-1.15	0.534	-1.78	0.509	-1.36	0.572	-0.77
1439964_at	D8Bwg1414e	DNA segment, Chr 8, Brigham & Women's Genetics 1414 expressed	-1.12	0.504	-1.07	0.59	-1.23	0.34	1.15	0.247	-0.57
1429168_at	Btbd4	BTB (POZ) domain containing 4	-1.16	0.564	1.03	0.863	-1.35	0.16	-1.08	0.652	-0.64
1434996_at	Slc25a16	solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen), mem	-1.06	0.663	-1.29	0.224	-1.09	0.603	1.01	0.964	-0.61
1417596_at	Eppb9	endothelial precursor protein B9	1.05	0.678	-1.58	0.351	-1.04	0.865	-1.27	0.188	-0.71
1428810_at	2700097O09Rik	RIKEN cDNA 2700097O09 gene	-1.2	0.504	-1.07	0.351	-1.15	0.18	1.56	0.194	-0.46
1425938_a_at	Fkbp11	FK506 binding protein 11	-2.2	0.111	-1.13	0.842	1.3	0.654	-2.18	0.068	-1.05
1438397_a_at	Rbm39	RNA binding motif protein 39	-1.3	0.6	-1.2	0.327	1.04	0.904	-2.18	0.1	-0.91
1452551_at	---	---	1.29	0.451	-1.39	0.47	-1.6	0.272	-2.26	0.255	-0.99
1419211_s_at	4933424B01Rik	RIKEN cDNA 4933424B01 gene	-1.33	0.137	-1.03	0.732	-1.09	0.323	1.22	0.616	-0.56
1438809_at	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	-1.38	0.221	1.08	0.798	-1.2	0.36	-1.63	0.279	-0.78
1429122_a_at	1700040I03Rik	RIKEN cDNA 1700040I03 gene	-1.11	0.468	-1.09	0.402	-1.22	0.019	1.3	0.389	-0.53
1420922_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	-1.15	0.062	-1.15	0.155	-1.12	0.347	1.26	0.174	-0.54
1454958_at	Gsk3b	glycogen synthase kinase 3 beta	-1.11	0.015	-1.08	0.628	-1.22	0.374	1.14	0.514	-0.57
1418378_at	Bpil1	bactericidal/permeability-increasing protein-like 1	-1.12	0.751	-1.25	0.279	-1.06	0.709	1.07	0.848	-0.59
1459929_at	Zfp568	zinc finger protein 568	-1.05	0.954	-1.09	0.791	-1.3	0.464	1.26	0.321	-0.54

1418359_at	Wbscr27	Williams Beuren syndrome chromosome region 27 (human)	-1.21	0.317	-1.11	0.336	-1.09	0.517	2.98	0.231	-0.11
1455486_at	Pias1	protein inhibitor of activated STAT 1	-1.17	0.66	1.07	0.576	-1.41	0.046	-1.21	0.51	-0.68
1456933_at	Smg7	Smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.08	0.831	1.21	0.508	-2.02	0.005	-1.41	0.444	-0.82
1424326_at	Lemd2	LEM domain containing 2	-1.16	0.439	-1.29	0.086	-1	0.997	1.05	0.18	-0.6
1438089_a_at	Bclaf1	BCL2-associated transcription factor 1	1.09	0.452	-1.28	0.247	-1.31	0.063	-1.18	0.175	-0.67
1453252_at	Dus4l	dihydrouridine synthase 4-like (S. cerevisiae)	-1.49	0.327	-1.36	0.356	1.23	0.669	-1.92	0.286	-0.88
1441298_at	---	---	-1.14	0.742	-1.18	0.65	-1.09	0.657	1.52	0.469	-0.47
1444908_at	Habp4 /// LOC6717	hyaluronic acid binding protein 4 /// similar to hyaluronic acid binding protein 4	-1.23	0.11	-1.21	0.257	1	0.996	-1.25	0.067	-0.67
1458031_at	B230315F11Rik	RIKEN cDNA B230315F11 gene	1.15	0.026	-1.18	0.678	-1.57	0.068	-1.03	0.789	-0.66
1425457_a_at	Grb10	growth factor receptor bound protein 10	-1.1	0.67	-2.07	0.236	1.24	0.706	-1.02	0.958	-0.73
1423513_at	Neo1 /// E030041M	neogenin /// RIKEN cDNA E030041M21 gene	-1.16	0.288	-1.04	0.787	-1.22	0.195	1.07	0.635	-0.59
1450264_a_at	Chka	choline kinase alpha	-1.19	0.015	1.09	0.809	-1.4	0.159	-1.52	0.159	-0.76
1446490_at	Ptbp2	Polypyrimidine tract binding protein 2	1.12	0.491	-1.35	0.272	-1.28	0.219	-1.23	0.401	-0.69
1444611_at	U2af1-rs2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 2	-1.04	0.781	1.01	0.954	-1.5	0.003	-1.15	0.206	-0.67
1451397_at	---	---	-1.81	0.406	-1.22	0.466	1.27	0.498	-1.33	0.475	-0.77
1457793_a_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	1.06	0.611	-1.24	0.435	-1.29	0.076	-1	0.988	-0.62
1416035_at	---	---	-1.34	0.221	1.02	0.847	-1.15	0.091	-1.31	0.226	-0.69
1454950_at	B930006L02Rik	RIKEN cDNA B930006L02 gene	-1.03	0.915	-1.17	0.716	-1.23	0.632	1.12	0.368	-0.58
1443400_at	Mier1	Mesoderm induction early response 1 homolog (Xenopus laevis	1.15	0.066	-1.21	0.262	-1.52	0.031	-1.05	0.591	-0.66
1458204_at	Sparc	secreted acidic cysteine rich glycoprotein	1.37	0.145	-1.44	0.631	-1.72	0.155	-1	0.988	-0.7
1434771_at	0610011F06Rik	RIKEN cDNA 0610011F06 gene	1.02	0.857	-1.57	0.085	-1.02	0.926	-1.22	0.291	-0.7
1449799_s_at	Pkp2	plakophilin 2	-1.08	0.591	-1.12	0.296	-1.21	0.219	1.65	0.279	-0.44
1436826_at	Tmtc3	transmembrane and tetratricopeptide repeat containing 3	-1.34	0.175	-1.08	0.68	-1.03	0.865	1.32	0.148	-0.53
1444839_at	---	---	-1.48	0.426	1.39	0.495	-1.72	0.411	-1.63	0.529	-0.86
1418454_at	Mfap5	microfibrillar associated protein 5	1.14	0.723	-1.03	0.923	-1.89	0.048	-1.48	0.283	-0.81
1459283_at	6430510B20Rik	RIKEN cDNA 6430510B20 gene	-1.07	0.694	1.1	0.758	-1.65	0.058	-1.15	0.582	-0.69
1457367_at	Amy2	Amylase 2, pancreatic	1.01	0.918	-1.21	0.275	-1.25	0.361	-1.21	0.287	-0.66
1425990_a_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-2.4	0.031	-1.01	0.974	1.23	0.384	-1.34	0.528	-0.88
1440091_at	Mrg1	myeloid ecotropic viral integration site-related gene 1	-1.19	0.052	1.16	0.099	-1.56	0.247	-1.07	0.781	-0.67
1458183_at	2810039B14Rik	RIKEN cDNA 2810039B14 gene	-1.15	0.102	-1.14	0.61	-1.11	0.331	1.41	0.453	-0.5
1434607_at	Ddx52	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	1.08	0.71	-1.2	0.114	-1.37	0.166	-1.78	0.127	-0.82
1443698_at	Fbxo39	F-box protein 39	-1.1	0.594	1.05	0.623	-1.46	0.013	-1.26	0.302	-0.69
1435919_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	-1.08	0.449	-1.55	0.467	1.07	0.477	-1.06	0.581	-0.66
1427139_at	Adamts10	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.03	0.627	1.06	0.359	-1.62	0.021	-1.71	0.172	-0.83
1433364_at	A930036I15Rik	RIKEN cDNA A930036I15 gene	-2.16	0.072	-1.61	0.466	1.56	0.495	-1.01	0.967	-0.81
1417116_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	-1.31	0.011	1.04	0.72	-1.19	0.333	-1.13	0.538	-0.65
1460233_at	Guca2b	guanylate cyclase activator 2b (retina)	1.24	0.122	-1.39	0.468	-1.46	0.31	-1.48	0.144	-0.77
1452297_at	Ccnt2	cyclin T2	-1.07	0.68	-1.32	0.204	-1.05	0.818	1.29	0.383	-0.54
1416319_at	Adk	adenosine kinase	-1.13	0.202	-1.01	0.898	-1.31	0.155	1.9	0.163	-0.39
1429708_at	Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	-1.22	0.312	-1.06	0.281	-1.14	0.072	1.08	0.509	-0.58
1443959_at	C230095G01Rik	RIKEN cDNA C230095G01 gene	-1.17	0.647	1.29	0.599	-2	0.113	-1.44	0.191	-0.83
1456995_at	2700045P11Rik	RIKEN cDNA 2700045P11 gene	-1.15	0.894	-1.13	0.554	-1.12	0.499	1.23	0.562	-0.54
1436877_at	Lrch2	leucine-rich repeats and calponin homology (CH) domain containing 2	-1.5	0.334	1.15	0.799	-1.21	0.606	-2.17	0.036	-0.93
1419010_x_at	Klk1b5	kallikrein 1-related peptidase b5	-1.35	0.411	-1.14	0.661	1.02	0.962	-1.51	0.517	-0.74
1416367_at	1110001J03Rik	RIKEN cDNA 1110001J03 gene	-1.13	0.31	-1.24	0.101	-1.05	0.768	1.1	0.443	-0.58
1416369_at	Hiatl1	hippocampus abundant transcript-like 1	-1.18	0.096	-1.17	0.118	-1.07	0.297	1.18	0.402	-0.56
1431736_at	4933405D12Rik	RIKEN cDNA 4933405D12 gene	1.03	0.957	-1.18	0.723	-1.3	0.605	-1.03	0.828	-0.62
1445031_at	Tbc1d8	TBC1 domain family, member 8	1.07	0.889	-1.02	0.951	-1.69	0.285	-1.19	0.386	-0.71
1421148_a_at	Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	-1.19	0.235	-1.25	0.206	1	1	-1.08	0.738	-0.63
1418885_a_at	Idh3b	isocitrate dehydrogenase 3 (NAD+) beta	-1.18	0.056	-1.28	0.08	1.01	0.889	-1.43	0.048	-0.72
1428925_at	Senp1	SUMO1/sentrin specific peptidase 1	-1.19	0.57	-1.07	0.688	-1.16	0.474	1.34	0.206	-0.52
1420035_at	Aqp6	Aquaporin 6	-1.03	0.823	-1.21	0.636	-1.18	0.715	1.03	0.959	-0.6
1441071_at	Kcnq5	potassium voltage-gated channel, subfamily Q, member 5	1.65	0.566	-1.48	0.461	-3.1	0.014	-1.35	0.512	-1.07

1443929_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420432F0	-1.39	0.199	1	0.989	-1.09	0.808	-1.15	0.426	-0.66
1443057_at	---	---	-1.05	0.435	-1.01	0.97	-1.43	0.034	1.07	0.716	-0.61
1421621_at	Rasgrf2	RAS protein-specific guanine nucleotide-releasing factor 2	-1.45	0.565	-1.15	0.653	1.08	0.788	-1.49	0.133	-0.75
1439513_at	Pnrc1	proline-rich nuclear receptor coactivator 1	-1.12	0.842	-2.25	0.045	1.31	0.552	-1.26	0.449	-0.83
1441487_at	Trim2	tripartite motif protein 2	-1.04	0.944	-1.12	0.808	-1.26	0.324	1.42	0.202	-0.5
1425474_a_at	Vps39	vacuolar protein sorting 39 (yeast)	1.16	0.72	-1.33	0.374	-1.36	0.247	-1.41	0.192	-0.74
1429539_at	Bcl2l13	BCL2-like 13 (apoptosis facilitator)	-1.09	0.313	-1.17	0.028	-1.14	0.239	2.13	0.103	-0.32
1457243_at	1110032O16Rik	RIKEN cDNA 1110032O16 gene	-1.32	0.36	1.04	0.8	-1.18	0.543	-1.15	0.371	-0.65
1454995_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	-1.18	0.301	-1.38	0.321	1.07	0.723	-1.38	0.053	-0.72
1434005_at	Rbms1	RNA binding motif, single stranded interacting protein 1	1.02	0.872	-1.14	0.274	-1.34	0.039	-1.63	0.073	-0.77
1427850_x_at	Igh-VJ558	immunoglobulin heavy chain (J558 family)	-1.19	0.369	-1.08	0.846	-1.15	0.773	1.48	0.493	-0.48
1458567_at	D130017N08Rik	RIKEN cDNA D130017N08 gene	-1.42	0.18	1.18	0.496	-1.31	0.058	-1.3	0.417	-0.71
1424932_at	Egfr	epidermal growth factor receptor	-1.07	0.806	1.13	0.789	-1.73	0.025	-1.61	0.096	-0.82
1424434_at	BC024814	cDNA sequence BC024814	-1.11	0.592	-1.36	0.192	1.01	0.895	-1.03	0.754	-0.62
1442903_at	4732423E21Rik	RIKEN cDNA 4732423E21 gene	1.07	0.512	-1.09	0.765	-1.53	0.068	-1.01	0.941	-0.64
1458432_at	Nck2	Non-catalytic region of tyrosine kinase adaptor protein 2	1.21	0.465	-1.09	0.429	-1.93	0.055	-1.58	0.177	-0.85
1424085_at	Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	-1.16	0.219	-1.17	0.157	-1.08	0.748	1.32	0.104	-0.52
1423136_at	Fgf1	fibroblast growth factor 1	1.23	0.038	-1.45	0.053	-1.38	0.078	-1.71	0.014	-0.83
1434375_at	B930006L02Rik	RIKEN cDNA B930006L02 gene	1.08	0.501	-1.14	0.309	-1.45	0.011	-1.11	0.66	-0.66
1453830_at	---	---	-1.72	0.245	1.25	0.534	-1.23	0.622	-1.52	0.449	-0.8
1445106_at	Mbnl1	Muscleblind-like 1 (Drosophila)	-1.16	0.148	1.07	0.831	-1.41	0.12	-1.31	0.316	-0.7
1452694_at	Ihpk1	inositol hexaphosphate kinase 1	-1.32	0.262	-1.05	0.52	-1.07	0.758	1.05	0.752	-0.6
1457761_at	C79607	expressed sequence C79607	-1.07	0.809	-1.03	0.885	-1.34	0.176	1.07	0.648	-0.6
1451367_at	Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	-1.34	0.249	-1.2	0.423	1.06	0.614	-1.26	0.141	-0.68
1423725_at	Pls3	plastin 3 (T-isoform)	-1.12	0.002	1	0.953	-1.34	0.004	-1.47	0.285	-0.73
1428490_at	C1galt1	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransfe	-1.26	0.12	-1.04	0.745	-1.13	0.352	1.08	0.741	-0.59
1421227_at	Gzme	granzyme E	1.08	0.768	-1.01	0.976	-1.74	0.119	-1.71	0.354	-0.85
1445453_at	---	---	-1.08	0.774	1.07	0.716	-1.55	0.235	-1.27	0.657	-0.71
1457656_s_at	C230085N15Rik	RIKEN cDNA C230085N15 gene	1.36	0.39	-1.23	0.24	-2.13	0.043	-4.38	0.059	-1.6
1424601_at	Xrcc4	X-ray repair complementing defective repair in Chinese hamster cells 4	-1.27	0.309	1.03	0.678	-1.21	0.099	-1.03	0.802	-0.62
1455778_at	Zfp192	zinc finger protein 192	-1.05	0.65	-1.17	0.256	-1.2	0.203	1.02	0.948	-0.6
1435546_a_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	-1.18	0.192	-1.07	0.584	-1.16	0.206	1.19	0.43	-0.55
1451572_a_at	5230400G24Rik ///	RIKEN cDNA 5230400G24 gene /// hypothetical protein LOC637796	-1.12	0.461	-1.04	0.614	-1.27	0.003	1.11	0.684	-0.58
1419869_s_at	Hdlbp	high density lipoprotein (HDL) binding protein	-1.17	0.073	-1.04	0.456	-1.2	0.131	1.04	0.817	-0.59
1416662_at	Sardh	sarcosine dehydrogenase	1.04	0.899	-1.16	0.481	-1.34	0.505	-1.43	0.402	-0.72
1457983_s_at	Rwdd4a	RWD domain containing 4A	1.03	0.87	-1.1	0.411	-1.42	0.048	-1.01	0.94	-0.62
1436214_at	1110028C15Rik	RIKEN cDNA 1110028C15 gene	-1.2	0.335	1.13	0.43	-1.46	0.061	-1.08	0.279	-0.65
1453796_a_at	Ergic2	ERGIC and golgi 2	-1.04	0.61	-1.26	0.258	-1.12	0.409	1.4	0.254	-0.51
1458831_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	1.1	0.562	-1.27	0.492	-1.32	0.204	-1.44	0.147	-0.73
1436865_at	Slc26a11	solute carrier family 26, member 11	-1.73	0.084	-1.21	0.393	1.24	0.278	-1.23	0.568	-0.73
1419959_s_at	C330003B14Rik	RIKEN cDNA C330003B14 gene	-1.27	0.782	-1.16	0.586	-1	0.997	1.13	0.66	-0.58
1450891_at	Srp19	signal recognition particle 19	-1.04	0.448	-1.08	0.238	-1.32	0.029	1.2	0.035	-0.56
1422110_at	Hr	hairless	-1.35	0.274	1.05	0.803	-1.16	0.367	-1.2	0.444	-0.67
1438890_at	---	---	-1.1	0.711	-1.03	0.798	-1.3	0.174	1.04	0.78	-0.6
1458359_at	---	Transcribed locus	1.09	0.847	-1.19	0.697	-1.41	0.546	-2.68	0.049	-1.05
1431577_at	---	---	-1.4	0.622	1.07	0.902	-1.16	0.52	-1.84	0.213	-0.83
1452848_at	Gpr178	G protein-coupled receptor 178	-1.31	0.066	1.09	0.669	-1.26	0.447	-1.31	0.27	-0.7
1418931_at	Reg4	regenerating islet-derived family, member 4	-1.65	0.16	-1.36	0.248	1.31	0.522	-1.14	0.707	-0.71
1442038_at	Rbm26	RNA binding motif protein 26	-1.17	0.661	-1.13	0.352	-1.1	0.706	1.12	0.557	-0.57
1428228_at	Pgm3	phosphoglucomutase 3	1.08	0.669	-1.14	0.473	-1.45	0.156	-1.3	0.4	-0.7
1457827_at	Arsj	arylsulfatase J	1.48	0.363	-1.57	0.478	-1.87	0.213	-1.68	0.003	-0.91
1442087_at	H3f3a	H3 histone, family 3A	-1.02	0.924	-1.36	0.317	-1.08	0.62	1.35	0.336	-0.53
1441632_at	C130079B09Rik	RIKEN cDNA C130079B09 gene	1.44	0.24	-1.52	0.23	-1.81	0.032	-1.16	0.679	-0.76

1443236_at	B230118H07Rik	RIKEN cDNA B230118H07 gene	-1.59	0.177	-1.3	0.562	1.25	0.627	-1.79	0.512	-0.86
1424469_a_at	Cpsf4	cleavage and polyadenylation specific factor 4	-1.03	0.683	-1.06	0.71	-1.37	0.204	1.05	0.827	-0.6
1449961_at	Rph3a	rabphilin 3A	-1.3	0.357	1.01	0.931	-1.16	0.495	-1.56	0.461	-0.75
1444549_at	---	Adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:733040	1.3	0.535	-2.26	0.21	-1.11	0.866	-1.18	0.828	-0.81
1441455_at	Arpp19	CAMP-regulated phosphoprotein 19	-1.22	0.364	1.05	0.875	-1.28	0.124	-1.17	0.412	-0.66
1446383_at	Efna5	Ephrin A5	-1.17	0.616	1.08	0.791	-1.4	0.164	-1.83	0.305	-0.83
1428204_at	C030002O17Rik	RIKEN cDNA C030002O17 gene	-1.31	0.678	-1.05	0.921	-1.07	0.896	1.47	0.575	-0.49
1429664_at	Cdkl1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-1.11	0.829	-1.14	0.678	-1.16	0.616	1.35	0.311	-0.51
1437408_at	Gpr126	G protein-coupled receptor 126	1.5	0.299	-1.52	0.447	-2.03	0.053	-1.82	0.262	-0.97
1426126_a_at	MGC30332	hypothetical protein MGC30332	-1.39	0.188	-1.17	0.374	1.07	0.735	-1.47	0.174	-0.74
1457443_at	---	---	1.04	0.906	-1.44	0.291	-1.1	0.46	-1.06	0.814	-0.64
1430908_at	4933429O19Rik	RIKEN cDNA 4933429O19 gene	-1.96	0.12	1.28	0.167	-1.17	0.392	-1.3	0.202	-0.79
1431949_at	4930544F09Rik	RIKEN cDNA 4930544F09 gene	-1.62	0.61	1.35	0.529	-1.47	0.398	-2.01	0.304	-0.94
1438848_at	Rbpsuh	Recombining binding protein suppressor of hairless (Drosophila)	-1.26	0.407	1.19	0.631	-1.49	0.108	-1.22	0.158	-0.7
1434380_at	Gbp7	guanylate binding protein 7	1.22	0.475	-1.32	0.07	-1.49	0.08	-1.19	0.288	-0.7
1435209_at	BC057079	cDNA sequence BC057079	-1.3	0.281	-1.02	0.74	-1.11	0.171	1.16	0.598	-0.57
1441898_at	E530011F12Rik	RIKEN cDNA E530011F12 gene	1.31	0.492	-1.79	0.231	-1.29	0.538	-1.02	0.957	-0.7
1443331_at	Plekhg1	Pleckstrin homology domain containing, family G (with RhoGef domain) member	-1.28	0.059	1.26	0.07	-1.65	0.03	-1.09	0.683	-0.69
1416782_s_at	Praf2	PRA1 domain family 2	-1.06	0.468	-1.42	0.009	1	0.986	-1.05	0.818	-0.63
1436410_at	AI449023 /// Gm94	expressed sequence AI449023 /// gene model 941, (NCBI)	-1.52	0.331	-1.22	0.665	1.17	0.766	-2.34	0.092	-0.98
1442419_at	---	Transcribed locus	-1.17	0.684	-2.04	0.024	1.3	0.503	-1.17	0.769	-0.77
1449874_at	Ly96	lymphocyte antigen 96	-1.37	0.101	1.08	0.61	-1.19	0.559	-1.15	0.589	-0.66
1434313_at	6330407D12Rik	RIKEN cDNA 6330407D12 gene	-1.49	0.296	1.1	0.774	-1.13	0.516	-1.21	0.516	-0.69
1428186_at	Kctd6	potassium channel tetramerisation domain containing 6	-1.19	0.118	-1.02	0.895	-1.22	0.027	1.01	0.949	-0.6
1456027_at	Rbm41	RNA binding motif protein 41	-1.36	0.097	1.03	0.802	-1.14	0.215	-1.27	0.343	-0.68
1440982_at	LOC552909	hypothetical LOC552909	1.13	0.78	-1.11	0.709	-1.61	0.052	-1.3	0.285	-0.72
1433582_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	-1.16	0.498	-1.05	0.669	-1.2	0.482	1.66	0.175	-0.44
1453867_at	Fbxw2	F-box and WD-40 domain protein 2	1.18	0.462	-1.07	0.902	-1.87	0.379	-1.02	0.958	-0.7
1445658_at	---	Transcribed locus	-1.31	0.171	-1.08	0.766	-1.04	0.925	1.37	0.211	-0.52
1432650_at	2510019K15Rik	RIKEN cDNA 2510019K15 gene	-1.43	0.452	-1.35	0.207	1.21	0.534	-1.23	0.164	-0.7
1451105_at	Vash2	vasohibin 2	1.34	0.62	-2.17	0.074	-1.18	0.53	-1.79	0.168	-0.95
1449370_at	Sox4 /// LOC67227	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	1.3	0.521	-1.42	0.481	-1.55	0.256	-1.24	0.293	-0.73
1432899_at	4833408G04Rik	RIKEN cDNA 4833408G04 gene	-1.58	0.34	1.1	0.772	-1.09	0.816	-1.51	0.123	-0.77
1429777_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	-1.18	0.76	-1.37	0.244	1.07	0.746	-1.64	0.192	-0.78
1434329_s_at	Adipor2	adiponectin receptor 2	-1.11	0.129	-1.24	0.171	-1.06	0.716	1.14	0.183	-0.57
1416824_at	B230118H07Rik	RIKEN cDNA B230118H07 gene	-1.1	0.13	-1.03	0.294	-1.29	0.096	1.09	0.615	-0.58
1458910_at	---	---	1.21	0.847	-1.25	0.452	-1.56	0.254	-1.41	0.514	-0.75
1421320_a_at	Qtrtd1	queuine tRNA-ribosyltransferase domain containing 1	1.2	0.833	-2.15	0.281	-1.01	0.98	-1.52	0.005	-0.87
1438117_x_at	Tmem41b	transmembrane protein 41B	-1.21	0.014	-1.16	0.191	-1.05	0.797	1.17	0.433	-0.56
1442682_at	---	---	-1.03	0.888	-1.28	0.544	-1.12	0.671	1.57	0.296	-0.46
1460736_at	LOC665775 /// LOC	similar to CG5514-PB, isoform B /// region containing expressed sequence AF01	-1.17	0.16	1.03	0.899	-1.31	0.159	-1.1	0.561	-0.64
1437128_a_at	A630033E08Rik	RIKEN cDNA A630033E08 gene	-1.03	0.824	1.02	0.856	-1.5	0.061	-1.3	0.484	-0.71
1459939_at	---	Transcribed locus	-1.73	0.182	1.15	0.702	-1.09	0.812	-1.55	0.328	-0.8
1450903_at	Rad23b	RAD23b homolog (S. cerevisiae)	1.06	0.732	-1.26	0.008	-1.24	0.063	-1.17	0.143	-0.65
1446398_at	LOC433197	hypothetical gene supported by AK028463	1.53	0.111	-1.97	0.355	-1.62	0.453	-1.02	0.951	-0.77
1446960_at	LOC626082	Hypothetical protein LOC626082	1.12	0.829	-1.14	0.781	-1.54	0.488	-1.29	0.543	-0.71
1432578_at	4933440H19Rik	RIKEN cDNA 4933440H19 gene	-1.1	0.757	-1.04	0.86	-1.29	0.053	2.36	0.001	-0.27
1424761_at	BC011487	cDNA sequence BC011487	1.09	0.676	-1.41	0.482	-1.17	0.341	-1.34	0.014	-0.71
1437023_at	Zfp12	zinc finger protein 12	1.05	0.654	-1.16	0.064	-1.34	0.088	-1.09	0.715	-0.64
1458217_s_at	2210018M11Rik	RIKEN cDNA 2210018M11 gene	-1.29	0.391	1.04	0.867	-1.19	0.166	-1.1	0.157	-0.64
1449819_at	Dmc1h	disrupted meiotic cDNA 1 homolog	1.1	0.921	-1.52	0.534	-1.12	0.818	-1.88	0.602	-0.85
1436266_x_at	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	-1.08	0.414	-1.23	0.133	-1.09	0.469	1.07	0.7	-0.58
1428037_at	Otoa	otoancorin	-1.24	0.238	1.05	0.915	-1.26	0.657	-1.15	0.752	-0.65

1423534_at	Pdcd2	programmed cell death 2	1.02	0.944	-1.36	0.016	-1.11	0.333	-1.68	0.008	-0.78
1436521_at	Slc36a2	solute carrier family 36 (proton/amino acid symporter), member 2	-1.6	0.241	1.06	0.875	-1.04	0.882	-1.97	0.119	-0.89
1435812_at	Unc50	unc-50 homolog (C. elegans)	-1.46	0.293	-1.37	0.067	1.23	0.147	-1.07	0.847	-0.66
1451077_at	Rpl5 /// LOC38274(	ribosomal protein L5 /// similar to 60S ribosomal protein L5 /// similar to 60S ribos	-1.07	0.001	1.02	0.916	-1.42	0.102	-1.14	0.475	-0.65
1424726_at	Tmem150	transmembrane protein 150	-1.1	0.118	1.04	0.788	-1.42	0.037	-1.29	0.19	-0.69
1455075_at	Pigv	phosphatidylinositol glycan anchor biosynthesis, class V	-1.33	0.339	-1.19	0.662	1.06	0.542	-1.37	0.089	-0.71
1449203_at	Slco1a5	solute carrier organic anion transporter family, member 1a5	1.29	0.527	-1.14	0.65	-2.07	0.016	-1.26	0.674	-0.79
1437658_a_at	Snord22	small nucleolar RNA, C/D box 22	-1.53	0.37	-1.09	0.696	1.08	0.464	-1.06	0.876	-0.65
1439024_at	Bag4	BCL2-associated athanogene 4	1.02	0.927	-1.34	0.13	-1.12	0.096	-1.08	0.519	-0.63
1428279_a_at	Atxn7l4	ataxin 7-like 4	-1.05	0.771	-1.23	0.243	-1.13	0.369	1.13	0.483	-0.57
1442188_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	-1.41	0.163	1.26	0.347	-1.47	0.121	-1.8	0.144	-0.85
1420296_at	Clcn5	chloride channel 5	-1.19	0.205	-1.27	0.238	1.02	0.935	-1.68	0.315	-0.78
1457538_at	5930422O12Rik	RIKEN cDNA 5930422O12 gene	-1.08	0.513	-1.06	0.826	-1.28	0.113	2.19	0.09	-0.31
1457629_at	BC060631	cDNA sequence BC060631	-1.13	0.343	-1.97	0.068	1.26	0.523	-1.12	0.819	-0.74
1420507_a_at	3110031B13Rik	RIKEN cDNA 3110031B13 gene	-1.07	0.427	-1.09	0.403	-1.25	0.153	1.09	0.538	-0.58
1448544_at	Crat	carnitine acetyltransferase	-1.18	0.634	-1.07	0.856	-1.14	0.666	1.8	0.257	-0.4
1438061_at	4930523C07Rik	RIKEN cDNA 4930523C07 gene	1.1	0.216	-1.43	0.381	-1.18	0.191	-1.85	0.011	-0.84
1438113_at	Zmat4	zinc finger, matrin type 4	-1.2	0.183	1.1	0.874	-1.4	0.524	-1.1	0.869	-0.65
1434792_at	2010320M18Rik	RIKEN cDNA 2010320M18 gene	1	0.932	-1.13	0.476	-1.31	0.183	-1.18	0.476	-0.65
1457100_at	AW552889	expressed sequence AW552889	1.47	0.583	-1.5	0.34	-1.92	0.23	-1.02	0.971	-0.74
1456962_at	Cntn2	contactin 2	-1.96	0.17	-1.12	0.886	1.25	0.506	-1.82	0.406	-0.91
1430966_at	Cml3	camello-like 3	-1.19	0.601	-1	0.999	-1.24	0.536	1.23	0.293	-0.55
1458027_at	Mrpl17	mitochondrial ribosomal protein L17	-1.97	0.106	1.2	0.84	-1.06	0.791	-1.63	0.326	-0.86
1415791_at	Rnf34	ring finger protein 34	-1.55	0.011	-1.09	0.313	1.09	0.566	-1.2	0.088	-0.69
1452945_at	2610020C11Rik	RIKEN cDNA 2610020C11 gene	-1.1	0.337	1.12	0.313	-1.62	0.134	-1.85	0.09	-0.86
1428776_at	Slc10a6	solute carrier family 10 (sodium/bile acid cotransporter family), member 6	-1.05	0.872	1.04	0.784	-1.52	0.008	-1.2	0.177	-0.68
1452263_at	Slc35f4	solute carrier family 35, member F4	1.14	0.351	-1.33	0.398	-1.31	0.498	-1.4	0.701	-0.73
1430921_at	9130015G15Rik	RIKEN cDNA 9130015G15 gene	-1.24	0.701	-1.13	0.775	-1.04	0.924	1.65	0.319	-0.44
1429720_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-1.08	0.476	-1.48	0.027	1.05	0.815	-1.02	0.89	-0.63
1457418_at	Speer1-ps1	Spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1	-1.75	0.321	1.6	0.286	-2.08	0.115	-1.17	0.698	-0.85
1415689_s_at	Zfp306	zinc finger protein 306	-1.18	0.143	1.01	0.937	-1.25	0.158	-1.18	0.336	-0.65
1417671_at	Scly	selenocysteine lyase	-1.09	0.828	-1.21	0.331	-1.1	0.129	1.61	0.076	-0.45
1442209_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.57	0.435	-1.92	0.253	1.5	0.265	-2	0.134	-1
1457345_at	Polr3b	Polymerase (RNA) III (DNA directed) polypeptide B	-1.11	0.711	-1.08	0.901	-1.21	0.702	1.05	0.889	-0.59
1421844_at	---	---	-1.55	0.033	-1.01	0.886	1.02	0.895	-1.1	0.614	-0.66
1435374_at	---	Transcribed locus	-1.07	0.78	1.18	0.558	-1.86	0.032	-1.7	0.262	-0.86
1428694_at	5033413D16Rik	RIKEN cDNA 5033413D16 gene	-1.1	0.709	-1.32	0.309	-1.02	0.942	1.12	0.662	-0.58
1428233_at	Cpsf6	cleavage and polyadenylation specific factor 6	-1.17	0.553	-1.21	0.143	-1.03	0.774	1.17	0.454	-0.56
1431270_a_at	Aste1	asteroid homolog 1 (Drosophila)	-1.13	0.748	-1.34	0.412	1.02	0.964	-1.03	0.923	-0.62
1438646_x_at	2510039O18Rik	RIKEN cDNA 2510039O18 gene	-1.42	0.258	-1.11	0.452	1.05	0.705	-1.36	0.101	-0.71
1438916_x_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	1.05	0.766	-1.12	0.585	-1.41	0.066	-1.14	0.626	-0.65
1427946_s_at	Dpyd	dihydropyrimidine dehydrogenase	1.01	0.953	-1.04	0.661	-1.47	0.21	-1.47	0.378	-0.74
1446772_at	Sema5a	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmem	-1.37	0.297	1.4	0.448	-1.93	0.306	-1.3	0.372	-0.8
1423036_at	Txnl5	thioredoxin-like 5	-1.05	0.782	-1.21	0.529	-1.15	0.369	1.04	0.897	-0.59
1443050_at	BC032265	CDNA sequence BC032265	-1.19	0.243	1.22	0.655	-1.67	0.187	-2.01	0.099	-0.91
1419165_at	Zfp260 /// LOC635(	zinc finger protein 260 /// similar to Zinc finger protein OZF (Zinc finger protein 26	1.03	0.14	-1.09	0.25	-1.41	0.062	-1.55	0.043	-0.76
1417966_at	Mrpl39	mitochondrial ribosomal protein L39	-1.17	0.294	-1.38	0.034	1.07	0.615	-1.19	0.144	-0.67
1459728_at	5830446M03Rik	RIKEN cDNA 5830446M03 gene	-1.2	0.504	1.04	0.74	-1.29	0.29	-1.01	0.943	-0.61
1435170_at	Tsr2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	-1.19	0.501	-1.24	0.434	1.01	0.977	-1.07	0.84	-0.62
1425095_at	BC002059	cDNA sequence BC002059	-1.28	0.245	-1.22	0.264	1.05	0.463	-1.21	0.046	-0.66
1448547_at	Rassf3	Ras association (RalGDS/AF-6) domain family 3	-1.16	0.217	-1.26	0.148	1	0.999	-1.34	0.196	-0.69
1454790_at	Wdr35	WD repeat domain 35	-1.08	0.201	-1.32	0.479	-1.03	0.768	1.12	0.616	-0.58
1431063_at	---	---	-1.13	0.621	-1.14	0.716	-1.12	0.622	1.14	0.258	-0.56

1456579_x_at	1200003M09Rik	RIKEN cDNA 1200003M09 gene	-1.47	0.115	1.14	0.755	-1.21	0.417	-1.06	0.898	-0.65
1420222_at	---	---	-1.86	0.564	1.4	0.577	-1.4	0.456	-1.97	0.348	-0.96
1432771_at	Slc9a3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	-1.99	0.093	-1.74	0.17	1.58	0.09	-1.11	0.847	-0.82
1452255_at	Fbxo38	F-box protein 38	-1.25	0.137	-1.18	0.4	1.01	0.963	-1.11	0.51	-0.63
1428196_a_at	1200015F23Rik	RIKEN cDNA 1200015F23 gene	-1.12	0.158	-1.11	0.021	-1.16	0.218	1.34	0.454	-0.51
1445867_at	AL023008	expressed sequence AL023008	-1.01	0.779	1.02	0.805	-1.56	0.016	-1.57	0.038	-0.78
1454976_at	Sod2	superoxide dismutase 2, mitochondrial	-1.19	0.448	-1.06	0.706	-1.14	0.332	1.4	0.219	-0.5
1435576_at	AW413774	expressed sequence AW413774	-1.04	0.786	-1.19	0.189	-1.17	0.413	1.03	0.901	-0.59
1435135_at	Aadacl1	arylacetamide deacetylase-like 1	1.06	0.211	-1.41	0.049	-1.13	0.204	-1.6	0.123	-0.77
1449565_at	Cyp2g1	cytochrome P450, family 2, subfamily g, polypeptide 1	-1.92	0.241	-1.4	0.331	1.42	0.323	-1.1	0.867	-0.75
1455608_at	Sclt1	sodium channel and clathrin linker 1	-1.29	0.275	-1.19	0.104	1.04	0.735	-1.2	0.206	-0.66
1443954_at	Rad18	RAD18 homolog (S. cerevisiae)	-1.04	0.872	-1.1	0.768	-1.28	0.383	1.18	0.478	-0.56
1425197_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	-1.21	0.524	-1.08	0.868	-1.11	0.448	1.31	0.306	-0.52
1436326_at	Rora	RAR-related orphan receptor alpha	1.17	0.174	-1.26	0.051	-1.44	0.037	-1.3	0.331	-0.71
1442442_at	Thoc7	THO complex 7 homolog (Drosophila)	-1.29	0.403	-1.16	0.543	1.02	0.847	-1.01	0.877	-0.61
1424623_at	Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	1.07	0.816	-1.13	0.804	-1.44	0.199	-1.82	0.236	-0.83
1439758_at	Als2cr12	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (hum	-1.26	0.232	1.22	0.597	-1.56	0.156	-1.37	0.271	-0.74
1450953_at	Wdr39	WD repeat domain 39	-1.27	0.092	-1.24	0.094	1.06	0.485	-1.06	0.514	-0.63
1443163_at	Slc39a2	solute carrier family 39 (zinc transporter), member 2	-1.13	0.826	-1.38	0.079	1.04	0.85	-1.13	0.885	-0.65
1417573_at	2010311D03Rik	RIKEN cDNA 2010311D03 gene	-1.09	0.283	-1.18	0.015	-1.12	0.182	1.29	0.362	-0.53
1454988_s_at	Rab22a	RAB22A, member RAS oncogene family	-1.08	0.733	-1.06	0.821	-1.27	0.46	1.02	0.919	-0.6
1445677_x_at	Slc35f2	solute carrier family 35, member F2	-1.23	0.778	1.02	0.943	-1.22	0.499	-1.15	0.757	-0.64
1430723_at	Pdss2	prenyl (solanesyl) diphosphate synthase, subunit 2	1.25	0.237	-1.4	0.525	-1.44	0.416	-2.08	0.453	-0.92
1456932_at	B430201F14	Hypothetical protein B430201F14	-1.4	0.507	-1.14	0.837	1.06	0.723	-2.69	0.04	-1.04
1422443_at	Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-1.11	0.352	-1.21	0.026	-1.07	0.47	1.7	0.297	-0.43
1431959_x_at	Psg21	pregnancy-specific glycoprotein 21	-1.45	0.105	1.04	0.918	-1.08	0.83	-1.34	0.259	-0.71
1430627_at	5330420P17Rik	RIKEN cDNA 5330420P17 gene	1	0.989	-1.23	0.437	-1.19	0.461	-1.47	0.197	-0.72
1434435_s_at	Cox17	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	-1.11	0.037	-1.02	0.895	-1.3	0.056	1.22	0.319	-0.55
1439968_x_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.18	0.816	-1.41	0.657	-1.3	0.206	-1.26	0.292	-0.7
1442786_s_at	Rufy3	RUN and FYVE domain containing 3	-1.31	0.032	-1.08	0.631	-1.03	0.934	1.09	0.852	-0.58
1447085_s_at	Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	-1.25	0.469	-1.36	0.316	1.12	0.636	-1.34	0.142	-0.71
1428314_at	Pcnp	PEST proteolytic signal containing nuclear protein	-1	0.929	-1.24	0.157	-1.17	0.149	1.09	0.471	-0.58
1457202_at	---	---	-1.54	0.191	-2.14	0.18	1.54	0.429	-1.02	0.953	-0.79
1442622_at	Strbp	Spermatid perinuclear RNA binding protein	1.07	0.649	-1.07	0.603	-1.52	0.064	-2.3	0.063	-0.96
1451995_at	Taf11	TAF11 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.05	0.828	-1.3	0.137	-1.08	0.732	1.09	0.716	-0.58
1433442_at	Klhl9	Kelch-like 9 (Drosophila)	-1.03	0.827	1.03	0.738	-1.53	0	-1.13	0.554	-0.66
1455612_at	AI848218	expressed sequence AI848218	-1.17	0.448	-1.18	0.542	-1.05	0.845	1.33	0.461	-0.52
1456749_at	---	Transcribed locus	1.32	0.177	-1.33	0.57	-1.7	0.248	-1.93	0.306	-0.91
1434978_at	4933403F05Rik	RIKEN cDNA 4933403F05 gene	-1.06	0.717	-1.1	0.502	-1.25	0.191	1.32	0.482	-0.52
1435079_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	-1.15	0.41	1.05	0.719	-1.36	0.06	-1.22	0.258	-0.67
1429218_at	Det1	de-etiolated homolog 1 (Arabidopsis)	-1.43	0.155	-1.21	0.287	1.13	0.477	-1.13	0.355	-0.66
1446075_at	---	---	-1.03	0.882	-1.04	0.892	-1.38	0.024	1.5	0.134	-0.49
1440522_at	B930075F07	hypothetical protein B930075F07	-1.21	0.045	-1.02	0.891	-1.17	0.411	1.09	0.568	-0.58
1433910_at	Zcchc6	zinc finger, CCHC domain containing 6	-1.05	0.292	-1.12	0.139	-1.23	0.035	1.31	0.229	-0.52
1447060_at	Smyd3	SET and MYND domain containing 3	-1.28	0.225	1.05	0.68	-1.21	0.417	-1.73	0.043	-0.79
1437510_x_at	Rps17	ribosomal protein S17	-1.11	0.086	1.03	0.61	-1.38	0.018	-1.39	0.02	-0.71
1430425_at	Sdk2	sidekick homolog 2 (chicken)	1.07	0.751	-1.22	0.456	-1.31	0.334	-1.05	0.22	-0.63
1451558_at	Fbxw7	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	-1.14	0.28	-1.04	0.806	-1.22	0.295	1.09	0.143	-0.58
1426488_at	Bfar	bifunctional apoptosis regulator	1	0.997	-1.03	0.707	-1.45	0.012	-1.23	0.305	-0.68
1429191_at	Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	-1.18	0.088	-1.41	0.041	1.1	0.678	-1.1	0.298	-0.65
1446816_at	---	Transcribed locus	1.4	0.706	-1.48	0.536	-1.71	0.223	-1.18	0.623	-0.74
1455632_at	Gnb5	Guanine nucleotide binding protein, beta 5	-1.03	0.914	1.16	0.586	-1.9	0.09	-1.87	0.385	-0.91
1458696_at	Actr1a	ARP1 actin-related protein 1 homolog A (yeast)	-1.3	0.505	-2.68	0.225	1.52	0.2	-1.59	0.445	-1.02

1449723_at	Serpinb6e	serine (or cysteine) peptidase inhibitor, clade B, member 6e	1.22	0.667	-1.31	0.405	-1.47	0.09	-2.21	0.364	-0.94
1439068_at	Arts1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	1.03	0.908	-1.09	0.21	-1.4	0.011	-1.31	0.08	-0.69
1449880_s_at	Bglap-rs1 /// Bglap1	bone gamma-carboxyglutamate protein, related sequence 1 /// bone gamma carb	-1.07	0.784	-1.17	0.442	-1.16	0.205	1.58	0.29	-0.45
1422665_a_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	-1.02	0.906	-1.01	0.956	-1.47	0.066	1.15	0.509	-0.59
1456382_at	Atad1	ATPase family, AAA domain containing 1	-1.03	0.864	-1.1	0.829	-1.28	0.478	1.07	0.873	-0.59
1452994_at	Pip5k3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	-1.39	0.133	1.07	0.123	-1.15	0.378	-1.29	0.417	-0.69
1451621_at	5830417C01Rik	RIKEN cDNA 5830417C01 gene	-1.06	0.769	1.04	0.893	-1.47	0.064	-1.24	0.403	-0.68
1428256_at	2310047H23Rik	RIKEN cDNA 2310047H23 gene	1.02	0.634	-1.19	0.017	-1.25	0.106	-1.37	0.217	-0.7
1425033_at	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	1.18	0.398	-1.39	0.004	-1.32	0.364	-1.15	0.119	-0.67
1459946_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933015	-1.13	0.838	1.08	0.876	-1.44	0.212	-1.51	0.589	-0.75
1452505_at	Lamc2	laminin, gamma 2	1.44	0.689	-1.6	0.406	-1.7	0.431	-1.04	0.947	-0.72
1431886_at	Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	1.12	0.146	-1.27	0.665	-1.34	0.151	-1.26	0.658	-0.68
1432905_at	3110037C07Rik	RIKEN cDNA 3110037C07 gene	1.04	0.945	-1.42	0.559	-1.09	0.778	-1.55	0.246	-0.76
1456336_at	A330102K23Rik	RIKEN cDNA A330102K23 gene	-1.12	0.49	-1.31	0.752	1	0.991	-2.29	0.252	-0.93
1432153_at	4933426B08Rik	RIKEN cDNA 4933426B08 gene	1.04	0.523	-1.24	0.399	-1.23	0.499	-1.38	0.52	-0.7
1419110_at	Riok1	RIO kinase 1 (yeast)	-1.17	0.546	-1.2	0.401	-1.03	0.698	1.11	0.226	-0.57
1458327_x_at	Slc26a1	solute carrier family 26 (sulfate transporter), member 1	-1.16	0.66	-1.15	0.512	-1.08	0.91	3.72	0.041	0.08
1436780_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:p	1.13	0.785	-1.03	0.9	-1.81	0.081	-1.02	0.966	-0.68
1437885_at	D030029J20Rik	RIKEN cDNA D030029J20 gene	-1.09	0.528	1.03	0.721	-1.4	0.142	-1.06	0.827	-0.63
1426965_at	Rap2a	RAS related protein 2a	1.03	0.728	-1.34	0.193	-1.14	0.517	-1.1	0.557	-0.64
1455080_at	Ppp1r16b	protein phosphatase 1, regulatory (inhibitor) subunit 16B	1.1	0.795	-1.35	0.274	-1.23	0.308	-1.26	0.351	-0.68
1438407_at	9330132E09Rik	RIKEN cDNA 9330132E09 gene	-1.17	0.605	1.2	0.339	-1.66	0.011	-1.22	0.396	-0.71
1418158_at	Trp63	transformation related protein 63	-1.18	0.617	1.13	0.594	-1.46	0.289	-1.53	0.318	-0.76
1434924_at	Phf2	PHD finger protein 2	-1.06	0.658	-1.45	0.053	1.03	0.917	-1.1	0.648	-0.65
1455677_s_at	Clcnka /// LOC639(	chloride channel Ka /// similar to Chloride channel protein ClC-Ka (Chloride chanr	1.29	0.336	-1.26	0.759	-1.72	0.097	-1.49	0.486	-0.8
1437486_at	Gprc5a	G protein-coupled receptor, family C, group 5, member A	-1.07	0.571	-1.16	0.672	-1.15	0.288	1.43	0.538	-0.49
1416997_a_at	Hap1	huntingtin-associated protein 1	-1.26	0.626	-1.43	0.203	1.17	0.345	-1.17	0.722	-0.67
1442473_at	---	---	1.21	0.416	-1.25	0.276	-1.53	0.018	-1.57	0.393	-0.79
1446010_at	LOC668019 /// LOC	similar to F-box only protein 34 /// similar to F-box only protein 34 /// similar to F-b	1.12	0.909	-1.7	0.189	-1.05	0.898	-1.44	0.714	-0.77
1438159_x_at	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	1.02	0.806	-1.33	0.115	-1.13	0.631	-1.6	0.269	-0.76
1445349_at	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030049A20	1.26	0.669	-2.27	0.285	-1.04	0.922	-1.1	0.89	-0.79
1422636_at	Dmtf1	cyclin D binding myb-like transcription factor 1	-1.33	0.118	1.13	0.361	-1.28	0.011	-1.55	0.074	-0.76
1445541_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	-1.71	0.64	1.33	0.657	-1.34	0.298	-1.3	0.23	-0.75
1434518_at	Phka2	phosphorylase kinase alpha 2	-1.22	0.002	-1.1	0.161	-1.07	0.661	1.17	0.196	-0.56
1422032_a_at	Zfand6	zinc finger, AN1-type domain 6	-1.07	0.437	-1.3	0.006	-1.04	0.529	1.32	0.205	-0.52
1426976_at	Usp47	ubiquitin specific peptidase 47	-1.12	0.356	-1.05	0.389	-1.23	0.034	1.24	0.234	-0.54
1453373_at	6330532G10Rik	RIKEN cDNA 6330532G10 gene	1.29	0.732	-2.16	0.224	-1.11	0.82	-1.29	0.703	-0.82
1419693_at	Colec12	collectin sub-family member 12	1.05	0.82	-1.03	0.771	-1.56	0.054	-1.06	0.87	-0.65
1433585_at	Tnpo1	transportin 1	-1.17	0.292	1.03	0.742	-1.29	0.115	-1.19	0.315	-0.65
1437896_at	Zcrb1	Zinc finger CCHC-type and RNA binding motif 1	-1.19	0.549	-1.03	0.779	-1.18	0.466	1.15	0.434	-0.56
1440948_at	Frk	Fyn-related kinase	-1.4	0.088	-1.19	0.54	1.11	0.716	-1.37	0.426	-0.71
1449883_at	Fxyd2	FXYD domain-containing ion transport regulator 2	1.01	0.975	-1.15	0.252	-1.28	0.349	-1.21	0.752	-0.66
1425893_a_at	Fhit	fragile histidine triad gene	-1.23	0.204	-1.28	0.326	1.06	0.847	-1.21	0.35	-0.66
1433268_at	4930553M12Rik	RIKEN cDNA 4930553M12 gene	-3.01	0.012	-1.29	0.3	1.55	0.422	-1.2	0.812	-0.99
1457631_at	2310047N11Rik	RIKEN cDNA 2310047N11 gene	1.12	0.857	-1.11	0.831	-1.56	0.012	-1.83	0.288	-0.84
1418128_at	Adcy6	adenylate cyclase 6	-1.13	0.338	-1.26	0.388	-1.02	0.936	2.71	0.256	-0.17
1432246_at	4922502N22Rik	RIKEN cDNA 4922502N22 gene	1.35	0.761	-1.88	0.211	-1.28	0.624	-1.57	0.512	-0.85
1444417_at	9330101J02Rik /// I	RIKEN cDNA 9330101J02 gene /// similar to Protein C10orf93 /// similar to Protei	-1.26	0.689	-1.5	0.406	1.2	0.563	-1.15	0.772	-0.68
1429335_at	Snapc1	small nuclear RNA activating complex, polypeptide 1	-1.4	0.312	1.09	0.535	-1.16	0.1	-1.55	0.126	-0.76
1437047_at	Zfp664	zinc finger protein 664	1.21	0.694	-1.11	0.67	-1.84	0.238	-1.46	0.461	-0.8
1457269_at	Gm1123 /// LOC67	gene model 1123, (NCBI) /// similar to coxsackie-adenovirus receptor-like	-1.26	0.305	1.02	0.954	-1.18	0.712	-1.02	0.955	-0.61
1455765_a_at	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-1.34	0.489	-1.51	0.385	1.25	0.337	-1.62	0.298	-0.81
1416958_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	1	0.995	-1.16	0.618	-1.26	0.521	-1.12	0.837	-0.63

1435711_at	---	---	-1.24	0.066	-1.09	0.684	-1.07	0.733	1.14	0.652	-0.56
1451455_at	BC051244	cDNA sequence BC051244	-1.3	0.201	-1.1	0.641	-1.02	0.89	1.47	0.589	-0.49
1452619_a_at	Agbl3	ATP/GTP binding protein-like 3	-1.01	0.943	-1.26	0.541	-1.14	0.68	1.31	0.441	-0.52
1454680_at	D5Ertd579e	DNA segment, Chr 5, ERATO Doi 579, expressed	-1.05	0.79	-1.2	0.237	-1.14	0.267	1.64	0.151	-0.44
1416285_at	Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	-1.11	0.143	-1.16	0.014	-1.11	0.168	1.17	0.473	-0.55
1458575_at	Setbp1	SET binding protein 1	-1.04	0.889	1.14	0.436	-1.8	0.02	-1.22	0.68	-0.73
1452615_s_at	Trpt1	tRNA phosphotransferase 1	-1.07	0.15	-1.07	0.701	-1.26	0.007	1.18	0.06	-0.56
1425341_at	Kcnk3	potassium channel, subfamily K, member 3	-2.1	0.205	-1.06	0.894	1.24	0.317	-1.65	0.031	-0.89
1416770_at	Stk25	serine/threonine kinase 25 (yeast)	-1.04	0.818	-1.07	0.64	-1.31	0.251	1.19	0.402	-0.56
1452639_at	Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-1.46	0.545	1.02	0.949	-1.04	0.895	-1.22	0.577	-0.68
1442314_at	Nup188	nucleoporin 188	-1.2	0.486	-1.09	0.684	-1.1	0.778	1.46	0.118	-0.48
1421868_a_at	Pnlip	pancreatic lipase	-1.22	0.113	-1.5	0.356	1.18	0.786	-1.34	0.258	-0.72
1444765_at	Rbpms	RNA binding protein gene with multiple splicing	-1.08	0.664	1.13	0.656	-1.64	0.164	-2.32	0.156	-0.98
1441866_s_at	Ptdss1	phosphatidylserine synthase 1	-1.11	0.197	-1.1	0.394	-1.17	0.127	1.06	0.391	-0.58
1433513_x_at	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	-1.13	0.217	-1.25	0.01	-1.03	0.474	1.2	0.123	-0.55
1434876_at	Glt8d3	glycosyltransferase 8 domain containing 3	1.01	0.916	-1.06	0.476	-1.42	0.031	-1.3	0.106	-0.69
1433902_at	Kbtbd8	kelch repeat and BTB (POZ) domain containing 8	-1.15	0.054	-1.17	0.369	-1.07	0.551	1.08	0.775	-0.58
1458576_at	Nat11	N-acetyltransferase 11	1.11	0.665	-1.41	0.573	-1.19	0.684	-1.2	0.681	-0.67
1424970_at	Purg	purine-rich element binding protein G	-1.05	0.532	-1.09	0.581	-1.25	0.066	1.16	0.455	-0.56
1417147_at	B230317C12Rik	RIKEN cDNA B230317C12 gene	-1.09	0.738	-1.14	0.788	-1.15	0.318	1.08	0.845	-0.58
1460163_at	C1qtnf7	C1q and tumor necrosis factor related protein 7	-1.04	0.736	1.14	0.171	-1.79	0.019	-1.84	0.215	-0.88
1425691_at	B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-1.07	0.93	-1.41	0.65	1.02	0.975	-1.27	0.775	-0.68
1437342_x_at	Pttg1ip	pituitary tumor-transforming 1 interacting protein	1.01	0.933	-1.27	0.072	-1.15	0.395	-1.13	0.248	-0.64
1424807_at	Lama4	laminin, alpha 4	-1.02	0.961	1.07	0.884	-1.63	0.009	-2.03	0.007	-0.9
1441484_at	Tcf2	Transcription factor 2	-1.19	0.234	1.05	0.91	-1.29	0.334	-1.88	0.102	-0.83
1457288_at	Ank3	ankyrin 3, epithelial	-1.15	0.54	1.31	0.446	-2.09	0.142	-1.5	0.335	-0.86
1418973_at	Blzf1	basic leucine zipper nuclear factor 1	-1.08	0.484	-1.04	0.821	-1.29	0.259	1.12	0.542	-0.57
1453027_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	-1.18	0.25	1.3	0.509	-1.95	0.247	-1.14	0.542	-0.74
1425375_at	Tdpoz1	TD and POZ domain containing 1	-1.45	0.135	-1.05	0.926	1.02	0.953	-1.18	0.789	-0.67
1417975_at	Kpna4	karyopherin (importin) alpha 4	-1.14	0.64	1.02	0.971	-1.3	0.563	-1.59	0.279	-0.75
1433735_a_at	Tmem64	transmembrane protein 64	-1.61	0.181	-1.05	0.799	1.08	0.612	-1.05	0.778	-0.65
1433759_at	Dpy19l1	dpy-19-like 1 (C. elegans)	-1.12	0.137	-1.25	0.155	-1.03	0.833	1.05	0.734	-0.59
1439950_at	Dync1h1	dynein cytoplasmic 1 heavy chain 1	1.14	0.375	-1.32	0.203	-1.31	0.535	-1.07	0.742	-0.64
1424154_a_at	Hbld1	HESB like domain containing 1	-1.09	0.288	-1.16	0.122	-1.13	0.327	1.44	0.384	-0.49
1448860_at	Rem2	rad and gem related GTP binding protein 2	-1.73	0.272	1.23	0.453	-1.16	0.595	-1.04	0.884	-0.68
1439273_at	Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	1	0.989	-1.1	0.568	-1.32	0.008	-1.03	0.851	-0.62
1447393_at	---	PREDICTED: Mus musculus hypothetical LOC434436 (LOC434436), mRNA	-1.06	0.252	-1.23	0.636	-1.1	0.851	2.59	0.108	-0.2
1436130_s_at	4930523C11Rik ///	RIKEN cDNA 4930523C11 gene /// a disintegrin and metallopeptidase domain 6	-1.11	0.876	-1.98	0.224	1.26	0.665	-1.22	0.417	-0.76
1433889_at	Sox9	SRY-box containing gene 9	1.07	0.893	-1.37	0.626	-1.16	0.758	-2.41	0.433	-0.97
1444059_at	6330415G19Rik	RIKEN cDNA 6330415G19 gene	-1.06	0.87	-2.04	0.058	1.23	0.373	-1.35	0.305	-0.8
1455625_at	---	---	-1.24	0.258	-1.08	0.326	-1.08	0.379	1.04	0.823	-0.59
1453352_at	9030605H24Rik	RIKEN cDNA 9030605H24 gene	1.06	0.903	-1.01	0.964	-1.64	0.333	-1.62	0.365	-0.8
1441409_at	Gnn	Grp94 neighboring nucleotidase variant 4	-1.24	0.652	-1.07	0.826	-1.08	0.48	1.42	0.356	-0.49
1417434_at	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	-1.14	0.641	-1.55	0.101	1.14	0.54	-1.3	0.316	-0.71
1438866_at	Grin3a	glutamate receptor ionotropic, NMDA3A	-1.47	0.586	1.17	0.849	-1.23	0.583	-1.77	0.141	-0.83
1416070_a_at	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	1.07	0.707	-1.27	0.004	-1.23	0.09	-1.47	0.033	-0.73
1449934_at	Pura	purine rich element binding protein A	1.04	0.794	-1.2	0.022	-1.27	0.101	-1.05	0.839	-0.62
1459962_at	4930523C07Rik	RIKEN cDNA 4930523C07 gene	1.16	0.154	-1.1	0.745	-1.67	0.027	-2.45	0.021	-1.02
1448586_at	Hspa14	heat shock protein 14	-1.11	0.254	-1.16	0.246	-1.11	0.15	1.1	0.704	-0.57
1449474_a_at	Nelf	nasal embryonic LHRH factor	-1.15	0.291	-1.07	0.588	-1.16	0.325	1.02	0.708	-0.59
1440917_at	2900093K20Rik	RIKEN cDNA 2900093K20 gene	1.09	0.178	-1.27	0.341	-1.28	0.264	-2.27	0.033	-0.93
1440459_at	Setx	senataxin	-1.08	0.702	1.04	0.882	-1.44	0.078	-1.12	0.499	-0.65
1435890_at	5730596K20Rik	RIKEN cDNA 5730596K20 gene	-1.17	0.017	-1.08	0.135	-1.13	0.132	1.03	0.832	-0.59

1429742_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	-1.09	0.854	-1.5	0.522	1.08	0.886	-1.03	0.937	-0.63
1445430_at	Arhgap28	Rho GTPase activating protein 28	-1.11	0.065	1.02	0.66	-1.33	0.461	-1.34	0.244	-0.69
1437083_at	A830020B06Rik	RIKEN cDNA A830020B06 gene	-2.03	0.053	1.4	0.55	-1.3	0.671	-1.22	0.771	-0.79
1436149_at	Cox5b	cytochrome c oxidase, subunit Vb	-1.03	0.87	-1.49	0.119	1.02	0.906	-1.06	0.734	-0.64
1434836_at	Nfatc2ip	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interactir	-1.08	0.541	-1.25	0.129	-1.06	0.3	1.09	0.623	-0.58
1454108_at	4930524O08Rik	RIKEN cDNA 4930524O08 gene	-1.51	0.413	1.29	0.712	-1.4	0.445	-1.1	0.863	-0.68
1419547_at	Fahd1	fumarylacetoacetate hydrolase domain containing 1	-1.07	0.173	-1.35	0.051	-1.01	0.931	3.72	0.202	0.07
1427543_s_at	Ube1y1	ubiquitin-activating enzyme E1, Chr Y 1	-1.52	0.107	-1.17	0.501	1.15	0.651	-1.09	0.766	-0.65
1458484_at	A730020M07Rik	RIKEN cDNA A730020M07 gene	-1.3	0.164	-1.53	0.222	1.24	0.369	-1.46	0.034	-0.76
1456161_at	0610040B10Rik	RIKEN cDNA 0610040B10 gene	-1.06	0.82	-1.45	0.181	1.03	0.688	-1.09	0.857	-0.64
1457479_at	---	---	-1.55	0.053	1.3	0.028	-1.39	0.195	-1.77	0.1	-0.85
1443230_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	1.17	0.247	-1.12	0.844	-1.66	0.102	-1.18	0.479	-0.7
1450770_at	3632451O06Rik	RIKEN cDNA 3632451O06 gene	-1.31	0.546	-1.07	0.865	-1.04	0.861	1.63	0.484	-0.45
1458179_at	---	---	1.74	0.314	-1.72	0.108	-2.92	0.034	-1.11	0.785	-1
1445684_s_at	Hdac2	histone deacetylase 2	-1.08	0.177	-1.03	0.701	-1.3	0.014	1.26	0.148	-0.54
1429771_at	3110073H01Rik	RIKEN cDNA 3110073H01 gene	1.05	0.392	-1.07	0.192	-1.47	0	-1.01	0.929	-0.63
1444140_at	---	---	1.61	0.153	-1.71	0.264	-2.11	0.044	-1.02	0.943	-0.81
1430753_at	8030491N06Rik	RIKEN cDNA 8030491N06 gene	-1.48	0.367	1.16	0.52	-1.21	0.419	-1.28	0.575	-0.7
1421222_at	Fip1l1	FIP1 like 1 (S. cerevisiae)	-1.39	0.603	-1.24	0.498	1.14	0.663	-1.17	0.327	-0.66
1439631_at	---	---	-1.09	0.679	1.04	0.622	-1.41	0.042	-2.13	0.065	-0.9
1436498_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	-1.37	0.34	-1.28	0.141	1.16	0.566	-1.34	0.291	-0.71
1431154_at	Znrf2	zinc and ring finger 2	-1.28	0.522	1	0.99	-1.13	0.432	-1.21	0.557	-0.66
1451370_at	LOC622404	hypothetical protein LOC622403	1.02	0.849	-1.32	0.092	-1.12	0.235	-1.3	0.042	-0.68
1460171_at	Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (Arabidopsis thaliana)	-1.07	0.789	-1.13	0.282	-1.18	0.411	1.19	0.566	-0.55
1433789_at	Snhg3 /// LOC6704	small nucleolar RNA host gene (non-protein coding) 3 /// similar to RNA, U17d sn	-1.04	0.649	-1.2	0.678	-1.15	0.624	1.18	0.576	-0.55
1428100_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	-1.35	0.139	-1.03	0.781	-1.05	0.696	1.04	0.891	-0.6
1433243_at	2810421E14Rik	RIKEN cDNA 2810421E14 gene	1.01	0.929	-1.27	0.651	-1.15	0.72	-1.05	0.929	-0.62
1447026_at	Mas1	MAS1 oncogene	1.35	0.192	-1.48	0.073	-1.54	0.011	-1.16	0.591	-0.71
1456999_at	Wipi2	WD repeat domain, phosphoinositide interacting 2	-1.27	0.221	-1.03	0.887	-1.1	0.606	1.49	0.345	-0.48
1459583_at	Grip1	Glutamate receptor interacting protein 1	-1.14	0.408	1.15	0.511	-1.58	0.363	-1.13	0.438	-0.67
1434244_x_at	Htf9c	HpaII tiny fragments locus 9c	-1.48	0.043	1.04	0.512	-1.05	0.64	-1.3	0.007	-0.7
1436514_at	Gpc4	glypican 4	-1.1	0.61	-1.22	0.083	-1.07	0.79	1.26	0.643	-0.53
1458418_at	---	Mus musculus, clone IMAGE:5368497, mRNA	-1.2	0.415	-1.32	0.117	1.08	0.871	-1.91	0.23	-0.84
1457085_at	LOC665934 /// LOC	hypothetical protein LOC665934 /// hypothetical protein LOC669392 /// hypothetic	1.05	0.841	-1.34	0.546	-1.15	0.7	-1.23	0.159	-0.67
1418954_at	Camkk1	calcium/calmodulin-dependent protein kinase kinase 1, alpha	-1.36	0.635	-1.03	0.908	-1.04	0.77	1.08	0.749	-0.59
1416652_at	Aspn	asporin	1.06	0.842	-1.49	0.145	-1.06	0.876	-2.12	0.212	-0.91
1426919_at	---	---	-1.56	0.401	1.23	0.485	-1.26	0.313	-1.05	0.91	-0.66
1447786_at	Pscd1	pleckstrin homology, Sec7 and coiled-coil domains 1	-1.25	0.731	1.1	0.774	-1.31	0.56	-1.03	0.867	-0.62
1418388_s_at	4930548G07Rik	RIKEN cDNA 4930548G07 gene	1.02	0.881	-1.08	0.584	-1.4	0.096	-1.25	0.079	-0.68
1435388_at	Ndor1	NADPH dependent diflavin oxidoreductase 1	1.27	0.398	-1.57	0.115	-1.31	0.309	-1.06	0.639	-0.67
1416946_a_at	Acaa1a /// Acaa1b	acetyl-Coenzyme A acyltransferase 1A /// acetyl-Coenzyme A acyltransferase 1B	-1	0.99	-1.74	0.232	1.1	0.271	-1.5	0.044	-0.79
1454864_at	Zfp592	zinc finger protein 592	1.01	0.98	-1.29	0.017	-1.13	0.437	-1.15	0.517	-0.64
1459445_at	---	---	1.04	0.917	-1.3	0.674	-1.16	0.662	-3.96	0.324	-1.35
1430895_at	2010109A12Rik	RIKEN cDNA 2010109A12 gene	-1.02	0.953	-1.51	0.196	1.03	0.86	-1.38	0.042	-0.72
1427553_at	LOC628926	hypothetical protein LOC628926	-1.34	0.61	-2.65	0.217	1.54	0.114	-1.5	0.399	-0.99
1442044_at	---	Transcribed locus	1.06	0.799	-1.19	0.565	-1.3	0.263	-1.75	0.085	-0.79
1453407_at	1700018L24Rik	RIKEN cDNA 1700018L24 gene	-1.27	0.295	-1.36	0.433	1.14	0.341	-1.02	0.965	-0.63
1442910_at	AL033314	Expressed sequence AL033314	1.51	0.554	-2.31	0.064	-1.37	0.364	-2.53	0.17	-1.17
1442967_at	AU020147	expressed sequence AU020147	-1.03	0.909	1.02	0.967	-1.49	0.402	-1.08	0.776	-0.64
1442348_at	---	---	-1.09	0.618	-1.23	0.237	-1.07	0.616	1.87	0.259	-0.38
1418308_at	Hus1	Hus1 homolog (S. pombe)	-1.09	0.598	-1.05	0.719	-1.25	0.149	1.18	0.297	-0.55
1434549_at	---	---	-1.05	0.63	-1.05	0.735	-1.32	0.007	1.04	0.868	-0.59
1429665_at	6230416J20Rik	RIKEN cDNA 6230416J20 gene	-1	0.965	-1.04	0.89	-1.4	0.103	1.13	0.68	-0.58

1431477_at	4921515L22Rik	RIKEN cDNA 4921515L22 gene	-2.39	0.517	-1.21	0.718	1.42	0.217	-1.02	0.94	-0.8
1423709_s_at	Farslb	phenylalanine-tRNA synthetase-like, beta subunit	-1.03	0.741	-1.13	0.068	-1.24	0.132	1.01	0.979	-0.6
1453684_s_at	2610312B22Rik	RIKEN cDNA 2610312B22 gene	1	0.988	-1.18	0.187	-1.22	0.115	-1.37	0.448	-0.69
1449063_at	Sec22b	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	-1.19	0.062	1	0.995	-1.21	0.112	-1.15	0.369	-0.64
1457532_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.29	0.585	1.15	0.555	-1.34	0.405	-1.59	0.04	-0.77
1458463_at	---	---	-2.11	0.166	1.82	0.15	-2.67	0.176	-1.97	0.56	-1.23
1446280_at	Foxp1	Forkhead box P1	1.14	0.261	-1.07	0.636	-1.7	0.085	-2.02	0.121	-0.91
1438291_x_at	Rpl37 /// LOC38343	ribosomal protein L37 /// similar to ribosomal protein L37	-1.13	0.665	1.05	0.656	-1.36	0.005	-2.93	0.26	-1.09
1450702_at	Hfe	hemochromatosis	-1.18	0.642	1.14	0.197	-1.47	0.03	-1.05	0.77	-0.64
1424521_at	Zfand2b	zinc finger, AN1 type domain 2B	-1.18	0.073	-1.09	0.16	-1.11	0.456	1.29	0.385	-0.52
1425557_x_at	Tsc22d3	TSC22 domain family 3	1	0.997	-1.17	0.419	-1.23	0.479	-1.2	0.215	-0.65
1457574_at	LOC635668 /// LOC	similar to F-box and WD-40 domain protein FBXW14 /// similar to F-box and WD-	1.03	0.937	-1.04	0.807	-1.48	0.364	-1.42	0.499	-0.73
1443250_at	---	---	-1.34	0.496	1.25	0.595	-1.48	0.336	-1.59	0.346	-0.79
1441885_s_at	---	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:95300	1.37	0.661	-1.7	0.424	-1.41	0.428	-1.56	0.515	-0.82
1449523_at	Bcl7c	B-cell CLL/lymphoma 7C	-1.25	0.113	-1.03	0.702	-1.11	0.502	1.03	0.905	-0.59
1432445_at	2310016G11Rik	RIKEN cDNA 2310016G11 gene	1.05	0.869	-1.26	0.648	-1.21	0.456	-1.07	0.762	-0.62
1427123_s_at	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2	-1.04	0.907	1.22	0.129	-2.05	0.006	-1.89	0.206	-0.94
1448085_at	D5Ertd102e	DNA segment, Chr 5, ERATO Doi 102, expressed	1.27	0.535	-1.11	0.789	-1.97	0.245	-1.13	0.673	-0.74
1435718_at	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	-1.26	0.25	-1.18	0.382	1.03	0.928	-1.02	0.948	-0.61
1434503_s_at	Lamp2	lysosomal membrane glycoprotein 2	-1.01	0.968	-1.01	0.936	-1.46	0.109	1.1	0.59	-0.59
1449213_at	Lage3	L antigen family, member 3	1.03	0.883	-1.19	0.194	-1.25	0.052	-1.31	0.311	-0.68
1455047_at	Fbxo3	F-box only protein 3	-1.18	0.173	-1.04	0.454	-1.15	0.126	1.94	0.245	-0.36
1433111_at	Nhsl1	NHS-like 1	-1.72	0.021	1.16	0.704	-1.07	0.808	-1.02	0.964	-0.66
1435058_x_at	Stxbp3a	syntaxin binding protein 3A	-1.94	0.156	1.22	0.479	-1.07	0.743	-1.28	0.331	-0.77
1458039_at	Ncoa3	Nuclear receptor coactivator 3	-1.09	0.236	1.24	0.606	-1.95	0.013	-3.01	0.028	-1.2
1423042_at	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	-1.11	0.377	1.04	0.396	-1.38	0.011	-1.11	0.542	-0.64
1454226_at	4931403M11Rik	RIKEN cDNA 4931403M11 gene	-1.34	0.557	1.32	0.65	-1.65	0.467	-1.03	0.934	-0.68
1423236_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.04	0.319	-1.08	0.126	-1.29	0.021	1.25	0.186	-0.54
1441992_at	Rab14	RAB14, member RAS oncogene family	1.09	0.794	-1.06	0.866	-1.58	0.051	-1.23	0.563	-0.69
1426461_at	Ugp2	UDP-glucose pyrophosphorylase 2	-1.15	0.143	-1.32	0.262	1.04	0.734	-1.06	0.58	-0.62
1444879_at	---	PREDICTED: Mus musculus similar to long interspersed repetitive DNA sequenc	1.56	0.51	-2.38	0.354	-1.44	0.508	-2.26	0.212	-1.13
1429670_a_at	Lrriq2	leucine-rich repeats and IQ motif containing 2	-1.29	0.009	1.16	0.83	-1.35	0.239	-1.18	0.556	-0.67
1435478_at	Wdr26	WD repeat domain 26	-1.04	0.745	-1.19	0.226	-1.15	0.182	1.61	0.188	-0.44
1432955_at	4930444K16Rik	RIKEN cDNA 4930444K16 gene	-1.53	0.686	1.08	0.761	-1.07	0.866	-1.05	0.935	-0.64
1448597_at	Cstf1	cleavage stimulation factor, 3' pre-RNA, subunit 1	-1.21	0.416	-1.26	0.021	1.05	0.65	-1.02	0.919	-0.61
1442834_at	Ppp4r2	Protein phosphatase 4, regulatory subunit 2	1	0.982	-1.01	0.941	-1.48	0.014	-1.12	0.687	-0.65
1442993_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	-1.49	0.372	1.06	0.887	-1.06	0.866	-2.08	0.451	-0.89
1427143_at	Jarid1b	jumonji, AT rich interactive domain 1B (Rbp2 like)	1.02	0.903	-1.26	0.152	-1.16	0.126	-1.4	0.22	-0.7
1459634_at	A230048G03Rik	RIKEN cDNA A230048G03 gene	1.07	0.831	-1.56	0.127	-1.04	0.708	-1.5	0.411	-0.76
1420483_at	Cnnm3	cyclin M3	-1.03	0.964	-1.54	0.171	1.05	0.798	-1.17	0.366	-0.67
1418404_at	Rad9	RAD9 homolog (S. pombe)	-1.56	0.239	1.14	0.439	-1.12	0.386	-1.04	0.788	-0.65
1438785_at	Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	-1.39	0.12	1.15	0.624	-1.25	0.619	-1	0.996	-0.62
1460335_at	Lysmd3	LysM, putative peptidoglycan-binding, domain containing 3	-1.05	0.664	-1.03	0.733	-1.34	0.103	1.07	0.808	-0.59
1437507_at	Gatad2b	GATA zinc finger domain containing 2B	-1.48	0.254	-1.08	0.734	1.07	0.863	-1.6	0.142	-0.77
1416861_at	Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	-1.05	0.375	-1.03	0.511	-1.34	0.053	1.67	0.204	-0.44
1420571_at	Prlpb	prolactin-like protein B	-1.07	0.851	1.07	0.885	-1.5	0.235	-1.07	0.826	-0.64
1426460_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	-1.03	0.771	-1.33	0.358	-1.05	0.764	1.03	0.914	-0.6
1443152_at	Ptcd3	Pentatricopeptide repeat domain 3	1.2	0.648	-1.79	0.189	-1.09	0.806	-1.02	0.859	-0.68
1428194_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	-1.01	0.88	-1.1	0.028	-1.3	0.006	1.39	0.019	-0.5
1444714_at	2510006D16Rik	RIKEN cDNA 2510006D16 gene	-1.12	0.554	1.06	0.878	-1.39	0	-1.2	0.065	-0.66
1451740_at	Paip1	polyadenylate binding protein-interacting protein 1	-1.13	0.406	-1.12	0.443	-1.12	0.336	1.1	0.542	-0.57
1418658_at	2410005O16Rik	RIKEN cDNA 2410005O16 gene	-1.1	0.076	-1.33	0.043	1.02	0.911	-1.24	0.252	-0.67
1458515_at	Zfp128	zinc finger protein 128	-1.34	0.155	1.07	0.744	-1.17	0.354	-1.69	0.032	-0.78

1437323_a_at	Iapp	islet amyloid polypeptide	-1.53	0.304	1.3	0.697	-1.38	0.077	-1.19	0.142	-0.7
1452937_s_at	Ccdc28b	coiled coil domain containing 28B	-1.19	0.065	-1.33	0.25	1.08	0.722	-1.14	0.321	-0.65
1426053_a_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	-1.13	0.724	-1.08	0.882	-1.16	0.478	1.16	0.317	-0.55
1453613_at	A130006I12Rik	RIKEN cDNA A130006I12 gene	-1.5	0.348	1.27	0.524	-1.36	0.347	-1.27	0.09	-0.71
1423191_at	Fnbp4	formin binding protein 4	-1.23	0.084	-1.21	0.01	1.03	0.867	-1.23	0.42	-0.66
1426925_at	Mnab	membrane associated DNA binding protein	1.21	0.39	-1.2	0.619	-1.58	0.073	-1.65	0.252	-0.81
1441263_a_at	A930005H10Rik	RIKEN cDNA A930005H10 gene	-1.26	0.04	-1.17	0.315	1.03	0.852	-1.99	0.046	-0.85
1452124_at	Ank3 /// 2900054D0	ankyrin 3, epithelial /// RIKEN cDNA 2900054D09 gene	-1.11	0.536	1.29	0.231	-2.08	0.002	-1.56	0.106	-0.86
1424901_at	Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	-1.23	0.64	-1.76	0.487	1.29	0.497	-1.12	0.806	-0.7
1436616_at	R74740	expressed sequence R74740	-1.35	0.017	1.07	0.753	-1.16	0.455	-1.15	0.716	-0.65
1428096_at	Ipo11	importin 11	-1.22	0.142	-1.08	0.61	-1.08	0.643	1.22	0.537	-0.54
1415733_a_at	1110019J04Rik	RIKEN cDNA 1110019J04 gene	-1.3	0.081	1.02	0.794	-1.13	0.344	-1.24	0.303	-0.66
1451434_s_at	5430405G24Rik	RIKEN cDNA 5430405G24 gene	-1.14	0.062	-1	0.996	-1.26	0.111	1.12	0.474	-0.57
1447019_at	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	-1.5	0.332	-1.28	0.168	1.23	0.516	-1.25	0.323	-0.7
1434913_at	Hmgcll1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	-1.1	0.65	1	1	-1.3	0.118	-1.42	0.394	-0.71
1426747_at	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	-1.14	0.351	-1.3	0.029	1.02	0.831	-1.4	0.079	-0.7
1444104_at	---	---	1.13	0.91	-1.55	0.281	-1.11	0.841	-1.09	0.798	-0.65
1443804_at	Ppp2r2c	Protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isofor	-1.68	0.586	1.23	0.681	-1.17	0.391	-1.65	0.5	-0.82
1434266_at	AI847670	expressed sequence AI847670	-1.17	0.066	-1.15	0.491	-1.05	0.752	1	0.967	-0.59
1455708_at	Tmod3	Tropomodulin 3	-1.68	0.303	-1.04	0.947	1.12	0.768	-1.16	0.77	-0.69
1428592_s_at	Usp38	ubiquitin specific peptidase 38	-1.2	0.68	-1.26	0.041	1.05	0.728	-1.33	0.181	-0.69
1448304_a_at	Rab6	RAB6, member RAS oncogene family	-1.21	0.092	-1.08	0.159	-1.08	0.265	1.4	0.288	-0.49
1443114_at	A730059M13Rik	RIKEN cDNA A730059M13 gene	-1.18	0.535	1.19	0.115	-1.57	0.049	-1.1	0.609	-0.67
1419866_s_at	Atxn2	ataxin 2	-1.08	0.2	-1.15	0.364	-1.13	0.477	1.07	0.783	-0.58
1425250_a_at	Slc14a2	solute carrier family 14 (urea transporter), member 2	-1.07	0.644	-2.1	0.012	1.26	0.386	-1.1	0.415	-0.75
1443219_at	---	---	-1.26	0.611	-1.05	0.858	-1.07	0.728	1.22	0.344	-0.54
1424609_a_at	BC003993 /// LOC5	cDNA sequence BC003993 /// hypothetical LOC544818	1.01	0.977	-1.17	0.032	-1.23	0.207	-1.06	0.312	-0.61
1457459_at	AU014973	expressed sequence AU014973	1.05	0.77	-1.38	0.299	-1.12	0.414	-1.08	0.696	-0.63
1455033_at	B430201A12Rik	RIKEN cDNA B430201A12 gene	1.01	0.969	-1.05	0.887	-1.41	0.173	-1.06	0.735	-0.63
1436688_x_at	Rpl14	ribosomal protein L14	-1.39	0.443	1.07	0.363	-1.12	0.184	-1.53	0.102	-0.75
1431257_at	6230409E13Rik	RIKEN cDNA 6230409E13 gene	-1.94	0.205	-1.27	0.63	1.37	0.424	-1.32	0.549	-0.79
1429727_at	Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), member 9	-1.01	0.981	1.13	0.576	-1.82	0.062	-1.02	0.95	-0.68
1452288_at	BB128963	expressed sequence BB128963	1.1	0.504	-1.22	0.044	-1.33	0.174	-1.09	0.424	-0.63
1426871_at	Fbxo33	F-box only protein 33	-1.09	0.188	1.04	0.847	-1.38	0.085	-1.04	0.765	-0.62
1440083_at	A430061O12Rik	RIKEN cDNA A430061O12 gene	1.19	0.296	-1.22	0.31	-1.5	0.025	-1.62	0.084	-0.79
1416047_at	Fuca2	fucosidase, alpha-L- 2, plasma	1.1	0.869	-1.1	0.82	-1.49	0.323	-1.22	0.406	-0.68
1438019_at	Ippk	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	-1.32	0.366	-1.09	0.284	-1	0.96	1.3	0.227	-0.53
1436720_s_at	Oog3	oogenesin 3	-1.09	0.534	-2.04	0.089	1.26	0.601	-2.66	0.008	-1.13
1455206_at	C130006E23	Hypothetical protein C130006E23	-1.36	0.141	1.09	0.596	-1.18	0.301	-1.3	0.397	-0.69
1451747_a_at	Atg12	autophagy-related 12 (yeast)	-1.12	0.38	-1.15	0.307	-1.1	0.376	1.01	0.913	-0.59
1421432_at	Arl10	ADP-ribosylation factor-like 10	1.05	0.745	-1.34	0.47	-1.14	0.545	-1.81	0.296	-0.81
1438615_x_at	2010317E24Rik	RIKEN cDNA 2010317E24 gene	-1.02	0.933	-1.19	0.526	-1.17	0.483	1.82	0.041	-0.39
1458397_at	LOC622208	hypothetical LOC622208	1.14	0.385	-1.44	0.286	-1.19	0.601	-1.54	0.19	-0.76
1426089_a_at	BC003331	cDNA sequence BC003331	-1.06	0.587	-1.19	0.009	-1.13	0.335	1.01	0.949	-0.59
1451320_at	3110043J09Rik	RIKEN cDNA 3110043J09 gene	1.03	0.932	-1.41	0.623	-1.07	0.665	-1.51	0.61	-0.74
1438755_at	C80068	expressed sequence C80068	-1.35	0.237	1.01	0.959	-1.09	0.777	-1.06	0.816	-0.62
1440403_at	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	-1.11	0.833	-1.39	0.055	1.06	0.789	-2.28	0.05	-0.93
1455208_at	Pex19	peroxisome biogenesis factor 19	1.04	0.167	-1.11	0.544	-1.37	0.039	-1.14	0.414	-0.64
1448652_at	Ift88	intraflagellar transport 88 homolog (Chlamydomonas)	-1.09	0.395	-1.46	0.081	1.07	0.75	-1.21	0.225	-0.67
1443032_at	Mrps22	Mitochondrial ribosomal protein S22	-1.01	0.976	-1.11	0.776	-1.27	0.264	1.15	0.594	-0.56
1448312_at	Pcsk2	proprotein convertase subtilisin/kexin type 2	-1.07	0.917	-1.05	0.882	-1.28	0.555	1.44	0.6	-0.49
1447672_x_at	Pskh1	protein serine kinase H1	-1.1	0.662	-1	0.977	-1.3	0.336	1.06	0.491	-0.59
1423881_at	Saps3	SAPS domain family, member 3	-1.27	0.075	-1.05	0.459	-1.07	0.619	1.16	0.346	-0.56

1439033_at	Zcchc7	zinc finger, CCHC domain containing 7	1.08	0.046	-1.34	0.019	-1.18	0.537	-1.39	0.342	-0.71
1459967_at	---	Transcribed locus	-1.19	0.698	-1.11	0.713	-1.07	0.862	1.05	0.893	-0.58
1431273_at	2810417H13Rik	RIKEN cDNA 2810417H13 gene	1.24	0.737	-2.17	0.302	-1.03	0.889	-1.6	0.482	-0.89
1443737_at	Xpo6	Exportin 6	-2.73	0.296	-1.58	0.449	1.68	0.435	-1.08	0.893	-0.93
1436203_a_at	1110059G02Rik	RIKEN cDNA 1110059G02 gene	-1.21	0.108	-1.02	0.895	-1.15	0.175	1.12	0.366	-0.56
1429369_at	Tnpo3	transportin 3	-1.07	0.322	-1.43	0.051	1.04	0.586	-1.13	0.21	-0.65
1424955_at	Ccdc5	coiled-coil domain containing 5	-1.04	0.714	-1.23	0.236	-1.11	0.397	1.84	0.235	-0.39
1452282_at	Crsp7	cofactor required for Sp1 transcriptional activation, subunit 7	-1.24	0.236	-1.35	0.251	1.13	0.571	-1.03	0.718	-0.62
1429732_at	Ppp1r1c	protein phosphatase 1, regulatory (inhibitor) subunit 1C	-1.2	0.769	1.21	0.672	-1.59	0.253	-1.53	0.116	-0.78
1415781_a_at	Sumo2 /// LOC6723	SMT3 suppressor of mif two 3 homolog 2 (yeast) /// similar to SMT3 suppressor o	1.05	0.192	-1.19	0.096	-1.27	0.002	-1.05	0.345	-0.61
1432761_at	4930551I15Rik	RIKEN cDNA 4930551I15 gene	1.44	0.594	-2.49	0.216	-1.2	0.267	-1.42	0.021	-0.92
1423684_at	Hnrpk	heterogeneous nuclear ribonucleoprotein K	-1.1	0.267	-1.01	0.959	-1.3	0.099	1.06	0.62	-0.59
1442668_at	---	---	-2.34	0.159	-1.15	0.791	1.38	0.567	-1.2	0.551	-0.83
1457321_at	LOC667963	hypothetical protein LOC667963	-1.01	0.977	-1.23	0.435	-1.14	0.305	1.18	0.591	-0.55
1427805_at	---	---	-1.06	0.379	-1.12	0.568	-1.2	0.499	1.29	0.362	-0.52
1432926_at	2900069M18Rik	RIKEN cDNA 2900069M18 gene	-1.71	0.466	-1.45	0.366	1.4	0.193	-2.69	0.05	-1.11
1424820_a_at	Ndfip1	Nedd4 family interacting protein 1	-1.16	0.206	-1.24	0.026	1.01	0.932	-1.34	0.335	-0.68
1439553_s_at	Nutf2 /// LOC62183	nuclear transport factor 2 /// similar to Nuclear transport factor 2 (NTF-2) /// simila	-1.08	0.623	-1.04	0.712	-1.27	0.059	1.26	0.396	-0.53
1443861_at	Cgnl1 /// LOC6774	cingulin-like 1 /// similar to cingulin-like 1 isoform 1	-1.05	0.83	-1.42	0.576	1.02	0.979	-3.58	0.075	-1.26
1419568_at	Mapk1	mitogen activated protein kinase 1	-1.72	0.408	-1.19	0.57	1.26	0.515	-1.19	0.784	-0.71
1458355_x_at	AI553587	expressed sequence AI553587	-1.24	0.325	-1.21	0.334	1.05	0.762	-1.11	0.435	-0.63
1438045_at	Eea1	early endosome antigen 1	-1.07	0.594	-1.16	0.137	-1.15	0.459	1.2	0.021	-0.54
1450922_a_at	Tgfb2	transforming growth factor, beta 2	1.1	0.66	-1.57	0.375	-1.06	0.835	-1.58	0.308	-0.78
1435407_at	Zfp483	Zinc finger protein 483	1.1	0.546	-1.26	0.63	-1.27	0.49	-1.59	0.156	-0.76
1423251_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	-1.06	0.378	-1.12	0.484	-1.19	0.235	1.25	0.262	-0.53
1452880_at	Znhit3	zinc finger, HIT type 3	-1.16	0.354	-1.19	0.208	-1.02	0.83	1.36	0.408	-0.5
1425618_at	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-3.14	0.06	-1.85	0.214	1.82	0.145	-1.21	0.553	-1.09
1433679_at	Fubp3	far upstream element (FUSE) binding protein 3	-1.07	0.718	-1.08	0.416	-1.21	0.139	1	0.986	-0.59
1426413_at	Neurod1	neurogenic differentiation 1	1.19	0.755	-1.59	0.307	-1.16	0.746	-1.48	0.469	-0.76
1420108_at	---	---	-1.5	0.51	1.16	0.71	-1.19	0.717	-2.79	0.004	-1.08
1434075_at	BC030336	cDNA sequence BC030336	1.04	0.764	-1.13	0.357	-1.33	0.093	-1	0.985	-0.61
1452573_a_at	Sr278	stretch responsive protein 278	-1.16	0.066	-1.1	0.516	-1.11	0.514	1.27	0.113	-0.52
1451754_a_at	Wdr45	WD repeat domain 45	-1.09	0.695	-1.18	0.011	-1.1	0.421	1.08	0.14	-0.57
1438353_at	---	---	1.04	0.825	-1.09	0.526	-1.39	0.083	-1.2	0.598	-0.66
1420935_a_at	Srrm1	serine/arginine repetitive matrix 1	-1.13	0.693	-1.2	0.506	-1.04	0.881	1.79	0.003	-0.4
1440127_a_at	---	Transcribed locus	-1.35	0.542	-1.27	0.14	1.15	0.729	-2.07	0.136	-0.88
1452385_at	Usp53	ubiquitin specific peptidase 53	-1.16	0.626	1	0.992	-1.23	0.305	-1.86	0.15	-0.81
1438227_at	She	src homology 2 domain-containing transforming protein E	-1.1	0.855	1.06	0.855	-1.4	0.317	-2.23	0.069	-0.92
1428494_a_at	Polr2i	polymerase (RNA) II (DNA directed) polypeptide I	-1.02	0.868	-1.17	0.088	-1.2	0.406	1.09	0.071	-0.57
1427830_at	Zfp260	zinc finger protein 260	-1.26	0.752	1.13	0.802	-1.34	0.319	-1.5	0.095	-0.74
1428554_a_at	1810035L17Rik	RIKEN cDNA 1810035L17 gene	-1.06	0.545	1	0.95	-1.37	0.035	-1.08	0.749	-0.63
1422237_at	Mc3r	melanocortin 3 receptor	1.04	0.673	-1.46	0.004	-1.05	0.813	-1.16	0.008	-0.66
1445645_at	Adam22	A disintegrin and metallopeptidase domain 22	1.38	0.663	-1.85	0.117	-1.32	0.381	-1.35	0.295	-0.79
1452974_at	Nol8	nucleolar protein 8	-1.16	0.501	1.09	0.738	-1.38	0.141	-1.41	0.018	-0.71
1435854_at	Tmem10	transmembrane protein 10	1.06	0.912	-1.15	0.609	-1.34	0.292	-1.41	0.553	-0.71
1450622_at	Bcar1	breast cancer anti-estrogen resistance 1	-1.14	0.078	-1.22	0.223	-1.02	0.938	1.07	0.497	-0.58
1458114_at	Samd12	sterile alpha motif domain containing 12	-1.23	0.659	1.02	0.957	-1.19	0.427	-1.1	0.671	-0.62
1429494_at	Trim35	tripartite motif-containing 35	1.02	0.918	-1.04	0.94	-1.43	0.135	-1.97	0.073	-0.86
1422433_s_at	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	-1.38	0.259	-1.13	0.078	1.07	0.659	-1.15	0.388	-0.65
1429383_at	Csnk1g3	casein kinase 1, gamma 3	1.03	0.915	-1.02	0.848	-1.48	0.008	-1.64	0.095	-0.78
1428384_at	D4Bwg0951e	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	1.04	0.86	-1.09	0.679	-1.38	0.028	-1.86	0.273	-0.82
1458744_at	Taf1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-2.53	0.438	-1.22	0.017	1.46	0.625	-1.06	0.931	-0.84
1447223_at	---	Transcribed locus	-1.15	0.179	-1.19	0.09	-1.03	0.773	1.09	0.527	-0.57

1443490_at	D3Ertd34e	DNA segment, Chr 3, ERATO Doi 34, expressed	1.02	0.768	-1.17	0.254	-1.24	0.272	-1.41	0.273	-0.7
1446748_at	2010007H06Rik	RIKEN cDNA 2010007H06 gene	1.28	0.03	-2.29	0.055	-1.04	0.759	-1.79	0.243	-0.96
1460691_at	Zfp598	zinc finger protein 598	1.05	0.737	-1.28	0.016	-1.18	0.189	-1.02	0.875	-0.61
1459307_at	Sec24b	SEC24 related gene family, member B (S. cerevisiae)	-1.08	0.805	1.18	0.655	-1.73	0.053	-1.17	0.699	-0.7
1460032_at	4933407C03Rik	RIKEN cDNA 4933407C03 gene	-1.35	0.297	1.16	0.471	-1.28	0.152	-1.02	0.923	-0.62
1438647_x_at	Cetn2	centrin 2	-1.13	0.329	1.02	0.827	-1.29	0.187	-1.27	0.491	-0.67
1443467_at	Dock11	dedicator of cytokinesis 11	1.21	0.474	-1.58	0.167	-1.19	0.194	-1.8	0.235	-0.84
1433103_at	Hyls1	hydrolethalus syndrome 1	-1.73	0.166	1.27	0.57	-1.2	0.733	-1.92	0.338	-0.9
1455597_at	AI585793	Expressed sequence AI585793	1.08	0.468	-1.03	0.735	-1.59	0.013	-1.35	0.201	-0.72
1447477_at	3110006E14Rik	RIKEN cDNA 3110006E14 gene	-1.54	0.135	-1.05	0.795	1.08	0.865	-2.62	0.14	-1.03
1443898_at	Bcl7c	B-cell CLL/lymphoma 7C	-1.29	0.401	1.01	0.957	-1.12	0.528	-1.07	0.764	-0.62
1437368_at	Gtf2h4 /// LOC6403	general transcription factor II H, polypeptide 4 /// similar to general transcription fa	-1.33	0.369	-1.52	0.312	1.27	0.592	-2.24	0.313	-0.95
1430592_at	Tmem106b	transmembrane protein 106B	1.26	0.495	-1.37	0.09	-1.46	0.055	-1.16	0.563	-0.68
1416727_a_at	Cyb5	cytochrome b-5	-1.09	0.384	-1.14	0.46	-1.13	0.26	1.3	0.187	-0.52
1452579_at	Nifun	NifU-like N-terminal domain containing	1.01	0.942	-1.17	0.09	-1.23	0.129	-1.09	0.655	-0.62
1423854_a_at	Rasl11b	RAS-like, family 11, member B	1.02	0.808	-1.02	0.867	-1.48	0.072	-1.18	0.71	-0.66
1441830_x_at	---	---	1.14	0.508	-1.31	0.291	-1.29	0.201	-2.4	0.014	-0.96
1437550_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	1.07	0.586	-1.27	0.099	-1.22	0.34	-1.23	0.574	-0.66
1451983_at	Irx1	Iroquois related homeobox 1 (Drosophila)	-1.3	0.019	1.27	0.502	-1.57	0.158	-1.41	0.189	-0.75
1417965_at	Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specif	-1.19	0.059	1.03	0.703	-1.24	0.098	-1.56	0.164	-0.74
1419156_at	Sox4 /// LOC67227	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	1.16	0.378	-1.12	0.762	-1.6	0.078	-1.45	0.314	-0.75
1453225_at	A930038C07Rik	RIKEN cDNA A930038C07 gene	-2.71	0.131	1.6	0.35	-1.41	0.249	-1.27	0.732	-0.95
1455303_at	---	---	-1.33	0.21	-1.11	0.169	1.03	0.848	-1.08	0.551	-0.62
1450112_a_at	Gas2	growth arrest specific 2	-1.23	0.026	-1.01	0.967	-1.15	0.332	1.86	0.023	-0.38
1431983_at	Myo3a	myosin IIIA	-1.32	0.716	-1.29	0.47	1.15	0.716	-1.2	0.459	-0.67
1429593_at	Slc38a2	solute carrier family 38, member 2	-1.25	0.322	1.08	0.727	-1.25	0.18	-1.23	0.263	-0.66
1437295_at	Pkn2	protein kinase N2	-1.05	0.438	-1.03	0.726	-1.33	0.026	1.6	0.31	-0.45
1448896_at	Pigf	phosphatidylinositol glycan anchor biosynthesis, class F	-1.13	0.101	1.09	0.414	-1.41	0.123	-1.27	0.115	-0.68
1449746_s_at	Glipr1	GLI pathogenesis-related 1 (glioma)	-1.64	0.106	1.35	0.363	-1.39	0.222	-1.23	0.267	-0.73
1459114_at	Anks1	Ankyrin repeat and SAM domain containing 1	-1.39	0.753	-1.09	0.904	1.04	0.926	-1.44	0.16	-0.72
1427925_at	Stx17	syntaxin 17	-1.1	0.57	-1.07	0.744	-1.19	0.289	1.15	0.579	-0.55
1456145_at	Dleu2	deleted in lymphocytic leukemia, 2	-1.03	0.83	-1.34	0.097	-1.04	0.714	2.22	0.208	-0.3
1456698_s_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	-1.25	0.283	1.05	0.78	-1.21	0.176	-1.48	0.074	-0.72
1446275_at	Tnrc15	Trinucleotide repeat containing 15	-1.17	0.726	-1.42	0.561	1.12	0.832	-2.1	0.446	-0.89
1437876_at	Fndc6	fibronectin type III domain containing 6	-1.28	0.479	-1.29	0.63	1.13	0.427	-1.2	0.705	-0.66
1455295_at	BC031853	cDNA sequence BC031853	-1.34	0.192	-1.07	0.635	1	0.956	-1.2	0.53	-0.65
1457504_at	---	---	-1.62	0.446	1.16	0.56	-1.11	0.763	-1.06	0.88	-0.66
1443920_at	Ccdc66	coiled-coil domain containing 66	-1.04	0.776	-1.09	0.89	-1.26	0.291	1.06	0.622	-0.58
1458894_at	---	---	-1.23	0.546	-1.91	0.028	1.34	0.436	-1.96	0.081	-0.94
1456217_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	-1.06	0.85	-1.38	0.262	1.01	0.952	-1.14	0.522	-0.64
1454000_s_at	4930578N16Rik	RIKEN cDNA 4930578N16 gene	-1.01	0.989	-1.21	0.475	-1.16	0.459	1.01	0.987	-0.59
1419074_at	2510006C20Rik	RIKEN cDNA 2510006C20 gene	-1.11	0.617	-1.19	0.127	-1.06	0.539	4.37	0.205	0.25
1418886_s_at	Idh3b	isocitrate dehydrogenase 3 (NAD+) beta	-1.18	0.022	-1.3	0.076	1.07	0.524	-1.42	0.032	-0.71
1419108_at	Ophn1	oligophrenin 1	-1.03	0.904	-1.17	0.523	-1.16	0.544	1.11	0.506	-0.56
1424709_at	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	-1.16	0.503	-1.41	0.66	1.1	0.667	-1.45	0.33	-0.73
1424636_at	2610204L23Rik	RIKEN cDNA 2610204L23 gene	-1.42	0.214	-1.01	0.917	-1.01	0.962	1.13	0.65	-0.58
1437206_at	Setd5	SET domain containing 5	-1.73	0.374	-1.66	0.202	1.5	0.327	-1.98	0.184	-0.97
1430461_at	1700120E14Rik	RIKEN cDNA 1700120E14 gene	1.14	0.871	-1.03	0.958	-1.76	0.414	-1.61	0.08	-0.81
1438038_at	4930402H24Rik	RIKEN cDNA 4930402H24 gene	-1.08	0.016	-1.25	0.071	-1.05	0.848	1.17	0.235	-0.55
1440426_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-1.37	0.017	-1.42	0.378	1.25	0.515	-1.36	0.036	-0.73
1416362_a_at	Fkbp4	FK506 binding protein 4	1.01	0.898	-1.15	0.14	-1.24	0.209	-1.02	0.907	-0.6
1439907_at	Rdx	Radixin	1.07	0.8	-1.14	0.69	-1.37	0.193	-1.4	0.436	-0.71
1455999_at	C330003B14Rik	RIKEN cDNA C330003B14 gene	-1.12	0.421	-1.04	0.908	-1.22	0.629	1.17	0.227	-0.55

1416452_at	Oat	ornithine aminotransferase	1.03	0.825	-1.48	0.196	-1.02	0.915	-1.16	0.497	-0.66
1442068_at	---	Mus musculus, clone IMAGE:5363897, mRNA	1.04	0.913	-1.05	0.917	-1.46	0.294	-1.12	0.691	-0.65
1446341_at	6030403N03Rik	RIKEN cDNA 6030403N03 gene	-1.23	0.433	1.08	0.61	-1.27	0.127	-1.12	0.687	-0.63
1450144_at	Pla2r1	phospholipase A2 receptor 1	-1.05	0.754	-1.04	0.885	-1.31	0.067	1.5	0.069	-0.47
1439626_at	Tmod3	tropomodulin 3	1.19	0.683	-1.34	0.248	-1.34	0.189	-2.49	0.021	-1
1451512_s_at	Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	-1.05	0.615	-1.17	0.21	-1.14	0.409	1.12	0.593	-0.56
1436435_at	9530026P05Rik	RIKEN cDNA 9530026P05 gene	1.12	0.615	-1.08	0.892	-1.55	0.165	-1.43	0.225	-0.74
1426367_at	Cab39l	calcium binding protein 39-like	1.03	0.647	-1.27	0.003	-1.15	0.098	-1.11	0.377	-0.63
1443926_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	1.01	0.963	-1.21	0.452	-1.19	0.565	-2.07	0.064	-0.86
1419438_at	Sim2	single-minded homolog 2 (Drosophila)	1.44	0.229	-1.53	0.139	-1.72	0.118	-1.49	0.479	-0.82
1455558_at	Gm114	gene model 114, (NCBI)	-1.04	0.805	-1.22	0.293	-1.1	0.238	1.14	0.475	-0.56
1436308_at	Zfp292	zinc finger protein 292	-1.09	0.628	1.04	0.809	-1.38	0.053	-1.38	0.162	-0.7
1429461_at	Ints2	integrator complex subunit 2	-1.18	0.269	-1.12	0.644	-1.06	0.774	1.18	0.289	-0.54
1443551_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.43	0.241	-1.09	0.86	1.07	0.775	-1.37	0.28	-0.71
1439678_at	Gls	Glutaminase	-1.63	0.091	1.39	0.25	-1.47	0.078	-1.4	0.16	-0.78
1421282_at	Bmp5	bone morphogenetic protein 5	-1.27	0.349	1.14	0.575	-1.33	0.291	-2	0.575	-0.86
1420266_at	---	---	-1.63	0.192	-1.08	0.686	1.14	0.456	-1.27	0.247	-0.71
1434832_at	Foxo3a	forkhead box O3a	-1.14	0.739	-1.01	0.97	-1.23	0.264	2.01	0.171	-0.34
1429749_at	9330180L21Rik	RIKEN cDNA 9330180L21 gene	-1.11	0.457	-1.19	0.139	-1.06	0.611	1.24	0.468	-0.53
1447594_at	1810012K16Rik	RIKEN cDNA 1810012K16 gene	1.1	0.891	-1.29	0.721	-1.24	0.614	-1.08	0.859	-0.63
1430519_a_at	Cnot7	CCR4-NOT transcription complex, subunit 7	-1.05	0.684	-1.28	0.081	-1.05	0.855	1.1	0.726	-0.57
1424566_s_at	Polr3d	polymerase (RNA) III (DNA directed) polypeptide D	-1.42	0.358	-1.07	0.861	1.05	0.895	-1.08	0.397	-0.63
1449983_a_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	-1.17	0.308	-1.15	0.525	-1.04	0.817	1.03	0.836	-0.58
1423517_at	Cct6a	chaperonin subunit 6a (zeta)	-1.07	0.51	-1.15	0.019	-1.14	0.107	1.06	0.653	-0.57
1437891_at	Frs2	fibroblast growth factor receptor substrate 2	-1.14	0.281	-1.01	0.917	-1.22	0.072	1.03	0.83	-0.59
1425014_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	-1.23	0.733	-1.15	0.721	-1	0.991	1.04	0.914	-0.58
1429146_at	6620401M08Rik	RIKEN cDNA 6620401M08 gene	-1.02	0.883	-1.1	0.283	-1.26	0.195	3.6	0.22	0.06
1418005_at	Sdhb	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-1.19	0.302	-1.3	0.083	1.07	0.394	-1.14	0.1	-0.64
1434621_at	BC054438	cDNA sequence BC054438	-1.02	0.912	1.06	0.67	-1.56	0.047	-1.8	0.113	-0.83
1432034_at	Neurog3	neurogenin 3	-1.05	0.723	-1.47	0.325	1.05	0.919	-1.08	0.589	-0.64
1460246_at	Mecp2	methyl CpG binding protein 2	-1.02	0.898	-1.15	0.504	-1.2	0.533	1.17	0.582	-0.55
1459499_at	---	Transcribed locus	1.34	0.081	-2.32	0.377	-1.1	0.646	-1.79	0.53	-0.97
1443375_at	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	-1.04	0.917	-1.16	0.681	-1.16	0.165	1.05	0.886	-0.58
1457836_at	2600014M03Rik	RIKEN cDNA 2600014M03 gene	1.02	0.978	-1.3	0.304	-1.12	0.781	-1.1	0.531	-0.62
1446751_s_at	Impact	imprinted and ancient	1.16	0.802	-1.36	0.596	-1.26	0.367	-1.48	0.321	-0.74
1420396_at	Cd160	CD160 antigen	-1.43	0.244	1	0.988	-1.02	0.897	-1.43	0.152	-0.72
1447848_at	Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	1.1	0.903	-1.24	0.742	-1.28	0.48	-1.85	0.231	-0.82
1457369_at	Phactr4	Phosphatase and actin regulator 4	-1.04	0.92	-1.11	0.422	-1.21	0.504	1.26	0.45	-0.53
1453807_at	6330563C09Rik	RIKEN cDNA 6330563C09 gene	-1.01	0.992	-1.25	0.665	-1.12	0.266	2.1	0.23	-0.32
1435609_at	---	---	-1.23	0.081	-1.05	0.938	-1.09	0.617	1.12	0.56	-0.56
1427282_a_at	Fxn	frataxin	-1.15	0.431	-1.2	0.189	-1.02	0.842	2.54	0.231	-0.21
1423474_at	Top1	topoisomerase (DNA) I	-1.09	0.716	-1.06	0.488	-1.22	0.005	1.78	0.121	-0.4
1419159_at	Golga3	golgi autoantigen, golgin subfamily a, 3	1	0.984	-1.21	0.265	-1.17	0.553	-1.29	0.086	-0.67
1460044_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.03	0.975	-1.18	0.204	-1.23	0.582	-1.36	0.538	-0.69
1424520_at	2010305A19Rik	RIKEN cDNA 2010305A19 gene	-1.09	0.503	1.01	0.957	-1.32	0.316	-1.03	0.865	-0.61
1455336_at	Thap2	THAP domain containing, apoptosis associated protein 2	-1.13	0.052	1.08	0.608	-1.39	0.009	-1.05	0.431	-0.62
1458057_at	Cald1	Caldesmon 1	-1.01	0.979	1.19	0.312	-1.99	0.136	-1.2	0.044	-0.75
1441920_x_at	Htf9c	HpaII tiny fragments locus 9c	1.06	0.902	-1.22	0.698	-1.25	0.654	-1.62	0.224	-0.76
1425870_a_at	Kcnip2	Kv channel-interacting protein 2	1.32	0.144	-2.38	0.031	-1.06	0.924	-1.25	0.548	-0.84
1442299_at	---	---	-1.24	0.586	-1.13	0.637	-1.01	0.974	1.36	0.143	-0.51
1417937_at	Dact1	dapper homolog 1, antagonist of beta-catenin (xenopus)	1.17	0.26	-1.36	0.364	-1.28	0.175	-1.15	0.559	-0.65
1427670_a_at	Tcf12	transcription factor 12	-1.19	0.312	1.07	0.614	-1.29	0.002	-1.24	0.154	-0.66
1425052_at	---	CDNA, clone:Y2G0147N17, strand:unspecified	-1.05	0.69	-1.12	0.183	-1.19	0.165	1	0.937	-0.59

1432334_at	4930488P18Rik	RIKEN cDNA 4930488P18 gene	-3.36	0.017	1.72	0.426	-1.5	0.334	-2.04	0.301	-1.3
1458535_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330040D	-1.33	0.073	1.45	0.488	-2.07	0.054	-1.17	0.587	-0.78
1443909_at	Cstf3	Cleavage stimulation factor, 3' pre-RNA, subunit 3	1.09	0.847	-1.01	0.968	-1.65	0.003	-1.42	0.261	-0.75
1431175_at	1810019D21Rik	RIKEN cDNA 1810019D21 gene	-1.1	0.61	1.06	0.834	-1.39	0.025	-1.35	0.204	-0.7
1444563_at	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	-1.31	0.577	-1.32	0.613	1.16	0.729	-1.61	0.24	-0.77
1416373_at	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	-1.13	0.324	-1.15	0.121	-1.07	0.362	1.21	0.303	-0.54
1457564_at	Dffa	DNA fragmentation factor, alpha subunit	1.02	0.941	-1.1	0.538	-1.32	0.407	-1.09	0.66	-0.62
1447232_at	---	---	-1.09	0.869	-1.15	0.493	-1.12	0.765	1.62	0.2	-0.43
1456902_at	Satb1	Special AT-rich sequence binding protein 1	-1.03	0.488	-1.19	0.403	-1.14	0.302	1.03	0.932	-0.58
1442125_at	Krit1	KRIT1, ankyrin repeat containing	-1.07	0.84	1.01	0.962	-1.34	0.229	-1.4	0.162	-0.7
1428121_at	2610528K11Rik	RIKEN cDNA 2610528K11 gene	-1.11	0.48	-1.13	0.231	-1.11	0.493	1.33	0.391	-0.51
1455705_at	Tmem161a	transmembrane protein 161A	1.17	0.323	-1.51	0.044	-1.17	0.58	-1.19	0.406	-0.68
1452132_at	Tlcd1	TLC domain containing 1	-1.16	0.198	-1.11	0.647	-1.08	0.489	3.68	0.183	0.08
1427950_at	Zfp294	zinc finger protein 294	-1.14	0.642	-1.04	0.923	-1.17	0.741	1.12	0.778	-0.56
1450101_a_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	1.12	0.533	-1.74	0.282	-1.01	0.985	-1	0.99	-0.66
1450386_at	Kpna3	karyopherin (importin) alpha 3	-1.12	0.131	-1.09	0.056	-1.15	0.096	1.29	0.236	-0.52
1416972_at	Nhp2l1 /// LOC434	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae) /// similar to Nhp2	-1.08	0.472	1.01	0.89	-1.34	0.011	-1.08	0.385	-0.62
1453045_at	4921537D05Rik	RIKEN cDNA 4921537D05 gene	-1.03	0.814	-1.21	0.054	-1.13	0.32	1.18	0.511	-0.55
1423071_x_at	LOC270335 /// LOC	hypothetical gene supported by BC019681; BC027236 /// hypothetical LOC43432	-1.22	0.582	1.02	0.919	-1.19	0.481	-1.89	0.149	-0.82
1425020_at	Ubxd4 /// LOC6216	UBX domain containing 4 /// similar to UBX domain containing 4 /// similar to UBX	-1.09	0.366	-1.12	0.236	-1.15	0.254	1.29	0.241	-0.52
1451114_at	Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	-1.23	0.17	-1.22	0.019	1.05	0.606	-1.66	0.082	-0.76
1445103_at	Tmem23	Transmembrane protein 23	-1.19	0.393	-1.13	0.659	-1.04	0.826	1.14	0.592	-0.56
1457316_at	Mtap6	microtubule-associated protein 6	-1.2	0.632	1.08	0.84	-1.29	0.06	-1.81	0.397	-0.81
1433834_at	6-Mar	membrane-associated ring finger (C3HC4) 6	-1.08	0.358	-1.07	0.173	-1.21	0.145	1.24	0.094	-0.53
1434035_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	-1.27	0.438	-1.09	0.649	-1.02	0.943	1.29	0.365	-0.52
1417158_at	Zxdc	ZXD family zinc finger C	-1.35	0.01	1.07	0.579	-1.14	0.568	-1.62	0.183	-0.76
1444845_at	---	---	1.11	0.655	-1.35	0.11	-1.2	0.286	-1.43	0.052	-0.72
1449773_s_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	1.1	0.221	-1.12	0.53	-1.44	0.153	-1.45	0.389	-0.73
1415726_at	Ankrd17	ankyrin repeat domain 17	-1.09	0.376	-1.18	0.12	-1.08	0.502	1.15	0.053	-0.55
1420253_at	D2Ertd63e	DNA segment, Chr 2, ERATO Doi 63, expressed	1.22	0.248	-1.48	0.234	-1.27	0.289	-1.03	0.886	-0.64
1441893_at	Tex24	testis expressed gene 24	1.11	0.825	-1.18	0.721	-1.36	0.648	-1.01	0.985	-0.61
1420105_at	D13Ertd205e	DNA segment, Chr 13, ERATO Doi 205, expressed	-2.01	0.539	-1.42	0.302	1.49	0.106	-1.47	0.395	-0.85
1416963_at	Ubadc1	ubiquitin associated domain containing 1	-1.19	0.31	-1.07	0.416	-1.09	0.402	3.58	0.156	0.06
1449641_at	---	---	-1.05	0.911	-1.2	0.267	-1.11	0.73	1.64	0.169	-0.43
1439251_at	---	Transcribed locus	-1.21	0.266	-1.05	0.756	-1.11	0.61	1.85	0.204	-0.38
1455661_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430106B	-1.06	0.861	-1.49	0.035	1.07	0.768	-1.13	0.29	-0.65
1437586_at	Cnot4	CCR4-NOT transcription complex, subunit 4	-1.15	0.304	-1.19	0.263	-1.02	0.93	1.32	0.23	-0.51
1425196_a_at	Hint2	histidine triad nucleotide binding protein 2	1.01	0.978	-1.15	0.507	-1.24	0.43	-1.14	0.593	-0.63
1424641_a_at	Thoc1	THO complex 1	-1.21	0.304	1.11	0.211	-1.32	0.077	-1.33	0.038	-0.69
1432080_s_at	Myst1	MYST histone acetyltransferase 1	-1.21	0.003	-1.21	0.035	1.03	0.829	-1.28	0.211	-0.67
1454624_at	Dennd2a	DENN/MADD domain containing 2A	-1.15	0.844	-1.21	0.683	-1.01	0.982	1.1	0.534	-0.57
1440466_at	BC003965	cDNA sequence BC003965	-1.26	0.35	1.07	0.775	-1.21	0.673	-1.34	0.638	-0.68
1451504_at	Chchd3	coiled-coil-helix-coiled-coil-helix domain containing 3	-1.09	0.555	-1.27	0.057	-1.01	0.888	1.3	0.313	-0.52
1427259_at	Trim24	tripartite motif protein 24	-1.24	0.366	-1.08	0.814	-1.05	0.796	1.06	0.868	-0.58
1448292_at	Uqcr	ubiquinol-cytochrome c reductase (6.4kD) subunit	-1.13	0.254	-1.11	0.238	-1.11	0.151	1.13	0.509	-0.55
1422679_s_at	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.14	0.246	1.01	0.867	-1.26	0.023	-1.13	0.311	-0.63
1427675_at	V1ra2	vomeronasal 1 receptor, A2	-1.66	0.033	1.35	0.655	-1.37	0.592	-1.54	0.57	-0.8
1455204_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.18	0.081	1.11	0.454	-1.36	0.196	-1.11	0.286	-0.64
1437172_x_at	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl	-1.1	0.264	-1.26	0.274	-1.02	0.866	1.02	0.852	-0.59
1438567_at	Vwa2	von Willebrand factor A domain containing 2	1.44	0.201	-1.15	0.707	-2.6	0.034	-1.08	0.926	-0.85
1426411_a_at	Strbp /// C230082I2	spermatid perinuclear RNA binding protein /// RIKEN cDNA C230082I21 gene	-1.15	0.444	-1.29	0.059	1.04	0.64	-1.44	0.026	-0.71
1458562_at	---	---	-1.23	0.369	-1.03	0.93	-1.11	0.07	1.04	0.921	-0.58
1457914_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930016I24 product:	-1.13	0.151	-1.02	0.936	-1.22	0.332	2.78	0.101	-0.15

1427685_a_at	Synj2	synaptojanin 2	-1.44	0.261	-1.23	0.439	1.18	0.069	-1.37	0.016	-0.72
1446795_at	Vav3	Vav 3 oncogene	-1.49	0.396	1.23	0.569	-1.27	0.63	-1.6	0.484	-0.78
1423238_at	Itgb1bp2	integrin beta 1 binding protein 2	-1.07	0.811	-2.68	0.122	1.38	0.563	-1.15	0.77	-0.88
1438099_at	Trio	triple functional domain (PTPRF interacting)	1.53	0.493	-2.22	0.332	-1.41	0.448	-1.69	0.36	-0.95
1431395_a_at	Iqgap1	IQ motif containing GTPase activating protein 1	-1.34	0.551	-1.76	0.13	1.37	0.407	-2.92	0.187	-1.16
1447884_x_at	1300010M03Rik	RIKEN cDNA 1300010M03 gene	-1.12	0.814	-1.4	0.295	1.08	0.867	-1.25	0.399	-0.67
1447827_x_at	Spop	speckle-type POZ protein	-1.2	0.301	-1.17	0.352	1	0.964	-1.36	0.22	-0.68
1459053_at	Centg2	centaurin, gamma 2	1.05	0.626	-1.16	0.466	-1.29	0.589	-1.01	0.982	-0.6
1419889_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	1.24	0.107	-1.55	0.459	-1.24	0.554	-1.48	0.403	-0.76
1416816_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	1.02	0.839	-1.13	0.409	-1.27	0.182	-1.03	0.922	-0.6
1432435_s_at	C030004A17Rik	RIKEN cDNA C030004A17 gene	-1.26	0.407	1.03	0.925	-1.16	0.019	-1.06	0.353	-0.61
1421880_at	Mtmr1	myotubularin related protein 1	-1.19	0.186	-1.28	0.042	1.07	0.505	-1.29	0.251	-0.67
1443474_at	D7Ertd495e	DNA segment, Chr 7, ERATO Doi 495, expressed	-1.05	0.897	-1.1	0.883	-1.21	0.581	1.24	0.242	-0.53
1438460_at	Zmym4	zinc finger, MYM-type 4	-1.15	0.393	1.06	0.809	-1.32	0.044	-1.4	0.333	-0.7
1438578_a_at	Btbd10	BTB (POZ) domain containing 10	-1.06	0.707	-1.14	0.522	-1.15	0.095	1.08	0.498	-0.57
1416542_at	Phf1	PHD finger protein 1	-1.17	0.298	-1.4	0.155	1.12	0.501	-1.25	0.296	-0.67
1435786_at	Klhl12	kelch-like 12 (Drosophila)	-1.22	0.294	-1.13	0.392	-1.01	0.907	3.01	0.153	-0.09
1456177_x_at	Zfp706	zinc finger protein 706	-1.22	0.129	-1.22	0.09	1.05	0.641	-1.06	0.827	-0.61
1444516_at	Ppfibp2	Protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein	-1.13	0.532	1.12	0.544	-1.45	0.148	-1.56	0.133	-0.76
1431671_at	4930447A16Rik	RIKEN cDNA 4930447A16 gene	-2	0.067	-1.06	0.822	1.25	0.446	-1.53	0.031	-0.84
1456574_at	AA407452	EST AA407452	-1.16	0.681	-1.05	0.83	-1.14	0.212	1.05	0.823	-0.58
1454412_at	2810410P21Rik	RIKEN cDNA 2810410P21 gene	1.12	0.387	-1.35	0.248	-1.21	0.406	-1.22	0.614	-0.66
1426285_at	Lama2	laminin, alpha 2	-1.29	0.057	1.25	0.418	-1.5	0.147	-1.73	0.161	-0.82
1416176_at	Hmgb1	high mobility group box 1	-1.04	0.498	-1.07	0.335	-1.25	0.001	1.35	0.11	-0.51
1419551_s_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	1.09	0.751	-1.46	0.254	-1.09	0.764	-1.1	0.782	-0.64
1443251_at	Prdm16	PR domain containing 16	-1.96	0.027	1.45	0.455	-1.38	0.157	-1.1	0.852	-0.75
1450362_at	---	---	-1.15	0.855	1.33	0.645	-2.04	0.164	-1.01	0.973	-0.72
1442174_at	Tspan18	tetraspanin 18	-1.17	0.083	1.06	0.849	-1.3	0.179	-1.23	0.42	-0.66
1425076_at	Dnajc18	DnaJ (Hsp40) homolog, subfamily C, member 18	-1.29	0.054	1.05	0.737	-1.15	0.356	-1.19	0.506	-0.65
1415910_s_at	Ciapin1	cytokine induced apoptosis inhibitor 1	-1.11	0.405	-1.09	0.552	-1.15	0.151	1.74	0.149	-0.4
1447355_at	Acsl1	acyl-CoA synthetase long-chain family member 1	-2.06	0.283	-2.25	0.042	1.76	0.232	-1.72	0.504	-1.07
1416720_at	Sfrs6	splicing factor, arginine/serine-rich 6	-1.11	0.562	-1.23	0.015	-1.02	0.675	1.18	0.598	-0.55
1441512_at	6030445D17Rik	RIKEN cDNA 6030445D17 gene	-1.35	0.697	1.1	0.86	-1.18	0.629	-2.21	0.236	-0.91
1456094_at	Usp36	ubiquitin specific peptidase 36	-1.04	0.9	-1.32	0.634	-1.03	0.917	1.32	0.24	-0.52
1428931_a_at	Parp6	poly (ADP-ribose) polymerase family, member 6	1.03	0.76	-1.36	0.219	-1.08	0.461	-1.95	0.022	-0.84
1425402_at	Thop1	thimet oligopeptidase 1	1.62	0.518	-1.75	0.442	-2	0.259	-1.23	0.788	-0.84
1460367_at	Hbp1	high mobility group box transcription factor 1	-1.05	0.22	-1.07	0.355	-1.24	0.353	1.08	0.719	-0.57
1432827_x_at	Ubc	ubiquitin C	-1.17	0.227	-1.24	0.263	1.03	0.748	-1.04	0.508	-0.61
1452283_at	Rassf8	Ras association (RalGDS/AF-6) domain family 8	1.07	0.727	-1.21	0.211	-1.26	0.288	-1.47	0.045	-0.72
1451384_at	Jmjd5	jumonji domain containing 5	-1.04	0.553	-1.57	0.065	1.1	0.539	-1.05	0.77	-0.64
1455096_at	---	---	-1.34	0.387	-1.4	0.37	1.23	0.626	-1.1	0.551	-0.65
1436426_at	5730509K17Rik	RIKEN cDNA 5730509K17 gene	-1.13	0.313	-1.32	0.239	1.05	0.67	-1.63	0.138	-0.76
1428939_s_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	-1.11	0.626	1.06	0.6	-1.36	0.125	-1.56	0.059	-0.74
1417875_at	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	-1.11	0.453	1	0.971	-1.27	0.218	-1.35	0.091	-0.68
1458791_at	AU015849	expressed sequence AU015849	-1.66	0.054	1.27	0.485	-1.22	0.621	-2.07	0.547	-0.92
1437638_at	Srrm2	serine/arginine repetitive matrix 2	1.25	0.35	-1.26	0.415	-1.54	0.094	-1.19	0.639	-0.69
1449899_at	Grin3b	glutamate receptor, ionotropic, NMDA3B	-1.18	0.392	1.29	0.415	-1.82	0.219	-1.02	0.966	-0.68
1444760_at	Ncor1	nuclear receptor co-repressor 1	1.09	0.827	-1.1	0.608	-1.44	0.272	-1.25	0.502	-0.68
1438863_at	A530079E22Rik	RIKEN cDNA A530079E22 gene	-1.15	0.694	1.14	0.794	-1.46	0.003	-1.92	0.135	-0.85
1459601_at	Snf1lk	SNF1-like kinase	-1.3	0.395	1.13	0.794	-1.26	0.277	-1.96	0.059	-0.85
1449782_at	AA517650	expressed sequence AA517650	-1.21	0.709	-1.56	0.217	1.23	0.628	-1.58	0.31	-0.78
1447381_at	Cpsf6	Cleavage and polyadenylation specific factor 6	1.04	0.665	-1.11	0.588	-1.33	0.382	-1.37	0.34	-0.69
1417251_at	Palmd	palmdelphin	-1.01	0.934	-1.44	0.12	1.01	0.968	-1.29	0.044	-0.68

1417159_at	---	---	-1.04	0.967	-1.06	0.888	-1.28	0.615	1.3	0.51	-0.52
1454709_at	Tmem64	transmembrane protein 64	-1.4	0.139	-1.07	0.633	1.04	0.653	-1.17	0.404	-0.65
1440071_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.45	0.451	1.06	0.864	-1.07	0.858	-1.06	0.848	-0.63
1460033_at	C030002C11Rik	RIKEN cDNA C030002C11 gene	-1.05	0.875	-1.46	0.289	1.05	0.879	-1.22	0.672	-0.67
1426151_a_at	Stx3	syntaxin 3	-1.14	0.64	-1.05	0.86	-1.15	0.455	1.19	0.556	-0.54
1444321_at	Psmd9	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	-1.11	0.744	1.08	0.849	-1.4	0.18	-1.1	0.802	-0.63
1423472_at	2-Sep	septin 2	-1.21	0.367	1.04	0.742	-1.21	0.392	-1.2	0.311	-0.65
1433967_at	LOC433492	similar to RIKEN cDNA 5430413K10	-1.3	0.495	1.28	0.611	-1.55	0.173	-2.27	0.213	-0.96
1448542_at	Bccip	BRCA2 and CDKN1A interacting protein	-1.11	0.031	-1.17	0.031	-1.07	0.337	1.01	0.968	-0.59
1425875_a_at	Lepr	leptin receptor	1.21	0.682	-1.67	0.007	-1.14	0.393	-1.13	0.248	-0.68
1442110_at	Smyd3	SET and MYND domain containing 3	-1.69	0.348	1.21	0.64	-1.12	0.692	-1.42	0.333	-0.75
1434262_at	---	---	1.06	0.599	-1.46	0.364	-1.05	0.786	-1.45	0.243	-0.73
1428434_at	Zcchc12	zinc finger, CCHC domain containing 12	-1.2	0.418	1.02	0.971	-1.19	0.1	-1.33	0.455	-0.67
1417421_at	S100a1	S100 calcium binding protein A1	-1.13	0.183	1	0.982	-1.24	0.095	-1.2	0.357	-0.64
1416484_at	Ttc3	tetratricopeptide repeat domain 3	1.05	0.834	-1.38	0.128	-1.09	0.661	-1.63	0.367	-0.76
1452931_at	2810408M09Rik	RIKEN cDNA 2810408M09 gene	-1.41	0.184	1.13	0.565	-1.18	0.525	-1.7	0.096	-0.79
1453991_at	Cenpo	centromere protein O	1.08	0.8	-1.19	0.543	-1.29	0.301	-1.7	0.42	-0.78
1448331_at	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	-1.04	0.264	-1.23	0.019	-1.1	0.413	1.15	0.442	-0.55
1457704_at	Zfp533	zinc finger protein 533	-1.03	0.864	-1.14	0.654	-1.19	0.466	1.01	0.962	-0.59
1447405_at	AI449023	Expressed sequence AI449023	1.5	0.087	-4.61	0	-1.02	0.972	-1.12	0.814	-1.31
1416909_at	1810008A14Rik	RIKEN cDNA 1810008A14 gene	-1.03	0.818	-1.01	0.899	-1.37	0.169	1.02	0.743	-0.6
1416313_at	Mllt11	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	1.01	0.968	-1.03	0.939	-1.41	0.004	-1.6	0.053	-0.76
1452054_at	Ube2w	ubiquitin-conjugating enzyme E2W (putative)	-1.24	0.386	1.15	0.325	-1.35	0.077	-1.36	0.174	-0.7
1429513_at	1700019M22Rik	RIKEN cDNA 1700019M22 gene	-1.15	0.204	-1.44	0.305	1.13	0.587	-1.13	0.458	-0.65
1428052_a_at	Zmym1	zinc finger, MYM domain containing 1	1.03	0.8	-1.16	0.414	-1.25	0.073	-1.1	0.573	-0.62
1446585_at	Dlgh2	Discs, large homolog 2 (Drosophila)	-2.67	0	-1.4	0.262	1.6	0.158	-1.49	0.343	-0.99
1424403_a_at	Rufy3	RUN and FYVE domain containing 3	-1.11	0.003	-1.52	0.146	1.13	0.558	-1.04	0.862	-0.63
1441238_at	9030416H16Rik	RIKEN cDNA 9030416H16 gene	-1.04	0.874	-1.41	0.051	1.02	0.964	-1.13	0.774	-0.64
1442232_at	C530025M09Rik	RIKEN cDNA C530025M09 gene	-1.17	0.596	-1.38	0.243	1.11	0.617	-1.94	0.159	-0.84
1458133_at	---	---	1.2	0.242	-1.71	0.008	-1.11	0.583	-1.54	0.081	-0.79
1435894_at	C030014L02	hypothetical protein C030014L02	-1.05	0.957	-1.35	0.725	1	0.987	-1.08	0.929	-0.62
1435029_at	---	---	-1.06	0.607	-1.04	0.662	-1.28	0.237	1.59	0.096	-0.45
1426671_a_at	Rbm39	RNA binding motif protein 39	-1.11	0.559	1.01	0.912	-1.28	0.1	-1.31	0.086	-0.67
1442669_at	---	---	-1.65	0.49	1.11	0.803	-1.03	0.962	-1.29	0.712	-0.71
1431518_at	Ptchd3	patched domain containing 3	-1.83	0.161	-1.31	0.532	1.38	0.547	-1.05	0.832	-0.7
1435395_s_at	Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	-1.13	0.017	-1.03	0.724	-1.2	0.057	1.09	0.094	-0.57
1459004_at	---	---	-1.16	0.617	-1.72	0.051	1.25	0.221	-1.46	0.277	-0.77
1418115_s_at	Ifrg15	interferon alpha responsive gene	-1.1	0.085	-1.11	0.47	-1.14	0.331	1.07	0.713	-0.57
1443193_at	Ttll1	tubulin tyrosine ligase-like 1	1.21	0.561	-1.73	0.441	-1.1	0.801	-2.19	0.075	-0.95
1420367_at	Denr	density-regulated protein	-1.17	0.008	1.05	0.643	-1.26	0.235	-1.03	0.885	-0.6
1429731_at	6530403G13Rik	RIKEN cDNA 6530403G13 gene	-1.05	0.919	-1.09	0.793	-1.21	0.574	1.41	0.264	-0.49
1454541_at	4921522E08Rik	RIKEN cDNA 4921522E08 gene	1.31	0.511	-1.5	0.361	-1.4	0.269	-1.52	0.49	-0.78
1447143_at	Phf14	PHD finger protein 14	1.18	0.752	-1.31	0.458	-1.33	0.323	-1.27	0.372	-0.68
1441209_at	Rin2	Ras and Rab interactor 2	1.05	0.888	-1.11	0.777	-1.35	0.438	-1.56	0.066	-0.74
1436029_at	Bicc1	bicaudal C homolog 1 (Drosophila)	-1.06	0.751	1.11	0.49	-1.56	0.115	-1.4	0.166	-0.73
1424478_at	Bbs2	Bardet-Biedl syndrome 2 homolog (human)	1.11	0.333	-1.64	0.401	-1.02	0.726	-1.32	0.071	-0.72
1435754_at	2810482G21Rik	RIKEN cDNA 2810482G21 gene	-1.17	0.068	1.06	0.431	-1.27	0.159	-1.7	0.152	-0.77
1448839_at	Ankrd47	ankyrin repeat domain 47	1.07	0.785	-1.24	0.012	-1.22	0.376	-1.3	0.391	-0.67
1441935_at	Ankra2	ankyrin repeat, family A (RFXANK-like), 2	-1.49	0.218	-1.52	0.327	1.36	0.265	-1.11	0.38	-0.69
1448936_at	Stx12	syntaxin 12	-1.06	0.532	-1.08	0.351	-1.22	0.127	1.09	0.527	-0.56
1442745_x_at	C79248	expressed sequence C79248	-1.06	0.787	1.07	0.666	-1.46	0.009	-1.84	0.078	-0.82
1428385_at	8-Mar	membrane-associated ring finger (C3HC4) 8	-1.18	0.34	-1.11	0.508	-1.06	0.647	3.9	0.153	0.14
1439435_x_at	Pgk1 /// LOC43359	phosphoglycerate kinase 1 /// phosphoglycerate kinase 1-like /// phosphoglycerat	-1.2	0.416	-1.5	0.02	1.19	0.455	-1.21	0.439	-0.68

1426752_at	Phf17	PHD finger protein 17	-1.03	0.735	-1.13	0.414	-1.2	0.163	1.1	0.533	-0.56
1426878_at	Pb1	polybromo 1	-1.01	0.953	-1.08	0.575	-1.29	0.072	1.36	0.413	-0.5
1439716_at	Piwil4	piwi-like homolog 4 (Drosophila)	-1.48	0.44	1.34	0.613	-1.48	0.095	-2.14	0.335	-0.94
1455979_at	Arid1b	AT rich interactive domain 1B (Swi1 like)	-1.13	0.495	1.05	0.683	-1.32	0.054	-1.44	0.166	-0.71
1459871_x_at	2-Mar	membrane-associated ring finger (C3HC4) 2	-1.09	0.576	-1.14	0.359	-1.11	0.771	2.89	0.286	-0.11
1433798_a_at	E330034G19Rik	RIKEN cDNA E330034G19 gene	-1.02	0.941	-1.03	0.922	-1.34	0.368	1.01	0.979	-0.6
1425383_a_at	Pbx1 /// LOC67687	pre B-cell leukemia transcription factor 1 /// region containing RIKEN cDNA 2310(	-1.1	0.758	-1.12	0.585	-1.12	0.647	1.22	0.502	-0.53
1428961_a_at	Sfrs16	splicing factor, arginine/serine-rich 16 (suppressor-of-white-apricot homolog, Dros	-1.47	0.102	-1.03	0.789	1.05	0.649	-1.22	0.406	-0.67
1450581_at	Galr3	galanin receptor 3	-1.91	0.104	-1.11	0.544	1.27	0.224	-1.42	0.309	-0.79
1425108_a_at	BC004728	cDNA sequence BC004728	1.11	0.526	-1.26	0.034	-1.27	0.052	-1.04	0.863	-0.61
1450347_at	Syt10	synaptotagmin X	-2.42	0.089	1.34	0.526	-1.07	0.828	-1.44	0.209	-0.89
1432521_at	Mxra8	matrix-remodelling associated 8	-1.24	0.028	-1.25	0.49	1.09	0.523	-1.14	0.606	-0.64
1447244_at	Cybasc3	cytochrome b, ascorbate dependent 3	1.5	0.363	-1.37	0.362	-2.13	0.106	-2.2	0.271	-1.05
1436012_s_at	Scrn2	secernin 2	1.15	0.338	-1.6	0.136	-1.09	0.73	-1.22	0.186	-0.69
1415816_at	Cct7	chaperonin subunit 7 (eta)	-1.12	0.398	-1.19	0.006	-1.04	0.589	1.05	0.712	-0.58
1417247_at	AI597479	expressed sequence AI597479	-1.14	0.02	1.03	0.752	-1.27	0.129	-1.19	0.478	-0.64
1442942_at	Wbscr1	Williams-Beuren syndrome chromosome region 1 homolog (human)	-1.06	0.875	-1.61	0.435	1.13	0.68	-2.26	0.095	-0.95
1423649_at	Tmem68	transmembrane protein 68	1.06	0.601	-1.1	0.225	-1.38	0.082	-1.09	0.196	-0.63
1427389_at	BC021785	cDNA sequence BC021785	-1.14	0.428	1.1	0.88	-1.4	0.164	-1.31	0.015	-0.69
1437582_at	Acss1	acyl-CoA synthetase short-chain family member 1	1.12	0.827	-1.36	0.58	-1.19	0.77	-2.93	0.16	-1.09
1436610_at	Ankrd12	ankyrin repeat domain 12	1.11	0.349	-1.28	0.38	-1.25	0.556	-1.01	0.964	-0.61
1416610_a_at	Clcn3	chloride channel 3	-1.12	0.059	-1.09	0.088	-1.13	0.32	2.46	0.224	-0.22
1454161_s_at	0610007P14Rik	RIKEN cDNA 0610007P14 gene	-1.21	0.531	-1.05	0.592	-1.09	0.748	1.09	0.642	-0.57
1442928_at	Kpna4	Karyopherin (importin) alpha 4	1.5	0.075	-1.67	0.012	-1.67	0	-1.46	0.061	-0.83
1458776_at	---	---	-1.13	0.741	-1.1	0.747	-1.12	0.387	1.32	0.169	-0.51
1455773_at	Picalm	Phosphatidylinositol binding clathrin assembly protein	-1.03	0.91	-1.2	0.09	-1.13	0.54	1.9	0.12	-0.36
1441389_at	---	Transcribed locus	1.03	0.89	-1.14	0.764	-1.26	0.288	-1.18	0.371	-0.64
1425813_at	Pign	phosphatidylinositol glycan anchor biosynthesis, class N	-1.2	0.743	-1.39	0.653	1.14	0.743	-1.24	0.696	-0.67
1423159_at	Dld	dihydrolipoamide dehydrogenase	-1.18	0.224	-1.14	0.034	-1.03	0.877	1.09	0.569	-0.57
1428352_at	Arrdc2	arrestin domain containing 2	-1.09	0.775	-1.25	0.457	-1.02	0.967	1.13	0.613	-0.56
1443202_at	Cyb5b	Cytochrome b5 type B	-1.01	0.987	-1.06	0.846	-1.33	0.204	1.07	0.815	-0.58
1452669_at	2810012G03Rik	RIKEN cDNA 2810012G03 gene	-1.25	0.338	1.03	0.728	-1.16	0.451	-1.04	0.538	-0.6
1418560_at	Pdha1	pyruvate dehydrogenase E1 alpha 1	-1.18	0.028	-1.25	0.157	1.05	0.837	-1.03	0.855	-0.6
1433249_at	4931409D07Rik	RIKEN cDNA 4931409D07 gene	1.43	0.145	-1.89	0.343	-1.36	0.468	-1.28	0.773	-0.77
1459289_at	Pde4d	Phosphodiesterase 4D, cAMP specific	-1.56	0.318	1.58	0.495	-2.1	0.072	-1.44	0.381	-0.88
1443809_at	Ptn	Pleiotrophin	-1.34	0.739	-1.28	0.594	1.17	0.771	-2.01	0.247	-0.87
1424525_at	Grp	gastrin releasing peptide	-1.2	0.735	1.38	0.438	-2.1	0.06	-1.43	0.437	-0.83
1434587_x_at	Ptdss2	phosphatidylserine synthase 2	-1.07	0.338	-1.25	0.214	-1.04	0.82	4.07	0.192	0.18
1429291_at	Psmd1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	-1.1	0.19	-1.17	0.026	-1.07	0.186	1.47	0.149	-0.47
1417086_at	Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	-1.27	0.331	-1.24	0.064	1.1	0.663	-1.07	0.74	-0.62
1436724_a_at	Lgtn	ligatin	-1.02	0.611	-1.18	0.117	-1.16	0.134	1.1	0.385	-0.56
1446623_at	---	---	-1.04	0.867	-3.85	0.133	1.47	0.514	-2.12	0.346	-1.38
1435143_at	Pctk2	PCTAIRE-motif protein kinase 2	1.16	0.217	-1.28	0.397	-1.33	0.075	-1.57	0.097	-0.75
1447437_at	Acsm1	Acyl-CoA synthetase medium-chain family member 1	-1.13	0.747	-1.25	0.293	1.01	0.978	-1.12	0.794	-0.62
1421271_at	Sh3rf1	SH3 domain containing ring finger 1	-1.21	0.432	-1.52	0.428	1.21	0.545	-1.04	0.916	-0.64
1443729_at	Mtss1	metastasis suppressor 1	-1.17	0.305	1.07	0.112	-1.3	0.231	-1.31	0.163	-0.68
1443055_at	B230369F24Rik	RIKEN cDNA B230369F24 gene	-3.25	0.005	1.46	0.701	-1.08	0.901	-2.42	0.296	-1.32
1458018_at	Ppm1h	Protein phosphatase 1H (PP2C domain containing)	-1.07	0.838	1.18	0.619	-1.73	0.03	-1.28	0.477	-0.72
1454760_at	Htatsf1	HIV TAT specific factor 1	-1.17	0.457	1.04	0.734	-1.25	0.126	-1.07	0.607	-0.61
1442477_at	---	---	-1.48	0.224	1.29	0.376	-1.36	0.042	-1.29	0.036	-0.71
1433486_at	Clcn3	chloride channel 3	-1.03	0.819	-1.05	0.648	-1.3	0.013	2.4	0.188	-0.24
1431641_at	9330161L09Rik	RIKEN cDNA 9330161L09 gene	-1.12	0.865	-1.84	0.247	1.26	0.468	-1.13	0.515	-0.71
1455943_at	Zfp451	zinc finger protein 451	-1.08	0.778	1.03	0.882	-1.36	0.317	-1.1	0.549	-0.63

1451145_s_at	Tmem111	transmembrane protein 111	-1.08	0.102	-1.01	0.854	-1.28	0.001	1.06	0.474	-0.58
1416812_at	Tia1	cytotoxic granule-associated RNA binding protein 1	-1.07	0.47	1.02	0.88	-1.34	0.049	-1.54	0.15	-0.73
1426618_a_at	Pomgnt1	protein O-linked mannose beta1,2-N-acetylglucosaminyltransferase	1.01	0.912	-1.23	0.018	-1.14	0.109	-1.4	0.079	-0.69
1452343_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	-1.06	0.711	-1.44	0.149	1.06	0.782	-1.5	0.122	-0.73
1438644_x_at	Commd9	COMM domain containing 9	-1.14	0.382	1.08	0.36	-1.35	0.055	-1.27	0.111	-0.67
1458407_s_at	AI429294	Expressed sequence AI429294	-1.07	0.766	-1.14	0.812	-1.13	0.407	1.05	0.79	-0.57
1458568_at	Tusc3	Tumor suppressor candidate 3	1.15	0.791	-1.32	0.61	-1.27	0.511	-1.03	0.959	-0.62
1444086_at	E030049G20Rik	RIKEN cDNA E030049G20 gene	-1.13	0.594	1.02	0.96	-1.27	0.254	-1.48	0.307	-0.71
1456146_at	Osbpl10	oxysterol binding protein-like 10	-1.31	0.156	-1.36	0.478	1.2	0.167	-1.21	0.197	-0.67
1458524_at	Fndc3a	fibronectin type III domain containing 3a	-1.18	0.508	1.04	0.849	-1.24	0.134	-1.47	0.277	-0.71
1445165_at	1200003I07Rik	RIKEN cDNA 1200003I07 gene	1.33	0.725	-1.17	0.815	-1.94	0.05	-1.55	0.048	-0.83
1422742_at	Hivep1	human immunodeficiency virus type I enhancer binding protein 1	-1.13	0.544	-1.28	0.011	1.03	0.851	-1.31	0.062	-0.67
1419459_a_at	2610529C04Rik	RIKEN cDNA 2610529C04 gene	-1.03	0.896	-1.12	0.543	-1.2	0.438	1.63	0.031	-0.43
1420422_at	Pcdhb21	protocadherin beta 21	1.21	0.834	-1.39	0.605	-1.31	0.062	-1.36	0.182	-0.71
1424026_s_at	BC013529	cDNA sequence BC013529	-1.13	0.16	-1.1	0.582	-1.11	0.047	1.03	0.525	-0.58
1460072_at	---	Transcribed locus	-1.6	0.263	1.41	0.273	-1.52	0.205	-1.55	0.346	-0.81
1448882_at	Tmem93	transmembrane protein 93	1.01	0.658	-1.08	0.138	-1.32	0.075	-1.21	0.188	-0.65
1424121_at	Commd1	COMM domain containing 1	-1.06	0.75	-1.03	0.798	-1.28	0.277	1.13	0.581	-0.56
1439236_at	D15Ertd509e	DNA segment, Chr 15, ERATO Doi 509, expressed	1.27	0.637	-1.48	0.188	-1.32	0.096	-1.91	0.041	-0.86
1430091_at	1700001P01Rik	RIKEN cDNA 1700001P01 gene	-1.38	0.244	1.1	0.416	-1.15	0.551	-1.17	0.594	-0.65
1426017_a_at	0610011L14Rik	RIKEN cDNA 0610011L14 gene	-1.17	0.326	-1.19	0.225	1	0.971	-1.02	0.817	-0.6
1422285_at	Otp	orthopedia homolog (Drosophila)	-2.25	0.096	-1.68	0.059	1.66	0.181	-1.94	0.375	-1.05
1451251_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.06	0.357	-1.08	0.524	-1.21	0.225	1.04	0.814	-0.58
1424586_at	Ehbp1	EH domain binding protein 1	-1.13	0.487	-1.1	0.363	-1.1	0.685	1.07	0.816	-0.57
1428274_s_at	Abhd13	abhydrolase domain containing 13	1.04	0.859	-1.24	0.451	-1.18	0.177	-1.13	0.566	-0.63
1449007_at	Btg3 /// LOC64041(	B-cell translocation gene 3 /// similar to BTG3 protein (Tob5 protein) (Abundant in	-1.14	0.306	-1.06	0.707	-1.14	0.218	1.6	0.204	-0.43
1443529_at	Rutbc2	RUN and TBC1 domain containing 2	-1.06	0.059	1.01	0.994	-1.33	0.568	-1.21	0.776	-0.65
1427100_at	Metrn	meteorin, glial cell differentiation regulator	-1.82	0.346	-1.55	0.348	1.5	0.255	-1.69	0.329	-0.89
1444172_at	---	Transcribed locus	1.29	0.761	-1.34	0.536	-1.5	0.058	-1.28	0.651	-0.71
1454739_at	Cdc27	cell division cycle 27 homolog (S. cerevisiae)	-1.09	0.518	-1.01	0.899	-1.27	0.014	1.33	0.216	-0.51
1442025_a_at	---	---	1.02	0.987	-1.14	0.809	-1.24	0.718	-2.06	0.287	-0.86
1456752_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330038P	1.08	0.893	-1.54	0.477	-1.03	0.916	-1.03	0.899	-0.63
1446153_at	Zfp608	Zinc finger protein 608	-1.5	0.674	1.21	0.552	-1.22	0.53	-1.21	0.763	-0.68
1443712_x_at	Ccdc82	Coiled-coil domain containing 82	1.05	0.94	-1.12	0.817	-1.32	0.393	-2.11	0.161	-0.87
1451870_a_at	Brd4	bromodomain containing 4	1.17	0.705	-1.06	0.815	-1.69	0.308	-1.31	0.122	-0.72
1439830_at	LOC675366	similar to mitogen activated protein kinase kinase kinase 5	-1.26	0.609	-1.5	0.246	1.24	0.34	-1.34	0.194	-0.71
1428187_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	-1.01	0.963	-1.11	0.574	-1.25	0.315	1.09	0.687	-0.57
1439213_at	4921524J06Rik	RIKEN cDNA 4921524J06 gene	1.37	0.006	-1.25	0.558	-1.89	0.006	-1.41	0.15	-0.8
1437962_at	Gm443	gene model 443, (NCBI)	-2.97	0.334	1.43	0.391	-1.07	0.876	-1.2	0.707	-0.95
1435498_at	Arfip2	ADP-ribosylation factor interacting protein 2	1.07	0.453	-1.06	0.648	-1.46	0.045	-1.06	0.656	-0.63
1435567_at	Phka1	phosphorylase kinase alpha 1	-1.28	0.065	-1.04	0.599	-1.05	0.791	1.13	0.593	-0.56
1431501_at	1700037C18Rik	RIKEN cDNA 1700037C18 gene	-1.07	0.626	-1.74	0.294	1.19	0.486	-1.49	0.134	-0.78
1429751_at	Zswim2	zinc finger, SWIM domain containing 2	-1.24	0.576	-1.02	0.961	-1.1	0.84	1.52	0.014	-0.46
1423605_a_at	Mdm2	transformed mouse 3T3 cell double minute 2	-1.12	0.547	-1.01	0.849	-1.23	0.065	1.12	0.226	-0.56
1441573_at	Scmh1	Sex comb on midleg homolog 1	1.13	0.217	-1.11	0.468	-1.48	0.045	-1.64	0.163	-0.78
1423175_s_at	Pard6b	par-6 (partitioning defective 6) homolog beta (C. elegans)	-1.14	0.077	-1.42	0.335	1.11	0.701	-1.16	0.599	-0.65
1428410_at	Nat13	N-acetyltransferase 13	-1.11	0.441	-1.07	0.466	-1.16	0.29	1.26	0.334	-0.52
1416003_at	Cldn11	claudin 11	-1.29	0.581	-1.75	0.494	1.35	0.416	-1.42	0.598	-0.78
1432474_a_at	Krtcap3	keratinocyte associated protein 3	1	0.999	-1.07	0.824	-1.3	0.252	-1.35	0.132	-0.68
1456992_at	Ube3c	ubiquitin protein ligase E3C	1.05	0.818	-1	0.996	-1.53	0.031	-1.11	0.62	-0.65
1440627_at	Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	-2.03	0.127	-1.37	0.16	1.48	0.216	-1.21	0.417	-0.78
1444829_at	C78532	expressed sequence C78532	1.61	0.485	-3.09	0.016	-1.3	0.41	-1.04	0.864	-0.96
1444022_at	---	---	-1.37	0.5	-1.13	0.712	1.08	0.734	-1.5	0.105	-0.73

1415934_at	Cops8	COP9 (constitutive photomorphogenic) homolog, subunit 8 (Arabidopsis thaliana)	1	0.981	-1.13	0.342	-1.23	0.076	-1.19	0.128	-0.64
1449354_at	U2af1-rs1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 1	-1.13	0.251	-1.22	0.047	-1.01	0.942	1.1	0.709	-0.56
1438183_x_at	Sord	sorbitol dehydrogenase	-1.12	0.604	-1.2	0.421	-1.03	0.763	2.1	0.259	-0.31
1438520_at	Slc25a36	solute carrier family 25, member 36	-1.15	0.4	1.09	0.779	-1.35	0.096	-1.24	0.404	-0.66
1437265_at	5330438D12Rik	RIKEN cDNA 5330438D12 gene	-1.13	0.114	-1.35	0.276	1.07	0.729	-1.68	0.178	-0.77
1436852_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-1.05	0.71	-1.1	0.639	-1.2	0.225	1.26	0.523	-0.52
1455244_at	Daam1	dishevelled associated activator of morphogenesis 1	-1.01	0.85	-1.07	0.665	-1.29	0.111	2.77	0.229	-0.15
1430583_at	C130076O07Rik	RIKEN cDNA C130076O07 gene	1.3	0.494	-1.11	0.719	-1.98	0.087	-1.12	0.867	-0.73
1458838_at	4732468M13Rik	RIKEN cDNA 4732468M13 gene	-1.74	0.344	1.38	0.381	-1.35	0.316	-1.6	0.333	-0.82
1441108_at	---	12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D23003	-1.02	0.923	1.12	0.125	-1.69	0.021	-1.18	0.47	-0.69
1418083_at	0610009B22Rik	RIKEN cDNA 0610009B22 gene	-1.15	0.191	-1.03	0.779	-1.16	0.262	1.26	0.295	-0.52
1430951_at	2810011L19Rik	RIKEN cDNA 2810011L19 gene	-1.02	0.97	1	0.995	-1.4	0.215	-1.27	0.625	-0.67
1423481_at	Riok2	RIO kinase 2 (yeast)	-1.23	0.362	-1.17	0.097	1.03	0.825	-1.42	0.025	-0.7
1427443_at	LOC625794	Hypothetical protein LOC625794	-1.95	0.038	1.34	0.571	-1.18	0.694	-1.01	0.989	-0.7
1434025_at	---	---	-1.12	0.698	-1.16	0.761	-1.06	0.626	5.7	0.26	0.59
1441571_at	2410089E03Rik	RIKEN cDNA 2410089E03 gene	-1.1	0.819	1.15	0.601	-1.57	0.011	-1.2	0.491	-0.68
1437861_s_at	---	---	-1.19	0.187	1.04	0.747	-1.22	0.267	-1.52	0.075	-0.72
1418996_a_at	4930469P12Rik	RIKEN cDNA 4930469P12 gene	-1.07	0.693	-1.31	0.014	1	0.992	-1.12	0.482	-0.62
1427444_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	-1.13	0.715	-1.14	0.772	-1.07	0.829	1.39	0.287	-0.49
1433755_at	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis	-1.01	0.873	-1.02	0.836	-1.36	0.04	1.23	0.319	-0.54
1444758_at	Traf3	Tnf receptor-associated factor 3	1.04	0.895	-1.1	0.813	-1.33	0.368	-1.35	0.399	-0.69
1423010_at	Sacs	sacsin	-1.39	0.511	-1.12	0.226	1.09	0.459	-1.04	0.906	-0.62
1451696_at	Zfp64	zinc finger protein 64	-2.06	0.257	-1	0.998	1.22	0.559	-2.31	0.485	-1.04
1452845_at	Hif1an	hypoxia-inducible factor 1, alpha subunit inhibitor	1.43	0.075	-1.24	0.543	-2.16	0.084	-2.26	0.348	-1.06
1458563_at	Zfp668	zinc finger protein 668	-1.14	0.738	1.21	0.61	-1.63	0.432	-1.42	0.619	-0.74
1430393_at	2510017J16Rik	RIKEN cDNA 2510017J16 gene	-1.22	0.329	1.24	0.462	-1.56	0.165	-1.18	0.29	-0.68
1440081_at	4631422C13Rik	RIKEN cDNA 4631422C13 gene	1.09	0.818	-1.56	0.228	-1.03	0.778	-1.33	0.104	-0.71
1454734_at	---	---	1.11	0.581	-1.29	0.482	-1.22	0.332	-5.73	0.043	-1.78
1431355_s_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	1.13	0.346	-1.04	0.851	-1.63	0.082	-1.11	0.655	-0.66
1435159_at	9430038I01Rik	RIKEN cDNA 9430038I01 gene	-1.47	0.035	1.13	0.674	-1.12	0.578	-1.31	0.172	-0.69
1446506_at	B930041G04	hypothetical protein B930041G04	-1.26	0.597	-1.22	0.589	1.09	0.72	-1.85	0.12	-0.81
1434970_a_at	---	---	-1.12	0.289	-1.03	0.74	-1.2	0.176	1.07	0.731	-0.57
1442654_at	A530054K11Rik	RIKEN cDNA A530054K11 gene	1.04	0.836	-1.09	0.417	-1.34	0.266	-1.49	0.038	-0.72
1443825_x_at	Spaca3	sperm acrosome associated 3	-1.31	0.67	1.32	0.601	-1.61	0.306	-1.07	0.838	-0.67
1441370_at	H2afz	H2A histone family, member Z	-1.2	0.577	-1.02	0.906	-1.13	0.654	1	0.994	-0.59
1458154_at	---	Transcribed locus	1.39	0.665	-1.65	0.56	-1.41	0.556	-1.84	0.377	-0.88
1450519_a_at	Prkaca	protein kinase, cAMP dependent, catalytic, alpha	-1.15	0.751	-1.07	0.6	-1.11	0.621	1.47	0.009	-0.47
1423190_at	1810020G14Rik	RIKEN cDNA 1810020G14 gene	1.25	0.343	-1.36	0.239	-1.41	0.009	-1.87	0.069	-0.84
1418575_at	Shfm1	split hand/foot malformation (ectrodactyly) type 1	-1.06	0.511	1.02	0.847	-1.37	0.009	-1.22	0.127	-0.65
1439425_x_at	BC024814	cDNA sequence BC024814	1.12	0.723	-1.32	0.451	-1.2	0.617	-1.39	0.304	-0.7
1456668_at	Zcchc11	Zinc finger, CCHC domain containing 11	1.27	0.116	-1.47	0.096	-1.32	0.199	-2.13	0.124	-0.91
1420375_at	Kif3a	kinesin family member 3A	-1.04	0.727	-1.17	0.395	-1.13	0.376	1.45	0.142	-0.47
1424951_at	Baiap2l1	BAI1-associated protein 2-like 1	-1.01	0.956	-1.28	0.21	-1.07	0.533	1.04	0.81	-0.58
1452399_at	Rgs6	regulator of G-protein signaling 6	1.57	0.05	-1.5	0.18	-2.15	0.047	-1.03	0.91	-0.78
1453554_a_at	Wdr33	WD repeat domain 33	-1.23	0.259	-1.13	0.571	1	0.981	-1.18	0.585	-0.63
1444673_at	E030031F02Rik	RIKEN cDNA E030031F02 gene	1.03	0.959	-1.35	0.569	-1.07	0.714	-1.49	0.332	-0.72
1451718_at	Plp1	proteolipid protein (myelin) 1	1.01	0.974	-1.19	0.528	-1.17	0.491	-1.1	0.755	-0.61
1427278_at	Rsnl2	restin-like 2	-1.37	0.003	-1.02	0.9	-1.01	0.966	1.1	0.733	-0.57
1448629_at	Hps4	Hermansky-Pudlak syndrome 4 homolog (human)	-1.1	0.422	-1.13	0.15	-1.09	0.366	1.08	0.57	-0.56
1428587_at	Tmem41b	transmembrane protein 41B	-1.1	0.201	-1.06	0.713	-1.18	0.273	1.44	0.325	-0.47
1421587_at	Klk1b27	kallikrein 1-related peptidase b27	-1.1	0.842	1.1	0.574	-1.44	0.506	-1.28	0.386	-0.68
1450616_at	Ear5	eosinophil-associated, ribonuclease A family, member 5	-2.61	0.039	1.52	0.444	-1.25	0.471	-1.28	0.581	-0.91
1418320_at	Prss8	protease, serine, 8 (prostasin)	1.02	0.882	-1.16	0.711	-1.21	0.179	-2.34	0.164	-0.92

1431375_s_at	Parva	parvin, alpha	1.02	0.893	-1.1	0.348	-1.3	0.107	-1.61	0.228	-0.75
1449841_at	Kif3a	kinesin family member 3A	-1.18	0.07	-1	0.983	-1.17	0.261	1.28	0.291	-0.52
1425237_at	Krtap16-8	keratin associated protein 16-8	1.44	0.364	-1.64	0.364	-1.52	0.196	-1.55	0.514	-0.82
1416499_a_at	Dctn6	dynactin 6	-1.21	0.336	1.18	0.085	-1.44	0.192	-2.15	0.19	-0.9
1443344_at	4932409I22Rik	RIKEN cDNA 4932409I22 gene	1.18	0.728	-1.52	0.071	-1.15	0.574	-1.05	0.822	-0.64
1460286_at	6-Sep	septin 6	-1.05	0.753	-1.83	0.13	1.2	0.554	-2.09	0.038	-0.94
1445086_at	Cyp2j5	Cytochrome P450, family 2, subfamily j, polypeptide 5	1.17	0.794	-1.26	0.235	-1.35	0.554	-1.07	0.767	-0.63
1437997_x_at	Mrpl48	mitochondrial ribosomal protein L48	-1.13	0.537	1.08	0.267	-1.35	0.13	-1.11	0.619	-0.63
1448834_at	Foxm1	forkhead box M1	-1.08	0.786	-1.21	0.487	-1.05	0.658	4.25	0.133	0.23
1453890_at	---	---	-1.25	0.245	1.02	0.774	-1.14	0.453	-1.07	0.751	-0.61
1421029_a_at	Hbs1l	Hbs1-like (S. cerevisiae)	-1.23	0.03	-1.08	0.328	-1.03	0.887	1.21	0.489	-0.54
1442933_at	Foxk2	forkhead box K2	1.1	0.744	-1.15	0.683	-1.37	0.25	-1.06	0.717	-0.62
1435524_at	2010109N14Rik	RIKEN cDNA 2010109N14 gene	-1.05	0.506	1.02	0.843	-1.36	0.108	-1.19	0.154	-0.65
1425361_at	Zfp397	zinc finger protein 397	-1.56	0.055	-2.21	0	1.61	0	-1.21	0.142	-0.84
1435066_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.16	0.332	1.2	0.416	-1.56	0.061	-1.11	0.687	-0.66
1420134_at	RP23-289L21.1	Hypothetical protein LOC433719	-1.41	0.262	1.13	0.887	-1.16	0.737	-1.28	0.244	-0.68
1446496_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	1.27	0.446	-1.49	0.165	-1.32	0.656	-1.24	0.556	-0.69
1449085_at	Phf10	PHD finger protein 10	-1.03	0.892	-1.24	0.065	-1.08	0.58	2.33	0.213	-0.25
1422329_a_at	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	-1.09	0.712	-1.5	0.074	1.12	0.684	-1.45	0.394	-0.73
1428674_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-1.18	0.268	-1.23	0.068	1.04	0.743	-1.4	0.197	-0.69
1423563_at	Prrt1	proline-rich transmembrane protein 1	-1.21	0.552	-1.52	0.098	1.22	0.151	-1.35	0.333	-0.72
1418466_at	Rnf141	ring finger protein 141	-1.6	0.363	-1.43	0.133	1.38	0.284	-1.19	0.541	-0.71
1452645_x_at	Klra22	killer cell lectin-like receptor subfamily A, member 22	-1.33	0.737	-1.2	0.308	1.12	0.575	-1.53	0.631	-0.74
1444458_at	Mgea6	Meningioma expressed antigen 6 (coiled-coil proline-rich)	1.13	0.359	-1.02	0.92	-1.68	0.002	-1.29	0.184	-0.72
1434187_at	---	---	1.14	0.11	-1.18	0.2	-1.39	0.006	-1.23	0.152	-0.67
1458086_at	4732471D19Rik	RIKEN cDNA 4732471D19 gene	1.42	0.078	-1.5	0.208	-1.62	0.076	-1.28	0.446	-0.75
1447576_at	2010001K21Rik	RIKEN cDNA 2010001K21 gene	-1.02	0.983	-1.51	0.464	1.06	0.65	-1.28	0.746	-0.69
1457550_at	9530059O14Rik	RIKEN cDNA 9530059O14 gene	1.59	0.538	-1.58	0.45	-2.07	0.358	-1.8	0.23	-0.96
1436803_a_at	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	-1.04	0.442	-1.2	0.184	-1.1	0.135	1.33	0.163	-0.5
1455465_at	Snx12	Sorting nexin 12	-1.13	0.046	1.03	0.914	-1.26	0.152	-1.3	0.472	-0.67
1429468_at	1110018F16Rik	RIKEN cDNA 1110018F16 gene	-1.15	0.142	1.22	0.353	-1.63	0.037	-1.23	0.442	-0.7
1433656_a_at	Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)	-1.05	0.451	-1.2	0.218	-1.08	0.501	1.11	0.588	-0.56
1432868_at	2310047C04Rik	RIKEN cDNA 2310047C04 gene	1.15	0.616	-1.19	0.62	-1.4	0.401	-1.05	0.82	-0.62
1448822_at	Psmb6	proteasome (prosome, macropain) subunit, beta type 6	1.03	0.476	-1.24	0.028	-1.15	0.155	-1.1	0.368	-0.61
1426272_at	Lmbr1	limb region 1	-1	0.984	-1.07	0.515	-1.3	0.048	1.13	0.468	-0.56
1426360_at	Zc3h11a	zinc finger CCCH type containing 11A	1.03	0.87	-1.22	0.161	-1.18	0.431	-1.18	0.656	-0.63
1445405_at	---	---	1.12	0.69	-1.34	0.546	-1.19	0.297	-1.32	0.477	-0.68
1455769_at	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	1.01	0.941	-1.17	0.672	-1.19	0.392	-1.81	0.284	-0.79
1430006_x_at	1700024B05Rik	RIKEN cDNA 1700024B05 gene	-1.87	0.187	-1.76	0.389	1.6	0.252	-1.29	0.456	-0.83
1437402_x_at	Tmem41b	transmembrane protein 41B	-1.22	0.306	-1.09	0.322	-1.03	0.873	1.21	0.453	-0.53
1436033_at	BC031353	cDNA sequence BC031353	-1.32	0.344	-1.57	0.123	1.31	0.447	-1.34	0.539	-0.73
1436279_at	---	Transcribed locus	-1.16	0.691	1.06	0.873	-1.28	0.366	-1.41	0.719	-0.7
1449783_at	---	---	-1.21	0.203	1.03	0.867	-1.18	0.502	-1.5	0.411	-0.71
1420058_s_at	2410166I05Rik	RIKEN cDNA 2410166I05 gene	-1.25	0.198	1.06	0.416	-1.18	0.163	-1.27	0.065	-0.66
1432636_at	---	---	-1.57	0.018	1.25	0.567	-1.22	0.668	-1.31	0.211	-0.71
1451719_at	Crsp6	cofactor required for Sp1 transcriptional activation, subunit 6	1.4	0.521	-2.34	0.308	-1.14	0.477	-2.79	0.013	-1.22
1441341_at	---	Transcribed locus	-1.22	0.426	-1.19	0.695	1.05	0.697	-1.4	0.523	-0.69
1452144_a_at	Mrpl44	mitochondrial ribosomal protein L44	-1.19	0.088	-1.18	0.046	1.02	0.882	-1.14	0.143	-0.62
1451420_at	2610204L23Rik	RIKEN cDNA 2610204L23 gene	-1.14	0.318	-1.23	0.219	1.01	0.881	-1.31	0.048	-0.67
1429307_s_at	Lzic	leucine zipper and CTNNBIP1 domain containing	-1.43	0.005	1.05	0.811	-1.05	0.39	-1.08	0.229	-0.63
1419070_at	Cys1	cystin 1	-1.1	0.643	-1.49	0.271	1.13	0.733	-1.38	0.598	-0.71
1437038_x_at	1700029I08Rik	RIKEN cDNA 1700029I08 gene	-1.07	0.934	1.19	0.707	-1.72	0.165	-1.14	0.74	-0.69
1424325_at	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	-1.15	0.405	-2.26	0.12	1.4	0.387	-1.71	0.252	-0.93

1457673_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	-1.3	0.269	1.04	0.89	-1.12	0.571	-1.36	0.32	-0.68
1457734_at	Pou3f2	POU domain, class 3, transcription factor 2	1.39	0.718	-3	0.276	-1.01	0.978	-1.06	0.75	-0.92
1447472_at	---	Transcribed locus	1.21	0.647	-1.49	0.531	-1.22	0.216	-1.9	0.189	-0.85
1428937_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	-1.15	0.167	1.06	0.71	-1.28	0.211	-1.36	0.437	-0.68
1427933_at	Vps33b	vacuolar protein sorting 33B (yeast)	-1.05	0.82	1.08	0.806	-1.49	0.064	-1.2	0.392	-0.66
1433675_at	Snord22	small nucleolar RNA, C/D box 22	-1.05	0.872	-1.47	0.097	1.08	0.778	-1.03	0.918	-0.62
1435794_at	BC050254	cDNA sequence BC050254	-1.3	0.059	-1.12	0.505	1.04	0.607	-1.15	0.433	-0.63
1455524_at	2810046L04Rik	RIKEN cDNA 2810046L04 gene	-1.28	0.29	-1.17	0.384	1.07	0.642	-1.04	0.547	-0.61
1435225_s_at	Brpf3	bromodomain and PHD finger containing, 3	-1.16	0.422	-1.16	0.405	-1.02	0.952	3.94	0.105	0.15
1425149_a_at	Pdcl	phosducin-like	-1.13	0.472	1.03	0.796	-1.26	0.055	-1.12	0.378	-0.62
1418700_at	Lias	lipoic acid synthetase	-1.12	0.304	-1.16	0.05	-1.05	0.269	1.12	0.413	-0.55
1446315_at	Acly	ATP citrate lyase	-1.3	0.664	-1.62	0.089	1.32	0.529	-1.34	0.523	-0.74
1437192_x_at	Vdac1	voltage-dependent anion channel 1	-1.1	0.15	-1.18	0.228	-1.05	0.749	1.21	0.309	-0.53
1459833_x_at	Cib2	calcium and integrin binding family member 2	-1.08	0.874	-1.14	0.849	-1.11	0.838	3.66	0.093	0.08
1460404_at	Sr278	stretch responsive protein 278	-1.03	0.427	-1.12	0.293	-1.18	0.263	1.32	0.021	-0.5
1418763_at	Nit2	nitrilase family, member 2	-1.16	0.167	-1.27	0.03	1.06	0.688	-1.21	0.217	-0.65
1424780_a_at	D10Ucla1	DNA segment, Chr 10, University of California at Los Angeles 1	1	0.977	-1.07	0.111	-1.3	0.065	-1.72	0.183	-0.77
1426613_a_at	Snrpb2	U2 small nuclear ribonucleoprotein B	1.12	0.664	-1.28	0.213	-1.24	0.269	-1.48	0.121	-0.72
1457060_at	Anks1b /// LOC544	ankyrin repeat and sterile alpha motif domain containing 1B /// similar to AIDA-1b	-1.1	0.142	-1.21	0.063	-1.03	0.235	1.04	0.614	-0.57
1420916_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	-1.15	0.248	-1.41	0.014	1.13	0.53	-1.12	0.544	-0.64
1457945_at	Eif2s3y	Eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	-1.39	0.575	-1.44	0.262	1.3	0.304	-1.51	0.219	-0.76
1431734_a_at	Dnajb4	DnaJ (Hsp40) homolog, subfamily B, member 4	-1.17	0.413	-1.13	0.696	-1.03	0.924	3.26	0.236	-0.02
1454345_at	1700081H04Rik	RIKEN cDNA 1700081H04 gene	-1.09	0.92	1.08	0.852	-1.41	0.095	-1.2	0.465	-0.66
1436573_at	Scrn3	secernin 3	-1.07	0.652	-1.19	0.093	-1.07	0.554	2.52	0.265	-0.2
1426406_at	Setd8	SET domain containing (lysine methyltransferase) 8	-1.15	0.598	-1.06	0.363	-1.12	0.154	2.17	0.085	-0.29
1452761_a_at	8430436O14Rik	RIKEN cDNA 8430436O14 gene	-1	0.981	1.15	0.539	-1.78	0.024	-1.86	0.124	-0.87
1432284_at	Mipol1	mirror-image polydactyly gene 1 homolog (human)	1.22	0.636	-1.41	0.622	-1.28	0.411	-1.25	0.486	-0.68
1429763_at	Cnih4	cornichon homolog 4 (Drosophila)	-1.11	0.207	-1.03	0.745	-1.19	0.209	1.14	0.544	-0.55
1432427_at	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	-1.36	0.249	-1.11	0.725	1.08	0.758	-1.15	0.769	-0.64
1423976_at	4930453N24Rik	RIKEN cDNA 4930453N24 gene	-1.05	0.806	-1.04	0.842	-1.27	0.145	1.01	0.872	-0.59
1428883_at	Tmem57	transmembrane protein 57	-1.06	0.816	-1.2	0.255	-1.08	0.555	1.04	0.857	-0.57
1444100_at	Pdpn	podoplanin	-1.11	0.505	1.02	0.956	-1.27	0.097	-1.87	0.145	-0.81
1459707_at	Pacs1	Phosphofurin acidic cluster sorting protein 1	1.15	0.309	-1	0.998	-1.8	0.053	-1.39	0.208	-0.76
1434988_x_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	-1.51	0.475	-1.53	0.168	1.4	0.35	-1.01	0.96	-0.67
1417444_at	E2f5	E2F transcription factor 5	-1.31	0.052	1.07	0.517	-1.14	0.368	-1.41	0.014	-0.7
1447636_x_at	Tmco4	transmembrane and coiled-coil domains 4	-1.24	0.506	1.1	0.47	-1.25	0.389	-1.31	0.073	-0.68
1459681_at	---	---	-1.75	0.331	1.16	0.796	-1.02	0.937	-1.57	0.295	-0.8
1447188_at	---	Transcribed locus	-1.33	0.498	1.12	0.568	-1.19	0.752	-1.15	0.452	-0.64
1456355_s_at	2810002G02Rik ///	RIKEN cDNA 2810002G02 gene /// region containing RIKEN cDNA 2810002G02	-1.11	0.634	-1.11	0.477	-1.11	0.688	1.3	0.195	-0.51
1444299_at	A430093F15Rik	RIKEN cDNA A430093F15 gene	-1.01	0.872	-1.9	0.215	1.19	0.686	-1.36	0.472	-0.77
1452812_at	Lphn1	latrophilin 1	-1.73	0.016	-1.07	0.893	1.19	0.456	-1.16	0.634	-0.69
1440790_x_at	5033414K04Rik	RIKEN cDNA 5033414K04 gene	-1.01	0.976	1.35	0.443	-2.71	0.027	-1.94	0.105	-1.08
1430271_x_at	Josd3	Josephin domain containing 3	-1.04	0.852	-1.75	0.114	1.17	0.255	-1.44	0.274	-0.76
1435715_x_at	Tdg /// LOC545124	thymine DNA glycosylase /// similar to thymine DNA glycosylase isoform 2 /// simi	-1.08	0.566	-1.15	0.028	-1.1	0.501	1.33	0.211	-0.5
1440699_at	Mtap2	microtubule-associated protein 2	-2	0.309	1.32	0.622	-1.12	0.829	-3.61	0.059	-1.35
1426495_at	2410042D21Rik	RIKEN cDNA 2410042D21 gene	-1.04	0.853	-1.14	0.533	-1.16	0.491	1.22	0.588	-0.53
1444251_x_at	D4Ertd111e	DNA segment, Chr 4, ERATO Doi 111, expressed	-1.23	0.58	1.25	0.395	-1.56	0.091	-1.1	0.774	-0.66
1441415_at	Spred2	Sprouty-related, EVH1 domain containing 2	-1.02	0.882	-1.11	0.725	-1.21	0.651	1.1	0.695	-0.56
1433531_at	Acsl4	acyl-CoA synthetase long-chain family member 4	-1.1	0.358	-1.03	0.749	-1.2	0.1	1.07	0.419	-0.57
1429477_at	D15Ertd785e	DNA segment, Chr 15, ERATO Doi 785, expressed	-1.1	0.715	-1.07	0.776	-1.16	0.597	1.23	0.471	-0.53
1455427_at	Angpt4	angiopoietin 4	-1.04	0.876	1.03	0.889	-1.41	0.064	-1.31	0.465	-0.68
1459203_at	Ipo8	importin 8	1.06	0.851	-1.15	0.68	-1.28	0.294	-1.31	0.213	-0.67
1419643_s_at	2310057J18Rik /// 2	RIKEN cDNA 2310057J18 gene /// RIKEN cDNA 2310065H11 gene	-2.68	0.069	-1.14	0.635	1.46	0.413	-1.23	0.65	-0.9

1416170_at	Trap1	TNF receptor-associated protein 1	-1.1	0.639	-1.22	0.125	-1.02	0.836	1.12	0.508	-0.56
1454593_at	Fgd3	FYVE, RhoGEF and PH domain containing 3	-1.18	0.746	-1.2	0.263	1.03	0.934	-1.49	0.256	-0.71
1436911_at	Ss18l1	synovial sarcoma translocation gene on chromosome 18-like 1	-1.16	0.436	-1.27	0.076	1.06	0.825	-1.6	0.259	-0.74
1425363_at	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	-1.11	0.731	-1.28	0.727	1.03	0.941	-1.76	0.005	-0.78
1422350_at	Fpr-rs3	formyl peptide receptor, related sequence 3	-1.24	0.601	-1.05	0.931	-1.06	0.882	1.69	0.069	-0.41
1437613_s_at	AW456874	expressed sequence AW456874	-1.18	0.205	-1.11	0.851	-1.04	0.864	1.03	0.924	-0.58
1459976_s_at	Sod1	superoxide dismutase 1, soluble	-1.02	0.884	-1.02	0.885	-1.33	0.01	1.01	0.957	-0.59
1433196_at	9530006O14Rik	RIKEN cDNA 9530006O14 gene	-1.16	0.61	-1.03	0.93	-1.15	0.44	1.23	0.601	-0.53
1450169_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	-2.06	0.27	1.25	0.713	-1.03	0.959	-1.27	0.797	-0.78
1415704_a_at	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	-1.07	0.586	-1.11	0.459	-1.15	0.493	1.04	0.721	-0.57
1453982_at	Mdm4	transformed mouse 3T3 cell double minute 4	1.05	0.444	-1.45	0.449	-1.03	0.896	-1.37	0.527	-0.7
1440557_at	Ipw	imprinted gene in the Prader-Willi syndrome region	1.2	0.778	-1.88	0.016	-1.02	0.967	-1.17	0.788	-0.72
1426729_at	2900046G09Rik	RIKEN cDNA 2900046G09 gene	1.57	0.402	-2.89	0.004	-1.26	0.156	-1.17	0.657	-0.94
1436762_x_at	Elp3	Elongation protein 3 homolog (S. cerevisiae)	1.01	0.874	-1.1	0.326	-1.27	0.111	-1.35	0.121	-0.68
1442128_at	Reep5	Receptor accessory protein 5	-1.24	0.438	1.12	0.705	-1.28	0.178	-1.35	0.335	-0.69
1457057_at	1700042G07Rik	RIKEN cDNA 1700042G07 gene	1.05	0.901	-1.12	0.86	-1.31	0.298	-1.03	0.952	-0.6
1440153_at	---	Adult male brain cDNA, RIKEN full-length enriched library, clone:3526403L10 prc	-1.07	0.465	1.18	0.519	-1.68	0.02	-1.33	0.304	-0.72
1456297_at	Tscot	thymic stromal cotransporter	-2.04	0.409	1.42	0.206	-1.25	0.438	-1.65	0.404	-0.88
1435362_at	Foxj3	forkhead box J3	1.01	0.917	-1.18	0.217	-1.17	0.279	-1.07	0.747	-0.6
1457840_at	Plxna4	plexin A4	-1.02	0.973	-2.32	0.094	1.3	0.471	-2.84	0.458	-1.22
1450185_a_at	Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	1.15	0.329	-1.23	0.553	-1.35	0.333	-1.3	0.755	-0.68
1435483_x_at	Slc25a32	solute carrier family 25, member 32	-1.55	0.024	-1.18	0.394	1.22	0.391	-1.15	0.622	-0.66
1446462_at	Hars2	Histidyl tRNA synthetase 2	-1.5	0.375	-1.19	0.744	1.2	0.461	-3.17	0.26	-1.16
1441388_at	---	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C63002	1.03	0.629	-1.19	0.099	-1.2	0.342	-1.06	0.728	-0.6
1423591_at	Fgfr1op2	FGFR1 oncogene partner 2	-1.02	0.689	-1.13	0.086	-1.18	0.099	1.04	0.672	-0.57
1442414_at	Rnf103	Ring finger protein 103	1.32	0.166	-1.66	0.105	-1.27	0.517	-1.04	0.856	-0.66
1433995_s_at	D16Bwg1543e	DNA segment, Chr 16, Brigham & Women's Genetics 1543 expressed	-1.26	0.03	-1.13	0.126	1.04	0.865	-1.56	0.198	-0.73
1417841_at	Pxmp2	peroxisomal membrane protein 2	-1.05	0.705	-1.22	0.063	-1.07	0.659	1.92	0.155	-0.35
1426382_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	-1.03	0.8	-1.25	0.051	-1.06	0.266	1.31	0.263	-0.51
1445946_at	Pde4a	Phosphodiesterase 4A, cAMP specific	1.2	0.628	-1.48	0.1	-1.2	0.617	-1.14	0.607	-0.66
1458395_at	B930054O08	hypothetical protein B930054O08	-1.27	0.349	-1.07	0.554	-1.01	0.966	1.38	0.421	-0.49
1454803_a_at	Hdac11	histone deacetylase 11	-1.17	0.599	-1.29	0.093	1.09	0.52	-1.05	0.86	-0.61
1437561_at	Trat1	T cell receptor associated transmembrane adaptor 1	-2.03	0.233	-1.28	0.501	1.43	0.43	-4	0.028	-1.47
1423856_at	Popdc3	popeye domain containing 3	-1.45	0.572	-1.03	0.955	1.05	0.699	-1.26	0.425	-0.67
1455594_at	Exoc3	exocyst complex component 3	-1.29	0.093	1.09	0.46	-1.18	0.152	-1.45	0.157	-0.71
1452676_a_at	Pnpt1	polyribonucleotide nucleotidyltransferase 1	-1.11	0.026	-1.06	0.387	-1.15	0.138	1.05	0.751	-0.57
1448922_at	Dusp19	dual specificity phosphatase 19	-1.24	0.207	-1.11	0.172	1	0.997	-1.18	0.536	-0.63
1418370_at	Tnnc1	troponin C, cardiac/slow skeletal	-1.03	0.954	-1.26	0.087	-1.06	0.625	1.14	0.728	-0.55
1418654_at	Hao3	hydroxyacid oxidase (glycolate oxidase) 3	-1.08	0.417	1.09	0.932	-1.43	0.488	-1.57	0.177	-0.75
1421910_at	Tcf20	transcription factor 20	1.01	0.912	-1.22	0.391	-1.14	0.378	-1.11	0.636	-0.61
1442311_at	Zfr	Zinc finger RNA binding protein	1.07	0.706	-1.02	0.78	-1.5	0.134	-1.03	0.879	-0.62
1421724_at	V1rd7	vomeronasal 1 receptor, D7	1.16	0.697	-1.74	0.217	-1.02	0.943	-1.13	0.759	-0.68
1451868_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	-1.63	0.49	1.45	0.532	-1.55	0.344	-1.15	0.823	-0.72
1445305_at	---	---	-1.18	0.616	1.21	0.699	-1.53	0.257	-1.27	0.324	-0.69
1437275_at	Ctnna1	Catenin (cadherin associated protein), alpha 1	1.51	0.605	-2.39	0.409	-1.27	0.307	-1.51	0.52	-0.92
1446041_at	---	Transcribed locus	1.16	0.756	-1.18	0.784	-1.42	0.492	-1.09	0.817	-0.63
1430589_at	Pigh	phosphatidylinositol glycan anchor biosynthesis, class H	-1.04	0.932	-1.65	0.385	1.15	0.761	-1.25	0.296	-0.7
1426688_at	Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-1.23	0.265	-1.28	0.105	1.12	0.16	-1.15	0.025	-0.64
1418242_at	Faf1	Fas-associated factor 1	-1.11	0.337	-1.23	0.134	-1.01	0.95	1.37	0.241	-0.49
1434721_at	D5Ertd585e	DNA segment, Chr 5, ERATO Doi 585, expressed	1	0.993	-1.17	0.138	-1.17	0.039	-1.27	0.311	-0.65
1416565_at	Cox6b1	cytochrome c oxidase, subunit VIb polypeptide 1	-1.1	0.388	-1.12	0.143	-1.1	0.351	1.03	0.814	-0.57
1418387_at	4930548G07Rik	RIKEN cDNA 4930548G07 gene	-1.05	0.539	-1.04	0.875	-1.25	0.425	1.13	0.253	-0.55
1446001_at	Reps1	RalBP1 associated Eps domain containing protein	1.23	0.081	-1.23	0.298	-1.49	0.046	-1.43	0.425	-0.73

1452223_s_at	Gcap14	granule cell antiserum positive 14	-1.27	0.064	1.18	0.248	-1.35	0.265	-1.55	0.37	-0.75
1418485_at	Slc4a3	solute carrier family 4 (anion exchanger), member 3	1.22	0.279	-1.49	0.023	-1.23	0.108	-1.51	0.403	-0.75
1453693_at	Wdr20	WD repeat domain 20	-1.65	0.325	-1.42	0.414	1.4	0.206	-1.35	0.025	-0.75
1423168_at	Prei3	preimplantation protein 3	1.03	0.82	-1.06	0.504	-1.36	0.024	-1.17	0.538	-0.64
1424837_at	Rnf113a1	ring finger protein 113A1	1.04	0.888	-1.22	0.508	-1.17	0.381	-1.01	0.983	-0.59
1426563_at	Zfp553	zinc finger protein 553	1.2	0.707	-1.45	0.274	-1.21	0.63	-1.3	0.325	-0.69
1448574_at	Nme6	expressed in non-metastatic cells 6, protein	-1.05	0.64	-1.22	0.166	-1.07	0.543	1.48	0.258	-0.46
1424952_at	Ociad1	OCIA domain containing 1	-1.05	0.896	-1.03	0.928	-1.28	0.282	1.13	0.837	-0.56
1423169_at	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.08	0.752	-1.36	0.429	-1.12	0.294	-1.01	0.963	-0.6
1431271_at	2810428J06Rik	RIKEN cDNA 2810428J06 gene	1.32	0.703	-1.63	0.452	-1.28	0.367	-1.4	0.209	-0.75
1448938_at	Rpa3	replication protein A3	-1.16	0.329	-1.12	0.277	-1.04	0.711	1.4	0.299	-0.48
1432968_at	4930456A14Rik	RIKEN cDNA 4930456A14 gene	-1.3	0.1	1.01	0.919	-1.08	0.849	-1.44	0.137	-0.7
1439369_x_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	1.08	0.812	-1.25	0.29	-1.2	0.555	-1.45	0.296	-0.71
1456244_x_at	Txnl2	thioredoxin-like 2	-1.17	0.456	1	0.988	-1.17	0.217	-1.51	0.046	-0.71
1452055_at	Ctdsp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	1.06	0.724	-1.2	0.46	-1.22	0.237	-1.01	0.972	-0.59
1451330_a_at	Inpp5b	inositol polyphosphate-5-phosphatase B	-1.02	0.946	-1.08	0.047	-1.24	0.029	1.18	0.412	-0.54
1432109_at	4930578I07Rik	RIKEN cDNA 4930578I07 gene	-1.12	0.681	-1.25	0.683	1.02	0.963	-1.3	0.647	-0.66
1425624_at	Epm2aip1	EPM2A (laforin) interacting protein 1	-1.36	0.225	-1.1	0.832	1.07	0.857	-1.16	0.603	-0.64
1442495_at	Birc6	Baculoviral IAP repeat-containing 6	1.24	0.405	-1.2	0.562	-1.58	0.058	-1.08	0.855	-0.65
1419452_at	Uchl5	ubiquitin carboxyl-terminal esterase L5	-1.07	0.379	-1.16	0.008	-1.08	0.524	1.13	0.512	-0.55
1449666_at	Atrnl1	Attractin like 1	1.53	0.522	-2.16	0.232	-1.39	0.047	-1.08	0.637	-0.78
1438535_at	Phip	pleckstrin homology domain interacting protein	1.13	0.494	-1.18	0.411	-1.35	0.058	-1.63	0.006	-0.76
1435152_at	Leng8	leukocyte receptor cluster (LRC) member 8	-1.01	0.934	-1.13	0.528	-1.19	0.456	1.15	0.699	-0.55
1459589_at	Cryl1	crystallin, lamda 1	-1.09	0.764	-1.42	0.279	1.09	0.848	-1.27	0.726	-0.67
1451348_at	Depdc6	DEP domain containing 6	1.02	0.666	-1.29	0.041	-1.09	0.622	-1.47	0.038	-0.71
1420326_s_at	Cramp1l	Crm, cramped-like (Drosophila)	-1.16	0.23	-1.13	0.266	-1.04	0.773	1.15	0.474	-0.54
1449525_at	Fmo3	flavin containing monooxygenase 3	-1.2	0.765	-1.23	0.353	1.07	0.815	-1.62	0.144	-0.74
1421849_at	Stag2	stromal antigen 2	-1.08	0.458	-1.04	0.561	-1.21	0.173	1.11	0.262	-0.56
1438143_s_at	Atxn2	ataxin 2	-1.18	0.264	-1.02	0.91	-1.13	0.352	1.01	0.956	-0.58
1439824_at	Chm	choroidermia	-1	0.939	1.05	0.431	-1.49	0.045	-1.28	0.466	-0.68
1442997_at	Odz3	Odd Oz/ten-m homolog 3 (Drosophila)	1.32	0.704	-2.32	0.221	-1.04	0.866	-1.49	0.473	-0.88
1450659_at	Rgs7	regulator of G protein signaling 7	-1.28	0.045	-2.3	0.32	1.5	0.652	-2.02	0.272	-1.03
1416555_at	Ei24	etoposide induced 2.4 mRNA	1.03	0.572	-1.08	0.557	-1.31	0.012	-1.02	0.795	-0.6
1417096_at	2810430M08Rik	RIKEN cDNA 2810430M08 gene	-1.38	0.009	-1.16	0.296	1.13	0.48	-1.08	0.882	-0.62
1442642_at	4930413O22Rik	RIKEN cDNA 4930413O22 gene	1.04	0.766	-1.19	0.811	-1.2	0.682	-1.34	0.645	-0.67
1442294_at	A530053G22Rik	RIKEN cDNA A530053G22 gene	-2.48	0.132	-1.05	0.941	1.36	0.722	-1.57	0.616	-0.94
1452930_at	Dock3	dedicator of cyto-kinesis 3	1.02	0.974	-1.38	0.104	-1.04	0.953	-1.04	0.956	-0.61
1423438_at	Kptn	kaptin	-1.16	0.249	-1.19	0.274	1.01	0.962	-1.4	0.111	-0.69
1448428_at	Nbl1	neuroblastoma, suppression of tumorigenicity 1	1.43	0.279	-1.9	0.364	-1.32	0.173	-1.08	0.762	-0.72
1438275_at	C130046K22Rik	RIKEN cDNA C130046K22 gene	1.07	0.305	-1.5	0.009	-1.02	0.916	-1.2	0.219	-0.66
1430448_at	6720418B01Rik	RIKEN cDNA 6720418B01 gene	-1.7	0.37	1.59	0.165	-1.85	0.13	-3.54	0.02	-1.38
1438136_at	Astl	astacin-like metalloendopeptidase (M12 family)	-2.26	0.105	1.53	0.512	-1.35	0.452	-1.16	0.387	-0.81
1453097_a_at	Ubtf	upstream binding transcription factor, RNA polymerase I	-1.27	0.102	-1.01	0.913	-1.06	0.798	1.25	0.169	-0.52
1419350_at	Hook2	hook homolog 2 (Drosophila)	-1.08	0.705	-1.53	0.181	1.14	0.556	-1.03	0.914	-0.63
1456502_at	Dyrk2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	-1.2	0.132	-1.14	0.369	1	0.985	-1.9	0.24	-0.81
1433774_x_at	Cog1	component of oligomeric golgi complex 1	1.05	0.738	-1.28	0.155	-1.13	0.49	-1.09	0.514	-0.61
1446565_at	Man1a2	Mannosidase, alpha, class 1A, member 2	-1.07	0.153	-1.11	0.747	-1.13	0.62	1.35	0.078	-0.49
1445273_at	D10Ertd638e	DNA segment, Chr 10, ERATO Doi 638, expressed	1.14	0.511	-1.08	0.729	-1.53	0.138	-1.09	0.619	-0.64
1432585_at	4931428A05Rik	RIKEN cDNA 4931428A05 gene	1.55	0.33	-1.79	0.194	-1.65	0.102	-1.27	0.389	-0.79
1437566_at	LOC633966	similar to guanine nucleotide binding protein-like 2 (nucleolar)	1.05	0.873	-1.36	0.181	-1.08	0.499	-1.27	0.262	-0.66
1435815_at	Ldoc1	leucine zipper, down-regulated in cancer 1	-1.31	0.702	1.12	0.484	-1.21	0.694	-1.72	0.106	-0.78
1433891_at	Lgr4 /// LOC669588	leucine-rich repeat-containing G protein-coupled receptor 4 /// similar to Leucine-r	-1.19	0.384	1.06	0.574	-1.23	0.436	-1.22	0.254	-0.65
1452607_at	2610030H06Rik	RIKEN cDNA 2610030H06 gene	-1.07	0.488	-1.13	0.026	-1.11	0.285	1.38	0.003	-0.48

1429245_at	2510022D24Rik	RIKEN cDNA 2510022D24 gene	-1.04	0.764	-1.11	0.703	-1.17	0.484	1.12	0.158	-0.55
1440708_at	Myh9	myosin, heavy polypeptide 9, non-muscle	1.12	0.226	-1.04	0.921	-1.57	0.219	-1.13	0.49	-0.66
1460019_at	LOC627607	similar to leucine rich repeat containing 45	1.46	0.655	-1.78	0.561	-1.44	0.488	-1.4	0.565	-0.79
1450465_at	Cdk5r2	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	1.01	0.965	-1.08	0.737	-1.28	0.379	-1.41	0.326	-0.69
1454834_at	Nfib	nuclear factor I/B	1.16	0.023	-1.03	0.79	-1.71	0.013	-1.21	0.458	-0.7
1444317_at	Pcdh15	protocadherin 15	-1.46	0.257	-1.07	0.927	1.09	0.895	-1.49	0.465	-0.73
1447709_at	Epb4.1l3	Erythrocyte protein band 4.1-like 3	1.1	0.89	-1.11	0.787	-1.39	0.588	-2.59	0.29	-1
1434865_a_at	Exoc7	exocyst complex component 7	-1.26	0.001	-1.13	0.313	1.04	0.713	-1.31	0.154	-0.66
1435418_at	Slc22a8	solute carrier family 22 (organic anion transporter), member 8	-1.06	0.748	1.1	0.801	-1.49	0.268	-1.28	0.572	-0.68
1428552_at	2610001J05Rik	RIKEN cDNA 2610001J05 gene	-1.21	0.038	1.03	0.655	-1.15	0.308	-1.26	0.279	-0.65
1416849_at	Zcd1	zinc finger, CDGSH-type domain 1	-1.16	0.123	-1.13	0.347	-1.03	0.816	1.28	0.359	-0.51
1420142_s_at	Pa2g4	proliferation-associated 2G4	-1.01	0.969	-1.32	0.081	-1.03	0.834	1.26	0.4	-0.53
1453512_at	5830407P18Rik	RIKEN cDNA 5830407P18 gene	-1.02	0.889	1.13	0.684	-1.66	0.017	-1.44	0.203	-0.75
1435881_at	Pcbp2	poly(rC) binding protein 2	-1.07	0.451	-1.01	0.914	-1.25	0.22	1.33	0.111	-0.5
1431370_at	4930512B01Rik	RIKEN cDNA 4930512B01 gene	-1.23	0.463	-1.46	0.182	1.22	0.659	-1.12	0.615	-0.65
1442316_x_at	Trp53bp1	transformation related protein 53 binding protein 1	-1.16	0.64	1.16	0.527	-1.45	0.13	-1.04	0.92	-0.62
1433894_at	AI591476	expressed sequence AI591476	-1.12	0.64	-1.03	0.955	-1.17	0.537	1.07	0.832	-0.56
1444731_at	Pde4b	phosphodiesterase 4B, cAMP specific	1.04	0.888	-1.2	0.476	-1.19	0.281	-1.66	0.013	-0.75
1437433_at	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	-2.08	0.374	-1.44	0.254	1.54	0.515	-1.27	0.63	-0.81
1431413_at	9130218E19Rik	RIKEN cDNA 9130218E19 gene	-1.45	0.471	-1.27	0.497	1.24	0.577	-1.76	0.154	-0.81
1442027_at	Nbeal1	neurobeachin like 1	1.21	0.443	-1.23	0.38	-1.45	0.271	-1.45	0.489	-0.73
1440574_at	Rag1	Recombination activating gene 1	-1.34	0.107	-1.16	0.725	1.11	0.709	-1.2	0.627	-0.65
1441023_at	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	1.16	0.572	-1.3	0.011	-1.27	0.282	-1.02	0.94	-0.61
1415937_s_at	Pdcd6ip	programmed cell death 6 interacting protein	-1.09	0.126	-1.4	0.079	1.09	0.721	-1.35	0.282	-0.69
1419920_s_at	Usp7	ubiquitin specific peptidase 7	-1.05	0.039	-1.09	0.471	-1.18	0.205	1.6	0.308	-0.43
1436950_at	Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	-1.07	0.591	-1.09	0.482	-1.15	0.218	1.08	0.713	-0.56
1428383_a_at	2310021P13Rik	RIKEN cDNA 2310021P13 gene	1.01	0.955	-1.06	0.653	-1.3	0.254	-1.24	0.576	-0.65
1446013_at	Slc38a3	solute carrier family 38, member 3	-1.39	0.758	1.19	0.146	-1.24	0.711	-1.75	0.356	-0.8
1438657_x_at	Ptp4a1 /// LOC433	protein tyrosine phosphatase 4a1 /// protein tyrosine phosphatase 4a1-like /// prot	1.03	0.815	-1.16	0.392	-1.21	0.033	-1.05	0.64	-0.6
1433769_at	Als2cl	ALS2 C-terminal like	-1.11	0.411	1.02	0.625	-1.27	0.054	-3.22	0.024	-1.14
1451444_s_at	2700008B19Rik	RIKEN cDNA 2700008B19 gene	-1.22	0.049	-1.73	0.001	1.32	0.087	-1.3	0.044	-0.73
1428159_s_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-1.07	0.201	-1.19	0.021	-1.06	0.199	1.2	0.376	-0.53
1435089_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	1.06	0.744	-1.07	0.807	-1.37	0.212	-1.17	0.453	-0.64
1446429_at	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	1.33	0.454	-2.3	0.054	-1.05	0.861	-1.04	0.94	-0.76
1418725_at	Dnajc5b	DnaJ (Hsp40) homolog, subfamily C, member 5 beta	-1.02	0.929	-1.74	0.221	1.16	0.626	-1.6	0.316	-0.8
1451493_at	Ndfip1	Nedd4 family interacting protein 1	-1.05	0.452	-1.42	0.054	1.06	0.745	-1.29	0.415	-0.68
1454552_at	4930456K20Rik	RIKEN cDNA 4930456K20 gene	1.2	0.765	-1.33	0.235	-1.31	0.503	-1.52	0.003	-0.74
1428117_x_at	Gpr178	G protein-coupled receptor 178	1.02	0.937	-1.31	0.607	-1.07	0.708	-1.54	0.216	-0.73
1451994_s_at	3930401K13Rik	RIKEN cDNA 3930401K13 gene	-1.88	0.291	-1.32	0.262	1.43	0.273	-2.03	0.187	-0.95
1434753_at	Nfrkb	nuclear factor related to kappa B binding protein	-1.34	0.502	-1.34	0.188	1.23	0.426	-2.09	0.251	-0.89
1423062_at	Igfbp3	insulin-like growth factor binding protein 3	-1.13	0.516	1.36	0.45	-2.1	0.035	-2.12	0.208	-1
1429652_at	1190002C06Rik	RIKEN cDNA 1190002C06 gene	-1.14	0.126	1.04	0.813	-1.25	0.003	-1.12	0.347	-0.62
1451242_a_at	Ppp5c	protein phosphatase 5, catalytic subunit	-1.24	0.188	-1.46	0.045	1.23	0.182	-1.13	0.376	-0.65
1425035_s_at	Dnmt3l	DNA (cytosine-5-)-methyltransferase 3-like	1.12	0.804	-1.33	0.495	-1.18	0.548	-1.46	0.656	-0.71
1423210_a_at	Nola3	nucleolar protein family A, member 3	-1.11	0.444	1.04	0.591	-1.28	0.08	-1.12	0.083	-0.62
1441790_at	---	Transcribed locus	-1.08	0.909	-1.75	0.524	1.23	0.314	-1.18	0.765	-0.7
1434889_at	Plekha7	pleckstrin homology domain containing, family A member 7	-1.33	0.195	-1.65	0.162	1.37	0.317	-1.31	0.551	-0.73
1423889_at	MGC5739	similar to hypothetical protein FLJ20010	-1.21	0.173	-1.31	0.167	1.13	0.667	-1.09	0.749	-0.62
1416663_at	Ndufa9	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	-1.14	0.017	-1.16	0.105	-1.03	0.613	1.07	0.554	-0.56
1444562_at	Ube3c	Ubiquitin protein ligase E3C	-1.05	0.838	1.15	0.667	-1.62	0.059	-1.3	0.021	-0.7
1442648_at	D130054H01	hypothetical protein D130054H01	-1.33	0.268	-1.09	0.784	1.05	0.848	-1.18	0.661	-0.64
1429752_x_at	Rsnl2	restin-like 2	-1.54	0.256	1.25	0.701	-1.22	0.115	-2.03	0.346	-0.88
1447383_at	BC005471	CDNA sequence BC005471	-1.17	0.755	1.12	0.691	-1.35	0.455	-1.29	0.292	-0.67

1430088_at	3000002G13Rik	RIKEN cDNA 3000002G13 gene	-1.19	0.496	1.14	0.636	-1.36	0.3	-1.57	0.194	-0.74
1439077_at	Zxda /// LOC66817	zinc finger, X-linked, duplicated A /// similar to Zinc finger X-linked protein ZXDA	-1.09	0.139	-1.56	0.189	1.16	0.552	-1.56	0.355	-0.76
1449143_at	Rtp4	receptor transporter protein 4	-1.53	0.358	1.32	0.52	-1.34	0.233	-1.88	0.286	-0.86
1439153_at	Ibrdc2	IBR domain containing 2	-1.11	0.637	-1.11	0.548	-1.09	0.633	1.3	0.397	-0.5
1432347_at	4931428L18Rik	RIKEN cDNA 4931428L18 gene	-1.19	0.722	1.1	0.741	-1.29	0.573	-2.47	0.148	-0.96
1447294_at	Fbxw11	F-box and WD-40 domain protein 11	-1.08	0.295	1.04	0.88	-1.32	0.203	-1.04	0.777	-0.6
1418814_s_at	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	-1.07	0.608	-1.16	0.173	-1.09	0.589	1.26	0.178	-0.51
1457156_at	Trhde	TRH-degrading enzyme	-3.93	0.005	-1.03	0.936	1.5	0.467	-1.85	0.282	-1.33
1438658_a_at	Edg3	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	1.19	0.27	-1.28	0.059	-1.33	0.119	-2.39	0.097	-0.95
1442203_at	LOC552880	hypothetical LOC552880	-2.34	0.095	1.41	0.553	-1.13	0.818	-2.44	0.053	-1.13
1460450_at	E230022H04Rik	RIKEN cDNA E230022H04 gene	-1.07	0.535	-1.18	0.107	-1.07	0.645	1.1	0.061	-0.55
1430515_s_at	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-1	0.989	-1.31	0.011	-1.04	0.657	1.03	0.73	-0.58
1448692_at	Ubqln4	ubiquilin 4	-1.29	0.344	-1.03	0.875	-1.03	0.799	1.53	0.169	-0.45
1459095_at	---	---	1.28	0.763	-1.6	0.541	-1.23	0.485	-1.96	0.303	-0.88
1455972_x_at	Hadhsc	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-1.2	0.056	-1.31	0.343	1.12	0.302	-1.42	0.032	-0.7
1423818_a_at	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1	-1.18	0.085	-1.06	0.379	-1.08	0.6	1.26	0.291	-0.51
1434861_at	---	Transcribed locus	1.05	0.551	-1.07	0.644	-1.35	0.078	-1.19	0.379	-0.64
1456958_at	C230072F16Rik	RIKEN cDNA C230072F16 gene	-1.21	0.477	1.08	0.412	-1.23	0.3	-1.21	0.606	-0.64
1440456_at	LOC381255	similar to KIAA0944 protein	-1.01	0.976	-1.33	0.579	-1.02	0.938	1.15	0.791	-0.55
1434615_x_at	---	---	-1.11	0.864	1.03	0.96	-1.28	0.654	-1.01	0.96	-0.59
1452371_at	Sfrs11	splicing factor, arginine/serine-rich 11	-1.16	0.233	-1.18	0.013	1.01	0.964	-1.1	0.502	-0.61
1416731_at	Top2b	topoisomerase (DNA) II beta	-1.15	0.669	1.12	0.266	-1.37	0.03	-1.36	0.054	-0.69
1429847_a_at	4833418A01Rik	RIKEN cDNA 4833418A01 gene	-1.05	0.675	-1.42	0.041	1.06	0.755	-1.38	0.01	-0.7
1457292_at	Josd3	Josephin domain containing 3	-1.16	0.452	-1.13	0.335	-1.02	0.939	1.03	0.857	-0.57
1432965_at	4921507H08Rik	RIKEN cDNA 4921507H08 gene	-2	0.391	1.22	0.707	-1	0.996	-1.62	0.611	-0.85
1416211_a_at	Ptn	pleiotrophin	1.2	0.409	-1.26	0.492	-1.37	0.081	-1.11	0.116	-0.64
1428884_at	Tmem57	transmembrane protein 57	-1.1	0.582	-1.17	0.209	-1.05	0.453	1.31	0.287	-0.5
1417241_at	X83328	EST X83328	-1.15	0.086	-1.08	0.339	-1.08	0.38	1.2	0.111	-0.53
1444848_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	1.27	0.047	-1.26	0.449	-1.51	0.028	-1.31	0.154	-0.7
1435556_at	Zfp597	zinc finger protein 597	-1.08	0.535	-1.33	0.114	1.04	0.583	-1.48	0.02	-0.71
1427010_s_at	Lama5 /// LOC671	laminin, alpha 5 /// similar to Laminin alpha-5 chain precursor	-1.2	0.057	-1.15	0.612	1.02	0.918	-1.72	0.464	-0.76
1448474_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	1.12	0.04	-1.11	0.173	-1.43	0.162	-1.04	0.879	-0.62
1460702_at	Triap1	TP53 regulated inhibitor of apoptosis 1	1.03	0.864	-1.07	0.489	-1.32	0.138	-1.16	0.653	-0.63
1448905_at	Nme3	expressed in non-metastatic cells 3	-1.04	0.69	-1.17	0.07	-1.1	0.569	1.5	0.379	-0.45
1451893_s_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.44	0.263	1.08	0.595	-1.06	0.813	-1.67	0.113	-0.77
1423445_at	Rock1	Rho-associated coiled-coil containing protein kinase 1	-1.09	0.36	-1.16	0.129	-1.06	0.542	1.11	0.349	-0.55
1417512_at	Evi5	ecotropic viral integration site 5	-1.09	0.537	-1.06	0.563	-1.16	0.26	2.23	0.171	-0.27
1434305_at	U2af1l4	U2 small nuclear RNA auxiliary factor 1-like 4	-1.08	0.634	-1.22	0.041	-1.02	0.846	1.01	0.975	-0.58
1430463_a_at	Sncaip	synuclein, alpha interacting protein (synphilin)	-1.38	0.538	-1.34	0.575	1.25	0.616	-1.44	0.334	-0.73
1450497_at	Apc2	adenomatosis polyposis coli 2	-1.2	0.179	-1.08	0.781	-1.04	0.863	1.38	0.347	-0.49
1428582_at	2010208K18Rik	RIKEN cDNA 2010208K18 gene	1.02	0.606	-1.02	0.751	-1.39	0.038	-1.36	0.068	-0.69
1451125_at	BC017133	cDNA sequence BC017133	-1.14	0.504	1	0.92	-1.19	0.141	-1.5	0.026	-0.71
1423200_at	Ncor1	nuclear receptor co-repressor 1	1.01	0.922	-1.13	0.017	-1.21	0.065	-1.14	0.025	-0.62
1422215_at	4930542C12Rik	RIKEN cDNA 4930542C12 gene	-1.03	0.639	-1.81	0.136	1.2	0.547	-1.12	0.392	-0.69
1428382_at	Smarcc2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.26	0.214	-1.06	0.834	-1.02	0.948	1.21	0.368	-0.53
1454109_a_at	Ptdsr	phosphatidylserine receptor	-1.11	0.05	-1.07	0.28	-1.13	0.666	1.03	0.944	-0.57
1436910_at	Rasal2	RAS protein activator like 2	-1.02	0.893	1.13	0.69	-1.65	0.018	-1.37	0.51	-0.73
1427264_at	Crygb	crystallin, gamma B	-2.47	0.218	1.47	0.474	-1.18	0.472	-3.22	0.248	-1.35
1436401_at	---	---	-1.12	0.637	-1.28	0.373	1.05	0.773	-1.28	0.06	-0.66
1448492_a_at	Psmd12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	-1.04	0.517	-1.16	0.04	-1.12	0.415	1.19	0.485	-0.53
1426425_at	Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	-1.21	0.166	-1.16	0.056	1.03	0.885	-1.62	0.087	-0.74
1458912_at	Rbm6	RNA binding motif protein 6	-1.05	0.849	1.08	0.237	-1.46	0.025	-1.09	0.627	-0.63
1444112_at	---	6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430409O0	-1.14	0.399	-1.14	0.355	-1.03	0.814	1.02	0.942	-0.57

1452700_s_at	Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	-1.13	0.322	-1.16	0.079	-1.02	0.783	1.11	0.594	-0.55
1438179_s_at	Statip1	Signal transducer and activator of transcription interacting protein 1	-1.02	0.807	-1.13	0.182	-1.17	0.14	1.02	0.899	-0.57
1446525_at	Gpc3	Glypican 3	1.18	0.832	-1.04	0.898	-1.73	0.004	-1.96	0.166	-0.89
1423105_a_at	Yeats4	YEATS domain containing 4	-1.14	0.05	1	0.965	-1.19	0.21	-1.32	0.015	-0.66
1444863_at	Nhlrc2	NHL repeat containing 2	-1.27	0.275	-1.83	0.355	1.39	0.17	-1.05	0.803	-0.69
1448774_at	Stoml2	stomatin (Epb7.2)-like 2	-1.1	0.02	-1.08	0.151	-1.13	0.151	1.11	0.662	-0.55
1441591_at	---	---	-1.46	0.523	1.25	0.63	-1.26	0.596	-1.08	0.87	-0.64
1460507_at	4930552P12Rik	RIKEN cDNA 4930552P12 gene	-2.02	0.272	-1.1	0.826	1.32	0.486	-1.06	0.934	-0.72
1433552_a_at	Polr2b	polymerase (RNA) II (DNA directed) polypeptide B	1.04	0.803	-1.21	0.031	-1.16	0.131	-1.16	0.3	-0.62
1453120_at	Txndc13	thioredoxin domain containing 13	-1.05	0.822	-1.19	0.204	-1.08	0.504	1.99	0.213	-0.33
1428499_at	2810454L23Rik	RIKEN cDNA 2810454L23 gene	-1.14	0.299	1.13	0.441	-1.41	0.068	-1.03	0.94	-0.61
1441959_s_at	1200003C05Rik	RIKEN cDNA 1200003C05 gene	-1.05	0.087	1.05	0.279	-1.38	0.005	-1.56	0.058	-0.74
1418260_at	Hunk /// LOC63056	hormonally upregulated Neu-associated kinase /// similar to hormonally upregulat	-1.44	0.074	1.25	0.376	-1.28	0.102	-1.14	0.061	-0.65
1430221_at	9130008F23Rik	RIKEN cDNA 9130008F23 gene	-1.17	0.411	-1.04	0.915	-1.11	0.554	1.01	0.909	-0.57
1447536_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	1.39	0.644	-1.35	0.329	-1.68	0.038	-1.01	0.972	-0.66
1435818_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030(	-1.17	0.204	1.05	0.69	-1.22	0.069	-1.11	0.527	-0.61
1416859_at	Fkbp3	FK506 binding protein 3	-1.02	0.866	1	0.975	-1.34	0.058	-1.87	0.058	-0.81
1441049_at	Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	-1.28	0.716	-1.01	0.96	-1.05	0.901	1.5	0.304	-0.46
1434188_at	Slc16a12	solute carrier family 16 (monocarboxylic acid transporters), member 12	-1.36	0.231	1	0.982	-1.02	0.931	-1.02	0.958	-0.6
1433793_s_at	Nrip2	nuclear receptor interacting protein 2	-1.6	0.664	1.29	0.477	-1.23	0.761	-1.6	0.422	-0.79
1427065_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	-1.36	0.165	-1.04	0.772	1.03	0.833	-1.17	0.559	-0.64
1426717_at	Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	-1.28	0.014	1.07	0.454	-1.14	0.189	-1.02	0.682	-0.59
1452177_at	Abcf3	ATP-binding cassette, sub-family F (GCN20), member 3	-1.2	0.394	-1.49	0.198	1.22	0.143	-1.5	0.006	-0.74
1446647_at	---	---	-1.13	0.136	-1.31	0.486	1.07	0.838	-1.06	0.909	-0.61
1445937_at	A630001G21Rik	RIKEN cDNA A630001G21 gene	1.31	0.503	-1.49	0.473	-1.35	0.344	-1.1	0.501	-0.66
1451336_at	Lgals4	lectin, galactose binding, soluble 4	-1.01	0.965	-1.39	0.541	1.02	0.949	-1.09	0.747	-0.62
1429257_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	1.35	0.603	-1.6	0.441	-1.34	0.088	-1.27	0.573	-0.71
1433674_a_at	Snord22	small nucleolar RNA, C/D box 22	-1.1	0.567	-1.24	0.181	1.01	0.973	-1.11	0.644	-0.61
1431728_at	2310010I16Rik	RIKEN cDNA 2310010I16 gene	-1.82	0.097	1.65	0.261	-1.92	0.048	-1.03	0.951	-0.78
1422693_a_at	Sub1	SUB1 homolog (S. cerevisia	-1.14	0.316	-1.19	0.026	1.01	0.969	-1.27	0.175	-0.65
1440282_at	Tulp4 /// 2210038L1	tubby like protein 4 /// RIKEN cDNA 2210038L17 gene	1.26	0.665	-1.24	0.642	-1.52	0.511	-1.47	0.569	-0.74
1418439_at	D10Ertd322e	DNA segment, Chr 10, ERATO Doi 322, expressed	-1.1	0.342	-1.11	0.212	-1.1	0.297	1.26	0.22	-0.51
1450588_at	Olfr67	olfactory receptor 67	-1.15	0.754	-1.62	0.042	1.24	0.667	-1.03	0.892	-0.64
1436711_at	Actr5	ARP5 actin-related protein 5 homolog (yeast)	-1.33	0.099	-1.07	0.771	1.04	0.841	-1.23	0.006	-0.65
1455784_at	Sec1	secretory blood group 1	-1.25	0.717	1.03	0.883	-1.11	0.8	-1.12	0.835	-0.62
1428094_at	Lamp2	lysosomal membrane glycoprotein 2	-1.03	0.745	-1.04	0.725	-1.27	0.063	1.27	0.303	-0.52
1442917_at	---	Adult male vesicular gland cDNA, RIKEN full-length enriched library, clone:G630(	1.15	0.86	-1.29	0.706	-1.24	0.502	-4.38	0.237	-1.44
1433671_at	A130022J15Rik	RIKEN cDNA A130022J15 gene	1.04	0.55	-1.09	0.697	-1.3	0.08	-1.02	0.902	-0.59
1426180_a_at	Smr2	submaxillary gland androgen regulated protein 2	-1.26	0.696	-1.23	0.387	1.12	0.367	-1.04	0.759	-0.6
1431466_at	4930553D19Rik	RIKEN cDNA 4930553D19 gene	-1.36	0.714	-1.02	0.981	1.01	0.989	-1.17	0.864	-0.64
1421877_at	Mapk9	mitogen activated protein kinase 9	-1.1	0.133	-1.15	0.264	-1.06	0.589	1.07	0.345	-0.56
1425526_a_at	Prrx1	paired related homeobox 1	1.3	0.633	-1.75	0.223	-1.18	0.651	-1.08	0.837	-0.68
1427943_at	Acyp2	acylphosphatase 2, muscle type	1	0.977	-1.09	0.642	-1.24	0.229	-1.03	0.85	-0.59
1457926_at	Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	-1.6	0.056	-1.19	0.735	1.26	0.423	-1.14	0.688	-0.67
1457951_at	4930434E21Rik	RIKEN cDNA 4930434E21 gene	-2.08	0.33	1.65	0.542	-1.68	0.293	-2.91	0.074	-1.25
1428502_at	Actr6	ARP6 actin-related protein 6 homolog (yeast)	-1.34	0.389	-1.05	0.647	1.03	0.772	-1.2	0.108	-0.64
1416494_at	Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	-1.08	0.276	-1.29	0.024	1.02	0.648	-1.05	0.717	-0.6
1424910_at	Kif12	kinesin family member 12	-1.55	0.244	1.22	0.238	-1.17	0.547	-1.41	0.498	-0.73
1423833_a_at	Brp44	brain protein 44	-1.14	0.259	-1.16	0.045	-1.02	0.799	1.49	0.306	-0.46
1438806_at	Bcl9l	B-cell CLL/lymphoma 9-like	-1.4	0.475	1.27	0.674	-1.35	0.66	-2.77	0.115	-1.06
1419988_at	Map3k7	mitogen activated protein kinase kinase kinase 7	-1.2	0.256	-1.03	0.855	-1.09	0.392	1.1	0.305	-0.55
1447043_at	Erbb4	V-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	1.34	0.315	-1.57	0.511	-1.33	0.539	-1.11	0.848	-0.67
1428768_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	1.01	0.933	-1.18	0.557	-1.16	0.569	-1.01	0.978	-0.58

1443314_at	2410042D21Rik	RIKEN cDNA 2410042D21 gene	-1.05	0.743	1.09	0.656	-1.47	0.043	-1.37	0.111	-0.7
1446406_at	Paqr8	Progestin and adipoQ receptor family member VIII	-2.85	0.164	1.82	0.37	-1.8	0.067	-1.99	0.142	-1.2
1433659_at	Trp53bp1	Transformation related protein 53 binding protein 1	1.01	0.896	-1.22	0.016	-1.12	0.393	-1.25	0.169	-0.65
1436898_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associat	1.23	0.257	-1.07	0.739	-1.81	0.027	-1.03	0.931	-0.67
1435893_at	Vldlr	very low density lipoprotein receptor	-1.11	0.402	1.2	0.822	-1.59	0.065	-1.22	0.691	-0.68
1451916_s_at	Trim15	tripartite motif protein 15	1.63	0.416	-3.42	0.059	-1.25	0.508	-1	0.993	-1.01
1450791_at	Nppb	natriuretic peptide precursor type B	-3	0.352	-1.66	0.1	1.79	0.118	-1.12	0.751	-1
1458787_at	Map3k7	Mitogen activated protein kinase kinase kinase 7	-4.14	0.006	-3.35	0.133	2.19	0	-1.29	0.73	-1.65
1448399_at	Tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1	-1.14	0.436	-1.15	0.087	-1.02	0.729	1.02	0.914	-0.57
1456415_at	Zfp451	zinc finger protein 451	-1.22	0.053	1.14	0.398	-1.32	0.082	-1.28	0.211	-0.67
1434898_at	Tnrc6a	trinucleotide repeat containing 6a	1.04	0.779	-1.05	0.715	-1.36	0.016	-1.23	0.415	-0.65
1443790_x_at	4930414L22Rik	RIKEN cDNA 4930414L22 gene	-1.27	0.2	-1.18	0.223	1.09	0.513	-1.22	0.115	-0.65
1429081_at	Gcc2	GRIP and coiled-coil domain containing 2	-1.05	0.369	1.02	0.527	-1.33	0.036	-1.42	0.121	-0.69
1430118_at	2700046A07Rik	RIKEN cDNA 2700046A07 gene	-1.03	0.971	-2.51	0.186	1.36	0.452	-1.01	0.983	-0.8
1433293_at	1500032O14Rik	RIKEN cDNA 1500032O14 gene	1.26	0.307	-1.23	0.52	-1.54	0.149	-1.09	0.653	-0.65
1432729_at	5830415G21Rik	RIKEN cDNA 5830415G21 gene	-1.47	0.391	-1.19	0.655	1.21	0.364	-1.72	0.519	-0.79
1456762_at	---	---	1.25	0.35	-1.67	0.143	-1.15	0.805	-1.44	0.434	-0.75
1441349_at	LOC552904	hypothetical LOC552904	1.5	0.097	-1.53	0.174	-1.75	0.058	-1.38	0.396	-0.79
1444144_at	5530400K22Rik	RIKEN cDNA 5530400K22 gene	1.2	0.673	-1.17	0.549	-1.49	0.032	-1.14	0.69	-0.65
1437520_a_at	Nup85	nucleoporin 85	-1.03	0.922	-1.14	0.577	-1.14	0.424	1.42	0.415	-0.47
1439497_at	4933415E08Rik	RIKEN cDNA 4933415E08 gene	-1.03	0.782	-1.88	0	1.22	0.256	-1.18	0.025	-0.72
1420384_at	Col4a3bp	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-1.16	0.462	-1.3	0.052	1.1	0.698	-1.13	0.556	-0.62
1434892_x_at	Rbbp4	retinoblastoma binding protein 4	-1.08	0.063	-1.16	0.023	-1.06	0.404	1.29	0.166	-0.5
1448570_at	Gmfb	glia maturation factor, beta	-1.13	0.16	1.02	0.671	-1.21	0.098	-1.4	0.183	-0.68
1415740_at	Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	-1.05	0.197	-1.23	0.012	-1.04	0.726	1.12	0.288	-0.55
1433355_at	2610021J01Rik	RIKEN cDNA 2610021J01 gene	-2.31	0.103	-1.57	0.457	1.66	0.247	-3.12	0.219	-1.33
1426722_at	Slc38a2	solute carrier family 38, member 2	-1.08	0.776	-1.14	0.271	-1.08	0.705	1.05	0.39	-0.56
1418630_at	Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1	1.13	0.597	-1.17	0.776	-1.34	0.196	-1.72	0.031	-0.78
1426372_a_at	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like	1.11	0.581	-1.04	0.658	-1.52	0.012	-1.35	0.004	-0.7
1434833_at	Map4k2	Mitogen activated protein kinase kinase kinase kinase 2	-1.15	0.26	-1.27	0.35	1.07	0.81	-2.58	0.075	-0.98
1422819_at	Mrpl36	mitochondrial ribosomal protein L36	-1.27	0.312	-1.01	0.764	-1.05	0.742	1.02	0.898	-0.58
1423458_at	Slc35a5	solute carrier family 35, member A5	-1.16	0.422	1.16	0.532	-1.41	0.057	-1.07	0.848	-0.62
1460355_at	Bud13	BUD13 homolog (yeast)	-1.12	0.743	-1.36	0.251	1.1	0.053	-1.05	0.75	-0.61
1425631_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	-1.46	0.459	-1.34	0.421	1.3	0.567	-1.75	0.089	-0.81
1419316_s_at	Gnb1l	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-1.24	0.309	-1.2	0.169	1.08	0.801	-1	0.995	-0.59
1424642_at	Thoc1	THO complex 1	-1.15	0.254	1.08	0.585	-1.28	0.042	-1.32	0.021	-0.67
1447364_x_at	Myo1b	myosin IB	1.14	0.773	-1.11	0.35	-1.45	0.101	-1.36	0.443	-0.7
1453931_at	Col14a1	procollagen, type XIV, alpha 1	-1.01	0.827	-1.34	0.059	-1.01	0.902	1.06	0.693	-0.57
1440171_x_at	1700049G17Rik	RIKEN cDNA 1700049G17 gene	-1.24	0.166	1.14	0.592	-1.27	0.258	-1.16	0.214	-0.63
1453999_at	LOC670473	similar to Nucleolar preribosomal-associated protein 1	1.63	0.509	-1.58	0.105	-2.16	0.316	-1.92	0.336	-1.01
1432534_at	3300002I08Rik	RIKEN cDNA 3300002I08 gene	-1.45	0.311	-1.12	0.832	1.14	0.695	-1.03	0.854	-0.61
1432190_at	Sox5	SRY-box containing gene 5	-2.19	0.087	1.54	0.132	-1.36	0.437	-2.3	0.145	-1.08
1422711_a_at	Pnck	pregnancy upregulated non-ubiquitously expressed CaM kinase	-1.55	0.62	-1.2	0.234	1.25	0.427	-1.4	0.56	-0.72
1450765_a_at	Pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma	-1.16	0.807	-1.1	0.683	-1.04	0.873	1.04	0.937	-0.57
1451090_a_at	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	-1.16	0.167	-1.06	0.481	-1.08	0.662	1.21	0.147	-0.52
1439784_at	2310046O06Rik	RIKEN cDNA 2310046O06 gene	-1.14	0.029	1.02	0.934	-1.2	0.291	-1.42	0.221	-0.69
1423724_at	Zwint	ZW10 interactor	-1.11	0.24	-1.03	0.792	-1.17	0.189	1.64	0.113	-0.42
1426447_at	Nup35	nucleoporin 35	-1.16	0.058	-1.09	0.401	-1.05	0.614	1.51	0.188	-0.45
1423502_at	Brd2	bromodomain containing 2	-1.34	0.012	-1.12	0.159	1.09	0.552	-1.29	0.011	-0.67
1425503_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	-1.01	0.975	-1.13	0.477	-1.17	0.102	1.11	0.733	-0.55
1459306_at	Bfsp2	Beaded filament structural protein 2, phakinin	-1.32	0.403	-1.39	0.593	1.25	0.688	-1.18	0.768	-0.66
1436766_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	1.15	0.678	-1.09	0.609	-1.51	0.11	-1.25	0.457	-0.67
1424838_at	A330049M08Rik	RIKEN cDNA A330049M08 gene	-1.67	0.408	1.31	0.084	-1.23	0.704	-1.53	0.007	-0.78

1445542_at	4930579C12Rik	RIKEN cDNA 4930579C12 gene	-1.02	0.978	1.22	0.771	-1.91	0.376	-2.06	0.377	-0.94
1427174_at	3100002L24Rik /// S	RIKEN cDNA 3100002L24 gene /// RIKEN cDNA 9230108I15 gene /// hypothetica	-1.12	0.091	1.01	0.919	-1.21	0.393	-1.88	0.103	-0.8
1429077_x_at	Rpl21 /// LOC43312	ribosomal protein L21 /// similar to 60S ribosomal protein L21 /// similar to riboson	-1.13	0.135	1.08	0.344	-1.31	0.013	-1.35	0.022	-0.68
1434049_at	Entpd3	ectonucleoside triphosphate diphosphohydrolase 3	-1.97	0.191	-1.27	0.647	1.43	0.122	-2.49	0.078	-1.07
1420410_at	Nr5a2	nuclear receptor subfamily 5, group A, member 2	1.18	0.818	-1.1	0.341	-1.56	0.372	-1.17	0.767	-0.66
1450528_at	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	-1.02	0.979	1.42	0.647	-3.06	0.107	-1.03	0.968	-0.92
1427270_a_at	Bsdc1	BSD domain containing 1	-1.07	0.35	-1.18	0.213	-1.06	0.763	2.35	0.236	-0.24
1427680_a_at	Nfib	nuclear factor I/B	1.11	0.542	-1.1	0.575	-1.41	0.25	-1.2	0.666	-0.65
1437674_at	Rac1	RAS-related C3 botulinum substrate 1	-1.27	0.459	-1.08	0.792	1.02	0.834	-1.41	0.286	-0.69
1424459_at	Aytl2	acyltransferase like 2	-1.1	0.371	-1.05	0.784	-1.14	0.566	1.34	0.287	-0.49
1442806_at	9430030N17Rik	RIKEN cDNA 9430030N17 gene	-1.1	0.897	-1.84	0.309	1.27	0.223	-1.47	0.15	-0.78
1451343_at	Vps36	vacuolar protein sorting 36 (yeast)	-1.19	0.249	1.05	0.682	-1.2	0.369	-1.7	0.007	-0.76
1427171_at	Rlf	rearranged L-myc fusion sequence	-1.13	0.766	-1.15	0.142	-1.03	0.916	1.05	0.799	-0.56
1456845_at	Oxa1l	Oxidase assembly 1-like	1.34	0.735	-1.84	0.397	-1.19	0.75	-1.87	0.081	-0.89
1452805_at	D11Wsu47e	DNA segment, Chr 11, Wayne State University 47, expressed	-1.3	0.081	-1.3	0.067	1.19	0.395	-1.06	0.817	-0.62
1442324_at	---	PREDICTED: Mus musculus hypothetical LOC547070 (LOC547070), mRNA	1	0.937	-1.16	0.488	-1.16	0.229	-1.61	0.171	-0.73
1452911_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1.21	0.169	-1.07	0.823	-1.7	0.014	-1.03	0.9	-0.65
1422404_x_at	Ifna1 /// Ifna2 /// Ifna	interferon alpha 1 /// interferon alpha 2 /// interferon alpha 4 /// interferon alpha 5 /	1.07	0.22	-1.06	0.923	-1.39	0.552	-1.1	0.843	-0.62
1435934_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-1.36	0.041	-1.03	0.773	1.03	0.909	-1.52	0.087	-0.72
1448515_at	Tsn	translin	-1.12	0.05	-1.11	0.017	-1.06	0.069	1.23	0.193	-0.52
1419913_at	Strap	Serine/threonine kinase receptor associated protein	-1.03	0.941	-1.09	0.605	-1.2	0.467	1.34	0.309	-0.49
1454959_s_at	Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	1.02	0.849	-1.01	0.962	-1.39	0.191	-1.08	0.694	-0.62
1452209_at	Pkp4	plakophilin 4	1.02	0.872	-1.08	0.546	-1.27	0.058	-1.13	0.689	-0.62
1416976_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	-1.24	0.163	-1.15	0.108	1.05	0.547	-1.16	0.157	-0.62
1438903_at	Maea	Macrophage erythroblast attacher	-1.42	0.427	-1.14	0.763	1.15	0.773	-2.53	0.305	-0.99
1446134_at	C78115	expressed sequence C78115	-1.1	0.73	1.26	0.278	-1.76	0	-1.01	0.987	-0.65
1448628_at	Scg3	secretogranin III	-1.05	0.758	-1.24	0.277	-1.03	0.961	1.08	0.902	-0.56
1440273_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-1.41	0.227	-1.17	0.552	1.17	0.34	-1.06	0.652	-0.62
1444937_at	Aff1	AF4/FMR2 family, member 1	-1.28	0.304	1.3	0.388	-1.54	0.104	-1.52	0.144	-0.76
1425152_s_at	Serpini2	serine (or cysteine) peptidase inhibitor, clade I, member 2	-1.01	0.904	1.02	0.939	-1.39	0.3	-2.12	0.345	-0.87
1430105_at	1700042O10Rik	RIKEN cDNA 1700042O10 gene	1.08	0.819	-1	0.987	-1.54	0.371	-1.21	0.707	-0.67
1452898_at	---	---	-1.17	0.164	1.12	0.176	-1.32	0.021	-1.34	0.003	-0.68
1425991_a_at	Ankrd25	ankyrin repeat domain 25	1.19	0.656	-1.35	0.582	-1.25	0.234	-1.02	0.944	-0.61
1426645_at	Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1	-1.07	0.359	-1.08	0.709	-1.16	0.304	1.3	0.211	-0.5
1452683_at	Dnajc8 /// LOC6692	DnaJ (Hsp40) homolog, subfamily C, member 8 /// similar to DnaJ (Hsp40) homol	-1.23	0.023	1.07	0.083	-1.18	0.164	-1.05	0.603	-0.6
1426287_at	Atxn7	ataxin 7	1.08	0.863	-1.17	0.559	-1.26	0.543	-1.24	0.405	-0.65
1435737_a_at	Nde1	nuclear distribution gene E homolog 1 (A nidulans)	-1.15	0.493	-1.08	0.597	-1.07	0.662	1.39	0.294	-0.48
1430597_at	Jakmip1	janus kinase and microtubule interacting protein 1	-1.18	0.609	-1.29	0.667	1.11	0.876	-2.37	0.127	-0.93
1455578_x_at	Rpl41	ribosomal protein L41	-1.1	0.112	1.05	0.263	-1.29	0.001	-1.27	0.002	-0.65
1449471_at	Kcnmb4	potassium large conductance calcium-activated channel, subfamily M, beta meml	-1.34	0.592	-1.12	0.756	1.09	0.707	-1.06	0.854	-0.61
1454675_at	Thra	thyroid hormone receptor alpha	-1.11	0.582	-1.03	0.835	-1.16	0.073	1.43	0.044	-0.47
1429507_at	LOC671838	similar to naked cuticle 1 homolog	-1.3	0.259	1.1	0.639	-1.16	0.479	-1.01	0.981	-0.59
1441293_at	---	Adult male accessory axillary lymph node cDNA, RIKEN full-length enriched libra	-1.07	0.793	1.06	0.718	-1.36	0.061	-1.46	0.225	-0.71
1435311_s_at	Fbxo7	F-box only protein 7	-1.11	0.795	-1.13	0.63	-1.06	0.793	1.33	0.17	-0.49
1431411_a_at	Rai12	retinoic acid induced 12	-1.09	0.178	-1.06	0.38	-1.16	0.19	1.13	0.429	-0.54
1438486_at	Tssk4	testis-specific serine kinase 4	-2.33	0.384	1.43	0.686	-1.15	0.712	-2.34	0.241	-1.1
1430133_at	Tbc1d8b	TBC1 domain family, member 8B	-1.01	0.922	1.04	0.666	-1.42	0.015	-1.07	0.698	-0.62
1439106_at	Zfp462	zinc finger protein 462	-1.07	0.352	1.13	0.789	-1.5	0.153	-1.14	0.673	-0.64
1429981_a_at	4933426K21Rik	RIKEN cDNA 4933426K21 gene	-1.31	0.232	-2.76	0.033	1.6	0.26	-1.06	0.908	-0.88
1451957_at	Il1f10	interleukin 1 family, member 10	-1.28	0.638	-1.33	0.419	1.2	0.601	-1.03	0.86	-0.61
1452497_a_at	Nfatc3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	1.21	0.326	-1.42	0.106	-1.23	0.444	-1.69	0.35	-0.78
1457957_at	---	Transcribed locus	-1.06	0.888	-1.02	0.933	-1.24	0.496	1.12	0.706	-0.55
1455767_x_at	Rpl21	ribosomal protein L21	-1.08	0.418	1.08	0.292	-1.39	0.001	-1.5	0.029	-0.72

1442346_at	---	Transcribed locus	-1.22	0.844	1.47	0.46	-2.29	0.011	-1.95	0.322	-1
1448181_at	Klf15	Kruppel-like factor 15	1.05	0.876	-1.17	0.35	-1.21	0.604	-1.96	0.505	-0.82
1428189_at	5730494M16Rik	RIKEN cDNA 5730494M16 gene	-1.13	0.145	1.01	0.903	-1.2	0.218	-1.33	0.289	-0.66
1419262_at	Acad8	acyl-Coenzyme A dehydrogenase family, member 8	-1.08	0.703	-1.23	0.018	-1.01	0.952	1.07	0.793	-0.56
1428915_at	Sirt5	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	-1.15	0.411	-1.26	0.095	1.07	0.741	-1.39	0.463	-0.68
1449044_at	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	-1.14	0.511	-1.16	0.334	-1.01	0.974	1.47	0.274	-0.46
1427285_s_at	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	-1.39	0.165	-1.58	0.227	1.38	0.117	-1.23	0.388	-0.71
1452671_s_at	Lman1	lectin, mannose-binding, 1	-1.11	0.119	-1.01	0.662	-1.19	0.132	1.34	0.056	-0.49
1428408_a_at	D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed	1.01	0.765	-1.02	0.864	-1.35	0.04	-1.05	0.739	-0.6
1424804_at	BC020002	cDNA sequence BC020002	-1.28	0.105	1.02	0.851	-1.07	0.625	-1.02	0.892	-0.59
1452923_at	Ndufa12l	Ndufa12-like	-1.01	0.854	-1.05	0.621	-1.27	0.133	1.05	0.872	-0.57
1417305_at	Speg	SPEG complex locus	-1.46	0.453	-1.23	0.665	1.24	0.321	-1.04	0.939	-0.62
1417211_a_at	1110032A03Rik	RIKEN cDNA 1110032A03 gene	-1.04	0.774	-1.08	0.465	-1.18	0.284	1.14	0.5	-0.54
1449940_a_at	Eif2b4	eukaryotic translation initiation factor 2B, subunit 4 delta	-1.16	0.417	-1.2	0.249	1.03	0.747	-1.12	0.572	-0.61
1424678_at	Actl7b	actin-like 7b	-1.36	0.127	-1.23	0.421	1.18	0.47	-1.13	0.782	-0.63
1452398_at	Plce1	phospholipase C, epsilon 1	1.01	0.884	-1.02	0.907	-1.36	0.153	-1.05	0.781	-0.6
1436943_at	Cyb5d2	cytochrome b5 domain containing 2	-1.05	0.839	1.03	0.683	-1.33	0.366	-1.09	0.738	-0.61
1441856_x_at	Tysnd1	trypsin domain containing 1	-1.12	0.665	-1.13	0.453	-1.05	0.8	1.19	0.494	-0.53
1434888_a_at	Matr3	matrin 3	-1.02	0.744	1.04	0.408	-1.41	0.047	-1.05	0.672	-0.61
AFFX-r2-P1-cre-5_a	---	---	1.03	0.835	-1.03	0.888	-1.36	0.05	-1.07	0.53	-0.61
1416425_at	Pex19	peroxisome biogenesis factor 19	-1.07	0.641	-1.19	0.248	-1.05	0.638	1	0.975	-0.58
1439446_at	BC048507	cDNA sequence BC048507	-1.35	0.54	1.33	0.705	-1.51	0.439	-1.07	0.934	-0.65
1457846_at	Cox11	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	1.2	0.737	-1.01	0.984	-1.85	0.302	-1.76	0.2	-0.85
1448358_s_at	Snrpg /// LOC6666(	small nuclear ribonucleoprotein polypeptide G /// similar to small nuclear ribonucle	-1.12	0.044	1.05	0.38	-1.27	0.01	-1.22	0.092	-0.64
1425089_at	Kcnc4	potassium voltage gated channel, Shaw-related subfamily, member 4	1.59	0.147	-1.74	0.391	-1.76	0.118	-1.17	0.508	-0.77
1429544_at	1700029J11Rik	RIKEN cDNA 1700029J11 gene	-2.21	0.28	-1.31	0.658	1.52	0.327	-1.25	0.394	-0.81
1451954_at	---	---	-2.42	0.035	-1	0.993	1.32	0.495	-2.01	0.139	-1.03
1417782_at	Lass4	longevity assurance homolog 4 (S. cerevisiae)	-1.15	0.276	1.02	0.941	-1.19	0.309	-1.68	0.1	-0.75
1438182_x_at	Asb6	ankyrin repeat and SOCS box-containing protein 6	-1.38	0.592	-1.2	0.557	1.17	0.698	-1.74	0.109	-0.78
1437500_at	Slc39a12	Solute carrier family 39 (zinc transporter), member 12	-1.03	0.816	-1.11	0.601	-1.17	0.415	1.01	0.856	-0.57
1459016_at	Igf2bp3	Insulin-like growth factor 2, binding protein 3	1.72	0.527	-1.73	0.115	-2.28	0.071	-1.16	0.762	-0.86
1436204_at	1110059G02Rik	RIKEN cDNA 1110059G02 gene	-1.02	0.936	-1.11	0.533	-1.18	0.435	1.13	0.771	-0.54
1430288_x_at	Rps21	ribosomal protein S21	-1.1	0.268	1.07	0.244	-1.34	0.007	-1.44	0.027	-0.7
1446531_at	---	---	1.09	0.93	-1.05	0.954	-1.44	0.395	-1.34	0.554	-0.69
1427113_s_at	2700049H19Rik	RIKEN cDNA 2700049H19 gene	-1.22	0.318	1.05	0.806	-1.16	0.091	-1.13	0.382	-0.62
1437944_at	Shc2	Src homology 2 domain-containing transforming protein C2	-1.26	0.066	1.18	0.678	-1.31	0.638	-1.01	0.988	-0.6
1427131_s_at	Lrrc58	leucine rich repeat containing 58	-1.08	0.657	1.06	0.579	-1.35	0.043	-1.13	0.573	-0.62
1441141_at	C730024G19Rik	RIKEN cDNA C730024G19 gene	-1.07	0.35	1.04	0.857	-1.33	0.149	-1.32	0.26	-0.67
1440760_at	Lef1	Lymphoid enhancer binding factor 1	-1.15	0.409	1.36	0.573	-1.96	0.09	-3.32	0.166	-1.27
1419320_at	Chst5	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	1.4	0.644	-2.29	0.279	-1.11	0.584	-1.55	0.197	-0.89
1437679_a_at	Glrx2	glutaredoxin 2 (thioltransferase)	-1.03	0.345	-1.13	0.041	-1.13	0.286	1.01	0.962	-0.57
1439079_a_at	Erbb2ip	Erbb2 interacting protein	-1.02	0.849	1.06	0.757	-1.45	0.006	-1.41	0.128	-0.7
1460251_at	Fas	Fas (TNF receptor superfamily member)	-1.17	0.661	1.1	0.742	-1.29	0.374	-1.25	0.346	-0.65
1433866_x_at	Prdx1	peroxiredoxin 1	-1.27	0.206	1.1	0.087	-1.18	0.062	-1.47	0.148	-0.71
1447904_s_at	Fnta	farnesyltransferase, CAAX box, alpha	1.01	0.898	-1.05	0.504	-1.3	0.021	-1.22	0.147	-0.64
1453240_a_at	Gcap14	granule cell antiserum positive 14	-1.05	0.77	1.02	0.628	-1.32	0.033	-1.19	0.715	-0.63
1447212_at	Cnot2	CCR4-NOT transcription complex, subunit 2	-1.66	0.102	-1.09	0.867	1.21	0.583	-1.86	0.143	-0.85
1451192_a_at	Ttc4	tetratricopeptide repeat domain 4	1	0.979	-1.04	0.547	-1.31	0.165	-1.11	0.611	-0.61
1440122_at	LOC666504 /// LOC	hypothetical protein LOC666504 /// hypothetical protein LOC672638 /// hypothetic	1.11	0.89	-1.04	0.918	-1.5	0.583	-1.27	0.408	-0.67
1435580_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	-1.04	0.15	1.08	0.479	-1.44	0.203	-1.24	0.48	-0.66
1415840_at	Elovl5	ELOVL family member 5, elongation of long chain fatty acids (yeast)	1.15	0.126	-1.25	0.149	-1.28	0.093	-1.47	0.292	-0.71
1454971_x_at	Tsc22d1	TSC22 domain family, member 1	1.14	0.664	-1.22	0.155	-1.29	0.009	-1.36	0.137	-0.68
1427895_at	2310004N24Rik	RIKEN cDNA 2310004N24 gene	-1.01	0.913	-1.28	0.582	-1.04	0.811	1.07	0.668	-0.56

1452026_a_at	Pla2g12a	phospholipase A2, group XIIA	-1.02	0.911	-1.32	0.168	-1	0.969	2.34	0.306	-0.25
1434907_at	Tbpl1	TATA box binding protein-like 1	-1.25	0.366	1.05	0.642	-1.13	0.101	-1.02	0.805	-0.59
1424057_at	Gdap2	ganglioside-induced differentiation-associated-protein 2	-1.16	0.397	-1.06	0.681	-1.07	0.48	1.09	0.448	-0.55
1460635_at	Fastk	Fas-activated serine/threonine kinase	-1.26	0.314	-1.02	0.911	-1.05	0.748	1.02	0.896	-0.58
1458823_at	Lrig1	Leucine-rich repeats and immunoglobulin-like domains 1	1.4	0.622	-1.21	0.768	-1.95	0.186	-1.01	0.986	-0.69
1454967_at	---	Transcribed locus	1.01	0.847	-1.06	0.578	-1.29	0.288	-1.29	0.577	-0.65
1455376_at	1300010F03Rik	RIKEN cDNA 1300010F03 gene	1.04	0.774	-1.4	0.246	-1.02	0.857	-1.19	0.236	-0.64
1438502_x_at	Rps17 /// LOC3830	ribosomal protein S17 /// similar to 40S ribosomal protein S17	-1.43	0.258	-1.01	0.962	1.05	0.674	-1.63	0.083	-0.76
1443513_at	---	Transcribed locus	-1.03	0.88	-1.03	0.898	-1.25	0.543	1.39	0.172	-0.48
1452787_a_at	Prmt1	protein arginine N-methyltransferase 1	-1.28	0.365	-1.15	0.37	1.08	0.678	-1.55	0.227	-0.73
1423118_at	1200014J11Rik	RIKEN cDNA 1200014J11 gene	-1.17	0.262	1.03	0.89	-1.18	0.163	-1.39	0.104	-0.68
1417239_at	Cetn3	centrin 3	-1.21	0.058	-1.02	0.789	-1.08	0.273	1.08	0.72	-0.56
1435675_at	Tbc1d12	TBC1D12: TBC1 domain family, member 12	-1.02	0.817	-1.1	0.197	-1.17	0.236	1.28	0.353	-0.5
1415708_at	Tug1	taurine upregulated gene 1	1.01	0.92	-1.02	0.889	-1.34	0.022	-1.2	0.295	-0.64
1424615_at	Frag1	FGF receptor activating protein 1	1.04	0.441	-1.11	0.287	-1.26	0.137	-1.29	0.43	-0.66
1453969_at	Prlpc4	prolactin-like protein C 4	-2.13	0.386	-1.02	0.752	1.29	0.319	-1.12	0.083	-0.75
1444217_at	Mrpl38	mitochondrial ribosomal protein L38	-1.06	0.88	-1.21	0.218	-1.04	0.844	1.09	0.518	-0.55
1452374_at	Zfp322a	zinc finger protein 322a	-1.08	0.411	1.04	0.58	-1.3	0.001	-1.25	0.173	-0.65
1439368_a_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	1.01	0.958	-1.12	0.508	-1.2	0.195	-1.06	0.884	-0.59
1428076_s_at	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	-1.1	0.175	-1.05	0.399	-1.15	0.242	1.04	0.85	-0.56
1426003_at	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	1.02	0.931	-1.11	0.708	-1.23	0.622	-1.04	0.952	-0.59
1458847_at	---	---	-1.14	0.723	1.17	0.585	-1.45	0.097	-1.17	0.573	-0.65
1456247_x_at	Plp2 /// LOC62064	proteolipid protein 2 /// similar to Proteolipid protein 2 /// similar to Proteolipid prot	-1.32	0.561	1.32	0.31	-1.51	0.411	-1.24	0.708	-0.69
1423148_at	Skp1a	S-phase kinase-associated protein 1A	-1.03	0.779	-1.14	0.105	-1.12	0.249	1.07	0.575	-0.56
1437878_s_at	Ccdc39 /// Ttc14	coiled-coil domain containing 39 /// tetratricopeptide repeat domain 14	1.08	0.623	-1.2	0.206	-1.22	0.073	-1.15	0.467	-0.62
1448082_at	Clcn1	Chloride channel 1	-2.57	0.036	1.72	0.365	-1.61	0.505	-1.9	0.278	-1.09
1455213_at	4930488E11Rik	RIKEN cDNA 4930488E11 gene	-1.22	0.283	-1.1	0.7	1.01	0.976	-2	0.08	-0.83
1445523_at	Gje1	Gap junction membrane channel protein epsilon 1	-1.89	0.281	1.52	0.028	-1.46	0.42	-1.76	0.082	-0.9
1438271_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1.05	0.785	-1.01	0.966	-1.44	0.103	-1.21	0.396	-0.65
1429237_at	Stx16	syntaxin 16	-1.28	0.11	-1.1	0.139	1.04	0.727	-1.67	0.164	-0.75
1444013_at	5930412G12Rik	RIKEN cDNA 5930412G12 gene	-4.22	0.076	1.72	0.244	-1.28	0.759	-1.13	0.845	-1.23
1430780_a_at	Pmm1	phosphomannomutase 1	-1.18	0.2	-1.1	0.879	-1.02	0.935	1.49	0.326	-0.45
1415691_at	Dlgh1	discs, large homolog 1 (Drosophila)	1.01	0.747	-1.04	0.514	-1.31	0.021	-1.02	0.885	-0.59
1437357_at	Ythdc2	YTH domain containing 2	-1.18	0.202	-1.03	0.905	-1.09	0.28	1.07	0.649	-0.56
1444963_at	---	---	-1.54	0.375	-1.21	0.445	1.26	0.27	-1.87	0.059	-0.84
1430290_at	Rps15a /// LOC434	ribosomal protein S15a /// similar to ribosomal protein S15a /// similar to ribosoma	-1.25	0.304	1.35	0.569	-1.7	0.269	-1.69	0.209	-0.82
1443455_at	Cuedc1	CUE domain containing 1	-1.07	0.754	1.22	0.688	-1.73	0.153	-2.18	0.225	-0.94
1419302_at	Heyl	hairy/enhancer-of-split related with YRPW motif-like	-1.34	0.31	-1.08	0.77	1.07	0.632	-1.15	0.099	-0.63
1452111_at	Mrps35	mitochondrial ribosomal protein S35	-1.29	0.106	-1.35	0.02	1.22	0.217	-1.06	0.588	-0.62
1453435_a_at	Fmo2	flavin containing monooxygenase 2	-1.25	0.143	-1.13	0.398	1.05	0.77	-1.16	0.455	-0.62
1443775_x_at	Zfp406	zinc finger protein 406	-1.48	0.568	-1.06	0.876	1.12	0.665	-1.38	0.652	-0.7
1426133_a_at	Mitd1	MIT, microtubule interacting and transport, domain containing 1	-1.23	0.415	1.06	0.712	-1.17	0.264	-1.35	0.16	-0.67
1416106_at	Kti12	KTI12 homolog, chromatin associated (S. cerevisiae)	-1.2	0.128	-1.23	0.053	1.09	0.481	-1.09	0.587	-0.61
1451277_at	Zadh2	zinc binding alcohol dehydrogenase, domain containing 2	1.02	0.72	-1.33	0.087	-1.04	0.745	-1.24	0.136	-0.65
1460184_at	Hadhsc	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	-1.17	0.033	-1.37	0.033	1.15	0.303	-1.28	0.145	-0.67
1430334_at	Zfp192	zinc finger protein 192	1.2	0.67	-1.7	0.177	-1.06	0.922	-1.51	0.469	-0.77
1456431_at	Zfp64	zinc finger protein 64	-1.29	0.573	1.19	0.711	-1.3	0.319	-2.15	0.018	-0.89
1449113_at	Gpbp1l1	GC-rich promoter binding protein 1-like 1	-1.07	0.709	-1.12	0.348	-1.1	0.632	1.05	0.57	-0.56
1428315_at	Ebna1bp2	EBNA1 binding protein 2	-1.13	0.351	-1.22	0.025	1.03	0.74	-1.25	0.131	-0.64
1458302_at	---	Transcribed locus	-1.11	0.544	-1.22	0.342	1.02	0.883	-1.35	0.335	-0.67
1440115_at	Olfm1	Olfactomedin 1	-1.09	0.854	-1.38	0.615	1.1	0.833	-1.41	0.136	-0.7
1417694_at	Gab1	growth factor receptor bound protein 2-associated protein 1	-1.12	0.302	-1.04	0.78	-1.13	0.677	1.99	0.207	-0.33
1428277_at	Otud6b	OTU domain containing 6B	-1.12	0.09	-1.02	0.826	-1.16	0.275	1.12	0.512	-0.54

1423599_a_at	Pdcl	phosducin-like	-1.12	0.379	-1.08	0.573	-1.09	0.438	1.1	0.496	-0.55
1443046_at	Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	1.29	0.537	-1.46	0.542	-1.31	0.422	-3.52	0.01	-1.25
1457030_at	Mirg	miRNA containing gene	-1.23	0.718	1.38	0.635	-1.82	0.333	-1.36	0.7	-0.76
1428061_at	Hat1	histone aminotransferase 1	-1.12	0.39	-1.19	0.229	-1	0.994	1.36	0.329	-0.49
1431785_at	Rnaset2	ribonuclease T2	-1.15	0.661	-1.58	0.096	1.24	0.582	-1.07	0.838	-0.64
1427120_at	Zfp26	zinc finger protein 26	1.16	0.109	-1.17	0.109	-1.38	0.055	-1.2	0.196	-0.65
1446674_at	Kns2	Kinesin 2	-1.01	0.835	1.05	0.91	-1.43	0.145	-1.7	0.233	-0.77
1452703_at	4631427C17Rik	RIKEN cDNA 4631427C17 gene	-1.11	0.028	-1.13	0.093	-1.05	0.516	1.07	0.449	-0.55
1447831_s_at	Mtmr7	myotubularin related protein 7	-1.18	0.261	-1.05	0.855	-1.06	0.465	1.23	0.303	-0.52
1418048_at	1110059G10Rik	RIKEN cDNA 1110059G10 gene	1	0.823	-1.08	0.194	-1.24	0.057	-1.17	0.176	-0.62
1420377_at	St8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-1.5	0.017	-1.23	0.484	1.26	0.419	-1.15	0.673	-0.66
1435581_at	Bace2	beta-site APP-cleaving enzyme 2	-1.21	0.816	1.07	0.766	-1.19	0.489	-1.46	0.121	-0.7
1451379_at	Rab22a	RAB22A, member RAS oncogene family	-1.04	0.714	-1.13	0.185	-1.12	0.309	1.18	0.232	-0.53
1441221_at	1700008J07Rik	RIKEN cDNA 1700008J07 gene	1.45	0.359	-1.43	0.29	-1.71	0.332	-1.09	0.521	-0.69
1452179_at	Phf17	PHD finger protein 17	-1.07	0.755	-1.08	0.703	-1.14	0.116	1.01	0.954	-0.57
1457183_at	Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	-1.3	0.744	-1.18	0.793	1.12	0.773	-1.81	0.149	-0.79
1441829_s_at	Akap10	A kinase (PRKA) anchor protein 10	1.15	0.449	-1.2	0.188	-1.33	0.128	-1.33	0.091	-0.68
1430419_at	2310031A07Rik	RIKEN cDNA 2310031A07 gene	-1.47	0.111	-1.04	0.878	1.1	0.727	-1.59	0.186	-0.75
1432695_at	4921527H02Rik	RIKEN cDNA 4921527H02 gene	1.04	0.953	-1.15	0.713	-1.21	0.281	-3.76	0.016	-1.27
1449752_at	Spsb1	SpIA/ryanodine receptor domain and SOCS box containing 1	-1.15	0.29	1.47	0.396	-2.54	0.089	-2.12	0.221	-1.08
1457232_at	Fbxl21	F-box and leucine-rich repeat protein 21	-1.34	0.002	1	0.999	-1.01	0.987	-1.2	0.805	-0.64
1438265_at	---	---	-1.31	0.6	-1.2	0.538	1.14	0.791	-1.7	0.455	-0.77
1436053_at	Tbc1d22b	TBC1 domain family, member 22B	-1.02	0.935	1.05	0.858	-1.4	0.059	-1.08	0.087	-0.61
1418165_at	Itlna	intelectin a	1.07	0.874	-1.12	0.558	-1.29	0.183	-1.41	0.13	-0.69
1423584_at	Igfbp7	insulin-like growth factor binding protein 7	-1.15	0.07	1.19	0.054	-1.48	0.038	-1.43	0.184	-0.72
1443903_at	Ppm1a	Protein phosphatase 1A, magnesium dependent, alpha isoform	-1.62	0.18	1.24	0.626	-1.13	0.72	-1.63	0.389	-0.79
1439782_s_at	D930048N14Rik	RIKEN cDNA D930048N14 gene	-1.09	0.648	-1.22	0.764	1.01	0.991	-2.35	0.267	-0.91
1443172_at	Orc1l	origin recognition complex, subunit 1-like (S.cereviaiae)	-1.1	0.652	-1.05	0.876	-1.14	0.628	3.44	0.276	0.04
1457069_at	Ascc3	activating signal cointegrator 1 complex subunit 3	-1.1	0.828	-1.06	0.718	-1.13	0.42	1.04	0.737	-0.56
1432353_at	4933421B21Rik	RIKEN cDNA 4933421B21 gene	-1.25	0.294	1.07	0.879	-1.15	0.658	-1.3	0.597	-0.66
1459669_at	---	Transcribed locus	-1.04	0.864	-1.4	0.514	1.06	0.86	-1.15	0.38	-0.63
1424996_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.06	0.646	-1.03	0.828	-1.4	0.176	-1.51	0.129	-0.72
1449229_a_at	Cdkl2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	-1.11	0.506	1.07	0.594	-1.29	0.016	-1.11	0.76	-0.61
1458786_at	C79250	expressed sequence C79250	-1.2	0.829	-2.03	0.518	1.42	0.316	-1.59	0.032	-0.85
1426468_at	0610037L13Rik	RIKEN cDNA 0610037L13 gene	-1.1	0.005	1.05	0.126	-1.28	0.024	-1.15	0.066	-0.62
1433835_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	-1.19	0.288	-1.11	0.027	-1	0.994	1.67	0.219	-0.41
1452743_at	---	---	-1.07	0.777	-1.05	0.679	-1.17	0.215	2.52	0.16	-0.19
1419809_s_at	Cog4	component of oligomeric golgi complex 4	1.07	0.562	-1.25	0.26	-1.15	0.236	-1.02	0.799	-0.59
1441085_at	Rora	RAR-related orphan receptor alpha	-1.66	0.331	1.29	0.72	-1.18	0.74	-1.09	0.667	-0.66
1447298_at	C130071C03Rik	RIKEN cDNA C130071C03 gene	-1.04	0.967	1.08	0.924	-1.43	0.434	-3.15	0.117	-1.14
1448372_a_at	Tmem4	transmembrane protein 4	-1.11	0.205	-1.11	0.017	-1.07	0.526	1.2	0.086	-0.52
1440820_x_at	Tmco2	transmembrane and coiled-coil domains 2	1.37	0.354	-1.11	0.814	-2.16	0.059	-1.06	0.785	-0.74
1423994_at	Kif1b	kinesin family member 1B	-1.06	0.484	-1.3	0.029	1.03	0.809	-1.24	0.032	-0.64
1427642_at	Trpm6	transient receptor potential cation channel, subfamily M, member 6	1.23	0.357	-1.69	0.204	-1.09	0.721	-1.33	0.574	-0.72
1438850_at	Cldn1	claudin 1	-1.02	0.935	1.07	0.683	-1.44	0.561	-1.94	0.38	-0.83
1437983_at	---	---	-1.11	0.401	1.19	0.41	-1.54	0.352	-1.46	0.435	-0.73
1434131_at	Rufy1	RUN and FYVE domain containing 1	-1.17	0.337	-1.14	0.222	1.01	0.806	-1.54	0.098	-0.71
1427335_at	6720456H20Rik	RIKEN cDNA 6720456H20 gene	-1.16	0.582	-1.27	0.375	1.09	0.742	-1.16	0.566	-0.62
1441544_at	Cnnm3	Cyclin M3	-1.1	0.831	-1.58	0.011	1.19	0.489	-1.21	0.382	-0.67
1428628_at	1190002A17Rik	RIKEN cDNA 1190002A17 gene	-1.4	0.482	-1.5	0.62	1.36	0.386	-1.43	0.426	-0.74
1434383_at	Pja2	praja 2, RING-H2 motif containing	-1.05	0.602	-1.01	0.76	-1.25	0.003	1.06	0.543	-0.56
1438740_at	Nmt2	N-myristoyltransferase 2	-1.26	0.254	-1.19	0.572	1.11	0.462	-1.13	0.607	-0.62
1452828_at	Fbxo21	F-box only protein 21	-1.31	0.08	-1.26	0.207	1.18	0.496	-1.54	0.155	-0.73

1434688_x_at	Drg1	developmentally regulated GTP binding protein 1	-1.03	0.871	-1.08	0.297	-1.18	0.246	1.08	0.659	-0.55
1448007_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B	1.12	0.624	-1.27	0.189	-1.2	0.413	-1.3	0.136	-0.66
1450626_at	Manba	mannosidase, beta A, lysosomal	-1.2	0.093	1.01	0.957	-1.11	0.447	-1.38	0.261	-0.67
1448970_at	1200007B05Rik	RIKEN cDNA 1200007B05 gene	-1.07	0.319	-1.11	0.327	-1.11	0.36	1.03	0.719	-0.56
1431754_at	4930578N16Rik	RIKEN cDNA 4930578N16 gene	-1.06	0.465	-1.47	0.202	1.12	0.728	-1.43	0.17	-0.71
1448486_at	Mut	methylmalonyl-Coenzyme A mutase	-1.1	0.18	-1.11	0.214	-1.08	0.432	1.25	0.241	-0.51
1439025_at	Zfp446	zinc finger protein 446	-1.23	0.41	-1.14	0.65	1.05	0.703	-1.06	0.611	-0.6
1420907_at	Cd2ap	CD2-associated protein	-1.12	0.482	1.07	0.527	-1.29	0.072	-1.38	0.173	-0.68
1428366_at	1600027N09Rik	RIKEN cDNA 1600027N09 gene	-1.15	0.314	1.02	0.909	-1.17	0.354	-1.29	0.276	-0.65
1417865_at	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-1.04	0.801	1.06	0.599	-1.4	0.133	-1.44	0.36	-0.71
1441661_at	---	---	-1.26	0.3	1.18	0.627	-1.3	0.571	-1.19	0.652	-0.64
1449889_a_at	Ociad1	OCIA domain containing 1	-1.31	0.214	-1.34	0.062	1.24	0.39	-1.38	0.248	-0.7
1446354_at	C130098B18Rik	RIKEN cDNA C130098B18 gene	-1.34	0.147	1.19	0.608	-1.24	0.568	-1.13	0.785	-0.63
1432705_at	5330428N10Rik	RIKEN cDNA 5330428N10 gene	-1.07	0.637	-1.11	0.65	-1.1	0.85	1.23	0.732	-0.51
1457826_a_at	1810043H04Rik	RIKEN cDNA 1810043H04 gene	-1.09	0.383	1.07	0.092	-1.34	0.071	-1.48	0.209	-0.71
1439224_at	Ankib1	Ankyrin repeat and IBR domain containing 1	1.44	0.57	-1.36	0.595	-1.77	0.182	-1.47	0.533	-0.79
1425819_at	Zbtb7c	zinc finger and BTB domain containing 7C	-1.37	0.222	-1.3	0.642	1.24	0.528	-1.12	0.861	-0.64
1452507_at	Dlx6	distal-less homeobox 6	1.56	0.488	-1.89	0.141	-1.53	0.356	-1.07	0.834	-0.73
1423764_s_at	Mrpl37	mitochondrial ribosomal protein L37	-1.13	0.494	-1.07	0.53	-1.08	0.468	1.01	0.939	-0.57
1456996_at	1190005F20Rik	RIKEN cDNA 1190005F20 gene	-1.01	0.932	-1.42	0.261	1.04	0.6	-1.2	0.071	-0.64
1420095_s_at	Zipro1	zinc finger proliferation 1	-1.03	0.527	1.06	0.576	-1.41	0.015	-1.02	0.842	-0.6
1420576_at	Edg4	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 4	1.1	0.629	-1.44	0.666	-1.06	0.876	-1.39	0.289	-0.7
1425665_a_at	Srp54 /// LOC6651	signal recognition particle 54 /// similar to signal recognition particle 54	-1.38	0.137	-1	0.992	1.02	0.806	-1.21	0.11	-0.64
1444221_at	Tbc1d12	TBC1D12: TBC1 domain family, member 12	1.06	0.766	-1.31	0.266	-1.09	0.603	-1.04	0.785	-0.59
1435413_x_at	2700060E02Rik	RIKEN cDNA 2700060E02 gene	1	0.966	-1.03	0.629	-1.31	0.025	-1.55	0.044	-0.72
1423208_at	Tmem167	transmembrane protein 167	-1.11	0.176	-1.05	0.82	-1.13	0.459	1.01	0.949	-0.57
1447618_at	B630019K06Rik	RIKEN cDNA B630019K06 gene	1.04	0.058	-1.26	0.057	-1.1	0.308	-1.24	0.548	-0.64
1446775_at	---	---	-1.45	0.224	-1.1	0.352	1.14	0.365	-1.38	0.501	-0.7
1417690_at	Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	-1.21	0.315	-1.06	0.736	-1.03	0.813	1.8	0.174	-0.37
1437124_at	A630052C17Rik	RIKEN cDNA A630052C17 gene	-1.06	0.57	-1.27	0.153	1.01	0.972	-1.22	0.109	-0.63
1448509_at	3110001A13Rik	RIKEN cDNA 3110001A13 gene	-1.14	0.501	-1.5	0.137	1.2	0.007	-1.83	0.055	-0.82
1424433_at	Msrb2	methionine sulfoxide reductase B2	-1.02	0.867	-1.32	0.01	1.01	0.978	-1.5	0.085	-0.71
1436551_at	Fgfr1	fibroblast growth factor receptor 1	-1.24	0.274	-1.19	0.781	1.1	0.48	-1.37	0.547	-0.68
1455602_x_at	1110028C15Rik	RIKEN cDNA 1110028C15 gene	-1.36	0.142	1.21	0.197	-1.25	0.04	-1.2	0.168	-0.65
1420454_at	Rai1	retinoic acid induced 1	1.34	0.502	-1.31	0.742	-1.56	0.083	-1.01	0.967	-0.64
1416585_at	Ruvbl1	RuvB-like protein 1	-1.14	0.359	-1.17	0.02	1.01	0.876	-1.06	0.728	-0.59
1447626_x_at	Arid3b	AT rich interactive domain 3B (Bright like)	1.07	0.208	-1.33	0.652	-1.09	0.633	-2.38	0.481	-0.93
1445641_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	1.08	0.67	-1.12	0.777	-1.29	0.263	-1.19	0.018	-0.63
1437912_at	Iqsec3	IQ motif and Sec7 domain 3	-1.3	0.521	1.11	0.196	-1.15	0.207	-1.01	0.913	-0.59
1446176_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	1.18	0.402	-1.21	0.818	-1.36	0.488	-1.14	0.831	-0.63
1445857_at	BC026585	cDNA sequence BC026585	-1.24	0.17	-1.39	0.475	1.22	0.618	-1.28	0.518	-0.67
1437113_s_at	Pld1	phospholipase D1	-1.03	0.802	1.15	0.419	-1.62	0.136	-1.29	0.626	-0.7
1422559_at	Ube2n	ubiquitin-conjugating enzyme E2N	-1.2	0.13	1.02	0.789	-1.12	0.317	-1.03	0.834	-0.58
1450948_a_at	Mrpl1	mitochondrial ribosomal protein L1	-1.15	0.213	-1.18	0.124	1.03	0.837	-1.09	0.552	-0.6
1440936_at	Serac1	serine active site containing 1	-1.12	0.24	1.06	0.807	-1.26	0.248	-1.11	0.565	-0.61
1416059_at	Sec23b	SEC23B (S. cerevisiae)	-1.09	0.073	-1.14	0.426	-1.05	0.588	1.03	0.213	-0.56
1433718_a_at	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	-1.07	0.146	1.01	0.926	-1.26	0.099	-1.11	0.171	-0.61
1441136_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.01	0.965	-1.52	0.228	1.09	0.707	-1.24	0.201	-0.67
1449536_at	Kcnn1	potassium intermediate/small conductance calcium-activated channel, subfamily	-1.34	0.292	1.09	0.853	-1.1	0.672	-1.11	0.875	-0.62
1452081_a_at	9130017N09Rik	RIKEN cDNA 9130017N09 gene	1.18	0.615	-1.69	0.193	-1.02	0.903	-1.56	0.245	-0.77
1437868_at	BC023892	cDNA sequence BC023892	1.02	0.957	-1.21	0.506	-1.12	0.39	-1.64	0.13	-0.74
1441305_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030	1.03	0.815	-1.04	0.891	-1.32	0.25	-1.38	0.543	-0.68
1453288_at	Atf6	activating transcription factor 6	-1.1	0.635	-1.42	0.194	1.13	0.8	-1.07	0.792	-0.62

1429479_at	6430590I03Rik	RIKEN cDNA 6430590I03 gene	-1.13	0.672	-1	0.992	-1.17	0.513	1.19	0.345	-0.52
1426682_at	Cnot6	CCR4-NOT transcription complex, subunit 6	-1.03	0.702	-1.01	0.894	-1.28	0.049	1.14	0.205	-0.54
1444921_at	D15Ertd466e	DNA segment, Chr 15, ERATO Doi 466, expressed	1.09	0.618	-1.3	0.611	-1.13	0.458	-1.45	0.008	-0.7
1436075_at	Sfrp5	secreted frizzled-related sequence protein 5	-1.06	0.804	-1.44	0.371	1.11	0.672	-1.45	0.335	-0.71
1420902_at	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	1.22	0.688	-1.27	0.44	-1.36	0.309	-1.08	0.908	-0.62
1456089_at	Trim23	tripartite motif protein 23	-1.16	0.156	1.03	0.907	-1.17	0.56	-1	0.998	-0.58
1426266_s_at	Zbtb8os	zinc finger and BTB domain containing 8 opposite strand	-1.13	0.047	-1.17	0.058	1	0.999	-1.56	0.055	-0.71
1422686_s_at	Exoc4	exocyst complex component 4	-1.06	0.54	-1.1	0.253	-1.13	0.504	1.22	0.005	-0.52
1451602_at	Snx6	sorting nexin 6	1.01	0.971	-1.05	0.412	-1.29	0.022	-1.26	0.104	-0.64
1460628_at	Mapk8ip3	Mitogen-activated protein kinase 8 interacting protein 3	-1.16	0.149	-1.34	0.344	1.14	0.408	-1.5	0.052	-0.72
1439186_at	E130319B15Rik	RIKEN cDNA E130319B15 gene	1.05	0.872	-1.3	0.171	-1.08	0.712	-1.03	0.959	-0.59
1457040_at	Lgi2	leucine-rich repeat LGI family, member 2	1.14	0.79	-1.23	0.547	-1.27	0.229	-1.12	0.266	-0.62
1457865_at	Phr1	Pam, highwire, rpm 1	-1.93	0.368	1.63	0.01	-1.67	0.478	-1.56	0.558	-0.88
1458177_at	Ebpl	emopamil binding protein-like	-1	0.998	1.3	0.449	-2.26	0.079	-1.78	0.098	-0.94
1434446_at	D630014A15Rik	RIKEN cDNA D630014A15 gene	-1.12	0.648	1	0.991	-1.18	0.116	-1.04	0.897	-0.58
1427905_at	1810063B07Rik	RIKEN cDNA 1810063B07 gene	-1.1	0.051	1.05	0.618	-1.27	0.073	-1.37	0.267	-0.67
1454490_at	4930423C22Rik	RIKEN cDNA 4930423C22 gene	-1.21	0.45	-1.18	0.581	1.07	0.659	-1.3	0.509	-0.65
1428574_a_at	Chn2	chimerin (chimaerin) 2	-1.43	0.116	-1.23	0.097	1.23	0.565	-1.2	0.425	-0.66
1455317_at	Epc2	enhancer of polycomb homolog 2 (Drosophila)	1.05	0.715	-1.03	0.715	-1.4	0.009	-1.29	0.026	-0.66
1454725_at	Tra2a	transformer 2 alpha homolog (Drosophila)	-1.12	0.631	1.04	0.789	-1.24	0.034	-1.15	0.227	-0.62
1430342_at	4930518J20Rik	RIKEN cDNA 4930518J20 gene	1.63	0.419	-1.79	0.411	-1.79	0.203	-1.25	0.48	-0.8
1416924_at	Bri3	brain protein I3	1.02	0.89	-1.14	0.558	-1.17	0.035	-1.24	0.51	-0.63
1423744_x_at	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	-1.03	0.536	-1.12	0.313	-1.13	0.421	1.16	0.302	-0.53
1429448_s_at	Cxxc6	CXXC finger 6	-1.34	0.552	1.36	0.61	-1.57	0.294	-2.39	0.219	-0.98
1443232_at	---	Transcribed locus	1.02	0.929	-1.07	0.66	-1.27	0.28	-1.29	0.528	-0.65
1433676_at	Wnk1	WNK lysine deficient protein kinase 1	-1.14	0.007	-1.04	0.087	-1.11	0.387	1.21	0.218	-0.52
1424002_at	Pdcl3	phosducin-like 3	-1.11	0.005	1.03	0.696	-1.23	0.042	-1.36	0.004	-0.67
1436313_at	Scyl2	SCY1-like 2 (S. cerevisiae)	-1.1	0.36	-1.21	0.499	1.01	0.896	-1.05	0.841	-0.59
1429723_at	6330409N04Rik	RIKEN cDNA 6330409N04 gene	-1.04	0.671	-1.07	0.508	-1.19	0.332	1.31	0.454	-0.5
1457854_at	AU018877	expressed sequence AU018877	1.22	0.648	-1.23	0.505	-1.41	0.378	-1.57	0.088	-0.75
1459156_at	---	---	-1.16	0.403	1.3	0.564	-1.72	0.173	-1.92	0.105	-0.88
1435790_at	Olfm2	olfactomedin 2	1.37	0.505	-1.46	0.497	-1.44	0.117	-1.33	0.195	-0.72
1431318_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	-1.83	0.534	-1.27	0.651	1.42	0.161	-1.28	0.489	-0.74
1431337_a_at	1810055E12Rik	RIKEN cDNA 1810055E12 gene	-1.13	0.138	1.09	0.418	-1.29	0.097	-1.01	0.895	-0.59
1459002_at	Rpl21 /// LOC26867	ribosomal protein L21 /// similar to 60S ribosomal protein L21 /// similar to riboson	1.56	0.415	-1.73	0.074	-1.65	0.381	-2.07	0.094	-0.97
1456872_a_at	D230010M03Rik	RIKEN cDNA D230010M03 gene	-1.11	0.584	-1.03	0.79	-1.15	0.652	1.56	0.13	-0.43
1442978_at	Mpdz	Multiple PDZ domain protein	1.05	0.821	-1.24	0.63	-1.13	0.441	-1.1	0.816	-0.6
1434663_at	2410129H14Rik	RIKEN cDNA 2410129H14 gene	-1.11	0.421	-1.08	0.574	-1.09	0.459	2.34	0.158	-0.23
1431666_at	2610021K21Rik	RIKEN cDNA 2610021K21 gene	-1.63	0.296	1.3	0.584	-1.2	0.717	-1.65	0.614	-0.8
1422730_at	Limd1	LIM domains containing 1	1.06	0.729	-1.13	0.51	-1.25	0.376	-1.03	0.845	-0.59
1433077_at	2700078F05Rik	RIKEN cDNA 2700078F05 gene	-1.2	0.717	-1.1	0.602	1	0.953	-1.04	0.807	-0.58
1455222_a_at	Ubp1	upstream binding protein 1	-1.22	0.054	-1.02	0.836	-1.06	0.698	1.45	0.132	-0.46
1429085_at	Vezf1	vascular endothelial zinc finger 1	1.01	0.946	-1.19	0.002	-1.11	0.026	-1.31	0.14	-0.65
1423861_at	Plekhf2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	-1.14	0.481	-1.03	0.941	-1.12	0.555	1.46	0.24	-0.46
1445174_at	---	---	-1.27	0.724	-1.53	0.478	1.3	0.654	-3.18	0.311	-1.17
1456894_at	C130039O16Rik	RIKEN cDNA C130039O16 gene	-1.12	0.834	-1.08	0.817	-1.08	0.848	1.41	0.451	-0.47
1440641_at	Vps29	vacuolar protein sorting 29 (S. pombe)	-1.3	0.288	1.17	0.432	-1.24	0.418	-1.43	0.177	-0.7
1446950_at	Tox	Thymocyte selection-associated HMG box gene	-1.02	0.981	-1.43	0.223	1.07	0.861	-1.49	0.357	-0.72
1458298_at	Cadps	Ca<2+>dependent activator protein for secretion	-1.25	0.57	-1.1	0.85	1.04	0.94	-1.28	0.709	-0.65
1442295_at	Arpc2	Actin related protein 2/3 complex, subunit 2	1.13	0.598	-1.34	0.546	-1.14	0.617	-1.55	0.199	-0.73
1418400_at	Larp6	La ribonucleoprotein domain family, member 6	1.2	0.536	-1.62	0.409	-1.08	0.289	-1.2	0.487	-0.68
1456849_at	---	---	1.2	0.546	-1.33	0.144	-1.25	0.276	-1.24	0.334	-0.66
1415744_at	H2-Ke2	H2-K region expressed gene 2	-1.06	0.385	-1.18	0.061	-1.04	0.694	1.1	0.543	-0.55

1448864_at	Snrk	SNF related kinase	1.06	0.792	-1.3	0.386	-1.1	0.749	-1.57	0.111	-0.72
1432336_at	5033404E19Rik	RIKEN cDNA 5033404E19 gene	-1.7	0.105	1.38	0.438	-1.28	0.529	-1.34	0.299	-0.74
1454388_at	2900046F13Rik	RIKEN cDNA 2900046F13 gene	-1.09	0.833	1.24	0.59	-1.7	0.114	-1.28	0.273	-0.71
1455377_at	4921517B04Rik	RIKEN cDNA 4921517B04 gene	1.07	0.765	-1.04	0.923	-1.41	0.16	-1	0.985	-0.59
1434973_at	Car7	carbonic anhydrase 7	-1.16	0.748	-1.23	0.525	1.07	0.923	-1.12	0.665	-0.61
1424082_at	Tbc1d13	TBC1 domain family, member 13	1.01	0.947	-1.14	0.477	-1.17	0.389	-1.17	0.017	-0.62
1439896_at	Limk2	LIM motif-containing protein kinase 2	-1.34	0.674	1.24	0.462	-1.32	0.25	-2.7	0.103	-1.03
1423299_at	Txnl1	thioredoxin-like 1	-1.1	0.253	-1.19	0.009	-1	0.974	1.55	0.212	-0.44
1445005_at	C79491	expressed sequence C79491	-1.36	0.047	-1.08	0.452	1.08	0.615	-1.14	0.477	-0.62
1429119_at	4833421E05Rik	RIKEN cDNA 4833421E05 gene	1.06	0.481	-1.05	0.502	-1.35	0.045	-1.35	0.202	-0.67
1449689_at	C81600	expressed sequence C81600	-1.25	0.712	-1.54	0.473	1.3	0.391	-1.46	0.391	-0.74
1431822_a_at	Azi2	5-azacytidine induced gene 2	-1.14	0.229	-1.06	0.151	-1.07	0.18	1.04	0.807	-0.56
1419460_at	Rpp14	ribonuclease P 14 subunit (human)	-1.06	0.599	-1.05	0.436	-1.18	0.19	1.02	0.873	-0.57
1443874_at	2810002I04Rik	RIKEN cDNA 2810002I04 gene	-1.16	0.612	-1.28	0.001	1.1	0.755	-1.06	0.745	-0.6
1424828_a_at	Fh1	fumarate hydratase 1	-1.12	0.39	1.02	0.83	-1.2	0.315	-1.59	0.105	-0.72
1438880_at	1700012D14Rik	RIKEN cDNA 1700012D14 gene	1.06	0.806	-1.27	0.321	-1.12	0.513	-1.45	0.139	-0.69
1416747_at	D15Mgi27	DNA Segment, Chr 15, Mouse Genome Informatics 27	-1.07	0.528	-1.09	0.115	-1.11	0.427	1.03	0.686	-0.56
1458517_at	Akr1e1	Aldo-keto reductase family 1, member E1	-1.17	0.04	1.04	0.877	-1.17	0.659	-1.16	0.52	-0.62
1453174_at	2310076G13Rik	RIKEN cDNA 2310076G13 gene	-1.21	0.284	1.09	0.51	-1.21	0.146	-1.33	0.445	-0.66
1416005_at	Psmc1	protease (prosome, macropain) 26S subunit, ATPase 1	-1.05	0.597	-1.1	0.009	-1.13	0.243	1.06	0.698	-0.55
1419798_at	2610019E17Rik	RIKEN cDNA 2610019E17 gene	1.11	0.704	-1.56	0.164	-1	0.997	-1.14	0.715	-0.65
1452364_at	Suz12	suppressor of zeste 12 homolog (Drosophila)	-1.11	0.593	-1.02	0.888	-1.16	0.15	1.72	0.12	-0.39
1439430_x_at	4930403C10Rik	RIKEN cDNA 4930403C10 gene	1.02	0.959	-1.33	0.297	-1.02	0.913	-1.43	0.121	-0.69
1423538_at	Ntan1	N-terminal Asn amidase	1.07	0.165	-1.11	0.409	-1.29	0.054	-1.27	0.177	-0.65
1456626_a_at	1110005A23Rik ///	RIKEN cDNA 1110005A23 gene /// similar to cytokine induced protein 29 kDa ///	-1.25	0.236	1.07	0.498	-1.14	0.239	-1.18	0.702	-0.62
1418567_a_at	Srp14	signal recognition particle 14	1.02	0.862	-1.08	0.288	-1.23	0.061	-1.42	0.038	-0.68
1434625_at	4930432O21Rik	RIKEN cDNA 4930432O21 gene	1.08	0.749	-1.13	0.224	-1.28	0.086	-1.13	0.404	-0.61
1426352_s_at	Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	1.28	0.427	-1.44	0.396	-1.29	0.09	-1.6	0.01	-0.76
1430797_at	Xpo4	exportin 4	1.41	0.375	-2.07	0.031	-1.16	0.575	-1.03	0.962	-0.71
1446414_at	0910001A06Rik	RIKEN cDNA 0910001A06 gene	1.35	0.341	-1.37	0.483	-1.5	0.538	-1.89	0.314	-0.85
1450561_a_at	Surf1	surfeit gene 1	1.03	0.84	-1.22	0.013	-1.12	0.037	-1.26	0.271	-0.64
1455375_at	LOC669787	similar to Protein enabled homolog (NPC-derived proline-rich protein 1) (NDPP-1)	-1.33	0.488	1.06	0.783	-1.07	0.714	-1.38	0.084	-0.68
1429497_s_at	Snx6	sorting nexin 6	-1.21	0.181	1.1	0.39	-1.22	0.012	-1.45	0.09	-0.69
1429166_s_at	Clmn	calmin	-1.15	0.487	-1.29	0.258	1.11	0.744	-3.26	0.337	-1.15
1424200_s_at	Seh1l	SEH1-like (S. cerevisiae	-1.04	0.545	-1	0.976	-1.26	0.003	1.09	0.452	-0.55
1418584_at	Ccnh /// LOC67265	cyclin H /// similar to cyclin H	-1.07	0.713	-1.15	0.266	-1.06	0.575	1.07	0.638	-0.55
1439144_at	Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	-1.73	0.012	1.22	0.527	-1.05	0.813	-1.95	0.039	-0.88
1441927_at	Syt7	Synaptotagmin VII	-1.86	0.425	1.24	0.476	-1.03	0.919	-1.54	0.473	-0.8
1430518_at	5430402E10Rik	RIKEN cDNA 5430402E10 gene	-1.13	0.867	1.31	0.46	-1.8	0.301	-1.47	0.621	-0.77
1456981_at	Tmc7	transmembrane channel-like gene family 7	-1.6	0.38	-1.5	0.441	1.46	0.211	-1.03	0.883	-0.67
1456740_x_at	Cog1	component of oligomeric golgi complex 1	-1.25	0.569	1.03	0.844	-1.09	0.721	-1.3	0.486	-0.65
1444154_at	Ndufa11	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 11	-1.22	0.243	-1.06	0.851	-1.02	0.743	2.02	0.161	-0.32
1438776_x_at	Rps17 /// LOC2686	ribosomal protein S17 /// similar to ribosomal protein S17 /// similar to 40S ribosor	-1.09	0.581	1.04	0.724	-1.26	0.031	-1.52	0.09	-0.71
1416952_at	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	-1.09	0.397	-1.18	0.033	-1.02	0.79	1.02	0.867	-0.57
1454793_x_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-1.23	0.321	1.03	0.653	-1.1	0.267	-1.68	0.102	-0.75
1440240_at	Npb	neuropeptide B	-1	0.998	-1.43	0.439	1.05	0.732	-1.52	0.431	-0.72
1420890_at	Hccs	holocytochrome c synthetase	-1.09	0.018	-1.13	0.265	-1.05	0.656	1.09	0.395	-0.55
1438839_a_at	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsil	-1.08	0.493	-1.05	0.622	-1.15	0.058	1.04	0.799	-0.56
1457054_a_at	D130020L05Rik	RIKEN cDNA D130020L05 gene	-1.41	0.055	1.06	0.785	-1.02	0.65	-1.55	0.127	-0.73
1431557_at	4930488N15Rik	RIKEN cDNA 4930488N15 gene	-1.35	0.45	1.22	0.68	-1.27	0.471	-1.76	0.433	-0.79
1438420_at	Rbm39	RNA binding motif protein 39	1.14	0.295	-1.04	0.728	-1.52	0.046	-1.28	0.227	-0.68
1435267_at	A430108E01Rik	RIKEN cDNA A430108E01 gene	1.09	0.606	-1.19	0.135	-1.22	0.315	-1.31	0.319	-0.66
1448670_at	Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	-1.08	0.02	-1.09	0.11	-1.1	0.313	1.55	0.246	-0.43

1435004_at	Pank4	pantothenate kinase 4	-1.08	0.385	-1.41	0.067	1.12	0.003	-1.18	0.281	-0.64
1431830_at	Zfp329	zinc finger protein 329	-1.03	0.796	1.14	0.594	-1.56	0.134	-1.51	0.222	-0.74
1458121_at	A430107O13Rik	RIKEN cDNA A430107O13 gene	1.62	0.062	-1.97	0.149	-1.61	0.193	-1.1	0.705	-0.77
1421388_at	Mef2d	myocyte enhancer factor 2D	-1.07	0.627	-1.15	0.185	-1.06	0.868	1.21	0.07	-0.52
1460689_at	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed	-1.08	0.105	-1.06	0.697	-1.13	0.545	1.15	0.587	-0.53
1434312_at	AI788669	expressed sequence AI788669	-1.14	0.444	-1	0.988	-1.14	0.595	1	0.965	-0.57
1440838_at	AI852064	Expressed sequence AI852064	-1.1	0.731	-1.04	0.951	-1.14	0.625	1.33	0.059	-0.49
1432456_at	4930533B18Rik	RIKEN cDNA 4930533B18 gene	1.59	0.59	-3.48	0.002	-1.14	0.36	-1.68	0.513	-1.18
1415936_at	Bcar3	breast cancer anti-estrogen resistance 3	-1.29	0.218	-1.21	0.355	1.15	0.402	-1.96	0.074	-0.83
1439922_at	1190002C06Rik	RIKEN cDNA 1190002C06 gene	-1.33	0.493	1.11	0.774	-1.13	0.691	-1.07	0.718	-0.6
1434317_s_at	Tex10	testis expressed gene 10	-1.09	0.198	1.01	0.875	-1.22	0.144	-1.2	0.061	-0.62
1450341_at	Pcdhb8	protocadherin beta 8	1.24	0.35	-1.37	0.558	-1.28	0.546	-1.18	0.817	-0.65
1457078_at	Zfp473	zinc finger protein 473	-1.15	0.854	1.05	0.885	-1.2	0.566	-1.08	0.821	-0.6
1424588_at	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	-1.04	0.867	-1.45	0.228	1.1	0.686	-1.06	0.726	-0.61
1460580_at	Pcnx	pecanex homolog (Drosophila)	-1.05	0.741	1.02	0.915	-1.28	0.253	-1.43	0.15	-0.68
1437911_at	6330416L07Rik	RIKEN cDNA 6330416L07 gene	-1.34	0.176	-1.05	0.834	1.06	0.643	-1.09	0.575	-0.61
1436896_at	D14Ertd231e	DNA segment, Chr 14, ERATO Doi 231, expressed	-1.25	0.157	-1.08	0.26	1.02	0.773	-1.12	0.149	-0.61
1453515_at	4930511A21Rik	RIKEN cDNA 4930511A21 gene	1.75	0.386	-1.69	0.255	-2.42	0.28	-1.02	0.971	-0.85
1441265_at	Plekhm2	Pleckstrin homology domain containing, family M (with RUN domain) member 2	-1.06	0.813	-1.13	0.496	-1.08	0.749	1.29	0.13	-0.5
1435380_at	Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransf	-1.19	0.385	-1.1	0.678	-1	0.999	1.08	0.348	-0.55
1454860_x_at	Dad1	defender against cell death 1	1.15	0.43	-1.03	0.739	-1.58	0.006	-1.22	0.44	-0.67
1433377_at	5830445D09Rik	RIKEN cDNA 5830445D09 gene	-2.12	0.089	1.41	0.312	-1.15	0.631	-1.24	0.258	-0.78
1442757_at	Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1	-1.04	0.863	1.08	0.528	-1.42	0.088	-1.35	0.379	-0.68
1449624_at	Gm118	gene model 118, (NCBI)	1.05	0.568	-1.17	0.737	-1.18	0.553	-1.2	0.414	-0.63
1457264_at	Phf20l1	PHD finger protein 20-like 1	1.28	0.11	-1.19	0.465	-1.59	0.022	-1.74	0.052	-0.81
1434731_x_at	Prdx1	peroxiredoxin 1	-1.13	0.214	1.01	0.899	-1.18	0.104	-1.29	0.151	-0.65
1443620_at	Gpc4	Glypican 4	-1.04	0.806	-1.05	0.878	-1.2	0.339	1.5	0.046	-0.45
1450757_at	Cdh11	cadherin 11	1.16	0.404	-1.32	0.18	-1.2	0.472	-1.95	0.075	-0.83
1457073_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:p	1.29	0.15	-1.02	0.959	-2.07	0.008	-1.02	0.916	-0.71
1460574_at	Fat4	FAT tumor suppressor homolog 4 (Drosophila)	1.17	0.506	-1.62	0.098	-1.04	0.902	-1.39	0.268	-0.72
1422647_at	Ring1	ring finger protein 1	-1.07	0.827	1	0.968	-1.23	0.285	-1.33	0.359	-0.66
1455495_at	AA536808	Expressed sequence AA536808	1.02	0.881	-1.07	0.306	-1.25	0.167	-1.52	0.123	-0.71
1447866_x_at	2300009A05Rik	RIKEN cDNA 2300009A05 gene	1.12	0.621	-1.41	0.332	-1.09	0.862	-1.39	0.205	-0.69
1419899_at	Zc3h7a	Zinc finger CCCH type containing 7 A	1.63	0.094	-1.35	0.519	-2.66	0.191	-1.45	0.472	-0.96
1434093_at	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4	-1.04	0.872	1.01	0.95	-1.28	0.328	-1.12	0.565	-0.61
1458820_at	Zfp560	zinc finger protein 560	1.05	0.786	-1.03	0.934	-1.36	0.116	-1.22	0.334	-0.64
1438373_at	App	Amyloid beta (A4) precursor protein	-1.84	0.049	-1.2	0.73	1.38	0.311	-1.1	0.843	-0.69
1445416_at	Tsga14	Testis specific gene A14	-1.59	0.09	1.33	0.67	-1.26	0.406	-2.87	0.048	-1.1
1424993_at	8430410K20Rik	RIKEN cDNA 8430410K20 gene	-1.19	0.073	1.08	0.51	-1.21	0.099	-1.09	0.629	-0.6
1436622_at	Iqsec2	IQ motif and Sec7 domain 2	-1.07	0.664	-1.04	0.762	-1.17	0.41	1	0.995	-0.57
1450721_at	Acp1	acid phosphatase 1, soluble	-1.14	0.258	-1.05	0.185	-1.09	0.368	1.56	0.29	-0.43
1443059_at	Dhrs8	dehydrogenase/reductase (SDR family) member 8	-1.4	0.634	-1.12	0.257	1.15	0.639	-1.31	0.227	-0.67
1459234_at	Alox5ap	Arachidonate 5-lipoxygenase activating protein	-1.35	0.038	-1	0.995	1.01	0.911	-1.14	0.633	-0.62
1420936_s_at	Cpsf2	cleavage and polyadenylation specific factor 2	-1.19	0.171	-1.02	0.822	-1.07	0.69	1.36	0.334	-0.48
1425742_a_at	Tsc22d1	TSC22 domain family, member 1	1.11	0.75	-1.16	0.319	-1.28	0.025	-1.29	0.316	-0.66
1419354_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.08	0.616	-1.05	0.557	-1.39	0.069	-1.12	0.454	-0.62
1447850_x_at	Zfand3	zinc finger, AN1-type domain 3	-1.05	0.668	1.08	0.749	-1.4	0.36	-2.41	0.093	-0.94
1417709_at	Cyp46a1	cytochrome P450, family 46, subfamily a, polypeptide 1	1.26	0.108	-1.37	0.306	-1.31	0.231	-1.49	0.432	-0.73
1443150_at	Dnm2	Dynamin 2	1.07	0.831	-1.32	0.25	-1.08	0.747	-1.03	0.925	-0.59
1458585_at	---	Transcribed locus	-1.15	0.691	1.15	0.779	-1.37	0.079	-1.13	0.764	-0.62
1449694_s_at	Commd5	COMM domain containing 5	-1.24	0.167	-1.08	0.577	1.02	0.904	-1.19	0.248	-0.62
1442987_at	---	---	-1.49	0.524	1.26	0.618	-1.21	0.736	-1.02	0.968	-0.62
1424135_at	Rspry1	ring finger and SPRY domain containing 1	-1.11	0.423	-1.1	0.19	-1.06	0.705	1.05	0.405	-0.56

1427248_at	Whsc2	Wolf-Hirschhorn syndrome candidate 2 (human)	-1.09	0.702	-1.09	0.374	-1.09	0.645	1.02	0.925	-0.56
1455703_at	Akt2	thymoma viral proto-oncogene 2	-1.11	0.025	-1.23	0.018	1.04	0.687	-1.16	0.11	-0.61
1433627_at	Sec23ip	Sec23 interacting protein	-1.19	0.319	-1.08	0.367	-1.02	0.398	1.08	0.143	-0.55
1424904_at	1300010F03Rik	RIKEN cDNA 1300010F03 gene	-1.04	0.844	-1.83	0.057	1.24	0.236	-1.15	0.683	-0.69
1455039_a_at	Sin3b	transcriptional regulator, SIN3B (yeast)	1.04	0.814	-1.16	0.179	-1.17	0.308	-1.51	0.252	-0.7
1434605_at	Eif5b	eukaryotic translation initiation factor 5B	-1.04	0.746	-1.16	0.045	-1.08	0.646	1.13	0.375	-0.54
1433848_at	Cdc27	cell division cycle 27 homolog (S. cerevisiae)	-1	0.992	-1.1	0.42	-1.18	0.208	2.11	0.125	-0.29
1435625_at	Entpd7	ectonucleoside triphosphate diphosphohydrolase 7	-1.23	0.619	-1.44	0.16	1.24	0.315	-1.51	0.1	-0.73
1420115_at	Exosc8	exosome component 8	-1.24	0.555	-1.3	0.367	1.17	0.581	-1.11	0.565	-0.62
1458538_at	Sirt1	Sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	1.04	0.639	-1.16	0.269	-1.17	0.29	-1.15	0.489	-0.61
1425460_at	Mtmr2	myotubularin related protein 2	-1.1	0.511	1.08	0.582	-1.31	0.001	-1.18	0.102	-0.63
1415995_at	Casp6	caspase 6	-1.09	0.293	-1.27	0.214	1.05	0.69	-1.29	0.169	-0.65
1449744_at	Slc19a1	Solute carrier family 19 (sodium/hydrogen exchanger), member 1	-1.23	0.177	1.02	0.95	-1.08	0.746	-1.88	0.346	-0.79
1433909_at	Syt17	synaptotagmin XVII	-1.02	0.725	-1.03	0.953	-1.26	0.405	1.31	0.351	-0.5
1454769_at	Tatdn2	TatD DNase domain containing 2	-2.11	0.299	-1.31	0.527	1.51	0.219	-2.06	0.278	-0.99
1445346_at	Ank2	Ankyrin 2, brain	-1.37	0.538	1.31	0.631	-1.41	0.292	-1.14	0.817	-0.65
1417424_at	Ier3ip1	immediate early response 3 interacting protein 1	-1.02	0.455	1.01	0.924	-1.31	0.021	-1.37	0.181	-0.67
1455988_a_at	Cct6a	chaperonin subunit 6a (zeta)	-1.02	0.427	-1.06	0.334	-1.21	0.105	1.03	0.819	-0.56
1429623_at	Zfp644	zinc finger protein 644	-1.04	0.785	-1.1	0.441	-1.14	0.333	1.02	0.945	-0.56
1460176_at	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	1.13	0.583	-1.23	0.102	-1.24	0.199	-1.06	0.65	-0.6
1454644_at	6330569M22Rik	RIKEN cDNA 6330569M22 gene	-1.16	0.284	1.04	0.785	-1.18	0.222	-1.59	0.104	-0.72
1446343_at	---	Transcribed locus	-2.04	0.085	-1.58	0.033	1.63	0.082	-1.28	0.489	-0.82
1424472_at	Nol6	nucleolar protein family 6 (RNA-associated)	-1.45	0.188	-1.24	0.019	1.26	0.289	-1.04	0.66	-0.62
1427921_s_at	2310061C15Rik	RIKEN cDNA 2310061C15 gene	-1.1	0.275	-1.1	0.417	-1.07	0.169	2.01	0.229	-0.32
1416732_at	Top2b	topoisomerase (DNA) II beta	-1.13	0.425	-1.28	0.326	1.09	0.698	-1.28	0.449	-0.65
1459414_at	Wdfy3	WD repeat and FYVE domain containing 3	-1.1	0.589	-1.09	0.48	-1.08	0.834	1.6	0.168	-0.42
1450425_a_at	2700062C07Rik	RIKEN cDNA 2700062C07 gene	-1.21	0.316	-1.17	0.113	1.07	0.716	-1.11	0.294	-0.6
1423769_at	Ptcd2	pentatricopeptide repeat domain 2	-1.18	0.089	-1.14	0.031	1.03	0.822	-1.32	0.036	-0.65
1417672_at	Slc4a10	solute carrier family 4, sodium bicarbonate cotransporter-like, member 10	-1.02	0.856	1.22	0.497	-1.82	0.208	-3.04	0.223	-1.16
1430558_at	Zfp318	zinc finger protein 318	-1.18	0.248	1.09	0.556	-1.23	0.306	-1.81	0.138	-0.78
1424240_at	Arfip2	ADP-ribosylation factor interacting protein 2	-1.03	0.823	-1.03	0.762	-1.22	0.429	1.19	0.226	-0.53
1428871_at	4121402D02Rik	RIKEN cDNA 4121402D02 gene	-1.13	0.255	1.06	0.605	-1.23	0.331	-1.21	0.375	-0.63
1436152_a_at	Hbxip	hepatitis B virus x interacting protein	-1.15	0.024	1.04	0.587	-1.18	0.258	-1.39	0.137	-0.67
1415813_at	Api5	apoptosis inhibitor 5	-1.1	0.236	-1.09	0.256	-1.08	0.253	1.1	0.513	-0.54
1423490_at	Fbxo3	F-box only protein 3	-1.11	0.356	-1.1	0.247	-1.06	0.565	1.76	0.196	-0.38
1450583_s_at	Fprl1	formyl peptide receptor-like 1	1.08	0.775	-1.12	0.679	-1.28	0.66	-1.28	0.382	-0.65
1427990_at	Usp45	ubiquitin specific petidase 45	-1.11	0.531	-1.03	0.855	-1.13	0.396	1.87	0.242	-0.35
1436684_a_at	Riok2	RIO kinase 2 (yeast)	-1.16	0.638	1.09	0.425	-1.25	0.193	-1.22	0.39	-0.63
1426581_at	Ptpmt1	protein tyrosine phosphatase, mitochondrial 1	-1.08	0.545	-1.19	0.175	-1.01	0.94	1.06	0.733	-0.56
1435624_at	9030409G11Rik	RIKEN cDNA 9030409G11 gene	1.1	0.898	-1.36	0.399	-1.08	0.816	-1.2	0.78	-0.64
1448771_a_at	Fth1	ferritin heavy chain 1	-1.08	0.11	-1.09	0.641	-1.09	0.03	1.03	0.726	-0.56
1418693_at	Hnrpc /// LOC62088	heterogeneous nuclear ribonucleoprotein C /// similar to heterogeneous nuclear ri	-1.08	0.4	-1.1	0.108	-1.09	0.323	1.17	0.229	-0.52
1434517_at	Wdfy2	WD repeat and FYVE domain containing 2	-1.24	0.351	1.14	0.409	-1.24	0.164	-1.46	0.132	-0.7
1444280_at	A930001M12Rik	RIKEN cDNA A930001M12 gene	-1.5	0.605	1.44	0.493	-1.53	0.531	-1.1	0.859	-0.68
1417227_at	Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-1.16	0.132	-1.31	0.077	1.13	0.118	-1.3	0.049	-0.66
1459900_at	C79468	expressed sequence C79468	1.06	0.756	-1	0.991	-1.44	0.036	-1.69	0.175	-0.77
1440084_at	AI663975	Expressed sequence AI663975	-1.17	0.42	1.11	0.879	-1.27	0.455	-1.72	0.37	-0.76
1424740_at	Creb3	cAMP responsive element binding protein 3	1.01	0.897	-1.04	0.423	-1.27	0.098	-1.29	0.216	-0.65
1426696_at	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	1.02	0.822	-1.09	0.305	-1.23	0.07	-1.01	0.943	-0.58
1438157_s_at	Nfkbia	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	-1.28	0.571	1.01	0.953	-1.03	0.81	-2.22	0.067	-0.88
1428307_at	Zdhhc13	zinc finger, DHHC domain containing 13	-1.19	0.216	1	0.986	-1.1	0.379	-1.39	0.171	-0.67
1455505_at	Gatad2a	GATA zinc finger domain containing 2A	-1.23	0.331	1.1	0.623	-1.19	0.178	-1.03	0.877	-0.59
1448253_at	Glud1	glutamate dehydrogenase 1	-1.21	0.042	-1.12	0.052	1.04	0.736	-1.54	0.198	-0.71

1442953_at	---	Transcribed locus	-1.06	0.878	1.08	0.61	-1.38	0.049	-1.35	0.442	-0.68
1457370_at	Rabgap1	RAB GTPase activating protein 1	-1.03	0.915	1.21	0.33	-1.73	0.062	-1.44	0.202	-0.75
1431538_at	4931415C17Rik	RIKEN cDNA 4931415C17 gene	1.09	0.817	-1.19	0.302	-1.21	0.534	-1.2	0.819	-0.63
1435536_at	Rsc1a1	regulatory solute carrier protein, family 1, member 1	-1.02	0.756	-1.09	0.152	-1.17	0.07	1.21	0.24	-0.52
1433427_at	1700111A04Rik	RIKEN cDNA 1700111A04 gene	-1.26	0.529	-1.26	0.257	1.17	0.403	-1.88	0.007	-0.81
1445367_at	---	Transcribed locus	1.4	0.221	-1.52	0.217	-1.43	0.024	-1.23	0.27	-0.7
1460168_at	Slbp	stem-loop binding protein	-1.14	0.005	-1.07	0.108	-1.06	0.576	2.31	0.167	-0.24
1450701_a_at	Gtf2h2	general transcription factor II H, polypeptide 2	-1.16	0.545	-1.04	0.678	-1.08	0.278	1.02	0.895	-0.56
1454817_at	Utp18	UTP18, small subunit (SSU) processome component, homolog (yeast)	-1.3	0.177	-1.26	0.032	1.19	0.533	-1.09	0.514	-0.61
1447753_at	Cdc37l1	Cell division cycle 37 homolog (S. cerevisiae)-like 1	-1.41	0.345	1.25	0.254	-1.25	0.315	-1.17	0.71	-0.65
1417652_a_at	Tbca	tubulin cofactor a	-1.01	0.83	1.01	0.751	-1.33	0.02	-1.28	0.096	-0.65
1434579_x_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	-1.02	0.817	-1.08	0.194	-1.18	0.118	1.03	0.787	-0.56
1454975_at	Psrc2	proline/serine-rich coiled-coil 2	1.01	0.96	-1.04	0.751	-1.28	0.192	-1.16	0.534	-0.62
1426957_at	Trp53bp1	transformation related protein 53 binding protein 1	-1.23	0.134	-1.09	0.453	1.03	0.82	-1.06	0.697	-0.59
1423143_at	Gtpbp4	GTP binding protein 4	1.07	0.814	-1.32	0.104	-1.08	0.628	-1.39	0.261	-0.68
1433991_x_at	Dbi	diazepam binding inhibitor	-1.07	0.501	-1.04	0.803	-1.16	0.639	1.05	0.86	-0.56
1428261_at	2310042L06Rik	RIKEN cDNA 2310042L06 gene	-1.33	0.02	-1.22	0.054	1.18	0.137	-1.13	0.518	-0.62
1428876_at	Srp72	signal recognition particle 72	-1.07	0.512	-1.06	0.389	-1.13	0.146	1.15	0.165	-0.53
1452126_at	Zfp160	zinc finger protein 160	-1.22	0.143	-1.07	0.285	1	0.991	-1.25	0.095	-0.63
1425007_at	Zfp566	zinc finger protein 566	-1.35	0.251	-1.02	0.95	1.03	0.808	-1.41	0.324	-0.69
1449583_at	Pcdhb20	protocadherin beta 20	1.64	0.275	-1.74	0.169	-1.86	0.025	-1.5	0.445	-0.86
1434412_x_at	Stub1	STIP1 homology and U-Box containing protein 1	1.08	0.769	-1.05	0.804	-1.38	0.15	-1.34	0.068	-0.67
1417992_a_at	Svs3 /// 9530004A2	seminal vesicle secretion 3 /// RIKEN cDNA 9530004A22	-2.11	0.242	-1.03	0.97	1.31	0.626	-1.22	0.745	-0.76
1457371_at	5230400G24Rik	RIKEN cDNA 5230400G24 gene	-1.28	0.433	1.14	0.504	-1.2	0.118	-1.14	0.194	-0.62
1460350_at	Osbp	oxysterol binding protein	-1.14	0.262	-1.12	0.341	-1.01	0.808	1.03	0.56	-0.56
1454613_at	Dpysl3	dihydropyrimidinase-like 3	1.33	0.01	-1.25	0.541	-1.6	0.06	-1.18	0.246	-0.67
1427450_x_at	Myo1b	myosin IB	1.07	0.848	-1.16	0.327	-1.22	0.28	-1.04	0.883	-0.59
1448234_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	-1.04	0.373	-1.07	0.081	-1.17	0.162	1.12	0.362	-0.54
1446442_at	Rnmt	RNA (guanine-7-) methyltransferase	1.65	0.089	-1.73	0.361	-1.87	0.143	-1.46	0.562	-0.86
1434337_at	---	Transcribed locus	-1.08	0.416	-1.21	0.309	1.01	0.902	-1.11	0.636	-0.6
1427448_at	Rabep1	rabaptin, RAB GTPase binding effector protein 1	-1.11	0.621	1.03	0.859	-1.21	0.142	-1.29	0.077	-0.65
1426394_at	Eif3s1	eukaryotic translation initiation factor 3, subunit 1 alpha	-1.02	0.857	-1.16	0	-1.1	0.061	1.37	0.428	-0.48
1454214_a_at	2410019A14Rik	RIKEN cDNA 2410019A14 gene	-1.17	0.139	-1.15	0.015	1.03	0.801	-1.4	0.02	-0.67
1444601_at	---	---	-1.21	0.021	-1.09	0.773	1.01	0.934	-1.43	0.363	-0.68
1451532_s_at	Steap1	six transmembrane epithelial antigen of the prostate 1	-1.19	0.02	-1.21	0.685	1.09	0.688	-1.17	0.691	-0.62
1445111_at	Exoc4	Exocyst complex component 4	1.46	0.148	-1.14	0.558	-2.39	0.002	-1.14	0.63	-0.8
1441936_x_at	4930447M23Rik	RIKEN cDNA 4930447M23 gene	1.13	0.69	-1.06	0.905	-1.45	0.514	-1.67	0.085	-0.76
1448111_at	Ctps2	cytidine 5'-triphosphate synthase 2	1.01	0.948	-1.16	0.388	-1.13	0.074	-1.72	0.223	-0.75
1437982_x_at	Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-1.39	0.153	-1.12	0.532	1.14	0.379	-1.23	0.211	-0.65
1452222_at	Utrn	utrophin	1.09	0.132	-1.15	0.178	-1.26	0.392	-1.64	0.107	-0.74
1437991_x_at	Rusc1	RUN and SH3 domain containing 1	-1.17	0.481	-1.22	0.314	1.09	0.58	-1.52	0.102	-0.71
1424069_at	Napg	N-ethylmaleimide sensitive fusion protein attachment protein gamma	-1.17	0.037	1	0.997	-1.11	0.305	-1.19	0.398	-0.62
1426933_at	Oxsr1	oxidative-stress responsive 1	-1.15	0.505	-1.13	0.492	-1	0.992	1.56	0.133	-0.43
1416860_s_at	Ing1	inhibitor of growth family, member 1	1.05	0.852	-1.09	0.26	-1.27	0.258	-1.39	0.311	-0.67
1419755_at	Mfi2	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 an	-1.19	0.8	-2.89	0.049	1.57	0.102	-2.25	0.018	-1.19
1446342_at	2310001H17Rik	RIKEN cDNA 2310001H17 gene	1.01	0.971	-1.29	0.181	-1.03	0.944	-1.64	0.295	-0.74
1435810_at	5730455O13Rik	RIKEN cDNA 5730455O13 gene	1.06	0.444	-1.14	0.161	-1.22	0.037	-1.5	0.217	-0.7
1448366_at	Stx1a	syntaxin 1A (brain)	1.35	0.034	-1.65	0.126	-1.25	0.119	-1.55	0.259	-0.77
1439550_at	---	---	1.15	0.216	-1.27	0.282	-1.22	0.263	-2.51	0.069	-0.96
1453682_at	Gabpb2	GA repeat binding protein, beta 2	1.03	0.436	-1.09	0.156	-1.24	0.034	-1.19	0.368	-0.62
1434052_at	AI593442	expressed sequence AI593442	1.38	0.18	-1.65	0.512	-1.3	0.604	-1.19	0.247	-0.69
1449492_a_at	Lect2	leukocyte cell-derived chemotaxin 2	1.11	0.896	-1.53	0.093	-1	0.997	-1.94	0.272	-0.84
1422263_at	Bdkrb2	bradykinin receptor, beta 2	-1.62	0.527	-1.7	0.42	1.55	0.384	-1.1	0.875	-0.72

1451524_at	Fbxw2	F-box and WD-40 domain protein 2	-1.22	0.155	-1.03	0.855	-1.04	0.823	2.42	0.245	-0.22
1454459_at	4933423L19Rik	RIKEN cDNA 4933423L19 gene	1.33	0.032	-1.25	0.635	-1.59	0.342	-1.08	0.881	-0.65
1448654_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	-1.09	0.237	-1.06	0.328	-1.1	0.436	1.27	0.485	-0.5
1420368_at	Denr	density-regulated protein	1.04	0.735	-1.12	0.306	-1.22	0.191	-1.22	0.247	-0.63
1451152_a_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	1.01	0.958	-1.23	0.303	-1.06	0.738	-2.82	0.011	-1.03
1441592_at	Jmjd1c	Jumonji domain containing 1C	1.27	0.421	-1.07	0.782	-1.82	0	-1.78	0.121	-0.85
1415966_a_at	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	-1.02	0.779	-1.2	0.118	-1.06	0.646	1.12	0.55	-0.54
1453313_at	Sesn3	sestrin 3	1.13	0.846	-1.41	0.269	-1.09	0.892	-3.27	0.152	-1.16
1424787_a_at	Nrf1	nuclear respiratory factor 1	-1.04	0.869	-1.1	0.677	-1.12	0.292	1.14	0.713	-0.53
1419723_at	Opn1mw	opsin 1 (cone pigments), medium-wave-sensitive (color blindness, deutan)	-1.15	0.358	1.34	0.683	-1.81	0.286	-1.98	0.545	-0.9
1443630_at	---	---	1.25	0.48	-1.09	0.813	-1.71	0.077	-2	0.104	-0.89
1422756_at	Slc32a1	solute carrier family 32 (GABA vesicular transporter), member 1	-1.99	0.412	1.34	0.258	-1.09	0.758	-2.08	0.541	-0.96
1422968_at	Ihpk1	inositol hexaphosphate kinase 1	-1.28	0.196	-1.04	0.88	1.02	0.921	-1.45	0.119	-0.69
1439748_at	Dpp6	dipeptidylpeptidase 6	-1.19	0.402	-1.2	0.838	1.08	0.587	-1.15	0.725	-0.61
1436990_s_at	Ndg2	Nur77 downstream gene 2	-1.13	0.01	-1.33	0.242	1.12	0.39	-1.46	0.139	-0.7
1448262_at	Psmb2	proteasome (prosome, macropain) subunit, beta type 2	-1.02	0.93	-1.17	0.298	-1.08	0.705	1.39	0.112	-0.47
1440793_at	1700029M03Rik	RIKEN cDNA 1700029M03 gene	1.26	0.592	-1.56	0.107	-1.16	0.727	-1.1	0.872	-0.64
1454047_a_at	2410017P07Rik	RIKEN cDNA 2410017P07 gene	-1.06	0.744	1.02	0.787	-1.25	0.282	-1.07	0.61	-0.59
1447974_s_at	Aqp6	aquaporin 6	-1.28	0.429	1	0.992	-1.02	0.915	-1.11	0.854	-0.6
1423285_at	Coch	coagulation factor C homolog (Limulus polyphemus)	-1.44	0.371	-1.42	0.385	1.36	0.284	-2.06	0.201	-0.89
1453285_at	Tmem88	transmembrane protein 88	-1.23	0.469	-1.01	0.984	-1.05	0.805	1.22	0.204	-0.52
1438447_at	Ddx11	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like helicase homolog,	-1.17	0.255	-1.03	0.733	-1.07	0.805	1.33	0.118	-0.49
1423697_at	Psmd6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6	-1.04	0.092	-1.11	0.191	-1.12	0.178	1.07	0.562	-0.55
1420393_at	Nos2	nitric oxide synthase 2, inducible, macrophage	-1.16	0.266	-1.45	0.027	1.2	0.233	-1.04	0.936	-0.61
1427379_at	Nte	Neuropathy target esterase	-1.1	0.6	-1.06	0.685	-1.1	0.74	1.19	0.382	-0.52
1416566_at	Strap	serine/threonine kinase receptor associated protein	-1.09	0.099	-1.01	0.85	-1.17	0.075	1.13	0.451	-0.54
1421370_a_at	Il1f5	interleukin 1 family, member 5 (delta)	1.19	0.199	-1.23	0.661	-1.32	0.376	-1.26	0.68	-0.66
1441429_at	Irs4	insulin receptor substrate 4	-1.44	0.181	1.5	0.406	-1.75	0.188	-1.77	0.292	-0.87
1431563_at	2010003K10Rik	RIKEN cDNA 2010003K10 gene	-1.45	0.68	1.15	0.67	-1.08	0.824	-1.13	0.875	-0.63
1427194_a_at	Ercc8	excision repaiross-complementing rodent repair deficiency, complementation grou	-1.22	0.421	-1	0.961	-1.06	0.828	1.18	0.586	-0.52
1420786_a_at	Rbmy1a1	RNA binding motif protein, Y chromosome, family 1, member A1	1.26	0.633	-1.15	0.823	-1.58	0.593	-1.07	0.94	-0.64
1438505_s_at	Rnasen	ribonuclease III, nuclear	-1.28	0.09	1.06	0.694	-1.08	0.521	-1.06	0.723	-0.59
1423863_at	Abcf2	ATP-binding cassette, sub-family F (GCN20), member 2	-1.07	0.634	-1.05	0.624	-1.14	0.655	1.16	0.603	-0.53
1427150_at	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	1.04	0.658	-1.25	0.163	-1.09	0.668	-1.34	0.315	-0.66
1434870_at	2810004N23Rik	RIKEN cDNA 2810004N23 gene	1.05	0.642	-1.25	0.004	-1.09	0.404	-1.17	0.375	-0.62
1448392_at	Sparc	secreted acidic cysteine rich glycoprotein	-1.1	0.542	1.14	0.314	-1.41	0.363	-1.38	0.266	-0.69
1451129_at	Calb2	calbindin 2	-1.21	0.284	-1.33	0.308	1.18	0.713	-1.92	0.552	-0.82
1448783_at	Slc7a9	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	-1.07	0.568	-2.21	0.311	1.38	0.454	-1.87	0.12	-0.94
1436578_at	A330104H05Rik	RIKEN cDNA A330104H05 gene	-1.16	0.816	-1.08	0.82	-1.03	0.954	2.49	0.031	-0.19
1454778_x_at	Tia1	Cytotoxic granule-associated RNA binding protein 1	-1.08	0.429	1.05	0.63	-1.27	0.029	-1.2	0.03	-0.63
1457884_at	4732496C06Rik	RIKEN cDNA 4732496C06 gene	-1.12	0.63	-1.37	0.233	1.14	0.575	-1.33	0.289	-0.67
1421938_at	Serhl	serine hydrolase-like	-1.08	0.69	-1.03	0.794	-1.16	0.112	1.01	0.946	-0.56
1428090_at	Ptcd3	Pentatricopeptide repeat domain 3	-1.12	0.155	-1.16	0.066	1.01	0.94	-1.06	0.11	-0.58
1417725_a_at	Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	1.03	0.921	-1.15	0.42	-1.16	0.286	-1.36	0.326	-0.66
1460102_at	Clasp1	CLIP associating protein 1	-1.11	0.11	1.21	0.547	-1.53	0.02	-1.41	0.127	-0.71
1439726_at	4432406C05Rik	RIKEN cDNA 4432406C05 gene	-1.26	0.513	-1.53	0.118	1.31	0.184	-1.11	0.542	-0.65
1425600_a_at	Plcb1	phospholipase C, beta 1	-1.09	0.653	-1.17	0.377	-1.01	0.973	1.74	0.389	-0.38
1452271_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	-1.17	0.259	-1.11	0.122	1	0.98	-1.01	0.876	-0.57
1447052_at	---	---	1.01	0.949	-1.02	0.935	-1.29	0.306	-1.81	0.169	-0.78
1446819_at	Ran	RAN, member RAS oncogene family	-1.2	0.803	-1.14	0.68	1.05	0.89	-1.87	0.455	-0.79
1456215_at	Tfam	transcription factor A, mitochondrial	-1.07	0.194	-1.2	0.157	-1.01	0.962	1.11	0.68	-0.54
1435348_at	D930009K15Rik	RIKEN cDNA D930009K15 gene	1.07	0.74	-1.22	0.168	-1.15	0.262	-1.15	0.616	-0.61
1452833_at	Rapgef2	Rap guanine nucleotide exchange factor (GEF) 2	-1.16	0.582	1.03	0.795	-1.15	0.502	-1.4	0.363	-0.67

1446778_at	Hunk	Hormonally upregulated Neu-associated kinase	1.55	0.374	-1.32	0.472	-2.22	0.103	-2.14	0.159	-1.03
1436836_x_at	Cnn3	calponin 3, acidic	1.02	0.58	-1.03	0.649	-1.3	0.019	-2.45	0.038	-0.94
1416413_at	Ctsj	cathepsin J	-3.56	0.223	1.52	0.552	-1.04	0.896	-1.04	0.681	-1.03
1455957_x_at	Ceacam11	CEA-related cell adhesion molecule 11	-1.54	0.447	-1.53	0.479	1.46	0.567	-1.06	0.914	-0.67
1422033_a_at	Cntf /// Zfp91	ciliary neurotrophic factor /// zinc finger protein 91	-1.02	0.894	-1.25	0.375	-1.01	0.947	1.47	0.427	-0.46
1433296_at	2310045N14Rik	RIKEN cDNA 2310045N14 gene	-1.16	0.658	1.03	0.946	-1.15	0.781	-1.13	0.584	-0.6
1437261_at	2900024O10Rik	RIKEN cDNA 2900024O10 gene	-1.34	0.095	-1.1	0.645	1.1	0.562	-1.24	0.488	-0.64
1449390_at	Gpatc4	G patch domain containing 4	1.1	0.748	-1.11	0.777	-1.3	0.166	-1.47	0.001	-0.7
1415789_a_at	Ublcp1 /// LOC665(	ubiquitin-like domain containing CTD phosphatase 1 /// similar to ubiquitin-like do	1.14	0.66	-1.26	0.449	-1.21	0.552	-1.32	0.175	-0.66
1423901_at	Trip12	thyroid hormone receptor interactor 12	-1.11	0.413	-1.1	0.41	-1.05	0.68	1.11	0.649	-0.54
1455298_at	---	Transcribed locus	-1.11	0.77	1.04	0.862	-1.21	0.118	-1.47	0.203	-0.69
1457675_at	2510002D24Rik	RIKEN cDNA 2510002D24 gene	-1.02	0.898	-1.29	0.191	1.01	0.951	-1.24	0.383	-0.64
1429630_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	1.33	0.076	-1.77	0.363	-1.16	0.767	-1.24	0.721	-0.71
1439942_at	Prep	prolyl endopeptidase	-1.33	0.32	-1.04	0.87	1.04	0.647	-1.04	0.855	-0.59
1448537_at	Ttc1	tetratricopeptide repeat domain 1	-1.1	0.419	-1.02	0.86	-1.15	0.367	1.2	0.461	-0.52
1455000_at	Gpr68	G protein-coupled receptor 68	-1.05	0.881	-1.27	0.25	1.02	0.893	-1.88	0.089	-0.8
1432064_at	Ubox5	U box domain containing 5	-1.1	0.558	1.05	0.894	-1.24	0.511	-1.08	0.514	-0.59
1423385_at	Actr8	ARP8 actin-related protein 8 homolog (S. cerevisiae)	-1.16	0.257	-1.22	0.004	1.08	0.372	-1.19	0.191	-0.62
1420178_at	---	Transcribed locus	-1.65	0.327	-1.32	0.567	1.4	0.509	-1.13	0.62	-0.67
1446389_at	Nrip1	Nuclear receptor interacting protein 1	1.07	0.908	-1.04	0.902	-1.38	0.121	-1.73	0.18	-0.77
1457647_x_at	1600023N17Rik	RIKEN cDNA 1600023N17 gene	-1.54	0.437	1.2	0.762	-1.09	0.815	-1.09	0.627	-0.63
1438235_at	---	---	1.3	0.265	-1.14	0.639	-1.71	0.041	-1.66	0.071	-0.8
1448465_at	Nipsnap1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolo	-1.14	0.355	-1.17	0.136	1.03	0.784	-1.84	0.08	-0.78
1429018_at	3830408D24Rik	RIKEN cDNA 3830408D24 gene	-1.23	0.226	1.19	0.547	-1.32	0.121	-2.16	0.33	-0.88
1448463_at	4933434E20Rik	RIKEN cDNA 4933434E20 gene	1.01	0.85	-1.08	0.075	-1.2	0.041	-1.3	0.096	-0.65
1432372_a_at	Spr	sepiapterin reductase	-1.7	0.258	-1.26	0.255	1.38	0.381	-1.98	0.069	-0.89
1439977_at	4930515I15	hypothetical protein 4930515I15	-2.15	0.21	1.45	0.609	-1.18	0.562	-1.66	0.179	-0.89
1434423_at	---	---	-1.12	0.227	1.17	0.692	-1.43	0.068	-2.04	0.046	-0.86
1448193_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	-1.26	0.344	-1.11	0.692	1.07	0.738	-1.06	0.738	-0.59
1426048_s_at	Hrc /// Tcfap2a	histidine rich calcium binding protein /// transcription factor AP-2, alpha	1.36	0.125	-2.1	0.202	-1.08	0.723	-2.07	0.066	-0.97
1435492_at	Socs6	suppressor of cytokine signaling 6	-1.05	0.612	1.06	0.604	-1.34	0.099	-1.61	0.147	-0.73
1428576_at	Hif1an	hypoxia-inducible factor 1, alpha subunit inhibitor	-1.06	0.627	1.02	0.795	-1.26	0.186	-1.23	0.092	-0.63
1449710_s_at	Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform	-1.14	0.052	-1.16	0.021	1.02	0.743	-1.1	0.149	-0.59
1452823_at	Gstk1	glutathione S-transferase kappa 1	1.03	0.772	-1.13	0.349	-1.17	0.396	-1.21	0.54	-0.62
1437162_at	Gpiap1	GPI-anchored membrane protein 1	1.01	0.788	-1.09	0.475	-1.2	0.305	-1.05	0.582	-0.58
1431051_at	4930577N17Rik	RIKEN cDNA 4930577N17 gene	-1.12	0.546	-1.62	0.145	1.26	0.165	-1.44	0.252	-0.73
1452941_at	0610038F07Rik	RIKEN cDNA 0610038F07 gene	-1.25	0.44	-1.1	0.458	1.06	0.507	-1.27	0.023	-0.64
1417768_at	Pnpla8	patatin-like phospholipase domain containing 8	-1.1	0.725	-1.04	0.611	-1.12	0.48	1.02	0.917	-0.56
1446148_x_at	C79248	expressed sequence C79248	-1.01	0.973	1.11	0.369	-1.5	0.038	-1.17	0.393	-0.64
1453005_at	Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	-1.11	0.622	1.23	0.339	-1.58	0.034	-1.07	0.761	-0.63
1456759_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	-1.38	0.633	1.85	0.33	-5.27	0.014	-2.31	0.106	-1.78
1426187_a_at	Hax1	HCLS1 associated X-1	-1.09	0.414	-1.07	0.305	-1.09	0.398	1.04	0.828	-0.55
1435030_at	Upf2	UPF2 regulator of nonsense transcripts homolog (yeast)	-1.01	0.971	-1.13	0.323	-1.13	0.235	1.03	0.771	-0.56
1458577_at	---	---	-1.31	0.521	-1.64	0.488	1.39	0.079	-1.47	0.287	-0.76
1430199_at	1700007E05Rik	RIKEN cDNA 1700007E05 gene	-1.05	0.633	1	0.997	-1.24	0.734	-1.94	0.466	-0.81
1416519_at	LOC622534	similar to ribosomal protein L36	-1.15	0.117	1.03	0.625	-1.16	0.181	-1.39	0.003	-0.67
1436325_at	Rora	RAR-related orphan receptor alpha	-1.01	0.959	1.08	0.527	-1.43	0.148	-1.27	0.206	-0.66
1427085_at	2810432D09Rik	RIKEN cDNA 2810432D09 gene	1.02	0.899	-1.03	0.739	-1.3	0.073	-1.06	0.524	-0.59
1440193_at	Ankrd12	ankyrin repeat domain 12	1.06	0.847	-1.07	0.612	-1.3	0.326	-1.33	0.387	-0.66
1433002_at	9030613N10Rik	RIKEN cDNA 9030613N10 gene	1.05	0.938	-1.07	0.685	-1.28	0.58	-1.89	0.566	-0.8
1420096_at	Zipro1	Zinc finger proliferation 1	1.23	0.498	-1.39	0.28	-1.24	0.362	-1.19	0.611	-0.64
1418102_at	Hes1	hairy and enhancer of split 1 (Drosophila)	-1.21	0.436	-1.07	0.746	1	0.987	-1.11	0.51	-0.6
1435474_at	Taf5	TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.13	0.536	-1.01	0.967	-1.13	0.584	1.52	0.322	-0.44

1434706_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	-1.02	0.921	-1.15	0.218	-1.1	0.268	1.15	0.341	-0.53
1428836_at	2300009A05Rik	RIKEN cDNA 2300009A05 gene	-1.05	0.83	-1.02	0.875	-1.2	0.263	1.06	0.224	-0.55
1455876_at	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	1.36	0.216	-1.52	0.026	-1.35	0.245	-1.16	0.613	-0.66
1415747_s_at	Riok3	RIO kinase 3 (yeast)	-1.13	0.092	-1.09	0.256	-1.03	0.726	1.4	0.15	-0.46
1441059_at	1700049G17Rik	RIKEN cDNA 1700049G17 gene	-1.22	0.728	1.08	0.739	-1.16	0.339	-1.25	0.642	-0.64
1434170_at	Wdr40b	WD repeat domain 40B	-1.47	0.149	-1.07	0.707	1.15	0.577	-1.06	0.922	-0.61
1416892_s_at	3110001A13Rik	RIKEN cDNA 3110001A13 gene	-1.11	0.412	-1.52	0.086	1.2	0.388	-1.37	0.207	-0.7
1432589_at	---	---	1.33	0.391	-1.34	0.538	-1.45	0.081	-1.51	0.203	-0.74
1431266_at	5830433G22Rik	RIKEN cDNA 5830433G22 gene	-1.15	0.508	1.11	0.766	-1.28	0.295	-1.33	0.397	-0.66
1419661_at	1600012F09Rik /// I	RIKEN cDNA 1600012F09 gene /// hypothetical LOC624446	1.02	0.905	-1.3	0.475	-1.03	0.825	-1.02	0.945	-0.58
1426407_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	-1	0.979	-1.1	0.327	-1.17	0.197	1.19	0.178	-0.52
1451842_a_at	Chrnb3	cholinergic receptor, nicotinic, beta polypeptide 3	-1.81	0.585	1.45	0.164	-1.31	0.609	-1.31	0.745	-0.75
1448343_a_at	Nbr1	neighbor of Brca1 gene 1	-1.07	0.475	-1.06	0.341	-1.12	0.49	1.18	0.326	-0.52
1424759_at	Arrdc4	arrestin domain containing 4	-1.15	0.331	1.08	0.37	-1.23	0.447	-1.38	0.047	-0.67
1454044_a_at	Pex3	peroxisomal biogenesis factor 3	1.04	0.44	-1.14	0.179	-1.18	0.129	-1.09	0.598	-0.59
1431889_x_at	Psg21	pregnancy-specific glycoprotein 21	-1.14	0.554	1.1	0.731	-1.27	0.166	-1.06	0.861	-0.59
1436651_at	---	Transcribed locus	-1.29	0.299	1.01	0.98	-1.02	0.923	-1.58	0.043	-0.72
1458962_at	Tmed5	transmembrane emp24 protein transport domain containing 5	-1.18	0.644	-1.17	0.279	1.06	0.897	-1.21	0.122	-0.63
1416451_s_at	Tbn	taube nuss	-1.05	0.872	-1.38	0.266	1.09	0.625	-1.08	0.645	-0.61
1436424_at	1600020E01Rik	RIKEN cDNA 1600020E01 gene	-1.01	0.784	1.01	0.913	-1.3	0.109	-1.26	0.222	-0.64
1437690_x_at	Csnk1d	casein kinase 1, delta	-1.09	0.575	-1.33	0.046	1.1	0.54	-1.09	0.509	-0.6
1453593_at	1700110N18Rik	RIKEN cDNA 1700110N18 gene	1.27	0.494	-1.4	0.564	-1.28	0.342	-1.72	0.091	-0.78
1425506_at	Mylk	myosin, light polypeptide kinase	1.06	0.708	-1.2	0.167	-1.15	0.486	-1.04	0.799	-0.58
1457847_at	Rfxdc2	Regulatory factor X domain containing 2 homolog (human)	1.14	0.635	-1.08	0.71	-1.41	0.076	-1.85	0.171	-0.8
1453271_at	Phf14	PHD finger protein 14	-1.11	0.565	1.03	0.864	-1.2	0.267	-1.37	0.171	-0.66
1437900_at	4930523C07Rik	RIKEN cDNA 4930523C07 gene	1.09	0.103	-1.19	0.507	-1.19	0.183	-1.85	0.156	-0.79
1448172_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	-1.22	0.002	-1.29	0.017	1.17	0.234	-1.32	0.201	-0.67
1425044_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	-1.34	0.274	-1.76	0.15	1.45	0.272	-2.87	0.236	-1.13
1416716_at	Efs	embryonal Fyn-associated substrate	-1.15	0.495	-1.13	0.797	1.01	0.969	-1.88	0.171	-0.79
1434220_at	Nup98	nucleoporin 98	-1.07	0.509	-1.14	0.363	-1.05	0.754	1.08	0.537	-0.54
1420241_at	---	---	-2.26	0.372	-2.11	0.23	1.85	0.22	-1.02	0.95	-0.88
1438328_at	Hcfc2	host cell factor C2	1.13	0.631	-1.16	0.394	-1.3	0.122	-1.3	0.232	-0.66
1456334_s_at	A230106D06Rik	RIKEN cDNA A230106D06 gene	-1.54	0.083	1.39	0.607	-1.37	0.429	-2.15	0.239	-0.92
1452740_at	Myh10	myosin, heavy polypeptide 10, non-muscle	-1.1	0.304	-1.12	0.446	-1.04	0.894	5.72	0.129	0.62
1459787_at	---	---	1.16	0.184	-1.34	0.494	-1.16	0.692	-1.56	0.111	-0.73
1433655_at	Rnf141	ring finger protein 141	-1.01	0.876	-1.01	0.876	-1.27	0.095	1.1	0.679	-0.55
1436252_at	Slc45a1	solute carrier family 45, member 1	-1.38	0.424	1.05	0.836	-1	0.985	-1.62	0.13	-0.74
1417034_at	Trappc6a	trafficking protein particle complex 6A	1.02	0.911	-1.12	0.423	-1.17	0.126	-1.51	0.313	-0.69
1442700_at	Pde4b	phosphodiesterase 4B, cAMP specific	1.15	0.629	-1.37	0.241	-1.13	0.571	-2.58	0.106	-0.98
1439464_s_at	Tex10	testis expressed gene 10	-1.13	0.584	1.04	0.726	-1.18	0.25	-1.46	0.162	-0.68
1418614_at	Kcnj1	potassium inwardly-rectifying channel, subfamily J, member 1	1.19	0.738	-1.32	0.603	-1.22	0.723	-2.01	0.38	-0.84
1446949_at	4930431P19Rik	RIKEN cDNA 4930431P19 gene	1.33	0.131	-1.7	0.006	-1.18	0.221	-1.67	0.006	-0.8
1438545_at	Slc25a5 /// LOC433	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.3	0.488	-1.13	0.477	1.11	0.694	-1.09	0.75	-0.6
1435173_at	Ate1	arginine-tRNA-protein transferase 1	1.07	0.744	-1.09	0.707	-1.29	0.133	-1.33	0.088	-0.66
1448674_at	Rnf25	ring finger protein 25	-1.51	0.535	-1.26	0.633	1.31	0.589	-2.08	0.214	-0.88
1452659_at	Dek	DEK oncogene (DNA binding)	-1.08	0.48	-1.04	0.354	-1.14	0.141	1.66	0.15	-0.4
1426480_at	Sbds	Shwachman-Bodian-Diamond syndrome homolog (human)	-1.07	0.378	-1.24	0.016	1.03	0.416	-1.05	0.702	-0.58
1430242_at	Rwdd1	RWD domain containing 1	1.23	0.677	-1.78	0.425	-1.03	0.944	-1.42	0.281	-0.75
1427603_at	Atf7ip2	activating transcription factor 7 interacting protein 2	-1.61	0.128	-1.44	0.282	1.45	0.381	-1.02	0.962	-0.65
1417011_at	Sdc2	syndecan 2	1.15	0.31	-1.03	0.551	-1.55	0.136	-1.29	0.517	-0.68
1421918_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	1	0.997	-1.12	0.591	-1.15	0.432	-1.22	0.087	-0.62
1437978_at	Slit2	Slit homolog 2 (Drosophila)	-1.09	0.886	-1.1	0.776	-1.06	0.885	1.21	0.811	-0.51
1427310_at	Falz	fetal Alzheimer antigen	1.01	0.946	-1.2	0.081	-1.08	0.681	-1.63	0.084	-0.73

1435126_at	Dusp15	Dual specificity phosphatase-like 15	-1.44	0.312	1.14	0.809	-1.07	0.896	-1.44	0.37	-0.7
1452085_at	Gatad1	GATA zinc finger domain containing 1	-1.09	0.609	-1.09	0.502	-1.07	0.211	1.36	0.228	-0.47
1425971_at	---	(ORF 1) and reverse transcriptase (ORF 2) genes	-1.31	0.511	-1.04	0.94	1.04	0.903	-1.08	0.604	-0.6
1451101_a_at	Rps28	ribosomal protein S28	-1.07	0.24	1.02	0.789	-1.24	0.062	-1.22	0.016	-0.63
1442229_at	Pax9	Paired box gene 9	1.47	0.416	-1.33	0.266	-1.85	0.114	-1.93	0.105	-0.91
1435755_at	1110001A16Rik	RIKEN cDNA 1110001A16 gene	1.01	0.93	-1.07	0.47	-1.22	0.077	-1.17	0.622	-0.61
1415863_at	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	-1.17	0.117	1.05	0.491	-1.16	0.016	-1.04	0.478	-0.58
1433711_s_at	Sesn1	sestrin 1	-1.03	0.923	1.16	0.29	-1.58	0.158	-2	0.158	-0.86
1418187_at	Ramp2	receptor (calcitonin) activity modifying protein 2	-1.14	0.494	1.03	0.834	-1.16	0.24	-1.05	0.794	-0.58
1444735_at	---	---	1.09	0.373	-1.04	0.626	-1.39	0.405	-2.03	0.028	-0.84
1459783_s_at	Cno	cappuccino	1.01	0.892	-1.11	0.352	-1.16	0.358	-1.27	0.345	-0.63
1436958_x_at	Tpm3	Tropomyosin 3, gamma	1.11	0.602	-1.12	0.347	-1.3	0.355	-1.51	0.168	-0.71
1458082_at	Cd200	Cd200 antigen	-1.31	0.161	1.35	0.341	-1.53	0.405	-2.27	0.127	-0.94
1452668_x_at	Rab2b	RAB2B, member RAS oncogene family	1.08	0.467	-1.33	0.118	-1.06	0.694	-1.36	0.102	-0.67
1435836_at	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	-1.3	0.403	-1.18	0.491	1.15	0.479	-1.71	0.151	-0.76
1442342_at	Sp6	trans-acting transcription factor 6	-1.32	0.565	1.09	0.704	-1.09	0.779	-1.16	0.642	-0.62
1452012_a_at	Exosc1	exosome component 1	1.19	0.045	-1.21	0.259	-1.33	0.013	-1.48	0.102	-0.71
1431802_a_at	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	-1.06	0.569	-1.08	0.539	-1.11	0.454	1.38	0.243	-0.47
1439888_at	---	Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library,	1.26	0.732	-1.62	0.465	-1.12	0.785	-1.28	0.766	-0.69
1442762_at	Ttll10	tubulin tyrosine ligase-like family, member 10	-1.06	0.884	-1.61	0.31	1.21	0.332	-1	0.997	-0.62
1418382_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	-1.24	0.23	1.16	0.856	-1.25	0.417	-1.12	0.365	-0.61
1435116_at	4933403G14Rik	RIKEN cDNA 4933403G14 gene	1.07	0.841	-1.28	0.114	-1.09	0.663	-1.46	0.064	-0.69
1430516_at	4930428B01Rik	RIKEN cDNA 4930428B01 gene	-1.26	0.344	1.26	0.399	-1.4	0.053	-1.31	0.185	-0.68
1451381_at	1810020D17Rik	RIKEN cDNA 1810020D17 gene	-1.15	0.295	1.06	0.462	-1.19	0.195	-1.28	0.323	-0.64
1439936_at	---	---	-1.51	0.537	1.48	0.447	-1.6	0.333	-1.15	0.825	-0.69
1426020_at	Tmpo	thymopoietin	-1.11	0.496	-1.12	0.813	-1.03	0.918	2.01	0.198	-0.31
1416481_s_at	Higd1a	HIG1 domain family, member 1A	-1.01	0.941	1.01	0.949	-1.3	0.048	-1.18	0.539	-0.62
1436893_a_at	7-Mar	membrane-associated ring finger (C3HC4) 7	1.01	0.942	-1.02	0.898	-1.28	0.198	-1.56	0.018	-0.71
1427040_at	Mdfic	MyoD family inhibitor domain containing	1.07	0.643	-1.07	0.026	-1.3	0.086	-1.27	0.457	-0.64
1431151_at	LOC628236 /// LOC	similar to Gastric triacylglycerol lipase precursor (Gastric lipase) (GL) /// similar to	-1.69	0.325	-1.23	0.802	1.36	0.345	-1.26	0.564	-0.7
1426182_a_at	Klrc1	killer cell lectin-like receptor subfamily C, member 1	-1.24	0.028	-1.33	0.557	1.21	0.733	-1.04	0.948	-0.6
1436177_at	---	Transcribed locus	1.12	0.206	-1.12	0.539	-1.33	0.063	-1.78	0.117	-0.78
1420414_at	Hoxa11	homeo box A11	1.06	0.597	-1.05	0.886	-1.33	0.584	-1.24	0.532	-0.64
1446465_at	Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.84	0.397	1.55	0.205	-1.47	0.345	-1.4	0.178	-0.79
1438413_at	Senp7	SUMO1/sentrin specific peptidase 7	-1.32	0.096	1.14	0.411	-1.15	0.254	-1.33	0.031	-0.67
1452495_at	Adam28	a disintegrin and metallopeptidase domain 28	-1.94	0.027	-1.11	0.789	1.35	0.337	-2.25	0.228	-0.99
1434686_at	---	---	1.02	0.949	-1.27	0.138	-1.04	0.717	-1.44	0.061	-0.68
1415979_x_at	Rpl7	ribosomal protein L7	-1.06	0.152	1.02	0.457	-1.25	0.004	-1.33	0.013	-0.65
1456141_x_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	-1.21	0.243	1.14	0.344	-1.24	0.385	-1.13	0.508	-0.61
1444375_at	---	Transcribed locus	-1.94	0.188	-1.2	0.522	1.42	0.445	-1.4	0.02	-0.78
1430472_at	Armc1	armadillo repeat containing 1	-1.06	0.774	-1.71	0.327	1.24	0.7	-1.58	0.049	-0.78
1423864_at	Nrbp	nuclear receptor binding protein	1.09	0.79	-1	0.983	-1.46	0.053	-1.1	0.629	-0.62
1433812_at	Lix1l	Lix1-like	1.26	0.239	-1.1	0.684	-1.67	0.109	-1.24	0.155	-0.69
1428510_at	Lphn1	latrophilin 1	-1.13	0.124	-1.19	0.016	1.04	0.895	-1.17	0.276	-0.61
1440380_at	Capza1	Capping protein (actin filament) muscle Z-line, alpha 1	-1.14	0.464	1.22	0.277	-1.48	0.155	-1.35	0.122	-0.69
1451724_at	Ankmy2	ankyrin repeat and MYND domain containing 2	-1.02	0.716	-1.4	0.12	1.07	0.567	-1.05	0.747	-0.6
1460519_a_at	Mettl5	methyltransferase like 5	-1.03	0.373	-1.22	0.021	-1.02	0.876	1.24	0.501	-0.51
1432571_at	---	---	-1.34	0.649	1.3	0.238	-1.38	0.545	-1.01	0.988	-0.61
1452340_at	6820424L24Rik	RIKEN cDNA 6820424L24 gene	1.01	0.93	-1.04	0.855	-1.26	0.103	-1.17	0.153	-0.61
1441909_s_at	9530066K23Rik	RIKEN cDNA 9530066K23 gene	-1.34	0.677	-1.44	0.287	1.33	0.504	-3.31	0.024	-1.19
1434691_at	Sfrs2ip	splicing factor, arginine/serine-rich 2, interacting protein	-1.11	0.586	-1.11	0.235	-1.03	0.585	1.15	0.244	-0.53
1438185_at	---	---	-1.01	0.992	-1.4	0.251	1.06	0.792	-4.13	0.054	-1.37
1455485_x_at	Rpl13a	ribosomal protein L13a	-1.03	0.827	1.01	0.913	-1.27	0.045	-1.45	0.027	-0.68

1440818_s_at	Sf3b1	splicing factor 3b, subunit 1	-1.31	0.283	1.04	0.76	-1.03	0.805	-1.52	0.033	-0.71
1452576_at	Igh	Immunoglobulin heavy chain complex	-1.35	0.685	-1.8	0.102	1.47	0.301	-2.15	0.135	-0.96
1419492_s_at	Defb1	defensin beta 1	-1.08	0.294	-2.4	0.008	1.43	0.439	-2.26	0.156	-1.08
1429469_at	A930013F10Rik	RIKEN cDNA A930013F10 gene	-1.04	0.828	1.2	0.071	-1.64	0.031	-1.39	0.23	-0.72
1428847_a_at	Macf1	microtubule-actin crosslinking factor 1	-1.12	0.125	1.08	0.545	-1.24	0.263	-1.69	0.27	-0.74
1437450_x_at	2700060E02Rik	RIKEN cDNA 2700060E02 gene	-1.02	0.844	1.02	0.812	-1.29	0.009	-1.48	0.082	-0.69
1438226_at	AU022252	expressed sequence AU022252	-1.23	0.254	-1.14	0.315	1.09	0.738	-1.01	0.977	-0.57
1425537_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	-1.02	0.837	-1.1	0.421	-1.14	0.435	1.03	0.839	-0.56
1416671_a_at	Mcoln1	mucolipin 1	-1.84	0.115	-1.34	0.293	1.48	0.282	-1.31	0.344	-0.75
1451654_x_at	BC012278	cDNA sequence BC012278	-1.31	0.4	-1.03	0.306	1.04	0.88	-1.07	0.413	-0.59
1456737_x_at	Acaa1a	acetyl-Coenzyme A acyltransferase 1A	-1.51	0.009	-1.2	0.321	1.27	0.467	-1.17	0.488	-0.65
1416158_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	1.16	0.327	-1.05	0.803	-1.51	0.079	-1.52	0.337	-0.73
1434084_at	5730601F06Rik	RIKEN cDNA 5730601F06 gene	-1	0.966	1.13	0.378	-1.55	0.004	-1.06	0.24	-0.62
1439526_at	---	Adult male cecum cDNA, RIKEN full-length enriched library, clone:9130022D06 p	-1.63	0.113	-1.29	0.593	1.38	0.252	-1.76	0.333	-0.82
1453783_at	Pura	purine rich element binding protein A	1.16	0.372	-1.4	0.403	-1.12	0.637	-1.3	0.252	-0.66
1431938_a_at	Pmm2	phosphomannomutase 2	-1.02	0.905	-1.07	0.435	-1.16	0.337	1.18	0.318	-0.52
1433432_x_at	Rps12 /// LOC6707	ribosomal protein S12 /// similar to ribosomal protein S12 /// similar to ribosomal p	-1.09	0.493	1.09	0.061	-1.31	0.013	-1.32	0.02	-0.66
1432461_at	Eya4	eyes absent 4 homolog (Drosophila)	1.24	0.764	-1.14	0.284	-1.52	0.183	-1.07	0.859	-0.62
1425568_a_at	Tmem33	transmembrane protein 33	-1.08	0.487	-1.11	0.255	-1.06	0.762	1.36	0.25	-0.47
1434581_at	---	---	1.18	0.68	-1.29	0.473	-1.22	0.544	-1.04	0.822	-0.59
1448536_at	Lsm3	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.19	0.13	-1.04	0.465	-1.03	0.868	1.03	0.778	-0.56
1415715_at	Tmem129	transmembrane protein 129	-1.11	0.413	-1.01	0.903	-1.13	0.439	1.26	0.172	-0.5
1450191_a_at	Sox13	SRY-box containing gene 13	-1.13	0.403	-1.14	0.726	1.01	0.966	-1.22	0.465	-0.62
1421675_at	1700123K08Rik	RIKEN cDNA 1700123K08 gene	-1.24	0.546	1.09	0.763	-1.13	0.522	-1.11	0.182	-0.6
1435257_at	Klhl17	kelch-like 17 (Drosophila)	-1.33	0.137	-1.12	0.646	1.12	0.53	-1.03	0.797	-0.59
1426771_at	Tug1	taurine upregulated gene 1	-1.41	0.038	-1.1	0.532	1.16	0.303	-1.01	0.94	-0.59
1420642_a_at	2010100O12Rik	RIKEN cDNA 2010100O12 gene	-1.06	0.392	1.02	0.826	-1.24	0.137	-1.19	0.311	-0.62
1437511_x_at	Clcc1	chloride channel CLIC-like 1	-1.15	0.234	1.02	0.805	-1.13	0.293	-1.13	0.49	-0.6
1417105_at	Trappc2l	trafficking protein particle complex 2-like	-1.03	0.801	1	0.958	-1.26	0.162	-1.08	0.575	-0.59
1457249_at	Ubap2l	Ubiquitin associated protein 2-like	-1.06	0.841	1.19	0.538	-1.55	0.104	-1.84	0.035	-0.82
1416476_a_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	-1.38	0.238	1.1	0.458	-1.06	0.761	-1.13	0.318	-0.62
1454923_at	AW214353	expressed sequence AW214353	1.03	0.454	-1.1	0.39	-1.2	0.1	-1.08	0.783	-0.59
1420043_s_at	Thoc1	THO complex 1	1.05	0.941	-1.11	0.801	-1.21	0.74	-1.03	0.846	-0.58
1448813_at	Aadac	arylacetamide deacetylase (esterase)	-1.13	0.38	-1.57	0.007	1.25	0.548	-1.01	0.971	-0.62
1451431_a_at	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2	-1.07	0.315	1.16	0.257	-1.48	0.056	-1.37	0.044	-0.69
1418210_at	Pfn2	profilin 2	-1.14	0.42	1.05	0.847	-1.18	0.246	-1.29	0.456	-0.64
1423201_at	Ncor1	nuclear receptor co-repressor 1	-1.13	0.499	-1.18	0.054	1.04	0.703	-1.17	0.491	-0.61
1452563_a_at	Jarid1d	jumonji, AT rich interactive domain 1D (Rbp2 like)	-1.01	0.994	-1.38	0.501	1.05	0.887	-1.12	0.763	-0.61
1421965_s_at	Notch3	Notch gene homolog 3 (Drosophila)	1.01	0.929	-1.25	0.456	-1.04	0.803	-1.36	0.345	-0.66
1426504_a_at	Rnf121	ring finger protein 121	1.04	0.034	-1.09	0.276	-1.23	0.196	-1.18	0.154	-0.61
1433561_at	Centb2	centaurin, beta 2	-1.2	0.272	1.04	0.605	-1.12	0.502	-1.49	0.107	-0.69
1447414_at	---	---	-2.61	0.21	1.56	0.523	-1.2	0.215	-1.24	0.469	-0.87
1442739_at	BC031441	cDNA sequence BC031441	-1.24	0.626	1.16	0.566	-1.24	0.453	-1.76	0.137	-0.77
1439399_a_at	Snord22	small nucleolar RNA, C/D box 22	-1.11	0.601	-1.08	0.626	-1.05	0.833	1.17	0.613	-0.52
1458402_at	Pts	6-pyruvoyl-tetrahydropterin synthase	-1.27	0.439	1.04	0.931	-1.06	0.712	-1.92	0.364	-0.8
1452125_at	Thrap3	thyroid hormone receptor associated protein 3	1.17	0.38	-1.06	0.664	-1.52	0.06	-1.26	0.019	-0.67
1417248_at	Ralbp1	ralA binding protein 1	1.05	0.665	-1.06	0.24	-1.28	0.129	-1.12	0.648	-0.6
1431498_at	9530097N15Rik	RIKEN cDNA 9530097N15 gene	-1.88	0.233	-1.26	0.051	1.45	0.374	-1.22	0.802	-0.73
1435400_at	2900075B16Rik	RIKEN cDNA 2900075B16 gene	-1.06	0.796	1.09	0.7	-1.35	0.038	-1.5	0.28	-0.7
1422976_x_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	1.04	0.602	-1.26	0.22	-1.06	0.635	-1.1	0.786	-0.6
1448740_at	2400006H24Rik	RIKEN cDNA 2400006H24 gene	-1.16	0.42	-1.09	0.143	-1	0.994	1.88	0.274	-0.34
1455816_a_at	Kctd3	potassium channel tetramerisation domain containing 3	-1.18	0.452	1	0.979	-1.08	0.454	-1.13	0.681	-0.6
1423572_at	Bcl2l2	Bcl2-like 2	-1.03	0.11	-1.08	0.483	-1.14	0.551	1.02	0.915	-0.56

1447868_x_at	Txnl2 /// LOC62001	thioredoxin-like 2 /// similar to thioredoxin-like 2	-1.18	0.765	-1.29	0.229	1.15	0.142	-1.29	0.31	-0.65
1424293_s_at	Tmem55a	transmembrane protein 55A	-1.08	0.427	-1.03	0.756	-1.14	0.204	1.17	0.072	-0.52
1460737_at	Igbp1	immunoglobulin (CD79A) binding protein 1	-1.17	0.239	-1.1	0.381	1.01	0.911	-1.5	0.171	-0.69
1457271_at	Gm131 /// LOC634	gene model 131, (NCBI) /// similar to prochymosin	1.11	0.386	-1.12	0.658	-1.3	0.146	-1.22	0.422	-0.63
1419231_s_at	Krt12	keratin 12	-1.26	0.698	-1.44	0.445	1.29	0.61	-1.76	0.462	-0.79
1455607_at	Rspo3	R-spondin 3 homolog (Xenopus laevis)	-1.22	0.553	1.1	0.385	-1.17	0.607	-1.8	0.169	-0.77
1454823_at	Wdr37	WD repeat domain 37	-1.24	0.503	-1.39	0.174	1.25	0.259	-1	0.989	-0.6
1419016_at	1700034I23Rik	RIKEN cDNA 1700034I23 gene	1.01	0.952	-1.25	0.664	-1.04	0.913	-1.34	0.7	-0.65
1441615_at	Cbfa2t2h	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 homolog (hur	1.12	0.52	-1.09	0.671	-1.36	0.061	-1.3	0.143	-0.66
1434323_at	Eif3s3 /// LOC6250	eukaryotic translation initiation factor 3, subunit 3 (gamma) /// similar to eukaryoti	-1.45	0.45	-1.83	0.429	1.54	0.18	-1.1	0.834	-0.71
1449827_at	Agc1	aggrecan 1	-2.12	0.079	1.44	0.092	-1.15	0.645	-1.16	0.765	-0.75
1416115_at	Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	-1.15	0.24	-1.24	0.103	1.1	0.114	-1.14	0.073	-0.61
1437925_at	2210018M03Rik	RIKEN cDNA 2210018M03 gene	-1.01	0.995	-1.93	0.243	1.26	0.563	-1.13	0.416	-0.7
1416125_at	Fkbp5	FK506 binding protein 5	-1.31	0.782	-1.23	0.556	1.19	0.679	-1.2	0.714	-0.64
1434776_at	---	---	1.19	0.039	-1.35	0.062	-1.18	0.243	-1.35	0.485	-0.67
1426557_at	Mesp1	mesoderm posterior 1	-1.27	0.414	1.33	0.282	-1.52	0.026	-1.2	0.323	-0.67
1416825_at	Snta1	syntrophin, acidic 1	1.05	0.773	-1.04	0.601	-1.3	0.303	-1.56	0.147	-0.71
1427904_s_at	2410091C18Rik	RIKEN cDNA 2410091C18 gene	-1.09	0.339	-1.11	0.31	-1.05	0.77	1.16	0.157	-0.52
1422654_at	Sgca	sarcoglycan, alpha (dystrophin-associated glycoprotein)	-1.96	0.466	-1.18	0.123	1.42	0.269	-1.62	0.429	-0.83
1434222_at	Sipa1l1	signal-induced proliferation-associated 1 like 1	-1.12	0.264	-1.35	0.01	1.14	0.538	-1.26	0.422	-0.65
1457612_at	LOC14433 /// LOC2	similar to glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyd	-1.46	0.272	-1.02	0.878	1.11	0.635	-1.3	0.009	-0.67
1438257_at	Zfp313	Zinc finger protein 313	-1.13	0.178	1.02	0.889	-1.15	0.402	-1.56	0.067	-0.7
1415925_a_at	Nup62	nucleoporin 62	-1.05	0.786	-1.21	0.088	-1	0.983	1.19	0.589	-0.52
1415772_at	Ncl	nucleolin	1.03	0.876	-1.05	0.823	-1.25	0.047	-1.07	0.636	-0.59
1425873_a_at	Lepr	leptin receptor	1.28	0.541	-1.63	0.526	-1.14	0.545	-1.07	0.821	-0.64
1446215_at	Zfhx2as	zinc finger homeobox 2, antisense	-1.36	0.668	-1.08	0.718	1.11	0.569	-1.49	0.091	-0.7
1427257_at	Cspg2	chondroitin sulfate proteoglycan 2	-1.05	0.871	-1.11	0.407	-1.09	0.581	3.32	0.155	0.02
1415790_at	Ublcp1	ubiquitin-like domain containing CTD phosphatase 1	1.02	0.913	-1.1	0.687	-1.18	0.423	-1.29	0.207	-0.64
1447563_at	Rps3	ribosomal protein S3	-2.29	0.363	1.59	0.378	-1.34	0.503	-1.05	0.787	-0.77
1434016_at	Znrf2	zinc and ring finger 2	-1.13	0.07	-1.14	0.068	1.01	0.898	-1.23	0.398	-0.62
1418327_at	1110058L19Rik	RIKEN cDNA 1110058L19 gene	-1.07	0.507	1.02	0.779	-1.21	0.055	-1.1	0.288	-0.59
1429519_at	Fpgt	fucose-1-phosphate guanylyltransferase	-1.1	0.693	1.04	0.708	-1.21	0.173	-1.37	0.093	-0.66
1446906_at	C81615	expressed sequence C81615	-1.12	0.303	1.36	0.179	-1.9	0.042	-1.21	0.101	-0.72
1444485_at	Shq1	SHQ1 homolog (S. cerevisiae)	-1.12	0.644	-1.66	0.072	1.28	0.045	-1.16	0.449	-0.67
1456462_x_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	-1.1	0.779	-1.04	0.853	-1.1	0.451	1.33	0.375	-0.48
1420846_at	Mrps2	mitochondrial ribosomal protein S2	-1.27	0.003	-1.11	0.225	1.09	0.235	-1.3	0.18	-0.65
1441824_at	Mboat1	membrane bound O-acyltransferase domain containing 1	1.41	0.651	-1.72	0.388	-1.27	0.606	-1.25	0.618	-0.71
1457173_at	Ywhae	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eps	-1.41	0.338	1.42	0.193	-1.55	0.241	-1.25	0.455	-0.7
1416627_at	Spint1	serine protease inhibitor, Kunitz type 1	1	0.959	-1.23	0.386	-1.04	0.447	-1.01	0.915	-0.57
1460631_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:p	-1.07	0.522	1.01	0.965	-1.19	0.168	-1.25	0.378	-0.63
1455236_x_at	Serf2	small EDRK-rich factor 2	-1.13	0.437	1.05	0.578	-1.19	0.047	-1.36	0.054	-0.66
1444670_at	A130004G11Rik	RIKEN cDNA A130004G11 gene	-1.08	0.692	1.08	0.818	-1.29	0.034	-1.71	0.18	-0.75
1434289_at	Nsun5	NOL1/NOP2/Sun domain family, member 5	-1.02	0.939	-1.42	0.164	1.1	0.74	-1.18	0.365	-0.63
1444842_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	1.25	0.544	-1.22	0.625	-1.41	0.042	-1.03	0.93	-0.6
1446088_at	9430081I23Rik	RIKEN cDNA 9430081I23 gene	1.35	0.179	-1.34	0.437	-1.46	0.058	-1.95	0.186	-0.85
1438368_a_at	Matr3	matrin 3	-1.05	0.435	1.04	0.254	-1.29	0.035	-1.2	0.108	-0.62
1427897_s_at	2400003N08Rik	RIKEN cDNA 2400003N08 gene	-1.08	0.504	-1.17	0.08	1	0.993	-1.02	0.92	-0.57
1418618_at	En1	engrailed 1	1.54	0.107	-2.3	0.048	-1.25	0.664	-1.23	0.781	-0.81
1443666_at	Mid1	Midline 1	1.64	0.484	-1.42	0.511	-2.29	0.159	-1.8	0.393	-0.97
1425209_at	Zfp84	zinc finger protein 84	-1	0.996	-1.69	0.072	1.19	0.579	-1.21	0.277	-0.68
1453896_at	Pdzd2	PDZ domain containing 2	-1.17	0.538	1.01	0.984	-1.09	0.773	-1.01	0.981	-0.57
1448473_at	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	-1.14	0.444	-1.04	0.798	-1.06	0.799	1.49	0.298	-0.44
1457936_at	Mapk8	mitogen activated protein kinase 8	-1.04	0.924	1.04	0.894	-1.28	0.25	-2.11	0.017	-0.85

1450427_at	Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	1.46	0.634	-1.28	0.293	-1.85	0.112	-1.69	0.441	-0.84
1454730_at	4932414K18Rik	RIKEN cDNA 4932414K18 gene	-1.1	0.25	-1.01	0.864	-1.14	0.187	1.7	0.176	-0.39
1433737_at	LOC677213	similar to U2AF homology motif (UHM) kinase 1	1.03	0.807	-1.05	0.682	-1.26	0.074	-1.07	0.535	-0.59
1417591_at	Ptges2	prostaglandin E synthase 2	-1.18	0.359	-1	0.982	-1.07	0.591	1.32	0.262	-0.48
1448305_at	Rab6	RAB6, member RAS oncogene family	-1.09	0.281	-1.08	0.249	-1.08	0.553	1.31	0.069	-0.48
1437799_at	4933407H18Rik	RIKEN cDNA 4933407H18 gene	-1.29	0.459	1.14	0.7	-1.16	0.588	-1.39	0.312	-0.68
1444548_at	1600025M17Rik	RIKEN cDNA 1600025M17 gene	-2.46	0.314	1.52	0.594	-1.17	0.824	-1.53	0.519	-0.91
1426836_s_at	Metap1	methionyl aminopeptidase 1	-1.07	0.296	-1.05	0.727	-1.12	0.118	1.03	0.901	-0.55
1427001_s_at	Hnf4a	hepatic nuclear factor 4, alpha	-1.08	0.501	-1.11	0.543	-1.05	0.875	2.13	0.218	-0.28
1433926_at	Dync1li2	dynein, cytoplasmic 1 light intermediate chain 2	-1.05	0.544	-1.07	0.608	-1.13	0.332	1.05	0.705	-0.55
1460492_at	8030498B09Rik	RIKEN cDNA 8030498B09 gene	-1.4	0.439	1.12	0.735	-1.06	0.932	-2.05	0.545	-0.85
1435801_at	Fcmd	Fukuyama type congenital muscular dystrophy homolog (human)	1.01	0.689	-1.12	0.515	-1.14	0.546	-1.03	0.861	-0.57
1429446_at	Sdccag1	serologically defined colon cancer antigen 1	-1.12	0.579	1	0.956	-1.13	0.236	-1.34	0.123	-0.65
1440881_at	Brwd3	bromodomain and WD repeat domain containing 3	1.11	0.509	-1.27	0.498	-1.14	0.516	-1.2	0.476	-0.62
1442357_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	-3.06	0.057	-1.36	0.602	1.72	0.079	-1.53	0.382	-1.06
1453230_at	Zfp74	zinc finger protein 74	-1.08	0.766	1.16	0.168	-1.45	0.07	-1.57	0.157	-0.73
1438192_s_at	Baz2a	bromodomain adjacent to zinc finger domain, 2A	-1.48	0.065	-1.03	0.815	1.13	0.576	-1.13	0.608	-0.63
1448259_at	Fstl1	follistatin-like 1	-1.01	0.916	1.29	0.198	-2	0.02	-1.39	0.319	-0.78
1422609_at	Arpp19	cAMP-regulated phosphoprotein 19	-1.15	0.031	-1.01	0.959	-1.09	0.755	1	0.99	-0.56
1428286_at	---	---	-1.06	0.409	-1.04	0.717	-1.14	0.431	1.09	0.629	-0.54
1436385_at	Ganc	glucosidase, alpha; neutral C	-1.18	0.044	-1.14	0.459	1.06	0.835	-1.61	0.008	-0.72
1456402_at	A330076H08Rik	RIKEN cDNA A330076H08 gene	1.18	0.255	-1.06	0.939	-1.52	0.054	-1.56	0.601	-0.74
1427731_at	Gnrhr	gonadotropin releasing hormone receptor	-1.57	0.372	-1.02	0.949	1.17	0.601	-1.16	0.67	-0.65
1423383_a_at	Osbpl9	oxysterol binding protein-like 9	-1.26	0.621	1.14	0.141	-1.18	0.224	-1.62	0.143	-0.73
1418711_at	Pdgfa	platelet derived growth factor, alpha	-1.24	0.26	1.19	0.626	-1.28	0.372	-1.06	0.741	-0.6
1446430_at	Hectd2	HECT domain containing 2	-1.64	0.232	-1.01	0.961	1.18	0.641	-1.35	0.584	-0.71
1424977_at	4930418G15Rik	RIKEN cDNA 4930418G15 gene	-1.41	0.607	1.23	0.754	-1.19	0.585	-1.03	0.952	-0.6
1426827_at	A730098D12Rik	RIKEN cDNA A730098D12 gene	-1.13	0.127	-1.12	0.49	1.01	0.952	-1.17	0.284	-0.6
1443669_at	Zfyve28	Zinc finger, FYVE domain containing 28	-1.08	0.838	-1.73	0.259	1.27	0.521	-1.3	0.553	-0.71
1421272_at	Vav2	Vav2 oncogene	-1.08	0.887	-1.31	0.618	1.09	0.705	-1.96	0.399	-0.81
1426621_a_at	Ppp2r2b	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	-1.3	0.083	1.32	0.436	-1.45	0.09	-1.88	0.271	-0.83
1424147_at	Ahsa1	AHA1, activator of heat shock protein ATPase homolog 1 (yeast)	-1.19	0.182	-1.14	0.132	1.06	0.677	-1.03	0.856	-0.57
1435491_at	9830167H18Rik	RIKEN cDNA 9830167H18 gene	-1.01	0.96	1.13	0.226	-1.52	0.008	-1.09	0.679	-0.62
1416417_a_at	Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	-1.01	0.894	-1.19	0.266	-1.06	0.291	1.08	0.404	-0.54
1439217_at	Nalp9c	NACHT, LRR and PYD containing protein 9c	-1.02	0.976	-1.15	0.795	-1.08	0.503	1.9	0.165	-0.34
1433983_at	Cnksr3	Cnksr family member 3	1	0.986	-1.18	0.29	-1.07	0.352	-1.39	0.071	-0.66
1437907_a_at	Tbca	tubulin cofactor a	-1.06	0.074	1.04	0.661	-1.26	0.003	-1.39	0.111	-0.67
1428281_at	Trub1	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	-1.18	0.525	-1.32	0.088	1.17	0.229	-1.08	0.725	-0.6
1423144_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	-1.05	0.651	1.02	0.872	-1.23	0.37	-1.33	0.291	-0.65
1430849_a_at	Cgrrf1	cell growth regulator with ring finger domain 1	-1.03	0.852	-1.14	0.382	-1.08	0.68	1.41	0.352	-0.46
1435140_at	Ide	insulin degrading enzyme	-1.03	0.686	-1.11	0.119	-1.11	0.376	1.13	0.294	-0.53
1434523_x_at	Eif3s6	eukaryotic translation initiation factor 3, subunit 6	1.02	0.873	-1.06	0.371	-1.22	0.219	-1.32	0.068	-0.65
1420840_at	Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specif	-1.24	0.007	-1.03	0.749	1.01	0.94	-1.47	0.086	-0.68
1458972_at	9330112F22Rik	RIKEN cDNA 9330112F22 gene	-1.25	0.397	1.25	0.515	-1.37	0.221	-1.1	0.654	-0.62
1440236_at	A830039H05Rik	RIKEN cDNA A830039H05 gene	1.26	0.224	-1.12	0.581	-1.59	0.11	-1.31	0.432	-0.69
1430148_at	Rab19	RAB19, member RAS oncogene family	1.04	0.878	-1.32	0.704	-1.02	0.888	-1.62	0.049	-0.73
1415760_s_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	-1.07	0.536	-1.03	0.338	-1.14	0.298	1.05	0.894	-0.55
1451307_at	Mrpl14	mitochondrial ribosomal protein L14	-1	0.982	-1.17	0.286	-1.08	0.536	1.37	0.205	-0.47
1447323_at	LOC621954	Hypothetical protein LOC621954	-1.63	0.405	1.57	0.476	-1.67	0.237	-1.38	0.563	-0.78
1435698_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	-1.01	0.904	1.06	0.635	-1.36	0.287	-1.16	0.554	-0.62
1439994_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.01	0.981	-1.28	0.683	-1.01	0.983	-1.01	0.968	-0.57
1460567_at	Rfxdc2	regulatory factor X domain containing 2 homolog (human)	1.12	0.489	-1.18	0.437	-1.24	0.295	-1.98	0.134	-0.82
1448317_at	Tmem128	transmembrane protein 128	-1.22	0.092	1.03	0.586	-1.07	0.428	-1.13	0.146	-0.6

1416653_at	Stxbp3a	syntaxin binding protein 3A	-1.05	0.39	1.07	0.535	-1.32	0.039	-1.46	0.082	-0.69
1446847_at	0610010D24Rik	RIKEN cDNA 0610010D24 gene	1.12	0.837	-1.13	0.712	-1.29	0.183	-1.33	0.054	-0.66
1454814_s_at	AU021838	expressed sequence AU021838	-1.03	0.856	-1.1	0.193	-1.11	0.296	1.17	0.494	-0.52
1434737_at	Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	-1.31	0.091	1.07	0.798	-1.06	0.51	-1.27	0.158	-0.64
1456318_at	Clec1a	C-type lectin domain family 1, member a	-1.23	0.415	1.36	0.401	-1.64	0.055	-1.06	0.853	-0.64
1419246_s_at	Rab14	RAB14, member RAS oncogene family	-1.06	0.475	-1.25	0.021	1.04	0.575	-1.01	0.914	-0.57
1428797_at	0610039J04Rik	RIKEN cDNA 0610039J04 gene	-1.13	0.592	-1.21	0.114	1.07	0.443	-1.12	0.499	-0.6
1423152_at	Vapb	vesicle-associated membrane protein, associated protein B and C	-2	0.47	-1.45	0.367	1.59	0.46	-2.34	0.335	-1.05
1436390_a_at	Clcc1	chloride channel CLIC-like 1	-1.23	0.321	1.11	0.176	-1.17	0.245	-1.21	0.148	-0.62
1416631_at	Ap4b1	adaptor-related protein complex AP-4, beta 1	-1.16	0.584	-1.05	0.685	-1.04	0.803	1.07	0.752	-0.54
1459859_x_at	Chrac1	chromatin accessibility complex 1	1.04	0.698	-1.02	0.846	-1.33	0.085	-1.42	0.183	-0.68
1446362_at	---	---	1.17	0.13	-1.57	0.342	-1.03	0.933	-2.99	0.351	-1.1
1426402_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	-1.03	0.892	1.01	0.947	-1.25	0.126	-1.16	0.272	-0.61
1430573_s_at	Etohd2	ethanol decreased 2	-1.16	0.639	1.2	0.418	-1.39	0.133	-1.12	0.575	-0.62
1428051_a_at	Cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit	-1.21	0.619	-1.44	0.579	1.26	0.057	-1.24	0.538	-0.66
1454952_s_at	B130055D15Rik	RIKEN cDNA B130055D15 gene	-1.16	0.343	-1.02	0.831	-1.06	0.574	1.99	0.158	-0.31
1456374_x_at	Eif3s8	eukaryotic translation initiation factor 3, subunit 8	1.03	0.826	-1.11	0.072	-1.17	0.097	-1.21	0.163	-0.62
1425867_at	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specif	-1.14	0.809	1.29	0.618	-1.63	0.137	-1.6	0.491	-0.77
1422998_a_at	Glrx2	glutaredoxin 2 (thioltransferase)	-1.02	0.757	-1.04	0.598	-1.2	0.27	1.24	0.349	-0.5
1446158_at	Sec15l2	SEC15-like 2 (S. cerevisiae)	-1.21	0.363	1.39	0.205	-1.76	0.063	-1.51	0.392	-0.77
1422407_s_at	Hras1	Harvey rat sarcoma virus oncogene 1	-1.01	0.943	-1.09	0.263	-1.15	0.268	2.17	0.179	-0.27
1416426_at	Rab5a	RAB5A, member RAS oncogene family	-1.15	0.183	-1.05	0.559	-1.04	0.49	1.07	0.317	-0.54
1429278_at	Nubpl	nucleotide binding protein-like	-1.17	0.542	1.08	0.643	-1.18	0.379	-1.25	0.306	-0.63
1417593_at	Tusc2	tumor suppressor candidate 2	-1.15	0.32	-1.13	0.048	1.03	0.547	-1.04	0.829	-0.57
1453997_a_at	Nes	nestin	-1.37	0.628	-1.67	0.349	1.45	0.506	-2.28	0.465	-0.97
1428968_at	Cep57	centrosomal protein 57	-1.06	0.762	-1.03	0.85	-1.15	0.421	1.46	0.246	-0.45
1428715_at	2810423A18Rik	RIKEN cDNA 2810423A18 gene	1.03	0.58	-1.07	0.671	-1.22	0.02	-1.15	0.458	-0.6
1430125_s_at	Pqlc1	PQ loop repeat containing 1	-1.05	0.651	-1.12	0.557	-1.07	0.446	2.56	0.159	-0.17
1442309_at	Dnmt3a	DNA methyltransferase 3A	-1.06	0.791	1.19	0.578	-1.55	0.127	-1.42	0.354	-0.71
1437951_at	4930429A22Rik	RIKEN cDNA 4930429A22 gene	1.15	0.602	-1.04	0.829	-1.48	0.03	-1.27	0.338	-0.66
1427432_a_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	-1.05	0.656	-1.02	0.856	-1.18	0.139	1.04	0.696	-0.55
1443796_at	Il16	interleukin 16	-1.6	0.346	-1.01	0.989	1.16	0.237	-1.72	0.124	-0.79
1435265_at	---	Adult male cecum cDNA, RIKEN full-length enriched library, clone:9130204C03 p	-1.27	0.344	1.08	0.681	-1.09	0.797	-1.39	0.247	-0.67
1422911_at	Cbln3	cerebellin 3 precursor protein	-1.11	0.862	-1.3	0.243	1.11	0.78	-1	0.987	-0.58
1426467_s_at	0610037L13Rik	RIKEN cDNA 0610037L13 gene	1.11	0.381	-1.1	0.413	-1.3	0.144	-1.08	0.761	-0.59
1424220_a_at	Porcn	porcupine homolog (Drosophila)	-1.07	0.785	-1.08	0.704	-1.09	0.411	1.05	0.796	-0.55
1427397_at	2810046L04Rik	RIKEN cDNA 2810046L04 gene	-1.18	0.569	-1.13	0.281	1.05	0.545	-1.3	0.202	-0.64
1453590_at	Arl5b	ADP-ribosylation factor-like 5B	-1.35	0.392	-1.52	0.262	1.38	0.104	-1.52	0.086	-0.75
1428707_at	Ptms	parathymosin	1.03	0.918	-1.11	0.64	-1.16	0.184	-1.06	0.818	-0.58
1457293_at	Zbtb4	Zinc finger and BTB domain containing 4	-1.01	0.983	1.13	0.764	-1.51	0.023	-1.73	0.23	-0.78
1448055_at	Fndc7	fibronectin type III domain containing 7	-1.09	0.875	1.07	0.901	-1.25	0.67	-1.22	0.684	-0.62
1456473_x_at	Arf2	ADP-ribosylation factor 2	-1.15	0.751	1	0.993	-1.1	0.841	-1.52	0.433	-0.69
1437208_at	10-Sep	septin 10	-1.08	0.306	1.11	0.521	-1.34	0.286	-1.08	0.318	-0.6
1427593_at	Trim8	tripartite motif protein 8	-1.29	0.692	-2.18	0.063	1.55	0.392	-1.63	0.348	-0.89
1435811_a_at	Unc50	unc-50 homolog (C. elegans)	-1.1	0.186	1.09	0.519	-1.28	0.109	-1.1	0.63	-0.6
1459980_x_at	Rab3a	RAB3A, member RAS oncogene family	-1.14	0.03	1.05	0.287	-1.17	0.041	-1.11	0.411	-0.59
1432577_at	---	---	-1.77	0.015	-1.44	0.579	1.52	0.508	-1.43	0.524	-0.78
1430167_a_at	Rwdd3	RWD domain containing 3	-1.49	0.121	-1.12	0.277	1.22	0.212	-1.09	0.735	-0.62
1426398_at	Ube2w	ubiquitin-conjugating enzyme E2W (putative)	-1.04	0.785	-1.22	0.034	1	0.973	-1.39	0.022	-0.66
1445267_at	LOC626854	Similar to zinc finger protein 709	1.22	0.515	-1.39	0.187	-1.18	0.166	-1.61	0.067	-0.74
1445775_at	---	---	-1.27	0.487	1.13	0.798	-1.15	0.51	-1.05	0.488	-0.59
1418576_at	Yipf5	Yip1 domain family, member 5	-1.08	0.237	1.04	0.815	-1.21	0.129	-1.11	0.571	-0.59
1425022_at	Usp3	ubiquitin specific peptidase 3	-1.11	0.184	-1.21	0.069	1.05	0.791	-1.33	0.081	-0.65

1437850_a_at	Cnbp	cellular nucleic acid binding protein	-1.23	0.289	1.02	0.855	-1.05	0.728	-1.15	0.262	-0.6
1434443_at	---	---	-1.25	0.254	1.04	0.848	-1.06	0.793	-1.16	0.453	-0.61
1447897_x_at	Anapc11	Anaphase promoting complex subunit 11 homolog (yeast)	1.18	0.756	-1.01	0.96	-1.63	0.003	-1.54	0.244	-0.75
1435937_at	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	-1.08	0.147	1.04	0.856	-1.22	0.182	-1.01	0.948	-0.57
1438003_at	Pols	polymerase (DNA directed) sigma	-1.17	0.218	-1.07	0.526	-1.01	0.941	1.72	0.182	-0.38
1444336_at	Kcnj3	Potassium inwardly-rectifying channel, subfamily J, member 3	-2.45	0.116	-1.07	0.894	1.44	0.437	-1.1	0.302	-0.8
1447652_at	Slc35a4 /// LOC545	solute carrier family 35, member A4 /// similar to solute carrier family 35, member	-2.66	0.047	1.76	0.404	-1.56	0.462	-2.91	0.109	-1.34
1422156_a_at	Rps2 /// LOC54487	ribosomal protein S2 /// similar to 40S ribosomal protein S2 /// similar to 40S ribos	-1.2	0.066	-1.07	0.621	1.02	0.792	-1.13	0.014	-0.6
1438786_a_at	2610021A01Rik ///	RIKEN cDNA 2610021A01 gene /// similar to zinc finger protein 347	-1.15	0.419	1.14	0.64	-1.28	0.081	-1.3	0.289	-0.65
1455914_at	AI987944	expressed sequence AI987944	-1.1	0.693	1	0.979	-1.15	0.125	-1.82	0.056	-0.77
1439508_at	A730055L17Rik	RIKEN cDNA A730055L17 gene	-1.23	0.695	1.03	0.881	-1.07	0.639	-1.15	0.629	-0.6
1431372_at	Srpk2	serine/arginine-rich protein specific kinase 2	-1.16	0.674	1.24	0.47	-1.47	0.054	-1.26	0.54	-0.66
1456205_x_at	Tbca	tubulin cofactor a	-1.02	0.039	1.03	0.642	-1.29	0.006	-1.23	0.038	-0.63
1439978_at	D030022P06Rik	RIKEN cDNA D030022P06 gene	-1.34	0.325	1.27	0.54	-1.3	0.373	-1.45	0.259	-0.71
1454699_at	Sesn1	sestrin 1	1.01	0.975	-1.01	0.966	-1.28	0.334	-1.9	0.144	-0.79
1440263_at	Nrp	neural regeneration protein	1.05	0.836	-1.22	0.535	-1.1	0.602	-1.15	0.363	-0.6
1423028_at	Ifna2	interferon alpha 2	-1.16	0.872	-1.33	0.435	1.17	0.543	-2.25	0.191	-0.89
1429754_a_at	4933406F09Rik	RIKEN cDNA 4933406F09 gene	1.16	0.84	-1.43	0.553	-1.09	0.907	-2.33	0.091	-0.92
1446279_at	Negr1	Neuronal growth regulator 1	1.46	0.449	-1.77	0.26	-1.31	0.561	-1.33	0.728	-0.74
1435994_at	Kcnh1	potassium voltage-gated channel, subfamily H (eag-related), member 1	-1.27	0.427	-1.04	0.886	1.03	0.685	-1.4	0.265	-0.67
1423594_a_at	Ednrb	endothelin receptor type B	1.3	0.32	-1.36	0.023	-1.34	0.003	-1.13	0.602	-0.63
1451817_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.72	0.042	-1.78	0.338	1.64	0.253	-1.14	0.642	-0.75
1448861_at	Traf5 /// LOC62260	Tnf receptor-associated factor 5 /// similar to TNF receptor-associated factor 5	-1.32	0.256	-1.15	0.594	1.16	0.367	-1.81	0.025	-0.78
1417307_at	Dmd	dystrophin, muscular dystrophy	-1.07	0.654	1.03	0.74	-1.23	0.132	-1.26	0.397	-0.63
1417431_a_at	Sphk2	sphingosine kinase 2	-1.36	0.165	-1.25	0.238	1.25	0.077	-1.39	0.104	-0.69
1437683_x_at	Serf2	small EDRK-rich factor 2	-1.3	0.282	1.15	0.505	-1.16	0.486	-1.36	0.129	-0.67
1417062_at	2810037C14Rik	RIKEN cDNA 2810037C14 gene	-1.14	0.115	1.05	0.676	-1.16	0.207	-1.65	0.091	-0.73
1438650_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.39	0.176	1.39	0.159	-1.48	0.136	-1.5	0.026	-0.74
1450095_a_at	Acyp1	acylphosphatase 1, erythrocyte (common) type	-1.36	0.095	-1.01	0.933	1.06	0.694	-1.36	0.23	-0.67
1417532_at	Cyp2j5	cytochrome P450, family 2, subfamily j, polypeptide 5	-1.03	0.892	-1.32	0.006	1.06	0.918	-1.02	0.967	-0.58
1453292_at	4921501E09Rik	RIKEN cDNA 4921501E09 gene	-2.93	0.187	1.85	0.308	-1.68	0.269	-1.02	0.939	-0.94
1435255_at	Plxnb1	plexin B1	-1.24	0.298	-1.16	0.147	1.12	0.377	-1.24	0.249	-0.63
1418781_at	Nat9	NAT9	-1.02	0.884	-1.1	0.66	-1.12	0.561	1.12	0.56	-0.53
1419129_at	Slc22a13	solute carrier family 22 (organic cation transporter), member 13	1.49	0.172	-1.37	0.309	-1.77	0.238	-1.36	0.522	-0.75
1416864_at	Surf6	surfeit gene 6	-1.11	0.815	1.01	0.921	-1.15	0.473	-1.15	0.58	-0.6
1439309_at	9630044O09Rik	RIKEN cDNA 9630044O09 gene	-1.1	0.872	1.01	0.977	-1.15	0.484	-1.9	0.078	-0.79
1457805_at	---	---	1.27	0.558	-1.06	0.647	-1.73	0.073	-1.37	0.375	-0.72
1453725_a_at	Mrps7	mitchondrial ribosomal protein S7	-1.06	0.617	-1.2	0.02	1.01	0.954	-1.03	0.858	-0.57
1431737_at	LOC629820	hypothetical LOC629820	1.3	0.04	-1.34	0.574	-1.34	0.184	-1.16	0.589	-0.64
1440990_at	BC056349	cDNA sequence BC056349	-1.09	0.766	1.02	0.932	-1.18	0.392	-2.35	0.314	-0.9
1430655_at	4631405K08Rik	RIKEN cDNA 4631405K08 gene	1.46	0.618	-1.64	0.111	-1.4	0.507	-1.08	0.823	-0.66
1424394_at	Selm	selenoprotein M	1.04	0.622	-1	0.995	-1.34	0.071	-1.02	0.889	-0.58
1420231_at	---	---	-1.56	0.621	1.29	0.592	-1.17	0.734	-1.66	0.431	-0.78
1445360_at	Tgfb1	Transforming growth factor, beta 1	-1.09	0.594	-1.23	0.528	1.06	0.656	-1.57	0.017	-0.71
1434768_at	Tpp1	tripeptidyl peptidase I	-1.13	0.063	1.04	0.437	-1.16	0.33	-1.02	0.897	-0.57
1450671_at	Cryba1	crystallin, beta A1	1.41	0.389	-1.4	0.483	-1.51	0.588	-1.96	0.525	-0.87
1457877_at	Esr1	Estrogen receptor 1 (alpha)	-2.13	0.21	1.72	0.221	-1.67	0.287	-1.58	0.002	-0.92
1421374_a_at	Fxyd1	FXYD domain-containing ion transport regulator 1	1.23	0.538	-1.16	0.037	-1.45	0.029	-1.11	0.711	-0.62
1416814_at	Tia1	cytotoxic granule-associated RNA binding protein 1	-1.19	0.238	1.22	0.243	-1.38	0.147	-1.33	0.407	-0.67
1427021_s_at	Fth1	ferritin heavy chain 1	-1.11	0.256	-1.09	0.596	-1.04	0.334	1.15	0.248	-0.52
1449534_at	Sycp3	synaptonemal complex protein 3	1.18	0.553	-1.2	0.671	-1.29	0.566	-1.02	0.895	-0.58
1429799_at	Zfp606	zinc finger protein 606	1.14	0.621	-1.49	0.09	-1.03	0.948	-1	0.996	-0.59
1460545_at	Thrap3	thyroid hormone receptor associated protein 3	-1.18	0.095	-1.01	0.789	-1.05	0.508	1.1	0.167	-0.54

1454527_at	8430437B07Rik	RIKEN cDNA 8430437B07 gene	1.45	0.437	-1.65	0.361	-1.37	0.58	-1.46	0.594	-0.76
1455237_at	Usp36	ubiquitin specific peptidase 36	-1.39	0.023	-1.17	0.313	1.21	0.105	-1.16	0.416	-0.63
1458091_at	Dpp10	Dipeptidylpeptidase 10	1.68	0.269	-1.6	0.268	-2.07	0.127	-2.12	0.043	-1.03
1438917_x_at	Nup62	nucleoporin 62	-1.05	0.112	-1.1	0.453	-1.08	0.587	1.15	0.627	-0.52
1440634_at	Gpc6	Glypican 6	-1.05	0.81	1.1	0.66	-1.36	0.311	-1.49	0.5	-0.7
1440424_at	Tnnt2	Troponin T2, cardiac	-1.1	0.748	-1.13	0.67	-1	0.998	1.17	0.384	-0.52
1425009_at	Tcte2	t-complex-associated testis expressed 2	-1.51	0.165	-1.4	0.633	1.41	0.599	-1.29	0.712	-0.7
1423937_at	Kctd5	potassium channel tetramerisation domain containing 5	-1.18	0.443	-1.07	0.508	1.01	0.937	-1	0.978	-0.56
1420486_at	Nol7	nucleolar protein 7	-1.21	0.015	-1.08	0.428	1.03	0.818	-1.51	0.061	-0.69
1442484_at	D9Ertd306e	DNA segment, Chr 9, ERATO Doi 306, expressed	1.25	0.263	-1.07	0.578	-1.64	0.1	-1.13	0.486	-0.65
1449567_at	Tktl1	transketolase-like 1	-1.11	0.77	-1.13	0.623	1	0.997	-1.17	0.751	-0.6
1428063_at	Ankrd46	ankyrin repeat domain 46	-1.03	0.164	-1.18	0.15	-1.03	0.828	1.17	0.371	-0.52
1435093_at	Zfyve20	zinc finger, FYVE domain containing 20	1.02	0.912	-1.03	0.86	-1.25	0.052	-1.15	0.527	-0.6
1416276_a_at	Rps4x	ribosomal protein S4, X-linked	-1.04	0.424	1.04	0.598	-1.27	0.013	-1.35	0.051	-0.65
1442869_at	Dok7	docking protein 7	-1.48	0.456	-1.01	0.986	1.12	0.221	-1.33	0.358	-0.67
1456210_at	5430407P10Rik	RIKEN cDNA 5430407P10 gene	-1.02	0.926	-1.23	0.491	-1.01	0.955	1.13	0.631	-0.53
1428963_at	Rwdd2	RWD domain containing 2	-1.11	0.709	-1.21	0.174	1.06	0.655	-1.3	0.404	-0.64
1426770_at	Pex5	peroxisome biogenesis factor 5	-1.12	0.525	-1.15	0.213	1.02	0.926	-1	0.99	-0.56
1453795_at	Fahd2a	fumarylacetoacetate hydrolase domain containing 2A	-1.16	0.313	-1.43	0.049	1.23	0.187	-1.23	0.418	-0.65
1450694_at	Fkbp2	FK506 binding protein 2	-1.01	0.935	-1.15	0.004	-1.08	0.269	1.16	0.191	-0.52
1439022_at	Phactr1	phosphatase and actin regulator 1	-1.18	0.47	1.07	0.85	-1.15	0.729	-1.51	0.028	-0.69
1418310_a_at	Rlbp1	retinaldehyde binding protein 1	1.14	0.442	-1.47	0.331	-1.03	0.9	-1.07	0.879	-0.61
1454627_a_at	Rpl29 /// LOC4333	ribosomal protein L29 /// similar to 60S ribosomal protein L29 /// similar to 60S rib	-1.06	0.728	1.05	0.506	-1.26	0.03	-1.21	0.016	-0.62
1423035_s_at	Txnl5	thioredoxin-like 5	-1.13	0.124	1.02	0.755	-1.13	0.082	-1.13	0.32	-0.59
1455205_a_at	Usp19	ubiquitin specific peptidase 19	-1.17	0.031	-1.19	0.037	1.09	0.497	-1.17	0.388	-0.61
1439117_at	Clmn	calmin	-1.02	0.781	-1.27	0.373	1.02	0.925	-1.42	0.117	-0.67
1417580_s_at	Selenbp1	selenium binding protein 1	-1.08	0.483	-1.09	0.583	-1.06	0.68	2.08	0.108	-0.29
1417126_a_at	Rpl22l1	ribosomal protein L22 like 1	-1.15	0.127	1.02	0.856	-1.12	0.208	-1.47	0.007	-0.68
1440851_at	4933407N01Rik	RIKEN cDNA 4933407N01 gene	1.16	0.445	-1	0.995	-1.58	0.088	-1.15	0.266	-0.64
1434331_at	Eif2c1	eukaryotic translation initiation factor 2C, 1	1.01	0.895	-1.02	0.889	-1.25	0.262	-1.4	0.299	-0.67
1433886_at	Eif2b5	eukaryotic translation initiation factor 2B, subunit 5 epsilon	-1.07	0.72	-1.13	0.028	-1.04	0.442	1.02	0.922	-0.55
1416027_at	Pdcd6	programmed cell death 6	-1.09	0.214	1.01	0.855	-1.16	0.182	-1.03	0.772	-0.57
1452777_a_at	Nub1	negative regulator of ubiquitin-like proteins 1	1.06	0.356	-1.36	0.248	-1.01	0.975	-1.56	0.015	-0.72
1419935_s_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	-1.01	0.951	-1.02	0.934	-1.22	0.302	1.17	0.434	-0.52
1417530_a_at	Srp9	signal recognition particle 9	-1.01	0.81	1.03	0.368	-1.3	0.137	-1.25	0.291	-0.63
1438966_x_at	Fmod	fibromodulin	-1.33	0.7	-1.13	0.757	1.15	0.668	-1.88	0.126	-0.8
1428239_at	Ankrd16	ankyrin repeat domain 16	-1.32	0.06	1.07	0.376	-1.04	0.81	-1.5	0.323	-0.7
1430151_at	Nisch	nischarin	1.14	0.421	-1.05	0.812	-1.44	0.234	-1.55	0.005	-0.72
1448258_a_at	Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	-1.03	0.661	-1.06	0.427	-1.15	0.049	1.12	0.001	-0.53
1418874_a_at	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	-1.05	0.382	-1.16	0.022	-1.02	0.829	1.1	0.585	-0.53
1435235_at	Txnl1	thioredoxin-like 1	-1.02	0.692	-1.04	0.648	-1.18	0.266	1.48	0.142	-0.44
1451137_a_at	Brd8	bromodomain containing 8	-1.12	0.56	-1.21	0.197	1.07	0.579	-1.03	0.818	-0.57
1444923_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933015	1.2	0.676	-1.08	0.167	-1.5	0.399	-1.71	0.199	-0.77
1417099_at	Ftsj1	Ftsj homolog 1 (E. coli)	-1.07	0.184	-1.16	0.192	-1.01	0.941	1.87	0.23	-0.34
1416581_at	Wdr5	WD repeat domain 5	-1.08	0.492	-1.09	0.408	-1.06	0.703	1.05	0.642	-0.55
1420622_a_at	Hspa8 /// LOC6212	heat shock protein 8 /// similar to heat shock protein 8 /// heat shock protein 8 pse	-1.43	0.228	-1.08	0.666	1.16	0.253	-1.3	0.238	-0.66
1453153_at	Lins2	lines homolog 2 (Drosophila)	-1.05	0.845	-1.45	0.305	1.15	0.163	-1.53	0.16	-0.72
1424413_at	Ogfrl1	opioid growth factor receptor-like 1	-1.14	0.67	1.09	0.46	-1.23	0.103	-1.07	0.73	-0.59
1446493_at	Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-1.45	0.414	-1.45	0.287	1.41	0.542	-1.03	0.923	-0.63
1452635_x_at	Josd3	Josephin domain containing 3	-1.05	0.835	-1.31	0.242	1.07	0.703	-1.08	0.782	-0.59
1434637_x_at	Sin3b	transcriptional regulator, SIN3B (yeast)	1.04	0.796	-1.18	0.077	-1.11	0.369	-1.3	0.225	-0.64
1430959_at	4930546H06Rik	RIKEN cDNA 4930546H06 gene	-1.16	0.754	1.52	0.374	-2.45	0.378	-1.27	0.354	-0.84
1417145_at	Nfxl1	nuclear transcription factor, X-box binding-like 1	-1.07	0.708	-1.02	0.823	-1.14	0.555	1.4	0.171	-0.46

1441072_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.61	0.076	-1.43	0.219	-2.1	0.021	-1.12	0.543	-0.76
1419101_at	Sin3a	transcriptional regulator, SIN3A (yeast)	1.14	0.484	-1.14	0.389	-1.3	0.1	-1.21	0.193	-0.63
1448517_at	Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	-1.05	0.619	-1.14	0.331	-1.04	0.667	1.04	0.766	-0.55
1424653_at	LOC669875	similar to Tetraspanin-15 (Tspan-15) (Transmembrane 4 superfamily member 15)	-1.18	0.333	1.13	0.662	-1.22	0.396	-1.16	0.275	-0.61
1427875_a_at	1100001I22Rik	RIKEN cDNA 1100001I22 gene	-1.08	0.347	1.02	0.664	-1.19	0.024	-1.31	0.003	-0.64
1417306_at	Tyk2	tyrosine kinase 2	-1.33	0.052	-1.06	0.549	1.1	0.555	-1.32	0.316	-0.65
1439009_at	Gnl3l	guanine nucleotide binding protein-like 3 (nucleolar)-like	-1.11	0.353	-1.03	0.796	-1.09	0.367	1.17	0.054	-0.51
1424235_at	Ormdl2	ORM1-like 2 (S. cerevisiae)	-1.02	0.477	-1.07	0.496	-1.14	0.401	1.2	0.433	-0.51
1435243_at	Zfp746	zinc finger protein 746	-1.25	0.323	1.1	0.673	-1.13	0.341	-1.71	0.098	-0.75
1428322_a_at	Ndufb10	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-1.02	0.883	-1.2	0.181	-1.03	0.477	1.01	0.968	-0.56
1434510_at	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.12	0.437	-1.21	0.408	1.07	0.833	-1.59	0.252	-0.71
1430382_at	4833413G10Rik	RIKEN cDNA 4833413G10 gene	1.04	0.847	-1.14	0.525	-1.15	0.433	-1.15	0.596	-0.6
1447625_at	E2f5	E2F transcription factor 5	-1.11	0.717	-1.03	0.927	-1.09	0.884	1.39	0.441	-0.46
1445596_at	Adar	Adenosine deaminase, RNA-specific	-1.1	0.802	1.03	0.958	-1.18	0.74	-1.06	0.889	-0.58
1438812_x_at	Usp19	ubiquitin specific peptidase 19	-1.43	0.218	-1.22	0.692	1.27	0.512	-1.01	0.968	-0.6
1429645_at	1700017G19Rik	RIKEN cDNA 1700017G19 gene	-2	0.411	-1.31	0.67	1.53	0.503	-1.26	0.558	-0.76
1430187_at	Zfp60	zinc finger protein 60	-1.24	0.452	1.2	0.585	-1.29	0.301	-1.63	0.292	-0.74
1417103_at	Ddt	D-dopachrome tautomerase	-1.27	0.047	-1.18	0.267	1.16	0.209	-1.16	0.628	-0.62
1455722_at	---	---	1.61	0.099	-3.99	0.115	-1.08	0.813	-1.51	0.255	-1.24
1429588_at	2810474O19Rik	RIKEN cDNA 2810474O19 gene	-1.07	0.471	-1.03	0.874	-1.13	0.511	1.21	0.221	-0.51
1451514_at	Usp43	ubiquitin specific peptidase 43	-1.64	0.014	-1.65	0.416	1.57	0.219	-1.06	0.332	-0.69
1456925_at	---	---	-2.59	0.082	1.46	0.143	-1.06	0.849	-1.52	0.398	-0.93
1447704_s_at	D530033C11Rik	RIKEN cDNA D530033C11 gene	-1.16	0.56	1.13	0.378	-1.26	0.112	-1.07	0.754	-0.59
1442139_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933014	-1.07	0.382	1.13	0.51	-1.37	0.185	-1.18	0.518	-0.62
1454060_a_at	Nras	neuroblastoma ras oncogene	-1.12	0.445	1.02	0.936	-1.13	0.19	-1.23	0.266	-0.62
1429612_at	Eml4	echinoderm microtubule associated protein like 4	-1.08	0.332	1.03	0.85	-1.2	0.12	-1.54	0.212	-0.7
1452104_at	2600005N12Rik	RIKEN cDNA 2600005N12 gene	1.47	0.525	-1.39	0.577	-1.66	0.194	-1.39	0.505	-0.74
1452993_at	5430416O09Rik	RIKEN cDNA 5430416O09 gene	1.12	0.769	-1.15	0.776	-1.24	0.242	-1.15	0.592	-0.61
1433962_at	6720458F09Rik	RIKEN cDNA 6720458F09 gene	-1.24	0.432	-1.02	0.957	1	0.982	-1.2	0.479	-0.62
1422642_at	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	-1.02	0.933	-1.08	0.612	-1.12	0.342	1.62	0.083	-0.4
1428772_at	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	-1.09	0.009	-1.1	0.115	-1.04	0.551	1.21	0.259	-0.5
1418636_at	Etv3	ets variant gene 3	-1.31	0.273	-1.05	0.753	1.08	0.777	-1.57	0.168	-0.71
1454716_x_at	Cox5b	cytochrome c oxidase, subunit Vb	-1.05	0.565	-1.13	0.374	-1.05	0.724	1.16	0.293	-0.52
1428128_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	-1.16	0.001	1.09	0.463	-1.2	0.042	-1.07	0.313	-0.58
1435943_at	Dpep1	dipeptidase 1 (renal)	-1.02	0.896	-1.11	0.811	-1.1	0.601	1.45	0.598	-0.44
1458617_at	Prkcbp1	protein kinase C binding protein 1	-1.2	0.048	1.06	0.483	-1.11	0.605	-1.13	0.68	-0.6
1433960_at	Isg20l2	interferon stimulated exonuclease gene 20-like 2	-1.11	0.39	1	0.996	-1.12	0.494	-1.11	0.2	-0.59
1440894_at	LOC670793	similar to CG4050-PA, isoform A	-1.29	0.312	1.04	0.933	-1.02	0.969	-1.23	0.624	-0.63
1425505_at	Mylk	myosin, light polypeptide kinase	-1.05	0.869	-1.57	0.022	1.2	0.635	-1.48	0.22	-0.72
1430998_at	Sqrdl	sulfide quinone reductase-like (yeast)	-5.4	0.25	1.99	0.274	-1.61	0.429	-1.2	0.756	-1.56
1456068_at	Nfasc	neurofascin	1.45	0.582	-1.81	0.31	-1.27	0.253	-1.43	0.251	-0.76
1423424_at	Zic3	zinc finger protein of the cerebellum 3	-1.02	0.767	1.12	0.751	-1.45	0.152	-1.19	0.689	-0.63
1433786_x_at	Serf2	small EDRK-rich factor 2	-1.1	0.412	1.04	0.459	-1.19	0.095	-1.2	0.059	-0.61
1439140_at	1700019P01Rik	RIKEN cDNA 1700019P01 gene	1.05	0.932	-1.17	0.752	-1.13	0.659	-1.11	0.749	-0.59
1426678_at	Zfp706	zinc finger protein 706	1.02	0.869	-1.18	0.207	-1.08	0.154	-1.2	0.546	-0.61
1423792_a_at	Cmtm6	CKLF-like MARVEL transmembrane domain containing 6	-1.37	0.294	-1	0.991	1.06	0.617	-1.79	0.11	-0.77
1423902_s_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	-1.14	0.167	-1	0.987	-1.1	0.656	1.97	0.169	-0.32
1440933_at	4732460I02Rik	RIKEN cDNA 4732460I02 gene	-1.27	0.428	1.05	0.77	-1.05	0.615	-1.28	0.166	-0.64
1427695_a_at	Pou2f1	POU domain, class 2, transcription factor 1	-1.2	0.772	-1.06	0.92	1.01	0.969	-1.44	0.296	-0.67
1444204_at	Hoxb2	Homeo box B2	-1.08	0.609	-1.13	0.778	-1.02	0.944	1.35	0.541	-0.47
1429252_at	0610010K14Rik	RIKEN cDNA 0610010K14 gene	-1.12	0.546	1.14	0.36	-1.32	0.157	-1.93	0.244	-0.81
1455286_at	Btbd1	BTB (POZ) domain containing 1	1.01	0.958	-1.05	0.224	-1.19	0.144	-1.51	0.073	-0.69
1431071_at	Mtx3	metaxin 3	1.07	0.675	-1.31	0.194	-1.04	0.715	-1.1	0.414	-0.6

1427833_at	Spi16	serine protease inhibitor 16	-1.24	0.549	-3.83	0.044	1.73	0.093	-1.14	0.659	-1.12
1435101_at	Derl2	Der1-like domain family, member 2	1.17	0.025	-1.22	0.191	-1.24	0.368	-1.1	0.463	-0.6
1442266_at	AI662175	expressed sequence AI662175	-2.08	0.106	-1.22	0.763	1.49	0.407	-1.55	0.13	-0.84
1430944_at	A930030B08Rik	RIKEN cDNA A930030B08 gene	-1.75	0.141	-1.12	0.52	1.33	0.173	-1.19	0.692	-0.68
1435845_at	---	B16 F10Y cells cDNA, RIKEN full-length enriched library, clone:G370036C05 pro	-1.82	0.398	-1.34	0.197	1.5	0.414	-1.26	0.639	-0.73
1453318_at	Tmem102	transmembrane protein 102	-1	0.99	-1.19	0.375	-1.05	0.928	3.05	0.011	-0.05
1444881_at	Taok3	TAO kinase 3	-1.15	0.679	1.34	0.268	-1.71	0.006	-1.3	0.256	-0.71
1422457_s_at	Sumo3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	-1.1	0.385	-1.03	0.605	-1.09	0.2	1.1	0.162	-0.53
1432429_at	8430437N05Rik	RIKEN cDNA 8430437N05 gene	-1.25	0.784	-1.1	0.821	1.08	0.876	-2.2	0.314	-0.87
1460156_at	Aoah	Acyloxyacyl hydrolase	1.29	0.479	-1.41	0.653	-1.27	0.631	-1.25	0.575	-0.66
1455763_at	Rnf41	ring finger protein 41	-1.24	0.063	-1.3	0.185	1.22	0.3	-1.05	0.771	-0.59
1454540_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.03	0.897	1.02	0.941	-1.25	0.102	-1.38	0.276	-0.66
1453263_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	-1.04	0.872	-1.52	0.157	1.17	0.588	-1.3	0.447	-0.67
1434118_at	0610009K11Rik	RIKEN cDNA 0610009K11 gene	1.03	0.919	-1.06	0.806	-1.22	0.257	-1.16	0.265	-0.6
1456009_x_at	Top3b	topoisomerase (DNA) III beta	1.01	0.979	-1.21	0.045	-1.05	0.776	-1.01	0.946	-0.56
1417615_a_at	Rpl11	ribosomal protein L11	-1.06	0.659	1.03	0.713	-1.22	0.03	-1.56	0.041	-0.7
1460705_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	-1.11	0.51	-1	0.981	-1.12	0.668	1.06	0.801	-0.54
1452781_a_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	-1.33	0.1	1.15	0.232	-1.11	0.268	-1.04	0.542	-0.59
1430238_at	Got1l1	glutamic-oxaloacetic transaminase 1-like 1	-1.3	0.444	-1.89	0.158	1.5	0.241	-1.31	0.672	-0.75
1437250_at	Mreg	melanoregulin	-1.37	0.097	-1.21	0.156	1.23	0.455	-1.3	0.452	-0.66
1434310_at	Bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	-1.06	0.543	1.1	0.205	-1.33	0.047	-1.15	0.622	-0.61
1447337_at	Dapp1	Dual adaptor for phosphotyrosine and 3-phosphoinositides 1	1.33	0.331	-2.07	0.235	-1.02	0.949	-1.28	0.191	-0.76
1437007_x_at	Usp39	ubiquitin specific peptidase 39	-1.05	0.707	-1	0.983	-1.19	0.002	1.21	0.417	-0.51
1435163_at	9030612M13Rik	RIKEN cDNA 9030612M13 gene	1.42	0.53	-1.34	0.333	-1.6	0.253	-1.4	0.531	-0.73
1424781_at	D10Ucla1	DNA segment, Chr 10, University of California at Los Angeles 1	1.07	0.669	-1.11	0.155	-1.21	0.051	-1.16	0.651	-0.6
1424660_s_at	Crtc2	CREB regulated transcription coactivator 2	-1.15	0.676	-1.32	0.083	1.17	0.513	-2.1	0.054	-0.85
1428935_at	Canx	calnexin	1.15	0.131	-1.22	0.105	-1.21	0.219	-1.03	0.812	-0.58
1428697_at	Dpp8	dipeptidylpeptidase 8	-1.5	0.148	-1.28	0.375	1.34	0.464	-1.26	0.4	-0.67
1417685_at	Ankfy1	ankyrin repeat and FYVE domain containing 1	-1.13	0.186	1.06	0.606	-1.17	0.21	-1.17	0.112	-0.6
1421865_at	Dbil5	diazepam binding inhibitor-like 5	1.42	0.552	-2.53	0.027	-1.03	0.954	-1.09	0.811	-0.8
1437533_at	Birc4	baculoviral IAP repeat-containing 4	1.01	0.834	-1.06	0.421	-1.2	0.041	-1.18	0.364	-0.6
1418816_at	Chmp1b	chromatin modifying protein 1B	-1.14	0.313	1.01	0.948	-1.1	0.567	-1.03	0.865	-0.56
1448009_at	Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	-1.17	0.329	-1.22	0.298	1.12	0.39	-1.16	0.547	-0.61
1454742_at	Rasgef1b	RasGEF domain family, member 1B	-1.29	0.467	1.24	0.273	-1.28	0.171	-1.83	0.149	-0.79
1435036_at	A530050D06Rik	RIKEN cDNA A530050D06 gene	-1.17	0.614	-1.06	0.503	-1	0.988	1.19	0.775	-0.51
1448633_at	Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	-1.17	0.287	-1.06	0.733	-1.01	0.935	1.09	0.742	-0.54
1416131_s_at	C920006C10Rik	RIKEN cDNA C920006C10 gene	-1.19	0.149	1.03	0.744	-1.08	0.375	-1.34	0.161	-0.65
1447546_s_at	Maml2	Mastermind like 2 (Drosophila)	1.3	0.173	-1.09	0.68	-1.72	0.099	-3.27	0.009	-1.2
1446596_at	C130009A20Rik	RIKEN cDNA C130009A20 gene	-1.43	0.073	1.62	0.191	-2.1	0.009	-1.21	0.614	-0.78
1430764_at	1700023F06Rik	RIKEN cDNA 1700023F06 gene	-1.55	0.38	-1.19	0.741	1.31	0.385	-1.03	0.958	-0.62
1428852_at	Dock3	dedicator of cyto-kinesis 3	-1.18	0.805	-1.5	0.175	1.28	0.69	-1.29	0.493	-0.67
1447214_at	LOC666827 /// LOC	hypothetical protein LOC666827 /// hypothetical protein LOC670370 /// hypothetic	-1.75	0.613	-1.73	0.139	1.64	0.349	-1.29	0.715	-0.78
1458769_at	D7Ertd558e	DNA segment, Chr 7, ERATO Doi 558, expressed	-1.59	0.552	-1.02	0.983	1.19	0.71	-1.53	0.281	-0.74
1444740_at	4930550L11Rik	RIKEN cDNA 4930550L11 gene	1.2	0.792	-1.35	0.638	-1.17	0.608	-2.18	0.06	-0.88
1436462_at	LOC626832 /// LOC	similar to gonadotropin inducible ovarian transcription factor 1 /// similar to zinc fir	-1.07	0.704	1.02	0.861	-1.19	0.248	-1.08	0.69	-0.58
1426326_at	Zfp91	zinc finger protein 91	-1.25	0.554	1.12	0.244	-1.14	0.632	-1.1	0.76	-0.59
1451730_at	Zfp62	zinc finger protein 62	-1.15	0.63	-1.18	0.361	1.08	0.736	-1.55	0.2	-0.7
1436447_at	A630026N12Rik	RIKEN cDNA A630026N12 gene	-1.02	0.823	-1.47	0.071	1.13	0.629	-1.57	0.142	-0.73
1430294_at	Ssbp1	single-stranded DNA binding protein 1	-1.11	0.588	-1.19	0.254	1.06	0.818	-1.26	0.158	-0.63
1433614_at	Snx27	sorting nexin family member 27	-1.23	0.332	-1.26	0.276	1.19	0.26	-1.13	0.396	-0.61
1435759_at	Ctps2	cytidine 5'-triphosphate synthase 2	1.18	0.761	-1.13	0.729	-1.38	0.207	-1.59	0.114	-0.73
1445398_at	3732412D22Rik	RIKEN cDNA 3732412D22 gene	-1.07	0.705	1.49	0.336	-2.69	0.009	-1.87	0.261	-1.04
1428597_at	Tbc1d9b	TBC1 domain family, member 9B	-1.01	0.957	-1.02	0.9	-1.21	0.237	1.39	0.053	-0.46

1415767_at	Ythdf1	YTH domain family 1	-1.04	0.693	-1.16	0.261	-1.03	0.815	1.1	0.459	-0.53
1419397_at	Pola1	polymerase (DNA directed), alpha 1	-1.04	0.414	-1.15	0.377	-1.03	0.83	2.71	0.184	-0.13
1442109_at	---	---	1.43	0.081	-1.35	0.466	-1.61	0.088	-1.31	0.434	-0.71
1444365_at	Tsc22d3	TSC22 domain family 3	-1.3	0.267	1.36	0.504	-1.49	0.129	-1.27	0.476	-0.68
1441041_at	Zfp746	Zinc finger protein 746	1.11	0.697	-1.14	0.263	-1.23	0.439	-1.15	0.462	-0.6
1452797_at	Fastkd3	FAST kinase domains 3	-1.11	0.39	-1.19	0.433	1.06	0.683	-1.07	0.783	-0.58
1440480_at	AB182283	cDNA sequence AB182283	-1.39	0.127	-1.34	0.492	1.33	0.166	-1.44	0.052	-0.71
1447447_s_at	Srrm1	serine/arginine repetitive matrix 1	-1.09	0.495	-1.03	0.781	-1.1	0.515	1.07	0.47	-0.54
1420681_at	1700120K04Rik	RIKEN cDNA 1700120K04 gene	-1.82	0.2	1.38	0.535	-1.16	0.339	-1.17	0.208	-0.69
1452914_at	2410024N18Rik	RIKEN cDNA 2410024N18 gene	-1.47	0.607	-1.52	0.043	1.46	0.07	-1.09	0.631	-0.66
1442257_at	B130021B11Rik	RIKEN cDNA B130021B11 gene	1.37	0.403	-1.29	0.342	-1.53	0.054	-1.56	0.004	-0.75
1435038_s_at	Aak1	AP2 associated kinase 1	-1.6	0.136	1.41	0.103	-1.31	0.396	-1.47	0.019	-0.75
1460477_at	1700010C24Rik	RIKEN cDNA 1700010C24 gene	-1.06	0.7	1.15	0.842	-1.42	0.32	-1.17	0.818	-0.63
1450231_a_at	Birc4	baculoviral IAP repeat-containing 4	-1.39	0.206	-1.44	0.593	1.38	0.498	-1.08	0.851	-0.63
1416567_s_at	Atp5e	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit	1.01	0.807	-1.14	0.013	-1.09	0.261	-1.34	0.102	-0.64
1417801_a_at	Ppfibp2	protein tyrosine phosphatase, receptor-type, F interacting protein, binding protein	-1.28	0.024	1.05	0.824	-1.04	0.694	-1.29	0.277	-0.64
1433441_at	Fbxl5	F-box and leucine-rich repeat protein 5	-1.22	0.195	-1.04	0.572	1.01	0.918	-1.35	0.176	-0.65
1431368_at	4930404N11Rik	RIKEN cDNA 4930404N11 gene	-1.8	0.245	1.26	0.162	-1.02	0.967	-1.75	0.036	-0.83
1450464_at	E4f1	E4F transcription factor 1	-1.18	0.338	-1.14	0.538	1.07	0.511	-1.44	0.111	-0.67
1439557_s_at	Ldb2	LIM domain binding 2	-1.06	0.849	1.14	0.761	-1.39	0.262	-1.27	0.469	-0.65
1428551_at	2410075D05Rik	RIKEN cDNA 2410075D05 gene	-1.13	0.678	-1.06	0.389	-1.03	0.556	1.21	0.286	-0.5
1419353_at	Dpm1	dolichol-phosphate (beta-D) mannosyltransferase 1	-1.15	0.236	-1.23	0.347	1.11	0.264	-1.13	0.614	-0.6
1425334_at	Gorasp1	golgi reassembly stacking protein 1	-1.29	0.246	-1.41	0.029	1.31	0.114	-1.71	0.349	-0.77
1420428_at	Ager	advanced glycosylation end product-specific receptor	-1.29	0.679	1.17	0.543	-1.18	0.166	-2.14	0.016	-0.86
1454372_at	Cd80	CD80 antigen	-1.01	0.965	-1.38	0.421	1.08	0.853	-1.22	0.655	-0.63
1428075_at	Ndufb4	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 4	-1.04	0.609	-1.04	0.268	-1.15	0.155	1.01	0.932	-0.55
1438223_at	Vps54	Vacuolar protein sorting 54 (yeast)	-1.43	0.269	1.19	0.403	-1.1	0.636	-1.5	0.075	-0.71
1439438_a_at	1110005A23Rik ///	RIKEN cDNA 1110005A23 gene /// similar to cytokine induced protein 29 kDa ///	-1.04	0.436	1.06	0.287	-1.29	0.087	-1.11	0.276	-0.6
1437749_s_at	Mrpl9	mitochondrial ribosomal protein L9	-1.03	0.838	-1.13	0.302	-1.06	0.626	1.04	0.838	-0.54
1453251_at	Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	1.26	0.283	-1.5	0.114	-1.15	0.304	-1.24	0.087	-0.66
1444700_at	Nrxn3	Neurexin III	-1.25	0.755	-1.35	0.486	1.26	0.584	-1.7	0.192	-0.76
1439528_at	4833423E24Rik	RIKEN cDNA 4833423E24 gene	-1.14	0.609	1.11	0.72	-1.24	0.498	-1.37	0.526	-0.66
1441687_at	---	---	-1.33	0.586	-1.57	0.196	1.4	0.16	-1.48	0.308	-0.74
1455334_at	9830167H18Rik	RIKEN cDNA 9830167H18 gene	-1.09	0.538	1.02	0.896	-1.16	0.191	-1.06	0.584	-0.57
1436479_a_at	Dpp7	dipeptidylpeptidase 7	-1.25	0.005	-1.07	0.745	1.06	0.368	-1.48	0.169	-0.68
1433687_at	AI662250	expressed sequence AI662250	1.08	0.621	-1.18	0.044	-1.14	0.573	-1.18	0.406	-0.61
1459944_at	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	-1.2	0.791	1.14	0.721	-1.22	0.375	-1.21	0.102	-0.62
1455804_x_at	Oxct1	3-oxoacid CoA transferase 1	-1.51	0.172	1.2	0.523	-1.06	0.61	-1.14	0.26	-0.63
1453282_at	Cxadr	coxsackievirus and adenovirus receptor	1.08	0.528	-1.01	0.974	-1.38	0.093	-1.3	0.416	-0.65
1417185_at	Ly6a	lymphocyte antigen 6 complex, locus A	-1.21	0.301	1.12	0.568	-1.17	0.112	-1.22	0.389	-0.62
1450418_a_at	Yipf4	Yip1 domain family, member 4	-1.14	0.643	-1.05	0.792	-1.04	0.729	1.77	0.192	-0.36
1447828_x_at	2310005P05Rik	RIKEN cDNA 2310005P05 gene	-1.65	0.508	1.45	0.441	-1.35	0.509	-1.17	0.677	-0.68
1451193_x_at	Ttc4	tetratricopeptide repeat domain 4	1.03	0.648	-1.02	0.849	-1.26	0.273	-1.11	0.499	-0.59
1433204_at	2810436B12Rik	RIKEN cDNA 2810436B12 gene	-1.1	0.851	1.14	0.481	-1.34	0.462	-1.14	0.772	-0.61
1447349_s_at	Ep400	E1A binding protein p400	-1.01	0.943	-1.15	0.515	-1.07	0.815	1.06	0.654	-0.54
1452820_at	Brwd2	bromodomain and WD repeat domain containing 2	-1.16	0.333	-1.12	0.346	1.04	0.8	-1.35	0.358	-0.65
1428011_a_at	Erbb2ip	Erbb2 interacting protein	-1.13	0.305	1.08	0.499	-1.19	0.08	-1.36	0.037	-0.65
1438793_x_at	1200007D18Rik	RIKEN cDNA 1200007D18 gene	1.05	0.874	-1.14	0.424	-1.15	0.567	-1.03	0.869	-0.57
1433762_at	C630043F03Rik	RIKEN cDNA C630043F03 gene	1.25	0.32	-1.68	0.033	-1.05	0.815	-1.05	0.777	-0.63
1428212_x_at	Rpl31 /// LOC5448(	ribosomal protein L31 /// similar to ribosomal protein L31 /// similar to ribosomal p	-1.08	0.011	1.04	0.204	-1.2	0.035	-1.23	0	-0.62
1426860_at	Ep400	E1A binding protein p400	-1.21	0.13	-1.26	0.104	1.18	0.338	-1.14	0.461	-0.61
1439107_a_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5	-1.15	0.682	-1.35	0.117	1.18	0.557	-1.25	0.205	-0.64
1448546_at	Rassf3	Ras association (RalGDS/AF-6) domain family 3	1.07	0.61	-1.36	0.264	-1	0.986	-1.37	0.286	-0.67

1441260_a_at	---	---	-2.08	0.071	-1.21	0.694	1.49	0.203	-2.24	0.073	-1.01
1426759_at	Map4k3 /// LOC675	mitogen-activated protein kinase kinase kinase kinase 3 /// similar to mitogen-acti	-1.03	0.834	1.04	0.693	-1.27	0.231	-1.33	0.493	-0.65
1431287_at	Pcm1	pericentriolar material 1	-1.41	0.158	1.15	0.847	-1.06	0.791	-1.45	0.255	-0.69
1451259_at	Rexo2	REX2, RNA exonuclease 2 homolog (S. cerevisiae)	-1.05	0.617	-1.09	0.109	-1.07	0.559	1.6	0.086	-0.4
1453317_a_at	Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	-1.02	0.881	-1.35	0.172	1.08	0.754	-1.43	0.167	-0.68
1433598_at	9430010O03Rik	RIKEN cDNA 9430010O03 gene	-1.16	0.586	-1.25	0.183	1.13	0.537	-1.04	0.731	-0.58
1431423_a_at	Med8	mediator of RNA polymerase II transcription, subunit 8 homolog (yeast)	-1.15	0.181	-1.01	0.957	-1.07	0.623	1.21	0.307	-0.5
1421882_a_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	1.99	0.509	-1.8	0.295	-3.97	0	-2.31	0.021	-1.52
1455826_a_at	Bace1	beta-site APP cleaving enzyme 1	1.48	0.025	-1.48	0.052	-1.54	0.141	-1.28	0.126	-0.71
1431453_at	4933406K04Rik	RIKEN cDNA 4933406K04 gene	-1.08	0.92	1.01	0.986	-1.16	0.704	-1.2	0.431	-0.61
1425338_at	Plcb4	phospholipase C, beta 4	-1.09	0.821	-1.28	0.695	1.1	0.852	-1.53	0.195	-0.7
1449879_at	1700008F21Rik	RIKEN cDNA 1700008F21 gene	1.78	0.396	-2.71	0.199	-1.55	0.203	-1.59	0.409	-1.02
1448711_at	Mcm3ap	minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	-1.1	0.706	-1.15	0.16	1.02	0.908	-1.27	0.245	-0.63
1452612_at	Zfp294	zinc finger protein 294	1.06	0.515	-1.28	0.06	-1.04	0.443	-1.08	0.584	-0.59
1424531_a_at	Tcea3	transcription elongation factor A (SII), 3	-1.11	0.514	-1.4	0.162	1.18	0.24	-1.85	0.303	-0.79
1444695_at	---	Adult male colon cDNA, RIKEN full-length enriched library, clone:9030003C19 pr	1.32	0.225	-1.42	0.026	-1.29	0.09	-1.29	0.304	-0.67
1446993_at	Plin	Perilipin	-1.56	0.062	1.4	0.552	-1.33	0.521	-1.39	0.463	-0.72
1450275_x_at	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	-1.05	0.481	-1.05	0.642	-1.11	0.446	1.14	0.596	-0.52
1451622_at	Lmbrd1	LMBR1 domain containing 1	-1.15	0.31	-1.14	0.097	1.05	0.564	-1.67	0.098	-0.73
1434532_at	BC035295	cDNA sequence BC035295	-1.03	0.832	-1.07	0.388	-1.12	0.223	1.03	0.859	-0.55
1450433_at	Rbpsuhl	recombining binding protein suppressor of hairless-like (Drosophila)	-1.87	0.587	-1.08	0.718	1.34	0.344	-1.12	0.307	-0.68
1416300_a_at	Slc25a3	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	-1.2	0.014	-1.26	0.029	1.17	0.021	-1.02	0.844	-0.58
1415680_at	Anapc1	anaphase promoting complex subunit 1	-1.09	0.444	-1.06	0.326	-1.06	0.644	1.2	0.402	-0.5
1450732_a_at	Bicd2	bicaudal D homolog 2 (Drosophila)	1.07	0.794	-1.05	0.355	-1.28	0.407	-1.1	0.761	-0.59
1448848_at	Tor1b	torsin family 1, member B	-1.01	0.921	1.02	0.893	-1.27	0.045	-1.17	0.121	-0.61
1425370_a_at	Erg	avian erythroblastosis virus E-26 (v-ets) oncogene related	1.07	0.814	-1.23	0.239	-1.08	0.875	-1.12	0.35	-0.59
1458988_at	---	---	-1.7	0.378	1.47	0.323	-1.34	0.354	-1.4	0.574	-0.74
1435898_x_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	1.02	0.527	-1.01	0.943	-1.28	0.073	-1.31	0.255	-0.64
1435364_at	Cyhr1	cysteine and histidine rich 1	-1.01	0.864	-1.1	0.303	-1.11	0.246	1.21	0.35	-0.5
1416402_at	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	-1.04	0.711	-1.15	0.328	-1.03	0.837	5.08	0.17	0.47
1426368_at	Rin2	Ras and Rab interactor 2	-1.19	0.469	1.11	0.48	-1.18	0.481	-1.16	0.635	-0.6
1453942_at	1700123I01Rik	RIKEN cDNA 1700123I01 gene	-1.56	0.605	-1.97	0.312	1.65	0.229	-1.34	0.453	-0.8
1432693_at	4930517G19Rik	RIKEN cDNA 4930517G19 gene	1.18	0.577	-1.1	0.86	-1.39	0.343	-1.55	0.056	-0.72
1445698_at	Capn11	calpain 11	-1.36	0.383	1.25	0.296	-1.24	0.559	-1.31	0.303	-0.66
1442487_at	D14Ertd24e	DNA segment, Chr 14, ERATO Doi 24, expressed	-1.11	0.454	1.2	0.571	-1.43	0.172	-1.15	0.809	-0.62
1434646_s_at	Sap18	Sin3-associated polypeptide 18	-1.05	0.41	-1.11	0.019	-1.05	0.646	1.08	0.666	-0.53
1419611_at	---	---	-1.23	0.704	1.01	0.982	-1.02	0.937	-1.21	0.352	-0.61
1421204_a_at	Nudt16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-1.16	0.314	-1.23	0.243	1.12	0.564	-1.3	0.529	-0.64
1443448_x_at	2010110K16Rik	RIKEN cDNA 2010110K16 gene	-1.01	0.975	1.25	0.378	-1.79	0.22	-1.22	0.73	-0.69
1436038_a_at	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	-1.03	0.778	1.04	0.724	-1.25	0.238	-1.56	0.03	-0.7
1457842_at	Zfp292	Zinc finger protein 292	1.08	0.406	-1.02	0.931	-1.35	0.111	-1.67	0.003	-0.74
1437680_x_at	Glrx2	glutaredoxin 2 (thioltransferase)	-1.29	0.104	-1.03	0.854	1.05	0.776	-1.05	0.752	-0.58
1418491_a_at	Pus3	pseudouridine synthase 3	-1.23	0.02	-1.04	0.746	1.03	0.838	-1.46	0.23	-0.68
1438819_at	---	Transcribed locus	1.4	0.508	-1.33	0.237	-1.56	0.07	-2.16	0.054	-0.91
1449438_at	Dpm1	dolichol-phosphate (beta-D) mannosyltransferase 1	-1.1	0.362	-1.15	0.006	1.02	0.825	-1.09	0.376	-0.58
1420791_x_at	Speer4f	spermatogenesis associated glutamate (E)-rich protein 4f	1.36	0.609	-2.03	0.425	-1.05	0.763	-1.67	0.467	-0.85
1425776_a_at	C87436	expressed sequence C87436	1.02	0.921	-1.01	0.9	-1.26	0.096	-1.02	0.723	-0.57
1424574_at	Tmed5	transmembrane emp24 protein transport domain containing 5	1.01	0.962	-1.23	0.102	-1.03	0.707	-1.17	0.371	-0.6
1439403_x_at	Rnf12	ring finger protein 12	-1.13	0.665	1.15	0.581	-1.3	0.295	-1.32	0.173	-0.65
1422751_at	Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	1.44	0.247	-1.53	0.169	-1.41	0.179	-1.06	0.778	-0.64
1428802_at	Mgat3	mannoside acetylglucosaminyltransferase 3	-1.35	0.477	1.21	0.84	-1.18	0.627	-1.22	0.482	-0.63
1451613_at	Hrnr	hornerin	-1.03	0.821	1.27	0.161	-1.77	0.322	-1.87	0.362	-0.85
1417660_s_at	Vps29	vacuolar protein sorting 29 (S. pombe)	-1.1	0.22	1.05	0.572	-1.18	0.144	-1.42	0.043	-0.66

1438754_at	---	---	-1.05	0.562	1.1	0.843	-1.34	0.176	-1.44	0.246	-0.68
1458527_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	-1.35	0.021	-1.07	0.84	1.12	0.426	-1.45	0.348	-0.69
1460175_at	Rps23	ribosomal protein S23	-1.09	0.318	1.05	0.242	-1.21	0.011	-1.31	0.021	-0.64
1459244_at	AU014756	expressed sequence AU014756	-1.02	0.844	-1.08	0.496	-1.12	0.804	2.09	0.157	-0.28
1453146_at	Gapvd1	GTPase activating protein and VPS9 domains 1	-1.14	0.075	-1.07	0.355	-1	0.984	1.86	0.202	-0.34
1429327_at	Sdccag1	serologically defined colon cancer antigen 1	1.01	0.972	-1.07	0.825	-1.17	0.618	-1.16	0.716	-0.6
1424274_at	Vdp	vesicle docking protein	-1.1	0.451	1.02	0.878	-1.15	0.216	-1.15	0.175	-0.59
1442037_at	LOC668580	hypothetical protein LOC668580	1.19	0.628	-1.06	0.774	-1.49	0.482	-1.65	0.535	-0.75
1458197_x_at	Mapkapk5 /// Adam	MAP kinase-activated protein kinase 5 /// a disintegrin and metallopeptidase dom	-1.67	0.355	-1.24	0.767	1.4	0.522	-1.43	0.36	-0.74
1439147_at	1110049B09Rik	RIKEN cDNA 1110049B09 gene	-1.29	0.786	-1.67	0.404	1.43	0.025	-2.09	0.078	-0.91
1426994_at	Phlpp	PH domain and leucine rich repeat protein phosphatase	-1.01	0.879	-1.29	0.156	1.03	0.849	-1.35	0.25	-0.65
1423225_at	Selk	selenoprotein K	-1.14	0.017	1.15	0.247	-1.29	0.041	-1.1	0.486	-0.59
1438599_at	---	---	-1.36	0.64	1.1	0.5	-1.04	0.907	-2.05	0.431	-0.83
1422174_at	Ipf1	insulin promoter factor 1, homeodomain transcription factor	-2.54	0.431	-1.36	0.454	1.68	0.34	-2.94	0.201	-1.29
1430510_at	B130050I23Rik	RIKEN cDNA B130050I23 gene	-1.55	0.595	1.53	0.203	-1.59	0.281	-1.3	0.225	-0.73
1451735_at	Arfrp1	ADP-ribosylation factor related protein 1	-1.25	0.191	-1.42	0.14	1.3	0.232	-1.43	0.124	-0.7
1449672_s_at	Tufm /// LOC66983	Tu translation elongation factor, mitochondrial /// similar to Tu translation elongati	-1.97	0.068	-1.01	0.983	1.3	0.593	-2.68	0.038	-1.09
1419839_x_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	-1.13	0.28	-1.12	0.037	1.02	0.862	-1.49	0.056	-0.68
1419278_at	Usp48	ubiquitin specific peptidase 48	-1.14	0.54	-1.11	0.06	1.02	0.769	-1.03	0.879	-0.56
1438242_at	Usp40	ubiquitin specific peptidase 40	1	0.99	-1.17	0.093	-1.05	0.526	-1.18	0.439	-0.6
1455887_at	Alg8	asparagine-linked glycosylation 8 homolog (yeast, alpha-1,3-glucosyltransferase)	-1.69	0.318	-1.27	0.439	1.42	0.349	-1.21	0.551	-0.69
1423759_a_at	Tmco1	transmembrane and coiled-coil domains 1	-1.05	0.605	-1.01	0.777	-1.16	0.081	1.1	0.074	-0.53
1454908_x_at	Serf1	small EDRK-rich factor 1	-1.09	0.474	-1.09	0.675	-1.03	0.931	1.1	0.809	-0.53
1425774_at	1500001A10Rik	RIKEN cDNA 1500001A10 gene	-1.12	0.803	1.27	0.575	-1.54	0.181	-1.01	0.985	-0.6
1453904_at	4930528G09Rik	RIKEN cDNA 4930528G09 gene	-5.97	0.03	-1.21	0.423	1.81	0.32	-1	0.999	-1.59
1425231_a_at	Zfp46	zinc finger protein 46	-1.2	0.25	1.07	0.639	-1.12	0.297	-1.17	0.454	-0.6
1459350_at	Socs6	Suppressor of cytokine signaling 6	-1.09	0.821	-1.23	0.486	1.07	0.79	-1.25	0.292	-0.62
1456441_at	Ccdc87	coiled-coil domain containing 87	-1.53	0.252	1.2	0.396	-1.05	0.823	-1.14	0.569	-0.63
1425174_at	---	CDNA clone MGC:18942 IMAGE:3979577	1.01	0.979	-1.04	0.915	-1.2	0.665	-1.3	0.044	-0.63
1455922_at	Rab3gap1	RAB3 GTPase activating protein subunit 1	-1.17	0.086	-1.06	0.454	1	0.978	-1.32	0.137	-0.64
1422548_at	Dhdds	dehydrodolichyl diphosphate synthase	-1.11	0.716	-1.06	0.279	-1.04	0.837	1.35	0.006	-0.47
1455083_at	Atp11c	Atpase, class VI, type 11C	1.02	0.944	-1.05	0.643	-1.2	0.309	-1.11	0.249	-0.58
1422624_at	Rev1l	REV1-like (S. cerevisiae)	-1.14	0.714	-1.02	0.946	-1.06	0.762	1.1	0.696	-0.53
1429010_at	Snrp70	U1 small nuclear ribonucleoprotein polypeptide A	1.49	0.68	-1.74	0.32	-1.34	0.642	-2.46	0.43	-1.02
1416944_a_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	1.13	0.323	-1.15	0.046	-1.26	0.153	-1.23	0.189	-0.62
1428732_at	1700008J07Rik	RIKEN cDNA 1700008J07 gene	-1.04	0.445	-1.26	0.007	1.05	0.584	-1.23	0.046	-0.62
1437559_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	-1.06	0.913	1.16	0.758	-1.42	0.244	-1.07	0.778	-0.6
1434507_at	Npepl1	aminopeptidase-like 1	-1.18	0.154	-1.08	0.403	1.03	0.876	-1.3	0.304	-0.63
1422594_at	5730470L24Rik	RIKEN cDNA 5730470L24 gene	-1.13	0.44	1.09	0.238	-1.21	0.104	-1.74	0.164	-0.75
1448357_at	Snrpg /// LOC6666	small nuclear ribonucleoprotein polypeptide G /// similar to small nuclear ribonucl	-1.01	0.913	1.01	0.889	-1.25	0.168	-1.2	0.104	-0.61
1424920_at	Slc37a3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	-1.17	0.434	-1.16	0.26	1.09	0.666	-1.98	0.038	-0.81
1436968_x_at	Klhl24	kelch-like 24 (Drosophila)	-1.1	0.373	-1.14	0.562	1.02	0.936	-1.82	0.154	-0.76
1416884_at	Cbx3 /// LOC62957	chromobox homolog 3 (Drosophila HP1 gamma) /// similar to chromobox homolo	-1.03	0.77	-1	0.995	-1.2	0.356	1.22	0.145	-0.5
1457055_at	Nubp1	Nucleotide binding protein 1	1.07	0.488	-1.06	0.886	-1.26	0.087	-1.3	0.05	-0.64
1459926_at	C77068	expressed sequence C77068	1.62	0.227	-1.31	0.654	-2.36	0.109	-1.42	0.721	-0.87
1444932_at	---	---	-1.02	0.967	1.16	0.197	-1.51	0.353	-1.26	0.51	-0.66
1451338_at	Nisch	nischarin	-1.23	0.057	-1.06	0.577	1.05	0.5	-1.26	0.454	-0.63
1445035_at	Igk-V	immunoglobulin kappa chain complex variable region	1.23	0.682	-1.51	0.279	-1.09	0.778	-1.88	0.305	-0.81
1439228_at	Zfp407	zinc finger protein 407	1.3	0.788	-1.53	0.401	-1.18	0.779	-5.07	0	-1.62
1417245_at	Gpr180	G protein-coupled receptor 180	-1.12	0.085	1.09	0.343	-1.21	0.29	-1.43	0.202	-0.67
1455372_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	-1.21	0.573	-1.01	0.976	-1.02	0.943	3.96	0.085	0.18
1449148_a_at	Phtf1	putative homeodomain transcription factor 1	-1.22	0.107	1.06	0.597	-1.08	0.515	-1.11	0.591	-0.59
1437709_x_at	Ttc13	tetratricopeptide repeat domain 13	-1.07	0.492	1.02	0.802	-1.18	0.075	-1.38	0.18	-0.65

1433875_at	4732418C07Rik	RIKEN cDNA 4732418C07 gene	-1.07	0.288	1.08	0.248	-1.26	0.029	-1.04	0.722	-0.57
1427159_at	Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	-1.24	0.205	-1	0.984	1	0.976	-1.05	0.602	-0.57
1453470_a_at	Gna13	guanine nucleotide binding protein, alpha 13	-1.35	0.237	-1.11	0.599	1.16	0.53	-1.29	0.569	-0.65
1418135_at	Aff1	AF4/FMR2 family, member 1	-1.01	0.942	-1.13	0.189	-1.07	0.616	1.36	0.156	-0.46
1423491_at	Fbxo3	F-box only protein 3	-1.01	0.969	-1.12	0.469	-1.08	0.746	1.43	0.342	-0.45
1450178_at	Brdt	bromodomain, testis-specific	1.06	0.921	-1.01	0.97	-1.31	0.189	-2.24	0.038	-0.88
1419375_at	Wbp4	WW domain binding protein 4	-1.01	0.937	-1.05	0.36	-1.16	0.142	1.11	0.269	-0.53
1455185_s_at	---	---	-1.04	0.879	-1.08	0.674	-1.09	0.625	1.88	0.107	-0.33
1439184_s_at	Txnl5	thioredoxin-like 5	-1.08	0.581	1.05	0.641	-1.2	0.137	-1.2	0.365	-0.61
1458932_at	Pex2	peroxin 2	-1.84	0.156	1.27	0.554	-1	0.992	-1.09	0.874	-0.67
1440261_at	Ap4e1	adaptor-related protein complex AP-4, epsilon 1	1.02	0.899	-1.02	0.747	-1.24	0.032	-1.03	0.889	-0.57
1422487_at	Smad4	MAD homolog 4 (Drosophila)	1.05	0.501	-1.04	0.321	-1.26	0.023	-1.69	0.108	-0.74
1426588_at	Tspan10	tetraspanin 10	-1.25	0.326	-1.56	0.311	1.37	0.583	-2.02	0.271	-0.87
1437154_at	Cep170	centrosomal protein 170	-1.6	0.231	1.22	0.408	-1.04	0.722	-1.18	0.401	-0.65
1419134_at	Rhbg	Rhesus blood group-associated B glycoprotein	-1.44	0.292	-1	0.99	1.11	0.601	-1.19	0.037	-0.63
1436537_at	Zfp629	zinc finger protein 629	1.02	0.922	-1.07	0.705	-1.17	0.238	-1.25	0.061	-0.62
1446717_at	---	---	-1	0.977	-1.16	0.662	-1.06	0.891	1.03	0.917	-0.55
1441212_at	6720467C03Rik	RIKEN cDNA 6720467C03 gene	1.32	0.11	-1.37	0.3	-1.32	0.373	-1.21	0.468	-0.64
1447494_at	D7Bwg0826e	DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed	-1.24	0.233	1.11	0.755	-1.12	0.725	-1.47	0.043	-0.68
1441780_at	---	Transcribed locus	-2.32	0.405	-1.26	0.726	1.58	0.415	-1.6	0.509	-0.9
1417072_at	Slc22a6	solute carrier family 22 (organic anion transporter), member 6	-1.05	0.558	-1.44	0.328	1.15	0.873	-1.2	0.732	-0.63
1451848_a_at	Cryz	crystallin, zeta	-1.14	0.255	-1.22	0.205	1.11	0.528	-1.13	0.519	-0.6
1437881_at	6330416L07Rik	RIKEN cDNA 6330416L07 gene	-1.18	0.043	1.02	0.957	-1.07	0.872	-1.12	0.509	-0.58
1438612_a_at	Clps	colipase, pancreatic	1.46	0.575	-1.48	0.472	-1.48	0.41	-1.81	0.642	-0.83
1455906_at	6030446N20Rik	RIKEN cDNA 6030446N20 gene	-1.09	0.75	1.09	0.73	-1.24	0.148	-1.04	0.702	-0.57
1444218_at	D19Ertd737e	DNA segment, Chr 19, ERATO Doi 737, expressed	1.09	0.435	-1.02	0.746	-1.34	0.147	-1.52	0.23	-0.7
1437276_at	---	Transcribed locus	-1.27	0.635	1.05	0.814	-1.04	0.876	-1.08	0.686	-0.58
1433705_at	Zfp213	zinc finger protein 213	1.06	0.716	-1.26	0.209	-1.05	0.702	-1.2	0.443	-0.61
1436523_s_at	1810022K09Rik	RIKEN cDNA 1810022K09 gene	-1.11	0.27	1.03	0.755	-1.15	0.146	-1.3	0.059	-0.63
1446337_at	Hdh	Huntington disease gene homolog	1.14	0.637	-1.34	0.341	-1.09	0.853	-1.05	0.854	-0.58
1417006_at	Commd4	COMM domain containing 4	-1.2	0.374	-1.11	0.066	1.07	0.241	-1.5	0.1	-0.68
1460260_s_at	Kpna1	karyopherin (importin) alpha 1	-1.17	0.095	1.01	0.926	-1.06	0.637	-1.02	0.938	-0.56
1415887_at	Tfg	Trk-fused gene	-1.11	0.447	-1.04	0.699	-1.06	0.141	1.33	0.15	-0.47
1436855_at	Ptprs	protein tyrosine phosphatase, receptor type, S	-1.01	0.963	-1.11	0.69	-1.09	0.646	1.56	0.222	-0.41
1440828_x_at	Phf7	PHD finger protein 7	1.04	0.913	-1.16	0.744	-1.1	0.81	-1.14	0.853	-0.59
1458620_at	LOC332993	similar to ubiquitin A-52 residue ribosomal protein fusion product 1	1.56	0.469	-1.71	0.102	-1.52	0.439	-2.16	0.29	-0.96
1428806_at	Csnk1g1	casein kinase 1, gamma 1	1.01	0.954	-1.06	0.752	-1.16	0.302	-1.17	0.296	-0.6
1457893_at	Ptplad2	Protein tyrosine phosphatase-like A domain containing 2	-1.3	0.71	1.06	0.823	-1.02	0.935	-2.1	0.066	-0.84
1420167_at	---	---	-1.4	0.265	-1.18	0.728	1.24	0.605	-1.2	0.299	-0.63
1435525_at	Kctd17	potassium channel tetramerisation domain containing 17	-1.22	0.216	-1.01	0.924	-1.01	0.961	1.06	0.465	-0.54
1450055_at	Vsnl1	visinin-like 1	1.31	0.102	-1.09	0.808	-1.72	0.105	-1.52	0.404	-0.75
1435237_at	2310009A05Rik	RIKEN cDNA 2310009A05 gene	1.06	0.498	-1.06	0.305	-1.25	0.193	-1.29	0.069	-0.63
1420811_a_at	Ctnnb1	catenin (cadherin associated protein), beta 1	1	0.986	-1.01	0.835	-1.22	0.043	-1.17	0.121	-0.6
1451479_a_at	Tmem53	transmembrane protein 53	-1.09	0.682	1.14	0.333	-1.34	0.102	-1.17	0.691	-0.61
1456199_x_at	Ranbp9	RAN binding protein 9	-1.2	0.113	-1.12	0.044	1.08	0.619	-1.09	0.629	-0.58
1419038_a_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	1.19	0.671	-1.14	0.577	-1.36	0.39	-1.03	0.953	-0.58
1450898_at	Hiat1	hippocampus abundant gene transcript 1	-1.2	0.067	-1.13	0.508	1.09	0.62	-1.11	0.529	-0.59
1431059_x_at	Htatsf1	HIV TAT specific factor 1	-1.41	0.333	-1.23	0.406	1.29	0.379	-1.22	0.612	-0.64
1442922_at	Chfr	checkpoint with forkhead and ring finger domains	-1.04	0.856	-2.09	0.085	1.37	0.523	-2.71	0.079	-1.12
1433534_a_at	Cct2	chaperonin subunit 2 (beta)	-1.19	0.393	-1.05	0.776	1.02	0.898	-1.23	0.171	-0.61
1416582_a_at	Bad	Bcl-associated death promoter	-1.2	0.426	1.05	0.833	-1.08	0.567	-1.05	0.771	-0.57
1460025_at	Lrig2	leucine-rich repeats and immunoglobulin-like domains 2	-1.33	0.134	1.14	0.471	-1.09	0.218	-1.3	0.047	-0.64
1431310_s_at	Ttll10	tubulin tyrosine ligase-like family, member 10	1.28	0.196	-1.2	0.732	-1.45	0.052	-1.63	0.493	-0.75

1456492_at	9130404D08Rik	RIKEN cDNA 9130404D08 gene	1.17	0.56	-1.18	0.516	-1.26	0.031	-1.02	0.139	-0.57
1424557_at	Zcchc9	zinc finger, CCHC domain containing 9	1.03	0.814	-1.2	0.112	-1.06	0.356	-1.09	0.37	-0.58
1435266_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	-1.1	0.371	-1.15	0.606	1.03	0.859	-1.29	0.38	-0.63
1425746_at	D730039F16Rik	RIKEN cDNA D730039F16 gene	-1.03	0.659	1.08	0.544	-1.32	0.482	-1.01	0.984	-0.57
1428085_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	-1.14	0.335	-1.05	0.496	-1.02	0.815	1.1	0.219	-0.53
1439500_at	---	---	1.23	0.307	-1.27	0.631	-1.28	0.124	-1.13	0.707	-0.61
1424173_at	Tmem48	transmembrane protein 48	-1.04	0.446	-1.06	0.906	-1.11	0.76	1.94	0.317	-0.32
1456160_at	Nxn	Nucleoredoxin	1.43	0.003	-1.34	0.694	-1.57	0.185	-1.25	0.035	-0.68
1450869_at	Fgf1	fibroblast growth factor 1	1.13	0.429	-1.28	0.002	-1.12	0.478	-1.09	0.456	-0.59
1417900_a_at	Vldlr	very low density lipoprotein receptor	-1.11	0.254	1.18	0.805	-1.38	0.258	-1.33	0.393	-0.66
1459869_x_at	4930402E16Rik	RIKEN cDNA 4930402E16 gene	1.04	0.735	-1.24	0.306	-1.04	0.877	-1.16	0.459	-0.6
1455207_at	2410017P09Rik	RIKEN cDNA 2410017P09 gene	-1.15	0.224	1.07	0.399	-1.15	0.346	-1.12	0.536	-0.59
1420054_s_at	Slc35c2	solute carrier family 35, member C2	-1.19	0.604	1.06	0.873	-1.1	0.414	-1.36	0.335	-0.65
1426715_s_at	D11Ertd18e	DNA segment, Chr 11, ERATO Doi 18, expressed	-1.05	0.741	-1.13	0.162	-1.03	0.928	1.33	0.511	-0.47
1417016_at	Mapkapk5	MAP kinase-activated protein kinase 5	-1.11	0.465	-1.11	0.689	1	0.973	-1.07	0.759	-0.57
1416456_a_at	Chia	chitinase, acidic	-1.01	0.966	-1.39	0.327	1.11	0.329	-1.39	0.673	-0.67
1429993_s_at	Speer4b	spermatogenesis associated glutamate (E)-rich protein 4b	-1	0.999	-1.1	0.476	-1.11	0.736	2.73	0.288	-0.12
1436846_x_at	Ywhaq /// LOC5461	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	-1.06	0.496	-1.16	0.07	1.01	0.946	-1.07	0.778	-0.57
1459879_at	4921513D23Rik	RIKEN cDNA 4921513D23 gene	1.29	0.395	-1.06	0.808	-1.74	0.201	-1.03	0.636	-0.63
1454937_at	B630005N14Rik	RIKEN cDNA B630005N14 gene	-1.23	0.227	-1.13	0.197	1.11	0.52	-1.39	0.254	-0.66
1460632_at	---	---	-1.03	0.857	1.03	0.796	-1.23	0.11	-1.15	0.659	-0.6
1451141_at	Mettl8	methyltransferase like 8	-1.06	0.732	-1.01	0.943	-1.14	0.238	1.16	0.409	-0.51
1424222_s_at	Rad23b	RAD23b homolog (S. cerevisiae)	-1.1	0.159	-1.19	0.042	1.06	0.441	-1.18	0.204	-0.6
1422933_at	Xlr5d /// LOC62708	X-linked lymphocyte-regulated 5D /// similar to X-linked lymphocyte-regulated 5C	-1.2	0.613	1.15	0.531	-1.21	0.723	-1.21	0.452	-0.62
1437110_at	2810474O19Rik	RIKEN cDNA 2810474O19 gene	-1	0.986	-1.09	0.52	-1.11	0.26	1.43	0.106	-0.45
1427907_at	1110037F02Rik	RIKEN cDNA 1110037F02 gene	-1.26	0.438	1.05	0.663	-1.04	0.78	-1.2	0.485	-0.61
1446034_at	---	Adult male cortex cDNA, RIKEN full-length enriched library, clone:B530045B12 p	-1.2	0.297	-1.12	0.704	1.09	0.272	-1.16	0.035	-0.6
1429606_at	4930527B16Rik	RIKEN cDNA 4930527B16 gene	1.32	0.591	-1.48	0.412	-1.23	0.13	-1.09	0.761	-0.62
1455013_at	Arih2	ariadne homolog 2 (Drosophila)	-1.05	0.724	-1.08	0.071	-1.07	0.366	1.14	0.43	-0.52
1446679_at	Grm5	Glutamate receptor, metabotropic 5	1.39	0.582	-1.15	0.699	-1.8	0.146	-1.34	0.582	-0.73
1426107_at	Prdm9	VPR domain containing 9	-1.21	0.595	1.41	0.617	-1.73	0.363	-1.4	0.233	-0.73
1456432_at	Grap2	GRB2-related adaptor protein 2	-1.23	0.299	1.2	0.756	-1.26	0.33	-2.47	0.111	-0.94
1423456_at	Bzw2	basic leucine zipper and W2 domains 2	-1.26	0.22	1.13	0.483	-1.13	0.455	-1.07	0.808	-0.58
1446379_at	C79296	expressed sequence C79296	-1.73	0.288	1.32	0.232	-1.09	0.819	-1.38	0.517	-0.72
1427330_at	Cars	cysteinyl-tRNA synthetase	-1.24	0.007	-1.29	0.585	1.23	0.536	-1.74	0.376	-0.76
1446020_at	---	---	-1.12	0.4	1.13	0.499	-1.27	0.322	-1.08	0.596	-0.58
1428917_at	Stx17	syntaxin 17	1.12	0.37	-1.19	0.224	-1.18	0.259	-1.03	0.873	-0.57
1451880_at	LOC638575	hypothetical LOC638575	1.54	0.59	-2.28	0.293	-1.21	0.711	-1.13	0.793	-0.77
1453924_a_at	Ptgfr	prostaglandin F receptor	-1.01	0.941	-1.19	0.516	-1.02	0.924	1.36	0.537	-0.47
1426292_at	6330581L23Rik	RIKEN cDNA 6330581L23 gene	1.11	0.038	-1.16	0.064	-1.19	0.173	-1.37	0.296	-0.65
1442647_at	Yipf1	Yip1 domain family, member 1	-1.13	0.778	1.16	0.668	-1.31	0.132	-1.45	0.165	-0.68
1420727_a_at	Tmlhe	trimethyllysine hydroxylase, epsilon	-1.07	0.758	1.01	0.95	-1.16	0.332	-1.01	0.976	-0.56
1439599_at	Gal3st2	galactose-3-O-sulfotransferase 2	1.16	0.812	-1.21	0.473	-1.22	0.172	-1.91	0.091	-0.79
1434316_at	Chsy1	carbohydrate (chondroitin) synthase 1	-1.14	0.708	-1.03	0.876	-1.04	0.274	1.14	0.486	-0.52
1428476_a_at	Elac2	elaC homolog 2 (E. coli)	-1.24	0.398	-1.25	0.009	1.2	0.17	-1.04	0.676	-0.58
1436536_at	C730015A04Rik	RIKEN cDNA C730015A04 gene	1.1	0.535	-1.13	0.445	-1.21	0.407	-1	0.984	-0.56
1439670_at	B020006M18Rik	RIKEN cDNA B020006M18 gene	1.48	0.615	-1.62	0.417	-1.41	0.442	-2.38	0.322	-0.98
1456006_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	-1.09	0.754	-1.06	0.767	-1.06	0.506	1.2	0.524	-0.5
1433430_s_at	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	-1.04	0.832	-1.06	0.592	-1.1	0.569	1.12	0.504	-0.52
1418529_at	Osgep	O-sialoglycoprotein endopeptidase	-1.12	0.133	1.01	0.873	-1.11	0.4	-1.28	0.162	-0.62
1458557_at	Bcas3	breast carcinoma amplified sequence 3	-1.68	0.119	-1.04	0.937	1.26	0.484	-1.59	0.505	-0.76
1448235_s_at	Hmgb1 /// 4932431	high mobility group box 1 /// RIKEN cDNA 4932431P20 gene /// similar to High m	-1.04	0.786	-1.08	0.665	-1.08	0.667	1.15	0.516	-0.51
1430051_at	4930486L24Rik	RIKEN cDNA 4930486L24 gene	1.22	0.772	-1.25	0.666	-1.26	0.439	-1.28	0.509	-0.64

1434408_at	Mjd	Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3	1.18	0.635	-1.07	0.631	-1.43	0.028	-1.09	0.158	-0.6
1434585_at	2210038L17Rik	RIKEN cDNA 2210038L17 gene	1.06	0.656	-1.13	0.231	-1.16	0.157	-1.25	0.248	-0.62
1446861_at	Gns	glucosamine (N-acetyl)-6-sulfatase	-1.15	0.093	-1.15	0.437	1.07	0.731	-1.05	0.822	-0.57
1450473_at	Pcdh12	protocadherin 12	-1.34	0.575	1.3	0.532	-1.3	0.451	-1.06	0.863	-0.6
1458665_at	Clic1	Chloride intracellular channel 1	1.75	0.094	-4.02	0.197	-1.23	0.622	-1.02	0.936	-1.13
1434452_x_at	Eif2a	eukaryotic translation initiation factor 2a	-1.2	0.565	1.01	0.956	-1.03	0.834	-1.1	0.582	-0.58
1421480_a_at	Adarb1	adenosine deaminase, RNA-specific, B1	-1.5	0.362	-1.26	0.453	1.35	0.067	-1.12	0.754	-0.63
1455159_at	2900057D21Rik	RIKEN cDNA 2900057D21 gene	-1.13	0.337	1.17	0.288	-1.32	0.146	-1.78	0.13	-0.76
1460336_at	Ppargc1a	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	-1.27	0.227	-1.28	0.161	1.24	0.089	-1.88	0.253	-0.8
1439886_at	4632415L05Rik	RIKEN cDNA 4632415L05 gene	-1.23	0.144	-1.21	0.219	1.17	0.363	-1.28	0.055	-0.64
1440899_at	Fmo5	flavin containing monooxygenase 5	-1.17	0.687	-1.14	0.486	1.08	0.644	-1.31	0.352	-0.63
1443216_at	Tbc1d5	TBC1 domain family, member 5	-1.16	0.538	1.16	0.252	-1.27	0.292	-1.8	0.232	-0.77
1426620_at	Chst10	carbohydrate sulfotransferase 10	-1.12	0.482	-1.3	0.02	1.15	0.283	-1.56	0.07	-0.71
1430788_at	---	---	-1.25	0.796	1.09	0.488	-1.08	0.888	-2.12	0.27	-0.84
1447090_s_at	Arl1	ADP-ribosylation factor-like 1	-1.05	0.681	1.06	0.402	-1.26	0.006	-1.36	0.166	-0.65
1437280_s_at	Serbp1	Serpine1 mRNA binding protein 1	1.02	0.855	-1.07	0.395	-1.17	0.255	-1.08	0.109	-0.57
1416951_a_at	Atp6v1d	ATPase, H+ transporting, lysosomal V1 subunit D	-1.07	0.529	-1.03	0.787	-1.1	0.504	1.05	0.404	-0.54
1421115_a_at	Zdhhc16	zinc finger, DHHC domain containing 16	-1.03	0.29	-1.12	0.142	-1.05	0.715	1.04	0.83	-0.54
1448802_at	Nufip1	nuclear fragile X mental retardation protein interacting protein 1	-1.35	0.129	1.14	0.513	-1.08	0.612	-1.19	0.172	-0.62
1458349_s_at	---	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732488M:	1.24	0.12	-1.72	0.206	-1.01	0.977	-1.22	0.286	-0.68
1441401_at	C79329	expressed sequence C79329	1.2	0.781	-1.06	0.91	-1.48	0.407	-3.19	0.067	-1.13
1434104_at	6030458H05	hypothetical protein 6030458H05	-1.02	0.895	-1.17	0.431	-1.02	0.915	1.59	0.201	-0.41
1426894_s_at	C230093N12Rik	RIKEN cDNA C230093N12 gene	1.02	0.916	-1.24	0.387	-1.01	0.879	-1.76	0.155	-0.75
1438856_x_at	Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	1.16	0.713	-1.11	0.265	-1.33	0.381	-1.05	0.841	-0.58
1433555_at	Eaf1	ELL associated factor 1	-1.06	0.352	-1.12	0.148	-1.03	0.877	1.16	0.466	-0.51
1428263_a_at	Tceb2	transcription elongation factor B (SIII), polypeptide 2	-1.03	0.367	-1.05	0.064	-1.13	0.031	1.08	0.676	-0.53
1448352_at	Luzp1	leucine zipper protein 1	-1.14	0.598	1.1	0.773	-1.19	0.585	-1.06	0.691	-0.57
1426354_at	Bap1	Brca1 associated protein 1	-1.23	0.159	-1.03	0.741	1.03	0.817	-1.05	0.745	-0.57
1424280_at	Mospd1	motile sperm domain containing 1	-1.05	0.526	-1.02	0.847	-1.13	0.361	1.69	0.108	-0.38
1444178_at	LOC433237	hypothetical gene supported by AK028012	-1.18	0.365	-1.03	0.936	-1	0.996	3.98	0.204	0.19
1421733_a_at	Tpst1	protein-tyrosine sulfotransferase 1	1.05	0.863	-1.1	0.566	-1.17	0.519	-1.25	0.174	-0.62
1437499_at	Ankrd39	ankyrin repeat domain 39	-1.21	0.698	1.02	0.93	-1.04	0.906	-1.62	0.063	-0.71
1433897_at	AI597468	expressed sequence AI597468	-1.05	0.856	-1.01	0.954	-1.14	0.153	1.11	0.068	-0.53
1421489_a_at	2010106E10Rik	RIKEN cDNA 2010106E10 gene	1.64	0.302	-2.22	0.388	-1.38	0.225	-2.29	0.239	-1.06
1416891_at	Numb	numb gene homolog (Drosophila)	-1.07	0.083	-1.25	0.071	1.08	0.54	-1.26	0.216	-0.62
1434482_at	D4Ertd22e	DNA segment, Chr 4, ERATO Doi 22, expressed	-1.24	0.41	-1.06	0.598	1.06	0.759	-1.49	0.039	-0.68
1417642_at	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	-2.13	0.199	-1.01	0.979	1.36	0.35	-2.26	0.18	-1.01
1448527_at	Pdcd10	programmed cell death 10	-1.16	0.127	1.07	0.425	-1.12	0.163	-1.33	0.043	-0.64
1456143_at	Prkcbp1	protein kinase C binding protein 1	-1.09	0.551	-1.1	0.313	-1.01	0.97	1.02	0.907	-0.55
1426271_at	Smc5	structural maintenance of chromosomes 5	-1.08	0.646	-1.02	0.841	-1.1	0.283	1.12	0.427	-0.52
1418894_s_at	Pbx2	pre B-cell leukemia transcription factor 2	-1.07	0.715	-1.23	0.498	1.07	0.778	-1.78	0.134	-0.75
1427233_at	Tshz1	teashirt zinc finger family member 1	1.08	0.368	-1.15	0.217	-1.15	0.193	-1.07	0.7	-0.57
1448484_at	Amd1	S-adenosylmethionine decarboxylase 1	-1.08	0.227	-1.09	0.189	-1.04	0.639	1.97	0.216	-0.31
1452628_at	Bag5	BCL2-associated athanogene 5	-1	0.976	-1.07	0.435	-1.13	0.361	1.06	0.773	-0.54
1460674_at	Paqr7	progestin and adipoQ receptor family member VII	1.07	0.807	-1.24	0.604	-1.07	0.386	-1.19	0.204	-0.61
1426212_s_at	Tmem161a	transmembrane protein 161A	-1.06	0.526	-1.02	0.842	-1.12	0.074	1.01	0.928	-0.55
1420124_s_at	Tcta	T-cell leukemia translocation altered gene	-1.08	0.54	1.06	0.684	-1.21	0.004	-1.13	0.608	-0.59
1459705_at	Olfm3	Olfactomedin 3	1.14	0.836	-1.16	0.821	-1.24	0.559	-1.31	0.607	-0.64
1428946_at	Ube1l2	ubiquitin-activating enzyme E1-like 2	1.02	0.905	-1.1	0.606	-1.13	0.654	-1.05	0.839	-0.57
1436814_at	Tpcn2	Two pore segment channel 2	1.04	0.954	-1.05	0.918	-1.21	0.248	-2.66	0.123	-0.97
1432869_at	---	---	-1	0.999	-2.06	0.149	1.33	0.412	-2.6	0.311	-1.08
1454246_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.22	0.821	-1.55	0.069	1.35	0.678	-1.6	0.115	-0.76
1441454_at	Zhx3	zinc fingers and homeoboxes 3	-1.1	0.673	1.06	0.732	-1.18	0.51	-1.14	0.711	-0.59

1416074_a_at	Rpl28	ribosomal protein L28	-1.05	0.683	1.03	0.779	-1.2	0.139	-1.17	0.056	-0.6
1430838_x_at	Mbd1	methyl-CpG binding domain protein 1	-1.13	0.022	-1.15	0.431	1.07	0.716	-1.26	0.442	-0.62
1419371_s_at	Gosr2	golgi SNAP receptor complex member 2	-1.13	0.433	1.03	0.63	-1.11	0.225	-1.29	0.155	-0.63
1417635_at	Spa17	sperm autoantigenic protein 17	-1.01	0.927	-1.01	0.983	-1.19	0.478	1.23	0.617	-0.5
1433554_at	AU022870	expressed sequence AU022870	-1.03	0.241	1.03	0.364	-1.23	0.051	-1	0.983	-0.56
1455350_at	Tmem62	transmembrane protein 62	-1.16	0.021	1.09	0.665	-1.15	0.226	-1.29	0.187	-0.63
1453086_at	6330408A02Rik	RIKEN cDNA 6330408A02 gene	-1.03	0.932	-1.48	0.213	1.17	0.439	-1.28	0.133	-0.66
1429968_at	2310047L11Rik	RIKEN cDNA 2310047L11 gene	-1	0.981	1.12	0.65	-1.43	0.11	-1.43	0.398	-0.69
1440974_at	9030203C11Rik	RIKEN cDNA 9030203C11 gene	1.21	0.662	-1.2	0.329	-1.3	0.078	-1.42	0.258	-0.68
1442182_at	Dnajc19	DnaJ (Hsp40) homolog, subfamily C, member 19	1.08	0.62	-1.2	0.39	-1.1	0.635	-1.26	0.229	-0.62
1417476_at	Fbxw5	F-box and WD-40 domain protein 5	-1.1	0.555	-1.11	0.478	1.01	0.958	-1.16	0.336	-0.59
1448770_a_at	Atpif1	ATPase inhibitory factor 1	-1.06	0.27	-1.01	0.884	-1.14	0.255	2.38	0.159	-0.21
1424582_at	Mulk /// LOC66726	multiple substrate lipid kinase /// similar to multi-substrate lipid kinase /// similar to	-1.17	0.439	-1.01	0.926	-1.03	0.855	1.01	0.959	-0.55
1454605_a_at	Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	-1.25	0.217	-1.01	0.921	1.02	0.47	-1.07	0.596	-0.58
1453944_at	5430435K18Rik	RIKEN cDNA 5430435K18 gene	-1.36	0.152	1.09	0.821	-1.01	0.989	-1.24	0.563	-0.63
1435561_at	Erf	Ets2 repressor factor	-1.43	0.555	-1.07	0.817	1.18	0.562	-1.73	0.26	-0.76
1435690_at	2310008H09Rik	RIKEN cDNA 2310008H09 gene	-1.05	0.762	-1.13	0.646	-1.02	0.92	1.12	0.629	-0.52
1415984_at	Acadm	acyl-Coenzyme A dehydrogenase, medium chain	-1.09	0.411	-1.45	0.14	1.21	0.288	-1.39	0.228	-0.68
1425698_a_at	Zf	HCF-binding transcription factor Zhangfei	-1.26	0.561	-1.5	0.283	1.36	0.004	-1.45	0.185	-0.71
1452810_at	Ints10 /// LOC6748	integrator complex subunit 10 /// similar to integrator complex subunit 10	-1.02	0.928	-1.18	0.201	-1.01	0.894	1.05	0.325	-0.54
1421466_at	Asb10	ankyrin repeat and SOCS box-containing protein 10	-1.01	0.985	-1.02	0.958	-1.19	0.335	1.09	0.361	-0.53
1417703_at	Pvrl2	poliovirus receptor-related 2	1.1	0.473	-1.19	0.286	-1.15	0.203	-1.1	0.441	-0.58
1419242_at	9530002B09Rik	RIKEN cDNA 9530002B09 gene	-1.4	0.295	-1.09	0.82	1.18	0.654	-1.51	0.495	-0.7
1432863_a_at	Nkx2-4	NK2 transcription factor related, locus 4 (Drosophila)	-1.17	0.368	1.15	0.515	-1.24	0.279	-2.13	0.502	-0.85
1418106_at	Hey2	hairy/enhancer-of-split related with YRPW motif 2	-1.18	0.408	-1.05	0.901	1.01	0.962	-1.69	0.036	-0.73
1450531_at	H2-Bl	histocompatibility 2, blastocyst	-1.66	0.646	1.39	0.004	-1.21	0.452	-1.02	0.976	-0.62
1455087_at	D7Ertd715e	DNA segment, Chr 7, ERATO Doi 715, expressed	-1.24	0.125	1.13	0.723	-1.14	0.594	-1.04	0.744	-0.57
1422969_s_at	Ihpk1	inositol hexaphosphate kinase 1	-1.29	0.303	-1.79	0.268	1.49	0.506	-1.18	0.603	-0.7
1438969_x_at	Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-1.1	0.684	-1.14	0.341	1.03	0.705	-1.85	0.071	-0.76
1437067_at	Phtf2	putative homeodomain transcription factor 2	-1.15	0.567	-1.07	0.722	1.01	0.922	-1.65	0.052	-0.71
1454766_at	C730024G19Rik	RIKEN cDNA C730024G19 gene	1.04	0.543	-1.07	0.744	-1.19	0.263	-1.1	0.633	-0.58
1435740_at	Rai17	Retinoic acid induced 17	-1.07	0.226	-1.2	0.303	1.05	0.787	-1.4	0.347	-0.66
1446911_at	Itsn2	Intersectin 2	1.08	0.723	-1.2	0.403	-1.11	0.764	-1.43	0.369	-0.67
1421836_at	---	---	-1.23	0.07	-1.3	0.032	1.23	0.027	-1.27	0.188	-0.64
1423940_at	Yif1a	Yip1 interacting factor homolog A (S. cerevisiae)	-1.14	0.64	-1.1	0.527	1.04	0.671	-1.15	0.074	-0.59
1449441_a_at	Wbp1	WW domain binding protein 1	-1.03	0.886	-1.1	0.388	-1.07	0.655	1.24	0.239	-0.49
1419285_s_at	Cyhr1	cysteine and histidine rich 1	1.08	0.733	-1.26	0.169	-1.06	0.347	-1.14	0.283	-0.59
1417932_at	Il18	interleukin 18	-1.13	0.588	-1.13	0.535	1.05	0.408	-1.08	0.776	-0.57
1459686_at	---	---	1.11	0.728	-1.26	0.518	-1.09	0.82	-1.29	0.423	-0.63
1458844_at	4933415L06Rik	RIKEN cDNA 4933415L06 gene	1.18	0.172	-1.21	0.671	-1.23	0.2	-2.36	0.318	-0.91
1420271_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630030	-1.95	0.444	1.76	0.446	-1.82	0.336	-1.04	0.961	-0.77
1454954_at	Wdr61	WD repeat domain 61	-1.04	0.854	-1.08	0.737	-1.08	0.735	1.22	0.326	-0.49
1460743_at	Tigd5	tigger transposable element derived 5	-1.11	0.768	-1.16	0.774	1.05	0.758	-1.07	0.896	-0.57
1446336_at	---	---	-1.37	0.214	-1.05	0.865	1.14	0.69	-2.05	0.1	-0.83
1430731_at	Krtap2-4	keratin associated protein 2-4	1.81	0.394	-1.63	0.393	-2.52	0.165	-1.36	0.487	-0.92
1449350_at	Osr1	odd-skipped related 1 (Drosophila)	-1.03	0.918	1.18	0.774	-1.52	0.141	-1.52	0.503	-0.72
1423821_at	Tmem168	transmembrane protein 168	-1.18	0.404	1.06	0.271	-1.1	0.45	-1.38	0.179	-0.65
1422255_at	Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	1.15	0.738	-1.38	0.382	-1.06	0.745	-1.5	0.477	-0.7
1425036_a_at	Tnrc6a	trinucleotide repeat containing 6a	1.03	0.801	-1.03	0.771	-1.22	0.229	-1.58	0.045	-0.7
1449953_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	-1.43	0.024	1.13	0.702	-1.01	0.974	-1.32	0.544	-0.66
1436593_at	1700016K19Rik	RIKEN cDNA 1700016K19 gene	-1.2	0.462	1.02	0.929	-1.04	0.866	-2.03	0.369	-0.81
1446711_at	A130040G06Rik	RIKEN cDNA A130040G06 gene	1.08	0.685	-1.25	0.764	-1.07	0.826	-2.3	0.05	-0.88
1442001_at	Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	-1.26	0.327	-1.72	0.332	1.44	0.146	-1.24	0.325	-0.69

AFFX-r2-Bs-dap-3_a	---	---	1.08	0.853	-1.17	0.148	-1.13	0.417	-1.23	0.348	-0.61
1428817_at	Mon2	MON2 homolog (yeast)	-1.15	0.254	-1.14	0.119	1.07	0.495	-1.36	0.17	-0.64
1446091_at	Anp32b	Acidic nuclear phosphoprotein 32 family, member B	-1.31	0.616	1.06	0.834	-1.01	0.964	-1.22	0.125	-0.62
1426257_a_at	Sars	seryl-aminoacyl-tRNA synthetase	-1.07	0.693	-1.08	0.321	-1.05	0.735	1.26	0.014	-0.48
1449732_at	Zipro1	zinc finger proliferation 1	1.26	0.528	-1.04	0.807	-1.69	0.013	-1.6	0.255	-0.77
1435729_at	Mapbpip	mitogen activated protein binding protein interacting protein	1.03	0.336	-1.26	0.454	-1	0.984	-1.51	0.561	-0.69
1435956_at	A930004K21Rik	RIKEN cDNA A930004K21 gene	-2	0.149	-1.63	0.153	1.7	0.14	-1.92	0.36	-0.96
1418998_at	Kmo	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	1.08	0.598	-1.04	0.679	-1.28	0.042	-3.1	0.044	-1.09
1432164_a_at	Gcsh /// LOC67432	glycine cleavage system protein H (aminomethyl carrier) /// similar to Glycine clea	-1.01	0.883	1.01	0.849	-1.22	0.07	-1.09	0.564	-0.58
1427413_a_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	-1.03	0.881	-1.13	0.314	-1.04	0.789	1.01	0.952	-0.55
1434230_at	Polb /// A430088C0	polymerase (DNA directed), beta /// RIKEN cDNA A430088C08 gene	1.08	0.498	-1.04	0.644	-1.3	0.073	-1.26	0.194	-0.63
1428668_at	Acbd3	acyl-Coenzyme A binding domain containing 3	-1.06	0.334	1	0.993	-1.14	0.209	-1.33	0.029	-0.63
1458580_at	---	Transcribed locus	-1.39	0.524	1.21	0.617	-1.13	0.787	-1.35	0.274	-0.66
1418228_at	Hirip5	histone cell cycle regulation defective interacting protein 5	-1.11	0.66	-1.11	0.362	1.01	0.934	-1.25	0.241	-0.61
1436519_a_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	-1.15	0.678	-1.17	0.248	1.1	0.602	-1.01	0.982	-0.56
1424833_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	-1.43	0.215	-1.19	0.646	1.28	0.271	-1.36	0.42	-0.67
1450654_a_at	Dhdds	dehydrodolichyl diphosphate synthase	-1.08	0.581	-1.14	0.35	1.01	0.908	-1.02	0.84	-0.55
1419003_at	Bves	blood vessel epicardial substance	-1.19	0.595	-1.27	0.755	1.19	0.462	-1.5	0.597	-0.69
1416453_x_at	Rps12 /// LOC4328	ribosomal protein S12 /// similar to ribosomal protein S12 /// similar to ribosomal p	-1.07	0.484	1.02	0.842	-1.16	0.102	-1.32	0.001	-0.63
1440888_at	Oxtr	oxytocin receptor	-1.47	0.521	-1.24	0.53	1.34	0.519	-1.76	0.17	-0.78
1425713_a_at	Rnf146	ring finger protein 146	-1.52	0.294	-1.26	0.187	1.36	0.279	-1.24	0.461	-0.66
1416904_at	Mbnl1	muscleblind-like 1 (Drosophila)	1.03	0.754	-1.06	0.087	-1.18	0.158	-1.27	0.056	-0.62
1448149_at	Ctnna1	catenin (cadherin associated protein), alpha 1	-1.02	0.613	-1.01	0.822	-1.19	0.059	1.26	0.208	-0.49
1423931_s_at	Anapc4	anaphase promoting complex subunit 4	-1.13	0.457	1.14	0.109	-1.26	0.167	-1.27	0.359	-0.63
1442137_at	2010000I03Rik	RIKEN cDNA 2010000I03 gene	-1.1	0.521	-1.08	0.685	-1.01	0.853	1.17	0.675	-0.51
1440414_at	Mtf1	metal response element binding transcription factor 1	-1.39	0.393	-1.31	0.575	1.33	0.229	-1.36	0.206	-0.68
1456530_x_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.2	0.021	1.15	0.237	-1.21	0.245	-1.03	0.768	-0.57
1456347_at	Lnpep	Leucyl/cystinyl aminopeptidase	-1.22	0.443	-1.01	0.989	1.01	0.959	-1.31	0.417	-0.63
1432012_a_at	Nsun6	NOL1/NOP2/Sun domain family 6	1.04	0.957	-1.24	0.747	-1.03	0.89	-1.14	0.759	-0.59
1436007_a_at	Thumpd1	THUMP domain containing 1	-1.16	0.466	-1.11	0.62	1.05	0.736	-1.33	0.036	-0.63
1418392_a_at	Gbp4	guanylate nucleotide binding protein 4	-1.27	0.075	-1.37	0.271	1.3	0.474	-1.19	0.421	-0.63
1434894_at	Zc3h13	zinc finger CCCH type containing 13	1.02	0.909	-1.09	0.582	-1.13	0.572	-1.1	0.601	-0.58
1451510_s_at	Olah	oleoyl-ACP hydrolase	-1.24	0.364	-1	0.998	1.01	0.953	-1.01	0.977	-0.56
1460257_a_at	Mthfs	5, 10-methenyltetrahydrofolate synthetase	-1.17	0.306	-1.11	0.077	1.06	0.725	-1.56	0.093	-0.69
1444979_at	Proc	protein C	-1.08	0.917	-1.24	0.663	1.09	0.804	-1.15	0.595	-0.6
1440605_at	Fscn2	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus)	1.03	0.264	-1.13	0.774	-1.11	0.414	-1.06	0.68	-0.57
1438653_x_at	Atxn10	ataxin 10	-1.12	0.46	1.04	0.178	-1.13	0.175	-1.23	0.157	-0.61
1430124_x_at	Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	-1.22	0.155	-1.06	0.095	1.06	0.375	-1.1	0.512	-0.58
1430129_a_at	Commd8	COMM domain containing 8	-1.23	0.199	1.04	0.706	-1.03	0.759	-1.39	0.144	-0.65
1453457_at	2900070H08Rik	RIKEN cDNA 2900070H08 gene	-1.11	0.609	1.12	0.509	-1.26	0.125	-1.44	0.005	-0.67
1452013_at	Atp10a	ATPase, class V, type 10A	-1.07	0.409	-1.75	0.333	1.32	0.379	-1.93	0.107	-0.86
1448596_at	Slc6a8	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	-1.42	0.151	-1.18	0.646	1.27	0.384	-1	0.998	-0.58
1434500_at	Ttyh2	tweety homolog 2 (Drosophila)	-1.12	0.387	1.05	0.82	-1.14	0.515	-1.03	0.788	-0.56
1422072_a_at	Gstm6	glutathione S-transferase, mu 6	1.19	0.573	-1.47	0.403	-1.05	0.892	-1.79	0.065	-0.78
1449263_at	Ufm1	ubiquitin-fold modifier 1	1.02	0.867	-1.06	0.38	-1.17	0.11	-1.06	0.657	-0.57
1453536_at	1700034K16Rik	RIKEN cDNA 1700034K16 gene	-1.03	0.91	1.18	0.717	-1.48	0.396	-2.4	0.035	-0.94
1416908_s_at	Tsn	translin	-1.03	0.599	-1.08	0.444	-1.09	0.394	1.14	0.506	-0.51
1454365_at	4930554P06Rik	RIKEN cDNA 4930554P06 gene	-1.25	0.405	1.05	0.877	-1.03	0.863	-1.31	0.154	-0.63
1425179_at	Shmt1	serine hydroxymethyl transferase 1 (soluble)	-1.16	0.134	-1.19	0.259	1.12	0.547	-1.07	0.232	-0.58
1438047_at	Zfp384	zinc finger protein 384	-1.01	0.871	1.02	0.741	-1.24	0.167	-1.19	0.089	-0.6
1454647_at	Acad11	acyl-Coenzyme A dehydrogenase family, member 11	-1.14	0.595	-1.45	0.064	1.25	0.26	-1.05	0.496	-0.6
1441988_at	Ppm1k	protein phosphatase 1K (PP2C domain containing)	1.22	0.185	-1.24	0.099	-1.26	0.425	-1.08	0.785	-0.59
1458718_at	---	PREDICTED: Mus musculus hypothetical LOC243025 (LOC243025), mRNA	-2.07	0.363	1.47	0.037	-1.16	0.584	-1.9	0.116	-0.91

1457731_at	Snapc3	small nuclear RNA activating complex, polypeptide 3	1.13	0.513	-1.26	0.365	-1.12	0.549	-1.27	0.127	-0.63
1419743_s_at	Carm1	coactivator-associated arginine methyltransferase 1	-1.09	0.463	-1.06	0.225	-1.04	0.843	1.86	0.092	-0.33
1437204_a_at	Tcf25	transcription factor 25 (basic helix-loop-helix)	-1.09	0.668	-1.19	0.44	1.06	0.74	-1.63	0.158	-0.71
1446640_at	---	Transcribed locus	-1.1	0.658	-1.29	0.35	1.14	0.797	-1.17	0.513	-0.61
1453105_at	Zfp263	zinc finger protein 263	-1.31	0.012	-1.02	0.878	1.08	0.652	-1.78	0.151	-0.76
1424646_at	Uckl1	uridine-cytidine kinase 1-like 1	-1.11	0.282	-1.12	0.151	1.03	0.11	-1.41	0.087	-0.65
1430047_at	Brctd1	BRCT domain containing 1	-1.16	0.576	1.14	0.432	-1.22	0.311	-1.21	0.548	-0.61
1438557_x_at	Dnpep	aspartyl aminopeptidase	-1.23	0.058	-1.05	0.473	1.06	0.686	-1.12	0.298	-0.59
1424045_at	5730437N04Rik	RIKEN cDNA 5730437N04 gene	-1.37	0.348	-1.42	0.103	1.39	0.36	-2.16	0.19	-0.89
1448947_at	2810004N23Rik	RIKEN cDNA 2810004N23 gene	-1.13	0.272	-1.16	0.196	1.07	0.526	-1.12	0.667	-0.58
1416485_at	Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)	-1.06	0.431	-1.07	0.301	-1.06	0.391	1.1	0.484	-0.52
1454795_at	Cobll1	Cobl-like 1	-1.05	0.733	-1.18	0.28	1.02	0.819	-1.52	0.439	-0.68
1451310_a_at	Ctsl	cathepsin L	-1.16	0.209	1.08	0.522	-1.14	0.279	-1.6	0.165	-0.7
1416175_a_at	Vdac3	voltage-dependent anion channel 3	-1.05	0.048	-1.07	0.295	-1.08	0.276	1.13	0.383	-0.51
1435816_at	Rps6 /// LOC21473	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	1.01	0.936	-1.03	0.87	-1.19	0.453	-1.49	0.024	-0.67
1441033_at	Tmtc2	transmembrane and tetratricopeptide repeat containing 2	1.25	0.014	-1.16	0.458	-1.41	0.319	-1.2	0.524	-0.63
1435534_a_at	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.19	0.208	-1.01	0.856	-1	0.979	1	0.984	-0.55
1450612_a_at	Pemt	phosphatidylethanolamine N-methyltransferase	1.05	0.793	-1.03	0.853	-1.25	0.394	-1.17	0.245	-0.6
1421066_at	---	---	-1.05	0.627	1.02	0.871	-1.17	0.101	-1.27	0.26	-0.62
1456279_a_at	Bcap31	B-cell receptor-associated protein 31	1.02	0.291	-1.03	0.466	-1.21	0.103	-1.25	0.385	-0.62
1419963_at	Depdc6	DEP domain containing 6	1.15	0.777	-1.21	0.615	-1.18	0.594	-1.08	0.908	-0.58
1436480_at	Dpp7	dipeptidylpeptidase 7	-1.02	0.961	-1.23	0.069	1.03	0.875	-1.52	0.093	-0.69
1419922_s_at	Atrnl1	attractin like 1	1.06	0.765	-1.04	0.67	-1.24	0.367	-1.45	0.295	-0.67
1447773_x_at	6330409D20Rik	RIKEN cDNA 6330409D20 gene	1.54	0.617	-2.48	0.021	-1.13	0.748	-1.25	0.737	-0.83
1458042_at	---	---	-1.08	0.933	-1.51	0.34	1.23	0.728	-1.17	0.803	-0.63
1443911_at	---	---	-1.58	0.067	1.65	0.431	-1.84	0.067	-1.88	0.218	-0.91
AFFX-PheX-3_at	---	---	1.08	0.829	-1.13	0.211	-1.16	0.574	-1.67	0.366	-0.72
1449256_a_at	Rab11a	RAB11a, member RAS oncogene family	1.03	0.636	-1.07	0.321	-1.16	0.14	-1.16	0.034	-0.59
1450972_at	3110040N11Rik	RIKEN cDNA 3110040N11 gene	-1.03	0.765	-1.02	0.929	-1.15	0.22	1.04	0.738	-0.54
1422209_s_at	Krtap9-1 /// LOC43	keratin associated protein 9-1 /// similar to keratin associated protein 9-1 /// simila	1.1	0.769	-1.34	0.714	-1.03	0.913	-1.02	0.947	-0.57
1434461_at	Zfp715	zinc finger protein 715	-1.01	0.76	1	0.973	-1.21	0.135	-1.46	0.042	-0.67
AFFX-DapX-3_at	---	---	1.09	0.862	-1.34	0.045	-1.02	0.932	-1.41	0.206	-0.67
1437779_at	Foxh1	forkhead box H1	1.54	0.531	-1.66	0.381	-1.48	0.057	-1.53	0.509	-0.78
1435967_s_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	-1.14	0.38	-1.11	0.485	1.04	0.393	-1.25	0.194	-0.61
1424689_at	Prss32	protease, serine, 32	1.81	0.359	-1.53	0.337	-2.75	0.06	-1.19	0.637	-0.92
1437198_at	Lig3	ligase III, DNA, ATP-dependent	-1.02	0.939	-1.06	0.754	-1.12	0.663	1.05	0.842	-0.54
1456357_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	1.21	0.556	-1.41	0.366	-1.1	0.694	-1.06	0.088	-0.59
1459837_at	Cyb561d1	Cytochrome b-561 domain containing 1	-1.14	0.696	-1.26	0.374	1.15	0.238	-2.41	0.011	-0.91
1446141_at	Tgfb2	Transforming growth factor, beta 2	1.78	0.361	-1.47	0.434	-2.78	0.09	-1.74	0.544	-1.05
1445152_at	Cask	Calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-1.02	0.955	1.16	0.531	-1.47	0.072	-1.21	0.519	-0.64
1460551_at	Ran	RAN, member RAS oncogene family	-1.01	0.828	-1.15	0.076	-1.03	0.788	1.52	0.197	-0.42
1426375_s_at	Oxnad1	oxidoreductase NAD-binding domain containing 1	-1.08	0.723	-1.09	0.571	-1.02	0.79	1.44	0.307	-0.44
1453417_at	4933407K13Rik	RIKEN cDNA 4933407K13 gene	-1.13	0.743	-1.13	0.699	1.05	0.752	-1.26	0.009	-0.62
1452086_at	Trmt5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	-1.1	0.568	1.01	0.981	-1.1	0.402	-1.09	0.449	-0.57
1428167_a_at	Mpzl1	myelin protein zero-like 1	-1.13	0.539	1.17	0.48	-1.31	0.435	-1.9	0.189	-0.79
1416788_a_at	Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	-1.07	0.265	-1.13	0.238	1.01	0.699	-1	0.992	-0.55
1427253_s_at	Suz12	suppressor of zeste 12 homolog (Drosophila)	-1.11	0.217	-1.05	0.176	-1.03	0.668	1.72	0.094	-0.37
1416470_a_at	Rpn1	ribophorin I	-1.04	0.558	1.03	0.82	-1.2	0.064	-1.14	0.53	-0.59
1423717_at	Ak3	adenylate kinase 3	-1.09	0.151	-1.06	0.328	-1.03	0.606	1.08	0.494	-0.53
1439300_at	---	---	1.18	0.666	-1.33	0.327	-1.13	0.599	-1.27	0.578	-0.63
1417505_s_at	Il11ra1 /// Il11ra2 ///	interleukin 11 receptor, alpha chain 1 /// interleukin 11 receptor, alpha chain 2 /// s	1.05	0.575	-1	0.946	-1.28	0.044	-1.51	0.059	-0.69
1447943_x_at	Yeats2	YEATS domain containing 2	1.02	0.821	-1.03	0.863	-1.19	0.196	-1.25	0.149	-0.61
1427451_a_at	BC018473	cDNA sequence BC018473	1.19	0.798	-1.15	0.792	-1.3	0.669	-2.1	0.232	-0.84

1421195_at	Cckar	cholecystokinin A receptor	-1.14	0.007	1.02	0.98	-1.08	0.694	-2.13	0.499	-0.83
1426795_at	Ptprs	protein tyrosine phosphatase, receptor type, S	-2.14	0.163	-1.34	0.646	1.61	0.152	-2.61	0.234	-1.12
1450725_s_at	Car14	carbonic anhydrase 14	-1.4	0.115	-1.52	0.053	1.45	0.121	-1.37	0.484	-0.71
1456552_at	---	2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clo	1.4	0.55	-1.27	0.609	-1.56	0.123	-1.11	0.614	-0.64
1418817_at	Chmp1b	chromatin modifying protein 1B	-1.09	0.352	1.06	0.541	-1.19	0.113	-1.12	0.437	-0.58
1451233_at	Traf2	Tnf receptor-associated factor 2	-1.12	0.555	-1.21	0.085	1.1	0.346	-1.71	0.089	-0.73
1447014_at	---	---	1.51	0.611	-1.68	0.316	-1.39	0.099	-1.15	0.271	-0.68
1438643_at	Camk1d	Calcium/calmodulin-dependent protein kinase ID	-1.2	0.622	1.35	0.341	-1.56	0.077	-2.47	0.152	-0.97
1416146_at	Hspa4	heat shock protein 4	1.1	0.476	-1.21	0.013	-1.11	0.567	-1.11	0.303	-0.58
1452325_at	Trp73	transformation related protein 73	-1.31	0.366	-1.54	0.419	1.42	0.077	-1.42	0.344	-0.71
1425377_at	Wnt1	wingless-related MMTV integration site 1	-1.89	0.205	1.87	0.308	-2.35	0.152	-1.13	0.629	-0.87
1423692_at	Ndufa8	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	-1.12	0.099	-1.1	0.232	1.02	0.843	-1.13	0.431	-0.58
1436116_x_at	2900057D21Rik	RIKEN cDNA 2900057D21 gene	-1.6	0.524	1.29	0.557	-1.1	0.406	-2.31	0.053	-0.93
1442476_at	Ift81	Intraflagellar transport 81 homolog (Chlamydomonas)	1.09	0.373	-1.2	0.675	-1.11	0.758	-1.18	0.358	-0.6
1426449_a_at	Pja1	praja1, RING-H2 motif containing	1.03	0.704	-1.06	0.633	-1.17	0.289	-1.15	0.511	-0.59
1424662_at	Pmpca	peptidase (mitochondrial processing) alpha	-1.01	0.857	-1.17	0.201	-1.01	0.902	1.15	0.462	-0.51
1425838_at	Atp9a	ATPase, class II, type 9A	-1.21	0.733	1.26	0.61	-1.36	0.519	-2.78	0.128	-1.02
1417320_at	Grpel1	GrpE-like 1, mitochondrial	-1.02	0.279	-1.05	0.2	-1.12	0.298	1.12	0.683	-0.52
1435081_at	Sypl	synaptophysin-like protein	-1.09	0.331	-1.11	0.094	1.01	0.854	-1.04	0.784	-0.56
1449635_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	-1.14	0.333	-1.09	0.101	1.03	0.768	-1.43	0.292	-0.66
1455897_x_at	Hmgn1	high mobility group nucleosomal binding domain 1	-1.13	0.338	1.1	0.313	-1.19	0.025	-1.42	0.01	-0.66
1419169_at	Mapk6	mitogen-activated protein kinase 6	-1.18	0.111	-1.01	0.83	-1.01	0.928	1.11	0.677	-0.52
1426882_at	Ube3c	ubiquitin protein ligase E3C	-1.07	0.328	-1.07	0.329	-1.05	0.789	1.26	0.349	-0.48
1458168_at	---	Adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:733044	1.1	0.177	-1.04	0.888	-1.31	0.341	-1.32	0.39	-0.64
1426826_at	Rbm16	RNA binding motif protein 16	-1.1	0.165	-1.11	0.291	1.01	0.919	-1.43	0.097	-0.65
1458099_at	---	---	-1.25	0.051	-1.36	0.042	1.29	0.631	-2	0.105	-0.83
1447611_at	1700073E17Rik	RIKEN cDNA 1700073E17 gene	1.09	0.183	-1.3	0.115	-1.04	0.704	-1.07	0.663	-0.58
1428225_s_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	1.1	0.467	-1.09	0.573	-1.23	0.309	-1.58	0.046	-0.7
1434260_at	Fchsd2	FCH and double SH3 domains 2	1.01	0.954	-1.18	0.321	-1.03	0.817	-2.15	0.042	-0.84
1430326_s_at	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	-1.02	0.815	-1.05	0.56	-1.13	0.323	1.17	0.487	-0.5
1437014_x_at	LOC545161 /// LOC	similar to Peroxiredoxin 1 (Thioredoxin peroxidase 2) (Thioredoxin-dependent pe	-1.4	0.214	1.2	0.107	-1.1	0.397	-1.08	0.403	-0.59
1455109_at	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	1.24	0.585	-1.17	0.439	-1.36	0.443	-1.48	0.113	-0.69
1460607_at	Igsf11	immunoglobulin superfamily, member 11	-1.22	0.248	-1.01	0.965	1.01	0.979	-1.69	0.161	-0.73
1429074_at	1700026D08Rik	RIKEN cDNA 1700026D08 gene	-1.47	0.665	-1.13	0.835	1.26	0.53	-1.41	0.226	-0.69
1426019_at	Plaa	phospholipase A2, activating protein	1.47	0.557	-1.24	0.805	-1.82	0.427	-1.48	0.524	-0.77
1438507_x_at	Rpl14	ribosomal protein L14	-1.1	0.535	1.03	0.743	-1.12	0.206	-1.47	0.098	-0.67
1417083_at	Sec61b	Sec61 beta subunit	-1.06	0.432	1.08	0.291	-1.24	0.048	-1.33	0.182	-0.64
1425397_at	---	CDNA clone MGC:6909 IMAGE:2655941	-1.48	0.535	1.32	0.507	-1.21	0.576	-1.64	0.054	-0.75
1458371_at	E130006N16Rik	RIKEN cDNA E130006N16 gene	1.13	0.797	-1.21	0.485	-1.14	0.47	-1.36	0.218	-0.65
1423951_at	Tm2d3	TM2 domain containing 3	1.09	0.346	-1.12	0.27	-1.19	0.258	-1.41	0.059	-0.66
1448199_at	Ankrd10	ankyrin repeat domain 10	-1.22	0.028	1.16	0.535	-1.19	0.314	-1.53	0.056	-0.69
1439082_at	Ddx50	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	1.08	0.746	-1.16	0.683	-1.14	0.63	-1.15	0.646	-0.59
1427983_at	Suhw3	suppressor of hairy wing homolog 3 (Drosophila)	-1.15	0.293	1.05	0.557	-1.1	0.49	-1.09	0.789	-0.57
1447619_at	A830039H05Rik	RIKEN cDNA A830039H05 gene	-1.02	0.984	1.12	0.848	-1.38	0.71	-1.73	0.175	-0.75
1426478_at	Rasa1	RAS p21 protein activator 1	1.11	0.365	-1.3	0.449	-1.06	0.721	-1.16	0.453	-0.6
1455570_x_at	Cnn3	calponin 3, acidic	-1.08	0.531	1.14	0.456	-1.3	0.01	-2.56	0.071	-0.95
1445390_at	Pawr	PRKC, apoptosis, WT1, regulator	-1.26	0.568	1.44	0.285	-1.69	0.007	-1.05	0.897	-0.64
1420291_at	---	---	-1.72	0.394	1.67	0.219	-1.73	0.346	-1.2	0.785	-0.74
1437807_x_at	Ctnna1	catenin (cadherin associated protein), alpha 1	-1.1	0.592	1.09	0.454	-1.2	0.06	-1.05	0.688	-0.57
1417197_at	Wwc2	WW, C2 and coiled-coil domain containing 2	1.03	0.871	-1.2	0.71	-1.04	0.87	-1.39	0.521	-0.65
1449638_at	---	---	-1.52	0.211	1.35	0.445	-1.21	0.592	-1.07	0.889	-0.62
1451351_at	Ttc13	tetratricopeptide repeat domain 13	-1.12	0.146	1.03	0.852	-1.11	0.511	-1.19	0.16	-0.6
1439843_at	Camk4	calcium/calmodulin-dependent protein kinase IV	-1.03	0.953	1.18	0.406	-1.48	0.215	-3.67	0.048	-1.25

1448979_at	Muted	muted	-1.03	0.276	-1.04	0.658	-1.12	0.203	1.29	0.344	-0.48
1452045_at	Zfp281	zinc finger protein 281	1.01	0.869	-1.03	0.772	-1.19	0.23	-1.18	0.245	-0.6
1439092_at	Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	-1.03	0.944	1.03	0.937	-1.21	0.494	-1.35	0.137	-0.64
1454789_x_at	Prpf6	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	-1.15	0.629	-1.15	0.322	1.09	0.222	-1.38	0.125	-0.65
1444160_at	Pkd1l3	Polycystic kidney disease 1 like 3	-1.28	0.56	-1.45	0.329	1.36	0.382	-1.06	0.852	-0.61
1425740_at	---	---	-1.78	0.518	1.5	0.223	-1.3	0.33	-1.47	0.22	-0.76
1440967_at	Bri3 /// Baiap2l1	Brain protein I3 /// BAI1-associated protein 2-like 1	1.11	0.864	-1.11	0.735	-1.22	0.252	-1.61	0.167	-0.71
1445716_at	---	---	-1.28	0.159	-1.77	0.24	1.48	0.41	-2.03	0.118	-0.9
1455923_at	Kctd8	potassium channel tetramerisation domain containing 8	-1.17	0.752	1.03	0.948	-1.06	0.795	-1.46	0.334	-0.66
1452053_a_at	Tmem33	transmembrane protein 33	-1.02	0.843	-1.12	0.282	-1.05	0.642	1.44	0.276	-0.44
1420842_at	Ptprf	protein tyrosine phosphatase, receptor type, F	1	0.987	-1.01	0.75	-1.19	0.413	-1.04	0.861	-0.56
1441360_at	Rps6ka3	Ribosomal protein S6 kinase polypeptide 3	-1.03	0.771	1.17	0.707	-1.45	0.085	-1.26	0.594	-0.64
1446989_at	---	Transcribed locus	1.38	0.17	-1.1	0.845	-1.86	0.207	-2.01	0.439	-0.9
1439014_at	1600021P15Rik	RIKEN cDNA 1600021P15 gene	-1.06	0.874	1.21	0.329	-1.49	0.21	-2.97	0.092	-1.08
1448214_at	Pdhb /// LOC62000	pyruvate dehydrogenase (lipoamide) beta /// similar to pyruvate dehydrogenase (	-1.18	0.169	-1.22	0.264	1.16	0.362	-1.05	0.835	-0.57
1429781_s_at	Ccdc39	coiled-coil domain containing 39	1	0.995	-1.15	0.72	-1.04	0.881	-1.28	0.278	-0.62
1440234_at	1810012P15Rik	RIKEN cDNA 1810012P15 gene	-1.19	0.385	-1.01	0.981	-1	0.985	1.13	0.677	-0.52
1434647_at	AU040377	expressed sequence AU040377	1.38	0.018	-1.29	0.355	-1.49	0.204	-1.36	0.344	-0.69
1450932_s_at	Dock9 /// LOC6703	dedicator of cytokinesis 9 /// similar to Dedicator of cytokinesis protein 9 (Cdc42 g	-1.16	0.445	-1.06	0.633	1.02	0.935	-1.27	0.354	-0.62
1436402_at	Dohh	deoxyhypusine hydroxylase/monooxygenase	-1.4	0.112	-1.09	0.702	1.2	0.356	-1.51	0.053	-0.7
1439959_at	Fgf11	fibroblast growth factor 11	-1.08	0.749	-1.05	0.949	-1.05	0.788	1.13	0.436	-0.51
1449886_a_at	Timm9	translocase of inner mitochondrial membrane 9 homolog (yeast)	-1.14	0.742	-1.07	0.598	1.02	0.855	-1.21	0.54	-0.6
1441682_s_at	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	-1.05	0.666	-1.09	0.275	-1.04	0.603	1.07	0.615	-0.53
1449236_at	Dll3	delta-like 3 (Drosophila)	1.45	0.564	-2.16	0.263	-1.09	0.846	-1.3	0.432	-0.78
1425115_at	Rbbp6	retinoblastoma binding protein 6	-1.18	0.313	-1.14	0.504	1.1	0.518	-1.65	0.164	-0.72
1457562_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	1.53	0.137	-1.52	0.291	-1.57	0.001	-1.61	0.203	-0.79
1416151_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	-1.02	0.804	1.07	0.519	-1.28	0.003	-1.02	0.871	-0.56
1431600_at	4930564C03Rik	RIKEN cDNA 4930564C03 gene	-1.19	0.748	-1.26	0.748	1.19	0.442	-1.31	0.248	-0.64
1440964_s_at	AI465270	expressed sequence AI465270	-1.13	0.547	-1.07	0.698	1.01	0.925	-1.23	0.144	-0.61
1429610_a_at	Zfp511	zinc finger protein 511	1.03	0.763	-1.12	0.57	-1.1	0.33	-1.16	0.156	-0.59
1438930_s_at	Mecp2	methyl CpG binding protein 2	1.12	0.398	-1.11	0.584	-1.23	0.166	-1.06	0.837	-0.57
1454133_s_at	4930523O13Rik	RIKEN cDNA 4930523O13 gene	-1.24	0.537	-1.2	0.537	1.19	0.327	-1.52	0.181	-0.69
1453665_at	4930529M08Rik	RIKEN cDNA 4930529M08 gene	-1.67	0.086	-1.93	0.036	1.71	0.147	-1.1	0.854	-0.75
1446752_at	C78200	expressed sequence C78200	-1.04	0.875	-1.27	0.714	1.08	0.885	-1.43	0.645	-0.66
1440742_at	Epc1	Enhancer of polycomb homolog 1 (Drosophila)	-1.03	0.864	-1.23	0.379	1.05	0.677	-1.13	0.38	-0.59
1442557_at	Syt1	Synaptotagmin I	-2.79	0.027	-1.69	0.339	1.88	0.317	-1.14	0.809	-0.93
1444136_at	Rai12	Retinoic acid induced 12	-1.25	0.46	1.2	0.227	-1.21	0.407	-1.22	0.231	-0.62
1454682_at	A430005L14Rik	RIKEN cDNA A430005L14 gene	-1.04	0.408	-1.06	0.522	-1.07	0.394	1.75	0.232	-0.36
1424050_s_at	Fgfr1	fibroblast growth factor receptor 1	1.01	0.866	-1.07	0.759	-1.13	0.424	-1.04	0.84	-0.56
1437871_at	Pgm5	phosphoglucomutase 5	-1	0.995	1.01	0.991	-1.21	0.443	-2.51	0.347	-0.93
1448368_at	Dctn6	dynactin 6	-1.13	0.023	1.02	0.762	-1.08	0.326	-1.05	0.587	-0.56
1446397_at	Nup98	Nucleoporin 98	1.26	0.137	-1.2	0.543	-1.36	0.061	-1.2	0.453	-0.63
1455741_a_at	Ece1	endothelin converting enzyme 1	1.02	0.827	-1.04	0.601	-1.19	0.478	-1.08	0.702	-0.57
1454615_x_at	Srp14	signal recognition particle 14	-1.04	0.512	1.03	0.571	-1.19	0.152	-1.2	0.203	-0.6
1423733_a_at	Fiz1	Flt3 interacting zinc finger protein 1	-1.08	0.362	-1.16	0.04	1.04	0.37	-1.08	0.242	-0.57
1445330_at	Pdia3	protein disulfide isomerase associated 3	-1.47	0.155	1.24	0.303	-1.1	0.627	-1.09	0.686	-0.61
1432296_a_at	Itgav	integrin alpha V	-1.4	0.218	1.24	0.345	-1.13	0.755	-1.19	0.395	-0.62
1426655_a_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.12	0.466	-1.09	0.56	1.02	0.908	-1.07	0.787	-0.56
1457689_at	Sbf2	SET binding factor 2	-1.18	0.537	1.29	0.425	-1.45	0.143	-1.16	0.614	-0.62
1460324_at	Dnmt3a	DNA methyltransferase 3A	-1.25	0.277	-1.04	0.892	1.07	0.77	-1.28	0.387	-0.62
1424887_at	Klhdc4	kelch domain containing 4	-1.14	0.294	-1.08	0.598	1.03	0.835	-1.08	0.613	-0.57
1439352_at	Trim7	tripartite motif protein 7	-1.11	0.769	-1.76	0.073	1.36	0.512	-2.5	0.033	-1
1430755_at	4930452G13Rik	RIKEN cDNA 4930452G13 gene	1.46	0.564	-1.59	0.002	-1.35	0.013	-2.34	0.015	-0.96

1429821_at	2810046L04Rik	RIKEN cDNA 2810046L04 gene	-1.07	0.799	1.22	0.35	-1.49	0.228	-1.39	0.197	-0.68
1458505_at	LOC552901	hypothetical LOC552901	-1.26	0.705	1.52	0.141	-1.95	0.003	-1.22	0.345	-0.73
1442489_at	D1Ertd564e	DNA segment, Chr 1, ERATO Doi 564, expressed	1.35	0.413	-1.21	0.433	-1.53	0.109	-1.05	0.818	-0.61
1436596_at	H2afv	H2A histone family, member V	-1.03	0.713	-1.11	0.342	-1.04	0.833	1.37	0.324	-0.45
1428483_a_at	2610039C10Rik	RIKEN cDNA 2610039C10 gene	-1.08	0.848	1.04	0.768	-1.15	0.137	-1.03	0.812	-0.56
1444941_at	---	---	1.48	0.387	-1.2	0.332	-1.95	0.023	-1.08	0.839	-0.69
1418342_at	Recc1	replication factor C 1	1.13	0.419	-1.05	0.64	-1.34	0.07	-1.08	0.38	-0.58
1427896_at	2400003N08Rik	RIKEN cDNA 2400003N08 gene	-1.02	0.899	-1.1	0.464	-1.06	0.319	1.02	0.688	-0.54
1453877_at	4930467D21Rik	RIKEN cDNA 4930467D21 gene	1.11	0.643	-1.03	0.969	-1.33	0.269	-1.18	0.753	-0.61
1443346_at	---	---	-1.16	0.528	1.24	0.251	-1.38	0.221	-1.31	0.656	-0.65
1457121_at	AW822216	expressed sequence AW822216	-1.58	0.442	-1.01	0.976	1.21	0.523	-3.93	0.096	-1.33
1420717_at	A930018P22Rik	RIKEN cDNA A930018P22 gene	1.33	0.302	-1.16	0.729	-1.55	0.536	-1.61	0.381	-0.75
1452674_a_at	Eif3s12	eukaryotic translation initiation factor 3, subunit 12	1.04	0.778	-1.11	0.096	-1.13	0.448	-1.24	0.106	-0.61
1443945_at	C130073F10Rik	RIKEN cDNA C130073F10 gene	-1.01	0.99	1.1	0.75	-1.34	0.522	-1.95	0.275	-0.8
1457098_at	D2Ertd624e	DNA segment, Chr 2, ERATO Doi 624, expressed	1.24	0.486	-1.07	0.884	-1.53	0.019	-1.52	0.517	-0.72
1455155_at	Lsm14b	LSM14 homolog B (SCD6, S. cerevisiae)	-1.09	0.05	-1.21	0.214	1.09	0.749	-1.38	0.158	-0.65
1423741_at	Rbm10	RNA binding motif protein 10	-1.13	0.698	-1.09	0.407	1.03	0.836	-1.11	0.304	-0.58
1418964_at	Pigm	phosphatidylinositol glycan anchor biosynthesis, class M	1.05	0.766	-1.09	0.75	-1.15	0.268	-1.19	0.188	-0.6
1419716_a_at	Pou2f1	POU domain, class 2, transcription factor 1	1.06	0.657	-1.1	0.461	-1.16	0.506	-1.26	0.197	-0.62
1450140_a_at	Cdkn2a	cyclin-dependent kinase inhibitor 2A	-1.94	0.078	-1.21	0.687	1.49	0.039	-1.2	0.661	-0.72
1418687_at	Arc	activity regulated cytoskeletal-associated protein	1.05	0.941	-1.08	0.775	-1.17	0.624	-1.13	0.667	-0.58
1425702_a_at	Enpp5	ectonucleotide pyrophosphatase/phosphodiesterase 5	-1.25	0.238	-1.12	0.374	1.14	0.368	-1.31	0.253	-0.63
1419659_s_at	Chic2	cysteine-rich hydrophobic domain 2	-1.07	0.2	-1.11	0.194	1	0.998	-1.07	0.354	-0.56
1418672_at	Akr1c13	aldo-keto reductase family 1, member C13	1.02	0.937	-1.17	0.226	-1.04	0.853	-1.1	0.689	-0.57
1433277_at	D730048A03Rik	RIKEN cDNA D730048A03 gene	1.41	0.659	-1.41	0.551	-1.4	0.351	-1.37	0.316	-0.69
1454559_at	5430437A18Rik	RIKEN cDNA 5430437A18 gene	-3.4	0.103	1.59	0.344	-1.05	0.909	-2.04	0.07	-1.23
1451256_at	Gpr172b	G protein-coupled receptor 172B	-1.12	0.612	-1	0.997	-1.06	0.775	1.23	0.181	-0.49
1432494_a_at	1700019E19Rik	RIKEN cDNA 1700019E19 gene	-1.15	0.277	-1.05	0.697	1.01	0.964	-1.56	0.143	-0.69
1435807_at	Cdc42	cell division cycle 42 homolog (S. cerevisiae)	-1.09	0.623	-1.16	0.742	1.05	0.887	-1.37	0.317	-0.64
1417371_at	Peli1	pellino 1	1.04	0.406	-1.06	0.503	-1.18	0.046	-1.94	0.022	-0.79
1454123_at	4933406K04Rik	RIKEN cDNA 4933406K04 gene	-1.36	0.459	1.55	0.224	-1.81	0.053	-1.79	0.059	-0.85
1427410_at	Dleu2	deleted in lymphocytic leukemia, 2	1.13	0.485	-1.01	0.934	-1.4	0.116	-1.27	0.117	-0.64
1418646_at	Gna-rs1	guanine nucleotide binding protein, related sequence 1	-1.15	0.536	-1.1	0.62	1.05	0.736	-1.55	0.063	-0.69
1456019_at	Cwf19l2	CWF19-like 2, cell cycle control (S. pombe)	-1.04	0.665	1.06	0.419	-1.23	0.122	-1.34	0.244	-0.64
1457875_at	Hcfc1	host cell factor C1	-1.88	0.449	-2.13	0.367	1.83	0.205	-1.07	0.655	-0.81
1420613_at	Ptp4a2	protein tyrosine phosphatase 4a2	1.1	0.585	-1.11	0.021	-1.19	0.067	-1.3	0.167	-0.63
1425011_x_at	Stx18	syntaxin 18	1.04	0.745	-1.14	0.442	-1.09	0.338	-1.37	0.167	-0.64
1423993_at	Atp6v1f	ATPase, H+ transporting, lysosomal V1 subunit F	-1.16	0.291	1.02	0.709	-1.05	0.751	-1.25	0.361	-0.61
1417186_at	Hip2	huntingtin interacting protein 2	-1.03	0.692	-1.03	0.721	-1.12	0.187	1.07	0.564	-0.53
1424366_at	Tmem15	transmembrane protein 15	-1.01	0.947	-1.2	0.093	1.01	0.941	-1.01	0.935	-0.55
1437454_a_at	Txndc14 /// LOC43	thioredoxin domain containing 14 /// similar to thioredoxin-related transmembrane	1.01	0.843	-1.05	0.594	-1.16	0.211	-1.16	0.346	-0.59
1418730_at	Rnf12	ring finger protein 12	-1.53	0.007	1.22	0.284	-1.04	0.804	-1.07	0.71	-0.6
1439595_at	A430107P09Rik	RIKEN cDNA A430107P09 gene	-1.01	0.986	-1.3	0.694	1.08	0.73	-1.88	0.196	-0.78
1456875_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	-1.06	0.757	1.02	0.911	-1.14	0.09	-1.05	0.51	-0.56
1416856_at	3230401D17Rik	RIKEN cDNA 3230401D17 gene	1	0.945	-1.05	0.498	-1.14	0.131	-1.21	0.009	-0.6
1438649_x_at	Pebp1	phosphatidylethanolamine binding protein 1	-1.01	0.672	-1.11	0.491	-1.06	0.378	1.07	0.141	-0.53
1429118_a_at	4930429M06Rik	RIKEN cDNA 4930429M06Rik	-1.11	0.436	-1.31	0.396	1.17	0.582	-1.12	0.606	-0.59
1424914_at	---	---	-1.1	0.785	-1.08	0.728	1.01	0.983	-1.25	0.584	-0.61
1424329_a_at	Prrg2	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	1.06	0.63	-1.14	0.35	-1.11	0.162	-1	0.987	-0.55
1442347_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	-1.18	0.602	-1.75	0.515	1.42	0.364	-1.36	0.244	-0.72
1453557_at	4930562F07Rik	RIKEN cDNA 4930562F07 gene	-1.39	0.501	1.29	0.653	-1.2	0.658	-2.15	0.013	-0.87
1429939_at	Saps3	SAPS domain family, member 3	-1.09	0.594	-1.42	0.412	1.21	0.526	-1.32	0.25	-0.65
1420976_at	Man1a2	mannosidase, alpha, class 1A, member 2	-1.3	0.275	-1.05	0.923	1.11	0.723	-1.62	0.259	-0.72

1445307_at	Auts2	Autism susceptibility candidate 2	-1.09	0.751	1.39	0.575	-1.9	0.055	-2.26	0.148	-0.96
1426723_at	Wdr48	WD repeat domain 48	-1.1	0.523	-1.08	0.421	1	0.952	-1.14	0.055	-0.58
1436189_at	Nqo2	NAD(P)H dehydrogenase, quinone 2	-1.01	0.867	1.06	0.745	-1.27	0.108	-1.1	0.654	-0.58
1444326_at	P4hb	Prolyl 4-hydroxylase, beta polypeptide	1.27	0.343	-1.14	0.837	-1.46	0.037	-1.18	0.63	-0.63
1422509_at	U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	-1.23	0.397	-1.19	0.155	1.19	0.146	-1.08	0.751	-0.58
1438562_a_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	-1.05	0.826	1.02	0.818	-1.15	0.205	-1.09	0.652	-0.57
1434872_x_at	Rpl37 /// LOC3834	ribosomal protein L37 /// similar to ribosomal protein L37	-1.06	0.545	1.1	0.531	-1.27	0.072	-1.3	0.039	-0.63
1416960_at	B3gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	1.28	0.345	-1.19	0.04	-1.39	0.047	-1.01	0.927	-0.58
1455379_at	Dnali1	dynein, axonemal, light intermediate polypeptide 1	-1.72	0.573	-1.13	0.715	1.37	0.229	-1.8	0.345	-0.82
1452448_at	Aqr	aquarius	-1.25	0.607	-2.01	0.374	1.54	0.585	-1.11	0.875	-0.71
1422495_a_at	Hmgn1	high mobility group nucleosomal binding domain 1	-1.07	0.31	1.06	0.327	-1.2	0.059	-1.54	0.051	-0.68
1428789_at	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	1.07	0.518	-1.22	0.387	-1.06	0.807	-2.57	0.077	-0.94
1428297_at	Map4k2	mitogen activated protein kinase kinase kinase kinase 2	-1.43	0.135	-1.23	0.479	1.33	0.301	-2.14	0.034	-0.87
1436054_at	9130227C08Rik	RIKEN cDNA 9130227C08Rik gene	-1.58	0.07	-1.02	0.93	1.23	0.465	-1.12	0.785	-0.63
1455359_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	-1.15	0.179	-1.06	0.634	1.03	0.848	-1.12	0.702	-0.58
1459888_at	LOC545261	hypothetical protein LOC545261	-1.01	0.966	1.19	0.25	-1.51	0.013	-1.28	0.15	-0.65
1427287_s_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	-1.28	0.102	-1.29	0.114	1.28	0.191	-1.79	0.137	-0.77
1415794_a_at	Spin	spindlin	-1.07	0.529	1.04	0.784	-1.16	0.196	-1.59	0.078	-0.7
1451121_a_at	Gltscr2	glioma tumor suppressor candidate region gene 2	-1.14	0.176	-1.17	0.016	1.1	0.152	-1.89	0.085	-0.77
1416632_at	Mod1 /// LOC62489	malic enzyme, supernatant /// similar to NADP-dependent malic enzyme (NADP-M	-1.31	0.03	-1.72	0.164	1.49	0.408	-1.11	0.865	-0.66
1433887_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	-1.11	0.439	1.11	0.497	-1.22	0.227	-1.3	0.266	-0.63
1417064_at	Jagn1	jagunal homolog 1 (Drosophila)	-1.01	0.955	-1.2	0.044	1.01	0.922	-1.02	0.903	-0.55
1417473_a_at	Ppcs	phosphopantothenoylcysteine synthetase	1.02	0.955	-1.21	0.138	-1.01	0.979	-1.71	0.079	-0.73
1445363_at	2810055G20Rik	RIKEN cDNA 2810055G20 gene	-1.03	0.944	1.18	0.467	-1.46	0.087	-2	0.061	-0.83
1460201_a_at	Rpl24 /// LOC66882	ribosomal protein L24 /// similar to ribosomal protein L24 /// similar to ribosomal pr	-1.06	0.098	1.03	0.53	-1.16	0.05	-1.32	0.015	-0.63
1459798_x_at	4732479N06Rik	RIKEN cDNA 4732479N06 gene	-1.37	0.707	-1.44	0.615	1.41	0.448	-2.34	0.303	-0.93
1428737_s_at	Gramd3	GRAM domain containing 3	-1.24	0.152	-1.18	0.105	1.18	0.323	-2.06	0.091	-0.83
1455413_at	Zfp11	zinc finger protein 11	-1.16	0.612	-1.07	0.804	1.04	0.86	-1.1	0.363	-0.57
1437376_at	Adam32	a disintegrin and metallopeptidase domain 32	1.12	0.884	-1.09	0.89	-1.25	0.508	-1.07	0.905	-0.57
1437439_at	2410089E03Rik	RIKEN cDNA 2410089E03 gene	1.18	0.308	-1.09	0.795	-1.35	0.347	-1.17	0.573	-0.61
1434456_at	Gm440	gene model 440, (NCBI)	-1.15	0.082	-1.04	0.916	1	0.989	-2.35	0.094	-0.88
1422785_at	Rasa2	RAS p21 protein activator 2	1.05	0.83	-1.04	0.669	-1.21	0.09	-1.98	0.026	-0.79
1452252_at	Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast)	-1.4	0.457	1.15	0.595	-1.02	0.921	-1.16	0.05	-0.61
1443244_at	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	-1.25	0.388	-1.19	0.305	1.19	0.4	-1.02	0.944	-0.57
1443158_at	Scmh1	Sex comb on midleg homolog 1	-1.06	0.893	1.16	0.682	-1.37	0.183	-1.53	0.105	-0.7
1438049_at	A430108E01Rik	RIKEN cDNA A430108E01 gene	1.15	0.123	-1.16	0.318	-1.2	0.025	-1.28	0.384	-0.62
1437666_x_at	Ubc	ubiquitin C	-1.15	0.068	-1.15	0.31	1.1	0.267	-1.01	0.826	-0.55
1448651_at	Nudt5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	-1.08	0.516	-1.09	0.523	-1.01	0.908	1.38	0.275	-0.45
1441955_s_at	Paip1 /// LOC67667	polyadenylate binding protein-interacting protein 1 /// similar to poly(A) binding pro	-1.18	0.59	1.13	0.669	-1.17	0.524	-2.05	0.003	-0.82
1434165_at	Clic6	chloride intracellular channel 6	-1.83	0.049	-1.59	0.246	1.66	0.143	-1.61	0.012	-0.84
1455245_x_at	Rpl13	ribosomal protein L13	-1.02	0.569	1.09	0.058	-1.3	0.008	-1.38	0.02	-0.65
1454707_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	-1.17	0.123	1.12	0.608	-1.16	0.513	-1.27	0.084	-0.62
1436323_at	2810001A02Rik	RIKEN cDNA 2810001A02 gene	1.06	0.418	-1.18	0.156	-1.08	0.596	-1.09	0.371	-0.57
1460433_at	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	-1.3	0.223	-1.31	0.044	1.31	0.203	-1	0.977	-0.58
1458268_s_at	Igfbp3	insulin-like growth factor binding protein 3	-1.15	0.297	1.33	0.288	-1.57	0.154	-1.72	0.282	-0.78
1438209_at	4632404H12Rik	RIKEN cDNA 4632404H12 gene	1.14	0.415	-1.27	0.367	-1.1	0.521	-1.14	0.663	-0.59
1458591_at	Rasef	RAS and EF hand domain containing	-1.3	0.366	1.44	0.55	-1.58	0.072	-1.07	0.593	-0.63
1415686_at	Rab14	RAB14, member RAS oncogene family	-1.16	0.128	-1.03	0.676	1.01	0.973	-1	0.991	-0.55
1420494_x_at	Ubc	ubiquitin C	-1.2	0.368	-1.16	0.255	1.15	0.1	-1.02	0.836	-0.56
1453852_at	8430408E17Rik	RIKEN cDNA 8430408E17 gene	1.13	0.172	-1.12	0.336	-1.22	0.334	-1.21	0.174	-0.61
1416912_at	6330407G11Rik	RIKEN cDNA 6330407G11 gene	-1.23	0.226	1.08	0.661	-1.06	0.269	-1.13	0.547	-0.58
1417071_s_at	Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	1.36	0.04	-1.54	0.086	-1.21	0.162	-1.22	0.447	-0.65
1429185_at	4631416L12Rik	RIKEN cDNA 4631416L12 gene	-1.13	0.709	1.06	0.803	-1.12	0.333	-1.22	0.153	-0.6

1451068_s_at	Rps25	ribosomal protein S25	1.03	0.641	-1.05	0.414	-1.18	0.086	-1.37	0.019	-0.64
1450262_at	Clcf1	cardiotrophin-like cytokine factor 1	-1.13	0.82	1.07	0.806	-1.13	0.57	-2.24	0.169	-0.86
1433683_at	Rbm35b	RNA binding motif protein 35b	-1.11	0.346	-1.08	0.331	1.01	0.898	-1.69	0.37	-0.72
1437144_x_at	Psma6	proteasome (prosome, macropain) subunit, alpha type 6	-1.05	0.566	1.08	0.147	-1.24	0.113	-1.17	0.09	-0.6
1456678_at	Scap1	Src family associated phosphoprotein 1	-1.16	0.811	1.16	0.763	-1.23	0.651	-2.13	0.06	-0.84
1431698_at	Ubash3a	ubiquitin associated and SH3 domain containing, A	-1.13	0.285	-1.14	0.79	1.08	0.86	-1.86	0.158	-0.76
1458706_at	2610035D17Rik	RIKEN cDNA 2610035D17 gene	-1.11	0.545	1.14	0.79	-1.27	0.18	-1.91	0.137	-0.78
1435253_at	Rab11b	RAB11B, member RAS oncogene family	-1.06	0.842	1.11	0.73	-1.26	0.215	-1.06	0.486	-0.57
1459586_at	C78452	expressed sequence C78452	-1.4	0.237	-1.82	0.344	1.58	0.134	-1.28	0.364	-0.73
1431177_a_at	Rpl10a	ribosomal protein L10A	-1.06	0.528	1.02	0.577	-1.14	0.23	-1.51	0.123	-0.67
AFFX-r2-Bs-lys-3_at	---	---	1.06	0.926	-1.21	0.37	-1.05	0.878	-1.48	0.463	-0.67
1458241_at	Hmga2	High mobility group AT-hook 2	-1.91	0.197	1.49	0.46	-1.22	0.513	-2.3	0.338	-0.98
1453247_at	Zfp618 /// LOC667	zinc fingerprotein 618 /// similar to zinc finger protein 618	-1.22	0.338	-1.08	0.744	1.09	0.652	-1.32	0.666	-0.63
1451356_at	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-1.06	0.566	-1.09	0.231	-1.02	0.694	1.64	0.162	-0.38
1439883_at	Ncoa1	Nuclear receptor coactivator 1	-1.24	0.442	-1.95	0.001	1.52	0.449	-2.03	0.541	-0.93
1428547_at	Nt5e	5' nucleotidase, ecto	1.06	0.767	-1.14	0.347	-1.12	0.555	-1.13	0.765	-0.58
1439989_at	Tsc1	tuberous sclerosis 1	-1.04	0.755	-1.02	0.961	-1.11	0.376	1.05	0.744	-0.53
1451427_a_at	Egfl7	EGF-like domain 7	1	0.992	-1.02	0.878	-1.17	0.221	-1.04	0.532	-0.56
1443773_at	Ylpm1	YLP motif containing 1	1.05	0.829	-1.11	0.261	-1.12	0.554	-1.03	0.85	-0.55
1448599_s_at	D4Wsu114e	DNA segment, Chr 4, Wayne State University 114, expressed	-1.17	0.333	-1.09	0.64	1.07	0.604	-1.35	0.02	-0.64
1419971_s_at	Slc35a5	solute carrier family 35, member A5	-1.03	0.676	1.04	0.652	-1.2	0.218	-1.34	0.159	-0.63
1433636_at	Bms1l	BMS1-like, ribosome assembly protein (yeast)	-1.04	0.741	-1.28	0.208	1.09	0.488	-1.3	0.318	-0.63
1446586_at	8030463A06Rik	RIKEN cDNA 8030463A06 gene	-1.31	0.565	1.12	0.566	-1.05	0.931	-1.19	0.431	-0.61
1440488_at	---	---	1.34	0.358	-1.36	0.135	-1.3	0.089	-1.1	0.804	-0.61
1419821_s_at	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	-1.29	0.203	1.09	0.199	-1.03	0.887	-1.57	0.105	-0.7
1421801_at	---	---	-1.23	0.186	1.08	0.754	-1.05	0.673	-1.29	0.356	-0.63
1429959_at	---	---	1.18	0.328	-1.06	0.633	-1.39	0.306	-1.27	0.455	-0.64
1456373_x_at	Rps20	ribosomal protein S20	-1.04	0.573	1.09	0.453	-1.27	0.023	-1.28	0.015	-0.62
1460194_at	Phyh	phytanoyl-CoA hydroxylase	-1.26	0.071	-1.4	0.118	1.33	0.082	-1.35	0.194	-0.67
1441451_at	Brwd3	bromodomain and WD repeat domain containing 3	1.83	0.546	-2.36	0.238	-1.69	0.114	-1	0.997	-0.81
1438946_at	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	1.47	0.502	-1.72	0.161	-1.27	0.045	-1.25	0.539	-0.69
1428050_a_at	Tmbim4	transmembrane BAX inhibitor motif containing 4	-1.07	0.78	-1.05	0.647	-1.05	0.709	1.43	0.107	-0.44
1436626_at	Tspan11	tetraspanin 11	1.23	0.722	-1.52	0.039	-1.04	0.862	-1.24	0.734	-0.64
1423254_x_at	Rps27l	ribosomal protein S27-like	-1.06	0.299	-1.06	0.345	-1.05	0.749	1.2	0.285	-0.49
1416350_at	Klf16	Kruppel-like factor 16	-1.18	0.63	-1.1	0.859	1.09	0.568	-1.09	0.82	-0.57
1431694_a_at	Ctnnbip1	catenin beta interacting protein 1	-1.15	0.673	1.07	0.534	-1.11	0.465	-1.04	0.847	-0.56
1437992_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.32	0.279	1.38	0.15	-1.41	0.256	-1.62	0.072	-0.75
1459418_at	2810457I06Rik	RIKEN cDNA 2810457I06 gene	1.25	0.714	-1.2	0.54	-1.32	0.702	-1.25	0.608	-0.63
1420785_at	Gab2	growth factor receptor bound protein 2-associated protein 2	-1.18	0.577	1.05	0.286	-1.06	0.855	-1.03	0.742	-0.56
1456489_at	Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	1.34	0.256	-1.53	0.108	-1.18	0.589	-1.34	0.337	-0.68
1430889_a_at	Tpmt	thiopurine methyltransferase	-1.01	0.918	1.13	0.585	-1.39	0.197	-1.41	0.356	-0.67
1440852_at	4833405L16Rik	RIKEN cDNA 4833405L16 gene	1.59	0.53	-2.6	0.153	-1.15	0.754	-1.01	0.972	-0.79
1435284_at	Rtn4	reticulon 4	-1.01	0.939	1.25	0.324	-1.66	0.038	-1.45	0.178	-0.72
1425942_a_at	Gpm6b	glycoprotein m6b	-1.08	0.655	1.16	0.481	-1.31	0.262	-1.51	0.195	-0.69
1423729_a_at	2500002L14Rik	RIKEN cDNA 2500002L14 gene	1	0.977	-1.05	0.644	-1.13	0.032	-1.13	0.544	-0.58
1420688_a_at	Sgce	sarcoglycan, epsilon	1.07	0.352	-1.04	0.752	-1.23	0.232	-1.07	0.695	-0.57
1434457_at	Sp100	nuclear antigen Sp100	-1.11	0.663	-1.12	0.674	1.05	0.78	-1.94	0.113	-0.78
1448587_at	Tbc1d10a	TBC1 domain family, member 10a	-1.14	0.065	1.09	0.726	-1.15	0.243	-1.73	0.048	-0.73
1436567_a_at	Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	-1.07	0.221	-1.19	0.159	1.07	0.76	-1.26	0.421	-0.61
1459135_at	Dcps	Decapping enzyme, scavenger	1.1	0.711	-1.27	0.338	-1.05	0.778	-1.08	0.432	-0.57
1460738_at	Limd2	LIM domain containing 2	1.29	0.728	-1.43	0.379	-1.17	0.567	-3.38	0.092	-1.17
1438343_at	0610037L13Rik	RIKEN cDNA 0610037L13 gene	-1.09	0.542	1.41	0.359	-1.96	0.232	-1.39	0.034	-0.76
1441383_at	1500002O10Rik	RIKEN cDNA 1500002O10 gene	-1.57	0.146	1.38	0.156	-1.21	0.336	-1.67	0.281	-0.77

1433576_at	Mat2a	methionine adenosyltransferase II, alpha	1.13	0.758	-1.12	0.632	-1.22	0.399	-1.01	0.878	-0.56
1422463_a_at	Mrpl3	mitochondrial ribosomal protein L3	-1.21	0.213	-1.12	0.217	1.12	0.418	-1.09	0.6	-0.58
1420821_at	Sgpp1	sphingosine-1-phosphate phosphatase 1	-1.25	0.358	1.06	0.669	-1.01	0.689	-1.05	0.73	-0.56
1416635_at	Smpdl3a	sphingomyelin phosphodiesterase, acid-like 3A	-1.18	0.121	1.1	0.142	-1.12	0.338	-1.61	0.201	-0.7
1415758_at	Fryl	furry homolog-like (Drosophila)	-1.1	0.301	-1.06	0.465	-1.01	0.907	1.41	0.127	-0.44
1449755_at	D7Ertd183e	DNA segment, Chr 7, ERATO Doi 183, expressed	-1.19	0.06	1.36	0.37	-1.56	0.059	-1.95	0.048	-0.84
1446663_at	Camk2d	Calcium/calmodulin-dependent protein kinase II, delta	1.02	0.955	-1.15	0.745	-1.05	0.888	-1.97	0.262	-0.79
1429564_at	Pcgf5	polycomb group ring finger 5	-1.07	0.761	-1.03	0.477	-1.07	0.432	1.43	0.299	-0.43
1457267_at	---	---	-1.09	0.382	-1.27	0.315	1.14	0.261	-1.14	0.428	-0.59
1459626_at	---	Transcribed locus	-1.06	0.642	-1.06	0.863	-1.05	0.787	1.01	0.938	-0.54
1444776_at	2700005E23Rik	RIKEN cDNA 2700005E23 gene	-1.11	0.854	-1.33	0.426	1.19	0.632	-1.81	0.121	-0.76
1459166_at	---	---	-1.09	0.775	-1.04	0.851	-1.04	0.813	1.22	0.067	-0.49
1429887_at	2310005C01Rik	RIKEN cDNA 2310005C01 gene	-1.77	0.135	1.47	0.46	-1.23	0.328	-1.18	0.44	-0.68
1434017_at	---	---	-1.11	0.178	-1.11	0.164	1.03	0.839	-1.46	0.28	-0.66
1439174_at	Unc5c	Unc-5 homolog C (C. elegans)	-1.14	0.723	1.05	0.918	-1.1	0.659	-2.38	0.152	-0.89
1438546_x_at	Slc25a5 /// LOC433	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.18	0.178	-1.14	0.232	1.11	0.416	-1	0.984	-0.55
1425422_a_at	Parn	poly(A)-specific ribonuclease (deadenylation nuclease)	-1.22	0.472	-1.1	0.107	1.12	0.394	-1.04	0.829	-0.56
1419364_a_at	Rps7 /// LOC62169	ribosomal protein S7 /// similar to 40S ribosomal protein S7 (S8) /// similar to 40S	-1.09	0.121	1.06	0.124	-1.16	0.175	-1.29	0.005	-0.62
1420485_at	Nol7	nucleolar protein 7	-1.04	0.187	-1.05	0.772	-1.08	0.568	1.01	0.932	-0.54
1430038_at	Gphn	gephyrin	-1.11	0.203	-1.26	0.037	1.15	0.359	-1.46	0.032	-0.67
1439296_at	---	---	1.09	0.871	-1.06	0.931	-1.24	0.552	-1.24	0.395	-0.61
1446044_at	AU015581	expressed sequence AU015581	1.43	0.402	-1.58	0.493	-1.28	0.682	-1.41	0.676	-0.71
1453400_at	4933428D01Rik	RIKEN cDNA 4933428D01 gene	-1.44	0.386	-1.36	0.592	1.41	0.32	-2.65	0.032	-1.01
1447614_at	Slfn1	Schlafen 1	-1.19	0.828	1.05	0.94	-1.05	0.943	-1.02	0.969	-0.55
1426209_at	Strn4	striatin, calmodulin binding protein 4	-1.22	0.523	1.1	0.446	-1.08	0.563	-1.14	0.015	-0.58
1456083_x_at	Eif3s8	eukaryotic translation initiation factor 3, subunit 8	1.04	0.592	-1.2	0.022	-1.03	0.641	-1.12	0.341	-0.58
1435774_at	AV024533	expressed sequence AV024533	1.11	0.724	-1.07	0.802	-1.26	0.17	-1.21	0.399	-0.61
1446579_at	---	---	1.09	0.838	-1.04	0.932	-1.27	0.499	-1.47	0.348	-0.67
1429568_x_at	Ube2f	ubiquitin-conjugating enzyme E2F (putative)	-1.02	0.765	-1.08	0.515	-1.07	0.609	1.04	0.824	-0.53
1455792_x_at	Ndn	necdin	1.29	0.023	-1.18	0.409	-1.42	0.195	-1.54	0.199	-0.71
1421060_at	Mllt1	myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosoph	-1.27	0.627	-1.83	0.294	1.51	0.512	-1.12	0.783	-0.68
1436584_at	Spry2	sprouty homolog 2 (Drosophila)	-1.03	0.876	1.18	0.576	-1.44	0.111	-1.1	0.625	-0.6
1448677_at	Cox4nb	COX4 neighbor	-1.03	0.787	-1.06	0.591	-1.08	0.492	1.28	0.244	-0.47
1431584_at	1110028F18Rik	RIKEN cDNA 1110028F18 gene	-1.43	0.463	1.21	0.517	-1.06	0.872	-2.29	0.246	-0.9
1436185_at	AI314180	expressed sequence AI314180	-1.11	0.637	1.09	0.648	-1.17	0.361	-1.33	0.22	-0.63
1435376_at	Ddhd2	DDHD domain containing 2	-1.01	0.866	-1.12	0.197	-1.04	0.829	1.01	0.979	-0.54
1449668_s_at	A730024A03Rik	RIKEN cDNA A730024A03 gene	-1.16	0.494	-1.05	0.671	1.03	0.794	-1.13	0.441	-0.58
1436788_at	---	---	1.03	0.862	-1.04	0.654	-1.17	0.304	-1.07	0.853	-0.56
1434636_at	Homez	homeodomain leucine zipper-encoding gene	-1.09	0.56	-1.12	0.639	1.03	0.734	-1.18	0.217	-0.59
1454066_at	Mina	myc induced nuclear antigen	-1.77	0.146	1.3	0.184	-1.02	0.942	-1.33	0.259	-0.71
1447573_at	Slc32a1	Solute carrier family 32 (GABA vesicular transporter), member 1	-1.11	0.451	-1.13	0.732	1.06	0.355	-1.09	0.327	-0.57
1432152_at	2610109H07Rik	RIKEN cDNA 2610109H07 gene	1.43	0.081	-1.24	0.263	-1.64	0.496	-1.36	0.604	-0.7
1453343_s_at	Vrk2	vaccinia related kinase 2	-1.34	0.057	1.15	0.219	-1.06	0.651	-1.06	0.643	-0.58
1436378_at	Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	-1.07	0.62	-1.03	0.828	-1.06	0.798	1.26	0.409	-0.48
1441611_at	Zdhhc6 /// LOC669	zinc finger, DHHC domain containing 6 /// similar to Probable palmitoyltransferase	1.29	0.665	-1.07	0.837	-1.6	0.187	-1.17	0.653	-0.64
1422071_at	Lgals6	lectin, galactose binding, soluble 6	-1.31	0.658	-2.27	0.019	1.64	0.228	-1.33	0.65	-0.82
1460140_at	Cd2ap	CD2-associated protein	1.12	0.881	-1.04	0.952	-1.31	0.373	-1.06	0.831	-0.57
1434419_s_at	Tardbp	TAR DNA binding protein	-1.1	0.637	-1.25	0.276	1.14	0.638	-1.26	0.512	-0.62
1438931_s_at	Sesn1	sestrin 1	-1.2	0.625	1.1	0.636	-1.1	0.655	-1.82	0.045	-0.76
1451736_a_at	Map2k7	mitogen activated protein kinase kinase 7	-1.1	0.086	1.05	0.635	-1.13	0.352	-1.12	0.576	-0.57
1446617_at	St8sia4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	-1.1	0.408	-1.09	0.799	1.02	0.928	-1.52	0.446	-0.67
1448446_at	Deaf1	deformed epidermal autoregulatory factor 1 (Drosophila)	-1.11	0.698	-1.23	0.298	1.13	0.614	-1.06	0.671	-0.57
1449947_s_at	Atbf1	AT motif binding factor 1	1.02	0.958	-1.1	0.793	-1.09	0.782	-1.01	0.974	-0.55

1443141_at	---	---	-1.59	0.493	1.26	0.106	-1.04	0.766	-1.23	0.273	-0.65
1447146_s_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	-1.18	0.035	1.02	0.8	-1.02	0.906	-1.1	0.515	-0.57
1451665_a_at	Ap4s1	adaptor-related protein complex AP-4, sigma 1	-1.17	0.335	1.03	0.675	-1.04	0.68	-1.25	0.224	-0.61
1430869_a_at	Hoxc13 /// Habp4 //	homeo box C13 /// hyaluronic acid binding protein 4 /// similar to hyaluronic acid b	-1.07	0.807	-1.11	0.779	1.01	0.982	-1.07	0.821	-0.56
1425565_at	Rest	RE1-silencing transcription factor	1.02	0.91	-1.13	0.499	-1.07	0.728	-1.3	0.401	-0.62
1419562_at	Birc6	baculoviral IAP repeat-containing 6	-1.18	0.244	1.07	0.474	-1.08	0.579	-1.14	0.482	-0.58
1437573_at	---	Mus musculus, clone IMAGE:3493537, mRNA	1.26	0.205	-1.26	0.405	-1.27	0.081	-1.63	0.108	-0.72
1419703_at	Col5a3	procollagen, type V, alpha 3	-1.13	0.497	1.06	0.669	-1.11	0.484	-1.21	0.018	-0.6
1457989_at	Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	1.37	0.587	-1.03	0.936	-1.98	0.243	-2.77	0.113	-1.1
1416385_a_at	M6pr	mannose-6-phosphate receptor, cation dependent	-1.1	0.382	1.02	0.473	-1.1	0.504	-1.21	0.459	-0.6
1438864_at	C920006C10Rik	RIKEN cDNA C920006C10 gene	1.05	0.64	-1.14	0.344	-1.09	0.564	-1.5	0.256	-0.67
1450880_at	Mrpl16	mitochondrial ribosomal protein L16	-1.09	0.02	-1.1	0.145	1.02	0.845	-1.02	0.893	-0.55
1458989_at	Limk1	LIM-domain containing, protein kinase	1.24	0.549	-1.05	0.919	-1.53	0.533	-1.4	0.349	-0.68
1456769_at	Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	-1.1	0.772	-1	0.985	-1.06	0.691	1.19	0.397	-0.49
1424628_a_at	1500032D16Rik	RIKEN cDNA 1500032D16 gene	-1.08	0.416	-1.04	0.434	-1.04	0.602	1.09	0.377	-0.52
1416257_at	Capn2	calpain 2	-1	0.99	-1.17	0.006	-1.01	0.959	1.02	0.907	-0.54
1458118_at	D2Ertd391e	DNA segment, Chr 2, ERATO Doi 391, expressed	1.46	0.176	-1.28	0.693	-1.66	0.174	-2.03	0.015	-0.88
1443822_s_at	---	---	-1.08	0.634	-1.19	0.289	1.08	0.614	-1	0.992	-0.55
1452276_at	Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subf	-1.05	0.067	-1.02	0.837	-1.1	0.236	1.1	0.565	-0.52
1417883_at	Gstt2	glutathione S-transferase, theta 2	-1.06	0.699	-1.41	0.254	1.19	0.173	-1.3	0.137	-0.64
1433710_at	Edc3	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	1.15	0.486	-1.15	0.377	-1.21	0.402	-1.3	0.131	-0.63
1454676_s_at	Ticam1	toll-like receptor adaptor molecule 1	-1.21	0.538	-1.11	0.515	1.12	0.668	-1.36	0.122	-0.64
1416438_at	2410104I19Rik	RIKEN cDNA 2410104I19 gene	1.01	0.934	-1.16	0.061	-1.02	0.832	-1.24	0.355	-0.6
1431565_at	4930511J24Rik	RIKEN cDNA 4930511J24 gene	1.73	0.296	-2.63	0.373	-1.35	0.553	-1.8	0.415	-1.02
1431448_at	4930474N09Rik	RIKEN cDNA 4930474N09 gene	-1.16	0.72	-1.28	0.308	1.2	0.744	-1.83	0.493	-0.77
1433074_at	4931412I15Rik	RIKEN cDNA 4931412I15 gene	-1.14	0.488	1.01	0.94	-1.05	0.489	-1.8	0.448	-0.74
1435366_at	D430042O09Rik	RIKEN cDNA D430042O09 gene	-1.36	0.254	-1.23	0.527	1.29	0.54	-1.61	0.184	-0.73
1417438_at	Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	-1.14	0.385	-1.13	0.048	1.08	0.364	-1.48	0.048	-0.67
1447842_x_at	Tcn2	Transcobalamin 2	-1.2	0.011	1.06	0.087	-1.06	0.735	-1.79	0.187	-0.74
1421757_at	Htr6	5-hydroxytryptamine (serotonin) receptor 6	-1.07	0.864	1.02	0.963	-1.11	0.567	-1.43	0.576	-0.65
1418151_at	Mtmr4	myotubularin related protein 4	-1.06	0.625	-1.27	0.192	1.12	0.268	-1.19	0.013	-0.6
1442548_at	Crim1	Cysteine rich transmembrane BMP regulator 1 (chordin like)	1.28	0.662	-1.02	0.951	-1.71	0.328	-1.1	0.749	-0.64
1441172_at	Aff3	AF4/FMR2 family, member 3	-1.15	0.748	1.5	0.28	-2.09	0.093	-2.37	0.063	-1.03
1444121_at	---	Transcribed locus	-1.41	0.478	1.39	0.253	-1.34	0.18	-1.78	0.297	-0.78
1416948_at	Mrpl23	mitochondrial ribosomal protein L23	1.06	0.583	-1.08	0.544	-1.17	0.229	-1.32	0.273	-0.63
1442763_s_at	Ttll10	tubulin tyrosine ligase-like family, member 10	1	0.987	-1.07	0.87	-1.11	0.453	-1.33	0.455	-0.62
1436840_x_at	Rpl35	ribosomal protein L35	-1.05	0.522	1.08	0.237	-1.23	0.123	-1.32	0.02	-0.63
1418214_at	Klc2	kinesin light chain 2	1.15	0.587	-1.23	0.421	-1.13	0.477	-3.65	0.002	-1.22
1438787_at	Zfp206	zinc finger protein 206	-1.24	0.388	-1.12	0.837	1.15	0.575	-1.03	0.871	-0.56
1419657_a_at	Slc25a36	solute carrier family 25, member 36	-1.04	0.61	1.14	0.388	-1.34	0.072	-1.35	0.347	-0.65
1455198_a_at	Ppp2r3a	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha	1.08	0.625	-1.24	0.172	-1.04	0.661	-1.29	0.388	-0.62
1422171_at	Ptgdr	prostaglandin D receptor	-1.27	0.077	1.26	0.578	-1.26	0.342	-1.44	0.037	-0.68
1460497_a_at	4933413B09Rik	RIKEN cDNA 4933413B09 gene	1.15	0.885	-1.34	0.59	-1.05	0.848	-1.25	0.683	-0.62
1424684_at	Rab5c	RAB5C, member RAS oncogene family	-2.6	0.341	-1.8	0.275	1.91	0.33	-1.61	0.574	-1.03
1415964_at	Scd1	stearoyl-Coenzyme A desaturase 1	-1.3	0.211	1.08	0.808	-1	0.978	-2.36	0.11	-0.9
1437947_x_at	Vdac1	voltage-dependent anion channel 1	-1.11	0.352	-1.01	0.834	-1.04	0.766	1.19	0.224	-0.49
1421121_at	Akap10	A kinase (PRKA) anchor protein 10	-1.31	0.008	-1.21	0.432	1.26	0.077	-1.25	0.072	-0.63
1435583_at	9330182L06Rik	RIKEN cDNA 9330182L06 gene	-1.11	0.893	-1.26	0.666	1.16	0.78	-1.33	0.561	-0.64
1452869_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	-1.08	0.81	-1.09	0.654	1.01	0.956	-1.53	0.102	-0.67
1459137_at	Pml	promyelocytic leukemia	1.13	0.752	-1.31	0.264	-1.05	0.882	-1.23	0.436	-0.61
1423098_at	Capn7	calpain 7	-1.08	0.303	-1.12	0.273	1.03	0.763	-1.16	0.022	-0.58
1444385_at	Taok1	TAO kinase 1	1.39	0.125	-1.24	0.302	-1.54	0.042	-1.01	0.95	-0.6
1435738_x_at	Serf2	small EDRK-rich factor 2	-1.07	0.554	1.07	0.073	-1.19	0.037	-1.4	0.065	-0.65

1423097_s_at	Capn7	calpain 7	1.01	0.965	-1.06	0.393	-1.12	0.035	-1.22	0.104	-0.6
1434835_at	Wapal	wings apart-like homolog (Drosophila)	-1.07	0.6	-1.06	0.647	-1.03	0.808	1.82	0.276	-0.34
1430177_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	1.24	0.72	-1.11	0.606	-1.4	0.188	-1.01	0.983	-0.57
1415981_at	Herpud2	HERPUD family member 2	-1.14	0.07	1.03	0.619	-1.07	0.608	-1.09	0.319	-0.57
1428677_at	Wdr73	WD repeat domain 73	-1.17	0.375	-1.07	0.567	1.05	0.726	-1.14	0.68	-0.58
1438519_at	Klhl24	kelch-like 24 (Drosophila)	1.26	0.136	-1.18	0.109	-1.35	0.163	-1.17	0.624	-0.61
1447454_at	Kif5c	Kinesin family member 5C	-1.2	0.262	1.12	0.88	-1.12	0.748	-1.06	0.825	-0.56
1441688_at	6430537I21Rik	RIKEN cDNA 6430537I21 gene	-1.18	0.424	1.23	0.385	-1.3	0.121	-1.07	0.571	-0.58
1438714_at	Zfp207	zinc finger protein 207	1.17	0.733	-1.14	0.688	-1.26	0.476	-1.06	0.913	-0.57
1424979_at	Aph1a	anterior pharynx defective 1a homolog (C. elegans)	1.07	0.627	-1.09	0.55	-1.17	0.176	-1.21	0.479	-0.6
1457032_at	Ak5	adenylate kinase 5	1.24	0.399	-1.41	0.117	-1.11	0.753	-1.2	0.174	-0.62
1434995_s_at	Dedd	death effector domain-containing	-1.02	0.832	1.01	0.915	-1.17	0.217	-1.18	0.206	-0.59
1429079_a_at	2310045N01Rik	RIKEN cDNA 2310045N01 gene	-1.18	0.21	-1.18	0.257	1.15	0.25	-1.1	0.771	-0.58
1420010_at	LOC574418	hypothetical LOC574418	-1.83	0.445	1.4	0.486	-1.11	0.534	-1.42	0.181	-0.74
1440773_at	2410004P22Rik	RIKEN cDNA 2410004P22 gene	1.37	0.293	-1.22	0.136	-1.52	0.105	-1.08	0.382	-0.61
1449299_at	LOC670589	similar to Low-density lipoprotein receptor-related protein 5 precursor (LRP7) (Lr3	-1.15	0.65	-1.24	0.228	1.17	0.399	-1.42	0.413	-0.66
1452002_at	Zfp508	zinc finger protein 508	-1.26	0.029	-1.05	0.876	1.1	0.603	-1.03	0.887	-0.56
1443290_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	-1.88	0.309	1.47	0.526	-1.18	0.719	-1.21	0.661	-0.7
1438063_at	Mphosph9	M-phase phosphoprotein 9	-1.23	0.079	1.1	0.51	-1.07	0.637	-1	0.996	-0.55
1432958_at	5730407O05Rik	RIKEN cDNA 5730407O05 gene	-1.03	0.928	-1.2	0.599	1.04	0.935	-1.22	0.546	-0.6
1458611_at	---	Transcribed locus	2.05	0.374	-5.31	0.108	-1.64	0.197	-1.13	0.839	-1.51
1417203_at	Ethe1	ethylmalonic encephalopathy 1	-1.18	0.493	-1.28	0.404	1.22	0.494	-1.14	0.59	-0.59
1416208_at	Usp14	ubiquitin specific peptidase 14	-1.11	0.337	-1.04	0.56	-1.01	0.898	2.16	0.188	-0.25
1419456_at	Dcxr	dicarbonyl L-xylulose reductase	-1.11	0.606	-1.09	0.715	1.02	0.929	-1.16	0.382	-0.58
1424915_s_at	---	---	1.09	0.74	-1.27	0.207	-1.03	0.871	-1.29	0.159	-0.62
1432264_x_at	Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	-1.14	0.04	-1.03	0.333	1	0.978	-1.91	0.074	-0.77
1439145_at	Lck	lymphocyte protein tyrosine kinase	1.08	0.911	-1.25	0.397	-1.03	0.958	-2.51	0.221	-0.93
1447985_s_at	Ankib1	ankyrin repeat and IBR domain containing 1	-1.12	0.555	1.15	0.663	-1.23	0.074	-1.43	0.326	-0.66
1433586_at	Rgmb	RGM domain family, member B	-1.05	0.363	-1.12	0.754	1	0.997	-1.08	0.773	-0.56
1428331_at	2210016F16Rik	RIKEN cDNA 2210016F16 gene	-1.23	0.05	-1.11	0.098	1.13	0.364	-1.13	0.397	-0.58
1429062_at	Kif16b	kinesin family member 16B	-1.12	0.623	-1.17	0.446	1.1	0.456	-1.22	0.384	-0.6
1428938_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	1.25	0.226	-1.22	0.342	-1.28	0.073	-1.19	0.553	-0.61
1442558_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.61	0.574	1.35	0.361	-1.14	0.731	-1.24	0.544	-0.66
1435373_at	Csnk1e	casein kinase 1, epsilon	-1.14	0.879	1.24	0.7	-1.37	0.381	-1.71	0.533	-0.74
1456076_at	Defb19	defensin beta 19	-1.31	0.66	-1.06	0.479	1.14	0.692	-1.32	0.113	-0.64
1440867_at	Spry4	sprouty homolog 4 (Drosophila)	-1.08	0.676	-1.62	0.057	1.3	0.246	-1.36	0.297	-0.69
1446673_at	D330013E07Rik	RIKEN cDNA D330013E07 gene	-1.56	0.601	-1.02	0.958	1.23	0.261	-1.02	0.971	-0.59
1434705_at	Ctbp2 /// Zranb1	C-terminal binding protein 2 /// zinc finger, RAN-binding domain containing 1	-1.13	0.169	1.12	0.459	-1.18	0.098	-1.17	0.048	-0.59
1419710_at	Nxph3	neurexophilin 3	-1.34	0.036	-1.28	0.004	1.32	0.408	-1.54	0.2	-0.71
1457845_at	1110059P08Rik	RIKEN cDNA 1110059P08 gene	-1.06	0.823	1.08	0.66	-1.22	0.352	-1.21	0.202	-0.6
1452637_a_at	Bola1	bolA-like 1 (E. coli)	-1.05	0.458	-1.03	0.813	-1.08	0.516	1.1	0.708	-0.52
1423059_at	Ptk2	PTK2 protein tyrosine kinase 2	-1.02	0.708	1.03	0.791	-1.19	0.246	-1.19	0.31	-0.59
1458566_at	Gpatc2	G patch domain containing 2	-1.18	0.515	1.34	0.281	-1.5	0.188	-1.31	0.329	-0.66
1459423_at	Meis1	myeloid ecotropic viral integration site 1	-1.16	0.204	1.25	0.501	-1.36	0.131	-1.12	0.789	-0.6
1436860_at	Senp7	SUMO1/sentrin specific peptidase 7	-1.11	0.623	1.2	0.065	-1.34	0.058	-1.21	0.335	-0.61
1431516_at	4930565N06Rik	RIKEN cDNA 4930565N06 gene	-1.57	0.341	1.48	0.422	-1.36	0.314	-1.2	0.708	-0.66
1415996_at	Txnip	thioredoxin interacting protein	1.07	0.573	-1.12	0.639	-1.13	0.228	-1.51	0.297	-0.67
1442224_at	Plekha6	Pleckstrin homology domain containing, family A member 6	-1.1	0.3	1.24	0.553	-1.44	0.507	-2.88	0.075	-1.04
1460672_at	2410002F23Rik	RIKEN cDNA 2410002F23 gene	1.25	0.39	-1.37	0.329	-1.14	0.293	-1.25	0.189	-0.63
1451087_at	Wdr36	WD repeat domain 36	-1.35	0.419	-1.07	0.68	1.17	0.319	-1.45	0.021	-0.67
1441886_at	4930532D21Rik	RIKEN cDNA 4930532D21 gene	-1.1	0.588	1.28	0.659	-1.52	0.339	-2.95	0.086	-1.07
1441555_at	---	---	1.16	0.339	-1.15	0.616	-1.22	0.356	-1.32	0.337	-0.63
1451564_at	Parp14	poly (ADP-ribose) polymerase family, member 14	-1.12	0.038	1.13	0.345	-1.2	0.167	-1.41	0.041	-0.65

1435791_x_at	Rpl17	ribosomal protein L17	-1.05	0.103	1.03	0.066	-1.16	0.196	-1.27	0.08	-0.61
1430936_at	Chmp7	CHMP family, member 7	-1.37	0.301	1.18	0.555	-1.06	0.827	-2.63	0.397	-0.97
1423536_at	Strn3	striatin, calmodulin binding protein 3	-1.09	0.299	-1	0.972	-1.07	0.372	1.13	0.566	-0.51
1453819_x_at	Stx18	syntaxin 18	-1.07	0.264	-1.01	0.968	-1.09	0.602	1.06	0.458	-0.53
1433979_at	Rbms2	RNA binding motif, single stranded interacting protein 2	-1.03	0.647	1.02	0.773	-1.16	0.422	-1.26	0.221	-0.61
1428395_at	Smurf1 /// LOC640	SMAD specific E3 ubiquitin protein ligase 1 /// similar to Smad ubiquitination regu	-1.05	0.299	-1.36	0.045	1.16	0.595	-1.24	0.396	-0.62
1445483_at	Abl2	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	1.13	0.372	-1.21	0.073	-1.12	0.632	-1.09	0.743	-0.57
1451501_a_at	Ghr	growth hormone receptor	1.29	0.048	-1.36	0.085	-1.21	0.271	-1.04	0.887	-0.58
1449497_at	Il12b	interleukin 12b	-1.05	0.889	1.13	0.849	-1.3	0.151	-1.77	0.062	-0.75
1416105_at	Nnt	nicotinamide nucleotide transhydrogenase	-1.02	0.807	-1.18	0.322	1.03	0.87	-1.01	0.984	-0.55
1419558_at	Mdm4	transformed mouse 3T3 cell double minute 4	-1.18	0.025	-1.27	0.35	1.22	0.142	-1.12	0.586	-0.59
1436935_x_at	Clns1a	chloride channel, nucleotide-sensitive, 1A	-1.11	0.018	-1.09	0.084	1.03	0.613	-1.1	0.24	-0.57
1419544_at	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	-1.12	0.199	-1.1	0.13	1.05	0.668	-1.03	0.696	-0.55
1418229_s_at	Hirip5	histone cell cycle regulation defective interacting protein 5	-1.01	0.89	1.02	0.651	-1.19	0.1	-1.34	0.002	-0.63
1441564_at	---	Transcribed locus	1.67	0.356	-2.72	0.11	-1.23	0.533	-1.63	0.362	-0.98
1454767_at	D2Bwg1423e	DNA segment, Chr 2, Brigham & Women's Genetics 1423 expressed	1.07	0.774	-1.15	0.46	-1.1	0.688	-1.36	0.49	-0.63
1434465_x_at	Vldlr	very low density lipoprotein receptor	-1.09	0.173	1.23	0.782	-1.41	0.066	-1.08	0.464	-0.59
1420844_at	Ubqln2	ubiquilin 2	-1.1	0.524	-1.26	0.617	1.15	0.662	-1.25	0.457	-0.61
1449261_at	Pbx2	pre B-cell leukemia transcription factor 2	-1.21	0.458	-1.04	0.895	1.06	0.821	-1.47	0.096	-0.66
1449942_a_at	Ilk	integrin linked kinase	-1	0.979	-1.15	0.145	-1.01	0.74	1.25	0.377	-0.48
1441827_x_at	Hsp90aa1 /// LOC6	heat shock protein 90kDa alpha (cytosolic), class A member 1 /// similar to heat s	1.58	0.523	-1.91	0.463	-1.34	0.593	-1.62	0.277	-0.82
1428714_at	Pgrmc2	progesterone receptor membrane component 2	-1	0.977	-1.12	0.103	-1.04	0.656	1.06	0.446	-0.53
1438230_at	Pggt1b	protein geranylgeranyltransferase type I, beta subunit	1.08	0.528	-1.02	0.837	-1.26	0.048	-1.07	0.764	-0.57
1430897_at	4931428L18Rik	RIKEN cDNA 4931428L18 gene	-1.08	0.783	-1.66	0.319	1.33	0.537	-1.97	0.499	-0.85
1456189_x_at	Ltbp3	latent transforming growth factor beta binding protein 3	-1.42	0.549	1.33	0.577	-1.22	0.513	-1.11	0.856	-0.61
1444910_at	---	---	-1.13	0.558	1.03	0.944	-1.07	0.693	-1.6	0.065	-0.69
1428620_at	Ensa	endosulfine alpha	-1.01	0.934	-1.04	0.157	-1.12	0.298	1.02	0.855	-0.53
1455078_at	Hsp90aa1	Heat shock protein 90kDa alpha (cytosolic), class A member 1	-1.15	0.637	1.14	0.348	-1.19	0.072	-1.77	0.16	-0.74
1430845_at	2410018L13Rik	RIKEN cDNA 2410018L13 gene	-1.23	0.471	1.2	0.259	-1.19	0.206	-1.06	0.756	-0.57
1423957_at	Isg20l1	interferon stimulated exonuclease gene 20-like 1	-1.04	0.806	-1.14	0.5	1.01	0.861	-1.26	0.042	-0.61
1459627_at	Sc4mol	Sterol-C4-methyl oxidase-like	-1.12	0.798	-1.1	0.854	1.05	0.745	-1.23	0.605	-0.6
1419808_at	Cog4	component of oligomeric golgi complex 4	-1.26	0.095	-1.06	0.717	1.11	0.649	-1.11	0.511	-0.58
1418379_s_at	Gpr124	G protein-coupled receptor 124	-1.28	0.658	-1.16	0.59	1.21	0.738	-1.59	0.216	-0.7
1435889_at	Mark2	MAP/microtubule affinity-regulating kinase 2	1.03	0.802	-1.01	0.978	-1.19	0.433	-1.07	0.667	-0.56
1458882_at	Serpinb8	serine (or cysteine) peptdiase inhibitor, clade B, member 8	-1.05	0.593	1.05	0.756	-1.17	0.039	-1.23	0.537	-0.6
1425488_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	-1.06	0.661	-1.06	0.49	-1.03	0.819	1.16	0.499	-0.5
1441989_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	-1.1	0.785	1.03	0.804	-1.09	0.47	-1.04	0.908	-0.55
1428320_at	Jmjd1b	jumonji domain containing 1B	-1.19	0.061	1.04	0.849	-1.03	0.87	-1.17	0.516	-0.59
1458449_at	Fbxl11	F-box and leucine-rich repeat protein 11	-1.02	0.914	-1.03	0.945	-1.11	0.582	1.01	0.953	-0.54
1455107_at	Srpk1	serine/arginine-rich protein specific kinase 1	-1.14	0.451	1.13	0.381	-1.18	0.104	-1.22	0.237	-0.6
1417046_at	Tusc4	tumor suppressor candidate 4	-1.17	0.04	-1.01	0.858	1.01	0.884	-1.37	0.024	-0.64
1450220_a_at	Spdef	SAM pointed domain containing ets transcription factor	1.5	0.468	-1.2	0.71	-1.94	0.019	-2.22	0.246	-0.96
1426634_at	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	1.14	0.183	-1.14	0.78	-1.2	0.634	-1.41	0.651	-0.65
1453709_at	3426406O18Rik	RIKEN cDNA 3426406O18 gene	-1.14	0.481	1.16	0.507	-1.23	0.262	-1.18	0.59	-0.6
1421124_at	Cdk5r1	cyclin-dependent kinase 5, regulatory subunit (p35) 1	-1.3	0.541	1.62	0.213	-2.17	0.244	-1.15	0.79	-0.75
1454561_at	9430087B13Rik	RIKEN cDNA 9430087B13 gene	-1.47	0.508	1.52	0.376	-1.54	0.221	-1.08	0.542	-0.64
1453861_at	C030014K22Rik	RIKEN cDNA C030014K22 gene	-1.54	0.689	-1.23	0.658	1.39	0.301	-1.18	0.703	-0.64
1448718_at	2400001E08Rik	RIKEN cDNA 2400001E08 gene	-1.14	0.206	-1.04	0.728	1.01	0.942	-1.15	0.318	-0.58
1447612_x_at	Jmjd3	Jumonji domain containing 3	1.08	0.354	-1.27	0.495	-1.01	0.971	-1.43	0.193	-0.66
1443360_x_at	Arhgap4	Rho GTPase activating protein 4	-1.16	0.181	-1.13	0.627	1.11	0.829	-1.17	0.635	-0.59
1448361_at	Ttc3	tetratricopeptide repeat domain 3	-1.07	0.313	1.13	0.023	-1.27	0.192	-1.58	0.107	-0.7
1446226_at	Fancb	Fanconi anemia, complementation group B	-1.06	0.736	-1.28	0.393	1.12	0.616	-1.03	0.905	-0.56
1455945_at	A530094I17Rik	RIKEN cDNA A530094I17 gene	1.02	0.933	-1.06	0.784	-1.11	0.581	-1.77	0.077	-0.73

1454610_at	7-Sep	septin 7	1.01	0.955	-1.01	0.903	-1.17	0.1	-1.1	0.247	-0.57
1435709_at	Ssr4	signal sequence receptor, delta	-1.25	0.092	-1	0.999	1.05	0.764	-1.09	0.665	-0.57
1448135_at	Atf4	activating transcription factor 4	-1.01	0.909	-1.08	0.599	-1.06	0.651	1.35	0.169	-0.45
1443985_at	Zfp719	zinc finger protein 719	-1.03	0.943	1.17	0.793	-1.4	0.013	-1.24	0.447	-0.63
1448268_at	Tmed9	transmembrane emp24 protein transport domain containing 9	-1.77	0.403	-1.17	0.653	1.44	0.384	-2.06	0.299	-0.89
1428555_at	Setd2	SET domain containing 2	1.07	0.738	-1.2	0.084	-1.06	0.648	-1.14	0.158	-0.58
1446474_at	---	---	-1.07	0.474	-1.17	0.685	1.06	0.682	-1.47	0.137	-0.66
1425298_a_at	Birc1a	baculoviral IAP repeat-containing 1a	-1.04	0.919	-1.23	0.525	1.08	0.663	-1.7	0.22	-0.72
1450634_at	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	-1.01	0.963	-1.05	0.62	-1.1	0.544	1.1	0.698	-0.51
1458708_at	Brd4	Bromodomain containing 4	1.23	0.559	-1.01	0.95	-1.58	0.083	-1.08	0.843	-0.61
1425532_a_at	Bin1	bridging integrator 1	-1.07	0.586	-1.12	0.306	1.03	0.704	-2.37	0.075	-0.88
1435019_at	Atxn7l3	ataxin 7-like 3	-1.19	0.123	-1.26	0.024	1.22	0.012	-1.19	0.168	-0.6
1431446_at	0610009B14Rik	RIKEN cDNA 0610009B14 gene	-1.29	0.133	-1.04	0.939	1.12	0.724	-1.72	0.293	-0.73
1455247_at	Amotl1	angiomotin-like 1	1.07	0.674	-1.02	0.947	-1.25	0.277	-1.2	0.548	-0.6
1455721_at	Gspt2	G1 to S phase transition 2	-1.35	0.434	-1	0.993	1.12	0.657	-1.42	0.479	-0.66
1441894_s_at	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	-1.1	0.739	-1.26	0.212	1.15	0.204	-1.08	0.746	-0.57
1449526_a_at	Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3	1.49	0.064	-1.74	0.021	-1.26	0.247	-1.15	0.217	-0.66
1429102_at	Arrdc5	arrestin domain containing 5	1.05	0.851	-1.24	0.683	-1	0.997	-1.09	0.782	-0.57
1434008_at	Scn4b	sodium channel, type IV, beta	-1.11	0.017	-1.46	0.596	1.27	0.503	-1.28	0.614	-0.65
1424663_at	BC017647	cDNA sequence BC017647	1.13	0.331	-1.18	0.124	-1.14	0.504	-1.07	0.529	-0.56
1417357_at	Emd	emerin	-1.31	0.129	-1.09	0.509	1.17	0.16	-1.16	0.383	-0.6
1428926_at	1110003O08Rik	RIKEN cDNA 1110003O08 gene	-1.18	0.304	-1.34	0.424	1.26	0.313	-1.08	0.645	-0.59
1440825_s_at	Ccdc28a	coiled-coil domain containing 28A	1.04	0.632	-1.11	0.07	-1.09	0.373	-1.55	0.41	-0.68
1452172_at	Fastkd2	FAST kinase domains 2	-1.1	0.546	-1.04	0.512	-1.02	0.804	1.17	0.536	-0.5
1424043_at	Ppil4	peptidylprolyl isomerase (cyclophilin)-like 4	1.09	0.673	-1.05	0.567	-1.22	0.019	-1.08	0.649	-0.57
1434782_at	Usp42	ubiquitin specific peptidase 42	-1.18	0.305	-1.01	0.857	1.02	0.743	-1.34	0.145	-0.63
1421147_at	Terf2	telomeric repeat binding factor 2	-1.04	0.583	-1.12	0.22	1	0.99	-1.34	0.077	-0.63
1437395_at	Zcchc11	zinc finger, CCHC domain containing 11	-1.03	0.567	-1.15	0.231	1.02	0.916	-1.82	0.088	-0.75
1452182_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.03	0.586	-1.19	0.433	1.05	0.657	-1.11	0.658	-0.57
1454771_at	---	---	-1.66	0.294	-1.22	0.221	1.43	0.279	-1.11	0.545	-0.64
1440617_at	Cpa6	carboxypeptidase A6	-1.06	0.922	1.04	0.91	-1.15	0.505	-1.37	0.449	-0.63
1422541_at	Ptprm	protein tyrosine phosphatase, receptor type, M	-1.19	0.438	1.02	0.889	-1	0.989	-1.34	0.115	-0.63
1448665_at	Dmd	dystrophin, muscular dystrophy	-1.03	0.87	1.06	0.655	-1.21	0.089	-1.16	0.605	-0.58
1423453_at	Nol12	nucleolar protein 12	1	0.989	-1.13	0.108	-1.04	0.765	-1.53	0.19	-0.67
1448210_at	Rab1	RAB1, member RAS oncogene family	-1.11	0.389	-1	0.994	-1.04	0.668	1.01	0.856	-0.54
1436030_at	Cachd1	cache domain containing 1	-1.07	0.756	-1.08	0.6	-1	0.979	2.66	0.223	-0.12
1436224_at	---	18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110(	-1.03	0.891	-1.12	0.375	-1.01	0.974	1.01	0.951	-0.54
1447577_x_at	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	1.13	0.625	-1.22	0.624	-1.1	0.719	-1.42	0.202	-0.65
1436834_x_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	-1.19	0.129	-1.15	0.023	1.15	0.024	-1.25	0.266	-0.61
1421069_at	Phf2	PHD finger protein 2	1	0.999	-1.13	0.755	-1.03	0.953	-1.02	0.972	-0.55
1423403_at	Mapkbp1	mitogen activated protein kinase binding protein 1	1.21	0.068	-1.09	0.57	-1.37	0.324	-1.53	0.411	-0.7
1428824_at	2310003C23Rik	RIKEN cDNA 2310003C23 gene	-1.01	0.91	-1.11	0.03	-1.03	0.809	2.04	0.213	-0.28
1458793_at	Tns3	Tensin 3	1.94	0.206	-3.66	0.065	-1.55	0.205	-1.56	0.522	-1.21
1433692_at	Nat10	N-acetyltransferase 10	-1.41	0.221	-1.05	0.771	1.2	0.514	-1.01	0.951	-0.57
1416359_at	Snag1	sorting nexin associated golgi protein 1	-1.05	0.727	1.04	0.801	-1.15	0.188	-1.42	0.12	-0.65
1420767_at	1700019G17Rik	RIKEN cDNA 1700019G17 gene	-1.13	0.784	-1	0.98	-1.03	0.926	1.65	0.437	-0.38
1420493_a_at	Pcyt2	phosphate cytidylyltransferase 2, ethanolamine	-1.13	0.237	1.04	0.657	-1.08	0.265	-1.33	0.1	-0.62
AFFX-CreX-3_at	---	---	1.17	0.313	-1.07	0.745	-1.34	0.112	-1.09	0.514	-0.58
1455746_at	Kif13a	kinesin family member 13A	1.09	0.675	-1.19	0.396	-1.08	0.712	-1.1	0.737	-0.57
1454068_at	4930470H14Rik	RIKEN cDNA 4930470H14 gene	-1.07	0.879	1.27	0.504	-1.54	0.284	-2.05	0.169	-0.85
1456380_x_at	Cnn3	calponin 3, acidic	-1.33	0.584	1.34	0.297	-1.32	0.131	-2.58	0.027	-0.97
1438123_at	---	---	-1.08	0.707	1.06	0.883	-1.14	0.69	-1.29	0.446	-0.61
1427438_at	Pip5k2b	Phosphatidylinositol-4-phosphate 5-kinase, type II, beta	-1.19	0.773	1.53	0.532	-2.04	0.149	-1.32	0.684	-0.76

1433055_at	4931407J08Rik	RIKEN cDNA 4931407J08 gene	1.33	0.59	-1.14	0.751	-1.55	0.592	-1.32	0.6	-0.67
1436151_x_at	BC031781	cDNA sequence BC031781	-1	1	-1.15	0.678	-1.02	0.958	1.61	0.239	-0.39
1416738_at	Brap	BRCA1 associated protein	1.1	0.616	-1.06	0.626	-1.22	0.136	-1.1	0.366	-0.57
1451517_at	Rhobtb2	Rho-related BTB domain containing 2	-1.22	0.082	-2.2	0.026	1.58	0.072	-1.43	0.074	-0.82
1431752_a_at	2900073H19Rik	RIKEN cDNA 2900073H19 gene	1.04	0.893	-1.18	0.257	-1.03	0.888	-1.12	0.621	-0.57
1433970_at	Bola3	bolA-like 3 (E. coli)	-1.01	0.827	-1.03	0.559	-1.12	0.021	1.75	0.229	-0.35
1456544_at	---	---	-1.17	0.451	1.07	0.436	-1.08	0.335	-1.44	0.307	-0.65
1423738_at	Oxa1l	oxidase assembly 1-like	-1.21	0.038	-1.14	0.6	1.15	0.651	-1.34	0.057	-0.63
1440358_at	Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	1.08	0.738	-1.12	0.833	-1.13	0.582	-1.08	0.817	-0.56
1430098_at	6330409D20Rik	RIKEN cDNA 6330409D20 gene	1.26	0.558	-1.65	0.308	-1.01	0.987	-3.33	0.079	-1.18
1434739_at	Fmr1nb	fragile X mental retardation 1 neighbor	-1.11	0.692	-1.17	0.674	1.1	0.885	-1.05	0.925	-0.56
1447931_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	1.15	0.577	-1.28	0.379	-1.08	0.685	-1.47	0.125	-0.67
1458187_at	Zfp142	zinc finger protein 142	-1.17	0.653	-1.07	0.885	1.07	0.759	-1.08	0.59	-0.56
1444050_at	---	PREDICTED: Mus musculus WNT1 inducible signaling pathway protein 3 (Wisp3	-1.57	0.031	1.34	0.218	-1.13	0.487	-1.49	0.298	-0.71
1448923_at	Prkra	protein kinase, interferon inducible double stranded RNA dependent activator	-1.26	0.198	1.12	0.31	-1.06	0.337	-1.14	0.613	-0.59
1436251_at	Pde1c	phosphodiesterase 1C	-2.49	0.053	-1.89	0.527	1.93	0.315	-1.84	0.109	-1.07
1458016_at	---	---	1.34	0.321	-1.56	0.183	-1.14	0.564	-1.23	0.636	-0.65
1437901_a_at	Vps41	vacuolar protein sorting 41 (yeast)	1.01	0.977	-1.03	0.899	-1.14	0.322	-1.69	0.151	-0.71
1456313_x_at	Mrpl28	mitochondrial ribosomal protein L28	-1.31	0.337	-1.22	0.344	1.28	0.477	-1.29	0.082	-0.64
1428955_x_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	1.01	0.967	-1.08	0.84	-1.09	0.718	-1.17	0.572	-0.58
1419484_a_at	Gbas	glioblastoma amplified sequence	-1.02	0.945	-1.14	0.528	-1	0.985	1.2	0.222	-0.49
1452591_a_at	2410018G20Rik	RIKEN cDNA 2410018G20 gene	-1.13	0.52	-1.02	0.853	-1.01	0.927	1.28	0.326	-0.47
1448238_at	2700060E02Rik	RIKEN cDNA 2700060E02 gene	1.07	0.515	-1.08	0.219	-1.16	0.252	-1.32	0.113	-0.62
1429893_at	2810004A10Rik	RIKEN cDNA 2810004A10 gene	1.08	0.772	-1.23	0.571	-1.04	0.927	-1.47	0.256	-0.66
1422232_at	Phox2b	paired-like homeobox 2b	-1.34	0.685	-1.32	0.568	1.35	0.676	-1.06	0.856	-0.59
1416163_at	Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (Arabidopsis thaliana)	-1.15	0.199	-1.12	0.381	1.09	0.482	-1.13	0.69	-0.58
1428918_at	Scyl3	SCY1-like 3 (S. cerevisiae)	-1.15	0.035	-1.13	0.374	1.1	0.441	-1.49	0.048	-0.67
1452616_s_at	Ssbp1	single-stranded DNA binding protein 1	-1.21	0.083	-1.1	0.243	1.13	0.281	-1.41	0.014	-0.65
1453372_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	-1.04	0.728	1.11	0.386	-1.28	0.104	-1.16	0.223	-0.59
1451120_at	Rpo1-3	RNA polymerase 1-3	-1.01	0.922	-1.21	0.13	1.04	0.753	-1.13	0.478	-0.58
1418786_at	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	-1.03	0.95	-1.28	0.621	1.11	0.684	-5.38	0.002	-1.65
1460254_at	1810049H13Rik	RIKEN cDNA 1810049H13 gene	-1.01	0.969	-1.24	0.376	1.06	0.597	-1.34	0.115	-0.63
1444785_at	Ski	Sloan-Kettering viral oncogene homolog	-1.11	0.685	1.24	0.2	-1.4	0.325	-1.7	0.087	-0.74
1423974_at	Numa1	nuclear mitotic apparatus protein 1	-1.02	0.838	-1.28	0.356	1.1	0.547	-1.27	0.075	-0.62
1426956_a_at	Trp53bp1	transformation related protein 53 binding protein 1	-1.18	0.003	1.12	0.528	-1.12	0.498	-1.38	0.075	-0.64
1429002_at	Snw1	SNW domain containing 1	1.02	0.871	-1.01	0.877	-1.17	0.188	-1.27	0.096	-0.61
1421772_a_at	Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	-1.06	0.664	1.02	0.8	-1.12	0.466	-1.88	0.059	-0.76
1437624_x_at	Nudt16l1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	-1.02	0.894	1.05	0.591	-1.21	0.075	-1.49	0.154	-0.67
1437320_s_at	Xpa	xeroderma pigmentosum, complementation group A	-1.43	0.19	-1.18	0.608	1.31	0.642	-1.68	0.143	-0.74
1435357_at	---	---	-1.06	0.737	1.15	0.425	-1.3	0.001	-1.63	0.078	-0.71
1425241_a_at	Wsb1	WD repeat and SOCS box-containing 1	-1.51	0.072	1.31	0.33	-1.13	0.529	-1.37	0.128	-0.68
1442073_at	---	---	-1.17	0.63	-1.15	0.711	1.13	0.517	-1.31	0.416	-0.62
1449815_a_at	Ssbp2	single-stranded DNA binding protein 2	-1.02	0.665	-1	0.964	-1.13	0.343	1.89	0.218	-0.32
1427988_s_at	Safb2	scaffold attachment factor B2	1.02	0.882	-1.15	0.412	-1.04	0.791	-1.36	0.204	-0.63
1434896_at	Zfp422-rs1	zinc finger protein 422, related sequence 1	1.1	0.49	-1.08	0.269	-1.19	0.309	-1.26	0.116	-0.61
1417871_at	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	-1.26	0.437	-1.1	0.726	1.15	0.403	-1.19	0.091	-0.6
1458060_at	---	10 days lactation, adult female mammary gland cDNA, RIKEN full-length enriche	-1.13	0.207	-1.1	0.415	1.07	0.446	-1	0.992	-0.54
1423664_at	Qdpr	quininoid dihydropteridine reductase	-1.21	0.084	-1.07	0.668	1.1	0.444	-1.03	0.826	-0.55
1426636_a_at	Birc4	baculoviral IAP repeat-containing 4	1	0.998	-1.16	0.617	-1	0.99	-1.37	0.22	-0.63
1453731_a_at	Tmem77	transmembrane protein 77	-1.13	0.228	-1.09	0.351	1.06	0.756	-1.56	0.03	-0.68
1453020_at	1810048J11Rik	RIKEN cDNA 1810048J11 gene	-1.15	0.577	1.03	0.821	-1.04	0.881	-1.45	0.009	-0.65
1454925_x_at	Mdh1	malate dehydrogenase 1, NAD (soluble)	-1.29	0.01	-1.18	0.1	1.24	0.114	-1.9	0.142	-0.78
1448104_at	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	-1.12	0.461	-1.06	0.402	1.02	0.794	-1.17	0.439	-0.58

1421523_at	Fgf17	fibroblast growth factor 17	-1.29	0.56	-1.47	0.527	1.41	0.053	-1.25	0.399	-0.65
1439110_at	A930012O16Rik	RIKEN cDNA A930012O16 gene	-1.16	0.567	-1.15	0.338	1.13	0.545	-1.64	0.054	-0.71
1426303_at	B4galt7	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase	-1.19	0.325	-1.07	0.816	1.08	0.695	-1.65	0.315	-0.71
1421879_at	Mtmr1	myotubularin related protein 1	-1.23	0.387	-1.24	0.466	1.24	0.548	-1.12	0.633	-0.59
1456479_at	Snx30	sorting nexin family member 30	-1.19	0.179	1.05	0.706	-1.03	0.882	-1.73	0.177	-0.72
1456168_at	Ccnjl	Cyclin J-like	1.14	0.494	-1.08	0.828	-1.27	0.44	-1	0.997	-0.55
1436801_x_at	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	-1.05	0.864	-1.07	0.752	-1.02	0.873	1.05	0.325	-0.52
1424981_at	Nln	neurolysin (metallopeptidase M3 family)	-1.48	0.044	-1.05	0.601	1.23	0.279	-1.05	0.812	-0.59
1428913_at	D2Bwg1335e	DNA segment, Chr 2, Brigham & Women's Genetics 1335 expressed	-1.04	0.667	-1.1	0.171	-1.01	0.931	1.01	0.905	-0.54
1450756_s_at	Cul3	cullin 3	-1.11	0.393	-1.2	0.035	1.13	0.323	-1	0.962	-0.55
1456422_at	---	---	-1.33	0.118	-1.2	0.069	1.27	0.135	-1.2	0.582	-0.61
1433782_at	Cldn12	claudin 12	1.08	0.576	-1.1	0.34	-1.15	0.201	-1.29	0.443	-0.61
1418523_at	Arih2	ariadne homolog 2 (Drosophila)	1.1	0.768	-1.06	0.727	-1.22	0.088	-1.67	0.101	-0.71
1434750_at	Exoc3	exocyst complex component 3	1.04	0.67	-1.08	0.122	-1.12	0.475	-1.17	0.365	-0.58
1418788_at	Tek	endothelial-specific receptor tyrosine kinase	1.03	0.844	-1	0.977	-1.19	0.263	-1.23	0.322	-0.6
1437698_at	Myo5b	myosin Vb	-1.16	0.199	1.13	0.52	-1.15	0.313	-1.41	0.597	-0.65
1452718_at	Edd1	E3 ubiquitin protein ligase, HECT domain containing, 1	-1.12	0.432	-1.07	0.184	1.03	0.758	-1.06	0.633	-0.55
1434938_at	Rbm9	RNA binding motif protein 9	-1.22	0.307	1.21	0.122	-1.2	0.49	-1.12	0.618	-0.58
1455733_at	Taok3	TAO kinase 3	-1.2	0.073	-1.12	0.371	1.13	0.407	-1.19	0.251	-0.59
1444966_at	Raver1	Ribonucleoprotein, PTB-binding 1	-2.3	0.484	1.46	0.469	-1.04	0.831	-1.15	0.525	-0.76
1453467_s_at	Rps15a	ribosomal protein S15a	-1.06	0.082	1.1	0.344	-1.23	0.033	-1.32	0.057	-0.63
1417367_at	Ppp2ca	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	-1.1	0.32	-1.04	0.452	-1.01	0.855	1.07	0.315	-0.52
1423373_at	Rpp30	ribonuclease P/MRP 30 subunit (human)	1.03	0.76	-1.02	0.901	-1.17	0.109	-1.02	0.92	-0.55
1445919_at	AA409261	expressed sequence AA409261	1.06	0.586	-1.01	0.949	-1.23	0.443	-1.5	0.037	-0.67
1420520_x_at	Eral1	Era (G-protein)-like 1 (E. coli)	1.02	0.908	-1.08	0.689	-1.09	0.177	-1.05	0.602	-0.55
1440343_at	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	-1.14	0.524	1.21	0.448	-1.29	0.264	-1.27	0.193	-0.62
1445956_at	---	---	-1.45	0.325	1.54	0.519	-1.58	0.068	-1.14	0.785	-0.66
1460172_at	5730403B10Rik	RIKEN cDNA 5730403B10 gene	1.03	0.8	-1.05	0.827	-1.14	0.452	-1.54	0.152	-0.67
1441663_at	Prickle1	Prickle like 1 (Drosophila)	-1.41	0.46	1.35	0.193	-1.24	0.226	-1.38	0.316	-0.67
1416467_at	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	1.1	0.498	-1.16	0.472	-1.1	0.47	-1.19	0.294	-0.59
1426985_s_at	2810485I05Rik	RIKEN cDNA 2810485I05 gene	1.11	0.607	-1.11	0.293	-1.18	0.278	-1.11	0.43	-0.57
1428929_s_at	Slc25a26	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 26	-1.33	0.011	-1.13	0.364	1.22	0.325	-1.2	0.315	-0.61
1432841_at	E130116L18Rik	RIKEN cDNA E130116L18 gene	-1.36	0.666	-1.07	0.719	1.19	0.703	-1.71	0.364	-0.74
1434746_at	Mga	MAX gene associated	1.16	0.524	-1.04	0.817	-1.34	0.251	-1.29	0.399	-0.63
1435878_at	Stk38l	serine/threonine kinase 38 like	-1	0.961	1.13	0.302	-1.36	0.032	-1.17	0.325	-0.6
1426721_s_at	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	-1.24	0.479	1.15	0.489	-1.1	0.179	-1.23	0.376	-0.61
1417718_at	Eif3s4	eukaryotic translation initiation factor 3, subunit 4 (delta)	-1.09	0.122	-1.08	0.35	1.02	0.742	-1.08	0.428	-0.56
1418923_at	Slc17a3	solute carrier family 17 (sodium phosphate), member 3	1.17	0.107	-1.25	0.012	-1.12	0.691	-1.21	0.416	-0.6
1421783_a_at	Kcnip2	Kv channel-interacting protein 2	1.22	0.819	-1.27	0.653	-1.17	0.698	-1.25	0.635	-0.62
1423817_s_at	2010315L10Rik	RIKEN cDNA 2010315L10 gene	1.08	0.476	-1	0.963	-1.28	0.13	-1.86	0.063	-0.77
1423163_at	Bat4	HLA-B associated transcript 4	-1.17	0.251	-1.09	0.592	1.09	0.612	-1.16	0.51	-0.58
1439590_at	Xkr8	X Kell blood group precursor related family member 8 homolog	-1.21	0.292	-1.06	0.856	1.09	0.576	-1.22	0.422	-0.6
1429152_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1.11	0.402	-1.03	0.832	-1.28	0.166	-1.2	0.33	-0.6
1449890_at	Ugt2b37	UDP glucuronosyltransferase 2 family, polypeptide B37	-1.03	0.958	-1.87	0.044	1.36	0.302	-1.48	0.033	-0.76
1415752_at	BC031181	cDNA sequence BC031181	-1.01	0.897	-1.04	0.538	-1.1	0.455	1.11	0.474	-0.51
1416328_a_at	Atp6v0e	ATPase, H+ transporting, lysosomal V0 subunit E	-1.13	0.274	1.05	0.57	-1.08	0.502	-1.04	0.685	-0.55
1422580_at	Myl4	myosin, light polypeptide 4	-1.14	0.773	1.07	0.65	-1.09	0.684	-2.43	0.091	-0.9
1421406_at	---	---	-1.76	0.097	-1.18	0.564	1.45	0.367	-1.21	0.71	-0.67
1453431_at	2610206C17Rik	RIKEN cDNA 2610206C17 gene	1.27	0.09	-1.02	0.963	-1.62	0.154	-1.1	0.728	-0.62
1455777_x_at	Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	-1.06	0.287	-1.14	0.373	1.04	0.513	-1.15	0.581	-0.58
1421128_at	U2af1-rs2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 2	1.7	0.523	-1.86	0.498	-1.6	0.566	-1.6	0.53	-0.84
1417183_at	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	-1.13	0.516	-1.19	0.038	1.13	0.252	-1.23	0.143	-0.6
1452868_at	Usp24	ubiquitin specific peptidase 24	-1.28	0.328	-1.14	0.225	1.21	0.381	-1.06	0.665	-0.57

1447648_at	1700021N20Rik	RIKEN cDNA 1700021N20 gene	1.22	0.763	-1.05	0.936	-1.44	0.363	-1.08	0.909	-0.59
1455994_x_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.21	0.082	1.21	0.223	-1.21	0.265	-1.1	0.382	-0.58
1426047_a_at	Ptprr	protein tyrosine phosphatase, receptor type, R	-1.22	0.415	1.28	0.281	-1.31	0.201	-1.72	0.453	-0.74
1450697_at	Slc30a7	solute carrier family 30 (zinc transporter), member 7	1.06	0.679	-1.04	0.737	-1.19	0.021	-1.22	0.242	-0.6
1452069_a_at	Thap7	THAP domain containing 7	-1.04	0.848	1.02	0.93	-1.13	0.175	-1.29	0.381	-0.61
1425625_at	Il13ra1	interleukin 13 receptor, alpha 1	-1.39	0.382	-1.19	0.342	1.3	0.031	-1.4	0.511	-0.67
1436820_at	Kctd11	potassium channel tetramerisation domain containing 11	-1.45	0.26	-1.24	0.386	1.37	0.033	-1.35	0.133	-0.67
1421943_at	Tgfa	transforming growth factor alpha	1.09	0.758	-1.28	0	-1.01	0.957	-1.08	0.68	-0.57
1457500_at	Depdc5	DEP domain containing 5	1.11	0.745	-1.14	0.707	-1.14	0.684	-1.44	0.511	-0.65
1427241_at	Papolg	poly(A) polymerase gamma	-1.03	0.837	1.03	0.793	-1.16	0.146	-1.81	0.075	-0.74
1433069_at	---	---	-1.26	0.559	1.11	0.836	-1.04	0.883	-1.04	0.907	-0.56
1416897_at	Parp9	poly (ADP-ribose) polymerase family, member 9	-1.07	0.191	-1.1	0.118	1.02	0.881	-1.3	0.01	-0.61
1448701_a_at	Krit1	KRIT1, ankyrin repeat containing	-1.24	0.413	1.21	0.373	-1.19	0.099	-1.2	0.463	-0.6
1460554_s_at	Glg1	golgi apparatus protein 1	-1.1	0.59	1	0.989	-1.05	0.884	-1.17	0.393	-0.58
1433697_at	AV312086	expressed sequence AV312086	-1.15	0.431	-1.17	0.068	1.13	0.244	-1.08	0.594	-0.57
1446447_at	4921537D05Rik	RIKEN cDNA 4921537D05 gene	-1.04	0.935	1.2	0.704	-1.42	0.015	-1.3	0.139	-0.64
1435908_at	Nrxn2	neurexin II	-1.4	0.152	1.41	0.024	-1.36	0.194	-1.19	0.671	-0.63
1451505_at	Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	-1.07	0.784	-1.03	0.78	-1.04	0.791	1.2	0.354	-0.49
1436575_at	Grin3a	glutamate receptor ionotropic, NMDA3A	-1.86	0.374	1.97	0.116	-2.77	0.143	-1.33	0.721	-1
1435464_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	1.13	0.225	-1.04	0.644	-1.29	0.025	-1.61	0.217	-0.7
1428541_at	3321401G04Rik	RIKEN cDNA 3321401G04 gene	-1.21	0.624	1.29	0.663	-1.34	0.149	-1.62	0.2	-0.72
1441541_at	AW011752	Expressed sequence AW011752	1.05	0.906	-1.19	0.752	-1.03	0.901	-1.72	0.063	-0.72
1432139_at	Srpk3	serine/arginine-rich protein specific kinase 3	-2.95	0.009	-1.46	0.524	1.84	0.468	-1.17	0.811	-0.93
1419898_s_at	Zc3h7a	zinc finger CCCH type containing 7 A	1.01	0.946	-1.06	0.732	-1.1	0.681	-1.33	0.346	-0.62
1437166_at	Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	-1.09	0.766	1.04	0.89	-1.1	0.645	-1.02	0.866	-0.54
1426418_at	Atoh8	atonal homolog 8 (Drosophila)	-1.08	0.79	-1.74	0.128	1.36	0.256	-1.18	0.618	-0.66
1426403_at	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	1.03	0.839	-1.08	0.568	-1.1	0.539	-1.26	0.297	-0.6
1460323_at	Tars	threonyl-tRNA synthetase	-1.05	0.62	-1.01	0.935	-1.08	0.558	1.04	0.814	-0.53
1449650_at	Etnk1	Ethanolamine kinase 1	-1.14	0.208	-1.9	0.356	1.46	0.565	-1.16	0.627	-0.68
1421826_at	Dll4	delta-like 4 (Drosophila)	-1.13	0.538	1.12	0.801	-1.16	0.243	-1.12	0.57	-0.57
1440953_at	1700096K18Rik	RIKEN cDNA 1700096K18 gene	-1.06	0.836	-1.19	0.643	1.08	0.679	-1.58	0.064	-0.69
1453848_s_at	Zbed3	zinc finger, BED domain containing 3	-1.12	0.507	1.04	0.926	-1.07	0.703	-1.25	0.272	-0.6
1456643_at	9230114K14Rik	RIKEN cDNA 9230114K14 gene	-1.03	0.697	-1.07	0.542	-1.04	0.805	2.06	0.269	-0.27
1456314_x_at	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	1.01	0.957	-1.06	0.46	-1.1	0.39	-1.08	0.543	-0.56
1451316_a_at	Picalm	phosphatidylinositol binding clathrin assembly protein	-1.12	0.135	-1.02	0.633	-1.01	0.731	1.49	0.238	-0.41
1456495_s_at	Osbpl6	oxysterol binding protein-like 6	-1.14	0.489	-1.05	0.909	1.03	0.807	-1.07	0.877	-0.56
1432355_at	2210039B01Rik	RIKEN cDNA 2210039B01 gene	-1.06	0.519	-1.01	0.979	-1.07	0.821	1.25	0.652	-0.47
1444181_at	Gimap5	GTPase, IMAP family member 5	-1.09	0.449	1.33	0.411	-1.64	0.038	-1.57	0.265	-0.74
1439122_at	---	---	1.12	0.652	-1.12	0.692	-1.17	0.653	-1.28	0.512	-0.61
1427888_a_at	Spna2 /// LOC3813	spectrin alpha 2 /// similar to Spectrin alpha chain, brain (Spectrin, non-erythroid a	1.18	0.23	-1.05	0.628	-1.37	0.098	-1.66	0.075	-0.72
1448223_at	Fto	fatso	-1.23	0.03	-1.12	0.208	1.16	0.23	-1.22	0.135	-0.6
1415888_at	Hdgf	hepatoma-derived growth factor	-1.04	0.856	-1.04	0.749	-1.06	0.67	2.23	0.14	-0.23
1435032_at	Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	-1.03	0.846	-1.04	0.689	-1.07	0.628	1.03	0.9	-0.53
1431653_at	Tcrb-J	T-cell receptor beta, joining region	1.39	0.677	-1.44	0.316	-1.28	0.686	-1.35	0.61	-0.67
1460026_s_at	Zfyve27	zinc finger, FYVE domain containing 27	1.13	0.278	-1.19	0.327	-1.12	0.324	-1.2	0.26	-0.59
1430354_x_at	Scyl1	SCY1-like 1 (S. cerevisiae)	-1.01	0.59	1.02	0.914	-1.17	0.503	-1.13	0.575	-0.57
1456867_x_at	Ergic3	ERGIC and golgi 3	-1.1	0.536	-1.03	0.675	-1.02	0.923	1.12	0.198	-0.51
1457710_at	Zhx3	zinc fingers and homeoboxes 3	1.03	0.966	-1.08	0.883	-1.1	0.731	-1.59	0.108	-0.68
1448306_at	Nfkbia	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	-1.15	0.647	1.04	0.661	-1.05	0.735	-1.85	0.093	-0.75
1435187_at	Tomm20	Translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.01	0.946	1.03	0.781	-1.19	0.259	-1.17	0.263	-0.58
1437681_at	Grik4	glutamate receptor, ionotropic, kainate 4	-3.4	0.018	1.93	0.291	-1.55	0.057	-1.51	0.405	-1.14
1437769_at	Eps15l1	Epidermal growth factor receptor pathway substrate 15-like 1	-1.04	0.738	-1.05	0.901	-1.06	0.902	1.01	0.969	-0.53
1446003_at	---	---	-1.14	0.868	-1.17	0.557	1.13	0.779	-1.38	0.131	-0.64

1455888_at	Lrrn6c	leucine rich repeat neuronal 6C	1.1	0.759	-1.3	0.557	-1	0.914	-1.2	0.558	-0.6
1433280_at	4933417G07Rik	RIKEN cDNA 4933417G07 gene	-1.77	0.125	-1.05	0.915	1.35	0.477	-1.6	0.221	-0.77
1419563_at	Birc6	baculoviral IAP repeat-containing 6	-1.21	0.766	1.31	0.585	-1.36	0.322	-1.55	0.148	-0.71
1448501_at	Tspan6	tetraspanin 6	-1.07	0.656	1.28	0.538	-1.55	0.026	-1.01	0.983	-0.59
1426689_s_at	Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-1.12	0.072	-1.15	0.396	1.1	0.658	-1.04	0.727	-0.55
1444779_s_at	Zfp59	zinc finger protein 59	1.04	0.432	-1.21	0.366	-1	0.98	-1.61	0.14	-0.69
1460707_at	Ptp4a2	protein tyrosine phosphatase 4a2	-1.01	0.875	1.1	0.288	-1.29	0.029	-1.31	0.069	-0.63
1419641_at	Purb	purine rich element binding protein B	-1.07	0.702	-1.27	0.052	1.14	0.273	-1.07	0.779	-0.57
1450131_a_at	Bspry	B-box and SPRY domain containing	-1.13	0.509	1.03	0.91	-1.06	0.803	-1.52	0.334	-0.67
1443117_at	Eya1	eyes absent 1 homolog (Drosophila)	-1.6	0.139	-1.38	0.578	1.51	0.51	-2.16	0.031	-0.91
1427882_at	Dnttip2	deoxynucleotidyltransferase, terminal, interacting protein 2	-1.07	0.787	-1.15	0.497	1.07	0.757	-1.15	0.456	-0.58
1429514_at	Ppap2b	phosphatidic acid phosphatase type 2B	1.02	0.937	-1.01	0.719	-1.16	0.527	-1.37	0.124	-0.63
1448282_at	Plrg1	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	-1.04	0.555	1.06	0.671	-1.18	0.067	-1.08	0.658	-0.56
1440360_at	Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	-1.25	0.06	1.25	0.306	-1.21	0.333	-1.81	0.075	-0.76
1417578_a_at	Gmppa	GDP-mannose pyrophosphorylase A	-1.09	0.571	-1.01	0.964	-1.04	0.737	1.01	0.945	-0.53
1420423_at	Tcl1b4	T-cell leukemia/lymphoma 1B, 4	-1.55	0.607	-1.35	0.657	1.48	0.431	-1.06	0.675	-0.62
1434054_at	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	-1	0.98	-1.12	0.636	-1.02	0.92	1.79	0.361	-0.34
1434866_x_at	Cpt1a	carnitine palmitoyltransferase 1a, liver	-1.15	0.701	-1.22	0.562	1.18	0.147	-1.21	0.33	-0.6
1454985_at	D030051N19Rik	RIKEN cDNA D030051N19 gene	-1.13	0.711	-1.29	0.33	1.2	0.318	-1.29	0.273	-0.63
1431377_at	Atxn10	ataxin 10	1.44	0.345	-1.44	0.479	-1.37	0.347	-1.71	0.102	-0.77
1448161_a_at	Clcn4-2	chloride channel 4-2	-1.07	0.651	-1.17	0.163	1.08	0.638	-1.18	0.276	-0.59
1460647_a_at	Nr2f6	nuclear receptor subfamily 2, group F, member 6	-1.07	0.633	1.05	0.592	-1.14	0.506	-1.69	0.241	-0.71
1437088_at	Sdad1	SDA1 domain containing 1	-1.34	0.126	-1.08	0.817	1.19	0.232	-1.2	0.285	-0.61
1416586_at	Zfp239	zinc finger protein 239	-1.68	0.01	-1.17	0.724	1.42	0.156	-1.08	0.662	-0.63
1446416_at	Sulf1	sulfatase 1	-1.36	0.179	1.15	0.743	-1.02	0.962	-2.15	0.45	-0.85
1436015_s_at	Stk4	serine/threonine kinase 4	-1.1	0.587	1.05	0.463	-1.11	0.252	-1.76	0.049	-0.73
1452443_s_at	Helz	helicase with zinc finger domain	-1.23	0.054	-1.07	0.74	1.12	0.572	-1.34	0.064	-0.63
1425109_at	Slc44a3	solute carrier family 44, member 3	-1.14	0.564	-1.02	0.908	1.01	0.925	-1.08	0.93	-0.56
1418843_at	Slc30a4	solute carrier family 30 (zinc transporter), member 4	-1.08	0.637	1.24	0.151	-1.43	0.078	-1.86	0.098	-0.78
1434926_at	Arhgef11 /// LOC67	Rho guanine nucleotide exchange factor (GEF) 11 /// similar to Rho guanine nucl	-1.21	0.101	1.11	0.172	-1.08	0.578	-1.29	0.258	-0.62
1421151_a_at	Epha2	Eph receptor A2	-1.09	0.659	1.07	0.593	-1.13	0.649	-1.25	0.292	-0.6
1441096_at	Tusc5	tumor suppressor candidate 5	1.14	0.862	-1.03	0.964	-1.32	0.542	-1.04	0.808	-0.56
1424818_at	Alg12	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransfera	-1.12	0.635	-1.25	0.232	1.17	0.041	-1.12	0.323	-0.58
1429710_at	Styx	phosphoserine/threonine/tyrosine interaction protein	1.02	0.912	-1.05	0.479	-1.13	0.118	-1.26	0.163	-0.6
1450983_at	Akap8	A kinase (PRKA) anchor protein 8	-1.09	0.149	-1.19	0.061	1.11	0.354	-1.13	0.394	-0.57
1438317_a_at	Endog	endonuclease G	1.06	0.559	-1.11	0.256	-1.1	0.366	-1.61	0.125	-0.69
1432725_at	4930445G23Rik	RIKEN cDNA 4930445G23 gene	-1.17	0.703	1.16	0.745	-1.18	0.189	-1.58	0.506	-0.69
1423740_a_at	Rbm10	RNA binding motif protein 10	1.01	0.958	-1.13	0.29	-1.03	0.694	-1.11	0.07	-0.56
1455417_at	Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	-1.29	0.121	-1.1	0.181	1.18	0.513	-1.18	0.637	-0.6
1438598_at	Shc2	src homology 2 domain-containing transforming protein C2	-2.08	0.22	1.5	0.213	-1.13	0.645	-1.5	0.598	-0.8
1437449_at	Rsad1	radical S-adenosyl methionine domain containing 1	-1.16	0.054	-1.05	0.836	1.06	0.677	-1.11	0.693	-0.57
1418594_a_at	Ncoa1	nuclear receptor coactivator 1	-1.12	0.34	-1.07	0.263	1.04	0.806	-1.46	0.193	-0.65
1436064_x_at	Rps24	ribosomal protein S24	-1.07	0.353	1.1	0.041	-1.19	0.096	-1.34	0.01	-0.63
1445961_at	---	---	1.16	0.608	-1.2	0.338	-1.14	0.521	-1.16	0.345	-0.59
1439742_at	Stam2	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.37	0.204	-1.46	0.272	-1.23	0.618	-1.17	0.68	-0.62
1416088_a_at	Rps15	ribosomal protein S15	1.07	0.217	-1	0.985	-1.25	0.076	-1.7	0.031	-0.72
1449687_at	D10Ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed	-1.1	0.456	-1.03	0.941	-1.01	0.947	1.7	0.02	-0.36
1424381_at	Sf4	splicing factor 4	-1.03	0.616	-1.24	0.012	1.09	0.303	-1.12	0.471	-0.58
1431775_at	3100002H09Rik	RIKEN cDNA 3100002H09 gene	-2.48	0.306	-1.08	0.859	1.54	0.34	-1.99	0.157	-1
1431939_a_at	Mina	myc induced nuclear antigen	-1.22	0.309	1.07	0.667	-1.02	0.824	-1.17	0.567	-0.58
1456409_at	---	---	1.33	0.353	-1.2	0.651	-1.42	0.41	-1.38	0.518	-0.67
1431232_a_at	Mga	MAX gene associated	1.26	0.276	-1.04	0.826	-1.56	0.013	-1.57	0.066	-0.73
1426644_at	Tbc1d20	TBC1 domain family, member 20	1.01	0.919	-1.13	0.376	-1.03	0.892	-1.53	0.132	-0.67

1430684_s_at	Lrp2bp	Lrp2 binding protein	-1.12	0.611	-1.33	0.284	1.22	0.738	-1.47	0.452	-0.67
1459348_at	Ebf1	Early B-cell factor 1	-1.01	0.98	1.28	0.502	-1.69	0.06	-2.81	0.056	-1.06
1416091_at	Mtap4	microtubule-associated protein 4	-1.07	0.732	-1.15	0.627	1.07	0.834	-1.4	0.408	-0.64
1438195_at	Gpd1l /// LOC6725(	glycerol-3-phosphate dehydrogenase 1-like /// similar to glycerol-3-phosphate deh	-1.04	0.542	-1.17	0.445	1.05	0.278	-1.81	0.1	-0.74
1454681_at	Rbm35a	RNA binding motif protein 35A	1.18	0.341	-1.15	0.818	-1.23	0.134	-1.27	0.773	-0.62
1452189_at	Wdr82	WD repeat domain containing 82	-1.05	0.663	1.01	0.849	-1.1	0.331	-1.22	0.107	-0.59
1454808_at	Efha1	EF hand domain family A1	-1.01	0.796	-1.12	0.189	-1.01	0.845	1.06	0.603	-0.52
1442985_at	Hmcn1	Hemicentin 1	-1.1	0.65	-1.11	0.688	1.06	0.889	-1.44	0.318	-0.65
1438278_a_at	BC003993	cDNA sequence BC003993	-1.1	0.743	1.06	0.462	-1.11	0.157	-1.37	0.082	-0.63
1446969_at	9630037P07Rik	RIKEN cDNA 9630037P07 gene	-1.05	0.907	1.06	0.675	-1.18	0.494	-1.09	0.625	-0.56
1450761_s_at	Rims2	regulating synaptic membrane exocytosis 2	-1.09	0.834	-1.58	0.126	1.32	0.21	-1.15	0.657	-0.63
1457172_at	Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	-1.09	0.739	1.26	0.329	-1.44	0.278	-2.49	0.042	-0.94
1431284_a_at	2210013K02Rik	RIKEN cDNA 2210013K02 gene	-1.03	0.904	-1.13	0.103	1.01	0.945	-1.06	0.782	-0.55
1416099_at	Rpl27 /// LOC6211(	ribosomal protein L27 /// similar to ribosomal protein L27 /// similar to ribosomal pr	-1.05	0.316	1.03	0.509	-1.12	0.23	-1.26	0.057	-0.6
1417659_at	Vps29	vacuolar protein sorting 29 (S. pombe)	-1.02	0.735	1.07	0.313	-1.22	0.358	-1.13	0.32	-0.57
1423708_a_at	Farslb	phenylalanine-tRNA synthetase-like, beta subunit	1.21	0.438	-1.27	0.115	-1.14	0.084	-1.18	0.287	-0.6
1454222_a_at	Ccdc13	coiled-coil domain containing 13	-1.08	0.909	-1.13	0.709	1.06	0.86	-1.87	0.255	-0.76
1449040_a_at	Sephs2	selenophosphate synthetase 2	-1.09	0.752	1	0.996	-1.05	0.597	-1.07	0.668	-0.55
1456833_at	Gpr17	G protein-coupled receptor 17	-2.16	0.269	-1.01	0.986	1.42	0.441	-1.29	0.394	-0.76
1416988_at	Msh2	mutS homolog 2 (E. coli)	-1.18	0.329	-1	0.998	1.02	0.859	-1.21	0.423	-0.59
1447031_at	---	---	-1.01	0.982	1.09	0.799	-1.27	0.154	-1.21	0.42	-0.6
1428137_at	Arl8b	ADP-ribosylation factor-like 8B	-1.09	0.662	1.02	0.92	-1.06	0.369	-1	0.975	-0.54
1428380_at	0610007C21Rik	RIKEN cDNA 0610007C21 gene	-1.04	0.688	1.06	0.345	-1.18	0.046	-1.12	0.598	-0.57
1440944_at	Anks1b /// LOC544	ankyrin repeat and sterile alpha motif domain containing 1B /// similar to AIDA-1b	-1.21	0.857	-1.27	0.681	1.26	0.678	-1.24	0.773	-0.62
1437009_a_at	Zfp364	zinc finger protein 364	-1.12	0.295	-1.09	0.344	1.06	0.423	-1.49	0.013	-0.66
1424049_at	Lrrc42	leucine rich repeat containing 42	-1.16	0.289	1.18	0.35	-1.2	0.269	-1	0.993	-0.55
1428138_s_at	Arl8b	ADP-ribosylation factor-like 8B	-1.07	0.58	-1.03	0.584	-1.04	0.713	1.1	0.208	-0.51
1435003_at	Pik4ca	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	-1.2	0.191	-1.09	0.462	1.12	0.122	-1.32	0.123	-0.62
1442120_at	---	Lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730007D1	-1.28	0.186	1.17	0.723	-1.09	0.526	-1.37	0.313	-0.64
1434608_at	---	---	-1.04	0.506	1.04	0.437	-1.16	0.321	-1.11	0.283	-0.57
1450127_a_at	Gcgr	glucagon receptor	-1.03	0.886	1	0.96	-1.12	0.436	-1.07	0.82	-0.55
1447934_at	9630033F20Rik	RIKEN cDNA 9630033F20 gene	1.33	0.419	-1.09	0.576	-1.59	0.137	-1.44	0.402	-0.7
1418679_at	Gzmf	granzyme F	-1.17	0.773	-1.1	0.879	1.1	0.603	-1.01	0.982	-0.54
1446196_at	Hmga2	high mobility group AT-hook 2	1.38	0.37	-1.27	0.676	-1.43	0.442	-1.76	0.033	-0.77
1454472_at	2900092N22Rik	RIKEN cDNA 2900092N22 gene	-2.12	0.387	1.81	0.204	-1.69	0.101	-4.31	0.078	-1.58
1447420_at	Brd1	bromodomain containing 1	1.1	0.68	-1.15	0.477	-1.11	0.621	-1.14	0.466	-0.57
1423609_a_at	Mgat1	mannoside acetylglucosaminyltransferase 1	-1.2	0.018	-1.08	0.148	1.12	0.334	-1.3	0.179	-0.62
1417327_at	Cav2	caveolin 2	-1.34	0.018	1.45	0.109	-1.48	0.017	-1.27	0.424	-0.66
1454981_at	D4Ertd22e	DNA segment, Chr 4, ERATO Doi 22, expressed	-1.12	0.685	1.01	0.962	-1.03	0.744	-1.24	0.043	-0.6
1418428_at	Kif5b	kinesin family member 5B	-1.36	0.16	1.21	0.455	-1.08	0.346	-1.01	0.947	-0.56
1455168_a_at	Gnb2l1	guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	-1.02	0.553	1.01	0.887	-1.13	0.109	-1.3	0.013	-0.61
1450372_a_at	Rpl18	ribosomal protein L18	1.01	0.942	-1.08	0.439	-1.06	0.466	-1.66	0.067	-0.7
1457297_at	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4	1.63	0.065	-1.37	0.077	-1.96	0.008	-1.04	0.903	-0.69
1420160_s_at	Myo1e	myosin IE	1.47	0.192	-1.57	0.448	-1.31	0.58	-1.08	0.833	-0.62
1445261_at	D17Ertd763e	DNA segment, Chr 17, ERATO Doi 763, expressed	-1.38	0.732	-1.85	0.243	1.61	0.273	-1.45	0.566	-0.77
1442717_at	Tbc1d13	TBC1 domain family, member 13	-1.17	0.314	1.07	0.916	-1.06	0.869	-1.37	0.169	-0.63
1425313_at	Carf	calcium response factor	1.42	0.301	-1.43	0.555	-1.32	0.173	-1.11	0.828	-0.61
1450635_at	Akp5	alkaline phosphatase 5	1.06	0.606	-1.21	0.136	-1.02	0.77	-1.05	0.451	-0.55
1424765_at	Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	-1.26	0.194	-1.05	0.53	1.12	0.559	-1.08	0.501	-0.57
1454570_at	5830432F11Rik	RIKEN cDNA 5830432F11 gene	1.1	0.817	-1.16	0.796	-1.11	0.822	-1.88	0.174	-0.76
1437042_at	Arnt	aryl hydrocarbon receptor nuclear translocator	-1	0.995	1.2	0.242	-1.49	0.03	-1.05	0.746	-0.58
1416195_at	RP23-136K12.4	putative phosphatase	-1.03	0.844	1.09	0.527	-1.25	0.086	-1.27	0.259	-0.61
1454607_s_at	Psat1	phosphoserine aminotransferase 1	-1.46	0.504	1.26	0.599	-1.08	0.749	-1.43	0.495	-0.68

1439325_at	Blmh	Bleomycin hydrolase	1.33	0.065	-1.22	0.165	-1.39	0.188	-1.76	0.135	-0.76
1440804_at	Nktr	natural killer tumor recognition sequence	1.03	0.967	-1.07	0.924	-1.1	0.876	-1.38	0.492	-0.63
1450674_at	Cdk5	cyclin-dependent kinase 5	1.07	0.736	-1.15	0.399	-1.08	0.7	-1.31	0.152	-0.62
1447119_at	Ttf2	Transcription termination factor, RNA polymerase II	1.19	0.52	-1.36	0.577	-1.05	0.756	-1.04	0.762	-0.57
1439614_at	Htr4	5 hydroxytryptamine (serotonin) receptor 4	-1.04	0.784	1.23	0.661	-1.47	0.533	-1.11	0.855	-0.6
1430857_s_at	Pex11c	peroxisomal biogenesis factor 11c	-1.07	0.675	-1.1	0.593	1.03	0.907	-1.01	0.938	-0.54
1441543_at	Eya3	Eyes absent 3 homolog (Drosophila)	1.52	0.26	-1.27	0.504	-1.77	0.117	-1.36	0.392	-0.72
1434697_at	1110001P04Rik	RIKEN cDNA 1110001P04 gene	-1.2	0.623	-1.21	0.268	1.22	0.362	-1.75	0.106	-0.74
1422507_at	Cstb	cystatin B	-1.08	0.324	1.08	0.123	-1.16	0.309	-1.27	0.406	-0.61
1416553_at	Stra13	stimulated by retinoic acid 13	-1.02	0.899	-1.1	0.391	-1.01	0.931	1.1	0.472	-0.51
1447189_at	Gltscr1	Glioma tumor suppressor candidate region gene 1	-1.2	0.587	-1.3	0.543	1.27	0.72	-1.46	0.566	-0.67
1430830_at	A430105J06Rik	RIKEN cDNA A430105J06 gene	-1.04	0.814	-2.08	0.006	1.43	0.437	-1.13	0.755	-0.7
1423282_at	Pitpna	phosphatidylinositol transfer protein, alpha	-1.01	0.513	1.05	0.119	-1.2	0.057	-1.53	0.025	-0.67
1418651_at	Spata6	spermatogenesis associated 6	-1.1	0.535	1.09	0.803	-1.15	0.193	-1.17	0.558	-0.58
1424285_s_at	Arl6ip4	ADP-ribosylation factor-like 6 interacting protein 4	1.05	0.063	-1.13	0.283	-1.07	0.432	-1.16	0.072	-0.58
1431141_at	2610507I01Rik	RIKEN cDNA 2610507I01 gene	1.2	0.622	-1.42	0.095	-1.03	0.939	-1.2	0.803	-0.61
1450067_a_at	1810034K20Rik	RIKEN cDNA 1810034K20 gene	1.01	0.958	-1.13	0.385	-1.03	0.897	-1.17	0.363	-0.58
1427773_a_at	Rabac1	Rab acceptor 1 (prenylated)	1.07	0.821	-1.03	0.814	-1.2	0.238	-1.48	0.285	-0.66
1428259_at	Pxdn	peroxidasin homolog (Drosophila)	-1.05	0.571	-1.08	0.646	-1.01	0.973	1.01	0.891	-0.53
1446812_at	Hand2	Heart and neural crest derivatives expressed transcript 2	-1.37	0.163	-1.33	0.372	1.39	0.463	-1.45	0.266	-0.69
1443512_at	Spata5	Spermatogenesis associated 5	-1.04	0.892	1.26	0.559	-1.54	0.155	-1.08	0.525	-0.6
1426497_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	-1	0.951	1.03	0.761	-1.19	0.077	-1.25	0.302	-0.6
1419324_at	Lhx9	LIM homeobox protein 9	-1.52	0.017	1.43	0.323	-1.28	0.516	-1.04	0.938	-0.6
1455572_x_at	Rps18	ribosomal protein S18	-1	0.94	1.07	0.36	-1.24	0.119	-1.3	0.016	-0.62
1427903_at	Phpt1	phosphohistidine phosphatase 1	1.06	0.474	-1.06	0.437	-1.15	0.221	-1.35	0.304	-0.62
1428389_s_at	Wdr43	WD repeat domain 43	-1.09	0.632	-1.14	0.249	1.08	0.739	-1.23	0.149	-0.6
1458069_at	Tbc1d5	TBC1 domain family, member 5	1.23	0.374	-1.22	0.105	-1.22	0.34	-1.39	0.49	-0.65
1454042_a_at	Srpk1	serine/arginine-rich protein specific kinase 1	1.07	0.368	-1.06	0.655	-1.16	0.311	-1.33	0.006	-0.62
1445235_at	Ythdf3	YTH domain family 3	1.37	0.313	-1.37	0.47	-1.29	0.382	-1.17	0.44	-0.61
1458192_at	C130065N10Rik	RIKEN cDNA C130065N10 gene	-1.17	0.588	-1.49	0.167	1.35	0.392	-1.46	0.286	-0.69
1446054_at	Zmpste24	Zinc metallopeptidase, STE24 homolog (S. cerevisiae)	-1.29	0.358	-1.38	0.624	1.37	0.514	-1.16	0.564	-0.61
1460715_x_at	Tcfcp2l1	Transcription factor CP2-like 1	-1.1	0.897	1.05	0.92	-1.09	0.645	-1.04	0.908	-0.55
1437348_at	Fbxo28	F-box protein 28	-1.12	0.586	-1.07	0.537	1.05	0.669	-1.03	0.854	-0.54
1421671_at	Hsd17b3	hydroxysteroid (17-beta) dehydrogenase 3	-1.36	0.469	1.26	0.604	-1.13	0.361	-2.06	0.117	-0.83
1459300_at	---	Transcribed locus	-1.12	0.368	1.43	0.416	-1.82	0.049	-1.24	0.317	-0.69
1441773_at	1700061N14Rik	RIKEN cDNA 1700061N14 gene	1.71	0.403	-2.1	0.419	-1.45	0.592	-1.57	0.529	-0.85
1420127_s_at	Ccpg1	cell cycle progression 1	1.04	0.869	-1.07	0.765	-1.11	0.51	-1.19	0.254	-0.58
1437336_x_at	1110002E23Rik	RIKEN cDNA 1110002E23 gene	-1.05	0.35	1.04	0.169	-1.14	0.369	-1.08	0.433	-0.56
1459748_at	---	---	1.07	0.586	-1.17	0.603	-1.05	0.73	-1.2	0.286	-0.59
1429515_at	Ubr2	ubiquitin protein ligase E3 component n-recognin 2	-1.01	0.81	-1.14	0.451	1.01	0.948	-1.07	0.548	-0.55
1444148_at	LOC497253	hypothetical LOC497253	-1.1	0.688	1.06	0.848	-1.1	0.844	-1.87	0.007	-0.75
1418504_at	Hspa9a	heat shock protein 9A	-1.04	0.627	-1.16	0.039	1.05	0.538	-1.06	0.695	-0.55
1448243_at	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	-1.12	0.595	-1.01	0.89	-1.01	0.95	1.5	0.142	-0.41
1437136_at	5830436I19Rik	RIKEN cDNA 5830436I19 gene	1.48	0.593	-1.24	0.581	-1.68	0.204	-1.43	0.437	-0.72
1422362_s_at	Olfr68 /// Olfr69	olfactory receptor 68 /// olfactory receptor 69	-1.09	0.549	-1.24	0.454	1.14	0.329	-1.22	0.007	-0.6
1448206_at	Psma2	proteasome (prosome, macropain) subunit, alpha type 2	-1.05	0.759	-1.14	0.022	1.05	0.489	-1.01	0.912	-0.54
1434543_a_at	Bola2	bolA-like 2 (E. coli)	-1.03	0.71	1.04	0.754	-1.15	0.575	-1.39	0.148	-0.63
1426571_at	Tmem16a	transmembrane protein 16A	-1.1	0.918	1.09	0.797	-1.14	0.709	-1.12	0.847	-0.57
1438017_at	Rusc1	RUN and SH3 domain containing 1	-1.04	0.657	1	0.994	-1.1	0.277	-1.09	0.303	-0.56
1428335_a_at	Scfd1	sec1 family domain containing 1	-1.16	0.203	-1.01	0.852	1.03	0.826	-1.11	0.354	-0.57
1418603_at	Avpr1a	arginine vasopressin receptor 1A	-1.51	0.249	-1.09	0.714	1.3	0.192	-1.54	0.068	-0.71
1458218_s_at	Pde7a	phosphodiesterase 7A	1.11	0.441	-1.01	0.962	-1.29	0.076	-1.92	0.091	-0.78
1456227_x_at	Rbbp7	retinoblastoma binding protein 7	-1.07	0.378	-1.01	0.884	-1.06	0.293	1.02	0.549	-0.53

1437350_at	RP23-143A14.5	candidate tumor suppressor OVCA2	1.09	0.172	-1.15	0.106	-1.09	0.2	-1.08	0.693	-0.56
1437969_s_at	0610007P22Rik	RIKEN cDNA 0610007P22 gene	-1.04	0.861	1.01	0.861	-1.1	0.659	-1.42	0.154	-0.64
1457075_at	A830031M15Rik	RIKEN cDNA A830031M15 gene	1.23	0.408	-1.33	0.366	-1.12	0.452	-1.24	0.473	-0.62
1435340_at	Jmjd2a	jumonji domain containing 2A	-1.33	0.031	-1.1	0.35	1.21	0.209	-1.18	0.435	-0.6
1442564_at	---	---	1.78	0.45	-1.44	0.526	-2.46	0.078	-1.07	0.6	-0.8
1440072_at	E430022K19Rik	RIKEN cDNA E430022K19 gene	-1.31	0.505	-1.64	0.078	1.5	0.321	-1.06	0.877	-0.63
1426234_s_at	BC002199	cDNA sequence BC002199	-1.21	0.118	1.12	0.211	-1.07	0.189	-1	0.984	-0.54
1424741_s_at	Creb3	cAMP responsive element binding protein 3	1.02	0.091	-1.08	0.196	-1.08	0.425	-1.27	0.255	-0.6
1418473_at	Cutc	cutC copper transporter homolog (E.coli)	-1.14	0.47	-1.1	0.538	1.09	0.181	-1.65	0.018	-0.7
1420753_at	Tll1	tolloid-like	1.16	0.789	-1.1	0.829	-1.23	0.292	-1.42	0.603	-0.65
1432194_at	9530020I12Rik	RIKEN cDNA 9530020I12 gene	-1.05	0.671	-1.77	0.104	1.35	0.128	-1.56	0.413	-0.75
1436173_at	Dlc1	deleted in liver cancer 1	-1.13	0.387	1.05	0.601	-1.06	0.838	-1.19	0.349	-0.58
1426526_s_at	Ovgp1	oviductal glycoprotein 1	-1.01	0.916	-1.26	0.337	1.1	0.238	-1.16	0.193	-0.59
1451312_at	Ndufs7	NADH dehydrogenase (ubiquinone) Fe-S protein 7	-1.07	0.436	-1.24	0.051	1.14	0.085	-1.08	0.514	-0.56
1453578_at	Pter	phosphotriesterase related	-1.11	0.148	1.03	0.918	-1.06	0.696	-1.24	0.686	-0.59
1436850_at	Creg2	cellular repressor of E1A-stimulated genes 2	-1.11	0.837	1.07	0.92	-1.1	0.626	-2.28	0.076	-0.86
1446190_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	1.38	0.45	-1.33	0.764	-1.35	0.123	-2.04	0.151	-0.83
1423522_at	Npm3 /// Npm3-ps1	nucleoplasmin 3 /// nucleoplasmin 3, pseudogene 1 /// similar to Nucleoplasmin-3	-3.95	0.46	-1.62	0.521	2.01	0.365	-9.33	0.206	-3.22
1430274_a_at	Stard3nl	STARD3 N-terminal like	-1.01	0.904	-1.02	0.883	-1.11	0.579	1.06	0.614	-0.52
1445093_at	Tcf12	Transcription factor 12	1.8	0.039	-1.52	0.226	-2.39	0.109	-1.1	0.717	-0.8
1452644_at	Mbd3l2	methyl-CpG binding domain protein 3-like 2	-1.12	0.879	1.28	0.705	-1.42	0.476	-1.19	0.585	-0.61
1437898_at	C920009B18Rik	RIKEN cDNA C920009B18 gene	-1.03	0.948	-1.2	0.775	1.07	0.8	-1.33	0.324	-0.62
1423177_a_at	Abi1	abl-interactor 1	-1.16	0.182	-1.05	0.259	1.06	0.329	-1.58	0.02	-0.68
1454900_s_at	Phr1	pam, highwire, rpm 1	-1.09	0.403	1.03	0.722	-1.07	0.727	-1.69	0.104	-0.71
1456081_a_at	Aacs	acetoacetyl-CoA synthetase	-1.32	0.224	-1.32	0.344	1.36	0.055	-1.38	0.408	-0.66
1445301_at	BC028528	CDNA sequence BC028528	1.47	0.235	-1.24	0.739	-1.67	0.074	-2.14	0.066	-0.89
1433698_a_at	Txnl4	thioredoxin-like 4	-1.14	0.114	-1.05	0.498	1.04	0.532	-1.07	0.404	-0.55
1454631_at	6330549H03Rik	RIKEN cDNA 6330549H03 gene	-1.02	0.675	-1.01	0.716	-1.1	0.136	1.06	0.528	-0.52
1460178_at	1300002A08Rik	RIKEN cDNA 1300002A08 gene	-1.17	0.004	-1.46	0.027	1.34	0.039	-1.23	0.179	-0.63
1435475_at	Lman2l	lectin, mannose-binding 2-like	-1.16	0.198	-1.14	0.085	1.13	0.472	-1.14	0.319	-0.57
1439560_x_at	LOC432995	hypothetical gene supported by BC047216	-1.06	0.735	1.15	0.495	-1.28	0.29	-1.08	0.866	-0.57
1459840_s_at	Ccdc28b	coiled coil domain containing 28B	-1.27	0.087	-1.03	0.727	1.12	0.685	-1.06	0.77	-0.56
1439386_x_at	Mat2a	methionine adenosyltransferase II, alpha	-1.18	0.524	1.21	0.666	-1.22	0.36	-1.01	0.939	-0.55
1435082_at	Sypl	synaptophysin-like protein	1.18	0.428	-1.06	0.724	-1.33	0.051	-1.2	0.245	-0.6
1419834_x_at	Mark1	MAP/microtubule affinity-regulating kinase 1	-1.11	0.8	-1.08	0.673	1.05	0.85	-1.35	0.187	-0.62
1445361_at	---	---	-1.06	0.763	1.15	0.682	-1.27	0.434	-1.3	0.102	-0.62
1423857_at	Mrpl30	mitochondrial ribosomal protein L30	1.02	0.706	-1.05	0.333	-1.1	0.419	-1.22	0.226	-0.59
1446589_at	Rhbdd1	Rhomboid domain containing 1	-1.11	0.821	-1.18	0.529	1.13	0.818	-1.55	0.114	-0.68
1426676_s_at	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	-1.21	0.36	-1.13	0.086	1.16	0.441	-1.07	0.637	-0.56
1460562_at	Eftud1	elongation factor Tu GTP binding domain containing 1	-1.23	0.206	-1.11	0.525	1.17	0.101	-1.34	0.019	-0.63
1457789_at	Cln3	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	-1.27	0.336	-1.1	0.314	1.18	0.22	-1.07	0.747	-0.56
1429055_at	4930506M07Rik	RIKEN cDNA 4930506M07 gene	-1.09	0.835	-1.22	0.244	1.15	0.148	-1.47	0.284	-0.66
1422900_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	-1.11	0.588	-1.25	0.004	1.18	0.511	-1.42	0.092	-0.65
1432600_at	2310061A09Rik	RIKEN cDNA 2310061A09 gene	-1.21	0.711	1.16	0.742	-1.13	0.535	-1.23	0.487	-0.6
1449289_a_at	B2m	beta-2 microglobulin	1.14	0.364	-1.16	0.431	-1.15	0.111	-1.19	0.013	-0.59
1447973_at	Trip11	thyroid hormone receptor interactor 11	-1.19	0.499	-1.09	0.821	1.12	0.623	-1.1	0.734	-0.57
1428543_at	Ppat	phosphoribosyl pyrophosphate amidotransferase	-1.06	0.589	-1.05	0.814	-1.02	0.907	1.93	0.103	-0.3
1424815_at	Gys2 /// LOC63362	glycogen synthase 2 /// similar to glycogen synthase 2	-1.45	0.235	-1.26	0.282	1.4	0.598	-3.03	0.237	-1.09
1438029_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	-1.1	0.13	-1.15	0.169	1.1	0.452	-1.24	0.302	-0.6
1427737_a_at	1200011M11Rik	RIKEN cDNA 1200011M11 gene	-1.2	0.167	-1.09	0.494	1.13	0.503	-1.16	0.478	-0.58
1423316_at	Tmem39a	transmembrane protein 39a	-1.06	0.798	1.05	0.801	-1.14	0.435	-1.18	0.022	-0.58
1416826_a_at	Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	-1.16	0.063	1.05	0.388	-1.04	0.781	-1.01	0.906	-0.54
1431818_at	1700012B15Rik	RIKEN cDNA 1700012B15 gene	-1.09	0.049	-1.29	0.221	1.18	0.429	-1.07	0.632	-0.56

1450339_a_at	Bcl11b	B-cell leukemia/lymphoma 11B	-1.51	0.32	-1.61	0.058	1.6	0.286	-1.85	0.279	-0.84
1416845_at	Tmem132a	transmembrane protein 132A	-1.08	0.138	-1.1	0.816	1.05	0.825	-1.09	0.785	-0.56
1448891_at	Msr2	macrophage scavenger receptor 2	1.21	0.2	-1.27	0.707	-1.14	0.557	-2.01	0.348	-0.8
1435039_a_at	Pip5k1b	Phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-1.77	0.465	-1.38	0.472	1.59	0.344	-1.38	0.661	-0.74
1453316_at	4933401F05Rik	RIKEN cDNA 4933401F05 gene	-1.12	0.646	-1.13	0.734	1.1	0.83	-1.9	0.022	-0.76
1449062_at	Khk	ketohexokinase	-1.09	0.506	-1.06	0.686	1.02	0.899	-1.11	0.553	-0.56
1420216_at	1810012K16Rik	RIKEN cDNA 1810012K16 gene	-1.26	0.675	1.32	0.451	-1.3	0.391	-1.41	0.33	-0.66
1454724_x_at	5730446C15Rik	RIKEN cDNA 5730446C15 gene	1.02	0.888	-1.05	0.349	-1.11	0.691	-1.66	0.194	-0.7
1419217_at	Sergef	secretion regulating guanine nucleotide exchange factor	-1.07	0.597	-1.27	0.142	1.16	0.543	-1.17	0.371	-0.59
1423073_at	Cmpk	cytidylate kinase	1.01	0.914	-1.02	0.717	-1.12	0.329	-1.19	0.323	-0.58
1457901_at	D4Ertd76e	DNA segment, Chr 4, ERATO Doi 76, expressed	1.53	0.46	-1.46	0.407	-1.51	0.023	-1.25	0.292	-0.67
1428140_at	Oxct1	3-oxoacid CoA transferase 1	-1.14	0.433	1.24	0.198	-1.31	0.004	-1.15	0.496	-0.59
1455150_at	---	13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:593043	-1.13	0.738	1.47	0.284	-1.91	0.058	-1.26	0.745	-0.71
1425632_a_at	Pqlc2	PQ loop repeat containing 2	-1.08	0.599	-1.07	0.624	1.02	0.817	-1.74	0.144	-0.72
1423801_a_at	Aprt	adenine phosphoribosyl transferase	-1.26	0.107	-1.01	0.907	1.1	0.513	-1.25	0.343	-0.61
1434752_at	Zfp207	zinc finger protein 207	1.58	0.13	-1.32	0.277	-1.85	0.013	-1.23	0.487	-0.7
1442135_at	Gm237	Gene model 237, (NCBI)	1.04	0.366	-1.03	0.812	-1.15	0.192	-1.11	0.376	-0.56
1456587_x_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	-1.12	0.281	-1.16	0.138	1.12	0.488	-1.18	0.185	-0.58
1448548_at	Tulp4	tubby like protein 4	1	0.99	-1.06	0.628	-1.07	0.728	-1.27	0.359	-0.6
1451269_at	Pdzd11	PDZ domain containing 11	-1.02	0.893	-1.07	0.714	-1.03	0.805	1.55	0.172	-0.39
1417799_at	Atp6v1g2	ATPase, H+ transporting, lysosomal V1 subunit G2	-1.07	0.224	-1.19	0.167	1.11	0.586	-1.2	0.651	-0.59
1436764_at	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	1.01	0.921	-1	0.967	-1.15	0.684	-1.05	0.872	-0.55
1424872_at	2310001H12Rik ///	RIKEN cDNA 2310001H12 gene /// similar to zinc finger protein 709 /// similar to	1.02	0.906	-1.1	0.589	-1.05	0.673	-1.31	0.063	-0.61
1422104_at	Vsx1	visual system homeobox 1 homolog (zebrafish)	1.08	0.872	-1.02	0.962	-1.23	0.355	-1.3	0.587	-0.62
1432998_at	5830462O15Rik	RIKEN cDNA 5830462O15 gene	1.27	0.34	-1.54	0.072	-1.04	0.841	-1.32	0.391	-0.66
1421230_a_at	Msi2	Musashi homolog 2 (Drosophila)	-1.09	0.699	1.08	0.805	-1.14	0.702	-1.17	0.57	-0.58
1427969_s_at	Zfp654	zinc finger protein 654	1.06	0.49	-1.02	0.859	-1.2	0.399	-1.15	0.418	-0.57
1418927_a_at	LOC671769	similar to hyaluronic acid binding protein 4	1.01	0.885	-1.06	0.497	-1.08	0.454	-1.29	0.182	-0.6
1451398_at	Cbr4	carbonyl reductase 4	-1.26	0.025	-1.04	0.724	1.12	0.198	-1.05	0.785	-0.56
1445232_at	Dock9	Dedicator of cytokinesis 9	1.37	0.081	-1.21	0.597	-1.46	0.303	-1.35	0.231	-0.66
1420474_at	Mtpn	myotrophin	-1.14	0.021	-1.2	0.04	1.17	0.148	-1.22	0.156	-0.6
1439485_at	Zfp608 /// D430007	zinc finger protein 608 /// RIKEN cDNA D430007A19 gene	-1.18	0.349	1.24	0.405	-1.26	0.171	-1.63	0.032	-0.71
1423985_at	Gng5	guanine nucleotide binding protein (G protein), gamma 5 subunit	-1.03	0.789	1.05	0.085	-1.17	0.125	-1.05	0.432	-0.55
1427051_at	Tnks1bp1	tankyrase 1 binding protein 1	-1	0.991	-1.15	0.523	1.02	0.914	-1.92	0.212	-0.77
1452092_at	4631426J05Rik	RIKEN cDNA 4631426J05 gene	-1.08	0.604	1.06	0.682	-1.12	0.499	-1.6	0.098	-0.68
1449052_a_at	Dnmt3b	DNA methyltransferase 3B	-1.43	0.601	-1	0.996	1.18	0.604	-1.26	0.104	-0.63
1455796_x_at	Olfm1	olfactomedin 1	1.01	0.98	-1.09	0.754	-1.04	0.885	-1.1	0.754	-0.56
1438125_at	C230085N15Rik	RIKEN cDNA C230085N15 gene	-2.41	0.394	1.55	0.514	-1.09	0.695	-3.48	0.033	-1.36
1448487_at	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	-1.02	0.906	1.12	0.548	-1.28	0.209	-1.55	0.227	-0.68
1457848_at	A930016P21Rik	RIKEN cDNA A930016P21 gene	1.27	0.456	-1.4	0.33	-1.11	0.545	-1.13	0.592	-0.59
1454153_at	4930556J24Rik	RIKEN cDNA 4930556J24 gene	1.19	0.1	-1.07	0.873	-1.31	0.588	-1.05	0.952	-0.56
1443466_s_at	Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	-1.09	0.683	-1.09	0.526	1.05	0.632	-1.1	0.41	-0.56
1449972_s_at	Zfp97 /// BC018101	zinc finger protein 97 /// cDNA sequence BC018101	1.03	0.247	-1.1	0.563	-1.06	0.736	-1.39	0.23	-0.63
1416054_at	Rps5	ribosomal protein S5	-1	0.92	1.03	0.742	-1.17	0.133	-1.33	0	-0.62
1432206_at	9030404E10Rik	RIKEN cDNA 9030404E10 gene	-1.82	0.265	1.43	0.117	-1.11	0.458	-1.38	0.116	-0.72
1421713_at	Pramel1	preferentially expressed antigen in melanoma-like 1	1.06	0.932	-1.15	0.693	-1.05	0.929	-1.33	0.473	-0.62
1416140_a_at	Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-1.16	0.049	-1.11	0.132	1.12	0.297	-1.51	0.064	-0.66
1453076_at	9130211I03Rik	RIKEN cDNA 9130211I03 gene	-1.25	0.477	1.13	0.305	-1.05	0.859	-1.69	0.008	-0.71
1453983_a_at	Mett10d	methyltransferase 10 domain containing	-1.18	0.06	1.03	0.525	-1	0.993	-1.29	0.245	-0.61
1438820_at	Rnf17	ring finger protein 17	-1.11	0.434	-1.06	0.811	1.03	0.867	-1.44	0.251	-0.64
1456532_at	Pdgfd	Platelet-derived growth factor, D polypeptide	-1.01	0.97	1.06	0.76	-1.21	0.196	-1.11	0.781	-0.57
1451820_at	Diras1	DIRAS family, GTP-binding RAS-like 1	1.11	0.829	-1.03	0.929	-1.24	0.491	-1.17	0.757	-0.58
1435180_at	Podn	podocan	-1.24	0.119	-1.07	0.777	1.14	0.524	-1.12	0.381	-0.57

1429532_at	Morc2a	microrchidia 2A	-1.13	0.284	-1.06	0.666	1.05	0.762	-1.2	0.53	-0.58
1450198_at	Dusp13	dual specificity phosphatase 13	-1.1	0.799	-1.35	0.643	1.23	0.375	-1.05	0.928	-0.57
1437544_at	Fubp1	far upstream element (FUSE) binding protein 1	1.37	0.479	-1.14	0.635	-1.58	0.322	-1.47	0.247	-0.7
1436638_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	-1.06	0.819	-2.25	0.105	1.49	0.271	-2.16	0.294	-0.99
1437215_at	LOC667026 /// LOC	similar to MTH2 protein /// similar to MTH2 protein	-1.49	0.292	1.26	0.461	-1.05	0.938	-2.07	0.13	-0.84
1436184_at	Gm632	gene model 632, (NCBI)	-1.12	0.322	1.09	0.529	-1.11	0.59	-1.58	0.125	-0.68
1438417_at	Pwwp2	PWWP domain containing 2	-1.09	0.316	1.15	0.428	-1.22	0.24	-1.14	0.21	-0.58
1438031_at	Rasgrp3	RAS, guanyl releasing protein 3	-1.05	0.562	1.02	0.843	-1.1	0.772	-1.45	0.301	-0.64
1455860_at	Pigh	phosphatidylinositol glycan anchor biosynthesis, class H	-1.01	0.914	1	0.977	-1.12	0.405	-1.2	0.403	-0.58
1422782_s_at	Tlr3	toll-like receptor 3	-1.2	0.539	1.36	0.08	-1.44	0.061	-1.85	0.166	-0.78
1435397_at	BC038156	cDNA sequence BC038156	1.29	0.207	-1.04	0.835	-1.58	0.073	-1.07	0.487	-0.6
1448725_at	Parg	poly (ADP-ribose) glycohydrolase	1.02	0.822	-1.04	0.375	-1.11	0.148	-1.06	0.396	-0.55
1426895_at	Zfp191	zinc finger protein 191	1.02	0.908	-1.06	0.188	-1.09	0.508	-1.36	0.104	-0.62
1450848_at	Dap3	death associated protein 3	-1.09	0.34	-1	0.998	-1.03	0.716	1.1	0.559	-0.51
1448211_at	Atp6v0e2	ATPase, H+ transporting, lysosomal V0 subunit E2	-1.19	0.442	-1.07	0.883	1.11	0.668	-1.3	0.142	-0.61
1438914_at	2310028N02Rik	RIKEN cDNA 2310028N02 gene	2	0.379	-2.44	0.222	-2.1	0.234	-1.76	0.396	-1.08
1436500_at	Rps24	ribosomal protein S24	1.41	0.14	-1.43	0.351	-1.29	0.704	-1.53	0.509	-0.71
1417366_s_at	Calm1	calmodulin 1	-1.1	0.338	-1.05	0.609	1.02	0.89	-1.5	0.204	-0.66
1438952_x_at	Tarbp2	TAR (HIV) RNA binding protein 2	1.29	0.016	-1.4	0.237	-1.14	0.521	-2.1	0.048	-0.84
1423295_at	Tm9sf2	transmembrane 9 superfamily member 2	-1.01	0.977	1.11	0.573	-1.29	0.107	-1.14	0.302	-0.58
1418363_at	Lalba	lactalbumin, alpha	-1.7	0.135	1.37	0.322	-1.08	0.866	-2.04	0.584	-0.86
1438076_at	Rpl30	ribosomal protein L30	-1.13	0.491	-1.11	0.508	1.1	0.645	-1.07	0.665	-0.55
1451138_x_at	Mier2	mesoderm induction early response 1, family member 2	-1.09	0.702	1.03	0.841	-1.07	0.848	-1.01	0.914	-0.53
1451074_at	Rnf13	ring finger protein 13	-1.04	0.538	1.03	0.599	-1.12	0.332	-1.45	0.085	-0.64
1455324_at	LOC433022	hypothetical LOC433022	1.08	0.788	-1.17	0.461	-1.05	0.724	-1.7	0.17	-0.71
1425515_at	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	-1.55	0.54	-1.6	0.348	1.61	0.413	-1.63	0.339	-0.79
1459716_at	AI835735	expressed sequence AI835735	1.38	0.693	-1.2	0.768	-1.49	0.384	-1.63	0.501	-0.74
1460342_s_at	AA536749	expressed sequence AA536749	-1.05	0.482	-1.15	0.301	1.06	0.748	-1.24	0.182	-0.6
1455079_at	Dcun1d4	DCN1, defective in cullin neddylation 1, domain containing 4 (S. cerevisiae)	1.04	0.71	-1.13	0.169	-1.04	0.762	-1.38	0.401	-0.63
1459679_s_at	Myo1b	myosin IB	1.33	0.624	-1.19	0.134	-1.4	0.166	-1.21	0.826	-0.62
1432373_at	4930533B01Rik	RIKEN cDNA 4930533B01 gene	-1.3	0.475	1.33	0.344	-1.27	0.681	-2.14	0.182	-0.85
1435328_at	Cyhr1	cysteine and histidine rich 1	-1.04	0.811	1.02	0.856	-1.11	0.232	-1.02	0.92	-0.54
1456990_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430015G	1.16	0.857	-1	0.995	-1.37	0.359	-1.38	0.259	-0.65
1457713_at	Ercc5	Excision repair cross-complementing rodent repair deficiency, complementation g	-1.5	0.504	-1.15	0.315	1.35	0.583	-1.51	0.39	-0.7
1439257_x_at	Rpn1	ribophorin I	-1.09	0.571	1.06	0.629	-1.11	0.343	-1.13	0.558	-0.56
1438869_at	4930515G01Rik	RIKEN cDNA 4930515G01 gene	1.21	0.502	-1.35	0.465	-1.07	0.773	-1.1	0.339	-0.58
1421803_at	Apbh	androgen-binding protein eta	1.27	0.484	-1.27	0.709	-1.21	0.667	-1.17	0.623	-0.6
1434696_at	Ift52	intraflagellar transport 52 homolog (Chlamydomonas)	-1.15	0.022	-1	0.938	1.02	0.806	-1.25	0.13	-0.6
1421827_at	Dll4	delta-like 4 (Drosophila)	-1.32	0.273	1.23	0.463	-1.12	0.661	-1.06	0.86	-0.57
1431176_at	2310010I16Rik	RIKEN cDNA 2310010I16 gene	-1.14	0.454	1.23	0.399	-1.28	0.397	-1.28	0.788	-0.62
1428426_s_at	Tgfbrap1	transforming growth factor, beta receptor associated protein 1	-1.1	0.04	-1.04	0.437	1.01	0.924	-1.1	0.653	-0.56
1436342_a_at	D19Ertd721e	DNA segment, Chr 19, ERATO Doi 721, expressed	1.1	0.359	-1.1	0.072	-1.15	0.251	-1.1	0.6	-0.56
1460457_at	2810405F17Rik	RIKEN cDNA 2810405F17 gene	-1.07	0.88	-1.27	0.537	1.17	0.705	-1.12	0.575	-0.57
1443833_at	---	Transcribed locus	-1.15	0.466	-1.1	0.796	1.11	0.319	-1.61	0.069	-0.69
1424070_at	Napg	N-ethylmaleimide sensitive fusion protein attachment protein gamma	-1.11	0.504	-1.19	0.149	1.15	0.656	-1.09	0.669	-0.56
1457943_at	1700011J10Rik	RIKEN cDNA 1700011J10 gene	1.09	0.9	-1.09	0.75	-1.13	0.801	-1.18	0.44	-0.58
1428201_at	2310036O22Rik	RIKEN cDNA 2310036O22 gene	-1.01	0.875	1.04	0.481	-1.16	0.132	-1.02	0.841	-0.54
1452293_at	Snx19	sorting nexin 19	1.19	0.438	-1.16	0.169	-1.21	0.099	-1.12	0.426	-0.57
1420388_at	Prss12	protease, serine, 12 neurotrypsin (motopsin)	-1.09	0.54	-1.43	0.326	1.27	0.166	-1.45	0.257	-0.67
1442210_at	1700058C01Rik	RIKEN cDNA 1700058C01 gene	-1.43	0.546	-1.44	0.524	1.49	0.283	-1.24	0.697	-0.66
1423782_at	Mobk1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	-1.05	0.704	1.07	0.182	-1.16	0.074	-1.44	0.075	-0.64
1416603_at	Rpl22 /// LOC6234	ribosomal protein L22 /// similar to 60S ribosomal protein L22 (Heparin-binding pr	-1.06	0.567	1.12	0.545	-1.23	0.105	-1.92	0.048	-0.77
1449054_a_at	Pcbp4	poly(rC) binding protein 4	1.08	0.794	-1.18	0.343	-1.04	0.808	-1.29	0.403	-0.61

1455256_at	Tnik /// LOC665113	TRAF2 and NCK interacting kinase /// similar to [Segment 1 of 2] Traf2 and NCK-	-1.24	0.259	1.18	0.157	-1.11	0.371	-1.01	0.959	-0.55
1426900_at	Jmjd1c	jumonji domain containing 1C	-1.04	0.864	1.03	0.823	-1.12	0.291	-1.64	0.195	-0.69
1423341_at	Cspg4	chondroitin sulfate proteoglycan 4	1.12	0.351	-1.12	0.728	-1.14	0.802	-1.13	0.728	-0.57
1439700_at	Adam1b	A disintegrin and metallopeptidase domain 1b	1.13	0.459	-1.03	0.908	-1.27	0.69	-1.44	0.549	-0.65
1451104_a_at	Snrp70	U1 small nuclear ribonucleoprotein polypeptide A	-1.12	0.366	1.02	0.862	-1.02	0.921	-1.11	0.694	-0.56
1418273_a_at	Rpl30 /// LOC6668	ribosomal protein L30 /// similar to ribosomal protein L30 /// similar to ribosomal p	-1.03	0.884	1.11	0.033	-1.25	0.087	-1.59	0.067	-0.69
1437343_x_at	Atad3a	ATPase family, AAA domain containing 3A	-1.19	0.029	-1.12	0.269	1.15	0.222	-1.12	0.189	-0.57
1416600_a_at	Dscr1	Down syndrome critical region homolog 1 (human)	-1.1	0.431	1.04	0.663	-1.07	0.765	-1.12	0.305	-0.56
1457903_at	Hebp1	Heme binding protein 1	1.45	0.674	-1.31	0.213	-1.49	0.166	-1.51	0.206	-0.72
1439609_at	---	Transcribed locus	-1.31	0.655	1.17	0.829	-1.04	0.95	-3.58	0.043	-1.19
1453786_at	---	---	-1.3	0.638	-1.26	0.487	1.32	0.168	-1.56	0.324	-0.7
1452405_x_at	Tcra /// A430107P0	T-cell receptor alpha chain /// RIKEN cDNA A430107P09 gene	-1.03	0.954	-1.32	0.214	1.15	0.398	-2.09	0.114	-0.82
1429112_at	Tln2 /// LOC639214	talin 2 /// similar to talin 2	-1.14	0.748	1.23	0.064	-1.28	0.545	-1.17	0.336	-0.59
1436989_s_at	Slc12a6	solute carrier family 12, member 6	-1.03	0.947	-1.28	0.08	1.13	0.72	-1.89	0.08	-0.77
1448034_at	AI842396	expressed sequence AI842396	1.06	0.766	-1.16	0.113	-1.04	0.782	-1.15	0.677	-0.57
1423052_at	Arf4	ADP-ribosylation factor 4	1.03	0.714	-1.14	0.107	-1.02	0.904	-1.1	0.59	-0.56
1445456_at	---	---	1.27	0.45	-1.01	0.91	-1.6	0.099	-1.26	0.027	-0.65
1458412_at	Zfp78	zinc finger protein 78	1.01	0.961	-1.05	0.84	-1.09	0.712	-1.44	0.086	-0.64
1429247_at	Anxa6	annexin A6	-1.02	0.911	1.19	0.616	-1.41	0.173	-1.8	0.196	-0.76
1419448_at	Tbc1d1	TBC1 domain family, member 1	1.81	0.299	-1.63	0.349	-2.14	0.042	-2.15	0.427	-1.03
1431124_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	1.04	0.857	-1.02	0.881	-1.15	0.35	-1.35	0.431	-0.62
1423855_x_at	Rpl17	ribosomal protein L17	-1	0.974	1.04	0.054	-1.18	0.067	-1.33	0.078	-0.62
1419054_a_at	Ptpn21	protein tyrosine phosphatase, non-receptor type 21	-1.15	0.257	1.08	0.702	-1.07	0.778	-1.92	0.098	-0.76
1438844_x_at	Spata5	spermatogenesis associated 5	-1.1	0.664	1.02	0.946	-1.04	0.838	-1.08	0.78	-0.55
1435577_at	Dab1	disabled homolog 1 (Drosophila)	1.6	0.034	-1.48	0.372	-1.64	0.174	-1.67	0.31	-0.8
1433383_at	1500002K03Rik	RIKEN cDNA 1500002K03 gene	-1.18	0.775	1.43	0.222	-1.62	0.027	-1.08	0.765	-0.62
1438704_at	Trim63	tripartite motif-containing 63	-1.43	0.071	-1.28	0.551	1.41	0.036	-1.84	0.014	-0.79
1428516_a_at	Alkbh7	alkB, alkylation repair homolog 7 (E. coli)	-1.05	0.899	-1.1	0.241	1.03	0.873	-1.38	0.269	-0.63
1433622_at	Gemin4	gem (nuclear organelle) associated protein 4	-1.05	0.779	-1.26	0.049	1.14	0.06	-1.09	0.438	-0.56
1446417_at	Serpinb6a	Serine (or cysteine) peptidase inhibitor, clade B, member 6a	-1.17	0.477	1.32	0.339	-1.41	0.059	-1.18	0.559	-0.61
1442624_at	C920008N22Rik	RIKEN cDNA C920008N22 gene	1.44	0.333	-1.22	0.696	-1.6	0.111	-1.28	0.474	-0.67
1454758_a_at	Tsc22d1	TSC22 domain family, member 1	1.1	0.785	-1.09	0.438	-1.15	0.14	-1.29	0.258	-0.61
1447277_s_at	Pcyox1	prenylcysteine oxidase 1	1.08	0.611	-1.11	0.415	-1.1	0.641	-1.12	0.664	-0.56
1444885_at	---	Transcribed locus	-1.05	0.943	1.19	0.59	-1.33	0.61	-2.07	0.342	-0.82
1423806_at	Ints4	integrator complex subunit 4	-1.09	0.045	-1.11	0.054	1.07	0.402	-1.36	0.044	-0.62
1428422_at	Ubxd8	UBX domain containing 8	-1.17	0.243	-1.04	0.673	1.07	0.579	-1.1	0.631	-0.56
1456115_at	Phf3	PHD finger protein 3	1.24	0.667	-1.48	0.521	-1.02	0.95	-1.94	0.434	-0.8
1435981_at	E430014L09Rik	RIKEN cDNA E430014L09 gene	-1.02	0.957	-1.35	0.171	1.17	0.563	-1.08	0.841	-0.57
1454938_at	Snx13	sorting nexin 13	-1.1	0.392	1.08	0.561	-1.12	0.37	-1.05	0.751	-0.55
1457139_at	Auts2	autism susceptibility candidate 2	-1.01	0.942	-1.49	0.482	1.23	0.6	-1.13	0.832	-0.6
1451221_at	BC018507	cDNA sequence BC018507	1.04	0.76	-1.12	0.429	-1.05	0.857	-1.68	0.139	-0.7
1447029_at	---	---	-1.97	0.316	1.64	0.258	-1.36	0.34	-1.14	0.86	-0.71
1430426_at	4930540M05Rik	RIKEN cDNA 4930540M05 gene	1.05	0.864	-1.09	0.867	-1.09	0.846	-1.06	0.901	-0.55
1419164_at	Zfp260	zinc finger protein 260	1.02	0.916	-1.05	0.728	-1.09	0.242	-1.4	0.174	-0.63
1424391_at	Nrd1	nardilysin, N-arginine dibasic convertase, NRD convertase 1	-1.07	0.439	1.04	0.703	-1.09	0.594	-1	0.987	-0.53
1415861_at	Tyrp1	tyrosinase-related protein 1	-1.38	0.574	-1.02	0.971	1.19	0.692	-1.26	0.704	-0.62
1420477_at	Nap1l1	nucleosome assembly protein 1-like 1	1.03	0.856	-1.06	0.679	-1.09	0.529	-1.23	0.159	-0.59
1436421_s_at	Arpc5l	actin related protein 2/3 complex, subunit 5-like	1.1	0.516	-1.02	0.887	-1.24	0.155	-1.88	0.046	-0.76
1450845_a_at	Bzw1	basic leucine zipper and W2 domains 1	1.03	0.712	-1.11	0.365	-1.04	0.75	-1.23	0.41	-0.59
1422270_a_at	Il6ra	interleukin 6 receptor, alpha	-1.15	0.865	-1.26	0.257	1.23	0.676	-1.41	0.334	-0.65
1447278_at	Cep164	centrosomal protein 164	-1.27	0.138	1.12	0.36	-1.02	0.934	-1.4	0.094	-0.64
1417583_a_at	Crlz1	charged amino acid rich leucine zipper 1	1.13	0.432	-1.13	0.087	-1.14	0.502	-1.25	0.232	-0.6
1437026_at	BC057893	cDNA sequence BC057893	-1.07	0.705	1.02	0.807	-1.07	0.535	-1.14	0.095	-0.56

1431343_at	---	---	-1.38	0.518	-1.14	0.787	1.29	0.584	-1.14	0.832	-0.59
1423617_at	Cog8	component of oligomeric golgi complex 8	-1	0.978	-1.18	0.139	1.05	0.319	-1.17	0.202	-0.58
1448869_a_at	Mrps16	mitochondrial ribosomal protein S16	-1.07	0.464	-1.11	0.307	1.06	0.636	-1.14	0.539	-0.57
1441603_at	Sstr3	somatostatin receptor 3	-1.23	0.626	-1.14	0.731	1.2	0.428	-1.51	0.151	-0.67
1441551_at	Mypn	myopalladin	-1.05	0.794	1.12	0.852	-1.23	0.048	-1	0.979	-0.54
1456438_x_at	Rpn1	ribophorin I	-1.04	0.81	1.04	0.751	-1.13	0.216	-1.11	0.621	-0.56
1449355_a_at	Eps15l1	epidermal growth factor receptor pathway substrate 15-like 1	1.01	0.888	-1.1	0.391	-1.04	0.792	-1	0.99	-0.53
1430719_at	4833447P13Rik	RIKEN cDNA 4833447P13 gene	1.15	0.563	-1.06	0.912	-1.26	0.546	-1.26	0.473	-0.61
1418712_at	Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5	-1.03	0.732	-1.02	0.929	-1.06	0.602	1.2	0.526	-0.48
1454805_at	Wtap	Wilms' tumour 1-associating protein	-1.05	0.542	1.06	0.561	-1.14	0.338	-1.49	0.087	-0.66
1452316_at	Ints12	integrator complex subunit 12	-1.14	0.637	-1.02	0.819	1.03	0.878	-1.11	0.615	-0.56
1429337_at	2610301K12Rik	RIKEN cDNA 2610301K12 gene	-1.02	0.87	1.13	0.528	-1.28	0.212	-1.5	0.072	-0.67
1451363_a_at	Dennd2d	DENN/MADD domain containing 2D	-1.25	0.08	1.09	0.656	-1	0.98	-2.03	0.05	-0.8
1434141_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	1.35	0.385	-1.01	0.949	-1.8	0.074	-1.46	0.113	-0.73
1423034_at	Txnl5	thioredoxin-like 5	-1.1	0.392	-1.02	0.819	1.01	0.959	-1.21	0.274	-0.58
1431061_s_at	Peli1	pellino 1	-1.17	0.62	-1.23	0.601	1.22	0.581	-1.59	0.31	-0.69
1456079_x_at	Apex1	apurinic/apyrimidinic endonuclease 1	-1.27	0.38	-1.06	0.414	1.16	0.444	-1.13	0.259	-0.57
1455171_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	-1.08	0.613	-1.08	0.743	1.03	0.863	-1.38	0.152	-0.63
1435481_at	Zfp653	zinc finger protein 653	-1.11	0.489	1	0.985	-1.01	0.889	-1.32	0.198	-0.61
1435651_a_at	Smarcad1	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subf	-1.13	0.279	-1.31	0.227	1.24	0.41	-1.02	0.959	-0.55
1452519_a_at	Zfp36	zinc finger protein 36	-1.32	0.607	-1.01	0.945	1.14	0.56	-1.51	0.186	-0.67
1459950_at	Dcamkl2	Doublecortin and CaM kinase-like 2	-1.14	0.757	-1.05	0.912	1.06	0.899	-1.88	0.231	-0.75
1416541_at	Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	-1.03	0.908	-1.25	0.042	1.11	0.57	-1.12	0.592	-0.57
1449681_at	Hdgf	Hepatoma-derived growth factor	1.38	0.111	-1.24	0.694	-1.42	0.514	-1.15	0.712	-0.61
1430852_at	1600029I14Rik	RIKEN cDNA 1600029I14 gene	-1.02	0.958	-1.16	0.622	1.05	0.88	-1.04	0.925	-0.54
1436966_at	Peli2	pellino 2	1.2	0.108	-1.2	0.451	-1.16	0.318	-1.01	0.914	-0.54
1441186_at	Sall3	sal-like 3 (Drosophila)	-1.27	0.108	-1.17	0.865	1.25	0.629	-1.56	0.619	-0.69
1459755_x_at	1700082C02Rik	RIKEN cDNA 1700082C02 gene	-2.44	0.37	-1	0.994	1.48	0.272	-1.13	0.83	-0.77
1444795_at	AU015723	expressed sequence AU015723	-1.53	0.241	-2.2	0.107	1.78	0.268	-1.77	0.572	-0.93
1423811_at	Sf3a3	splicing factor 3a, subunit 3	1.04	0.614	-1.04	0.734	-1.12	0.032	-1	0.983	-0.53
1434386_at	Atp2c1	ATPase, Ca++-sequestering	-1.07	0.553	1.08	0.233	-1.15	0.069	-1.37	0.089	-0.63
1458604_at	Arhgef18	Rho/rac guanine nucleotide exchange factor (GEF) 18	-1.22	0.327	1.4	0.293	-1.49	0.177	-2.01	0.138	-0.83
1429197_s_at	Rabgap1l	RAB GTPase activating protein 1-like	1.27	0.634	-1.37	0.36	-1.13	0.436	-1.38	0.062	-0.65
1438630_x_at	Mat2a	methionine adenosyltransferase II, alpha	1.13	0.557	-1.03	0.832	-1.26	0.18	-1.25	0.308	-0.6
1450293_at	Mageb3	melanoma antigen, family B, 3	1.29	0.503	-1.1	0.853	-1.45	0.43	-1.4	0.598	-0.66
1453814_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	-1.98	0.1	-2.34	0.099	1.96	0.15	-1.29	0.267	-0.91
1449095_at	Vps54	vacuolar protein sorting 54 (yeast)	1.05	0.464	-1.01	0.897	-1.18	0.186	-1.06	0.791	-0.55
1447191_at	---	---	1.35	0.714	-1.37	0.281	-1.23	0.543	-1.99	0.05	-0.81
1428227_at	Rest	RE1-silencing transcription factor	-1.1	0.137	-1.08	0.608	1.05	0.837	-1.14	0.521	-0.57
1424134_at	Rspry1	ring finger and SPRY domain containing 1	-1.01	0.885	-1.07	0.229	-1.03	0.823	1.2	0.207	-0.48
1424315_at	1110004E09Rik	RIKEN cDNA 1110004E09 gene	-1.06	0.379	-1.21	0.071	1.12	0.649	-1.11	0.638	-0.56
1455657_at	2610207I05Rik	RIKEN cDNA 2610207I05 gene	-1.33	0.401	1.14	0.619	-1	0.999	-1.37	0.074	-0.64
1441842_s_at	Zfp707	zinc finger protein 707	-1.01	0.963	1.16	0.421	-1.35	0.29	-1.4	0.387	-0.65
1451663_a_at	Trim3	tripartite motif protein 3	-1.03	0.752	1.14	0.159	-1.27	0.012	-1.52	0.071	-0.67
1422794_at	Cul3	cullin 3	-1.12	0.412	1	0.964	-1.01	0.924	-1.09	0.101	-0.55
1459615_at	B130052P14Rik	RIKEN cDNA B130052P14 gene	1.46	0.247	-1.3	0.698	-1.51	0.303	-1.08	0.739	-0.61
1418634_at	Notch1	Notch gene homolog 1 (Drosophila)	-1.06	0.761	1.04	0.698	-1.11	0.508	-1.28	0.215	-0.6
1434038_at	Dnajc13	DnaJ (Hsp40) homolog, subfamily C, member 13	-1.17	0.44	-1.05	0.571	1.08	0.554	-1.2	0.221	-0.58
1456175_a_at	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	-1.08	0.336	1.34	0.095	-1.61	0.021	-1.41	0.476	-0.69
1442726_s_at	AI845619	expressed sequence AI845619	1.47	0.585	-1.01	0.974	-2.28	0.112	-1.4	0.67	-0.81
1422735_at	Foxq1	forkhead box Q1	1.1	0.229	-1.14	0.569	-1.09	0.658	-1.18	0.514	-0.58
1442906_at	---	---	1.13	0.823	-1.28	0.698	-1.02	0.946	-2.25	0.3	-0.85
1455647_at	Ar	androgen receptor	-1.16	0.659	1.15	0.166	-1.14	0.492	-1.12	0.772	-0.57

AFFX-ThrX-3_at	---	---	1.12	0.822	-1.2	0.262	-1.07	0.812	-1.52	0.301	-0.67
1451037_at	Ptpn9	protein tyrosine phosphatase, non-receptor type 9	1.01	0.929	-1.05	0.161	-1.07	0.766	-1.2	0.424	-0.58
1453835_at	4930505M18Rik	RIKEN cDNA 4930505M18 gene	-1.01	0.988	-1.31	0.575	1.14	0.8	-1.21	0.757	-0.6
1436859_at	2700007P21Rik	RIKEN cDNA 2700007P21 gene	1.01	0.829	-1.01	0.908	-1.12	0.357	-1.3	0.182	-0.6
1450772_at	Wnt11	wingless-related MMTV integration site 11	-2.39	0.031	-1.02	0.933	1.5	0.054	-1.31	0.055	-0.8
1423987_at	Cdc26	cell division cycle 26	-1.04	0.501	1.08	0.339	-1.19	0.135	-1.04	0.744	-0.54
1452262_at	Grpel2	GrpE-like 2, mitochondrial	1.06	0.801	-1.06	0.518	-1.12	0.584	-1.18	0.324	-0.58
1417912_at	Tmem93	transmembrane protein 93	-1.02	0.888	-1.07	0.541	-1.03	0.871	1	0.988	-0.53
1448758_at	LOC627232 /// LOC	similar to nuclear receptor binding factor 2 /// similar to nuclear receptor binding fa	-1.12	0.548	-1.05	0.745	1.05	0.435	-1.25	0.208	-0.59
1421399_at	Insm1	insulinoma-associated 1	-1.28	0.672	1.12	0.704	-1.01	0.984	-1.54	0.058	-0.68
1454296_at	4631402F24Rik	RIKEN cDNA 4631402F24 gene	1.08	0.847	-1.17	0.209	-1.04	0.873	-1.04	0.864	-0.54
1458246_at	---	---	-1.09	0.75	1.2	0.796	-1.28	0.661	-1.94	0.563	-0.78
1443759_at	---	---	-1.49	0.157	-1.27	0.576	1.44	0.422	-1.73	0.465	-0.76
1438167_x_at	Flcn	Folliculin	-1.24	0.145	1.1	0.544	-1.01	0.912	-1.45	0.149	-0.65
1449384_at	4931417E11Rik	RIKEN cDNA 4931417E11 gene	1.05	0.764	-1.13	0.793	-1.04	0.816	-1.12	0.832	-0.56
1429180_at	Gmpr2	guanosine monophosphate reductase 2	-1.02	0.938	1	0.996	-1.1	0.502	-1.46	0.014	-0.64
1448173_a_at	Top3b	topoisomerase (DNA) III beta	1.03	0.848	-1.06	0.611	-1.08	0.579	-1.56	0.08	-0.67
1424294_at	Ppp4r1	protein phosphatase 4, regulatory subunit 1	-1.13	0.075	1.02	0.665	-1.01	0.818	-1.27	0.104	-0.6
1460047_at	Fnbp1	Formin binding protein 1	1.17	0.474	-1.12	0.748	-1.21	0.409	-1.47	0.301	-0.66
1438371_x_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-1.16	0.445	1.14	0.108	-1.13	0.246	-1.52	0.117	-0.66
1428704_at	Zfp661	zinc finger protein 661	-1.09	0.447	-1.06	0.719	1.03	0.658	-1.29	0.338	-0.6
1434987_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	-1.06	0.929	-1.36	0.18	1.21	0.461	-1	0.977	-0.55
1431006_at	---	---	-1.37	0.553	-1.13	0.801	1.28	0.588	-1.39	0.36	-0.65
1453071_s_at	Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2	-1.23	0.222	1.27	0.009	-1.24	0.38	-1.19	0.45	-0.6
1450942_at	Ccdc16	coiled-coil domain containing 16	-1.08	0.53	-1.17	0.171	1.11	0.242	-1.07	0.738	-0.55
1418784_at	Grik5	glutamate receptor, ionotropic, kainate 5 (gamma 2)	1.17	0.848	-1.35	0.538	-1.01	0.98	-1.1	0.869	-0.58
1435623_at	Tmem118	transmembrane protein 118	-1.14	0.806	-1.17	0.638	1.16	0.563	-1.1	0.787	-0.56
1421323_a_at	E430034L04Rik	RIKEN cDNA E430034L04 gene	1.01	0.887	-1.02	0.623	-1.11	0.195	-1.2	0.487	-0.58
1419592_at	Unc5c	unc-5 homolog C (C. elegans)	-1.39	0.172	1.29	0.594	-1.13	0.713	-1.38	0.24	-0.65
1432242_at	4930447N08Rik	RIKEN cDNA 4930447N08 gene	-1.86	0.432	1.64	0.508	-1.39	0.568	-1.02	0.933	-0.66
1457272_at	---	Transcribed locus	-1.07	0.82	-1.13	0.597	1.07	0.682	-1.21	0.679	-0.58
1452699_at	Mett11d1	methyltransferase 11 domain containing 1	-1.33	0.13	-1.21	0.075	1.31	0.052	-1.59	0.149	-0.7
1451069_at	Pim3	proviral integration site 3	1.22	0.356	-1.08	0.764	-1.33	0.024	-1.02	0.929	-0.55
1455217_at	Lrig2	leucine-rich repeats and immunoglobulin-like domains 2	-1.07	0.691	1.21	0.463	-1.33	0.092	-1.21	0.516	-0.6
1420909_at	Vegfa	vascular endothelial growth factor A	-1.13	0.408	-1	0.962	1.02	0.94	-1.05	0.67	-0.54
1430329_at	Cgn	cingulin	1.29	0.786	-1.15	0.793	-1.37	0.153	-1.66	0.16	-0.72
1432657_at	Adam1b	a disintegrin and metallopeptidase domain 1b	-1.19	0.795	1.07	0.902	-1.02	0.954	-2.56	0.171	-0.92
1418124_at	Tmem85	transmembrane protein 85	1.06	0.48	-1.14	0.04	-1.05	0.656	-1.15	0.416	-0.57
1433871_at	R3hdm1	R3H domain 1 (binds single-stranded nucleic acids)	-1.1	0.153	-1	0.98	-1.01	0.945	1.19	0.281	-0.48
1426948_at	Tpr	translocated promoter region	-1.04	0.765	-1.2	0.062	1.09	0.476	-1.11	0.586	-0.56
1434159_at	Stk4	serine/threonine kinase 4	1.07	0.636	-1.18	0.267	-1.02	0.904	-1.44	0.084	-0.64
1452733_at	Pank2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	1.19	0.046	-1.09	0.495	-1.26	0.088	-1.14	0.291	-0.58
1428109_at	Vps11	vacuolar protein sorting 11 (yeast)	-1.07	0.73	-1.18	0.362	1.11	0.198	-1.27	0.131	-0.6
1431593_a_at	Tsen34	tRNA splicing endonuclease 34 homolog (SEN34, S. cerevisiae)	-1.05	0.608	-1.21	0.074	1.12	0.514	-1.26	0.137	-0.6
1438261_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	1.63	0.114	-2.64	0.025	-1.13	0.803	-1.13	0.802	-0.82
1426445_at	Mgea6	meningioma expressed antigen 6 (coiled-coil proline-rich)	-1.11	0.424	-1.09	0.272	1.08	0.116	-1.1	0.28	-0.56
1418131_at	Samhd1	SAM domain and HD domain, 1	1.01	0.832	-1.11	0.269	-1.02	0.869	-2	0.127	-0.78
1424683_at	1810015C04Rik	RIKEN cDNA 1810015C04 gene	-1.12	0.474	-1.02	0.932	1.02	0.906	-2.33	0.042	-0.86
1430206_at	4933407L21Rik	RIKEN cDNA 4933407L21 gene	-1.64	0.504	-1.05	0.951	1.33	0.146	-1.88	0.4	-0.81
1419116_at	Alg14	asparagine-linked glycosylation 14 homolog (yeast)	1.04	0.793	-1.08	0.723	-1.08	0.715	-1.06	0.85	-0.54
1430991_at	1810014B01Rik	RIKEN cDNA 1810014B01 gene	-1.16	0.713	-1.11	0.477	1.14	0.661	-1.01	0.966	-0.54
1456293_s_at	Ccnh /// LOC67265	cyclin H /// similar to cyclin H	1.09	0.504	-1.13	0.013	-1.08	0.379	-1.12	0.132	-0.56
1419816_s_at	Errfi1	ERBB receptor feedback inhibitor 1	-1.14	0.497	1.04	0.852	-1.02	0.949	-2.01	0.086	-0.78

1434525_at	Pkn3	protein kinase N3	1.18	0.818	-1.34	0.186	-1.03	0.91	-1.17	0.645	-0.59
1423688_at	Man2c1	mannosidase, alpha, class 2C, member 1	-1.12	0.314	-1.17	0.199	1.15	0.093	-1.14	0.011	-0.57
1432238_at	Spats1	spermatogenesis associated, serine-rich 1	-1.66	0.412	-2	0.396	1.79	0.343	-1.07	0.891	-0.73
1448176_a_at	Hnrpk	heterogeneous nuclear ribonucleoprotein K	1.06	0.472	-1.05	0.58	-1.12	0.219	-1.02	0.81	-0.53
1422675_at	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.07	0.652	-1.17	0.062	-1.03	0.854	-1.27	0.126	-0.6
1440039_at	Brwd3	Bromodomain and WD repeat domain containing 3	1.15	0.553	-1.07	0.896	-1.23	0.034	-1.53	0.147	-0.67
1433535_x_at	Cct2	chaperonin subunit 2 (beta)	1.06	0.399	-1.1	0.346	-1.08	0.488	-1.17	0.026	-0.57
1426656_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.12	0.229	-1.03	0.851	1.03	0.827	-1.1	0.455	-0.55
1452147_at	Sec24c	SEC24 related gene family, member C (S. cerevisiae)	-1.13	0.209	-1.02	0.829	1.04	0.795	-1.42	0.064	-0.63
1445702_x_at	Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	1.11	0.894	-1.03	0.956	-1.22	0.655	-1.22	0.518	-0.59
1458433_at	Rasd2	RASD family, member 2	-1.14	0.882	1.28	0.641	-1.34	0.496	-1.5	0.118	-0.68
1434014_at	Atg4c	autophagy-related 4C (yeast)	-1.01	0.945	1.01	0.956	-1.12	0.257	-1.23	0.152	-0.59
1438487_s_at	Zzz3	zinc finger, ZZ domain containing 3	-1.05	0.809	1.05	0.799	-1.12	0.413	-1.07	0.617	-0.55
1426437_s_at	Hdac3	histone deacetylase 3	1.02	0.923	-1.03	0.835	-1.1	0.325	-1.1	0.506	-0.55
1425420_s_at	Lats2	large tumor suppressor 2	-1.11	0.709	-1.27	0.594	1.21	0.239	-1.43	0.037	-0.65
1424245_at	Ces2 /// LOC66775	carboxylesterase 2 /// similar to carboxylesterase 2	-1.19	0.336	-1.81	0.214	1.5	0.34	-1.12	0.767	-0.65
1434442_at	D5Ertd593e	DNA segment, Chr 5, ERATO Doi 593, expressed	1.06	0.826	-1.07	0.769	-1.1	0.625	-1.54	0.209	-0.66
1428894_at	1300018J18Rik	RIKEN cDNA 1300018J18 gene	-1.12	0.178	-1.08	0.57	1.08	0.637	-1.27	0.118	-0.6
1458092_at	Ap3m1	Adaptor-related protein complex 3, mu 1 subunit	-1.3	0.549	-1.3	0.637	1.35	0.527	-1.03	0.93	-0.57
1439308_at	Got1l1	glutamic-oxaloacetic transaminase 1-like 1	-1.7	0.057	-1.04	0.902	1.35	0.225	-1.03	0.897	-0.6
1460321_at	Cntn4	contactin 4	-1.21	0.736	-2.61	0.008	1.68	0.034	-1.46	0.43	-0.9
1426874_at	Edc4	enhancer of mRNA decapping 4	1.05	0.635	-1.03	0.808	-1.13	0.545	-1.35	0.007	-0.62
1417521_at	Efna2	ephrin A2	-1.19	0.614	-1.09	0.759	1.14	0.504	-1.12	0.596	-0.57
1449459_s_at	Asb13	ankyrin repeat and SOCS box-containing protein 13	1.05	0.177	-1.04	0.83	-1.14	0.034	-1.65	0.185	-0.69
1434540_a_at	Clta	clathrin, light polypeptide (Lca)	-1.11	0.02	1.04	0.217	-1.04	0.723	-1.28	0.205	-0.6
1452951_at	2410089E03Rik	RIKEN cDNA 2410089E03 gene	-1.02	0.907	-1.02	0.919	-1.06	0.749	1.07	0.779	-0.51
1440198_at	Epc1	Enhancer of polycomb homolog 1 (Drosophila)	-1.26	0.689	-1.51	0.254	1.44	0.031	-1.2	0.47	-0.63
1446785_at	---	Transcribed locus, weakly similar to XP_220328.3 PREDICTED: similar to metall	1.03	0.886	-1.03	0.817	-1.11	0.493	-1.03	0.953	-0.54
1435873_a_at	Rpl13a /// Zfp526	ribosomal protein L13a /// zinc finger protein 526	-1.02	0.812	1.1	0.234	-1.22	0.055	-1.38	0.011	-0.63
1453413_at	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	-1.14	0.537	1.13	0.667	-1.13	0.574	-1.03	0.801	-0.54
1429013_at	2900002G04Rik	RIKEN cDNA 2900002G04 gene	-1.04	0.842	-1.08	0.834	1.01	0.985	-1.02	0.973	-0.53
1449309_at	Cyp8b1	cytochrome P450, family 8, subfamily b, polypeptide 1	1.54	0.473	-1.74	0.134	-1.28	0.393	-2.43	0.109	-0.98
1452264_at	Tenc1	tensin like C1 domain-containing phosphatase	1.06	0.861	-1.08	0.792	-1.1	0.773	-1.31	0.495	-0.61
1424475_at	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-1.1	0.507	1.06	0.719	-1.08	0.562	-1.02	0.948	-0.53
1451214_at	Kbtbd2	kelch repeat and BTB (POZ) domain containing 2	-1.02	0.882	-1.02	0.846	-1.07	0.548	1.29	0.061	-0.45
1417793_at	Iigp2	interferon inducible GTPase 2	-1.02	0.864	1.03	0.881	-1.13	0.409	-1.2	0.202	-0.58
1449648_s_at	Rpo1-1	RNA polymerase 1-1	-1.03	0.627	-1.12	0.104	1.03	0.88	-1.16	0.324	-0.57
1427190_at	2900057D21Rik	RIKEN cDNA 2900057D21 gene	-1.14	0.479	1.26	0.217	-1.33	0.222	-1.36	0.273	-0.64
1442245_at	Prmt4	Protein arginine N-methyltransferase 4	-1.41	0.249	1.27	0.172	-1.09	0.798	-1.49	0.299	-0.68
1426674_at	Eif3s9	eukaryotic translation initiation factor 3, subunit 9 (eta)	-1.08	0.444	-1.02	0.645	-1.01	0.893	1.14	0.136	-0.49
1417354_at	Sil1	endoplasmic reticulum chaperone SIL1 homolog (S. cerevisiae)	1.04	0.728	-1.09	0.084	-1.06	0.272	-1.18	0.589	-0.57
1450431_a_at	Nedd4	neural precursor cell expressed, developmentally down-regulted gene 4	-1.06	0.261	-1.1	0.047	1.05	0.827	-1.22	0.266	-0.58
1448698_at	Ccnd1	cyclin D1	1.52	0.002	-1.58	0.067	-1.34	0.029	-1.74	0.15	-0.79
1455539_at	---	---	1.12	0.332	-1.02	0.93	-1.26	0.193	-1.44	0.206	-0.65
1424843_a_at	Gas5	growth arrest specific 5	-1.25	0.237	-1.03	0.721	1.13	0.335	-1.52	0.045	-0.67
1417398_at	Rras2	related RAS viral (r-ras) oncogene homolog 2	1.05	0.803	-1.06	0.535	-1.11	0.425	-2.19	0.06	-0.83
1439166_at	Nol11	nucleolar protein 11	-1.15	0.201	-1.01	0.976	1.04	0.912	-1.42	0.19	-0.63
1424081_at	Pcgf6	polycomb group ring finger 6	-1.16	0.56	-1.35	0.222	1.3	0.127	-1.03	0.895	-0.56
1460244_at	Upb1	ureidopropionase, beta	1.04	0.577	-1.15	0.189	-1.01	0.955	-1.55	0.011	-0.67
1442458_at	---	Transcribed locus	-1.26	0.365	1.39	0.603	-1.4	0.44	-1.22	0.712	-0.62
1434058_at	Mtmr12	Vmyotubularin related protein 12	-1.19	0.147	1.09	0.444	-1.04	0.441	-1.04	0.574	-0.54
1448174_at	Cul1	cullin 1	-1.23	0.079	1.15	0.463	-1.06	0.316	-1.1	0.359	-0.56
1435593_x_at	Rps7	ribosomal protein S7	-1.07	0.506	1.09	0.158	-1.14	0.238	-1.4	0.016	-0.63

1442144_at	Emid1	EMI domain containing 1	-1.81	0.063	1.55	0.308	-1.25	0.488	-1.07	0.555	-0.65
1436663_at	---	---	-1.01	0.906	1.55	0.434	-2.77	0.023	-1.71	0.086	-0.99
1452071_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	-1.07	0.709	1.04	0.705	-1.08	0.558	-2.09	0.079	-0.8
1415873_a_at	Actr1a	ARP1 actin-related protein 1 homolog A (yeast)	1	0.939	-1.02	0.894	-1.1	0.224	-1.07	0.276	-0.55
1417209_at	Sertad2	SERTA domain containing 2	-1.02	0.925	-1.06	0.755	-1.03	0.801	1.84	0.206	-0.32
1438938_x_at	Phb2	prohibitin 2	-1.01	0.96	-1.08	0.379	-1.02	0.917	1.07	0.58	-0.51
1452874_at	2510003E04Rik	RIKEN cDNA 2510003E04 gene	-1.13	0.537	-1.19	0.056	1.17	0.219	-1.02	0.461	-0.54
1426162_a_at	Rpl7	ribosomal protein L7	-1.07	0.238	1.04	0.665	-1.08	0.02	-1.31	0.008	-0.61
1447941_x_at	Braf	Braf transforming gene	1.01	0.987	-1.1	0.638	-1.01	0.944	-1.27	0.336	-0.6
1455276_x_at	1110004E09Rik	RIKEN cDNA 1110004E09 gene	1.99	0.39	-4.55	0.341	-1.44	0.455	-1.19	0.735	-1.3
1434552_at	Wdr77	WD repeat domain 77	-1.19	0.138	-1.1	0.535	1.15	0.192	-1.02	0.914	-0.54
1448653_at	Eed	embryonic ectoderm development	-1.05	0.735	1.05	0.544	-1.11	0.083	-1.19	0.026	-0.58
1431753_x_at	2900073H19Rik	RIKEN cDNA 2900073H19 gene	1	0.997	-1	0.996	-1.11	0.595	-1.02	0.895	-0.53
1433775_at	C77080	expressed sequence C77080	-1.15	0.283	-1.13	0.299	1.14	0.292	-1.13	0.169	-0.57
1448360_s_at	Angel2	angel homolog 2 (Drosophila)	-1.04	0.576	1.05	0.452	-1.13	0.255	-1.54	0.173	-0.66
1427526_at	Fgfr1op2	FGFR1 oncogene partner 2	1.06	0.287	-1.07	0.344	-1.1	0.467	-1.37	0.286	-0.62
1443174_at	Tmtc2	Transmembrane and tetratricopeptide repeat containing 2	1.73	0.532	-3.22	0.184	-1.16	0.691	-1.3	0.256	-0.99
1444579_at	Gatad2b	GATA zinc finger domain containing 2B	1.4	0.657	-1.33	0.633	-1.33	0.444	-1.06	0.821	-0.58
1416331_a_at	Nfe2l1	nuclear factor, erythroid derived 2,-like 1	1.07	0.822	-1.14	0.555	-1.04	0.9	-1.1	0.746	-0.55
1439496_at	4921524J06Rik	RIKEN cDNA 4921524J06 gene	1.15	0.64	-1.14	0.299	-1.14	0.534	-1.17	0.7	-0.58
1452726_a_at	Nop17	NOP17	-1.03	0.856	1	0.999	-1.08	0.342	-1.16	0.187	-0.57
1443829_x_at	Coasy	Coenzyme A synthase	-1.11	0.454	-1.04	0.8	1.04	0.868	-1.25	0.257	-0.59
1431924_at	4930432N10Rik	RIKEN cDNA 4930432N10 gene	-1.32	0.138	-1.42	0.332	1.44	0.405	-1.68	0.355	-0.74
1438462_x_at	---	---	-1.18	0.334	-1.02	0.917	1.07	0.682	-1.66	0.076	-0.7
1423076_at	---	---	-1.2	0.346	-1.14	0.319	1.19	0.107	-1.24	0.318	-0.6
1415681_at	Mrpl43	mitochondrial ribosomal protein L43	-1.09	0.358	-1.07	0.503	1.05	0.495	-1.25	0.186	-0.59
1427902_at	Srrm2	serine/arginine repetitive matrix 2	-2.08	0.452	-1.31	0.465	1.66	0.488	-1.55	0.576	-0.82
1451070_at	Gdi1	guanosine diphosphate (GDP) dissociation inhibitor 1	-1.08	0.03	-1.14	0.32	1.1	0.12	-1.08	0.78	-0.55
1420093_s_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	-1.11	0.237	1.08	0.342	-1.09	0.453	-1.41	0.088	-0.63
1423317_at	3110001D03Rik	RIKEN cDNA 3110001D03 gene	-1.11	0.244	-1.01	0.833	1.01	0.907	-1.43	0.067	-0.64
1428473_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	1.04	0.271	-1.09	0.375	-1.06	0.378	-1	0.993	-0.53
1432154_at	4933407I08Rik	RIKEN cDNA 4933407I08 gene	1.32	0.59	-1.38	0.559	-1.17	0.46	-1.1	0.324	-0.58
1439993_at	Rsrc1	Arginine/serine-rich coiled-coil 1	-1.38	0.499	1.49	0.294	-1.45	0.316	-1.47	0.267	-0.7
1422450_at	Ctnnd1	catenin (cadherin associated protein), delta 1	-1.1	0.725	1.18	0.34	-1.23	0.27	-1.03	0.922	-0.55
1448273_at	Gss	glutathione synthetase	-1	0.997	-1.07	0.445	-1.03	0.876	1.41	0.464	-0.42
1434863_at	AU041129	expressed sequence AU041129	-1.17	0.417	1.1	0.735	-1.05	0.801	-1.14	0.444	-0.57
1428716_at	Pex1	peroxisome biogenesis factor 1	-1.08	0.457	-1.1	0.499	1.06	0.601	-1.25	0.151	-0.59
1438156_x_at	Cpt1a	carnitine palmitoyltransferase 1a, liver	-1.39	0.453	-1.08	0.838	1.26	0.241	-1.32	0.063	-0.63
1420827_a_at	Ccng1	cyclin G1	1.1	0.366	-1.14	0.411	-1.08	0.451	-1.1	0.716	-0.56
1456468_x_at	1110012N22Rik	RIKEN cDNA 1110012N22 gene	-1.12	0.482	-1.53	0.144	1.35	0.058	-1.32	0.259	-0.65
1419366_at	Zmat5	zinc finger, matrin type 5	1.2	0.384	-1.11	0.515	-1.25	0.242	-1.42	0.404	-0.64
1416799_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	-1.14	0.015	1.05	0.443	-1.02	0.812	-1.18	0.491	-0.57
1423924_s_at	Tspan14	tetraspanin 14	-1.08	0.486	1.24	0.138	-1.35	0.007	-1.35	0.04	-0.64
1454829_at	Rundc1	RUN domain containing 1	-1.14	0.5	-1.12	0.196	1.13	0.132	-1.08	0.562	-0.55
1427016_at	4932438A13Rik ///	RIKEN cDNA 4932438A13 gene /// similar to CG4841-PA	-1.31	0.144	1.14	0.483	-1	0.975	-1.54	0.168	-0.68
1433104_at	5730412F04Rik	RIKEN cDNA 5730412F04 gene	1.38	0.063	-1.23	0.247	-1.41	0.185	-1.62	0.023	-0.72
1452409_at	Gltscr2	glioma tumor suppressor candidate region gene 2	-1.17	0.723	-1.1	0.513	1.14	0.355	-1.26	0.418	-0.6
1422505_at	Chrac1	chromatin accessibility complex 1	1.03	0.513	-1.03	0.601	-1.11	0.407	-1.05	0.691	-0.54
1442980_at	Srpk2	Serine/arginine-rich protein specific kinase 2	-1.13	0.459	-1.05	0.912	1.07	0.631	-1.15	0.627	-0.57
1438943_x_at	Rpn1	ribophorin I	-1.06	0.421	1.09	0.513	-1.15	0.058	-1.12	0.496	-0.56
1449821_a_at	0610016J10Rik /// I	RIKEN cDNA 0610016J10 gene /// hypothetical LOC619602	-1.01	0.875	-1.06	0.133	-1.03	0.647	3.11	0.189	0
1434116_at	Cbx2	chromobox homolog 2 (Drosophila Pc class)	-1.29	0.33	1.17	0.4	-1.04	0.833	-1.08	0.587	-0.56
1457481_at	---	Transcribed locus	-1.1	0.892	-1.81	0.11	1.44	0.35	-1.09	0.897	-0.64

1420547_at	Galc	galactosylceramidase	-1.04	0.67	-1.03	0.934	-1.03	0.916	2.16	0.154	-0.24
1416982_at	Foxo1	forkhead box O1	-1.12	0.626	-1.16	0.46	1.14	0.376	-1.84	0.141	-0.74
1448056_at	Huwe1	HECT, UBA and WWE domain containing 1	1.35	0.427	-1.1	0.714	-1.54	0.014	-1.33	0.083	-0.66
1455433_at	MGC107415	hypothetical protein LOC383216	-1.15	0.396	1.26	0.066	-1.3	0.252	-1.43	0.074	-0.65
1452838_at	Ddx10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	1.04	0.754	-1.07	0.659	-1.08	0.662	-1.4	0.089	-0.63
1447480_at	Fgf14	Fibroblast growth factor 14	1.82	0.333	-2.24	0.314	-1.57	0.557	-4.56	0.066	-1.64
1424514_at	Rnf126	ring finger protein 126	1.06	0.797	-1.14	0.494	-1.04	0.849	-1.04	0.709	-0.54
1435422_at	4933433P14Rik	RIKEN cDNA 4933433P14 gene	-1.11	0.598	1.16	0.55	-1.19	0.314	-1	0.985	-0.54
1432155_at	Wasl	Wiskott-Aldrich syndrome-like (human)	-1.44	0.067	-1.48	0.429	1.53	0.101	-1.99	0.163	-0.85
1445776_at	---	---	-1.84	0.205	-2.16	0.228	1.9	0.102	-1.28	0.589	-0.85
1434489_at	Elmo3	engulfment and cell motility 3, ced-12 homolog (C. elegans)	-1.06	0.691	-1.01	0.935	-1.04	0.319	1.57	0.263	-0.38
1452225_at	2010106G01Rik	RIKEN cDNA 2010106G01 gene	-1	0.973	1.09	0.517	-1.22	0.009	-1.3	0.215	-0.61
1444503_at	Gbas	Glioblastoma amplified sequence	1.21	0.639	-1.05	0.829	-1.35	0.009	-1.23	0.398	-0.61
1455183_at	Stk38l	serine/threonine kinase 38 like	-1.12	0.572	1.08	0.77	-1.07	0.69	-1.19	0.205	-0.58
1439001_at	LOC665286 /// LOC	hypothetical protein LOC665286 /// hypothetical protein LOC677425	-1.1	0.274	-1	0.98	-1	0.974	1.05	0.618	-0.51
1426641_at	Trib2	tribbles homolog 2 (Drosophila)	-1.05	0.888	-1.84	0.141	1.4	0.438	-1.86	0.103	-0.84
1452863_at	1700003F12Rik	RIKEN cDNA 1700003F12 gene	-1	0.961	-1.05	0.857	-1.05	0.766	1.18	0.544	-0.48
1433467_at	Slc7a6	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-1.11	0.74	1.01	0.978	-1.01	0.925	-1.77	0.035	-0.72
1436275_at	---	---	-1.36	0.013	-1.73	0.328	1.59	0.434	-1.09	0.729	-0.65
1436494_x_at	Trmt1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	-1.01	0.905	-1.1	0.281	1.01	0.97	-1.63	0.046	-0.68
1427009_at	Lama5 /// LOC671	laminin, alpha 5 /// similar to Laminin alpha-5 chain precursor	-1.09	0.071	-1.31	0.371	1.22	0.218	-1.02	0.891	-0.55
1439441_x_at	Lats2	large tumor suppressor 2	-1.08	0.589	1.04	0.779	-1.06	0.614	-1.51	0.089	-0.65
1424852_at	Mef2c	myocyte enhancer factor 2C	1.11	0.482	-1.13	0.683	-1.1	0.736	-2.05	0.095	-0.79
1416999_at	Smpd2	sphingomyelin phosphodiesterase 2, neutral	-1.01	0.652	-1.15	0.448	1.05	0.776	-1.36	0.183	-0.62
1449663_at	---	---	-1.33	0.475	-1.25	0.365	1.35	0.39	-1.4	0.282	-0.66
1433481_at	Fkbp14	FK506 binding protein 14	-1.05	0.698	1.16	0.267	-1.25	0.529	-1.05	0.88	-0.55
1428341_at	Zfp655	zinc finger protein 655	1.04	0.522	-1.01	0.946	-1.15	0.172	-1.16	0.114	-0.57
1435169_at	A930001N09Rik	RIKEN cDNA A930001N09 gene	-1.06	0.533	1.04	0.519	-1.08	0.707	-1.6	0.103	-0.68
1451282_at	Centd3	centaurin, delta 3	-1.14	0.661	1.1	0.68	-1.08	0.81	-1	0.999	-0.53
1427986_a_at	Col16a1	procollagen, type XVI, alpha 1	-1.08	0.698	1.14	0.534	-1.19	0.479	-1.32	0.148	-0.61
1430809_at	Fzd5	Frizzled homolog 5 (Drosophila)	-1.09	0.836	1.15	0.614	-1.2	0.784	-1.08	0.852	-0.55
1455225_at	Syne1	synaptic nuclear envelope 1	-1.01	0.985	-1.6	0.255	1.29	0.268	-1.35	0.67	-0.67
1423995_at	Kif1b	kinesin family member 1B	1.4	0.004	-1.36	0.244	-1.3	0.24	-1.12	0.542	-0.59
1452167_at	2810407C02Rik	RIKEN cDNA 2810407C02 gene	-1.01	0.897	1.02	0.698	-1.12	0.028	-1.12	0.105	-0.56
1455726_at	Gm71	gene model 71, (NCBI)	-1.05	0.685	-1.09	0.648	1.04	0.793	-1.39	0.199	-0.62
1422955_at	Syt17	synaptotagmin XVII	-1.04	0.849	-1.21	0.43	1.12	0.625	-2.26	0.394	-0.85
1450710_at	Jarid2	jumonji, AT rich interactive domain 2	-1.05	0.275	-1.5	0.141	1.29	0.2	-1.29	0.044	-0.64
1443786_at	Utf1	undifferentiated embryonic cell transcription factor 1	-1.73	0.482	1.44	0.523	-1.13	0.436	-1.28	0.503	-0.67
1423765_at	Athl1	ATH1, acid trehalase-like 1 (yeast)	-1.2	0.313	-1.2	0.261	1.24	0.294	-1.17	0.555	-0.58
1454324_at	4930487N04Rik	RIKEN cDNA 4930487N04 gene	-2.37	0.278	-1.2	0.205	1.65	0.016	-1.7	0.245	-0.9
1451265_at	Ccdc115	coiled-coil domain containing 115	-1.08	0.607	-1.11	0.285	1.08	0.226	-1.24	0.033	-0.59
1437236_a_at	Zfp110	zinc finger protein 110	1.1	0.695	-1.03	0.802	-1.2	0.103	-1.38	0.16	-0.63
1450817_at	Solh	small optic lobes homolog (Drosophila)	-1.87	0.51	-1.67	0.163	1.77	0.356	-1.02	0.972	-0.7
1424412_at	Ogfrl1	opioid growth factor receptor-like 1	1.06	0.555	-1.16	0.411	-1.02	0.936	-1.3	0.176	-0.6
1447045_at	---	---	-1.09	0.799	-2.22	0.167	1.54	0.33	-1.2	0.623	-0.74
1438027_at	---	---	-1.09	0.747	1.36	0.204	-1.59	0.022	-2.19	0.095	-0.88
1416532_at	Trrap	transformation/transcription domain-associated protein	1	0.999	-1.06	0.603	-1.03	0.872	-1.71	0.007	-0.7
1436908_at	Pcm1	pericentriolar material 1	-1.21	0.359	1.18	0.239	-1.11	0.348	-1.07	0.824	-0.55
1438739_at	Cnbp	cellular nucleic acid binding protein	1.08	0.851	-1.11	0.509	-1.09	0.718	-1.2	0.646	-0.58
1432851_at	Phactr1	phosphatase and actin regulator 1	-1.06	0.841	1.03	0.936	-1.07	0.753	-1.4	0.415	-0.62
1449509_at	Serf1	small EDRK-rich factor 1	-1.29	0.292	-1.68	0.426	1.54	0.149	-2.18	0.071	-0.9
1432625_at	5830487K18Rik	RIKEN cDNA 5830487K18 gene	-1.25	0.576	1.19	0.686	-1.1	0.717	-1.22	0.707	-0.59
1424651_at	BC021611	cDNA sequence BC021611	-1.11	0.564	-1.52	0.123	1.34	0.25	-1.29	0.26	-0.64

1451247_at	Mfsd1	major facilitator superfamily domain containing 1	-1.17	0.006	-1.02	0.784	1.07	0.339	-1.08	0.429	-0.55
1434352_at	B630005N14Rik	RIKEN cDNA B630005N14 gene	-1.21	0.321	-1.08	0.336	1.16	0.463	-1.45	0.209	-0.65
1455815_a_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	-1.09	0.382	1.05	0.316	-1.07	0.496	-1.16	0.35	-0.57
1434226_at	Cyb561d1	cytochrome b-561 domain containing 1	-1.22	0.725	-1.04	0.916	1.12	0.6	-2.07	0.194	-0.8
1426414_a_at	Rnf7	ring finger protein 7	1.03	0.831	-1.04	0.705	-1.09	0.358	-1.36	0.268	-0.62
1417313_at	Lsm7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.05	0.873	-1.07	0.718	1.02	0.898	-1.22	0.616	-0.58
1434654_at	Cog3	component of oligomeric golgi complex 3	-1.02	0.652	1.04	0.309	-1.12	0.364	-1.2	0.237	-0.58
1426574_a_at	Add3	adducin 3 (gamma)	-1.11	0.621	-1.11	0.627	1.1	0.637	-1.63	0.253	-0.69
1419817_s_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	-1.13	0.732	-1.04	0.698	1.05	0.8	-1.26	0.472	-0.59
1438638_x_at	1700027J05Rik	RIKEN cDNA 1700027J05 gene	-1.55	0.034	1.33	0.255	-1.07	0.785	-1.03	0.901	-0.58
1454960_at	Smad3	MAD homolog 3 (Drosophila)	1.01	0.796	-1.08	0.61	-1.04	0.706	-1.28	0.187	-0.59
1427653_at	Tcra /// A430107P0	T-cell receptor alpha chain /// RIKEN cDNA A430107P09 gene /// gene model 12	-1.08	0.402	1.04	0.785	-1.06	0.778	-2.49	0.115	-0.9
1417475_at	Atp13a1	ATPase type 13A1	-1.11	0.471	-1.15	0.018	1.13	0.429	-1.34	0.046	-0.62
1459406_at	Cept1	Choline/ethanolaminephosphotransferase 1	1.15	0.791	-1.14	0.81	-1.14	0.587	-1.07	0.802	-0.55
1453016_at	2900042B11Rik	RIKEN cDNA 2900042B11 gene	-1	0.995	1.11	0.43	-1.25	0.275	-1.66	0.229	-0.7
1437046_x_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.11	0.252	-1.03	0.787	1.03	0.747	-1.11	0.602	-0.55
1431774_a_at	4930404J24Rik	RIKEN cDNA 4930404J24 gene	-1.13	0.513	-1.01	0.946	1.03	0.722	-1.61	0.036	-0.68
1458898_at	---	---	-1.59	0.503	1.76	0.325	-1.93	0.166	-2.31	0.283	-1.02
1432244_at	4930507D10Rik	RIKEN cDNA 4930507D10 gene	-1.2	0.85	1.59	0.377	-2.05	0.122	-1.03	0.971	-0.67
1420000_s_at	Igbp1	immunoglobulin (CD79A) binding protein 1	-1.12	0.391	1.14	0.068	-1.14	0.247	-1.52	0.182	-0.66
1451692_at	2410015B03Rik	RIKEN cDNA 2410015B03 gene	-1.03	0.892	-1.14	0.4	1.06	0.829	-1.03	0.918	-0.53
1421537_at	Hoxd3	homeo box D3	-1.16	0.385	1.38	0.468	-1.5	0.368	-1.48	0.06	-0.69
1426482_at	Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, rep	1.14	0.222	-1.03	0.68	-1.26	0.02	-1.08	0.492	-0.56
1428967_at	Igf1r	insulin-like growth factor I receptor	-1.06	0.87	-1.03	0.865	-1	0.983	1.38	0.174	-0.43
1417135_at	Srpk2	serine/arginine-rich protein specific kinase 2	1.13	0.313	-1.09	0.457	-1.16	0.144	-1.19	0.532	-0.58
1424562_a_at	Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.26	0.034	1.23	0.244	-1.13	0.512	-1.52	0.201	-0.67
1428953_at	Otud7b	OTU domain containing 7B	-1.1	0.089	-1.03	0.779	1.03	0.801	-1.02	0.937	-0.53
1444978_at	---	---	1.16	0.849	-1.19	0.738	-1.09	0.775	-1.06	0.833	-0.55
1436809_a_at	Spin	spindlin	-1.07	0.667	1.06	0.761	-1.09	0.61	-1.51	0.165	-0.65
1429389_at	Setmar	SET domain and mariner transposase fusion gene	1.05	0.714	-1.07	0.637	-1.08	0.669	-1.14	0.347	-0.56
1457849_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.53	0.62	-1.2	0.783	1.42	0.45	-1.77	0.013	-0.77
1418642_at	Lcp2	lymphocyte cytosolic protein 2	-1.08	0.814	-1.02	0.935	1	0.994	-1.02	0.92	-0.53
1435383_x_at	Ndn	necdin	1.17	0.244	-1.09	0.821	-1.22	0.415	-1.33	0.352	-0.62
1439028_at	Ufm1	ubiquitin-fold modifier 1	-1.17	0.837	1.74	0.306	-3.18	0.163	-1.21	0.558	-0.96
1430691_at	4632411P08Rik	RIKEN cDNA 4632411P08 gene	1.1	0.342	-1.24	0.663	-1	0.996	-4.28	0.002	-1.35
1430020_x_at	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	-1.09	0.317	-1.15	0.084	1.12	0.568	-1.09	0.347	-0.55
1448263_a_at	Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)	1.05	0.674	-1.03	0.727	-1.12	0.19	-1.05	0.854	-0.54
1437688_x_at	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	-1.12	0.477	1.07	0.735	-1.07	0.34	-1.05	0.741	-0.54
1422770_at	Rad51l3	RAD51-like 3 (S. cerevisiae)	-1.22	0.249	-1.26	0.101	1.29	0.156	-1.04	0.875	-0.56
1433688_x_at	Rpl14	ribosomal protein L14	-1.07	0.413	1.06	0.485	-1.09	0.379	-1.4	0.071	-0.62
1460559_at	Ankrd25	ankyrin repeat domain 25	-1.03	0.615	1.05	0.803	-1.12	0.572	-1.39	0.364	-0.63
1428171_at	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	1.06	0.681	-1	0.963	-1.17	0.09	-1.34	0.045	-0.61
1418049_at	Ltbp3	latent transforming growth factor beta binding protein 3	-1.13	0.713	1.21	0.69	-1.23	0.533	-1.29	0.257	-0.61
1419846_at	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.14	0.75	-1.13	0.758	1.14	0.521	-1.1	0.51	-0.55
1422139_at	Plau	plasminogen activator, urokinase	1.14	0.804	-1.23	0.733	-1.04	0.765	-1.72	0.411	-0.71
1440088_at	---	Transcribed locus	-1.54	0.488	-1.72	0.159	1.68	0.043	-1.68	0.2	-0.82
1432150_at	Tmem59	transmembrane protein 59	1.24	0.781	-1.23	0.681	-1.17	0.603	-1.17	0.72	-0.58
1446407_at	Mysm1	Myb-like, SWIRM and MPN domains 1	-1.18	0.467	1.49	0.055	-1.75	0.044	-1.45	0.065	-0.72
1438956_x_at	Pim3	proviral integration site 3	-1.34	0.024	-1.26	0.581	1.37	0.093	-1.42	0.133	-0.66
1452857_at	---	---	-1.28	0.19	-1.11	0.637	1.23	0.405	-1.27	0.369	-0.61
1431718_at	Kif15	kinesin family member 15	-1.46	0.155	-1.21	0.525	1.4	0.332	-1.03	0.943	-0.57
1459329_at	Ttc7	tetratricopeptide repeat domain 7	-1.15	0.185	-1.05	0.885	1.08	0.805	-1.65	0.23	-0.69
1451237_s_at	Rbm7	RNA binding motif protein 7	-1.05	0.418	1.06	0.381	-1.12	0.052	-1.18	0.174	-0.57

1451575_a_at	Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	1.03	0.888	-1.04	0.788	-1.1	0.389	-1.01	0.964	-0.53
1456720_at	1500041B16Rik	RIKEN cDNA 1500041B16 gene	1.66	0.296	-1.65	0.211	-1.55	0.148	-1.37	0.445	-0.73
1437105_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	-1	0.937	1.06	0.42	-1.17	0.213	-1.21	0.035	-0.58
1430037_at	Snx27	sorting nexin family member 27	1.28	0.506	-1.3	0.041	-1.16	0.607	-1.09	0.281	-0.57
1417442_a_at	Pex3	peroxisomal biogenesis factor 3	-1.18	0.12	-1.12	0.275	1.17	0.588	-1.09	0.356	-0.56
1442925_at	2610207I05Rik	RIKEN cDNA 2610207I05 gene	-1.51	0.52	1.48	0.481	-1.3	0.52	-2.28	0.411	-0.9
1447131_at	LOC666453 /// LOC	hypothetical protein LOC666453 /// hypothetical protein LOC671074 /// hypothetic	1.09	0.68	-1	0.987	-1.21	0.695	-2.19	0.347	-0.83
1431618_a_at	D14Ertd581e	DNA segment, Chr 14, ERATO Doi 581, expressed	1.23	0.214	-1.26	0.504	-1.12	0.693	-1.18	0.483	-0.58
1438723_a_at	Rps10 /// LOC6365	ribosomal protein S10 /// similar to ribosomal protein S10 /// similar to ribosomal p	-1.03	0.41	1.06	0.529	-1.14	0.33	-1.31	0.004	-0.61
1418772_at	BC016423	cDNA sequence BC016423	-1.05	0.847	1.14	0.562	-1.22	0.271	-1.7	0.066	-0.71
1417090_at	Rcn1	reticulocalbin 1	-1.03	0.172	1.19	0.317	-1.33	0.03	-1.08	0.559	-0.56
1432291_at	0610033M10Rik	RIKEN cDNA 0610033M10 gene	-1.35	0.376	1.39	0.586	-1.28	0.529	-1.01	0.992	-0.56
1429186_a_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.16	0.045	-1.11	0.645	1.15	0.591	-1.04	0.902	-0.54
1417524_at	Cnih2	cornichon homolog 2 (Drosophila)	1.45	0.437	-1.59	0.434	-1.2	0.188	-1.02	0.955	-0.59
1459239_at	Ascc3	Activating signal cointegrator 1 complex subunit 3	1.65	0.638	-3.43	0.227	-1.03	0.914	-2.67	0.261	-1.37
1445659_at	Ppgb	Protective protein for beta-galactosidase	1.17	0.351	-1.02	0.953	-1.32	0.208	-1.4	0.357	-0.64
1441803_at	A130090K04Rik	RIKEN cDNA A130090K04 gene	1.54	0.188	-2.1	0.039	-1.12	0.801	-2.26	0.157	-0.99
1417843_s_at	Eps8l2	EPS8-like 2	-1.23	0.245	-1.47	0.095	1.42	0.201	-1.05	0.836	-0.58
1425296_a_at	Rgs3 /// LOC43623	regulator of G-protein signaling 3 /// similar to Regulator of G-protein signaling 3 (	-1.15	0.644	-1.26	0.553	1.25	0.301	-1.1	0.735	-0.57
1419947_at	D4Ertd117e	DNA segment, Chr 4, ERATO Doi 117, expressed	-1.15	0.716	1.08	0.655	-1.04	0.614	-1.13	0.595	-0.56
1429560_at	Zfp422-rs1	zinc finger protein 422, related sequence 1	1.03	0.78	-1.14	0.157	-1	0.995	-1.01	0.929	-0.53
1423247_at	Txndc4	thioredoxin domain containing 4 (endoplasmic reticulum)	-1.03	0.773	-1.1	0.175	1.03	0.648	-1.01	0.96	-0.53
1447160_at	Nono /// LOC38235	non-POU-domain-containing, octamer binding protein /// hypothetical gene suppo	-1.32	0.051	-1.19	0.116	1.31	0.186	-1.03	0.821	-0.56
1445612_at	---	---	1.41	0.696	-1.53	0.136	-1.18	0.409	-1.03	0.898	-0.58
1434108_at	Fbxo11	F-box protein 11	-1.13	0.267	1.05	0.53	-1.03	0.835	-1.51	0.136	-0.65
1440296_at	LOC666250 /// LOC	hypothetical protein LOC666250 /// hypothetical protein LOC669419	-1.07	0.863	1.01	0.968	-1.03	0.797	-1.65	0.287	-0.69
1435358_at	Cuedc1	CUE domain containing 1	-1.17	0.374	1.11	0.742	-1.05	0.76	-1.04	0.782	-0.54
1453099_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	1.19	0.42	-1.08	0.472	-1.26	0.186	-1.27	0.064	-0.6
1422773_at	Myt1	myelin transcription factor 1	1.3	0.545	-1.08	0.841	-1.46	0.508	-1.49	0.442	-0.68
1445480_at	Gpr19	G protein-coupled receptor 19	-1.24	0.124	-1.02	0.958	1.13	0.261	-1.14	0.439	-0.57
1420386_at	Seh1l	SEH1-like (S. cerevisiae	1.21	0.671	-1.24	0.142	-1.12	0.275	-1.12	0.608	-0.57
1452257_at	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	-1.08	0.815	-2.28	0.018	1.55	0.114	-1.66	0.291	-0.87
1458036_at	C77576	Expressed sequence C77576	1.43	0.593	-2.05	0.058	-1.01	0.976	-1.28	0.771	-0.73
1451833_a_at	Setdb1	SET domain, bifurcated 1	-1.05	0.094	-1.07	0.282	1.03	0.81	-1.04	0.769	-0.53
1436750_a_at	Oxct1	3-oxoacid CoA transferase 1	-1.34	0.107	1.18	0.52	-1.01	0.892	-1.14	0.524	-0.58
1445878_at	C920006O11Rik	RIKEN cDNA C920006O11 gene	-1.18	0.58	-1.14	0.732	1.19	0.61	-1.08	0.738	-0.55
1448255_a_at	Surf4	surfeit gene 4	-1.07	0.557	1.1	0.149	-1.14	0.197	-1.32	0.312	-0.61
1452918_at	D19Ertd737e	DNA segment, Chr 19, ERATO Doi 737, expressed	-1.11	0.38	1.07	0.741	-1.06	0.54	-1.16	0.496	-0.57
1458853_at	Pbx1	Pre B-cell leukemia transcription factor 1	-1.24	0.771	1.61	0.479	-2	0.08	-1.54	0.274	-0.79
1451362_at	Rab7l1	RAB7, member RAS oncogene family-like 1	1	0.986	-1.01	0.847	-1.08	0.452	-1.46	0.031	-0.64
1416709_a_at	Ngrn	neugrin, neurite outgrowth associated	1.06	0.668	-1.12	0.316	-1.05	0.653	-1.25	0.116	-0.59
1438666_at	Ldlrad3	low density lipoprotein receptor class A domain containing 3	-1.41	0.022	1.28	0.281	-1.08	0.567	-1.8	0.033	-0.75
1415718_at	Sap30l	SAP30-like	1.05	0.602	-1.01	0.887	-1.15	0.118	-1.36	0.233	-0.62
1452049_at	Rpl7l1	ribosomal protein L7-like 1	1.11	0.467	-1.01	0.91	-1.22	0.168	-1.26	0.393	-0.6
1426435_at	Tmem135	transmembrane protein 135	-1.19	0.092	-1.1	0.317	1.16	0.267	-1.09	0.613	-0.55
1422954_at	Zfp60	zinc finger protein 60	1.3	0.356	-1.4	0.525	-1.11	0.719	-1.15	0.811	-0.59
1459607_at	2900001O04Rik	RIKEN cDNA 2900001O04 gene	-1.11	0.86	1.53	0.455	-2.05	0.18	-1.55	0.681	-0.8
1447529_at	---	---	-2.33	0.159	-1.18	0.763	1.64	0.437	-1.23	0.756	-0.78
1452680_at	Snrpd2	small nuclear ribonucleoprotein D2	-1.04	0.591	-1.07	0.225	1.01	0.931	-1.24	0.227	-0.58
1417661_at	Rdm1	RAD52 motif 1	1.19	0.502	-1.28	0.119	-1.06	0.715	-1.04	0.513	-0.55
1415895_at	Snrpn	small nuclear ribonucleoprotein N	-1.14	0.547	-1.12	0.591	1.15	0.488	-2.08	0.134	-0.8
1435741_at	Pde8b	phosphodiesterase 8B	-1.16	0.481	1.45	0.092	-1.66	0.101	-1.18	0.794	-0.64
1445212_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630021	1.18	0.628	-1.32	0.387	-1.03	0.907	-1.4	0.45	-0.64

1436522_at	Map3k3	mitogen activated protein kinase kinase kinase 3	1.03	0.594	-1.03	0.736	-1.09	0.228	-1.67	0.107	-0.69
1447475_at	Gm967	gene model 967, (NCBI)	1.44	0.116	-1.39	0.143	-1.32	0.349	-1.37	0.543	-0.66
1419260_a_at	Snrpb	small nuclear ribonucleoprotein B	-1.04	0.888	-1.12	0.37	1.06	0.767	-1.17	0.485	-0.57
1419545_a_at	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	-1.13	0.321	1.07	0.279	-1.04	0.815	-1.21	0.043	-0.58
1460682_s_at	Ceacam1 /// Ceaca	CEA-related cell adhesion molecule 1 /// CEA-related cell adhesion molecule 2	1.35	0.048	-1.16	0.016	-1.41	0.112	-1.61	0.101	-0.71
1426052_at	Mlh3	mutL homolog 3 (E coli)	-1.15	0.389	1.1	0.391	-1.06	0.658	-1.05	0.72	-0.54
1428468_at	3110043O21Rik	RIKEN cDNA 3110043O21 gene	-1.14	0.345	1.09	0.588	-1.05	0.778	-1.06	0.675	-0.54
1424014_at	2900092E17Rik	RIKEN cDNA 2900092E17 gene	-1.06	0.782	-1.03	0.752	1	0.987	-1.02	0.906	-0.53
1440106_at	Tcf4	Transcription factor 4	-1.07	0.831	1.14	0.695	-1.19	0.434	-1.14	0.755	-0.57
1423356_at	Snap29	synaptosomal-associated protein	-1.26	0.598	-1.03	0.901	1.15	0.394	-1.61	0.246	-0.69
1426476_at	Rasa1	RAS p21 protein activator 1	-1.03	0.668	1.09	0.302	-1.17	0.034	-1.29	0.144	-0.6
1428110_x_at	Vps11	vacuolar protein sorting 11 (yeast)	-1.09	0.191	-1.16	0.051	1.13	0.358	-1.45	0.046	-0.64
1421236_at	Ripk2	receptor (TNFRSF)-interacting serine-threonine kinase 2	-1.14	0.429	-1.15	0.669	1.17	0.179	-1.31	0.003	-0.61
1455939_x_at	Srp14	signal recognition particle 14	-1.05	0.695	1.11	0.167	-1.16	0.124	-1.4	0.138	-0.63
1428249_at	Pygo2	pygopus 2	-1.04	0.759	-1.1	0.322	1.05	0.737	-1.24	0.251	-0.58
1430089_at	5830469G19Rik	RIKEN cDNA 5830469G19 gene	1.18	0.407	-1.06	0.551	-1.27	0.375	-1.68	0.095	-0.71
1451863_at	Uts2r	urotensin 2 receptor	-1.12	0.815	-1.21	0.428	1.2	0.573	-1.93	0.365	-0.77
1430000_at	B230117O15Rik	RIKEN cDNA B230117O15 gene	-1.19	0.001	1.44	0.294	-1.59	0.133	-1.21	0.288	-0.64
1454460_at	5730433N10Rik	RIKEN cDNA 5730433N10 gene	1.59	0.121	-1.41	0.128	-1.63	0.117	-1.25	0.287	-0.68
1416219_at	Rpl19	ribosomal protein L19	1	0.95	-1.01	0.803	-1.09	0.311	-1.36	0.011	-0.61
1457972_at	C87436	Expressed sequence C87436	-1.4	0.143	1.37	0.541	-1.2	0.535	-1.3	0.15	-0.63
1453358_s_at	5830467E07Rik ///	RIKEN cDNA 5830467E07 gene /// RIKEN cDNA C730024G19 gene	-1.1	0.671	1.01	0.94	-1	0.99	-1.42	0.172	-0.63
1459523_at	C85403	expressed sequence C85403	1.25	0.569	-1.21	0.177	-1.2	0.3	-1.01	0.946	-0.54
1452702_at	Clcn7	chloride channel 7	-1.12	0.232	-1.04	0.752	1.06	0.726	-1.04	0.876	-0.53
1434218_at	C330019G07Rik	RIKEN cDNA C330019G07 gene	-1.12	0.603	1.09	0.684	-1.07	0.533	-1.01	0.943	-0.53
1428056_at	Klra4	Killer cell lectin-like receptor, subfamily A, member 4	-1.06	0.884	-1.52	0.416	1.31	0.684	-1.63	0.438	-0.72
1452871_at	Neil1	nei endonuclease VIII-like 1 (E. coli)	-1.19	0.188	-1.07	0.364	1.15	0.141	-1.55	0.286	-0.67
1428636_at	Steap2	six transmembrane epithelial antigen of prostate 2	-1.12	0.147	1.14	0.686	-1.13	0.496	-1.34	0.448	-0.61
1452024_a_at	Ldb1	LIM domain binding 1	1.37	0.283	-1.24	0.497	-1.34	0.095	-1.02	0.921	-0.56
1428999_at	Phf3	PHD finger protein 3	1.18	0.583	-1.23	0.449	-1.08	0.637	-1.11	0.745	-0.56
1443200_at	A930011G24	hypothetical protein A930011G24	-1.31	0.539	-2.59	0.129	1.77	0.177	-1.37	0.519	-0.88
1421429_a_at	Npnt	nephronectin	1.14	0.756	-1.03	0.742	-1.25	0.518	-1.56	0.51	-0.67
1450608_at	Hist1h1t	histone 1, H1t	1.11	0.785	-1.05	0.905	-1.16	0.709	-1.34	0.269	-0.61
1429162_at	1500015A07Rik	RIKEN cDNA 1500015A07 gene	-1.15	0.333	-1.24	0.19	1.24	0.271	-1.27	0.136	-0.61
1457079_at	---	CDNA clone IMAGE:30014192	-1.12	0.75	-1.22	0.678	1.2	0.728	-1.81	0.215	-0.74
1422083_at	Tlr9	toll-like receptor 9	-1.22	0.35	1.5	0.279	-1.67	0.085	-1.74	0.011	-0.78
1460249_at	Lnx2	ligand of numb-protein X 2	-1.12	0.71	1.2	0.249	-1.21	0.138	-1.31	0.297	-0.61
1427464_s_at	Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)	-1.03	0.869	1.02	0.935	-1.08	0.575	-1	0.966	-0.52
1419271_at	Pax6	paired box gene 6	-1.05	0.948	-1.38	0.501	1.24	0.373	-1.17	0.762	-0.59
1421841_at	Fgfr3	fibroblast growth factor receptor 3	-1.09	0.504	-1.13	0.213	1.11	0.488	-1.46	0.009	-0.64
1429589_at	6330404F12Rik	RIKEN cDNA 6330404F12 gene	1.1	0.859	-1.2	0.509	-1.02	0.967	-1.05	0.909	-0.54
1429422_at	4933412E12Rik	RIKEN cDNA 4933412E12 gene	-1.26	0.534	-1.29	0.288	1.35	0.067	-1.73	0.048	-0.73
1416546_a_at	Rpl6	ribosomal protein L6	-1.02	0.769	1.02	0.794	-1.1	0.034	-1.29	0.035	-0.6
1448216_at	Syngr3	synaptogyrin 3	-1.08	0.775	1.08	0.771	-1.1	0.489	-1.15	0.552	-0.56
1457585_at	Tmem24	transmembrane protein 24	-1.47	0.148	-1.14	0.42	1.36	0.382	-4.29	0.147	-1.38
1439176_at	E130120F12Rik	RIKEN cDNA E130120F12 gene	-1.2	0.269	-1.01	0.846	1.09	0.435	-1.32	0.045	-0.61
1421340_at	Map3k5 /// LOC675	mitogen activated protein kinase kinase kinase 5 /// similar to mitogen activated p	-1.03	0.917	-1.57	0.286	1.31	0.272	-1.06	0.863	-0.59
1443080_at	Adcy5	Adenylate cyclase 5	-1.48	0.638	1.33	0.576	-1.09	0.547	-1.48	0.131	-0.68
1419680_a_at	Elac2	elaC homolog 2 (E. coli)	-1.26	0.061	-1.07	0.229	1.19	0.057	-1	0.973	-0.54
1432708_at	---	---	1.38	0.704	-1.45	0.267	-1.17	0.215	-1.29	0.619	-0.63
1457773_at	Slamf6	SLAM family member 6	-1.11	0.843	-1.16	0.757	1.16	0.438	-1.81	0.183	-0.73
1423556_at	Akr1b7	aldo-keto reductase family 1, member B7	-1.5	0.228	1.3	0.142	-1.05	0.341	-1.27	0.461	-0.63
1447915_x_at	BC054438	cDNA sequence BC054438	-1.1	0.679	1.29	0.248	-1.4	0.092	-1.9	0.078	-0.78

1436270_at	Gm740	gene model 740, (NCBI)	-1.02	0.849	-1.02	0.814	-1.04	0.755	1.23	0.236	-0.46
1417176_at	Csnk1e	casein kinase 1, epsilon	-1.06	0.745	-1.16	0.398	1.11	0.521	-1.17	0.252	-0.57
1423689_a_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-1.07	0.853	1.17	0.765	-1.23	0.243	-1.44	0.281	-0.64
1431503_at	4930513O06Rik	RIKEN cDNA 4930513O06 gene	1.28	0.739	-1.38	0.339	-1.09	0.826	-1.51	0.185	-0.67
1451974_at	Osbpl2	oxysterol binding protein-like 2	-1.09	0.102	-1.07	0.371	1.07	0.65	-1.17	0.202	-0.57
1453341_a_at	4930425N13Rik	RIKEN cDNA 4930425N13 gene	-1.16	0.441	1.29	0.182	-1.32	0.551	-1.1	0.912	-0.57
1418277_at	Rp9h	retinitis pigmentosa 9 homolog (human)	-1.12	0.507	1.19	0.144	-1.2	0.061	-1.51	0.009	-0.66
1446082_at	Jarid2	Jumonji, AT rich interactive domain 2	-1.17	0.601	1.3	0.632	-1.3	0.435	-1.52	0.529	-0.67
1427619_a_at	Sh3tc1	SH3 domain and tetratricopeptide repeats 1	-1.23	0.093	1.28	0.693	-1.22	0.564	-2.03	0.278	-0.8
1437475_at	BC028454	cDNA sequence BC028454	-1.05	0.465	-1.21	0.078	1.15	0.313	-1.03	0.722	-0.54
1456497_x_at	Rps10	ribosomal protein S10	-1.08	0.272	1.08	0.165	-1.09	0.463	-1.26	0.04	-0.59
1446792_at	---	Transcribed locus, moderately similar to XP_579119.1 PREDICTED: ATP-binding	-1.02	0.963	-1.24	0.8	1.14	0.726	-2.33	0.255	-0.87
1452678_a_at	Ccbl1	cysteine conjugate-beta lyase 1	1.02	0.867	-1.06	0.748	-1.05	0.446	-1.58	0.297	-0.67
1448742_at	Snai1	snail homolog 1 (Drosophila)	-1.01	0.979	-1.55	0.162	1.28	0.224	-1.34	0.042	-0.65
1425481_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	-1.04	0.69	-1.2	0.104	1.13	0.443	-1.38	0.171	-0.62
1454544_at	9530078B04Rik	RIKEN cDNA 9530078B04 gene	-1.78	0.538	1.74	0.182	-1.62	0.322	-1.47	0.265	-0.78
1435270_x_at	2510005D08Rik	RIKEN cDNA 2510005D08 gene	-1	0.998	1.01	0.895	-1.1	0.669	-1.03	0.594	-0.53
1427440_a_at	Afm	afamin	-1.26	0.002	-1.2	0.035	1.29	0.185	-1.16	0.638	-0.58
1454078_a_at	Gal3st1	galactose-3-O-sulfotransferase 1	1.08	0.722	-1	0.997	-1.19	0.176	-1.05	0.567	-0.54
1459223_at	B930095G15Rik	RIKEN cDNA B930095G15 gene	-1.05	0.541	-1.09	0.835	1.05	0.876	-1.07	0.945	-0.54
1459366_at	Rgmb	RGM domain family, member B	-1.17	0.359	1.36	0.423	-1.42	0.057	-1.62	0.473	-0.71
1425332_at	Zfp106	zinc finger protein 106	1	0.991	-1.01	0.926	-1.07	0.519	-1.28	0.304	-0.59
1438800_at	Nagk	N-acetylglucosamine kinase	-1.06	0.812	-1.26	0.599	1.18	0.647	-1.52	0.319	-0.66
1428629_at	Zfp518	zinc finger protein 518	1.13	0.523	-1.04	0.779	-1.2	0.103	-1.23	0.148	-0.59
1417408_at	F3	coagulation factor III	-1	0.985	-1.09	0.808	1	0.997	-1.24	0.385	-0.58
1425135_a_at	Dnm2	dynamin 2	-1.11	0.593	-1.1	0.232	1.11	0.578	-1.11	0.112	-0.55
1454802_x_at	Arih2	ariadne homolog 2 (Drosophila)	-1.1	0.69	-1.18	0.069	1.16	0.254	-1.07	0.8	-0.55
1426074_at	LOC434536	LOC434536	-1.1	0.716	1.19	0.337	-1.22	0.448	-1.52	0.177	-0.66
1422381_at	Olfr160	olfactory receptor 160	-1.04	0.935	-1.28	0.601	1.18	0.434	-1.66	0.286	-0.7
1428753_a_at	Dgcr6	DiGeorge syndrome critical region gene 6	1.03	0.553	-1.01	0.93	-1.11	0.498	-1.16	0.518	-0.56
1436072_at	---	---	-1.24	0.243	1.2	0.435	-1.09	0.619	-1.49	0.373	-0.65
1460041_at	D630040I23Rik	RIKEN cDNA D630040I23 gene	-1.19	0.617	-1.03	0.919	1.11	0.686	-1.39	0.149	-0.62
1453481_at	Zdhhc2	zinc finger, DHHC domain containing 2	-1	0.996	-1.21	0.455	1.1	0.884	-1.95	0.021	-0.77
1424368_s_at	Ubqln1	ubiquilin 1	-1.06	0.154	-1.09	0.055	1.06	0.349	-1.15	0.211	-0.56
1438798_at	4931406P16Rik	RIKEN cDNA 4931406P16 gene	1.17	0.245	-1.16	0.713	-1.13	0.769	-1.1	0.857	-0.55
1455756_at	F730014I05Rik	RIKEN cDNA F730014I05 gene	-1.09	0.535	1.08	0.544	-1.09	0.643	-1.03	0.916	-0.53
1455915_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.06	0.742	-1.06	0.498	-1.1	0.563	-1.37	0.156	-0.62
1437625_at	Rps6ka5	Ribosomal protein S6 kinase, polypeptide 5	1.28	0.419	-1.06	0.91	-1.43	0.361	-1.32	0.556	-0.63
1429712_at	Etohi1 /// 6230416C	ethanol induced 1 /// RIKEN cDNA 6230416C02 gene /// similar to zinc finger prot	-1.11	0.529	1.26	0.312	-1.31	0.083	-1.31	0.408	-0.62
1457774_at	2310079N02Rik	RIKEN cDNA 2310079N02 gene	-1.05	0.327	-1.03	0.893	-1	0.981	1.07	0.77	-0.5
1423245_at	Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana	1.02	0.88	-1.07	0.625	-1.04	0.759	-1.16	0.05	-0.56
1417243_at	2310065K24Rik	RIKEN cDNA 2310065K24 gene	-1.07	0.518	-1.15	0.039	1.12	0.018	-1.14	0.238	-0.56
1417267_s_at	Fkbp11	FK506 binding protein 11	1.17	0.588	-1.26	0.291	-1.05	0.638	-1.02	0.89	-0.54
1449548_at	Efnb2	ephrin B2	-1.33	0.568	-1.61	0.292	1.55	0.3	-4.72	0.017	-1.53
1422662_at	Lgals8	lectin, galactose binding, soluble 8	-1.06	0.754	1.03	0.805	-1.06	0.336	-1.36	0.077	-0.61
1431611_a_at	Igsf4a	immunoglobulin superfamily, member 4A	-1.01	0.978	-1.25	0.032	1.13	0.566	-1.01	0.947	-0.53
1428253_at	Chmp2b	chromatin modifying protein 2B	-1.18	0.394	-1.04	0.536	1.11	0.271	-1.28	0.293	-0.6
1420843_at	Ptprf	protein tyrosine phosphatase, receptor type, F	-1.12	0.315	-1.05	0.333	1.07	0.688	-1.42	0.315	-0.63
1420869_at	Mllt10	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosop	1.04	0.858	-1.14	0.782	-1	0.996	-1.13	0.722	-0.56
1450855_at	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	-1.13	0.697	1.04	0.661	-1	0.965	-1.16	0.332	-0.56
1422106_a_at	Spsb2	splA/ryanodine receptor domain and SOCS box containing 2	-1.13	0.219	1.17	0.242	-1.16	0.198	-1.01	0.931	-0.53
1430825_at	E130102C15Rik	RIKEN cDNA E130102C15 gene	1.15	0.387	-1.05	0.898	-1.21	0.301	-1.33	0.537	-0.61
1428092_at	Cdc5l	cell division cycle 5-like (S. pombe)	-1.08	0.725	-1.24	0.068	1.19	0.219	-1.12	0.621	-0.56

1455666_at	A230042K10Rik	RIKEN cDNA A030001O10 gene	1.17	0.125	-1.29	0.213	-1.02	0.932	-1.38	0.043	-0.63
1436549_a_at	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	-1.07	0.423	-1.01	0.851	1	0.982	-1.32	0.12	-0.6
1439509_at	2900008C10Rik	RIKEN cDNA 2900008C10 gene	-1.07	0.811	-1.52	0.091	1.32	0.197	-1.02	0.938	-0.57
1454163_at	5730420D15Rik	RIKEN cDNA 5730420D15 gene	1.4	0.722	-1.32	0.734	-1.31	0.715	-1.08	0.833	-0.58
1440530_at	AU019752	expressed sequence AU019752	1.07	0.616	-1.1	0.72	-1.06	0.788	-1.07	0.665	-0.54
1417142_at	4932442K08Rik	RIKEN cDNA 4932442K08 gene	-1.1	0.738	-1.07	0.828	1.08	0.69	-1.33	0.304	-0.6
1444828_at	Ppp2r5c	Protein phosphatase 2, regulatory subunit B (B56), gamma isoform	1.36	0.1	-1.28	0.494	-1.27	0.455	-1.36	0.212	-0.64
1436528_at	Kazald1	Kazal-type serine peptidase inhibitor domain 1	-1.08	0.456	1.2	0.614	-1.26	0.028	-1.32	0.358	-0.61
1429961_at	1700021C14Rik	RIKEN cDNA 1700021C14 gene	1.22	0.473	-1.24	0.36	-1.11	0.664	-1.33	0.048	-0.62
1440135_at	Apbb2	Amyloid beta (A4) precursor protein-binding, family B, member 2	1.42	0.236	-1.14	0.675	-1.59	0.204	-2.5	0.262	-0.95
1428971_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	1	0.999	-1.04	0.446	-1.04	0.792	-1.11	0.066	-0.55
1417953_at	D6Wsu176e	DNA segment, Chr 6, Wayne State University 176, expressed	1.15	0.191	-1.08	0.423	-1.18	0.128	-1.21	0.429	-0.58
1457008_at	Chrnb4	cholinergic receptor, nicotinic, beta polypeptide 4	-1.14	0.856	1.05	0.946	-1.01	0.99	-1.16	0.835	-0.56
1444191_at	---	---	1.06	0.905	-1.02	0.891	-1.13	0.499	-1.33	0.236	-0.6
1439995_at	C80638	expressed sequence C80638	-2	0.149	1.5	0.428	-1.08	0.814	-1.02	0.943	-0.65
1428763_at	Smug1	single-strand selective monofunctional uracil DNA glycosylase	1.06	0.418	-1.12	0.371	-1.04	0.726	-1.3	0.273	-0.6
1455720_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-5.68	0.145	2.06	0.426	-1.46	0.152	-1.65	0.151	-1.68
1451040_at	Hars2	histidyl tRNA synthetase 2	-1.07	0.42	-1.08	0.381	1.06	0.713	-1.21	0.266	-0.57
1448106_at	Necap1	NECAP endocytosis associated 1	-1.13	0.19	-1.1	0.334	1.13	0.218	-1.27	0.421	-0.59
1449617_at	2900092E17Rik	RIKEN cDNA 2900092E17 gene	-1.31	0.056	1.3	0.42	-1.16	0.677	-1.06	0.756	-0.56
1445765_at	9430011C21Rik	RIKEN cDNA 9430011C21 gene	1.5	0.396	-1.31	0.43	-1.5	0.487	-1.18	0.587	-0.63
1449124_at	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	-1.19	0.003	1.29	0.198	-1.26	0.148	-1.08	0.822	-0.56
1434829_at	Cbl	Casitas B-lineage lymphoma	1.08	0.578	-1.01	0.911	-1.16	0.347	-1.29	0.335	-0.6
1441210_at	Myo1b	Myosin IB	1.28	0.772	-1.4	0.025	-1.08	0.838	-1.11	0.719	-0.58
1425270_at	Kif1b	kinesin family member 1B	1.44	0.376	-1.15	0.662	-1.61	0.049	-1.31	0.526	-0.66
1434407_at	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	-1.14	0.704	-1.07	0.837	1.11	0.564	-1.12	0.76	-0.55
1437505_at	Trio	Triple functional domain (PTPRF interacting)	-1.37	0.462	1.45	0.295	-1.34	0.07	-1.49	0.245	-0.69
1451592_at	P42pop	Myb protein P42POP	-1.06	0.415	1.01	0.97	-1.02	0.912	-1.45	0.068	-0.63
1428880_at	0610038F07Rik	RIKEN cDNA 0610038F07 gene	-1.02	0.941	-1.14	0.458	1.07	0.618	-1.17	0.418	-0.57
1441764_at	Prdm10	PR domain containing 10	1.15	0.702	-1.06	0.922	-1.2	0.569	-1.34	0.337	-0.61
1456699_s_at	A730098D12Rik	RIKEN cDNA A730098D12 gene	-1.07	0.58	1.02	0.807	-1.02	0.825	-1.23	0.221	-0.58
1444850_at	RP23-248K2.4	hepatitis A virus cellular receptor 1-like	1.43	0.435	-1.93	0.164	-1.02	0.966	-1.03	0.942	-0.64
1455118_at	D9Ertd402e	DNA segment, Chr 9, ERATO Doi 402, expressed	-1.06	0.379	1.02	0.859	-1.03	0.858	-1.5	0.248	-0.64
1453110_at	Wdr51b	WD repeat domain 51B	-1.08	0.165	-1.11	0.774	1.1	0.489	-1.18	0.454	-0.57
1444075_at	Filip1	filamin A interacting protein 1	1.21	0.285	-1.13	0.83	-1.21	0.552	-1.47	0.59	-0.65
1451540_at	Mpi1	mannose phosphate isomerase 1	-1.06	0.649	1.03	0.894	-1.05	0.805	-1.02	0.94	-0.52
1423540_at	Rbms2	RNA binding motif, single stranded interacting protein 2	1.03	0.74	-1.03	0.451	-1.08	0.669	-1.08	0.782	-0.54
1428687_at	Zfp687	zinc finger protein 687	-1.03	0.807	-1.19	0.355	1.11	0.472	-1.1	0.573	-0.55
1441333_at	Trps1	Trichorhinophalangeal syndrome I (human)	-1.28	0.619	-1.46	0.379	1.46	0.49	-1.67	0.457	-0.74
1423754_at	Ifitm3	interferon induced transmembrane protein 3	1.13	0.627	-1.05	0.508	-1.18	0.148	-1.18	0.069	-0.57
1440324_at	Mrpl19	mitochondrial ribosomal protein L19	-1.25	0.345	-1.12	0.549	1.24	0.381	-1	0.993	-0.54
1425280_at	Leng1	leukocyte receptor cluster (LRC) member 1	-1.11	0.665	-1.02	0.804	1.05	0.824	-1.09	0.505	-0.54
1425194_a_at	6330577E15Rik	RIKEN cDNA 6330577E15 gene	1.02	0.652	-1	0.989	-1.1	0.466	-1.06	0.373	-0.54
1438862_at	A630005I04Rik	RIKEN cDNA A630005I04 gene	-1.14	0.817	1.27	0.55	-1.28	0.298	-1.65	0.175	-0.7
1428332_at	1500004A08Rik	RIKEN cDNA 1500004A08 gene	1.19	0.463	-1.37	0.423	-1	1	-2.62	0.093	-0.95
1451042_a_at	Mina	myc induced nuclear antigen	-1.21	0.063	-1.18	0.179	1.26	0.022	-1.49	0.017	-0.66
1424896_at	Gpr85	G protein-coupled receptor 85	-1.25	0.276	1.36	0.325	-1.3	0.342	-1.38	0.679	-0.64
1434690_at	Lycat	lysocardiolipin acyltransferase	1.05	0.664	-1.11	0.489	-1.03	0.792	-1.03	0.929	-0.53
1455669_at	Wdr19	WD repeat domain 19	-1.07	0.719	-1.05	0.896	1.04	0.758	-1.12	0.668	-0.55
1436359_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	1.31	0.77	-1.27	0.738	-1.2	0.526	-2.21	0.239	-0.84
1435544_at	Exosc6	exosome component 6	1.29	0.206	-1.25	0.2	-1.2	0.317	-1.09	0.723	-0.56
1452292_at	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	-3.27	0.421	-1.43	0.535	1.92	0.387	-3.26	0.302	-1.51
1418098_at	Adcy4	adenylate cyclase 4	-1.43	0.259	1.24	0.396	-1.02	0.91	-1.84	0.073	-0.76

1448553_at	LOC671894 /// LOC	similar to myosin, heavy polypeptide 4, skeletal muscle /// similar to myosin, heav	-1.72	0.268	1.39	0.57	-1.04	0.916	-2.01	0.49	-0.85
1455738_at	Ccdc55	coiled-coil domain containing 55	1.29	0.524	-1.07	0.705	-1.43	0.216	-1.33	0.081	-0.63
1450706_a_at	Arl3	ADP-ribosylation factor-like 3	1.1	0.241	-1.03	0.821	-1.17	0.26	-1.08	0.35	-0.55
1446039_at	---	Transcribed locus	1.28	0.655	-1.25	0.673	-1.19	0.64	-2.19	0.221	-0.84
1416078_s_at	Raf1	v-raf-leukemia viral oncogene 1	-1.04	0.103	-1.06	0.207	1.03	0.688	-1.14	0.273	-0.55
1436727_x_at	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	-1.03	0.916	-1.02	0.939	-1.03	0.938	1	0.977	-0.52
1456547_at	Ski	Sloan-Kettering viral oncogene homolog	-1.24	0.322	1.37	0.136	-1.33	0.477	-1.64	0.144	-0.71
1447271_at	Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	-1.19	0.547	1.33	0.106	-1.32	0.247	-1.07	0.652	-0.56
1419447_s_at	Tbc1d1	TBC1 domain family, member 1	-1.28	0.057	1.26	0.239	-1.13	0.588	-1.7	0.089	-0.71
1429262_at	Rassf6	Ras association (RalGDS/AF-6) domain family 6	-1.12	0.246	1.05	0.816	-1.02	0.939	-1.91	0.173	-0.75
1418735_at	Krt4	keratin 4	-1.12	0.615	1.42	0.634	-1.62	0.178	-1.22	0.524	-0.64
1436570_at	---	Transcribed locus	-1.15	0.506	1.21	0.166	-1.18	0.416	-2.54	0.068	-0.91
1435863_at	Commd6	COMM domain containing 6	-1.15	0.058	-1.08	0.247	1.13	0.427	-1.25	0.217	-0.59
1432081_at	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	-1.31	0.482	1.42	0.573	-1.35	0.052	-1.51	0.001	-0.69
1438498_at	Zmynd15	zinc finger, MYND-type containing 15	-1.29	0.254	1.23	0.132	-1.09	0.825	-1.64	0.087	-0.7
1436959_x_at	Nelf	nasal embryonic LHRH factor	1.17	0.269	-1.19	0.013	-1.09	0.435	-1.43	0.217	-0.63
1439672_at	Synj1	Synaptojanin 1	1.34	0.553	-1.07	0.731	-1.53	0.065	-1.04	0.853	-0.58
1438286_at	Thrap3	Thyroid hormone receptor associated protein 3	-1.36	0.47	1.3	0.268	-1.13	0.123	-1.05	0.779	-0.56
1420830_x_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	1.01	0.916	-1.02	0.793	-1.07	0.111	-1.05	0.742	-0.53
1448264_a_at	Eif3s2	eukaryotic translation initiation factor 3, subunit 2 (beta)	-1.06	0.414	1.06	0.233	-1.09	0.641	-1.22	0.113	-0.57
1444965_at	E130002L11Rik	RIKEN cDNA E130002L11 gene	1.05	0.889	-1.02	0.969	-1.12	0.755	-1.06	0.902	-0.54
1431832_x_at	Exosc10	exosome component 10	-1.07	0.54	-1.03	0.903	1.02	0.908	-1.3	0.016	-0.59
1437173_at	Edg3	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	1.21	0.213	-1.17	0.525	-1.16	0.49	-2.55	0.084	-0.92
1438441_at	Id4	Inhibitor of DNA binding 4	-1.04	0.815	1.04	0.92	-1.08	0.47	-1.11	0.524	-0.55
1445787_at	5033413D22Rik	RIKEN cDNA 5033413D22 gene	-1.28	0.128	-1.33	0.193	1.4	0.241	-1.12	0.54	-0.59
1443914_at	Lipl2	Lipase-like, ab-hydrolase domain containing 2	-2.14	0.493	-1.08	0.902	1.53	0.456	-1.2	0.71	-0.72
1424061_at	Manbal	mannosidase, beta A, lysosomal-like	1.15	0.473	-1.26	0.018	-1.02	0.704	-1.2	0.429	-0.58
1458452_at	Ankrd11	ankyrin repeat domain 11	-1.24	0.611	1.24	0.334	-1.14	0.625	-1.44	0.102	-0.64
1420370_s_at	Csn2	casein beta	-2.09	0.012	-1.29	0.714	1.68	0.296	-1.38	0.41	-0.77
1427968_at	Tgifx1	TGIF homeobox 1	-1.25	0.769	-1.13	0.835	1.24	0.507	-1.44	0.516	-0.64
1421402_at	Mta3	metastasis associated 3	1.03	0.954	-1.01	0.977	-1.1	0.463	-1.17	0.666	-0.56
1438979_s_at	1700029I15Rik	RIKEN cDNA 1700029I15 gene	-1.02	0.529	-1.09	0.731	1.03	0.785	-1.08	0.61	-0.54
1432760_at	Bat2d	BAT2 domain containing 1	-1.45	0.282	1.52	0.249	-1.39	0.222	-1.83	0.18	-0.79
1425694_at	Tbx5	T-box 5	-1.25	0.705	-1.63	0.355	1.51	0.237	-1.06	0.782	-0.61
1440266_at	5830428M24Rik	RIKEN cDNA 5830428M24 gene	1.44	0.485	-1.81	0.162	-1.07	0.787	-1.86	0.158	-0.83
1454773_at	Rxra	retinoid X receptor alpha	1.03	0.709	-1.09	0.344	-1.02	0.891	-1	0.986	-0.52
1450874_at	Matr3	matrin 3	-1	0.971	-1.08	0.223	1.01	0.944	-1.21	0.07	-0.57
1456605_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	1.3	0.376	-1.3	0.492	-1.17	0.453	-1.24	0.16	-0.6
1444206_at	A230042K10Rik	RIKEN cDNA A030001O10 gene	1.21	0.282	-1.06	0.646	-1.29	0.191	-1.37	0.201	-0.63
1417334_at	Stk19	serine/threonine kinase 19	-1.09	0.585	-1.04	0.833	1.04	0.507	-1.19	0.3	-0.57
1426163_x_at	Rpl7	ribosomal protein L7	1.22	0.566	-1.18	0.322	-1.17	0.558	-1.32	0.302	-0.61
1458258_at	---	---	1.1	0.891	-1	0.997	-1.21	0.655	-1.58	0.384	-0.67
1424999_at	1700022C21Rik	RIKEN cDNA 1700022C21 gene	1.12	0.662	-1.1	0.444	-1.12	0.603	-1.15	0.289	-0.56
1448073_at	LOC541456	hypothetical LOC541456	-1.94	0.519	1.7	0.214	-1.41	0.152	-1.19	0.751	-0.71
1416185_a_at	Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	1.02	0.838	-1.03	0.68	-1.07	0.456	-1.4	0.055	-0.62
1456813_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.13	0.668	-1.06	0.918	1.1	0.387	-2.13	0.129	-0.8
1450566_at	Il3	interleukin 3	1.38	0.166	-1.43	0.535	-1.18	0.542	-1.68	0.246	-0.73
1426093_at	Trim34	tripartite motif protein 34	1.61	0.423	-2.15	0.003	-1.18	0.599	-2.17	0.048	-0.97
1442042_at	Tcf20	Transcription factor 20	-1.03	0.898	-1.23	0.616	1.15	0.584	-2.14	0.01	-0.81
1416127_a_at	Dnpep	aspartyl aminopeptidase	-1.04	0.89	1.13	0.454	-1.19	0.33	-1.09	0.56	-0.55
1431904_at	4933427G17Rik	RIKEN cDNA 4933427G17 gene	1.35	0.134	-1.64	0.262	-1.03	0.926	-1.63	0.316	-0.74
1442723_at	---	Transcribed locus	1.37	0.614	-1.06	0.935	-1.63	0.004	-2.24	0.203	-0.89
1452844_at	Pou6f1	POU domain, class 6, transcription factor 1	-1.51	0.1	-1.04	0.777	1.31	0.054	-1.3	0.528	-0.64

1455330_at	Nol9	nucleolar protein 9	-1.1	0.697	-1.23	0.07	1.21	0.328	-1.08	0.447	-0.55
1458350_at	Opa3	Optic atrophy 3 (human)	-1.28	0.151	-1.07	0.673	1.21	0.025	-1.08	0.717	-0.55
1416422_a_at	Ssb	Sjogren syndrome antigen B	-1.07	0.608	1.19	0.105	-1.24	0.082	-1.12	0.287	-0.56
1424096_at	Krt5	keratin 5	-1.35	0.1	-1.03	0.917	1.21	0.526	-1.23	0.172	-0.6
1435448_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	1.01	0.853	-1.08	0.744	-1.01	0.956	-1.03	0.743	-0.53
1442011_at	A230065H16Rik	RIKEN cDNA A230065H16 gene	1.51	0.409	-1.51	0.562	-1.32	0.574	-1.76	0.059	-0.77
1429416_at	Ttc9b	tetratricopeptide repeat domain 9B	-1.41	0.336	1.28	0.645	-1.07	0.386	-1.24	0.184	-0.61
1419198_at	Cbx8	chromobox homolog 8 (Drosophila Pc class)	1.03	0.898	-1.1	0.574	-1.01	0.907	-1.83	0.021	-0.73
1451972_at	Glcci1	glucocorticoid induced transcript 1	-1.14	0.318	-1.14	0.509	1.17	0.441	-1.4	0.064	-0.63
1453696_at	4921508A21Rik	RIKEN cDNA 4921508A21 gene	-1.11	0.83	1.31	0.252	-1.39	0.258	-1.24	0.75	-0.61
1438544_at	1700001G11Rik	RIKEN cDNA 1700001G11 gene	-1.59	0.069	-1.07	0.784	1.37	0.204	-1.22	0.391	-0.63
1443365_at	Htr4	5 hydroxytryptamine (serotonin) receptor 4	-1.25	0.836	-1.07	0.89	1.19	0.511	-3.04	0.037	-1.04
1443082_at	---	---	-1.16	0.327	-1.06	0.766	1.13	0.574	-1.21	0.167	-0.58
1452791_at	Coq2	coenzyme Q2 homolog, prenyltransferase (yeast)	-1.01	0.968	1.07	0.547	-1.15	0.035	-1.28	0.057	-0.59
1449196_a_at	Rps27a /// LOC619	ribosomal protein S27a /// similar to ribosomal protein S27a /// similar to ubiquitin	-1.04	0.052	1.17	0.04	-1.25	0.04	-1.31	0.004	-0.61
1433258_at	A330102K18Rik	RIKEN cDNA A330102K18 gene	1.78	0.572	-1.53	0.594	-2.01	0.12	-1.04	0.9	-0.7
1426213_at	Imp4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.18	0.286	-1.02	0.679	1.1	0.366	-1.15	0.237	-0.56
1451628_a_at	Ank3	ankyrin 3, epithelial	-1.16	0.393	1.3	0.244	-1.29	0.007	-1.13	0.596	-0.57
1426781_at	Tyw1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	-1.08	0.421	-1.15	0.508	1.13	0.405	-1.04	0.823	-0.53
1444498_at	---	---	1.33	0.16	-1.48	0.432	-1.08	0.636	-1.52	0.302	-0.69
1418899_at	Ufm1	ubiquitin-fold modifier 1	-1.15	0.358	-1.07	0.725	1.13	0.384	-1.14	0.459	-0.56
1428889_at	Alkbh3	alkB, alkylation repair homolog 3 (E. coli)	-1.09	0.403	1.03	0.539	-1.02	0.863	-1.19	0.319	-0.57
1418391_at	Phf21a	PHD finger protein 21A	-1.07	0.424	1.07	0.751	-1.08	0.596	-1.54	0.324	-0.65
1420650_at	Atbf1	AT motif binding factor 1	1.2	0.322	-1.09	0.385	-1.23	0.373	-1.05	0.895	-0.54
1446988_at	Nup98	Nucleoporin 98	-1.01	0.99	1.23	0.649	-1.42	0.346	-1.31	0.65	-0.63
1447914_x_at	4833411O04Rik	RIKEN cDNA 4833411O04 gene	-1.75	0.266	1.36	0.197	-1	0.99	-1.43	0.37	-0.71
1438364_x_at	Ang4	angiogenin, ribonuclease A family, member 4	-1.34	0.614	1.27	0.451	-1.1	0.725	-1.78	0.173	-0.74
1437972_s_at	Sf3b5	splicing factor 3b, subunit 5	1.12	0.253	-1.06	0.613	-1.15	0.512	-1.5	0.156	-0.65
1420587_at	Tsga13	testis specific gene A13	1.4	0.087	-1.31	0.109	-1.31	0.176	-3.49	0.177	-1.18
1454898_s_at	4833421E05Rik	RIKEN cDNA 4833421E05 gene	-1	0.983	1.08	0.304	-1.17	0.226	-1.49	0.066	-0.65
1434193_at	Zmym6	zinc finger, MYM-type 6	1	0.994	-1.06	0.688	-1.01	0.944	-1.14	0.009	-0.55
1416233_at	Eif3s2	eukaryotic translation initiation factor 3, subunit 2 (beta)	-1.04	0.31	-1.05	0.526	1.02	0.852	-1.07	0.44	-0.54
1417232_at	Cldn2	claudin 2	1.52	0.478	-1.1	0.864	-1.98	0.092	-1.15	0.807	-0.68
1423090_x_at	Sec61g	SEC61, gamma subunit	-1.04	0.744	1.13	0.017	-1.19	0.322	-1.02	0.61	-0.53
1456890_at	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.22	0.408	-1.28	0.12	-1.07	0.582	-1.52	0.323	-0.66
1456959_at	1700034H15Rik	RIKEN cDNA 1700034H15 gene	-1.19	0.345	-1.18	0.749	1.24	0.429	-1.27	0.695	-0.6
1433981_s_at	Htatip	HIV-1 tat interactive protein, homolog (human)	-1.03	0.836	-1.11	0.329	1.06	0.629	-1.21	0.029	-0.57
1417192_at	Tomm70a	translocase of outer mitochondrial membrane 70 homolog A (yeast)	-1.06	0.639	-1.09	0.465	1.07	0.14	-1.19	0.558	-0.57
1422470_at	Bnip3	BCL2/adenovirus E1B interacting protein 1, NIP3	1.03	0.719	-1.04	0.723	-1.07	0.72	-1.14	0.595	-0.55
1418723_at	Edg7	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 7	-1.17	0.294	-1.02	0.964	1.1	0.564	-2.87	0.083	-0.99
1421347_at	Ftmt	ferritin mitochondrial	1.63	0.469	-1.97	0.188	-1.26	0.641	-1.06	0.93	-0.66
1452035_at	Col4a1	procollagen, type IV, alpha 1	-1.01	0.965	1.17	0.28	-1.3	0.16	-1.56	0.042	-0.67
1458028_at	---	Transcribed locus	-1.11	0.726	-1.21	0.351	1.21	0.295	-1.06	0.645	-0.54
1458120_at	Cdh18 /// B230220I	cadherin 18 /// RIKEN cDNA B230220E17 gene	-1.43	0.414	-1.51	0.206	1.57	0.391	-1.92	0.4	-0.82
1450011_at	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	-1.37	0.377	-1.32	0.173	1.45	0.23	-1.72	0.223	-0.74
1455326_at	4932416N17Rik	RIKEN cDNA 4932416N17 gene	-1.07	0.79	-1.1	0.571	1.09	0.66	-1.7	0.322	-0.7
1451081_a_at	Tcf25	transcription factor 25 (basic helix-loop-helix)	-1.07	0.624	1.09	0.05	-1.1	0.449	-1.38	0.083	-0.62
1436183_at	9830115L13Rik	RIKEN cDNA 9830115L13 gene	1.17	0.446	-1.12	0.429	-1.16	0.283	-1.14	0.565	-0.56
1423767_at	2810410M20Rik	RIKEN cDNA 2810410M20 gene	-1.03	0.696	-1.02	0.797	-1.02	0.839	1.3	0.397	-0.44
1456939_at	1700129I04Rik	RIKEN cDNA 1700129I04 gene	-1.53	0.138	-1.06	0.921	1.33	0.734	-1.95	0.585	-0.8
1425210_s_at	Zfp84	zinc finger protein 84	1.08	0.702	-1.09	0.061	-1.07	0.28	-1.21	0.275	-0.57
1424983_a_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	-1.02	0.596	-1.25	0.227	1.15	0.34	-1.32	0.257	-0.61
1416722_at	Hmg20a	high mobility group 20A	-1.03	0.681	-1.06	0.486	1.01	0.942	-1.09	0.509	-0.54

1428390_at	Wdr43	WD repeat domain 43	-1.07	0.365	1.04	0.76	-1.05	0.801	-1.08	0.477	-0.54
1455450_at	Ptpn3	protein tyrosine phosphatase, non-receptor type 3	-1.12	0.656	1.16	0.456	-1.12	0.407	-1.11	0.649	-0.55
1452062_at	Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	-1.09	0.436	-1.04	0.748	1.05	0.084	-1.46	0.177	-0.63
1451254_at	Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associate	-1.17	0.524	-1.06	0.511	1.14	0.377	-1.64	0.068	-0.68
1417619_at	Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	-1.05	0.818	-1.02	0.697	-1	0.983	1.03	0.837	-0.51
1421840_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	-1.07	0.723	1.08	0.651	-1.08	0.687	-1.6	0.19	-0.67
1423447_at	Clpx	caseinolytic peptidase X (E.coli)	-1.14	0.598	1.1	0.788	-1.04	0.601	-1.09	0.75	-0.54
1436411_at	Atp13a5	ATPase type 13A5	-1.26	0.276	-1.31	0.356	1.38	0.261	-1.14	0.333	-0.58
1443160_at	Sbf2	SET binding factor 2	1.39	0.321	-1.16	0.504	-1.48	0.073	-1.15	0.472	-0.6
1440439_at	AI591476	Expressed sequence AI591476	1.43	0.462	-1.44	0.203	-1.24	0.329	-1.43	0.253	-0.67
1455444_at	Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	1.57	0.332	-2.32	0.089	-1.07	0.756	-1.5	0.501	-0.83
1424360_at	BC019943	cDNA sequence BC019943	-1.12	0.575	-1.32	0.07	1.28	0.014	-1.33	0.036	-0.62
1449907_at	Bcmo1	beta-carotene 15,15'-monooxygenase	-1.13	0.239	1.09	0.378	-1.04	0.871	-1.72	0.01	-0.7
1432816_s_at	4930413G21Rik	RIKEN cDNA 4930413G21 gene	-1	0.998	-2.73	0.223	1.57	0.17	-1.67	0.169	-0.96
1418713_at	Pcbd1	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuc	-1.16	0.107	-1.09	0.511	1.16	0.433	-1.33	0.345	-0.61
1449724_s_at	D8Ertd738e	DNA segment, Chr 8, ERATO Doi 738, expressed	1.23	0.116	-1.13	0.05	-1.22	0.263	-1.08	0.79	-0.55
1419228_at	Elac1	elaC homolog 1 (E. coli)	-1.06	0.812	-1.06	0.594	1.05	0.66	-1.33	0.325	-0.6
1455695_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	1.45	0.054	-1.35	0.483	-1.34	0.261	-3.4	0.048	-1.16
1448775_at	Ifi203	interferon activated gene 203	-1.03	0.825	1.1	0.313	-1.16	0.53	-2.12	0.16	-0.8
1438789_s_at	Dpysl3	dihydropyrimidinase-like 3	-1.08	0.752	-1.03	0.929	1.04	0.91	-1.19	0.675	-0.57
1422855_at	Cpsf3	cleavage and polyadenylation specificity factor 3	-1.04	0.686	-1.07	0.111	1.04	0.776	-1.51	0.095	-0.65
1439246_x_at	Tnrc6a	trinucleotide repeat containing 6a	1.09	0.46	-1.07	0.677	-1.1	0.784	-1.15	0.265	-0.56
1432630_at	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	1.21	0.796	-1.37	0.215	-1	0.997	-1.1	0.771	-0.57
1416989_at	Vps53	vacuolar protein sorting 53 (yeast)	-1.1	0.24	-1.04	0.56	1.07	0.157	-1.23	0.293	-0.58
1455082_at	Cblb	Casitas B-lineage lymphoma b	1.06	0.718	-1.03	0.845	-1.1	0.369	-1.19	0.524	-0.57
1419017_at	Corin	corin	-2.14	0.075	-1.04	0.937	1.51	0.326	-1.27	0.654	-0.74
1424036_at	Prpf6	PRP6 pre-mRNA splicing factor 6 homolog (yeast)	-1.13	0.295	-1.28	0.038	1.27	0.019	-1.15	0.181	-0.57
1450024_at	---	---	-1.18	0.083	1.1	0.527	-1.01	0.965	-2.42	0.003	-0.88
1448267_at	Stx5a	syntaxin 5A	-1.01	0.979	-1	0.984	-1.06	0.736	1.09	0.317	-0.5
1449696_at	Arnt	Aryl hydrocarbon receptor nuclear translocator	1.18	0.745	-1.12	0.831	-1.16	0.347	-1.15	0.588	-0.56
1425507_at	Arfrp1	ADP-ribosylation factor related protein 1	-1.05	0.721	-1.2	0.06	1.15	0.425	-1.29	0.295	-0.6
1424212_at	9430023L20Rik	RIKEN cDNA 9430023L20 gene	1.01	0.836	-1.05	0.691	-1.03	0.876	-1.33	0.073	-0.6
1447517_at	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	-1.04	0.915	1.38	0.553	-1.68	0.016	-1.51	0.48	-0.71
1458669_at	---	Transcribed locus	-2.1	0.12	1.55	0.072	-1.1	0.76	-1.54	0.479	-0.8
1447535_at	Btbd4	BTB (POZ) domain containing 4	1.46	0.613	-2.01	0.427	-1.02	0.879	-1.73	0.516	-0.83
1439047_s_at	Recql	RecQ protein-like	-1.27	0.298	1.15	0.317	-1	0.99	-1.27	0.27	-0.6
1435916_at	2210410P13Rik	RIKEN cDNA 2210410P13 gene	-1.09	0.614	1.18	0.19	-1.19	0.283	-1.37	0.172	-0.62
1455468_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630029P(	-1.12	0.608	-1.03	0.928	1.08	0.664	-1.48	0.077	-0.64
1421858_at	Adam17	a disintegrin and metallopeptidase domain 17	-1.16	0.221	1.22	0.209	-1.18	0.263	-1.43	0.138	-0.64
1435023_at	Itsn2	intersectin 2	1.06	0.817	-1.01	0.948	-1.12	0.163	-1.7	0.064	-0.69
1453937_at	4933407G14Rik	RIKEN cDNA 4933407G14 gene	-1.09	0.844	1.26	0.578	-1.3	0.302	-1.82	0.46	-0.74
1447570_s_at	Akap10	A kinase (PRKA) anchor protein 10	2.19	0.124	-2.26	0.322	-3.34	0.302	-3.34	0.01	-1.69
1423041_a_at	Bzw1	basic leucine zipper and W2 domains 1	-1.14	0.003	-1.08	0.582	1.13	0.315	-1.03	0.857	-0.53
1437237_x_at	Zfp110	zinc finger protein 110	1.08	0.452	-1.15	0.187	-1.01	0.95	-1.32	0.145	-0.6
1448244_at	Lypla1	lysophospholipase 1	-1.08	0.531	1.01	0.833	-1	0.988	-1.35	0.183	-0.6
1439651_at	Lmo4	LIM domain only 4	1.38	0.329	-1.28	0.748	-1.29	0.086	-1.49	0.396	-0.67
1428168_at	Mpzl1	myelin protein zero-like 1	-1.09	0.639	1.21	0.491	-1.24	0.383	-1.22	0.6	-0.58
1452100_at	Dullard	Dullard homolog (Xenopus laevis)	-1.14	0.41	-1.04	0.753	1.1	0.596	-1.06	0.211	-0.54
1434113_a_at	Rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	-1.06	0.729	1.06	0.63	-1.08	0.684	-1.49	0.03	-0.64
1427280_at	Scn2a1	sodium channel, voltage-gated, type II, alpha 1	-1.16	0.403	1.58	0.375	-2.01	0.438	-1.08	0.878	-0.67
1427411_s_at	Dleu2	deleted in lymphocytic leukemia, 2	-1.01	0.878	1.14	0.349	-1.23	0.382	-1.08	0.311	-0.55
1457442_at	AW125324	expressed sequence AW125324	-1.03	0.867	1	0.968	-1.04	0.908	-1.5	0.268	-0.64
1443797_at	Agps	Alkylglycerone phosphate synthase	-1.11	0.734	1.11	0.816	-1.08	0.775	-1.03	0.935	-0.53

1423579_a_at	Trpc4	transient receptor potential cation channel, subfamily C, member 4	-1.14	0.871	1.19	0.767	-1.16	0.857	-1.87	0.364	-0.74
1428113_at	Tmtc4	transmembrane and tetratricopeptide repeat containing 4	-1.1	0.12	-1.15	0.202	1.15	0.217	-1.08	0.564	-0.54
1421513_at	Tdrd1	tudor domain containing 1	-1.32	0.163	1.29	0.198	-1.12	0.651	-1.03	0.793	-0.55
1417802_at	1110032A04Rik	RIKEN cDNA 1110032A04 gene	-1.83	0.242	1.46	0.429	-1.07	0.543	-1.96	0.322	-0.85
1453714_a_at	Shroom3	shroom family member 3	-1.27	0.161	1.8	0.105	-2.9	0.011	-1.9	0.221	-1.07
1460243_at	Sptlc2	serine palmitoyltransferase, long chain base subunit 2	-1.08	0.062	1.07	0.565	-1.06	0.446	-1.17	0.154	-0.56
1417140_a_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	-1.05	0.835	1.11	0.482	-1.15	0.266	-1.24	0.071	-0.58
1443935_at	BC032203	cDNA sequence BC032203	-1.12	0.704	-1.09	0.396	1.13	0.377	-1.14	0.246	-0.56
1428191_s_at	Mett11d1	methyltransferase 11 domain containing 1	-1.25	0.2	-1.12	0.461	1.24	0.12	-1.33	0.218	-0.61
1459901_at	6820429M01	hypothetical protein 6820429M01	-1.07	0.549	-1.16	0.119	1.14	0.517	-1.28	0.018	-0.59
1449677_s_at	Tmem38b	transmembrane protein 38B	-1.15	0.323	1.07	0.426	-1	0.987	-1.09	0.705	-0.54
1447667_x_at	Map3k4	mitogen activated protein kinase kinase kinase 4	-1.01	0.979	1.03	0.906	-1.09	0.084	-1.16	0.65	-0.56
1424688_at	Creb3l3	cAMP responsive element binding protein 3-like 3	1.37	0.259	-1.28	0.122	-1.28	0.699	-4.02	0.281	-1.3
1434545_x_at	Bola2	bolA-like 2 (E. coli)	-1.05	0.799	1.05	0.58	-1.06	0.784	-1.2	0.455	-0.57
1419301_at	Fzd4	frizzled homolog 4 (Drosophila)	1.28	0.424	-1.14	0.655	-1.28	0.428	-1.22	0.501	-0.59
1415677_at	Dhrs1	dehydrogenase/reductase (SDR family) member 1	-1	0.99	-1.16	0.275	1.08	0.448	-1.21	0.292	-0.57
1428648_at	Cand1	cullin associated and neddylation disassociated 1	-1.13	0.332	-1.03	0.56	1.08	0.315	-1.04	0.568	-0.53
1434418_at	Lass6	longevity assurance homolog 6 (S. cerevisiae)	-1.05	0.814	1.12	0.6	-1.16	0.295	-1.36	0.127	-0.61
1415912_a_at	Rps13 /// LOC6252	ribosomal protein S13 /// similar to ribosomal protein S13 /// similar to ribosomal p	-1.03	0.714	1.11	0.22	-1.16	0.032	-1.85	0.057	-0.73
1430205_a_at	Cdc37l1	cell division cycle 37 homolog (S. cerevisiae)-like 1	-1.18	0.56	-1.15	0.558	1.23	0.637	-1.62	0.262	-0.68
1445789_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630046H	1.14	0.582	-1.09	0.724	-1.13	0.47	-1.61	0.337	-0.67
1418343_at	Gtf2ird2	GTF2I repeat domain containing 2	-1.24	0.375	1.14	0.45	-1	0.982	-1.63	0.123	-0.68
1426242_at	Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	-1.12	0.645	-1.13	0.582	1.16	0.63	-1.07	0.795	-0.54
1430931_at	4933403O03Rik	RIKEN cDNA 4933403O03 gene	-1.15	0.689	1.21	0.718	-1.16	0.581	-1.15	0.764	-0.56
1415940_at	Zfand2a	zinc finger, AN1-type domain 2A	1.1	0.053	-1.04	0.593	-1.15	0.36	-1.06	0.622	-0.53
1455862_at	9630054F20Rik	RIKEN cDNA 9630054F20 gene	-1.02	0.941	1.14	0.559	-1.22	0.101	-1.45	0.109	-0.64
1443398_at	Snap25	Synaptosomal-associated protein 25	-1.19	0.828	-1.14	0.787	1.22	0.62	-1.29	0.646	-0.6
1439842_at	Zfp287	Zinc finger protein 287	1.7	0.567	-1.41	0.568	-1.88	0.226	-2.24	0.031	-0.96
1424168_a_at	Capzb	capping protein (actin filament) muscle Z-line, beta	-1.07	0.552	1.07	0.316	-1.06	0.433	-1.47	0.131	-0.63
1434076_at	Wdr37	WD repeat domain 37	1.03	0.867	-1.01	0.929	-1.09	0.342	-1.32	0.117	-0.6
1432801_at	4930418C01Rik	RIKEN cDNA 4930418C01 gene	-1.2	0.605	1.21	0.517	-1.11	0.59	-1.15	0.51	-0.56
1432546_at	4930529I22Rik	RIKEN cDNA 4930529I22 gene	1.41	0.493	-1.05	0.921	-1.73	0.205	-1.42	0.462	-0.7
1452856_at	Zf	HCF-binding transcription factor Zhangfei	-1.06	0.67	-1.01	0.903	1.01	0.966	-1.2	0.427	-0.56
1440057_at	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	-1.31	0.689	1.3	0.396	-1.14	0.762	-1.13	0.314	-0.57
1438777_a_at	AA881470	EST AA881470	-1.37	0.398	-1	0.995	1.21	0.378	-1.37	0.399	-0.63
1443543_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:64305(	1.18	0.197	-1.25	0.281	-1.05	0.813	-1.33	0.317	-0.61
1448948_at	Rag1ap1	recombination activating gene 1 activating protein 1	1.12	0.412	-1.02	0.908	-1.19	0.031	-1.57	0.223	-0.66
1440498_at	Rabif	RAB interacting factor	1.26	0.555	-1.21	0.338	-1.17	0.757	-1.1	0.298	-0.56
1434649_at	Ccm2	cerebral cavernous malformation 2 homolog (human)	-1	0.947	-1.14	0.143	1.07	0.658	-1.83	0.085	-0.73
1418105_at	Stmn4	stathmin-like 4	-1.1	0.413	-1.35	0.329	1.29	0.31	-1.28	0.218	-0.61
1423904_a_at	Pvr	poliovirus receptor	-1.04	0.892	1.02	0.924	-1.04	0.908	-1.12	0.661	-0.55
1441985_at	4933416C03Rik	RIKEN cDNA 4933416C03 gene	1.81	0.263	-1.4	0.556	-2.4	0.289	-2.1	0.227	-1.02
1451586_at	Tegt	testis enhanced gene transcript	-1.13	0.342	-1.1	0.499	1.15	0.371	-1.02	0.947	-0.53
1449628_s_at	Stard7	START domain containing 7	-1.17	0.129	-1.08	0.309	1.17	0.222	-1.25	0.023	-0.58
1435291_at	Lemd3	LEM domain containing 3	-1.14	0.52	1.11	0.419	-1.04	0.409	-1.34	0.209	-0.6
1425040_at	Cybrd1	cytochrome b reductase 1	-1.2	0.805	1.19	0.7	-1.09	0.719	-1.29	0.048	-0.6
1459355_at	Tgfbr3	Transforming growth factor, beta receptor III	1.81	0.34	-1.33	0.551	-2.66	0.01	-1.88	0.412	-1.01
1441765_at	---	PREDICTED: Mus musculus similar to Heterogeneous nuclear ribonucleoprotein	1.16	0.577	-1.08	0.729	-1.17	0.047	-1.84	0.011	-0.73
1455671_at	Commd8	COMM domain containing 8	1.14	0.519	-1.01	0.9	-1.23	0.43	-1.19	0.309	-0.57
1418673_at	Snai2	snail homolog 2 (Drosophila)	-1.61	0.157	1.46	0.158	-1.17	0.58	-2.36	0.114	-0.92
1453664_at	9130017K11Rik	RIKEN cDNA 9130017K11 gene	-1.49	0.608	-3.37	0.297	1.97	0.035	-1.35	0.391	-1.06
1430579_at	Tnik /// LOC665113	TRAF2 and NCK interacting kinase /// similar to [Segment 1 of 2] Traf2 and NCK-	1.76	0.216	-3.19	0.185	-1.14	0.362	-1.48	0.117	-1.01
1438412_at	---	---	-1.03	0.924	-1.8	0.097	1.42	0.098	-1.22	0.624	-0.66

1424444_a_at	1600014C10Rik	RIKEN cDNA 1600014C10 gene	-1.16	0.202	-1.14	0.251	1.2	0.052	-1.07	0.781	-0.54
1448761_a_at	Copg2	coatomer protein complex, subunit gamma 2	-1.22	0.376	-1.22	0.062	1.3	0.275	-1.17	0.498	-0.58
1424286_at	Prkx	protein kinase, X-linked	-1.09	0.137	1.22	0.154	-1.24	0.046	-1.08	0.76	-0.55
1456542_s_at	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	-1.18	0.343	-1.37	0.095	1.37	0.329	-1.55	0.115	-0.68
1449695_at	A830082K12Rik	RIKEN cDNA A830082K12 gene	1.23	0.562	-1.26	0.773	-1.08	0.876	-1.12	0.816	-0.56
1432439_at	Zfp715	zinc finger protein 715	-1.13	0.862	1.23	0.497	-1.2	0.69	-1.47	0.539	-0.64
1424457_at	Apbb3	amyloid beta (A4) precursor protein-binding, family B, member 3	1.08	0.714	-1.09	0.383	-1.06	0.765	-1.52	0.411	-0.65
1447247_at	Ppp1r9b	Protein phosphatase 1, regulatory subunit 9B	1.45	0.161	-1.68	0.378	-1.12	0.484	-1.3	0.479	-0.66
1447757_x_at	Inpp5f	inositol polyphosphate-5-phosphatase F	1.19	0.122	-1.04	0.888	-1.26	0.366	-2.37	0.094	-0.87
1457089_at	---	---	1.53	0.353	-1.28	0.594	-1.59	0.018	-1.04	0.771	-0.59
1446702_at	Ktn1	Kinectin 1	1.47	0.027	-1.15	0.726	-1.65	0.221	-1.82	0.216	-0.79
1424842_a_at	Arhgap24	Rho GTPase activating protein 24	-1.12	0.19	1.08	0.706	-1.03	0.905	-1.32	0.474	-0.6
1438984_x_at	Psmb4	proteasome (prosome, macropain) subunit, beta type 4	-1.04	0.496	1.04	0.679	-1.06	0.611	-1.1	0.382	-0.54
1454571_at	A930036A04Rik	RIKEN cDNA A930036A04 gene	-1.63	0.237	-1.01	0.98	1.34	0.217	-1.34	0.415	-0.66
1438693_at	Tmem110	transmembrane protein 110	1.13	0.611	-1.16	0.136	-1.05	0.845	-1.48	0.079	-0.64
1418717_at	Mrps25	mitochondrial ribosomal protein S25	1.33	0.495	-1.46	0.454	-1.08	0.795	-1.32	0.056	-0.63
1429541_at	2500002G23Rik	RIKEN cDNA 2500002G23 gene	-1.05	0.791	1.04	0.807	-1.05	0.875	-1	0.995	-0.52
1419181_at	Zfp326	zinc finger protein 326	-1.09	0.638	-1.03	0.776	1.06	0.501	-1.06	0.709	-0.53
1419488_at	Tnip2	TNFAIP3 interacting protein 2	-1.48	0.085	1.44	0.004	-1.2	0.345	-2.1	0.085	-0.84
1454539_at	4933417G07Rik	RIKEN cDNA 4933417G07 gene	1.44	0.603	-1.69	0.225	-1.09	0.823	-1.26	0.314	-0.65
1434895_s_at	Ppp1r13b	protein phosphatase 1, regulatory (inhibitor) subunit 13B	-1.03	0.884	-1.06	0.077	1.03	0.672	-1.44	0.197	-0.62
1432030_at	4930434J06Rik	RIKEN cDNA 4930434J06 gene	1.29	0.511	-1.22	0.646	-1.2	0.671	-1.24	0.597	-0.59
1434080_at	Aebp2	AE binding protein 2	1.01	0.955	-1.01	0.906	-1.06	0.559	-1.2	0.444	-0.57
1417734_at	Akap8l	A kinase (PRKA) anchor protein 8-like	1.12	0.325	-1.14	0.384	-1.05	0.672	-1.19	0.507	-0.57
1433915_s_at	Epn2	epsin 2	-1.01	0.89	1.22	0.091	-1.36	0.159	-1.18	0.542	-0.58
1416037_a_at	Cct2	chaperonin subunit 2 (beta)	-1.08	0.466	-1.19	0.069	1.17	0.026	-1.19	0.007	-0.57
1442828_at	Ifi203	Interferon activated gene 203	-1.03	0.89	1.03	0.889	-1.06	0.69	-1.42	0.234	-0.62
AFFX-MURINE_b1_	---	---	1.16	0.557	-1.11	0.588	-1.13	0.245	-1.6	0.022	-0.67
1427160_at	Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	1.26	0.274	-1.03	0.833	-1.4	0.017	-1.17	0.24	-0.58
1430348_at	2900019E01Rik	RIKEN cDNA 2900019E01 gene	1.02	0.95	-1.06	0.877	-1.02	0.93	-2.05	0.241	-0.78
1421875_a_at	Mrps23	mitochondrial ribosomal protein S23	-1.16	0.1	-1.05	0.728	1.13	0.17	-1.09	0.48	-0.54
1437458_x_at	Clu	clusterin	-1.14	0.237	-1.1	0.618	1.15	0.159	-1.81	0.217	-0.72
1416008_at	Satb1	special AT-rich sequence binding protein 1	1.06	0.444	-1.05	0.909	-1.07	0.768	-2.75	0.076	-0.95
1427058_at	Eif4a1	eukaryotic translation initiation factor 4A1	-1.25	0.348	-1.32	0.181	1.39	0.193	-1.16	0.484	-0.59
1443090_at	Cept1	Choline/ethanolaminephosphotransferase 1	1.18	0.658	-1.06	0.744	-1.22	0.159	-1.35	0.11	-0.61
1436095_at	Chd5	chromodomain helicase DNA binding protein 5	-1.17	0.758	-1.6	0.167	1.47	0.175	-1.21	0.817	-0.63
1420510_at	---	---	-1.21	0.161	-1.01	0.968	1.13	0.57	-1.5	0.015	-0.65
1437421_at	6330509M05Rik	RIKEN cDNA 6330509M05 gene	-1.12	0.542	-1.03	0.888	1.08	0.806	-1.84	0.288	-0.73
1430675_at	2900055J20Rik	RIKEN cDNA 2900055J20 gene	1.59	0.53	-1.73	0.226	-1.28	0.54	-2.29	0.208	-0.93
1441271_at	Idh3b	Isocitrate dehydrogenase 3 (NAD+) beta	-1.11	0.864	-1.31	0.09	1.28	0.428	-2.17	0.193	-0.83
1455221_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	-1.04	0.907	1.24	0.362	-1.35	0.166	-1.79	0.193	-0.73
1433549_x_at	Rps21	ribosomal protein S21	-1.02	0.82	1.22	0.056	-1.35	0.043	-1.75	0.074	-0.72
1425259_x_at	Klra12	killer cell lectin-like receptor subfamily A, member 12	-1	0.994	-1.56	0.354	1.31	0.344	-1.83	0.204	-0.77
1425495_at	Zfp62	zinc finger protein 62	-1.2	0.655	1.18	0.388	-1.08	0.719	-1.55	0.059	-0.66
1458968_at	C80283	expressed sequence C80283	-1.05	0.942	-1.02	0.964	1.01	0.986	-1.07	0.888	-0.53
1428966_at	2610204K14Rik	RIKEN cDNA 2610204K14 gene	-1.01	0.911	-1.12	0.364	1.06	0.739	-1.05	0.773	-0.53
1443274_at	4932435O22Rik	RIKEN cDNA 4932435O22 gene	1.34	0.67	-1.36	0.531	-1.15	0.795	-1.04	0.952	-0.55
1451521_x_at	Wbscr1	Williams-Beuren syndrome chromosome region 1 homolog (human)	-1.03	0.679	-1.1	0.006	1.07	0.34	-1.02	0.823	-0.52
1435657_at	AI425999	expressed sequence AI425999	-1.02	0.959	1.09	0.634	-1.14	0.589	-1.16	0.465	-0.56
1438940_x_at	Hmgn1	high mobility group nucleosomal binding domain 1	-1.03	0.601	1.18	0.095	-1.26	0.004	-1.39	0.123	-0.62
1415825_s_at	Csnk1d	casein kinase 1, delta	-1.1	0.587	-1.12	0.083	1.15	0.401	-1.17	0.278	-0.56
1428166_at	Cdan1	congenital dyserythropoietic anemia, type I (human)	-1.02	0.915	-1.01	0.958	-1.03	0.867	1.23	0.439	-0.46
1448266_at	Edf1	endothelial differentiation-related factor 1	1.08	0.615	-1.1	0.083	-1.04	0.778	-1.47	0.285	-0.63

1418893_at	Pbx2	pre B-cell leukemia transcription factor 2	-1.01	0.962	1.1	0.421	-1.17	0.195	-1.33	0.187	-0.6
1416589_at	Sparc	secreted acidic cysteine rich glycoprotein	-1.12	0.355	1.19	0.179	-1.15	0.657	-1.33	0.037	-0.6
1455975_x_at	Zfp313	zinc finger protein 313	-1.03	0.809	1.11	0.158	-1.16	0.173	-1.72	0.05	-0.7
1457575_at	AU021128	expressed sequence AU021128	1.56	0.385	-1.37	0.421	-1.51	0.216	-1.24	0.478	-0.64
1459617_at	Mapk14	Mitogen activated protein kinase 14	1.48	0.14	-1.27	0.407	-1.46	0.06	-1.06	0.834	-0.58
1447662_x_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	-1.65	0.304	1.53	0.45	-1.24	0.637	-1.66	0.139	-0.75
1438958_x_at	Fkbp1a	FK506 binding protein 1a	-1.18	0.003	1.15	0.298	-1.05	0.536	-1.46	0.138	-0.64
1422516_a_at	Fibp	fibroblast growth factor (acidic) intracellular binding protein	-1.02	0.906	-1.1	0.321	1.06	0.486	-1.48	0.024	-0.64
1425684_at	2310005E10Rik	RIKEN cDNA 2310005E10 gene	-1.16	0.441	1.17	0.192	-1.09	0.717	-1.65	0.23	-0.68
1432662_at	0610042E11Rik	RIKEN cDNA 0610042E11 gene	-1.08	0.883	-1.19	0.585	1.18	0.32	-1.24	0.703	-0.58
1452428_a_at	B2m	beta-2 microglobulin	1.18	0.415	-1.18	0.229	-1.09	0.078	-1.15	0.046	-0.56
1460374_at	Adam2	a disintegrin and metallopeptidase domain 2	-1.13	0.73	-1.21	0.695	1.24	0.665	-1.86	0.206	-0.74
1437327_x_at	2310057D15Rik	RIKEN cDNA 2310057D15 gene	-1.09	0.462	1.14	0.467	-1.12	0.166	-1.02	0.889	-0.52
1451722_s_at	Smyd5	SET and MYND domain containing 5	-1.08	0.646	-1.13	0.478	1.14	0.488	-1.25	0.017	-0.58
1437468_x_at	Fbxw11	F-box and WD-40 domain protein 11	-1	0.986	1.06	0.549	-1.13	0.103	-1.13	0.542	-0.55
1450698_at	Dusp2	dual specificity phosphatase 2	-1.36	0.251	1.26	0.295	-1.05	0.797	-2.79	0.052	-0.98
1417226_at	Fbxw4	F-box and WD-40 domain protein 4	-1.04	0.58	-1.14	0.195	1.11	0.469	-1.08	0.556	-0.54
1440067_at	Ncam1	Neural cell adhesion molecule 1	-1.31	0.365	1.5	0.394	-1.46	0.539	-1.13	0.745	-0.6
1434335_at	AI317237	expressed sequence AI317237	1.04	0.775	-1.08	0.471	-1.02	0.94	-1.49	0.277	-0.64
1441810_at	---	Transcribed locus	1.28	0.329	-1.41	0.111	-1.04	0.882	-1.63	0.333	-0.7
1457493_at	Pten	phosphatase and tensin homolog	1.36	0.071	-1.15	0.462	-1.39	0.086	-1.3	0.2	-0.62
1434205_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	-1.06	0.71	-1	0.979	1.01	0.939	-1.33	0.087	-0.6
1448422_at	Tmed4	transmembrane emp24 protein transport domain containing 4	1.09	0.271	-1.05	0.222	-1.11	0.138	-1.13	0.416	-0.55
1445931_at	---	---	1.6	0.363	-2.37	0.084	-1.08	0.89	-1.32	0.717	-0.79
1455940_x_at	Wdr6	WD repeat domain 6	-1	0.99	-1.08	0.337	1.02	0.904	-1.39	0.101	-0.61
1454442_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	-1.64	0.619	-2.21	0.128	1.89	0.164	-1.52	0.438	-0.87
1425168_at	Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polype	-1.1	0.894	1.07	0.871	-1.03	0.943	-1.13	0.754	-0.55
1419103_a_at	Abhd6	abhydrolase domain containing 6	-1.01	0.909	-1.49	0.081	1.29	0.019	-1.3	0.488	-0.63
1416477_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	-1.01	0.808	-1.05	0.324	1.01	0.863	-1.27	0.04	-0.58
1418676_at	Isl2	insulin related protein 2 (islet 2)	1.07	0.561	-1.01	0.963	-1.12	0.779	-1.44	0.484	-0.62
1440725_at	Gpr63	G protein-coupled receptor 63	-2.4	0.183	2.03	0.069	-1.97	0.271	-1.35	0.427	-0.92
1415876_a_at	Rps26	ribosomal protein S26	-1.03	0.688	1.04	0.38	-1.07	0.628	-1.17	0.003	-0.56
1423952_a_at	Krt7	keratin 7	-1.17	0.299	1.25	0.229	-1.19	0.307	-1.11	0.627	-0.55
1421878_at	Mapk9	mitogen activated protein kinase 9	-1.11	0.026	-1.25	0.384	1.25	0.206	-1.05	0.397	-0.54
1436693_x_at	Slc35e4	solute carrier family 35, member E4	-1.12	0.538	1.09	0.874	-1.04	0.86	-1.18	0.764	-0.56
1444699_at	Sf4	splicing factor 4	-1.22	0.236	-1.49	0.378	1.46	0.156	-1.05	0.878	-0.58
1442175_at	C030027H14Rik	RIKEN cDNA C030027H14 gene	-1.11	0.469	-1.25	0.242	1.25	0.261	-1.42	0.006	-0.63
1419274_at	C80913	expressed sequence C80913	-1.06	0.761	-1.07	0.686	1.07	0.635	-1.17	0.061	-0.56
1424573_at	Tmed5	transmembrane emp24 protein transport domain containing 5	1.1	0.526	-1.08	0.534	-1.09	0.617	-1.4	0.485	-0.62
1459186_at	C80165	expressed sequence C80165	1.51	0.667	-1.11	0.836	-1.83	0.256	-1.19	0.517	-0.66
1449768_at	---	---	-1.03	0.968	1.18	0.803	-1.26	0.606	-1.8	0.265	-0.72
1459282_at	---	---	1.04	0.525	-1.03	0.904	-1.06	0.825	-1.88	0.37	-0.73
1446250_at	Pparbp	peroxisome proliferator activated receptor binding protein	-2.57	0.312	-1.51	0.635	1.9	0.4	-2.09	0.33	-1.07
1417361_at	Asb3	ankyrin repeat and SOCS box-containing protein 3	-1.11	0.54	1.16	0.224	-1.13	0.203	-1.12	0.128	-0.55
1451130_at	2010315L10Rik	RIKEN cDNA 2010315L10 gene	1.12	0.412	-1.02	0.636	-1.18	0.303	-1.82	0.098	-0.72
1451334_at	1810009O10Rik	RIKEN cDNA 1810009O10 gene	-1.06	0.299	1.03	0.789	-1.02	0.807	-1.13	0.329	-0.55
1424339_at	Oasl1	2'-5' oligoadenylate synthetase-like 1	-1.39	0.227	1.29	0.269	-1.06	0.753	-1.92	0.194	-0.77
1417041_at	Rpo1-1	RNA polymerase 1-1	-1.21	0.175	-1.12	0.381	1.23	0.265	-1.24	0.204	-0.58
1425498_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1.03	0.797	-1	0.973	-1.08	0.387	-1.17	0.108	-0.56
1448968_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	-1.11	0.547	-1.06	0.801	1.11	0.605	-1.22	0.306	-0.57
1423384_s_at	Tex261	testis expressed gene 261	-1.14	0.583	-1.05	0.66	1.12	0.76	-1.02	0.942	-0.52
1427486_at	Ptprb	protein tyrosine phosphatase, receptor type, B	-1.03	0.686	1.04	0.721	-1.07	0.701	-1.25	0.198	-0.58
1438010_at	D4Ertd429e	DNA segment, Chr 4, ERATO Doi 429, expressed	-1.29	0.365	-1.18	0.225	1.33	0.191	-1.09	0.53	-0.56

1419521_at	Zfp94	zinc finger protein 94	-1.03	0.924	-1.1	0.783	1.08	0.576	-1.72	0.3	-0.69
1426096_at	Prmt7	protein arginine N-methyltransferase 7	1.33	0.162	-1.18	0.426	-1.3	0.563	-1.12	0.589	-0.57
1458352_at	A830039H10Rik	RIKEN cDNA A830039H10 gene	1.14	0.644	-1.04	0.867	-1.17	0.491	-1.04	0.788	-0.53
1450526_at	Tlx1	T-cell leukemia, homeobox 1	-1.33	0.557	1.23	0.499	-1.04	0.91	-1.35	0.256	-0.62
1430935_at	4933413G19Rik	RIKEN cDNA 4933413G19 gene	-1.28	0.359	-1.59	0.161	1.54	0.383	-1.15	0.783	-0.62
1444126_at	Pja2	Praja 2, RING-H2 motif containing	1.35	0.302	-1.19	0.395	-1.32	0.076	-1.16	0.39	-0.58
1450964_a_at	Osbpl9	oxysterol binding protein-like 9	-1.21	0.604	1.13	0.225	-1.01	0.925	-1.38	0.354	-0.62
1424612_at	Npal2	NIPA-like domain containing 2	1.42	0.197	-1.71	0.225	-1.05	0.612	-1.06	0.771	-0.6
1423648_at	Pdia6	protein disulfide isomerase associated 6	-1.01	0.93	1.11	0.623	-1.17	0.21	-1.25	0.124	-0.58
1458812_at	Ak3	Adenylate kinase 3	-1.3	0.327	-1.11	0.713	1.28	0.428	-1.44	0.427	-0.64
1417129_a_at	Mrg1	myeloid ecotropic viral integration site-related gene 1	-1.06	0.319	1.16	0.448	-1.19	0.619	-1.15	0.738	-0.56
1439102_at	Falz	fetal Alzheimer antigen	-1.01	0.919	1.16	0.438	-1.24	0.272	-1.82	0.031	-0.73
1447290_at	2610042O14Rik	RIKEN cDNA 2610042O14 gene	1.02	0.964	-1.07	0.893	-1.01	0.956	-1.61	0.145	-0.67
1423340_at	Tcfap2b	transcription factor AP-2 beta	-1.01	0.98	1.08	0.906	-1.13	0.788	-1.18	0.421	-0.56
1430390_x_at	4930444G20Rik ///	RIKEN cDNA 4930444G20 gene /// similar to sentrin 18 /// similar to Sumo1/sentr	-1.42	0.508	1.28	0.224	-1.03	0.938	-1.24	0.531	-0.6
1420634_a_at	Smad2	MAD homolog 2 (Drosophila)	-1.14	0.18	-1.09	0.14	1.16	0.079	-1.4	0.109	-0.62
1457231_at	Hif1a	Hypoxia inducible factor 1, alpha subunit	1.16	0.591	-1.17	0.395	-1.06	0.648	-1.38	0.328	-0.61
1429048_at	Bloc1s2	biogenesis of lysosome-related organelles complex-1, subunit 2	1.06	0.544	-1.09	0.072	-1.03	0.854	-1.68	0.025	-0.68
1426914_at	Marveld2	MARVEL (membrane-associating) domain containing 2	-1.16	0.383	-1.03	0.731	1.12	0.435	-2.06	0.097	-0.78
1427395_a_at	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	-1.14	0.427	1.11	0.723	-1.04	0.839	-1.11	0.51	-0.54
1434509_at	Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	1.1	0.281	-1.06	0.638	-1.1	0.569	-1.56	0.152	-0.66
1451142_at	Exoc1	exocyst complex component 1	-1.13	0.031	-1.07	0.546	1.13	0.254	-1.05	0.804	-0.53
1433665_at	Vps41	vacuolar protein sorting 41 (yeast)	-1.05	0.134	-1.15	0.066	1.13	0.262	-1.03	0.804	-0.52
1419333_at	1110008J03Rik	RIKEN cDNA 1110008J03 gene	-1.06	0.809	-1	0.982	1.01	0.947	-1.09	0.476	-0.53
1421873_s_at	Rab24	RAB24, member RAS oncogene family	-1.18	0.365	-1.2	0.048	1.27	0.156	-1.15	0.235	-0.56
1435156_at	BC046331	cDNA sequence BC046331	-1.16	0.508	-1.02	0.844	1.12	0.443	-1.02	0.832	-0.52
1430637_at	2210016H18Rik	RIKEN cDNA 2210016H18 gene	-1.04	0.839	1.12	0.472	-1.15	0.306	-1.27	0.5	-0.59
1446081_at	Zzef1	Zinc finger, ZZ-type with EF hand domain 1	-1.47	0.091	1.56	0.133	-1.4	0.216	-1.22	0.237	-0.63
1458789_at	---	---	-1.18	0.791	-1.36	0.579	1.37	0.738	-2.67	0.401	-0.96
1450660_at	Pts	6-pyruvoyl-tetrahydropterin synthase	-1.12	0.485	-1.03	0.771	1.09	0.386	-1.45	0.1	-0.63
1428609_at	Mylc2b /// LOC6307	myosin light chain, regulatory B /// similar to myosin regulatory light chain-like /// s	1.39	0.11	-1.33	0.152	-1.23	0.245	-1.35	0.544	-0.63
1440478_at	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	-1.41	0.365	1.28	0.399	-1.04	0.754	-1.21	0.374	-0.59
1456193_x_at	Gpx4 /// LOC67127	glutathione peroxidase 4 /// similar to Phospholipid hydroperoxide glutathione per	-1	0.991	-1	0.976	-1.04	0.874	1.07	0.866	-0.49
1428272_at	Eif1b	eukaryotic translation initiation factor 1B	1.05	0.746	-1.01	0.915	-1.09	0.431	-1.13	0.025	-0.55
1417955_at	Ccdc71	coiled-coil domain containing 71	-1.48	0.29	-1.21	0.27	1.45	0.286	-1.64	0.254	-0.72
1455515_at	1810041L15Rik	RIKEN cDNA 1810041L15 gene	-1.08	0.883	1.08	0.826	-1.06	0.087	-1.34	0.04	-0.6
1436330_x_at	LOC278757 /// LOC	similar to reduced expression 2 /// similar to reduced expression 2	-1.11	0.533	1.2	0.272	-1.17	0.343	-1.47	0.247	-0.64
1417180_at	Pcsk7	proprotein convertase subtilisin/kexin type 7	-1.09	0.21	1.12	0.319	-1.09	0.224	-1.04	0.767	-0.52
1421427_at	Col25a1	procollagen, type XXV, alpha 1	-1.86	0.356	1.74	0.205	-1.48	0.287	-1.73	0.355	-0.83
1424071_s_at	BC018507	cDNA sequence BC018507	-1.08	0.658	-1.03	0.849	1.06	0.561	-1.63	0.06	-0.67
1437745_at	Chd7	chromodomain helicase DNA binding protein 7	1.2	0.221	-1.27	0.5	-1.03	0.892	-1.73	0.278	-0.71
1449913_at	Zfp2	zinc finger protein 2	1.19	0.328	-1.09	0.729	-1.18	0.523	-2.52	0.139	-0.9
1437662_at	C730027J19Rik	RIKEN cDNA C730027J19 gene	-1.2	0.482	-1.37	0.128	1.39	0.543	-1.34	0.649	-0.63
1426208_x_at	Plagl1	pleiomorphic adenoma gene-like 1	-1.19	0.035	1.3	0.014	-1.22	0.215	-1.11	0.715	-0.56
1423626_at	Dst	dystonin	-1.06	0.464	-1.04	0.736	1.05	0.763	-1.1	0.782	-0.54
1440397_at	---	---	1.03	0.853	-1.05	0.929	-1.03	0.922	-2	0.175	-0.76
1437270_a_at	Clcf1	cardiotrophin-like cytokine factor 1	-1.17	0.438	1.42	0.56	-1.48	0.3	-2.99	0.059	-1.05
1433717_at	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	-1.08	0.696	-1.13	0.35	1.14	0.216	-1.22	0.15	-0.57
1417616_at	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	-1.05	0.68	1.32	0.406	-1.46	0.177	-1.3	0.55	-0.62
1431145_a_at	Cuedc2	CUE domain containing 2	1.04	0.696	-1.04	0.742	-1.05	0.727	-1.02	0.916	-0.52
1452377_at	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	-1.13	0.499	-1.23	0.087	1.26	0.558	-1.39	0.254	-0.62
1424835_at	Gstm4	glutathione S-transferase, mu 4	-1.31	0.401	-1.06	0.665	1.25	0.359	-1.37	0.06	-0.62
1416574_at	5730589K01Rik	RIKEN cDNA 5730589K01 gene	-1.12	0.232	-1.09	0.273	1.15	0.172	-1.07	0.545	-0.53

1415742_at	Aup1	ancient ubiquitous protein	1.09	0.639	-1.03	0.133	-1.11	0.211	-1.11	0.252	-0.54
1416783_at	Tac1	tachykinin 1	-1.42	0.637	1.43	0.286	-1.23	0.511	-1.56	0.441	-0.69
1434176_x_at	Poldip3	polymerase (DNA-directed), delta interacting protein 3	-1.11	0.045	-1.01	0.965	1.06	0.575	-1.07	0.386	-0.53
1448508_at	Traf3ip2	Traf3 interacting protein 2	-1.14	0.584	-1.24	0.413	1.27	0.075	-1.92	0.107	-0.76
1443137_at	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030034L15	1.47	0.357	-1.31	0.549	-1.39	0.357	-1.66	0.257	-0.72
1455458_x_at	Gmppa	GDP-mannose pyrophosphorylase A	-1.23	0.496	-1.03	0.801	1.17	0.325	-1.02	0.912	-0.53
1435970_at	Nlk	nemo like kinase	-1.03	0.849	1.07	0.325	-1.09	0.505	-1.49	0.064	-0.63
1450647_at	Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	-1.12	0.269	-1.02	0.844	1.08	0.382	-1.66	0.177	-0.68
1430949_at	9130231A04Rik	RIKEN cDNA 9130231A04 gene	-1.09	0.612	1.21	0.393	-1.21	0.559	-1.1	0.695	-0.55
1454855_at	Magi2	membrane associated guanylate kinase, WW and PDZ domain containing 2	-1.09	0.075	1.16	0.533	-1.13	0.426	-1.4	0.292	-0.62
1453630_at	Galnt14	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.1	0.48	1.43	0.567	-1.61	0.275	-1.03	0.894	-0.58
1419032_at	2610018G03Rik	RIKEN cDNA 2610018G03 gene	-1.73	0.11	-1.12	0.81	1.49	0.108	-1.02	0.954	-0.6
1435394_s_at	Rhoc	ras homolog gene family, member C	-1.17	0.423	1.23	0.11	-1.15	0.353	-1.21	0.134	-0.58
1418430_at	Kif5b	kinesin family member 5B	1.18	0.061	-1.03	0.677	-1.24	0.008	-1.08	0.742	-0.54
1456246_x_at	Tpbpb	trophoblast specific protein beta	1.63	0.61	-1.72	0.057	-1.34	0.465	-1.02	0.977	-0.61
1456061_at	Gimap8	GTPase, IMAP family member 8	-1.23	0.343	1.19	0.178	-1.05	0.796	-1.82	0.243	-0.73
1458991_at	Slc37a1	Solute carrier family 37 (glycerol-3-phosphate transporter), member 1	-1.94	0.187	1.8	0.227	-1.55	0.163	-1.43	0.142	-0.78
1437427_at	4933405O20Rik	RIKEN cDNA 4933405O20 gene	-1.29	0.449	-1.12	0.66	1.29	0.325	-1.06	0.822	-0.54
1435817_x_at	Rps6 /// LOC21473	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	-1	0.994	1.06	0.532	-1.12	0.602	-1.21	0.243	-0.57
1417567_at	Ctnnbip1	catenin beta interacting protein 1	-1.03	0.736	1.12	0.659	-1.16	0.665	-1.03	0.893	-0.52
1423368_at	Laptm4a	lysosomal-associated protein transmembrane 4A	-1.24	0.234	-1.16	0.43	1.28	0.342	-1.17	0.451	-0.57
1438342_at	A930025D01Rik	RIKEN cDNA A930025D01 gene	-1.27	0.219	1.24	0.699	-1.08	0.708	-1.36	0.147	-0.62
1415933_a_at	Cox5a	cytochrome c oxidase, subunit Va	-1.18	0.071	-1.14	0.013	1.24	0.099	-1.02	0.78	-0.53
1435240_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B	-1.02	0.874	-1.04	0.76	1.01	0.874	-1.53	0.017	-0.64
1444895_at	Jam3	Junction adhesion molecule 3	-1.26	0.266	-1.12	0.754	1.27	0.394	-1.26	0.268	-0.59
1434114_at	Rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	-1.01	0.946	1.03	0.742	-1.06	0.656	-1.35	0.06	-0.6
1455010_at	1500012F01Rik	RIKEN cDNA 1500012F01 gene	-1.13	0.501	-1.52	0.226	1.41	0.429	-1.31	0.107	-0.64
1452162_at	Wdr48	WD repeat domain 48	-1.03	0.916	-1.06	0.824	1.04	0.923	-1.03	0.901	-0.52
1444386_at	Pde1c	phosphodiesterase 1C	-1.27	0.677	1.3	0.626	-1.15	0.712	-3.67	0.026	-1.2
1436843_at	C430048L16Rik	RIKEN cDNA C430048L16 gene	-1.49	0.008	1.29	0.24	-1	0.998	-1.27	0.474	-0.62
1441020_at	2900056M20Rik	RIKEN cDNA 2900056M20 gene	1.23	0.33	-1.11	0.467	-1.21	0.405	-1.21	0.497	-0.58
1425926_a_at	Otx2	orthodenticle homolog 2 (Drosophila)	-1.25	0.353	1.55	0.207	-1.65	0.473	-1.18	0.546	-0.63
1424066_at	Dus3l	dihydrouridine synthase 3-like (S. cerevisiae)	-1.08	0.211	-1.25	0.01	1.24	0.356	-1.3	0.002	-0.6
1458608_at	Tpst2	Protein-tyrosine sulfotransferase 2	-1.3	0.594	1.27	0.729	-1.09	0.842	-1.25	0.257	-0.59
1419535_at	Slco6b1	solute carrier organic anion transporter family, member 6b1	1.33	0.631	-1	0.997	-1.59	0.247	-1.08	0.919	-0.58
1445150_at	BC023744	cDNA sequence BC023744	-1.05	0.941	-1.09	0.873	1.09	0.818	-1.48	0.367	-0.63
1431449_at	Slco6d1	solute carrier organic anion transporter family, member 6d1	1.13	0.755	-1.04	0.945	-1.15	0.553	-1.06	0.841	-0.53
1445586_at	Cadps	Ca<2+>dependent activator protein for secretion	-1.65	0.501	1.6	0.2	-1.32	0.5	-1.23	0.764	-0.65
1415949_at	Cpe	carboxypeptidase E	-1.09	0.784	1.13	0.753	-1.1	0.706	-1.42	0.392	-0.62
1455583_at	Gne	glucosamine	1.14	0.67	-1.19	0.342	-1.02	0.883	-1.23	0.29	-0.57
1423068_at	Ift172	intraflagellar transport 172 homolog (Chlamydomonas)	-1.04	0.734	-1.33	0.083	1.25	0.104	-1.37	0.105	-0.63
1424115_at	Ppp5c	protein phosphatase 5, catalytic subunit	-1.09	0.653	-1.19	0.254	1.2	0.341	-1.3	0.171	-0.6
1433626_at	Plscr4	phospholipid scramblase 4	-1.34	0.313	1.4	0.194	-1.23	0.373	-1.15	0.491	-0.58
1446870_at	D4Ertd510e	DNA segment, Chr 4, ERATO Doi 510, expressed	-1.15	0.204	-1.32	0.595	1.33	0.509	-1.29	0.152	-0.61
1453915_a_at	Slc37a3	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	-1.08	0.43	-1.01	0.942	1.04	0.845	-1.54	0.131	-0.65
1447887_x_at	Cspg2	chondroitin sulfate proteoglycan 2	-1.02	0.96	1.55	0.564	-2.35	0.008	-1.21	0.812	-0.76
1426138_a_at	Ube2j2	ubiquitin-conjugating enzyme E2, J2 homolog (yeast)	-1.09	0.216	-1.12	0.194	1.15	0.142	-1.1	0.573	-0.54
1417287_at	H13	histocompatibility 13	1.24	0.221	-1.15	0.097	-1.17	0.441	-1	0.991	-0.52
1447207_at	2810482G21Rik	RIKEN cDNA 2810482G21 gene	1.21	0.069	-1.17	0.471	-1.11	0.488	-1.39	0.156	-0.62
1457678_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	1.21	0.874	-1.2	0.696	-1.09	0.761	-1.24	0.505	-0.58
1428093_at	Trabd	TraB domain containing	-1.23	0.302	-1.01	0.956	1.16	0.527	-1.23	0.069	-0.58
1435728_at	Tyw3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	1.11	0.244	-1.09	0.773	-1.07	0.728	-1.09	0.573	-0.54
1433617_s_at	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	-1.07	0.683	-1.41	0.22	1.31	0.226	-1.66	0.094	-0.71

1454197_a_at	Ccdc86	coiled-coil domain containing 86	-1.09	0.35	-1.09	0.804	1.12	0.664	-1	0.994	-0.51
1426687_at	Map3k3	mitogen activated protein kinase kinase kinase 3	-1.13	0.049	-1	0.997	1.07	0.826	-1.26	0.409	-0.58
1455066_s_at	9130229H14Rik	RIKEN cDNA 9130229H14 gene	-1.01	0.736	-1.13	0.135	1.08	0.168	-1.29	0.329	-0.59
1460438_at	Lysmd1	LysM, putative peptidoglycan-binding, domain containing 1	-1.13	0.854	-1.09	0.736	1.16	0.431	-1.24	0.521	-0.58
1418032_at	Itfg2	integrin alpha FG-GAP repeat containing 2	-1.06	0.871	-1.08	0.743	1.09	0.568	-1.04	0.833	-0.52
1432731_at	5830437K03Rik	RIKEN cDNA 5830437K03 gene	-2.2	0.184	1.72	0.093	-1.27	0.226	-1.25	0.577	-0.75
1419151_at	4930449I24Rik	RIKEN cDNA 4930449I24 gene	-1.4	0.652	1.26	0.545	-1.02	0.933	-2.89	0.087	-1.01
1450688_at	Rgl2	ral guanine nucleotide dissociation stimulator-like 2	-1.21	0.001	1.23	0.26	-1.11	0.219	-1.78	0.037	-0.72
1446649_at	Centd1	Centaurin, delta 1	-1.37	0.148	1.23	0.541	-1	0.995	-1.75	0.181	-0.72
1440869_x_at	6720489N17Rik	RIKEN cDNA 6720489N17 gene	-1.68	0.374	1.4	0.387	-1.04	0.876	-1.17	0.633	-0.62
1434101_at	Nfib	nuclear factor I/B	1.56	0.045	-1.16	0.395	-1.85	0.04	-1.22	0.637	-0.67
1419896_at	BB001228	expressed sequence BB001228	-1.06	0.706	-1.74	0.226	1.44	0.012	-1.09	0.827	-0.61
1436043_at	Scn7a	sodium channel, voltage-gated, type VII, alpha	1.48	0.221	-1.04	0.87	-1.93	0.025	-1.06	0.826	-0.64
1433773_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	1.14	0.412	-1.02	0.897	-1.18	0.16	-1.43	0.151	-0.63
1434967_at	Zswim6	zinc finger, SWIM domain containing 6	-1.1	0.41	1.08	0.665	-1.03	0.836	-1.39	0.147	-0.61
1441725_at	6530402F18Rik	RIKEN cDNA 6530402F18 gene	-1.4	0.567	-1.47	0.512	1.57	0.053	-1.17	0.287	-0.62
1438738_at	BC010584	CDNA sequence BC010584	-1.01	0.957	-1.18	0.752	1.12	0.633	-1.38	0.321	-0.61
1458772_at	Lphn3	Latrophilin 3	-1.05	0.919	1.47	0.348	-1.86	0.093	-1.84	0.457	-0.82
1418525_at	Pcm1	pericentriolar material 1	-1.18	0.32	1.22	0.528	-1.12	0.58	-1.32	0.376	-0.6
1423183_at	Lgi1	leucine-rich repeat LGI family, member 1	-1.17	0.828	1.33	0.399	-1.29	0.618	-1.14	0.491	-0.57
1427228_at	Palld	palladin, cytoskeletal associated protein	-1.08	0.597	-1.06	0.695	1.09	0.793	-1.09	0.831	-0.53
1418045_at	Inpp1	inositol polyphosphate-1-phosphatase	-1.09	0.647	-1.1	0.196	1.14	0.578	-1.24	0.169	-0.57
1455623_at	A930031D07Rik	RIKEN cDNA A930031D07 gene	-1.04	0.781	1.17	0.777	-1.21	0.427	-1.74	0.279	-0.71
1435220_s_at	Cdc42se2	CDC42 small effector 2	-1.01	0.917	-1.05	0.592	1.02	0.912	-1.42	0.335	-0.62
1421614_at	Zan	zonadhesin	1.34	0.5	-1.07	0.691	-1.46	0.057	-1	0.992	-0.55
1448419_at	Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	-1.04	0.698	1.04	0.347	-1.04	0.545	-1.31	0.102	-0.59
1415991_a_at	Klhdc3	kelch domain containing 3	-1.1	0.057	1.07	0.09	-1.02	0.8	-1.02	0.89	-0.52
1422220_at	Pit1	pituitary specific transcription factor 1	1.55	0.18	-1.31	0.068	-1.55	0.413	-1.1	0.863	-0.6
1435725_x_at	LOC241053 /// Rpl1	similar to 60S ribosomal protein L12 /// ribosomal protein L12 /// similar to 60S rib	-1.05	0.576	1.1	0.158	-1.11	0.317	-1.48	0.046	-0.63
1435704_at	C920006O11Rik	RIKEN cDNA C920006O11 gene	-1.01	0.951	-1.06	0.685	1.03	0.832	-1.26	0.623	-0.58
1448901_at	Cpxm1	carboxypeptidase X 1 (M14 family)	-1.1	0.772	-1.2	0.729	1.22	0.606	-1.03	0.889	-0.53
1428702_at	Ddx28	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	-1.29	0.404	-1.01	0.983	1.19	0.316	-1	0.994	-0.53
1458529_at	LOC215714	hypothetical protein A930010C09	1.56	0.07	-1.06	0.871	-2.2	0.153	-1.3	0.668	-0.75
1459247_at	Agbl3	ATP/GTP binding protein-like 3	-1.03	0.9	-1.11	0.769	1.09	0.449	-1.3	0.434	-0.59
1448190_at	Mrpl33	mitochondrial ribosomal protein L33	-1.02	0.914	1.08	0.684	-1.1	0.324	-1.26	0.419	-0.58
1429084_at	Vezf1	vascular endothelial zinc finger 1	-1.13	0.68	1.18	0.595	-1.11	0.519	-1.51	0.041	-0.64
1421135_a_at	Cnot8	CCR4-NOT transcription complex, subunit 8	-1.16	0.606	-1.14	0.272	1.22	0.373	-1.08	0.53	-0.54
1444048_at	Rp9h	Retinitis pigmentosa 9 homolog (human)	1.34	0.559	-1.09	0.731	-1.42	0.205	-1.21	0.647	-0.59
1449072_a_at	2510005D08Rik	RIKEN cDNA 2510005D08 gene	-1.08	0.109	1.21	0.096	-1.22	0.275	-1.09	0.601	-0.54
1456236_s_at	Commd10	COMM domain containing 10	-1.07	0.647	1.18	0.111	-1.18	0.16	-1.13	0.486	-0.55
1437682_x_at	1110004E09Rik	RIKEN cDNA 1110004E09 gene	-1.06	0.835	-1.04	0.898	1.06	0.896	-1.65	0.437	-0.67
1455395_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	-1.03	0.697	-1.03	0.64	1.02	0.9	-1.24	0.127	-0.57
1426961_at	Phf20	PHD finger protein 20	-1.04	0.655	1.13	0.365	-1.15	0.301	-1.36	0.192	-0.6
1418667_at	2410002O22Rik	RIKEN cDNA 2410002O22 gene	1.17	0.489	-1.02	0.869	-1.24	0.273	-1.06	0.636	-0.54
1420778_at	Tas1r3	taste receptor, type 1, member 3	1.4	0.437	-1.62	0.091	-1.05	0.886	-1.32	0.485	-0.65
1436340_at	9630041G16Rik	RIKEN cDNA 9630041G16 gene	1.14	0.701	-1.03	0.953	-1.17	0.71	-1.47	0.523	-0.63
1455569_at	---	CDNA clone IMAGE:1548559	-1.06	0.803	1.26	0.503	-1.32	0.233	-1.07	0.806	-0.55
1434786_at	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-1.01	0.973	-1.24	0.261	1.16	0.524	-1.04	0.89	-0.53
1429470_at	Spdya	speedy homolog A (Drosophila)	1.45	0.247	-1.72	0.285	-1.07	0.833	-1.27	0.574	-0.65
1417692_at	Drg2	developmentally regulated GTP binding protein 2	-1.03	0.939	-1.14	0.338	1.12	0.486	-1.34	0.054	-0.6
1435025_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	-1.05	0.706	-1.26	0.015	1.22	0.219	-1.44	0.19	-0.63
1427640_a_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	-1.24	0.432	1.51	0.394	-1.54	0.171	-1.12	0.814	-0.6
1423176_at	Tob1	transducer of ErbB-2.1	-1.04	0.845	-1.22	0.231	1.19	0.125	-1.44	0.068	-0.63

1427906_at	1110037F02Rik	RIKEN cDNA 1110037F02 gene	-1.04	0.56	1.01	0.895	-1.01	0.907	-1.28	0.192	-0.58
1448221_at	Bat1a	HLA-B-associated transcript 1A	-1.01	0.903	-1.18	0.201	1.12	0.454	-1.2	0.258	-0.57
1417223_at	Cd2bp2	CD2 antigen (cytoplasmic tail) binding protein 2	-1.09	0.385	-1.07	0.267	1.12	0.291	-1.02	0.932	-0.52
1425200_at	Clcc1	chloride channel CLIC-like 1	-1.34	0.411	-1.64	0.246	1.61	0.328	-1.15	0.459	-0.63
1440857_at	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorot	1.46	0.675	-1.55	0.556	-1.16	0.689	-1.17	0.681	-0.61
1436322_a_at	2810001A02Rik	RIKEN cDNA 2810001A02 gene	1.15	0.049	-1.03	0.876	-1.18	0.461	-1.26	0.308	-0.58
1435352_at	Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	-1.12	0.385	-1.04	0.722	1.11	0.617	-1.13	0.346	-0.55
1424713_at	Calml4	calmodulin-like 4	-1.06	0.371	-1.12	0.698	1.12	0.613	-1.07	0.805	-0.53
1420569_at	Chad	chondroadherin	-1.6	0.015	-1.01	0.98	1.35	0.338	-1.48	0.531	-0.69
1454428_at	4930467D19Rik	RIKEN cDNA 4930467D19 gene	-1.07	0.609	1.07	0.785	-1.04	0.875	-1.19	0.655	-0.56
1432651_at	2510019K15Rik	RIKEN cDNA 2510019K15 gene	-1.25	0.481	1.24	0.554	-1.09	0.758	-1.05	0.851	-0.54
1448658_at	Sart1	squamous cell carcinoma antigen recognized by T-cells 1	-1.09	0.523	-1.15	0.52	1.18	0.224	-1.12	0.311	-0.54
1438252_at	Qscn6	quiescin Q6	1.42	0	-1.81	0.246	-1.01	0.96	-1.08	0.169	-0.62
1459824_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.73	0.341	-1.88	0.334	-1.42	0.631	-1.32	0.692	-0.72
1451405_at	Pcca	propionyl-Coenzyme A carboxylase, alpha polypeptide	-1.01	0.93	-1.17	0.41	1.11	0.519	-1.23	0.224	-0.57
1415851_a_at	Impdh2	inosine 5'-phosphate dehydrogenase 2	-1.06	0.416	1.04	0.458	-1.02	0.823	-1.03	0.879	-0.52
1415951_at	Fkbp10	FK506 binding protein 10	1	0.934	-1.03	0.965	-1.01	0.963	-1.01	0.965	-0.51
1424547_at	Car10	carbonic anhydrase 10	1.25	0.816	-1.24	0.781	-1.1	0.899	-1.58	0.224	-0.67
1447864_s_at	Pogk	pogo transposable element with KRAB domain	-1.01	0.971	1.28	0.407	-1.45	0.058	-1.17	0.726	-0.59
1451292_at	Zfp212	Zinc finger protein 212	-1.03	0.857	1.02	0.884	-1.02	0.759	-1.01	0.874	-0.51
1455046_a_at	Pogz	pogo transposable element with ZNF domain	-1.09	0.341	1.05	0.511	-1.01	0.946	-1.3	0.011	-0.58
1444205_at	Smad4	MAD homolog 4 (Drosophila)	1.48	0.298	-1.54	0.557	-1.19	0.571	-1.7	0.362	-0.74
1442855_at	Dopey1	dopey family member 1	-1.01	0.882	1.17	0.441	-1.23	0.063	-1.56	0.086	-0.66
1433443_a_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-1.07	0.663	1.28	0.368	-1.32	0.084	-1.86	0.101	-0.74
1448920_at	Zfp535	zinc finger protein 535	-1.21	0.25	1.24	0.306	-1.11	0.124	-1.99	0.113	-0.77
1448600_s_at	Vav3	vav 3 oncogene	-1.02	0.915	1.29	0.108	-1.44	0.259	-1.03	0.897	-0.55
1433595_at	---	---	-1.02	0.875	-1.01	0.679	-1	0.961	1.39	0.379	-0.41
1456379_x_at	Dner	delta/notch-like EGF-related receptor	-1.52	0.37	1.78	0.417	-1.9	0.088	-1.08	0.745	-0.68
1443655_s_at	Pik3c2a	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide	-1.17	0.779	-3.55	0.026	1.83	0.321	-1.1	0.498	-1
1428023_at	3110009E18Rik	RIKEN cDNA 3110009E18 gene	-1.06	0.518	1.04	0.681	-1.02	0.848	-1.34	0.243	-0.59
1436825_a_at	A630095E13Rik	RIKEN cDNA A630095E13 gene	-1.06	0.898	-1.27	0.583	1.23	0.686	-1.05	0.954	-0.54
1425190_a_at	Phospho2	phosphatase, orphan 2	1.01	0.865	-1.01	0.965	-1.03	0.881	-1.09	0.587	-0.53
1442273_at	4932413O14Rik	RIKEN cDNA 4932413O14 gene	-1.24	0.479	1.46	0.495	-1.43	0.111	-1.3	0.168	-0.63
1422503_s_at	Parp1	poly (ADP-ribose) polymerase family, member 1	-1.22	0.215	-1.09	0.339	1.23	0.381	-1.41	0.097	-0.62
1415880_a_at	Lamp1	lysosomal membrane glycoprotein 1	-1.05	0.367	1.17	0.005	-1.18	0.091	-1.11	0.545	-0.54
1448029_at	Tbx3	T-box 3	-1.24	0.059	1.23	0.454	-1.07	0.718	-1.36	0.339	-0.61
1426401_at	Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	1.17	0.126	-1.14	0.087	-1.09	0.302	-1.43	0.143	-0.62
1434393_at	Usp34	ubiquitin specific peptidase 34	1.2	0.29	-1.12	0.782	-1.14	0.646	-1.04	0.851	-0.53
1421434_at	Dnahc5	dynein, axonemal, heavy chain 5	-1.08	0.391	-2.87	0.136	1.7	0.124	-2.34	0.173	-1.15
1423217_a_at	2510049I19Rik	RIKEN cDNA 2510049I19 gene	-1.04	0.699	1.11	0.362	-1.12	0.451	-1.19	0.126	-0.56
1422506_a_at	Cstb	cystatin B	-1.01	0.828	1.11	0.07	-1.14	0.293	-1.3	0.411	-0.59
1453359_at	Exosc1	exosome component 1	-1.08	0.313	-1.02	0.948	1.06	0.782	-1.33	0.062	-0.59
1449440_at	Lpin3	lipin 3	1.36	0.286	-1.2	0.655	-1.29	0.12	-1.26	0.633	-0.6
1460203_at	Itpr1	inositol 1,4,5-triphosphate receptor 1	-1.1	0.313	1.16	0.185	-1.12	0.192	-1.34	0.246	-0.6
1442310_at	Pip5k2a	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	-1.02	0.933	-1.12	0.553	1.1	0.566	-1.16	0.333	-0.55
1459646_at	Hs3st6	heparan sulfate (glucosamine) 3-O-sulfotransferase 6	-1.19	0.58	-1.52	0.434	1.47	0.263	-1.14	0.818	-0.6
1454557_at	6720454L07Rik	RIKEN cDNA 6720454L07 gene	-1.81	0.058	1.59	0.03	-1.21	0.138	-1.3	0.506	-0.68
1439772_at	D1Bwg0212e	DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed	-1.54	0.441	-1.04	0.906	1.36	0.483	-1.73	0.244	-0.74
1452679_at	Tubb2b	tubulin, beta 2b	1.13	0.596	-1.18	0.858	-1.02	0.893	-1.73	0.2	-0.7
1429553_at	Cilp2	cartilage intermediate layer protein 2	-1.13	0.766	-2.66	0.069	1.71	0.137	-1.6	0.608	-0.92
1443840_x_at	1700010H22Rik	RIKEN cDNA 1700010H22 gene	-1.77	0.126	-1.01	0.976	1.41	0.411	-1.02	0.96	-0.6
1434248_at	Prkch	protein kinase C, eta	-1.08	0.372	-1.02	0.864	1.06	0.419	-1.24	0.381	-0.57
1420101_at	2610020H08Rik	RIKEN cDNA 2610020H08 gene	1.33	0.733	-1.37	0.44	-1.1	0.602	-1.12	0.611	-0.56

1437410_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	1.25	0.445	-1.11	0.425	-1.23	0.216	-1.17	0.502	-0.57
1451102_at	Cnot8	CCR4-NOT transcription complex, subunit 8	-1.08	0.482	1.07	0.575	-1.02	0.783	-1.3	0.153	-0.58
1455905_at	2610507B11Rik	RIKEN cDNA 2610507B11 gene	-2	0.515	-1.83	0.164	1.92	0.08	-1.1	0.85	-0.75
1450360_at	Plcg1	phospholipase C, gamma 1	-1.4	0.357	1.47	0.406	-1.27	0.559	-1.04	0.83	-0.56
1449129_a_at	Kcnip3	Kv channel interacting protein 3, calsenilin	-1.12	0.846	1.09	0.877	-1.02	0.939	-2.25	0.127	-0.82
1449594_at	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	1.25	0.781	-1.06	0.803	-1.29	0.645	-1.1	0.877	-0.55
1456131_x_at	Dag1	dystroglycan 1	-1.08	0.255	-1.07	0.444	1.11	0.656	-1.47	0.082	-0.63
1433884_at	Syt1	synaptotagmin I	-1.35	0.418	-1.41	0.269	1.52	0.246	-1.57	0.277	-0.7
1442075_at	AI314604	expressed sequence AI314604	-1.36	0.034	1.54	0.249	-1.44	0.127	-1.27	0.427	-0.63
1434439_at	Gsk3b	glycogen synthase kinase 3 beta	-1.23	0.341	1.37	0.132	-1.27	0.173	-1.86	0.096	-0.75
1426269_at	Sybl1	synaptobrevin like 1	-1.01	0.926	-1	0.969	-1.02	0.831	1.06	0.657	-0.49
1446765_at	C77973	expressed sequence C77973	-1.05	0.902	-1.32	0.315	1.26	0.647	-1.06	0.924	-0.54
1447315_at	---	---	1.63	0.547	-1.22	0.138	-1.93	0.032	-1.16	0.819	-0.67
1456085_x_at	Cd151	CD151 antigen	-1.04	0.443	1.2	0.022	-1.24	0.063	-1.29	0.056	-0.59
1426300_at	Alcam	activated leukocyte cell adhesion molecule	1.11	0.566	-1.08	0.42	-1.07	0.653	-1.09	0.598	-0.53
1423080_at	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.07	0.11	-1.05	0.491	1.08	0.453	-1.39	0.083	-0.61
1435744_at	6720401G13Rik	RIKEN cDNA 6720401G13 gene	-1.19	0.044	-1.05	0.209	1.18	0.585	-1.12	0.449	-0.55
1445785_at	---	---	1.36	0.523	-1.14	0.704	-1.36	0.138	-1.38	0.116	-0.63
1451741_a_at	Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	-1.21	0.249	1.22	0.311	-1.09	0.58	-1.08	0.662	-0.54
1454723_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	-1.11	0.294	-1.19	0.287	1.23	0.236	-1.04	0.757	-0.53
1416009_at	Tspan3	tetraspanin 3	-1.07	0.086	-1.08	0.465	1.1	0.343	-1.5	0.23	-0.64
1423894_a_at	Dalrd3	DALR anticodon binding domain containing 3	-1.11	0.545	-1.11	0.163	1.17	0.44	-1.35	0.1	-0.6
1454662_at	A230106M15Rik	RIKEN cDNA A230106M15 gene	-1.04	0.835	-1.1	0.586	1.1	0.604	-1.19	0.332	-0.56
1447801_x_at	---	---	1.39	0.011	-1.02	0.969	-1.68	0.015	-1.12	0.548	-0.61
1421062_s_at	Clta	clathrin, light polypeptide (Lca)	-1.03	0.793	1.04	0.543	-1.04	0.687	-1.24	0.128	-0.57
1430368_s_at	1700019D03Rik	RIKEN cDNA 1700019D03 gene	-1.08	0.784	-1	0.994	1.05	0.892	-1.21	0.726	-0.56
1416048_at	Phc2	polyhomeotic-like 2 (Drosophila)	1.08	0.466	-1.02	0.815	-1.1	0.184	-1.48	0.106	-0.63
1437542_at	A730095J18Rik	RIKEN cDNA A730095J18 gene	-1.14	0.513	1.12	0.51	-1.03	0.682	-1.07	0.802	-0.53
1427467_a_at	Rpgr	retinitis pigmentosa GTPase regulator	-1.01	0.957	-1.02	0.917	1	0.991	-1.22	0.398	-0.56
1441817_at	1700099I09Rik	RIKEN cDNA 1700099I09 gene	1.37	0.609	-1.34	0.448	-1.17	0.828	-3.06	0.085	-1.05
1456573_x_at	Nnt	nicotinamide nucleotide transhydrogenase	-1.1	0.698	-1.06	0.698	1.12	0.279	-1.18	0.453	-0.56
1448257_at	Slc29a2	solute carrier family 29 (nucleoside transporters), member 2	-1.39	0.411	-2.49	0.202	1.85	0.225	-2.83	0.027	-1.22
1425580_a_at	Pik3c3	phosphoinositide-3-kinase, class 3	-1.14	0.545	-1.14	0.061	1.22	0.339	-1.33	0.085	-0.6
1421213_at	Edaradd	EDAR (ectodysplasin-A receptor)-associated death domain	1.31	0.168	-1.44	0.463	-1.03	0.908	-2.36	0.114	-0.88
1452386_at	Sall3	sal-like 3 (Drosophila)	-1.04	0.922	1.05	0.858	-1.04	0.852	-1.03	0.895	-0.51
1458778_at	Wdsof1	WD repeats and SOF domain containing 1	-1.22	0.613	-1.37	0.575	1.42	0.014	-1.69	0.176	-0.71
1448513_a_at	Npc2	Niemann Pick type C2	-1.04	0.159	1.23	0.008	-1.28	0.062	-1.33	0.21	-0.61
1428026_at	Tshz2	teashirt zinc finger family member 2	-1.07	0.776	-1.28	0.547	1.26	0.515	-1.94	0.24	-0.76
1441436_at	Dusp12	dual specificity phosphatase 12	-1.21	0.716	1.4	0.533	-1.35	0.114	-1.1	0.648	-0.57
1442407_at	---	---	1.22	0.06	-1.04	0.881	-1.26	0.001	-1.21	0.152	-0.57
1431932_s_at	Trim44	tripartite motif-containing 44	-1.14	0.655	-1.05	0.885	1.14	0.2	-1.29	0.409	-0.58
1439965_at	---	Transcribed locus	-1.3	0.046	1.21	0.082	-1.01	0.94	-1.11	0.678	-0.55
1426039_a_at	Alox12e	arachidonate lipoxygenase, epidermal	-2.24	0.272	-1.33	0.276	1.78	0.287	-1.12	0.841	-0.73
1434156_at	---	---	-1.36	0.102	-1.2	0.512	1.4	0.271	-1.16	0.577	-0.58
1453718_at	Bcl2l12	BCL2-like 12 (proline rich)	-1.6	0.634	1.78	0.298	-1.76	0.408	-1.36	0.705	-0.74
1447771_at	---	---	2.2	0.182	-4.02	0.15	-1.91	0.176	-2.53	0.283	-1.57
1415932_x_at	Atp9a	ATPase, class II, type 9A	1.04	0.857	-1.05	0.715	-1.02	0.931	-1.17	0.628	-0.55
1434362_at	AW550831	expressed sequence AW550831	-1.02	0.809	1.21	0.039	-1.28	0.038	-1.42	0.309	-0.63
1421610_at	Cx3cl1	chemokine (C-X3-C motif) ligand 1	1.5	0.552	-1.22	0.624	-1.53	0.159	-1.42	0.42	-0.67
1435456_at	Ttc28	tetratricopeptide repeat domain 28	-1.26	0.226	-1.03	0.719	1.2	0.306	-1.28	0.482	-0.59
1433695_at	1500041B16Rik	RIKEN cDNA 1500041B16 gene	-1.3	0.395	1.24	0.235	-1.04	0.715	-1.09	0.684	-0.55
1438663_at	Bat2d	BAT2 domain containing 1	-1.03	0.803	-1.04	0.797	1.04	0.842	-1.17	0.122	-0.55
1436499_at	Tmem23	transmembrane protein 23	-1.08	0.532	1.12	0.579	-1.07	0.795	-1.76	0.026	-0.7

1438745_at	LOC666945	hypothetical protein LOC666945	-1.48	0.708	-1.24	0.538	1.49	0.286	-2.14	0.513	-0.84
1448850_a_at	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	1.08	0.366	-1.06	0.059	-1.05	0.723	-1.37	0.039	-0.6
1422511_a_at	Ogfr	opioid growth factor receptor	-1.06	0.435	-1	0.989	1.03	0.499	-1.48	0.072	-0.63
1430050_at	Ddx23	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	-1.26	0.28	1.6	0.422	-1.72	0.001	-1.13	0.048	-0.63
1437630_at	Lsg1	large subunit GTPase 1 homolog (S. cerevisiae)	-1.01	0.861	-1.13	0.536	1.1	0.552	-1.08	0.793	-0.53
1427663_a_at	Clk4	CDC like kinase 4	-1.2	0.384	-1.13	0.514	1.25	0.311	-1.04	0.834	-0.53
1429797_at	5730596K20Rik	RIKEN cDNA 5730596K20 gene	1.14	0.261	-1.09	0.685	-1.1	0.658	-1.02	0.919	-0.52
1435591_at	AI426330	expressed sequence AI426330	-1.2	0.547	-1.2	0.65	1.3	0.519	-1.01	0.932	-0.53
1423484_at	Bicc1	bicaudal C homolog 1 (Drosophila)	-1.03	0.892	1.35	0.39	-1.53	0.158	-1.07	0.477	-0.57
1417456_at	Gnpat	glyceronephosphate O-acyltransferase	-1.09	0.536	-1.21	0.131	1.23	0.084	-1.14	0.386	-0.55
1448041_at	Rnf2	ring finger protein 2	-1.05	0.812	1.26	0.573	-1.3	0.344	-1.07	0.639	-0.54
1415730_at	5730453I16Rik	RIKEN cDNA 5730453I16 gene	-1.13	0.419	1.12	0.406	-1.04	0.826	-1.19	0.507	-0.56
1425589_at	Hsd17b13	hydroxysteroid (17-beta) dehydrogenase 13	1.29	0.437	-1.28	0.266	-1.11	0.751	-1.28	0.121	-0.59
1434450_s_at	Adrbk2	adrenergic receptor kinase, beta 2	-1.09	0.508	1.3	0.45	-1.32	0.202	-1.25	0.627	-0.59
1452916_at	Wbp7	WW domain binding protein 7	-1.14	0.245	-1.09	0.506	1.18	0.327	-1.06	0.747	-0.53
1431772_a_at	Itsn2	intersectin 2	-1.13	0.503	-1.09	0.466	1.17	0.48	-1.78	0.046	-0.71
1434203_at	BC055107	cDNA sequence BC055107	1.26	0.028	-1.07	0.831	-1.28	0.651	-3.46	0.202	-1.14
1455788_x_at	Poldip3	Polymerase (DNA-directed), delta interacting protein 3	-1.19	0.324	-1.03	0.788	1.16	0.381	-1.09	0.186	-0.54
1442382_at	Mast4	microtubule associated serine/threonine kinase family member 4	-1.2	0.515	1.46	0.032	-1.47	0.118	-1.96	0.062	-0.79
1427283_at	Mll1	myeloid/lymphoid or mixed-lineage leukemia 1	-1.03	0.585	-1.05	0.798	1.05	0.868	-1.27	0.485	-0.57
1426032_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	1.34	0.697	-1.42	0.359	-1.08	0.647	-1.64	0.168	-0.7
1457284_at	---	CDNA clone IMAGE:5256843	-1.16	0.705	-1.17	0.455	1.26	0.138	-1.17	0.612	-0.56
1435930_at	Zfp291	zinc finger protein 291	-1	0.989	1.14	0.582	-1.19	0.091	-1.44	0.283	-0.62
1452976_a_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	-1.01	0.975	-1.13	0.633	1.1	0.676	-1.16	0.464	-0.55
1448454_at	Sfrs6	splicing factor, arginine/serine-rich 6	-1.1	0.339	-1.06	0.642	1.12	0.205	-1.12	0.465	-0.54
1458235_at	Akap12	A kinase (PRKA) anchor protein (gravin) 12	-1.01	0.968	1.34	0.048	-1.54	0.087	-1.21	0.528	-0.61
1435132_at	Disp1	dispatched homolog 1 (Drosophila)	1.25	0.431	-1.08	0.795	-1.25	0.209	-1.2	0.38	-0.57
1426944_at	Fbxw8	F-box and WD-40 domain protein 8	-1.06	0.84	-1.1	0.353	1.12	0.472	-1.04	0.865	-0.52
1436811_at	Kctd3	potassium channel tetramerisation domain containing 3	-1.31	0.042	-1.06	0.764	1.27	0.309	-1.01	0.961	-0.53
1435222_at	Foxp1	forkhead box P1	1.14	0.031	-1.13	0.255	-1.05	0.754	-2.21	0.094	-0.81
1428099_a_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	-1.06	0.678	1.07	0.325	-1.04	0.77	-1.01	0.946	-0.51
1417539_at	Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member 1	-1	0.986	-1.09	0.337	1.06	0.702	-1.08	0.35	-0.53
1419574_at	Zfp292	zinc finger protein 292	-1.01	0.758	1.18	0.455	-1.25	0.168	-1.42	0.227	-0.62
AFFX-LysX-M_at	---	---	1.21	0.706	-1.23	0.145	-1.05	0.886	-1.7	0.448	-0.69
1425521_at	Paip1	polyadenylate binding protein-interacting protein 1	1.41	0.047	-1.27	0.736	-1.28	0.587	-1	0.995	-0.54
1439900_at	Thtpa	Thiamine triphosphatase	-1.17	0.573	-1.14	0.669	1.24	0.519	-1.1	0.606	-0.54
1442676_at	Maoa	monoamine oxidase A	1.11	0.774	-1.09	0.813	-1.06	0.867	-1.35	0.197	-0.6
1444595_at	Zxda /// LOC66817	zinc finger, X-linked, duplicated A /// similar to Zinc finger X-linked protein ZXDA	1.32	0.484	-1.28	0.493	-1.15	0.542	-1.21	0.392	-0.58
1436919_at	Trp53i11	Trp53 inducible protein 11	-1.03	0.861	-1.06	0.648	1.06	0.824	-1.17	0.603	-0.55
1453151_at	Slc26a3	solute carrier family 26, member 3	-1.29	0.751	1.41	0.545	-1.27	0.71	-1.48	0.296	-0.66
1457632_s_at	Mrg1	myeloid ecotropic viral integration site-related gene 1	-1.12	0.482	1.14	0.487	-1.06	0.819	-1.59	0.254	-0.66
1420036_at	Ate1	Arginine-tRNA-protein transferase 1	-1.12	0.703	-1.18	0.766	1.24	0.238	-1.41	0.205	-0.62
1437152_at	Rkhd3	ring finger and KH domain containing 3	-1.12	0.829	1.34	0.667	-1.34	0.337	-1.51	0.212	-0.66
1423712_a_at	Qars	glutaminyl-tRNA synthetase	1.08	0.682	-1.06	0.453	-1.05	0.722	-1.18	0.045	-0.55
1424099_at	2310016C16Rik	RIKEN cDNA 2310016C16 gene	-1.1	0.506	1.43	0.168	-1.57	0.019	-1.53	0.296	-0.69
1438688_at	Srrm2	serine/arginine repetitive matrix 2	-1.04	0.859	-1.09	0.171	1.1	0.457	-1.06	0.688	-0.52
1430501_at	C030047K22Rik	RIKEN cDNA C030047K22 gene	-2.7	0.065	-1.4	0.53	1.89	0.044	-1.49	0.388	-0.92
1435720_at	Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	-1.37	0.05	-1.06	0.808	1.3	0.416	-1.45	0.07	-0.64
1441785_at	Gm879	gene model 879, (NCBI)	1.11	0.901	-1.14	0.837	-1	0.977	-1.62	0.12	-0.67
1451470_s_at	Eif5a	eukaryotic translation initiation factor 5A	1.05	0.739	-1	0.981	-1.08	0.606	-1.01	0.897	-0.51
1460177_at	Cndp2	CNDP dipeptidase 2 (metallopeptidase M20 family)	-1.07	0.696	-1.03	0.673	1.07	0.275	-1	0.992	-0.51
1433118_at	2300004M11Rik	RIKEN cDNA 2300004M11 gene	-1.66	0.132	1.6	0.011	-1.28	0.57	-1.32	0.419	-0.67
1440483_at	Plekhm2	Pleckstrin homology domain containing, family M (with RUN domain) member 2	-1.01	0.982	1.07	0.88	-1.09	0.652	-1.1	0.538	-0.53

1445984_at	Pftk1	PFTAIRE protein kinase 1	1.73	0.113	-1.2	0.514	-2.43	0.029	-1.29	0.585	-0.8
1415820_x_at	Nono	non-POU-domain-containing, octamer binding protein	-1.02	0.855	1.11	0.046	-1.13	0.254	-1.19	0.236	-0.56
1452203_at	5830411E10Rik	RIKEN cDNA 5830411E10 gene	-1.07	0.782	-1.07	0.351	1.11	0.413	-1.47	0.291	-0.63
1419026_at	Daxx	Fas death domain-associated protein	-1.04	0.672	1.03	0.678	-1.02	0.917	-1.3	0.151	-0.58
1420826_at	Letm1	leucine zipper-EF-hand containing transmembrane protein 1	-1.06	0.637	-1.27	0.045	1.25	0.251	-1.15	0.224	-0.56
1447886_at	0610040B09Rik	RIKEN cDNA 0610040B09 gene	1.17	0.227	-1.06	0.833	-1.16	0.224	-1.19	0.619	-0.56
1442677_at	---	Transcribed locus	-1.2	0.657	-1.01	0.969	1.16	0.373	-1.22	0.59	-0.57
1458544_at	BC059841	cDNA sequence BC059841	-1.08	0.836	1.44	0.394	-1.64	0.337	-1.61	0.502	-0.72
1431206_at	5730601F06Rik	RIKEN cDNA 5730601F06 gene	1.26	0.439	-1.25	0.523	-1.09	0.753	-1.35	0.33	-0.61
1459093_at	Fras1	Fraser syndrome 1 homolog (human)	-1	0.995	1.19	0.508	-1.27	0.424	-1.14	0.269	-0.56
1455812_x_at	Vasn	vasorin	-1.03	0.901	1.26	0.283	-1.33	0.031	-2.17	0.107	-0.82
1437281_x_at	Xab2	XPA binding protein 2	1.08	0.797	-1.04	0.797	-1.06	0.742	-1.33	0.166	-0.59
1442014_at	Ifrd1	Interferon-related developmental regulator 1	1.75	0.161	-1.29	0.57	-2.18	0.012	-1.18	0.685	-0.73
1431256_at	5033423O07Rik	RIKEN cDNA 5033423O07 gene	1.31	0.06	-1.26	0.303	-1.14	0.685	-1.11	0.777	-0.55
1434566_a_at	4732496O08Rik	RIKEN cDNA 4732496O08 gene	-1.11	0.342	1.15	0.404	-1.08	0.536	-1.37	0.17	-0.6
1420427_a_at	Dhx32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	-1.15	0.271	-1.01	0.95	1.12	0.476	-1.22	0.293	-0.57
1451378_at	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	-1.1	0.23	-1.26	0.043	1.28	0.08	-1.1	0.625	-0.54
1456037_x_at	Preb	prolactin regulatory element binding	-1.24	0.329	-1.07	0.523	1.24	0.314	-1.3	0.299	-0.59
1443165_at	Mrps31	mitochondrial ribosomal protein S31	1.52	0.385	-1.16	0.655	-1.68	0.165	-1.04	0.866	-0.59
1437305_at	6430601A21Rik	RIKEN cDNA 6430601A21 gene	-2.2	0.122	1.78	0.222	-1.34	0.314	-1.23	0.569	-0.75
1427135_at	Sfrs12	splicing factor, arginine/serine-rich 12	-1.08	0.722	1.22	0.325	-1.19	0.358	-1.1	0.5	-0.54
1453357_at	Tdrd9	tudor domain containing 9	-1.21	0.793	-1.17	0.573	1.3	0.32	-1.01	0.979	-0.52
1446857_at	C87115	expressed sequence C87115	-1.01	0.994	1.56	0.441	-2.33	0.225	-2.56	0.259	-1.09
1455598_at	Usp30	ubiquitin specific peptidase 30	-1.19	0.074	-1.25	0.142	1.34	0.209	-1.15	0.603	-0.56
1452601_a_at	Acbd6	acyl-Coenzyme A binding domain containing 6	-1.22	0.08	-1.03	0.721	1.19	0.019	-1.15	0.446	-0.55
1419163_s_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	-1.09	0.033	1.12	0.467	-1.06	0.526	-1.08	0.659	-0.53
1441884_x_at	Cx3cl1	chemokine (C-X3-C motif) ligand 1	1.48	0.548	-1.37	0.636	-1.3	0.537	-1.06	0.928	-0.56
1437043_a_at	1110012M11Rik	RIKEN cDNA 1110012M11 gene	1.05	0.588	-1.06	0.447	-1.02	0.941	-1.34	0.17	-0.59
1420815_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	-1.12	0.384	1.11	0.122	-1.02	0.826	-1.18	0.215	-0.55
1455984_at	Rai17	retinoic acid induced 17	-1.34	0.696	-1.06	0.738	1.29	0.628	-1.27	0.644	-0.6
1433462_a_at	Pi4k2a	phosphatidylinositol 4-kinase type 2 alpha	-1.03	0.924	-1.05	0.763	1.06	0.772	-1.15	0.034	-0.54
1419347_x_at	Svs5	seminal vesicle secretion 5	-1.89	0.484	-1.38	0.596	1.72	0.489	-1.08	0.902	-0.65
1441742_at	Kcnh5	potassium voltage-gated channel, subfamily H (eag-related), member 5	1.91	0.451	-1.93	0.201	-1.81	0.312	-1.81	0.461	-0.91
1451694_at	Ttll3	tubulin tyrosine ligase-like family, member 3	-1.25	0.705	1.31	0.587	-1.15	0.583	-1.04	0.874	-0.53
1427230_at	B930041F14Rik	RIKEN cDNA B930041F14 gene	-1.21	0.108	-1.47	0.342	1.48	0.075	-1.41	0.306	-0.65
AFFX-r2-Bs-thr-3_s_	---	---	1.19	0.779	-1.17	0.423	-1.07	0.799	-1.49	0.313	-0.63
1447374_at	Ube2h	Ubiquitin-conjugating enzyme E2H	-1.44	0.311	1.4	0.482	-1.13	0.384	-1.37	0.433	-0.63
1455238_at	Mum1l1	melanoma associated antigen (mutated) 1-like 1	-1.59	0.014	1.59	0.402	-1.3	0.187	-1.01	0.965	-0.58
1437989_at	Pde8b	phosphodiesterase 8B	-1.08	0.426	1.5	0.305	-1.79	0.051	-1.03	0.937	-0.6
1455533_at	A930025D01Rik	RIKEN cDNA A930025D01 gene	1.01	0.93	-1	0.968	-1.03	0.809	-1.32	0.166	-0.58
1439253_x_at	2610524G07Rik	RIKEN cDNA 2610524G07 gene	1.03	0.663	-1.04	0.646	-1	0.977	-1.35	0.221	-0.59
1452259_at	Phf20	PHD finger protein 20	-1.02	0.738	1.04	0.463	-1.04	0.681	-1.65	0.153	-0.67
1427494_at	Hoxb7 /// Hoxb8	homeo box B7 /// homeo box B8	-2.42	0.013	-1.21	0.477	1.75	0.085	-1.15	0.673	-0.76
1449000_at	D10Jhu81e	DNA segment, Chr 10, Johns Hopkins University 81 expressed	-1.26	0.31	-1.1	0.294	1.28	0.319	-1.43	0.154	-0.63
1430836_at	4933437G19Rik	RIKEN cDNA 4933437G19 gene	1.31	0.605	-1.08	0.801	-1.34	0.043	-1.15	0.632	-0.56
1446130_at	Pctk2	PCTAIRE-motif protein kinase 2	1.46	0.205	-1.03	0.884	-1.83	0.105	-1.56	0.099	-0.74
1424728_at	BC011248	cDNA sequence BC011248	1.07	0.7	-1.09	0.268	-1.01	0.957	-1.18	0.45	-0.55
1448496_a_at	Ing1	inhibitor of growth family, member 1	1.18	0.398	-1.18	0.403	-1.05	0.748	-1.06	0.759	-0.53
1446466_at	Mrc2	Mannose receptor, C type 2	-1.06	0.638	1.76	0.505	-3.57	0.089	-1.12	0.88	-1
1434281_at	1500034J01Rik	RIKEN cDNA 1500034J01 gene	-1.12	0.171	-1.1	0.445	1.18	0.018	-1.12	0.436	-0.54
1440534_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.54	0.085	-1.14	0.518	1.46	0.475	-1.35	0.349	-0.64
1422432_at	Dbi	diazepam binding inhibitor	-1.16	0.195	-1.05	0.609	1.17	0.47	-1.14	0.36	-0.55
1426377_at	Zfp281	zinc finger protein 281	-1.07	0.615	1.21	0.311	-1.2	0.155	-1.28	0.008	-0.58

1445739_at	9430080K19Rik	RIKEN cDNA 9430080K19 gene	-1.05	0.898	-1.01	0.994	1.04	0.923	-1.65	0.319	-0.67
1426883_at	AW491445	expressed sequence AW491445	-1.26	0.119	-1.1	0.057	1.28	0.032	-1.56	0.06	-0.66
1426535_at	9630046K23Rik	RIKEN cDNA 9630046K23 gene	-1.07	0.386	1.3	0.023	-1.34	0.029	-1.57	0.08	-0.67
1422497_at	Slc30a5	solute carrier family 30 (zinc transporter), member 5	-1.23	0.485	1.17	0.214	-1	0.979	-1.29	0.189	-0.59
1419286_s_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	-1.06	0.744	1.06	0.611	-1.02	0.893	-1.54	0.183	-0.64
1453167_at	1700013G24Rik	RIKEN cDNA 1700013G24 gene	-1.15	0.39	1.55	0.048	-1.78	0.057	-1.46	0.341	-0.71
1452947_at	Gprc5c	G protein-coupled receptor, family C, group 5, member C	-1.26	0.216	-1.02	0.879	1.21	0.579	-1.04	0.903	-0.53
1416026_a_at	Rpl12	ribosomal protein L12	-1.01	0.829	1.16	0.135	-1.2	0.235	-1.31	0.009	-0.59
1416637_at	Slc4a2	solute carrier family 4 (anion exchanger), member 2	-1.06	0.648	1.09	0.367	-1.05	0.491	-1.22	0.271	-0.56
1431708_a_at	Tia1	cytotoxic granule-associated RNA binding protein 1	-1.01	0.937	1.42	0.038	-1.75	0.074	-1.66	0.202	-0.75
1459391_at	Abca5	ATP-binding cassette, sub-family A (ABC1), member 5	-1.36	0.387	1.72	0.174	-1.88	0.036	-1.35	0.222	-0.72
1419431_at	Ereg	epiregulin	-2.27	0.183	1.57	0.322	-1.03	0.891	-1.5	0.363	-0.81
1450670_at	Dbh	dopamine beta hydroxylase	-1.75	0.308	-1.18	0.56	1.56	0.035	-1.2	0.443	-0.64
1428287_at	Cul5	cullin 5	-1.03	0.183	-1.01	0.92	1.02	0.93	-1.06	0.681	-0.52
1438008_at	Gga3	Golgi associated, gamma adaptin ear containing, ARF binding protein 3	-1.02	0.871	-1.13	0.348	1.12	0.63	-1.18	0.189	-0.55
1428600_at	3110068G20Rik	RIKEN cDNA 3110068G20 gene	1.13	0.178	-1.01	0.978	-1.16	0.114	-1.32	0.129	-0.59
1447800_x_at	Tcn2	Transcobalamin 2	-1.2	0.087	1.24	0.002	-1.1	0.665	-1.41	0.364	-0.62
1440609_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	-1.44	0.144	1.75	0.182	-1.87	0.076	-1.84	0.243	-0.85
1422469_at	Tbk1	TANK-binding kinase 1	-1.15	0.247	1.17	0.407	-1.06	0.625	-1.09	0.468	-0.53
1426828_at	1300018I17Rik	RIKEN cDNA 1300018I17 gene	-1.05	0.691	-1.12	0.61	1.14	0.376	-1.06	0.797	-0.52
1453733_a_at	4933434E20Rik	RIKEN cDNA 4933434E20 gene	-1.12	0.327	1.13	0.362	-1.04	0.359	-1.13	0.499	-0.54
1433003_at	4933423N03Rik	RIKEN cDNA 4933423N03 gene	-1.57	0.305	1.92	0.174	-2.35	0.127	-2.08	0.235	-1.02
1419405_at	Nmb	neuromedin B	1.06	0.797	-1.05	0.906	-1.03	0.908	-1.28	0.434	-0.57
1426626_at	Gtf2f2	general transcription factor IIF, polypeptide 2	1.1	0.279	-1.07	0.64	-1.06	0.733	-1.09	0.726	-0.53
1434252_at	Tmcc3	transmembrane and coiled coil domains 3	1.26	0.553	-1.04	0.787	-1.31	0.122	-1.29	0.465	-0.59
1438974_x_at	Pitpnm1	phosphatidylinositol membrane-associated 1	-1.05	0.477	1.15	0.482	-1.14	0.196	-1.16	0.056	-0.55
1417122_at	Vav3	vav 3 oncogene	-1.01	0.943	1.28	0.349	-1.4	0.169	-1.4	0.189	-0.63
1455545_at	1110065P20Rik	RIKEN cDNA 1110065P20 gene	1.13	0.236	-1.02	0.799	-1.15	0.325	-1.04	0.817	-0.52
1422047_at	Cdh5	cadherin 5	-1.02	0.906	-1.27	0.55	1.22	0.645	-1.11	0.772	-0.55
1450177_at	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	-1.59	0.157	1.37	0.526	-1.01	0.924	-2.36	0.548	-0.9
1446542_at	Acss2	acyl-CoA synthetase short-chain family member 2	-1.37	0.445	1.32	0.278	-1.07	0.857	-1.04	0.955	-0.54
1441533_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933016	1.62	0.27	-1.09	0.843	-2.23	0.262	-1.02	0.935	-0.68
1442776_at	2310009E04Rik	RIKEN cDNA 2310009E04 gene	1.29	0.417	-1.15	0.691	-1.22	0.187	-1.05	0.922	-0.53
1434643_at	Tbl1x	transducin (beta)-like 1 X-linked	1.42	0.283	-1.35	0.363	-1.21	0.486	-1.39	0.463	-0.63
1433955_at	Brwd1	bromodomain and WD repeat domain containing 1	-1.22	0.365	1.2	0.495	-1.04	0.754	-1.6	0.114	-0.66
1454097_at	Zcwpw2	zinc finger, CW type with PWWP domain 2	-1.11	0.869	1.28	0.645	-1.23	0.474	-1.09	0.552	-0.54
1444084_at	Prrg4 /// LOC67696	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane) /// similar to Transm	-1.16	0.299	1.32	0.307	-1.25	0.39	-1.17	0.4	-0.56
1417917_at	Cnn1	calponin 1	1.37	0.27	-1.01	0.993	-1.61	0.147	-1.47	0.474	-0.68
1451917_a_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	-1.1	0.76	-1.11	0.757	1.17	0.407	-3.82	0.156	-1.21
1433815_at	Jakmip1	janus kinase and microtubule interacting protein 1	-1	0.979	-1.55	0.419	1.35	0.558	-2.16	0.084	-0.84
1416260_a_at	Snx1	sorting nexin 1	-1.15	0.254	1.28	0.001	-1.19	0.076	-1.16	0.217	-0.55
1426833_at	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	-1.23	0.085	-1.07	0.451	1.24	0.191	-1.35	0.277	-0.6
1455163_at	Guf1	GUF1 GTPase homolog (S. cerevisiae)	-1	0.991	-1.07	0.741	1.05	0.728	-1.02	0.957	-0.51
1420251_at	---	---	1.44	0.19	-1.29	0.561	-1.31	0.44	-3.17	0.083	-1.08
1425433_a_at	Nrp2	neuropilin 2	-1.36	0.679	1.34	0.697	-1.1	0.841	-1.06	0.8	-0.54
1424654_at	Acp2	acid phosphatase 2, lysosomal	1.16	0.243	-1.13	0.309	-1.06	0.446	-1.01	0.971	-0.51
1428712_at	Mon1b	MON1 homolog b (yeast)	-1.24	0.313	-1.02	0.939	1.2	0.476	-1.55	0.261	-0.65
1449875_s_at	H2-T22 /// H2-T9	histocompatibility 2, T region locus 22 /// histocompatibility 2, T region locus 9	-1.09	0.418	1.09	0.326	-1.01	0.849	-1.7	0.149	-0.68
1424773_at	1110012M11Rik	RIKEN cDNA 1110012M11 gene	-1.01	0.866	1.04	0.687	-1.05	0.844	-1.12	0.6	-0.53
1459058_at	Siae	sialic acid acetylesterase	-2.41	0.42	2.16	0.413	-2.44	0.186	-2.02	0.03	-1.18
1458274_at	Zfp69	zinc finger protein 69	-1.16	0.681	1.15	0.443	-1.02	0.946	-1.52	0.478	-0.64
1460190_at	Ap1m2	adaptor protein complex AP-1, mu 2 subunit	-1.11	0.428	1.18	0.596	-1.09	0.469	-1.54	0.418	-0.64
1418219_at	Il15	interleukin 15	-1.27	0.299	-1.2	0.615	1.37	0.001	-1.3	0.237	-0.6

1415724_a_at	Cdc42	cell division cycle 42 homolog (S. cerevisiae)	-1.12	0.334	-1.1	0.24	1.19	0.095	-1.29	0.122	-0.58
1437677_at	AI449595	EST AI449595	-1.28	0.336	-1.06	0.317	1.26	0.445	-1.1	0.602	-0.54
1431264_at	---	---	1.39	0.491	-1.13	0.838	-1.41	0.464	-1.64	0.552	-0.7
1448141_at	1110014J01Rik	RIKEN cDNA 1110014J01 gene	-1.1	0.392	-1.21	0.051	1.25	0.228	-1.56	0.073	-0.65
1438512_at	BC048679	cDNA sequence BC048679	-1.29	0.553	1.35	0.505	-1.16	0.663	-1.14	0.706	-0.56
1416901_at	Npc2	Niemann Pick type C2	-1.01	0.887	1.23	0.009	-1.31	0.006	-1.43	0.101	-0.63
1456039_at	Snx14	sorting nexin 14	-1.06	0.578	-1.02	0.476	1.07	0.634	-1.24	0.171	-0.56
1431864_at	Fbxo24	F-box only protein 24	-1	0.997	-1.5	0.151	1.32	0.665	-1.04	0.851	-0.55
1420981_a_at	Lmo4	LIM domain only 4	-1.1	0.529	1.09	0.191	-1.01	0.94	-1.48	0.005	-0.63
1428292_at	Ndor1	NADPH dependent diflavin oxidoreductase 1	-1.12	0.822	-1.06	0.767	1.15	0.366	-1.04	0.452	-0.52
1445859_at	Bcl9	B-cell CLL/lymphoma 9	-1.18	0.551	1.2	0.642	-1.06	0.465	-1.15	0.383	-0.55
1445252_at	Kremen1	kringle containing transmembrane protein 1	-1.16	0.488	1.43	0.308	-1.43	0.117	-1.27	0.361	-0.61
1457739_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	-1.04	0.968	1.08	0.885	-1.06	0.85	-1.18	0.592	-0.55
1444564_at	Apod	apolipoprotein D	-2.17	0.384	1.61	0.488	-1.09	0.81	-1.36	0.567	-0.75
1423212_at	Phc1	polyhomeotic-like 1 (Drosophila)	-1.07	0.38	-1.12	0.849	1.16	0.525	-1.44	0.264	-0.62
1450309_at	Astn2	astrotactin 2	1.27	0.676	-1.15	0.569	-1.17	0.604	-2.66	0.408	-0.93
1454259_s_at	4931433A01Rik	RIKEN cDNA 4931433A01 gene	-1.3	0.637	1.46	0.521	-1.32	0.575	-1.62	0.382	-0.69
1438048_at	Myct1	myc target 1	1.05	0.874	-1.05	0.822	-1.01	0.934	-1.04	0.754	-0.51
1450872_s_at	Lip1	lysosomal acid lipase 1	1.13	0.542	-1.05	0.503	-1.1	0.362	-1.38	0.196	-0.6
1458269_at	Pcdh9 /// LOC6382	protocadherin 9 /// similar to protocadherin 9 isoform 1 precursor	-1.43	0.631	-2.16	0.023	1.83	0.349	-1.06	0.737	-0.7
1419623_at	Prss21	protease, serine, 21	-1.11	0.759	-1.22	0.689	1.27	0.351	-1.12	0.325	-0.54
1460023_at	---	---	1.19	0.396	-1.01	0.957	-1.22	0.57	-1.11	0.778	-0.54
1419819_s_at	Sec63	SEC63-like (S. cerevisiae)	1.11	0.392	-1.07	0.364	-1.06	0.472	-1.11	0.502	-0.53
1438043_at	Eif2c2	eukaryotic translation initiation factor 2C, 2	1.44	0.429	-1.19	0.721	-1.41	0.661	-1.17	0.663	-0.58
1428251_at	Smchd1	SMC hinge domain containing 1	-1	0.997	1.1	0.385	-1.12	0.128	-1.29	0.131	-0.58
1417863_at	Spata19	spermatogenesis associated 19	-1.14	0.483	-1.28	0.313	1.34	0.459	-1.05	0.892	-0.53
1450117_at	Tcf3	transcription factor 3	-1.02	0.929	-1.78	0.001	1.45	0.134	-1.64	0.168	-0.75
1447102_at	Ninj2	Ninjurin 2	-1.25	0.009	-1.01	0.985	1.2	0.507	-1.03	0.908	-0.52
1442655_at	Dnmt3b	DNA methyltransferase 3B	-1.94	0.086	1.56	0.032	-1.09	0.68	-1.23	0.391	-0.68
1434459_at	BC057627	cDNA sequence BC057627	-1.15	0.237	-1.11	0.208	1.22	0.139	-1.04	0.803	-0.52
1452356_at	Iqcc	IQ motif containing C	-1.1	0.435	-1.02	0.914	1.1	0.319	-1.04	0.788	-0.52
1445066_at	Ttc7b	Tetratricopeptide repeat domain 7B	-1.21	0.658	-1.15	0.703	1.3	0.292	-1.23	0.485	-0.57
1452416_at	Il6ra	interleukin 6 receptor, alpha	1.14	0.725	-1.17	0.628	-1	0.979	-1.56	0.246	-0.65
1454277_at	1700049J03Rik	RIKEN cDNA 1700049J03 gene	1.93	0.253	-4.81	0.147	-1.17	0.406	-1.75	0.506	-1.45
1444696_at	BC059841	CDNA sequence BC059841	-1.2	0.716	1.46	0.442	-1.42	0.516	-1.37	0.626	-0.63
1453799_at	9430038I01Rik	RIKEN cDNA 9430038I01 gene	1.08	0.786	-1.07	0.758	-1.03	0.86	-1.26	0.521	-0.57
1457343_at	Strn3	Striatin, calmodulin binding protein 3	-1.35	0.671	1.63	0.442	-1.59	0.173	-1.01	0.958	-0.58
1434720_at	9530033F24Rik	RIKEN cDNA 9530033F24 gene	1.21	0.44	-1.11	0.345	-1.13	0.578	-1.34	0.217	-0.59
1422838_at	Kcnu1	potassium channel, subfamily U, member 1	1.31	0.307	-1.37	0.398	-1.05	0.813	-3.47	0.123	-1.14
1438238_at	2010315B03Rik	RIKEN cDNA 2010315B03 gene	1.05	0.467	-1.02	0.782	-1.04	0.813	-1.55	0.292	-0.64
1439358_a_at	Nrxn1	neurexin I	1.55	0.284	-1.33	0.22	-1.45	0.147	-1.1	0.534	-0.58
1457976_at	2010002M12Rik	RIKEN cDNA 2010002M12 gene	-1.45	0.628	-1.02	0.951	1.32	0.397	-1.44	0.272	-0.65
1458318_at	3110047M12Rik	RIKEN cDNA 3110047M12 gene	-1.29	0.643	1.48	0.468	-1.36	0.46	-1.43	0.412	-0.65
1436606_at	---	Adult male colon cDNA, RIKEN full-length enriched library, clone:9030003C19 pr	-1.14	0.535	-1.05	0.499	1.17	0.28	-1.26	0.046	-0.57
1435363_at	Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	-1.22	0.482	1.24	0.168	-1.07	0.779	-1.01	0.968	-0.51
1440883_at	---	Transcribed locus	1.07	0.291	-1.03	0.728	-1.05	0.812	-1.12	0.609	-0.53
1457953_at	---	PREDICTED: Mus musculus hypothetical protein LOC629238 (LOC629238), mR	-1.32	0.246	-1.27	0.716	1.45	0.522	-2.04	0.36	-0.79
1437040_at	Etnk2	ethanolamine kinase 2	1.24	0.596	-1.1	0.601	-1.18	0.485	-1.23	0.563	-0.57
1445140_at	AU022804	expressed sequence AU022804	-2.51	0.019	-1.26	0.691	1.8	0.139	-1.39	0.562	-0.84
1433223_at	5830442K09Rik	RIKEN cDNA 5830442K09 gene	1.09	0.919	-1.04	0.927	-1.06	0.893	-1.16	0.84	-0.54
1421885_at	Sos1	Son of sevenless homolog 1 (Drosophila)	1.18	0.639	-1.13	0.765	-1.08	0.867	-1.69	0.197	-0.68
1418796_at	Clec11a	C-type lectin domain family 11, member a	1.37	0.153	-1.03	0.908	-1.55	0.073	-1.18	0.621	-0.6
1460142_at	D13Ertd324e	DNA segment, Chr 13, ERATO Doi 324, expressed	-2.04	0.153	1.51	0.297	-1.01	0.969	-1.35	0.623	-0.72

1416330_at	Cd81	CD 81 antigen	1.08	0.193	-1.04	0.64	-1.04	0.618	-1.13	0.543	-0.53
1448131_at	Mfn2	mitofusin 2	-1.05	0.524	-1.24	0.124	1.23	0.261	-1.25	0.179	-0.57
1427532_at	Trat1	T cell receptor associated transmembrane adaptor 1	1.83	0.233	-1.58	0.239	-1.89	0.056	-6.67	0.018	-2.08
1445971_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	-1.13	0.869	-1	0.987	1.11	0.862	-1.3	0.554	-0.58
1451094_at	Ggtl3	gamma-glutamyltransferase-like 3	-1.68	0.018	-2.01	0.069	1.9	0.47	-1.72	0.49	-0.88
1433557_at	Cbx7	chromobox homolog 7	-1.02	0.87	-1.05	0.92	1.06	0.812	-1.7	0.195	-0.68
1454670_at	Rere	arginine glutamic acid dipeptide (RE) repeats	-1.32	0.278	-1.04	0.813	1.27	0.466	-1.21	0.609	-0.57
1444034_at	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	-1.29	0.486	1.78	0.335	-2.27	0.005	-2.58	0.082	-1.09
1426852_x_at	Nov	nephroblastoma overexpressed gene	1.5	0.278	-1.13	0.849	-1.64	0.029	-1.15	0.822	-0.6
1448844_at	Cyb5b	cytochrome b5 type B	-1.22	0.493	-1.12	0.663	1.29	0.469	-1.35	0.141	-0.6
1442204_at	Panx2	Pannexin 2	-1.24	0.572	1.64	0.187	-1.84	0.267	-1.01	0.959	-0.61
1444543_at	---	Transcribed locus	1.37	0.225	-1.02	0.97	-1.55	0.363	-1.84	0.247	-0.76
1429834_a_at	1110014N23Rik	RIKEN cDNA 1110014N23 gene	-1.06	0.275	-1.26	0.693	1.26	0.548	-1.15	0.805	-0.55
1423991_at	2610033H07Rik	RIKEN cDNA 2610033H07 gene	-1.23	0.488	-1.05	0.83	1.23	0.086	-1.01	0.975	-0.51
1427258_at	Trim24	tripartite motif protein 24	-1.04	0.692	-1.12	0.47	1.14	0.377	-1.03	0.791	-0.51
1416071_at	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-1.15	0.142	-1.11	0.297	1.22	0.072	-1.2	0.053	-0.56
1452387_a_at	Amotl2	angiomotin like 2	-1.08	0.548	-1.27	0.236	1.28	0.408	-1.3	0.243	-0.59
1418522_at	Mtx1	metaxin 1	-1.02	0.928	-1.03	0.85	1.05	0.67	-1.01	0.965	-0.5
1430641_at	9030605I04Rik /// A	RIKEN cDNA 9030605I04 gene /// expressed sequence AI987692	1.34	0.053	-1.26	0.674	-1.15	0.654	-1.15	0.897	-0.56
1425861_x_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	-1.29	0.729	-1.03	0.955	1.26	0.67	-1.94	0.098	-0.75
1436991_x_at	Gsn	gelsolin	-1.08	0.4	1.23	0.258	-1.18	0.094	-1.38	0.292	-0.6
1453013_at	Zfp740	zinc finger protein 740	-1.09	0.063	-1.12	0.559	1.18	0.441	-1.27	0.161	-0.57
1419775_at	---	---	2.24	0.066	-2.07	0.006	-3.62	0.01	-1.63	0.501	-1.27
1434047_x_at	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	-1.08	0.786	1.18	0.205	-1.13	0.398	-1.01	0.977	-0.51
1422676_at	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.11	0.524	1.16	0.208	-1.07	0.386	-1.18	0.189	-0.55
1439287_at	---	---	-1.22	0.514	-1.57	0.36	1.54	0.152	-2.27	0.346	-0.88
1431895_at	4933434M16Rik	RIKEN cDNA 4933434M16 gene	-2.04	0.419	-1.44	0.27	1.81	0.444	-1.19	0.678	-0.71
1425823_at	BC026782 /// LOC6	cDNA sequence BC026782 /// similar to complement factor H-related protein B	1.31	0.596	-1.11	0.219	-1.27	0.197	-1.01	0.982	-0.52
1422157_a_at	Itgb1bp1	integrin beta 1 binding protein 1	-1.04	0.469	1.15	0.189	-1.13	0.187	-1.38	0.114	-0.6
1457883_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	-1.17	0.703	-1.03	0.827	1.18	0.253	-1.32	0.43	-0.59
1430924_at	4933440M02Rik	RIKEN cDNA 4933440M02 gene	-1.1	0.917	1.61	0.087	-2.09	0.156	-1.21	0.593	-0.7
1419936_at	Csnk2a2	Casein kinase II, alpha 2, polypeptide	-1.31	0.611	1.46	0.118	-1.29	0.621	-1.26	0.703	-0.6
1433281_at	Prune	prune homolog (Drosophila)	-1.08	0.017	1.09	0.778	-1.02	0.945	-1.05	0.918	-0.52
1416535_at	Mcrs1 /// LOC4337	microspherule protein 1 /// similar to Microspherule protein 1 (58 kDa microspheru	-1.02	0.919	-1.14	0.379	1.14	0.391	-1.08	0.441	-0.52
1419824_a_at	A230062G08Rik	RIKEN cDNA A230062G08 gene	-1.01	0.977	-1.04	0.787	1.05	0.742	-1.56	0.264	-0.64
1430364_at	Atf7ip2	activating transcription factor 7 interacting protein 2	1.36	0.586	-1.43	0.133	-1.07	0.465	-1.88	0.256	-0.75
1438169_a_at	Frmd4b	FERM domain containing 4B	-1.16	0.769	1.19	0.425	-1.06	0.592	-1.01	0.976	-0.51
1421238_a_at	Ptprt	protein tyrosine phosphatase, receptor type, T	1.71	0.406	-1.83	0.096	-1.35	0.404	-1.05	0.913	-0.63
1455928_x_at	Lztr1	leucine-zipper-like transcriptional regulator, 1	-1.07	0.608	1.16	0.506	-1.11	0.688	-1.07	0.727	-0.52
1456603_at	1500005K14Rik	RIKEN cDNA 1500005K14 gene	1.07	0.379	-1.01	0.987	-1.07	0.75	-1.73	0.034	-0.68
1436467_at	D230004N17Rik	RIKEN cDNA D230004N17 gene	-1.5	0.665	-1.36	0.658	1.59	0.141	-1.18	0.701	-0.61
1418477_at	Matn1	matrilin 1, cartilage matrix protein 1	-1.04	0.791	-1.07	0.855	1.11	0.839	-1.64	0.473	-0.66
1417138_s_at	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	-1.07	0.294	-1.07	0.453	1.13	0.039	-1.15	0.48	-0.54
1446463_at	BC024969	CDNA sequence BC024969	1.63	0.326	-1.25	0.527	-1.77	0.05	-1.43	0.18	-0.7
1428728_at	Ddx51	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	-1.26	0.017	-1.15	0.381	1.34	0.12	-1.34	0.004	-0.6
1424506_at	BC026432	cDNA sequence BC026432	1.11	0.516	-1.03	0.782	-1.08	0.637	-1.02	0.767	-0.51
1433187_at	B230112I24Rik	RIKEN cDNA B230112I24 gene	-1.66	0.333	1.42	0.603	-1.03	0.937	-1.14	0.371	-0.6
1442212_at	Cpd	carboxypeptidase D	1.08	0.903	-1.02	0.976	-1.07	0.821	-1.14	0.645	-0.54
1425204_s_at	Ddx19a /// Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a /// DEAD (Asp-Glu-Ala-Asp) box p	-1.11	0.615	-1.13	0.451	1.21	0.536	-1.1	0.588	-0.53
1428267_at	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	-1.01	0.889	1.02	0.732	-1	0.972	-1.3	0.275	-0.58
1447520_at	---	---	-1.41	0.678	1.58	0.217	-1.41	0.132	-1.75	0.487	-0.75
1457709_a_at	A930005H10Rik	RIKEN cDNA A930005H10 gene	1.12	0.184	-1.05	0.605	-1.07	0.715	-1.95	0.082	-0.74
1415962_at	Eif3s3	eukaryotic translation initiation factor 3, subunit 3 (gamma)	-1.02	0.414	-1.02	0.32	1.05	0.52	-1.31	0.135	-0.58

1441195_at	6030487A22Rik	RIKEN cDNA 6030487A22 gene	-1.33	0.194	1.62	0.06	-1.6	0.221	-1.08	0.667	-0.6
1449420_at	Pde1b	phosphodiesterase 1B, Ca2+-calmodulin dependent	-1.04	0.924	-1.22	0.588	1.22	0.506	-1.28	0.195	-0.58
1428017_at	Pknox2	Pbx/knotted 1 homeobox 2	-1.11	0.837	-1.98	0.233	1.6	0.203	-1.21	0.734	-0.68
1416061_at	Tbc1d15	TBC1 domain family, member 15	-1.03	0.4	-1.14	0.221	1.15	0.298	-1.03	0.844	-0.51
1416065_a_at	Ankrd10	ankyrin repeat domain 10	-1.12	0.662	1.13	0.607	-1.03	0.874	-1.89	0.037	-0.73
1417349_at	Pldn	pallidin	-1.18	0.147	-1.03	0.726	1.18	0.016	-1.23	0.357	-0.56
1435208_at	Dtx3l	deltex 3-like (Drosophila)	-1.03	0.886	-1.02	0.836	1.04	0.752	-1.21	0.357	-0.55
1435382_at	Ndn	necdin	1.24	0.047	-1	0.994	-1.31	0.299	-1.55	0.124	-0.66
1428457_at	5830472M02Rik	RIKEN cDNA 5830472M02 gene	-1.09	0.59	1.09	0.665	-1.01	0.954	-1.57	0.283	-0.64
1424422_s_at	Lenep /// Flad1	lens epithelial protein /// RFad1, flavin adenine dinucleotide synthetase, homolog	-1.05	0.804	-1.04	0.682	1.1	0.582	-1.73	0.105	-0.68
1429529_at	Tsen54	tRNA splicing endonuclease 54 homolog (SEN54, S. cerevisiae)	-1.04	0.741	-1.04	0.77	1.08	0.643	-1.26	0.153	-0.57
1442297_at	BB212172	expressed sequence BB212172	-1.16	0.09	1.17	0.746	-1.03	0.883	-1.11	0.591	-0.53
1444122_at	4930518F03Rik	RIKEN cDNA 4930518F03 gene	-1.02	0.982	-1.22	0.644	1.2	0.758	-1.12	0.875	-0.54
1438415_s_at	Yipf2	Yip1 domain family, member 2	-1.03	0.668	1.31	0.008	-1.4	0.112	-1.03	0.906	-0.54
1429246_a_at	Anxa6	annexin A6	-1.1	0.627	-1.04	0.829	1.14	0.583	-1.7	0.25	-0.68
1452273_at	AA409316	expressed sequence AA409316	-1.02	0.897	-1.02	0.885	1.04	0.688	-1.01	0.986	-0.5
1423925_at	Dhx16	DEAH (Asp-Glu-Ala-His) box polypeptide 16	-1.03	0.664	-1.12	0.301	1.14	0.021	-1.26	0.032	-0.57
1417258_at	Cct5	chaperonin subunit 5 (epsilon)	1.01	0.775	-1.01	0.745	-1	0.999	-1.1	0.393	-0.52
1440831_at	Bach1	BTB and CNC homology 1	1.15	0.335	-1.05	0.68	-1.1	0.149	-1	0.975	-0.5
1450504_a_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	-1.04	0.306	-1.09	0.58	1.12	0.137	-1.29	0.332	-0.57
1424559_at	AW060207	expressed sequence AW060207	-1.12	0.432	-1.01	0.908	1.12	0.249	-1	0.999	-0.5
1423762_at	Adck1	aarF domain containing kinase 1	-1.22	0.272	-1.14	0.471	1.31	0.082	-1.24	0.048	-0.57
1429627_at	Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3	-1.05	0.787	1.08	0.477	-1.03	0.855	-1.18	0.255	-0.54
1429370_a_at	Psmd11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	-1.11	0.619	-1.15	0.066	1.24	0.216	-1.1	0.549	-0.53
1455108_at	Eif4e2	eukaryotic translation initiation factor 4E member 2	-1.05	0.87	-1.23	0.179	1.23	0.3	-1.04	0.781	-0.52
1454550_at	4930478M09Rik	RIKEN cDNA 4930478M09 gene	-2.04	0.015	-1.06	0.905	1.57	0.172	-1.37	0.519	-0.73
1456766_at	C330001K17Rik	RIKEN cDNA C330001K17 gene	-1.04	0.893	1.12	0.84	-1.08	0.608	-2.13	0.109	-0.78
1424028_at	5830457O10Rik	RIKEN cDNA 5830457O10 gene	-1.36	0.158	-1.12	0.663	1.38	0.25	-1.25	0.261	-0.59
1416024_x_at	Cct3	chaperonin subunit 3 (gamma)	-1.04	0.386	-1.03	0.701	1.07	0.593	-1.19	0.016	-0.55
1459753_x_at	Tra2a	transformer 2 alpha homolog (Drosophila)	-1.03	0.974	1.19	0.728	-1.19	0.55	-1.57	0.061	-0.65
1460001_at	Pgpep1	pyroglutamyl-peptidase I	-1.06	0.469	-1.04	0.674	1.1	0.542	-1.36	0.061	-0.59
1428438_s_at	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	1.3	0.317	-1.12	0.127	-1.24	0.023	-1.1	0.339	-0.54
1434702_at	2600009E05Rik	RIKEN cDNA 2600009E05 gene	1.1	0.387	-1.1	0.208	-1.01	0.935	-1.11	0.345	-0.53
1456582_x_at	5230400G24Rik ///	RIKEN cDNA 5230400G24 gene /// hypothetical protein LOC637796	-1.34	0.126	1.35	0.242	-1.11	0.477	-1.2	0.417	-0.57
1441749_at	4930447F24Rik	RIKEN cDNA 4930447F24 gene	2.06	0.33	-2.64	0.111	-1.78	0.15	-1.79	0.366	-1.04
1445547_at	---	Transcribed locus	-1.53	0.719	1.88	0.133	-2.11	0	-1.11	0.587	-0.72
1418629_a_at	---	---	-1.06	0.192	-1.2	0.096	1.23	0.092	-1.15	0.422	-0.54
1459352_at	2410003P15Rik	RIKEN cDNA 2410003P15 gene	-1.15	0.873	1.3	0.532	-1.2	0.631	-2.42	0.04	-0.87
1424537_at	1700017G21Rik ///	RIKEN cDNA 1700017G21 gene /// similar to Germ cell-less protein-like 2 (mGcll	-1.32	0.721	1.34	0.287	-1.11	0.818	-1.07	0.752	-0.54
1459215_at	Laptm4b	Lysosomal-associated protein transmembrane 4B	1.34	0.379	-1.16	0.775	-1.25	0.542	-1.22	0.235	-0.57
1433841_at	KIAA0415	KIAA0415 protein	-1.03	0.916	-1.04	0.702	1.07	0.658	-1.16	0.346	-0.54
1456105_at	Mnab	membrane associated DNA binding protein	-1.09	0.58	1.28	0.33	-1.23	0.402	-1.02	0.946	-0.52
1433602_at	Gabra5	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 5	-2.02	0.117	1.6	0.374	-1.1	0.651	-3.58	0.22	-1.27
1428710_at	Rit1	Ras-like without CAAX 1	1.18	0.108	-1.02	0.855	-1.19	0.425	-1.33	0.302	-0.59
1457906_at	Rbm13	RNA binding motif protein 13	-1	0.998	1.7	0.35	-3.26	0.069	-1.97	0.393	-1.13
1423005_a_at	Espn	espin	-1.2	0.523	-1.81	0.176	1.62	0.094	-1.11	0.887	-0.62
1428530_x_at	Rps24 /// LOC6291	ribosomal protein S24 /// similar to ribosomal protein S24 /// similar to ribosomal p	-1.03	0.197	1.17	0.042	-1.16	0.209	-1.5	0.025	-0.63
1441448_at	Pum2	Pumilio 2 (Drosophila)	-1.14	0.101	1.41	0.29	-1.4	0.174	-1.26	0.57	-0.6
1437935_at	4930486G11Rik	RIKEN cDNA 4930486G11 gene	-1.02	0.958	-1.15	0.824	1.16	0.625	-1.63	0.348	-0.66
1442765_at	---	Transcribed locus	1.41	0.011	-1.22	0.702	-1.29	0.579	-1.57	0.549	-0.67
1426378_at	Eif4b	eukaryotic translation initiation factor 4B	-1.05	0.389	-1.07	0.383	1.13	0.398	-1.13	0.185	-0.53
1458592_at	Auts2	Autism susceptibility candidate 2	-1.34	0.276	1.41	0.578	-1.18	0.176	-1.61	0.096	-0.68
1456290_x_at	Ccm2	cerebral cavernous malformation 2 homolog (human)	-1.19	0.224	1.19	0.214	-1.02	0.945	-1.29	0.111	-0.58

1424645_at	Tnrc6c	trinucleotide repeat containing 6C	1.08	0.601	-1.06	0.67	-1.01	0.942	-1.36	0.22	-0.59
1441250_at	---	---	-1.21	0.801	1.53	0.045	-1.55	0.301	-1.86	0.14	-0.77
1430581_at	---	---	1.51	0.229	-1.06	0.855	-1.79	0.11	-1.36	0.318	-0.68
1418335_a_at	Dph1 /// RP23-143/	DPH1 homolog (S. cerevisiae) /// candidate tumor suppressor OVCA2	-1.01	0.963	-1.15	0.446	1.15	0.573	-1.41	0.273	-0.61
1460402_at	Brpf1	bromodomain and PHD finger containing, 1	-1.05	0.375	-1.02	0.789	1.08	0.525	-1.12	0.491	-0.53
1435224_at	Crebbp	CREB binding protein	-1.06	0.523	-1.02	0.843	1.09	0.604	-1.07	0.396	-0.52
1433148_at	4930513N20Rik	RIKEN cDNA 4930513N20 gene	-1.36	0.107	1.91	0.145	-2.77	0.014	-1.71	0.476	-0.98
1448969_at	Ftsj2	FtsJ homolog 2 (E. coli)	1.21	0.461	-1.15	0.294	-1.07	0.334	-1.08	0.52	-0.53
1424610_at	Trub2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	-1.25	0.018	-1.13	0.602	1.32	0.234	-1.4	0.17	-0.61
1426851_a_at	Nov	nephroblastoma overexpressed gene	1.39	0.334	-1.21	0.485	-1.27	0.28	-1.15	0.807	-0.56
1446908_at	Il28ra	Interleukin 28 receptor alpha	-1.36	0.447	1.59	0.554	-1.46	0.336	-1.52	0.27	-0.69
1435417_at	AI464131	expressed sequence AI464131	-1.19	0.195	-1.11	0.46	1.27	0.394	-1.09	0.888	-0.53
1442205_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930031I16 product:	-1.24	0.501	1.47	0.158	-1.36	0.108	-1.26	0.328	-0.6
1446486_at	Dtwd2	DTW domain containing 2	1.23	0.185	-1.01	0.963	-1.26	0.304	-1.05	0.855	-0.52
1454718_at	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	-1.13	0.326	-1.06	0.548	1.18	0.01	-1.06	0.655	-0.52
1428199_at	Adal	adenosine deaminase-like	-1.34	0.706	-1.08	0.768	1.33	0.634	-1.02	0.95	-0.53
1438797_at	6330509M05Rik	RIKEN cDNA 6330509M05 gene	-1.18	0.418	1.36	0.001	-1.25	0.285	-1.29	0.415	-0.59
1443680_at	Otx2os1	Otx2 opposite strand transcript 1	-1.9	0.018	-1.15	0.228	1.62	0.106	-1	0.999	-0.61
1425880_x_at	Zfp352	zinc finger protein 352	-1.01	0.986	1.16	0.768	-1.16	0.498	-2.28	0.31	-0.82
1436327_a_at	Vps53	vacuolar protein sorting 53 (yeast)	-1.13	0.108	1.18	0.811	-1.06	0.83	-1.26	0.631	-0.57
1424776_a_at	Slc25a28	solute carrier family 25, member 28	1.05	0.641	-1	0.987	-1.04	0.751	-1.29	0.115	-0.57
1458581_at	LOC553093	hypothetical LOC553093	1.46	0.357	-1.13	0.577	-1.5	0.486	-1.19	0.589	-0.59
1448710_at	Cxcr4	chemokine (C-X-C motif) receptor 4	-1.11	0.724	1.24	0.6	-1.15	0.665	-1.22	0.04	-0.56
1432327_at	9530067L11Rik	RIKEN cDNA 9530067L11 gene	-1.74	0.419	-1.01	0.975	1.45	0.372	-1	0.98	-0.58
1415674_a_at	Trappc4	trafficking protein particle complex 4	-1.06	0.548	1.12	0.432	-1.06	0.645	-1.2	0.168	-0.55
1423780_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	-1.08	0.595	-1.17	0.217	1.23	0.09	-1.02	0.841	-0.51
1449023_a_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	-1.03	0.802	1.12	0.284	-1.09	0.298	-1.12	0.465	-0.53
1433246_at	6720475M21Rik	RIKEN cDNA 6720475M21 gene	1.65	0.512	-1.48	0.401	-1.46	0.186	-1.01	0.934	-0.58
1443308_at	Unc13b	unc-13 homolog B (C. elegans)	-1.36	0.312	-1.13	0.745	1.39	0.269	-1.09	0.873	-0.55
1428691_at	5630401D06Rik	RIKEN cDNA 5630401D06 gene	-1.01	0.942	1.11	0.324	-1.1	0.372	-1.51	0.028	-0.63
1423061_at	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	1.05	0.696	-1.01	0.968	-1.03	0.875	-1.12	0.718	-0.53
1452400_a_at	Hoxa11os	homeo box A11, opposite strand transcript	1.31	0.634	-1.04	0.952	-1.36	0.52	-1.02	0.974	-0.53
1422861_s_at	LOC669660	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ an	-1.03	0.954	-1.17	0.521	1.18	0.653	-1.4	0.115	-0.6
1442511_at	Ipo7	importin 7	1.57	0.315	-1.35	0.318	-1.43	0.091	-1.08	0.534	-0.57
1431367_at	1-Mar	membrane-associated ring finger (C3HC4) 1	-1.3	0.229	1.38	0.281	-1.17	0.685	-1.93	0.207	-0.75
1433011_at	4921506L19Rik	RIKEN cDNA 4921506L19 gene	-1.13	0.533	-1.25	0.522	1.33	0.656	-1.59	0.24	-0.66
1434925_at	4833424O15Rik	RIKEN cDNA 4833424O15 gene	-1.75	0.266	1.51	0.484	-1.08	0.919	-3.64	0.012	-1.24
1423523_at	Aass	aminoadipate-semialdehyde synthase	-1.15	0.444	-1.12	0.079	1.25	0.392	-1.57	0.4	-0.65
1416885_at	1110038F14Rik	RIKEN cDNA 1110038F14 gene	-1.09	0.404	1.1	0.499	-1	0.964	-1.27	0.157	-0.57
1448139_at	Mlc1	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)	-1.08	0.477	1.22	0.157	-1.16	0.649	-4.74	0.161	-1.44
1448155_at	Pdcd6ip	programmed cell death 6 interacting protein	-1.08	0.54	-1.03	0.7	1.11	0.385	-1.16	0.367	-0.54
1454391_at	6030442K20Rik	RIKEN cDNA 6030442K20 gene	1.4	0.655	-1.17	0.657	-1.31	0.533	-1.17	0.779	-0.57
1428736_at	Gramd3	GRAM domain containing 3	-1.06	0.712	-1.11	0.462	1.16	0.478	-1.68	0.286	-0.67
1452946_a_at	3222401M22Rik	RIKEN cDNA 3222401M22 gene	1.24	0.487	-1	0.989	-1.29	0.03	-1.6	0.228	-0.66
1442343_at	Txndc11	Thioredoxin domain containing 11	-1.08	0.761	-1.66	0.067	1.48	0.357	-2.59	0.008	-0.96
1438794_x_at	Rps13 /// LOC6252	ribosomal protein S13 /// similar to ribosomal protein S13 /// similar to ribosomal p	-1.04	0.755	1.14	0.205	-1.09	0.544	-1.35	0.08	-0.59
1456943_a_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.09	0.871	1.32	0.694	-1.28	0.396	-1.7	0.222	-0.69
1445389_at	Zp3r	Zona pellucida 3 receptor	-1.14	0.886	-1.07	0.877	1.2	0.57	-1.29	0.66	-0.58
1456298_at	---	---	-1.23	0.634	1.41	0.582	-1.28	0.433	-1.36	0.537	-0.61
1452929_at	Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	1.09	0.355	-1.06	0.658	-1.03	0.882	-1.17	0.167	-0.54
1434710_at	Dhx29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	-1.02	0.667	1.06	0.458	-1.02	0.878	-1.26	0.242	-0.56
1441361_at	Mpdz	multiple PDZ domain protein	-2.24	0.405	1.57	0.095	-1	0.992	-2.2	0.055	-0.97
1451926_at	Mrgpra4	MAS-related GPR, member A4	1.49	0.527	-1.64	0.317	-1.09	0.854	-3.45	0.236	-1.17

1437877_at	Ccdc39 /// Ttc14	coiled-coil domain containing 39 /// tetratricopeptide repeat domain 14	-1.23	0.023	1.25	0.356	-1.04	0.682	-1.05	0.805	-0.52
1432177_a_at	Mnat1	menage a trois 1	1.06	0.646	-1.03	0.763	-1.01	0.941	-1.01	0.924	-0.5
1442896_at	Hspa12a	Heat shock protein 12A	1.62	0.218	-1.31	0.68	-1.57	0.4	-1.31	0.666	-0.65
1443487_at	AU022238	expressed sequence AU022238	-1.21	0.409	1.57	0.337	-1.62	0.434	-2.81	0.247	-1.02
1423973_a_at	Arf3	ADP-ribosylation factor 3	-1.1	0.599	-1.11	0.417	1.2	0.334	-1.15	0.685	-0.54
1460159_at	Mysm1	myb-like, SWIRM and MPN domains 1	1.31	0.679	-1.03	0.925	-1.37	0.234	-1.72	0.201	-0.7
1425570_at	Slamf1	signaling lymphocytic activation molecule family member 1	-1.64	0.244	-2.01	0.05	1.91	0.166	-1.46	0.175	-0.8
1456137_at	Nrxn3	neurexin III	1.66	0.228	-1.17	0.77	-2.01	0.263	-1.54	0.536	-0.77
1434934_at	Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	-1.03	0.717	-1	0.971	1.05	0.833	-1.41	0.008	-0.6
1444182_at	2210010C17Rik	RIKEN cDNA 2210010C17 gene	1.51	0.657	-1.13	0.864	-1.61	0.422	-1.73	0.016	-0.74
1444346_at	Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	1.82	0.52	-3.06	0.189	-1.15	0.527	-1.61	0.096	-1
1436903_at	Ubqln3	ubiquilin 3	-2.1	0.509	-1.14	0.737	1.66	0.331	-3.24	0.165	-1.2
1434277_a_at	6430570G24	Hypothetical protein 6430570G24	-1.07	0.834	1.24	0.474	-1.19	0.085	-1.06	0.875	-0.52
1456023_at	2210010B09Rik	RIKEN cDNA 2210010B09 gene	1.37	0.347	-1.1	0.81	-1.36	0.156	-1.56	0.137	-0.66
1415908_at	Tspyl1	testis-specific protein, Y-encoded-like 1	1.11	0.284	-1.01	0.91	-1.09	0.562	-1.11	0.752	-0.52
1449516_a_at	Rgs3	regulator of G-protein signaling 3	-1.07	0.769	-1.05	0.73	1.12	0.661	-1.07	0.824	-0.52
1419190_at	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	-1.01	0.969	-1.27	0.388	1.24	0.564	-1.14	0.639	-0.55
1435935_at	---	Transcribed locus	-1.4	0.269	1.47	0.026	-1.2	0.419	-1.55	0.088	-0.67
1438246_at	Csnk1g1	casein kinase 1, gamma 1	-1.19	0.36	-1.09	0.401	1.26	0.03	-1.08	0.4	-0.53
1427145_at	Iqsec1	IQ motif and Sec7 domain 1	-1.65	0.209	1.54	0.233	-1.15	0.618	-1.02	0.969	-0.57
1437532_at	2810055G22Rik ///	RIKEN cDNA 2810055G22 gene /// similar to ubiquitin conjugating enzyme 7 inte	-1.16	0.282	-1	0.933	1.16	0.195	-1.29	0.209	-0.57
1449738_s_at	Exosc8	Exosome component 8	-1.08	0.237	-1.03	0.73	1.12	0.511	-1.49	0.17	-0.62
1436556_at	Tmem139	transmembrane protein 139	-1.08	0.305	1.19	0.657	-1.11	0.699	-1.1	0.736	-0.53
1445414_at	---	Transcribed locus	-1.02	0.946	1.18	0.641	-1.17	0.574	-1.21	0.64	-0.55
1438106_at	Pcdhb22	protocadherin beta 22	-1.32	0.65	1.57	0.349	-1.45	0.185	-1.36	0.54	-0.64
1445422_at	LOC621549	hypothetical protein LOC621549	-1	0.99	1.23	0.466	-1.26	0.45	-1.52	0.263	-0.64
1444235_at	1700025G04Rik	RIKEN cDNA 1700025G04 gene	-1.01	0.983	1.06	0.804	-1.04	0.883	-1.36	0.49	-0.59
1450679_at	5730470L24Rik	RIKEN cDNA 5730470L24 gene	1.17	0.387	-1.04	0.788	-1.13	0.171	-1.44	0.24	-0.61
1424933_at	Myo5c	myosin VC	-1.06	0.786	1.27	0.63	-1.24	0.038	-1	0.999	-0.51
1417585_at	Nup210	nucleoporin 210	-1.05	0.764	-1.05	0.688	1.11	0.644	-1.04	0.577	-0.51
1431673_at	4930557A04Rik	RIKEN cDNA 4930557A04 gene	1.48	0.587	-1.64	0.496	-1.08	0.726	-2.84	0.35	-1.02
1426240_at	Chmp4b	chromatin modifying protein 4B	-1.11	0.165	1.14	0.415	-1.03	0.774	-1.15	0.361	-0.54
1428650_at	Tns1	tensin 1	-1.16	0.573	-1.11	0.678	1.25	0.39	-1	0.993	-0.5
1416820_at	Cdc37	cell division cycle 37 homolog (S. cerevisiae)	-1.9	0.278	1.56	0.541	-1.08	0.906	-1.5	0.22	-0.73
1419401_at	Asb13	ankyrin repeat and SOCS box-containing protein 13	-1.12	0.373	-1.02	0.874	1.14	0.441	-1.8	0.083	-0.7
1423532_at	Rnf44	ring finger protein 44	-1.12	0.238	-1.15	0.153	1.26	0.209	-1.32	0.283	-0.58
1427546_at	Abca8b	ATP-binding cassette, sub-family A (ABC1), member 8b	1.5	0.185	-1.38	0.216	-1.26	0.373	-1.05	0.881	-0.55
1448781_at	Nab1	Ngfi-A binding protein 1	1.14	0.72	-1.08	0.484	-1.05	0.848	-1.33	0.243	-0.58
1459212_at	Anapc11	anaphase promoting complex subunit 11 homolog (yeast)	1.3	0.593	-1.27	0.62	-1.08	0.878	-1.56	0.187	-0.65
1437400_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030(	-1.34	0.294	1.53	0.328	-1.35	0.223	-1.74	0.346	-0.72
1418299_at	Dpysl4	dihydropyrimidinase-like 4	1.29	0.314	-1.01	0.972	-1.36	0.681	-1.2	0.649	-0.57
1452204_at	Anks1	ankyrin repeat and SAM domain containing 1	-1.04	0.096	-1.17	0.371	1.2	0.314	-1.24	0.296	-0.56
1450885_at	Dffa	DNA fragmentation factor, alpha subunit	-1.11	0.474	-1.15	0.126	1.25	0.052	-1.04	0.819	-0.51
1457583_at	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	1.4	0.409	-1.01	0.935	-1.59	0.176	-1.11	0.702	-0.58
1434899_s_at	Tnrc6a	trinucleotide repeat containing 6a	1.14	0.203	-1.02	0.889	-1.11	0.343	-1.46	0.028	-0.61
1423922_s_at	Ints3	integrator complex subunit 3	-1.1	0.636	-1.01	0.895	1.12	0.31	-1.24	0.1	-0.56
1457266_at	AW322671	expressed sequence AW322671	-1.09	0.58	1.25	0.05	-1.16	0.108	-1.19	0.565	-0.55
1437291_at	2700081O15Rik	RIKEN cDNA 2700081O15 gene	-1.05	0.626	1.18	0.696	-1.13	0.688	-1.53	0.18	-0.63
1439952_at	3110082M05Rik	RIKEN cDNA 3110082M05 gene	1.37	0.494	-1.09	0.762	-1.37	0.359	-1.5	0.074	-0.65
1429310_at	Flrt3	fibronectin leucine rich transmembrane protein 3	1.61	0.429	-1.4	0.129	-1.44	0.102	-1.59	0.18	-0.71
1453480_at	D630002J15Rik	RIKEN cDNA D630002J15 gene	-1.12	0.504	1.25	0.055	-1.14	0.54	-1.68	0.128	-0.67
1431579_at	4933421D24Rik	RIKEN cDNA 4933421D24 gene	1.36	0.291	-1.18	0.272	-1.22	0.303	-2.1	0.105	-0.79
1418492_at	Grem2	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	1.38	0.602	-1.37	0.331	-1.1	0.75	-1.08	0.812	-0.54

1434821_at	Brd1	bromodomain containing 1	-1.11	0.474	-1.09	0.394	1.2	0.34	-1.15	0.257	-0.54
1433514_at	Etnk1	ethanolamine kinase 1	-1.13	0.306	1.14	0.37	-1.01	0.946	-1.53	0.275	-0.63
1424597_at	ORF19	open reading frame 19	-1.12	0.351	-1.02	0.739	1.15	0.062	-1.23	0.191	-0.56
1458662_at	Daam1	dishevelled associated activator of morphogenesis 1	-1.13	0.839	-2.75	0.073	1.77	0.187	-1.12	0.824	-0.81
1417558_at	Fyn	Fyn proto-oncogene	-1.11	0.412	1.14	0.344	-1.02	0.917	-1.26	0.599	-0.56
1457158_at	0610039J04Rik	RIKEN cDNA 0610039J04 gene	-1.1	0.793	1.45	0.541	-1.5	0.01	-3.51	0.278	-1.17
1454281_at	4930506C02Rik	RIKEN cDNA 4930506C02 gene	-1.15	0.024	1.52	0.241	-1.6	0.225	-1.26	0.621	-0.62
1457101_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430035F	-1.54	0.034	1.95	0.438	-2.35	0.262	-1.23	0.625	-0.79
1449103_at	Tex101	testis expressed gene 101	1.26	0.613	-1.12	0.814	-1.15	0.65	-1.25	0.473	-0.57
1432929_at	4930453O09Rik	RIKEN cDNA 4930453O09 gene	1.36	0.09	-1.15	0.794	-1.26	0.404	-1.08	0.687	-0.53
1433191_at	A430105P17Rik	RIKEN cDNA A430105P17 gene	-1.37	0.531	1.79	0.397	-1.98	0.177	-1.21	0.546	-0.7
1458899_at	Usp53	ubiquitin specific peptidase 53	1.54	0.26	-1.36	0.171	-1.33	0.303	-1.29	0.346	-0.61
1426778_at	Dag1	dystroglycan 1	-1.04	0.788	1.1	0.082	-1.03	0.856	-1.19	0.234	-0.54
1428020_at	Bxdc5	brix domain containing 5	1.64	0.253	-2.31	0.33	-1.05	0.935	-2.55	0.101	-1.07
1428724_at	Pcf11	cleavage and polyadenylation factor subunit homolog (S. cerevisiae)	-1.27	0.091	-1.14	0.688	1.35	0.272	-1.11	0.565	-0.54
1458999_at	Mrps10	Mitochondrial ribosomal protein S10	-1.35	0.743	1.85	0.267	-2.32	0.018	-1.5	0.193	-0.83
1455347_at	Rtel1	regulator of telomere elongation helicase 1	1.24	0.84	-1.04	0.951	-1.22	0.143	-1.03	0.911	-0.51
1437921_x_at	Zfp516	zinc finger protein 516	-1	1	-1.05	0.744	1.07	0.721	-1.44	0.102	-0.6
1431221_at	5830405M20Rik	RIKEN cDNA 5830405M20 gene	-1.03	0.905	-1.34	0.361	1.3	0.522	-1.64	0.024	-0.68
1416243_a_at	Rpl35	ribosomal protein L35	-1.05	0.389	1.14	0.146	-1.08	0.547	-1.46	0.011	-0.61
AFFX-r2-Bs-phe-3_a	---	---	1.09	0.867	-1.04	0.729	-1.03	0.915	-1.45	0.428	-0.61
1450843_a_at	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	-1.03	0.876	1.32	0.168	-1.37	0.278	-1.18	0.414	-0.56
1457456_at	Map3k10	mitogen activated protein kinase kinase kinase 10	-1.35	0.637	-1.56	0.132	1.64	0.406	-3.28	0.205	-1.14
1456900_at	---	---	1.32	0.451	-1.07	0.713	-1.31	0.008	-1.7	0.006	-0.69
1424569_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1.23	0.067	-1.25	0.062	-1.01	0.925	-1.12	0.427	-0.54
1435821_s_at	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8	-1.01	0.762	1.11	0.309	-1.07	0.699	-1.15	0.496	-0.53
1440767_at	Defb41	defensin beta 41	1.18	0.706	-1.11	0.812	-1.06	0.893	-1.97	0.274	-0.74
1417039_a_at	Cul7	cullin 7	-1.03	0.616	-1.07	0.552	1.12	0.468	-1.02	0.901	-0.5
1435315_s_at	2900034E22Rik	RIKEN cDNA 2900034E22 gene	-1.15	0.224	1.44	0.161	-1.39	0.016	-1.2	0.521	-0.58
1455845_at	BC030477	cDNA sequence BC030477	1.21	0.682	-1.14	0.611	-1.07	0.819	-1.15	0.378	-0.54
1423613_at	---	---	-1.07	0.606	-1.02	0.837	1.11	0.524	-1.48	0.092	-0.61
1451149_at	Pgm2	phosphoglucomutase 2	-1.11	0.199	-1.07	0.453	1.19	0.236	-1.25	0.237	-0.56
1427570_at	Srpr	signal recognition particle receptor ('docking protein')	-1.46	0.353	-1.15	0.765	1.47	0.4	-1.62	0.5	-0.69
1438547_x_at	Tor2a	torsin family 2, member A	-1.01	0.963	1.14	0.152	-1.11	0.556	-1.29	0.177	-0.57
1456687_at	Rp9h	Retinitis pigmentosa 9 homolog (human)	1.17	0.724	-1.06	0.819	-1.1	0.357	-1.47	0.275	-0.62
1425617_at	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-1.05	0.719	-1.21	0.056	1.25	0.354	-1.39	0.255	-0.6
1428034_a_at	Tnfrsf9	tumor necrosis factor receptor superfamily, member 9	-1.78	0.363	-1.44	0.685	1.77	0.078	-2.41	0.218	-0.97
1456858_at	Gpr149	G protein-coupled receptor 149	1.06	0.645	-1.02	0.961	-1.01	0.983	-1.99	0.322	-0.74
1435838_at	Agxt2	alanine-glyoxylate aminotransferase 2	-1.91	0.004	-1.03	0.85	1.53	0.212	-1.15	0.524	-0.64
1424974_at	Zfp418	zinc finger protein 418	-1.15	0.722	1.36	0.174	-1.26	0.088	-1.72	0.26	-0.69
1460240_a_at	Hnrpc	heterogeneous nuclear ribonucleoprotein C	-1.02	0.269	1.13	0.096	-1.09	0.475	-1.04	0.693	-0.51
1440243_at	Cpne7	copine VII	-1.22	0.815	-1.18	0.823	1.35	0.535	-1.43	0.056	-0.62
1437808_x_at	Il10ra	Interleukin 10 receptor, alpha	1.6	0.286	-1.78	0.209	-1.16	0.724	-1.03	0.787	-0.59
1427585_at	---	---	-1.44	0.66	-1.78	0.441	1.77	0.143	-1.05	0.943	-0.63
1420772_a_at	Tsc22d3	TSC22 domain family 3	1.19	0.781	-1.08	0.623	-1.09	0.741	-1.75	0.229	-0.69
1437913_at	Bcl2a1a /// Bcl2a1b	B-cell leukemia/lymphoma 2 related protein A1a /// B-cell leukemia/lymphoma 2 r	1.73	0.401	-3.32	0.063	-1.01	0.991	-1.23	0.601	-0.95
1455547_at	Zc3h7b	zinc finger CCCH type containing 7B	-3.74	0.391	-1.88	0.247	2.23	0.349	-2.82	0.317	-1.55
1447725_at	C030034E14Rik	RIKEN cDNA C030034E14 gene	1.31	0.065	-1.08	0.868	-1.27	0.231	-1.06	0.899	-0.52
1454856_x_at	Rpl35	ribosomal protein L35	-1.02	0.754	1.18	0.24	-1.15	0.268	-1.27	0.029	-0.56
1432345_at	1700048F04Rik	RIKEN cDNA 1700048F04 gene	-1.36	0.609	1.44	0.158	-1.18	0.572	-1.04	0.93	-0.53
1452091_a_at	Rbm28	RNA binding motif protein 28	-1.01	0.945	-1.02	0.674	1.06	0.754	-1.57	0.107	-0.64
1458916_at	Slc12a6	Solute carrier family 12, member 6	-1.26	0.133	1.69	0.114	-1.85	0.049	-1.62	0.061	-0.76
1449376_at	Nicn1	nicolin 1	-1.05	0.785	-1.05	0.77	1.12	0.669	-1.18	0.547	-0.54

1438214_at	Trps1	trichorhinophalangeal syndrome I (human)	1.51	0.237	-1.15	0.504	-1.56	0.197	-1.22	0.61	-0.6
1440505_at	Plcxd1	phosphatidylinositol-specific phospholipase C, X domain containing 1	-1.05	0.917	1.15	0.622	-1.08	0.887	-1.65	0.554	-0.66
1448270_at	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	-1.02	0.945	-1.02	0.827	1.07	0.748	-1.09	0.302	-0.52
1428527_at	Snx7	sorting nexin 7	-1.04	0.697	1.19	0.224	-1.14	0.278	-1.08	0.769	-0.52
1415814_at	Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.18	0.29	-1.01	0.946	1.18	0.249	-1.08	0.373	-0.52
1452034_at	Prepl	prolyl endopeptidase-like	1.15	0.209	-1.09	0.565	-1.04	0.896	-1.21	0.126	-0.55
1423659_a_at	Tbc1d17	TBC1 domain family, member 17	-1.06	0.842	-1.03	0.681	1.11	0.509	-1.15	0.395	-0.53
1435515_at	---	Transcribed locus	1.36	0.629	-1.38	0.494	-1.06	0.885	-2.72	0.114	-0.95
1416055_at	Amy2 /// 1810008N	amylase 2, pancreatic /// RIKEN cDNA 1810008N23 gene	1.3	0.486	-1.07	0.929	-1.25	0.643	-1.73	0.451	-0.69
1425189_a_at	Mrpl15	mitochondrial ribosomal protein L15	-1.09	0.222	-1.03	0.757	1.15	0.45	-1.01	0.94	-0.5
1444827_at	Btbd9	BTB (POZ) domain containing 9	1.3	0.545	-1.12	0.785	-1.2	0.39	-1.24	0.492	-0.56
1449422_at	Cdh4	cadherin 4	-1.05	0.894	-1.05	0.872	1.12	0.605	-1.3	0.208	-0.57
1427458_at	Bmp1	bone morphogenetic protein 1	1.57	0.352	-1.02	0.806	-2.08	0.132	-1.42	0.308	-0.74
1428131_a_at	Cdc42se1	CDC42 small effector 1	-1.12	0.474	-1.02	0.881	1.15	0.074	-1.73	0.073	-0.68
1424827_a_at	Csnk1a1	casein kinase 1, alpha 1	-1.03	0.757	1.1	0.347	-1.04	0.494	-1	0.966	-0.49
1443695_at	Habp2	hyaluronic acid binding protein 2	-1.23	0.244	-1.29	0.024	1.44	0.445	-3.51	0.213	-1.15
1444625_at	LOC545822	Hypothetical LOC545822	-1.58	0.379	-1.17	0.534	1.54	0.132	-1.68	0.423	-0.72
1447976_at	AI596198	expressed sequence AI596198	-1.11	0.571	1.45	0.05	-1.46	0.275	-1.16	0.457	-0.57
1454840_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	-1	0.971	-1.33	0.09	1.28	0.019	-1.31	0.3	-0.59
1458170_at	---	---	-1.45	0.395	-1	1	1.34	0.251	-2.06	0.227	-0.79
1447234_s_at	Snx6	sorting nexin 6	-1.04	0.05	1.27	0.015	-1.25	0.063	-1.57	0.047	-0.65
1446757_at	Sugt1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	-1.65	0.216	1.61	0.451	-1.24	0.452	-1.85	0.044	-0.78
1416607_at	4931406C07Rik	RIKEN cDNA 4931406C07 gene	-1.08	0.123	-1.14	0.311	1.22	0.214	-1.27	0.434	-0.57
1450268_at	Fign	fidgetin	-1.07	0.798	-1.26	0.383	1.3	0.319	-1.16	0.632	-0.55
1427476_a_at	Trim32	tripartite motif protein 32	1.04	0.893	-1.01	0.976	-1	0.993	-1.2	0.508	-0.54
1428156_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	-1.14	0.641	1.5	0.237	-1.53	0.092	-1.11	0.797	-0.57
1456351_at	Brd8	bromodomain containing 8	-1.02	0.933	1.22	0.587	-1.21	0.38	-1.02	0.911	-0.51
1439000_at	Acsbg2	acyl-CoA synthetase bubblegum family member 2	1.43	0.385	-1.01	0.989	-1.64	0.38	-2.15	0.48	-0.84
1446055_at	---	---	-1.2	0.074	-1.08	0.762	1.27	0.424	-1.31	0.424	-0.58
1459042_at	Rims3	regulating synaptic membrane exocytosis 3	1.12	0.854	-1.03	0.894	-1.07	0.848	-1.06	0.881	-0.51
1435368_a_at	Parp1	poly (ADP-ribose) polymerase family, member 1	-1.16	0.074	-1.01	0.945	1.17	0.461	-1.35	0.052	-0.59
1456016_x_at	BC005624	CDNA sequence BC005624	-1.19	0.363	-1.52	0.035	1.53	0.42	-1.07	0.707	-0.56
1443941_at	LOC433886	hypothetical gene supported by AK049058; BC025881	1.21	0.157	-1	0.996	-1.22	0.433	-1.54	0.361	-0.64
1443378_s_at	Mapkapk5 /// Adam	MAP kinase-activated protein kinase 5 /// a disintegrin and metallopeptidase dom	-1.28	0.448	-1.6	0.512	1.62	0.213	-1.17	0.453	-0.61
1431627_at	Kif27	kinesin family member 27	-1.03	#DIV/0!	1.36	0.004	-1.42	0.367	-1.02	0.729	-0.53
1428957_at	2300008B03Rik	RIKEN cDNA 2300008B03 gene	-1.06	0.67	-1.14	0.621	1.21	0.489	-1.18	0.542	-0.54
1415679_at	Psenen	presenilin enhancer 2 homolog (C. elegans)	-1.01	0.841	-1.04	0.253	1.09	0.519	-1.26	0.157	-0.56
1436760_a_at	Rps8	ribosomal protein S8	-1.06	0.576	1.13	0.082	-1.05	0.671	-1.29	0.027	-0.57
1416248_at	Nadk	NAD kinase	-1.06	0.185	-1.09	0.274	1.17	0.357	-1.42	0.074	-0.6
1419044_at	Cntnap4	contactin associated protein 4	-1.05	0.64	1.38	0.568	-1.45	0.175	-1.23	0.534	-0.59
1450048_a_at	Idh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-1.1	0.094	-1.21	0.534	1.29	0.21	-1.22	0.143	-0.56
1422049_at	Nkx1-2	NK1 transcription factor related, locus 2 (Drosophila)	-4.73	0.023	-1.36	0.527	2.08	0.154	-1	0.999	-1.25
1422871_at	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	-1.07	0.881	-1.41	0.595	1.39	0.266	-1.01	0.99	-0.53
1458457_at	---	---	1.11	0.279	-1.05	0.7	-1.03	0.91	-1.19	0.696	-0.54
1444309_at	Suclg2	Succinate-Coenzyme A ligase, GDP-forming, beta subunit	1.18	0.664	-1.16	0.769	-1.01	0.98	-1.37	0.411	-0.59
1428425_at	Tgfbrap1	transforming growth factor, beta receptor associated protein 1	-1.23	0.074	-1.26	0.011	1.42	0.023	-1.03	0.83	-0.52
1433405_at	---	---	-1.05	0.761	-1.25	0.612	1.28	0.494	-1.44	0.412	-0.62
1438799_at	Dlx6os1	Dlx6 opposite strand transcript 1	-1.64	0.327	1.58	0.372	-1.2	0.645	-1.75	0.2	-0.75
1422901_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	-1.2	0.157	-1.14	0.31	1.32	0.191	-1.14	0.391	-0.54
1439204_at	Scn3a	sodium channel, voltage-gated, type III, alpha	-1.39	0.678	1.76	0.387	-1.81	0.036	-3.29	0.018	-1.18
1419185_a_at	Mlxipl	MLX interacting protein-like	-1.27	0.103	-1.23	0.268	1.43	0.667	-2.07	0.287	-0.78
1457691_at	Ebi2	Epstein-Barr virus induced gene 2	-1.3	0.681	1.34	0.482	-1.09	0.769	-1.62	0.338	-0.67
1434236_at	Zdhhc20	zinc finger, DHHC domain containing 20	1.15	0.513	-1.1	0.333	-1.03	0.774	-1.76	0.093	-0.68

1437335_x_at	Poldip3	polymerase (DNA-directed), delta interacting protein 3	-1.22	0.001	-1.06	0.239	1.26	0.122	-1.06	0.561	-0.52
1416177_at	Rbmxrt	RNA binding motif protein, X chromosome retrogene	-1.02	0.763	1.11	0.167	-1.06	0.653	-1.09	0.576	-0.51
1424157_at	Ehd2 /// LOC67325	EH-domain containing 2 /// similar to EH-domain containing 2	-1.1	0.741	-1.33	0.379	1.37	0.358	-1.44	0.02	-0.63
1422712_a_at	Ube2i	ubiquitin-conjugating enzyme E2I	-1.03	0.791	-1.03	0.825	1.09	0.452	-1.04	0.717	-0.5
1428846_at	Ttc14	tetratricopeptide repeat domain 14	-1.07	0.782	-1.1	0.382	1.19	0.448	-1.26	0.297	-0.56
1433975_at	Cdk10	cyclin-dependent kinase (CDC2-like) 10	-1	0.979	-1.03	0.467	1.07	0.169	-1.1	0.627	-0.52
1437216_at	A430106J12Rik	RIKEN cDNA A430106J12 gene	-1.01	0.946	1.35	0.102	-1.44	0.014	-1.34	0.24	-0.61
1435141_at	Sft2d2	SFT2 domain containing 2	-1.09	0.525	-1.02	0.864	1.13	0.231	-1.27	0.262	-0.56
1422053_at	Inhba	inhibin beta-A	-1.63	0.57	-1.22	0.715	1.6	0.465	-2.63	0.035	-0.97
1454234_at	Wbscr28	Williams-Beuren syndrome chromosome region 28 (human)	-1.91	0.293	1.69	0.131	-1.23	0.194	-1.01	0.985	-0.61
1417419_at	Ccnd1	cyclin D1	1.5	0.331	-1.67	0.048	-1.07	0.82	-1.58	0.327	-0.7
1435896_at	Sfxn2 /// LOC67714	sideroflexin 2 /// similar to Sideroflexin-2	-1	0.953	-1	0.989	1.04	0.83	-1.11	0.339	-0.52
1437419_at	Bmp2k	BMP2 inducible kinase	-1.11	0.321	-1.15	0.268	1.26	0.174	-1.52	0.05	-0.63
1447459_at	Aatf	Apoptosis antagonizing transcription factor	1.44	0.356	-1.32	0.45	-1.19	0.298	-1.21	0.377	-0.57
1415743_at	Hdac5	histone deacetylase 5	-1	0.99	-1	0.979	1.04	0.696	-1.2	0.624	-0.54
1423069_at	Adnp	activity-dependent neuroprotective protein	-1.02	0.445	-1.02	0.838	1.07	0.5	-1.13	0.266	-0.52
1424967_x_at	Tnnt2	troponin T2, cardiac	-1.32	0.762	1.32	0.527	-1.05	0.824	-1.15	0.802	-0.55
1448622_at	Lsm4	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.14	0.232	-1.07	0.268	1.22	0.147	-1.32	0.334	-0.58
1445376_at	Spast	Spastin	-2.8	0.467	-1.41	0.535	1.97	0.332	-1.12	0.827	-0.84
1426342_at	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisia	-1.02	0.788	1.13	0.387	-1.09	0.475	-1.08	0.298	-0.51
1434405_at	A730024A03Rik	RIKEN cDNA A730024A03 gene	1.22	0.114	-1.1	0.5	-1.11	0.278	-1	0.991	-0.5
1415953_s_at	Mark2	MAP/microtubule affinity-regulating kinase 2	-1.24	0.374	-1.1	0.421	1.32	0.249	-1.07	0.711	-0.52
1444006_at	Setd2	SET domain containing 2	1.51	0.082	-1.23	0.542	-1.42	0.021	-1.15	0.646	-0.57
1424420_at	Ccpg1	cell cycle progression 1	-1.06	0.602	1.19	0.245	-1.12	0.441	-1.07	0.763	-0.51
1437243_at	D2hgdh /// LOC673	D-2-hydroxyglutarate dehydrogenase /// similar to CG3835-PA, isoform A	-1.22	0.271	-1.1	0.41	1.31	0.264	-1.28	0.353	-0.57
1435875_at	Prkab2	protein kinase, AMP-activated, beta 2 non-catalytic subunit	-1.21	0.469	1.23	0.234	-1.02	0.866	-1.26	0.285	-0.56
1419927_s_at	Rabif	RAB interacting factor	1.18	0.209	-1.05	0.568	-1.12	0.471	-1.08	0.701	-0.51
1433850_at	Ppp4r2 /// LOC627	protein phosphatase 4, regulatory subunit 2 /// similar to protein phosphatase 4, r	1.07	0.351	-1	0.983	-1.03	0.356	-1.05	0.532	-0.51
1421328_at	Mtap2 /// A730034C	microtubule-associated protein 2 /// hypothetical protein A730034C02	1.34	0.503	-1.07	0.864	-1.32	0.106	-1.02	0.9	-0.52
1426606_at	Crtac1	cartilage acidic protein 1	1.17	0.778	-1.02	0.978	-1.12	0.547	-1.53	0.087	-0.63
1448667_x_at	Tob2	transducer of ERBB2, 2	-1.22	0.372	-1.11	0.383	1.31	0.061	-1.18	0.622	-0.55
1428119_a_at	Rap2c	RAP2C, member of RAS oncogene family	-1	0.999	-1.19	0.134	1.19	0.065	-1.05	0.673	-0.51
1444388_at	---	Transcribed locus	-1.87	0.214	-1.33	0.561	1.75	0.063	-1.4	0.444	-0.71
1445489_at	5830472M02Rik	RIKEN cDNA 5830472M02 gene	1.68	0.407	-1.75	0.009	-1.28	0.456	-1.22	0.625	-0.64
1438356_x_at	4933432K03Rik	RIKEN cDNA 4933432K03 gene	-1.01	0.932	-1.05	0.871	1.09	0.674	-1.52	0.069	-0.62
1418869_a_at	Pus1	pseudouridine synthase 1	-1.29	0.031	-1.35	0.005	1.52	0.041	-1.17	0.426	-0.57
1441471_at	2810002D19Rik	RIKEN cDNA 2810002D19 gene	-1	0.943	1.24	0.587	-1.25	0.225	-1.19	0.223	-0.55
1453298_at	Ptpn21	protein tyrosine phosphatase, non-receptor type 21	1.64	0.292	-1.61	0.283	-1.29	0.199	-1.53	0.241	-0.7
1430260_at	---	---	1.26	0.658	-1.21	0.706	-1.05	0.781	-1.41	0.503	-0.6
1419799_at	Psmd1	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	-1.46	0.645	-1.66	0.172	1.74	0.191	-1.52	0.662	-0.72
1422759_a_at	Xpo6	exportin 6	-1.19	0.051	-1.15	0.312	1.33	0.056	-1.39	0.186	-0.6
1440349_at	Dmtf1	Cyclin D binding myb-like transcription factor 1	-1.16	0.361	1.3	0.109	-1.14	0.419	-1.39	0.246	-0.6
1440140_at	Nfic	Nuclear factor I/C	1.73	0.26	-1.52	0.066	-1.53	0.366	-1.58	0.332	-0.73
1431530_a_at	Tspan5	tetraspanin 5	-1.01	0.99	1.05	0.946	-1.01	0.979	-2.01	0.159	-0.74
1439686_at	Mbnl1	Muscleblind-like 1 (Drosophila)	1.59	0.121	-1.11	0.57	-1.83	0.002	-1.52	0.358	-0.72
1453770_at	Cpa4	carboxypeptidase A4	-1.11	0.766	-2.24	0.073	1.69	0.287	-2.4	0.007	-1.02
1449206_at	Sypl2	synaptophysin-like 2	-1.12	0.637	-1.29	0.269	1.36	0.482	-1.18	0.642	-0.55
1420678_a_at	Il17rb	interleukin 17 receptor B	-1.38	0.083	1.36	0.089	-1.05	0.868	-1.3	0.001	-0.59
1442628_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930002E	-1.04	0.784	1.3	0.392	-1.3	0.29	-1.13	0.767	-0.54
1435923_at	Gm237	gene model 237, (NCBI)	-1.01	0.915	1.12	0.211	-1.09	0.112	-1.09	0.559	-0.51
1423984_a_at	Mrg2 /// LOC67077	myeloid ecotropic viral integration site-related gene 2 /// similar to Homeobox prot	1.2	0.417	-1.15	0.65	-1.03	0.794	-1.7	0.262	-0.67
1447605_at	Zfp457	Zinc finger protein 457	1.38	0.581	-1.52	0.521	-1	0.998	-1.43	0.303	-0.64
1436697_at	---	Transcribed locus	1.15	0.696	-1.01	0.943	-1.12	0.575	-1.72	0.117	-0.67

1422576_at	Atxn10	ataxin 10	-1.05	0.252	-1.06	0.297	1.14	0.104	-1.07	0.436	-0.51
1421522_at	B4galnt2	beta-1,4-N-acetyl-galactosaminyl transferase 2	-1.65	0.427	1.78	0.043	-1.54	0.356	-1.35	0.688	-0.69
1422835_at	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	-1.52	0.472	-1.1	0.886	1.47	0.609	-1.11	0.893	-0.56
1458173_at	Centd1	Centaurin, delta 1	1.42	0.702	-1.3	0.676	-1.18	0.673	-1.64	0.315	-0.67
1416776_at	Crym	crystallin, mu	-1.22	0.422	1.23	0.406	-1.01	0.975	-3.33	0.152	-1.08
1460394_a_at	Inppl1	inositol polyphosphate phosphatase-like 1	-1.25	0.092	-1.15	0.111	1.37	0.065	-1.36	0.168	-0.6
1426023_a_at	Rabep1	rabaptin, RAB GTPase binding effector protein 1	-1	0.989	-1.17	0.24	1.19	0.401	-1.41	0.176	-0.6
1437840_s_at	LOC673662	similar to CG3835-PA, isoform A	-1.09	0.607	-1.15	0.133	1.25	0.023	-1.2	0.35	-0.55
1419362_at	Mrpl35	mitochondrial ribosomal protein L35	-1.01	0.961	-1.13	0.416	1.16	0.421	-1.33	0.096	-0.58
1436571_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930525M22 pr	-1.08	0.136	-1.06	0.653	1.17	0.075	-1.41	0.049	-0.59
1458952_at	Wdfy3	WD repeat and FYVE domain containing 3	-1.55	0.19	1.43	0.451	-1.04	0.93	-1.35	0.107	-0.63
1453618_at	4933424N20Rik	RIKEN cDNA 4933424N20 gene	-1.06	0.67	1.14	0.336	-1.04	0.727	-1	0.996	-0.49
1446330_at	---	---	1.62	0.015	-1.21	0.499	-1.68	0.16	-1.67	0.315	-0.74
1423966_at	Cd99l2	Cd99 antigen-like 2	1.64	0.366	-1.56	0.1	-1.31	0.233	-1.08	0.672	-0.58
1454400_at	4632432E15Rik	RIKEN cDNA 4632432E15 gene	1.48	0.49	-1.6	0.527	-1.07	0.917	-1.3	0.407	-0.62
1438315_x_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	-1.02	0.826	-1.15	0.476	1.19	0.139	-1.21	0.322	-0.55
1427784_at	Defb13	defensin beta 13	-1.27	0.649	1.61	0.546	-1.55	0.209	-2.25	0.477	-0.87
1419340_at	Mov10l1	Moloney leukemia virus 10-like 1	-1.04	0.951	-1.04	0.952	1.11	0.733	-1.38	0.583	-0.59
1450963_at	Hnrpf	heterogeneous nuclear ribonucleoprotein F	-1.12	0.275	-1.08	0.223	1.22	0.119	-1.22	0.12	-0.55
1445711_at	BB163080	expressed sequence BB163080	1.61	0.224	-1.1	0.731	-1.92	0.028	-2.44	0.102	-0.96
1438365_x_at	Laptm4b	lysosomal-associated protein transmembrane 4B	1.09	0.16	-1.02	0.902	-1.04	0.766	-1.1	0.508	-0.52
1431129_at	Usp31	ubiquitin specific peptidase 31	-1.15	0.178	1.18	0.58	-1.01	0.967	-1.07	0.383	-0.51
1459209_at	Rnf10	Ring finger protein 10	-1.2	0.772	-1.51	0.374	1.54	0.466	-1.82	0.079	-0.74
1455611_at	Pias1	protein inhibitor of activated STAT 1	-1.06	0.806	1.18	0.465	-1.08	0.454	-1.02	0.909	-0.5
1449300_at	Cttnbp2nl	CTTNBP2 N-terminal like	1.13	0.651	-1.07	0.716	-1.02	0.93	-1.2	0.173	-0.54
1424752_x_at	Zfp71-rs1	zinc finger protein 71, related sequence 1	-1.06	0.349	1.2	0.003	-1.12	0.104	-1.46	0.105	-0.61
1428973_s_at	0610012D17Rik	RIKEN cDNA 0610012D17 gene	-1.29	0.173	1.39	0.318	-1.15	0.525	-1.32	0.272	-0.59
1422057_at	Nodal	nodal	-1.77	0.319	1.55	0.296	-1.08	0.077	-1.4	0.594	-0.67
1429350_at	1700027M21Rik	RIKEN cDNA 1700027M21 gene	-1.66	0.399	1.55	0.519	-1.13	0.779	-2.25	0.331	-0.87
1457124_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.05	0.722	-1.25	0.657	1.29	0.594	-1.25	0.565	-0.57
1451357_at	E130307M08Rik	RIKEN cDNA E130307M08 gene	-1.13	0.321	1.21	0.161	-1.06	0.615	-2.24	0.112	-0.8
1448010_at	A430104N18Rik	RIKEN cDNA A430104N18 gene	-1.29	0.333	-1.22	0.598	1.44	0.252	-2.33	0.11	-0.85
1415756_a_at	Snapap	SNAP-associated protein	-1	0.987	1.13	0.029	-1.1	0.207	-1.25	0.274	-0.55
1450187_a_at	Galt	galactose-1-phosphate uridyl transferase	-1.07	0.365	-1.06	0.602	1.16	0.039	-1.38	0.001	-0.59
1446543_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	-1.35	0.169	-1.04	0.902	1.34	0.338	-1.19	0.466	-0.56
1430656_a_at	Asnsd1	asparagine synthetase domain containing 1	-1.09	0.243	-1.07	0.243	1.19	0.193	-1.23	0.062	-0.55
1454147_at	2810429I04Rik	RIKEN cDNA 2810429I04 gene	1.71	0.379	-2.44	0.284	-1.08	0.833	-1.56	0.298	-0.84
1459213_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	-1.1	0.602	1.24	0.457	-1.12	0.653	-1.54	0.495	-0.63
1440870_at	Prdm16	PR domain containing 16	1.16	0.324	-1.03	0.909	-1.1	0.458	-1.3	0.066	-0.57
1425487_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	-1.06	0.851	-1.29	0.183	1.33	0.411	-1	0.992	-0.51
1438945_x_at	Gja1	gap junction membrane channel protein alpha 1	-1.32	0.52	1.59	0.067	-1.45	0.093	-1.48	0.08	-0.66
1456499_at	LOC552912	hypothetical LOC552912	-1.04	0.906	-1.51	0.397	1.42	0.032	-2	0.351	-0.78
1429248_at	2810002N01Rik	RIKEN cDNA 2810002N01 gene	1.16	0.445	-1.07	0.469	-1.06	0.46	-1.02	0.874	-0.5
1423345_at	Degs1	degenerative spermatocyte homolog 1 (Drosophila)	-1.05	0.352	1.14	0.372	-1.05	0.738	-1.04	0.601	-0.5
1456482_at	Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	-1.04	0.862	1.28	0.171	-1.25	0.328	-1.48	0.021	-0.62
1419127_at	Npy	neuropeptide Y	1.43	0.361	-1.46	0.428	-1.08	0.866	-1.69	0.172	-0.7
1439036_a_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-1.11	0.473	-1.04	0.511	1.18	0.225	-2.99	0.02	-0.99
1439191_at	---	---	-1.03	0.639	1.52	0.539	-1.81	0.127	-1.33	0.502	-0.66
1444918_at	---	---	-1.49	0.688	-1.69	0.299	1.78	0.043	-1.38	0.517	-0.7
1416139_at	Reg2	regenerating islet-derived 2	-1.15	0.178	1.38	0.545	-1.26	0.594	-1.11	0.654	-0.54
1459132_at	Bnc2	basonuclin 2	-1.12	0.871	1.29	0.449	-1.15	0.715	-1.18	0.605	-0.54
1456681_at	AI848149	expressed sequence AI848149	-1.04	0.828	1.32	0.503	-1.31	0.253	-1.35	0.407	-0.59
1422897_at	Slc22a12	solute carrier family 22 (organic anion/cation transporter), member 12	-1.34	0.093	-2.45	0.367	1.89	0.28	-1.05	0.958	-0.74

1449891_a_at	Dcbld2	discoidin, CUB and LCCL domain containing 2	1.61	0.036	-1.62	0.049	-1.23	0.587	-1.32	0.613	-0.64
1430866_at	4921537D05Rik	RIKEN cDNA 4921537D05 gene	-1.02	0.953	1.16	0.683	-1.1	0.634	-1.57	0.458	-0.63
1457502_at	Qk	Quaking	-1.55	0.349	-1.25	0.499	1.6	0.164	-1.51	0.386	-0.68
1429008_at	1810074P20Rik	RIKEN cDNA 1810074P20 gene	-1.01	0.9	-1.08	0.725	1.12	0.359	-1.38	0.112	-0.59
1452649_at	Rtn4	reticulon 4	-1.07	0.586	-1.02	0.821	1.14	0.132	-1.07	0.666	-0.51
1420765_a_at	Foxp3	forkhead box P3	-1.1	0.572	1.34	0.683	-1.26	0.379	-1.25	0.456	-0.57
1426380_at	Eif4b	eukaryotic translation initiation factor 4B	-1.02	0.864	-1.12	0.202	1.17	0.288	-1.13	0.462	-0.52
1451818_at	Mib1	mindbomb homolog 1 (Drosophila)	-1.24	0.605	-1.07	0.705	1.31	0.097	-1.23	0.326	-0.56
1447852_x_at	2900002H16Rik	RIKEN cDNA 2900002H16 gene	-1.27	0.205	1.43	0.094	-1.21	0.151	-1.48	0.098	-0.63
1451299_at	Prkx	protein kinase, X-linked	-1.09	0.064	1.18	0.059	-1.05	0.634	-1.03	0.934	-0.5
1427608_a_at	Tcrg-C	T-cell receptor gamma, constant region	1.43	0.136	-1.57	0.111	-1.02	0.9	-1.51	0.137	-0.67
1427064_a_at	Scrib	scribbled homolog (Drosophila)	-1.07	0.556	-1.13	0.561	1.23	0.337	-1.05	0.712	-0.51
1460669_at	Ilf3	interleukin enhancer binding factor 3	-1.19	0.064	-1.04	0.868	1.24	0.307	-1.27	0.11	-0.56
1424929_a_at	Trim26	tripartite motif protein 26	-1.09	0.575	-1.13	0.172	1.24	0.091	-1.19	0.498	-0.54
1431137_at	Rusc1	RUN and SH3 domain containing 1	-1.4	0.277	-1.35	0.318	1.59	0.319	-1.2	0.635	-0.59
1428252_at	Chmp2b	chromatin modifying protein 2B	-1.13	0.399	1.23	0.019	-1.07	0.373	-1.38	0.067	-0.59
1452097_a_at	Dusp7 /// LOC6749	dual specificity phosphatase 7 /// similar to dual specificity phosphatase 7	1.41	0.49	-1.17	0.77	-1.28	0.247	-1.44	0.416	-0.62
1416648_at	Dync1h1	dynein cytoplasmic 1 heavy chain 1	-1.07	0.527	-1.04	0.657	1.15	0.503	-1.56	0.097	-0.63
1456750_at	B230303O12Rik	RIKEN cDNA B230303O12 gene	1.26	0.703	-1.15	0.677	-1.09	0.78	-1.06	0.893	-0.51
1437169_at	Pdlim1 /// LOC5457	PDZ and LIM domain 1 (elfin) /// similar to PDZ and LIM domain protein 1 (Elfin) (	-1.04	0.959	-1.22	0.675	1.27	0.56	-1.22	0.41	-0.55
1456628_x_at	Rps24	ribosomal protein S24	-1.01	0.968	1.22	0.2	-1.2	0.127	-1.51	0.025	-0.62
1433572_a_at	BC010304	cDNA sequence BC010304	-1.01	0.94	-1.05	0.548	1.1	0.332	-1.05	0.619	-0.5
1458090_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.15	0.729	-1.03	0.963	1.21	0.73	-1.17	0.755	-0.53
1448429_at	Gyg	glycogenin	-1.03	0.874	-1	0.988	1.08	0.803	-1.01	0.906	-0.49
1458198_at	C81508	expressed sequence C81508	1.67	0.364	-1.64	0.203	-1.3	0.666	-1.45	0.275	-0.68
1446851_at	Col22a1	collagen, type XXII, alpha 1	-1.04	0.866	-1.04	0.943	1.12	0.576	-1.37	0.169	-0.58
1417447_at	Tcf21	transcription factor 21	-1.09	0.725	1.16	0.43	-1.03	0.897	-1.43	0.472	-0.6
1445722_at	Manbal	mannosidase, beta A, lysosomal-like	-1.1	0.902	1.63	0.234	-1.98	0.184	-1.27	0.273	-0.68
1439004_at	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	1.24	0.619	-1.18	0.78	-1.04	0.799	-1.71	0.183	-0.67
1453210_at	5730507C01Rik	RIKEN cDNA 5730507C01 gene	-1.08	0.856	-1.2	0.63	1.29	0.528	-1.56	0.349	-0.64
1433451_at	Cdk5r1	cyclin-dependent kinase 5, regulatory subunit (p35) 1	-1.36	0.76	-1.34	0.359	1.57	0.049	-1.08	0.572	-0.55
1445266_at	Ercc1	excision repair cross-complementing rodent repair deficiency, complementation g	1.52	0.179	-1.09	0.826	-1.61	0.506	-2.87	0.248	-1.01
1440562_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.27	0.476	1.32	0.254	-1.06	0.734	-1.15	0.776	-0.54
1447012_at	---	---	1.18	0.787	-1.1	0.839	-1.04	0.911	-1.42	0.48	-0.59
1419652_s_at	2610200G18Rik	RIKEN cDNA 2610200G18 gene	-1.18	0.186	-1.19	0.489	1.36	0.412	-1.71	0.228	-0.68
1433746_at	Wdr3	WD repeat domain 3	-1.15	0.619	1.21	0.195	-1.03	0.804	-1.33	0.184	-0.57
1430629_at	Slc16a14	solute carrier family 16 (monocarboxylic acid transporters), member 14	-2.82	0.501	-1.12	0.781	1.8	0.005	-2.2	0.412	-1.08
1426530_a_at	Klhl5	kelch-like 5 (Drosophila)	1.09	0.22	-1.03	0.79	-1	0.88	-1.29	0.154	-0.56
1445458_at	Mrgprg	MAS-related GPR, member G	1.88	0.329	-1.25	0.244	-2.67	0.006	-3.58	0.197	-1.41
1448765_at	Fyn	Fyn proto-oncogene	-1.25	0.594	1.28	0.078	-1.02	0.874	-1.21	0.552	-0.55
1416399_a_at	Hmox2	heme oxygenase (decycling) 2	-1.07	0.154	-1	0.99	1.12	0.263	-1.48	0.09	-0.61
1429554_at	Sdccag3	serologically defined colon cancer antigen 3	1.13	0.561	-1.07	0.716	-1.01	0.91	-1.07	0.733	-0.51
1416724_x_at	Tcf4	transcription factor 4	-1	0.949	1.28	0.031	-1.3	0.118	-1.23	0.456	-0.56
1423735_a_at	Wdr36	WD repeat domain 36	-1.04	0.913	1.15	0.347	-1.07	0.71	-1.06	0.703	-0.5
1441895_x_at	---	Transcribed locus	1.14	0.119	-1.02	0.955	-1.07	0.763	-1.77	0.136	-0.68
1430147_a_at	Josd3	Josephin domain containing 3	-1.01	0.968	-1.21	0.417	1.24	0.206	-1.59	0.102	-0.64
1456840_at	---	---	-1.21	0.577	-1.37	0.363	1.5	0.345	-1.14	0.732	-0.56
1417133_at	Pmp22	peripheral myelin protein	-1.03	0.623	1.4	0.007	-1.46	0.036	-1.1	0.72	-0.55
1454353_at	4833420D23Rik	RIKEN cDNA 4833420D23 gene	-1.21	0.753	-1.2	0.677	1.39	0.582	-1.56	0.063	-0.64
1436680_s_at	Ddb2	damage specific DNA binding protein 2	-1.03	0.831	1.22	0.466	-1.16	0.419	-2.2	0.035	-0.79
1436172_at	9530028C05	hypothetical protein 9530028C05	1.23	0.081	-1.05	0.725	-1.15	0.183	-2.37	0.072	-0.84
1416386_a_at	M6pr	mannose-6-phosphate receptor, cation dependent	-1.1	0.547	-1.03	0.789	1.17	0.317	-1.1	0.693	-0.51
1424159_at	1300010M03Rik	RIKEN cDNA 1300010M03 gene	-1.3	0.433	-1.04	0.923	1.33	0.554	-1.01	0.98	-0.51

1458874_at	Fat3	FAT tumor suppressor homolog 3 (Drosophila)	-1.21	0.538	1.6	0.15	-1.59	0.162	-1.28	0.706	-0.62
1447658_x_at	Synpo2l	synaptopodin 2-like	-1.05	0.928	-1.51	0.162	1.44	0.312	-1.92	0.244	-0.76
1451156_s_at	Vldlr	very low density lipoprotein receptor	-1.11	0.511	1.22	0.809	-1.07	0.802	-2.21	0.243	-0.79
1426592_a_at	Fbxo22	F-box only protein 22	-1.02	0.511	-1.07	0.409	1.14	0.309	-1.38	0.172	-0.58
1440769_at	2010305A19Rik	RIKEN cDNA 2010305A19 gene	1.17	0.586	-1.05	0.682	-1.07	0.786	-1.35	0.092	-0.58
1441080_at	---	Transcribed locus	-1.59	0.666	1.72	0.334	-1.42	0.203	-2.93	0.007	-1.05
1427255_s_at	Zfp445	zinc finger protein 445	-1.16	0.482	-1.11	0.626	1.29	0.337	-1.21	0.495	-0.55
1424982_a_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	-1.07	0.656	-1.1	0.66	1.21	0.329	-1.01	0.934	-0.49
1421049_at	0610009O20Rik	RIKEN cDNA 0610009O20 gene	-1.57	0.241	-1	0.998	1.42	0.096	-1.02	0.768	-0.54
1452932_at	Zbtb7a	zinc finger and BTB domain containing 7a	-1.14	0.649	-1.18	0.454	1.33	0.203	-1.12	0.286	-0.53
1443574_at	6530439I21	hypothetical protein 6530439I21	-1.13	0.403	1.18	0.348	-1.01	0.964	-1.77	0.605	-0.68
1451703_s_at	---	---	-1.05	0.557	1.13	0.301	-1.03	0.764	-1.33	0.088	-0.57
1433439_at	Cpne1	copine I	-1.03	0.707	-1.06	0.214	1.14	0.052	-1	0.999	-0.49
1423319_at	Hhex	hematopoietically expressed homeobox	-1.1	0.761	-1.41	0.273	1.44	0.23	-1.84	0.122	-0.73
1443024_at	---	PREDICTED: Mus musculus hypothetical protein LOC623199 (LOC623199), mR	-1.11	0.67	1.38	0.555	-1.28	0.666	-1.08	0.874	-0.52
1452246_at	Ostf1	osteoclast stimulating factor 1	-1.07	0.452	-1.04	0.424	1.16	0.271	-1.52	0.14	-0.62
1444532_at	---	---	-1.04	0.965	1.28	0.476	-1.24	0.536	-1.48	0.171	-0.62
1448142_x_at	Rps13 /// LOC6252	ribosomal protein S13 /// similar to ribosomal protein S13 /// similar to ribosomal p	-1	0.967	1.18	0.013	-1.14	0.258	-1.52	0.022	-0.62
1453508_at	1700104B16Rik	RIKEN cDNA 1700104B16 gene	-1.72	0.401	-1.44	0.073	1.78	0.037	-1.04	0.745	-0.6
1448026_at	---	---	-1.05	0.913	1.12	0.734	-1.01	0.94	-1.22	0.541	-0.54
1418132_a_at	D7Wsu128e	DNA segment, Chr 7, Wayne State University 128, expressed	-2.02	0.122	-1.03	0.965	1.59	0.332	-1.92	0.384	-0.85
1437592_x_at	Ccdc101	coiled-coil domain containing 101	-1.14	0.403	-1.02	0.855	1.2	0.231	-1.09	0.347	-0.51
1416620_at	Smarcal1	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfa	-1	0.993	-1.03	0.813	1.09	0.396	-1.4	0.094	-0.59
1418825_at	Irgm	immunity-related GTPase family, M	1.09	0.067	-1.02	0.876	-1.02	0.875	-1.18	0.382	-0.53
1425419_a_at	Raf1	v-raf-leukemia viral oncogene 1	-1.12	0.123	-1.04	0.672	1.2	0.168	-1.1	0.627	-0.51
1420453_at	Crygs	crystallin, gamma S	-1.26	0.588	-1.31	0.574	1.5	0.451	-1.03	0.977	-0.52
1418364_a_at	Ftl1	ferritin light chain 1	-1.02	0.779	-1.06	0.809	1.13	0.174	-1.12	0.382	-0.52
1444482_at	A130078K24Rik	RIKEN cDNA A130078K24 gene	1.22	0.714	-1.09	0.878	-1.09	0.817	-1.5	0.072	-0.61
1452658_at	Krr1	KRR1, small subunit (SSU) processome component, homolog (yeast)	-1.06	0.322	-1.07	0.44	1.18	0.366	-1.03	0.882	-0.5
1432913_at	Lrrc52	leucine rich repeat containing 52	1.82	0.354	-2.05	0.134	-1.34	0.606	-1.55	0.557	-0.78
1435428_at	BC037112	cDNA sequence BC037112	-1.03	0.854	1.15	0.496	-1.07	0.674	-1.12	0.752	-0.52
1420196_s_at	Tbc1d14	TBC1 domain family, member 14	-1.19	0.4	-1.02	0.747	1.24	0.017	-1.61	0.135	-0.65
1438153_x_at	Coq10a	coenzyme Q10 homolog A (yeast)	-1.23	0.362	-1.44	0.112	1.55	0.256	-1.71	0.435	-0.71
1434361_at	Sh3px3	SH3 and PX domain containing 3	1.08	0.349	-1.02	0.838	-1	0.988	-1.24	0.514	-0.55
1427225_at	Epn2	epsin 2	1.45	0.597	-1.24	0.263	-1.25	0.552	-2.58	0.038	-0.91
1447669_s_at	Gng4	guanine nucleotide binding protein (G protein), gamma 4 subunit	-1.92	0.286	1.59	0.278	-1.05	0.776	-1.51	0.167	-0.72
1433021_at	5830413G11Rik	RIKEN cDNA 5830413G11 gene	-1.09	0.689	-1.01	0.93	1.15	0.447	-1.44	0.234	-0.6
1417744_a_at	Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	-1.09	0.314	1.35	0	-1.27	0.068	-1.16	0.081	-0.54
1453170_at	Sft2d3	SFT2 domain containing 3	-1.28	0.763	1.66	0.189	-1.63	0.252	-1.74	0.311	-0.75
1433791_at	Rab9b	RAB9B, member RAS oncogene family	-1.02	0.978	-1.16	0.754	1.22	0.688	-1.24	0.786	-0.55
1439267_x_at	Cox5a	cytochrome c oxidase, subunit Va	-1.19	0.047	-1.11	0.021	1.32	0.003	-1.02	0.666	-0.5
1432178_at	4933431I19Rik	RIKEN cDNA 4933431I19 gene	1.18	0.864	-1.1	0.845	-1.03	0.961	-2.08	0.566	-0.76
1443553_at	---	---	1.83	0.415	-2.13	0.13	-1.32	0.18	-1.75	0.413	-0.84
1449228_at	Sh3gl2	SH3-domain GRB2-like 2	1.39	0.326	-1.12	0.757	-1.3	0.395	-1.16	0.672	-0.54
1451659_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	-1.35	0.373	1.49	0.465	-1.2	0.677	-1.5	0.232	-0.64
1440839_x_at	1700065I16Rik	RIKEN cDNA 1700065I16 gene	-1.33	0.594	1.71	0.137	-1.66	0.193	-1.23	0.573	-0.63
1442411_at	Glcci1	Glucocorticoid induced transcript 1	1.4	0.131	-1.15	0.573	-1.26	0.219	-1.46	0.205	-0.62
1417854_at	Map2k5	mitogen activated protein kinase kinase 5	-1.19	0.371	-1.11	0.498	1.32	0.034	-1.17	0.534	-0.54
1460474_at	2610028L16Rik	RIKEN cDNA 2610028L16 gene	1.27	0.526	-1.23	0.277	-1.03	0.826	-1.13	0.507	-0.53
1458889_at	Evl	Ena-vasodilator stimulated phosphoprotein	1.62	0.209	-1.15	0.845	-1.75	0.082	-1.8	0.098	-0.77
1446318_at	Slc44a1	Solute carrier family 44, member 1	-1.23	0.579	1.43	0.394	-1.23	0.232	-1.02	0.929	-0.51
1422387_at	V1rc2	vomeronasal 1 receptor, C2	1.92	0.469	-2.01	0.202	-1.56	0.593	-1.92	0.414	-0.89
1435805_at	Lin7a	lin-7 homolog A (C. elegans)	-1	0.992	-1.2	0.131	1.23	0.517	-1.38	0.769	-0.59

1434139_at	Parp11	poly (ADP-ribose) polymerase family, member 11	-1.2	0.24	1.33	0.008	-1.11	0.257	-1.2	0.156	-0.55
1434743_x_at	Rusc1	RUN and SH3 domain containing 1	-1.06	0.731	-1.1	0.712	1.2	0.112	-1.31	0.359	-0.56
1433754_at	Mbnl2	muscleblind-like 2	-1	0.99	1.18	0.155	-1.14	0.474	-1.3	0.265	-0.56
1416160_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	1.21	0.126	-1.03	0.939	-1.14	0.293	-1.07	0.766	-0.51
1445471_at	Tada2l	Transcriptional adaptor 2 (ADA2 homolog, yeast)-like	1.38	0.345	-1.09	0.892	-1.31	0.59	-1.2	0.166	-0.56
1448436_a_at	Irf1	interferon regulatory factor 1	-1.15	0.311	1.27	0.021	-1.09	0.44	-1.51	0.258	-0.62
1447375_at	---	Transcribed locus	-1.76	0.414	1.91	0.483	-1.71	0.334	-1.46	0.055	-0.76
1450429_at	Capn6	calpain 6	-1.11	0.501	1.6	0.175	-1.79	0.024	-1.07	0.821	-0.59
1435472_at	Kremen1	kringle containing transmembrane protein 1	-1.23	0.269	-1.04	0.522	1.29	0.007	-1.22	0.369	-0.55
1424304_at	Tpcn2	two pore segment channel 2	-1.21	0.612	-1.16	0.606	1.37	0.301	-1.68	0.316	-0.67
1459804_at	Crebbp	CREB binding protein	-1.49	0.671	-1.93	0.082	1.87	0.23	-3.31	0.197	-1.22
1439087_a_at	1500004A08Rik	RIKEN cDNA 1500004A08 gene	-1.08	0.633	-1.31	0.439	1.37	0.286	-2.8	0.01	-0.95
1450152_at	Zfp316	zinc finger protein 316	-1.21	0.621	1.28	0.471	-1.05	0.878	-1.2	0.655	-0.54
1450167_at	Rab37	RAB37, member of RAS oncogene family	-1.08	0.896	-1.83	0.182	1.59	0.059	-1.6	0.187	-0.73
1452819_at	Lphn3	latrophilin 3	-1.12	0.894	1.44	0.518	-1.38	0.078	-1.26	0.366	-0.58
1449878_a_at	Slc12a6	solute carrier family 12, member 6	-1	0.993	1.13	0.44	-1.07	0.748	-2.02	0.103	-0.74
1431619_a_at	Dtnbp1	dystrobrevin binding protein 1	-1.08	0.133	-1.08	0.553	1.21	0.098	-1.07	0.428	-0.5
1433605_at	Inpp5a	inositol polyphosphate-5-phosphatase A	1.11	0.599	-1.03	0.801	-1.02	0.84	-1.1	0.574	-0.51
1447194_at	---	Transcribed locus	-1.54	0.377	-1.11	0.864	1.51	0.422	-1.4	0.135	-0.63
1437021_at	Arl13b	ADP-ribosylation factor-like 13B	-1.43	0.339	1.48	0.172	-1.13	0.364	-1.47	0.073	-0.64
1418168_at	Zcchc14	zinc finger, CCHC domain containing 14	-1.02	0.761	-1.02	0.906	1.1	0.417	-1.06	0.771	-0.5
1445818_at	4930544M13Rik	RIKEN cDNA 4930544M13 gene	1.57	0.485	-1.16	0.716	-1.59	0.394	-1.11	0.907	-0.57
1417987_at	Btd	biotinidase	-1.01	0.948	1.09	0.337	-1.02	0.887	-1.09	0.69	-0.51
1422713_a_at	Ube2i	ubiquitin-conjugating enzyme E2I	1.1	0.731	-1.01	0.957	-1.03	0.728	-1.3	0.262	-0.56
1449009_at	Tgtp	T-cell specific GTPase	-1.03	0.866	1.28	0.286	-1.23	0.212	-1.41	0.004	-0.6
1436543_at	BC034507	cDNA sequence BC034507	-1.17	0.02	-1.21	0.004	1.38	0.346	-1.07	0.748	-0.52
1447749_at	Smyd5	SET and MYND domain containing 5	-1.5	0.347	1.6	0.289	-1.25	0.396	-1.03	0.838	-0.54
1415780_a_at	Armcx2	armadillo repeat containing, X-linked 2	-1.03	0.68	1.31	0.285	-1.27	0.37	-1.32	0.402	-0.58
1428344_at	Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	-1.05	0.605	-1.09	0.581	1.2	0.235	-1.41	0.214	-0.59
1454807_a_at	Snx12	sorting nexin 12	-1.01	0.967	1.17	0.123	-1.11	0.276	-1.03	0.834	-0.49
1415707_at	Anapc2	anaphase promoting complex subunit 2	-1.04	0.74	-1.05	0.387	1.16	0.001	-1.01	0.913	-0.49
1436900_x_at	Leprot	leptin receptor overlapping transcript	-1.1	0.339	1.33	0.024	-1.21	0.003	-1.17	0.304	-0.54
1454979_at	Diap1 /// LOC6715	diaphanous homolog 1 (Drosophila) /// similar to Protein diaphanous homolog 1 (I	-1.05	0.243	-1.01	0.924	1.12	0.035	-1.18	0.204	-0.53
1450396_at	Stag2	stromal antigen 2	-1.03	0.837	-1.18	0.411	1.26	0.384	-1.11	0.67	-0.52
1452498_at	Gpatc2	G patch domain containing 2	1.47	0.076	-1.15	0.657	-1.38	0.282	-1.29	0.485	-0.59
1422437_at	Col5a2	procollagen, type V, alpha 2	-1.02	0.953	1.64	0.11	-2.22	0.033	-1.12	0.597	-0.68
1424035_at	Rora	RAR-related orphan receptor alpha	1.63	0.001	-1.36	0.255	-1.42	0.301	-1.31	0.404	-0.61
1447674_at	2900080J11Rik	RIKEN cDNA 2900080J11 gene	-1	0.989	-1.25	0.492	1.27	0.423	-1.33	0.463	-0.58
1423139_at	Wdr4	WD repeat domain 4	-1.04	0.763	-1	0.996	1.11	0.721	-1.1	0.727	-0.51
1432985_at	5430402M21Rik	RIKEN cDNA 5430402M21 gene	-1.24	0.727	-1.05	0.948	1.31	0.453	-1.01	0.96	-0.5
1445560_at	---	Transcribed locus	-1.19	0.544	1.29	0.166	-1.07	0.748	-1.02	0.937	-0.5
1445050_at	AU015247	expressed sequence AU015247	-2.88	0.165	1.81	0.08	-1.1	0.478	-1.06	0.927	-0.81
1447165_at	Ankrd12	Ankyrin repeat domain 12	1.48	0.181	-1.28	0.68	-1.24	0.207	-1.36	0.404	-0.6
1434091_at	Faah	fatty acid amide hydrolase	-1.23	0.476	-1.29	0.041	1.48	0.069	-1.54	0.18	-0.65
1417627_a_at	Limk1	LIM-domain containing, protein kinase	-1.17	0.628	-1.2	0.474	1.38	0.212	-1.42	0.306	-0.6
1441670_at	Tiam2	T-cell lymphoma invasion and metastasis 2	-1.18	0.8	-1.02	0.968	1.24	0.607	-1.18	0.833	-0.54
1437044_a_at	Gba	glucosidase, beta, acid	-1.09	0.175	1.15	0.166	-1	0.978	-1.29	0.21	-0.56
1424116_x_at	Ppp5c	protein phosphatase 5, catalytic subunit	-1.05	0.721	-1.18	0.191	1.27	0.195	-1.2	0.304	-0.54
1438024_at	6230416A05Rik	RIKEN cDNA 6230416A05 gene	-1.12	0.093	-1.11	0.055	1.27	0.015	-1.32	0.115	-0.57
1417874_at	Tmem9b	TMEM9 domain family, member B	-1.06	0.656	1.17	0.419	-1.04	0.887	-1.07	0.838	-0.5
1429927_at	5830409B07Rik	RIKEN cDNA 5830409B07 gene	-1.03	0.88	1.1	0.805	-1	0.993	-1.03	0.858	-0.49
1422546_at	Ilf3	interleukin enhancer binding factor 3	1.28	0.771	-1.19	0.635	-1.05	0.854	-1.08	0.913	-0.51
1437768_at	Ankib1	ankyrin repeat and IBR domain containing 1	-1.16	0.785	-1.11	0.901	1.3	0.261	-1.49	0.431	-0.61

1444904_at	Runx1t1	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	-1.05	0.932	-1.2	0.823	1.29	0.445	-1.04	0.946	-0.5
1435964_a_at	Taok3	TAO kinase 3	-1.02	0.848	-1.18	0.382	1.24	0.124	-1.32	0.225	-0.57
1459384_at	Dnmt3b	DNA methyltransferase 3B	-1.54	0.646	1.59	0.298	-1.21	0.641	-2.35	0.03	-0.88
1424352_at	Cyp4a12	cytochrome P450, family 4, subfamily a, polypeptide 12	1.95	0.135	-2.89	0.384	-1.3	0.524	-1.59	0.197	-0.96
1416216_at	Reps1	RalBP1 associated Eps domain containing protein	-1.09	0.096	-1.14	0.096	1.27	0.092	-1.15	0.282	-0.53
1418561_at	Sf3b1	splicing factor 3b, subunit 1	-1.01	0.974	1.39	0.068	-1.45	0.001	-1.27	0.384	-0.59
1440955_at	Crim2	cysteine rich BMP regulator 2 (chordin like)	-1.24	0.186	-1.06	0.794	1.32	0.027	-1.01	0.939	-0.5
1422866_at	Col13a1	procollagen, type XIII, alpha 1	-1.03	0.908	-1.03	0.835	1.13	0.503	-1.43	0.355	-0.59
1423352_at	Crispld1	cysteine-rich secretory protein LCCL domain containing 1	1.32	0.299	-1.23	0.456	-1.07	0.718	-1.12	0.489	-0.52
1446151_at	---	---	-1.53	0.051	1.53	0.493	-1.13	0.836	-2.18	0.455	-0.83
1426842_at	Ythdf3	YTH domain family 3	-1.05	0.463	-1.01	0.929	1.14	0.624	-1.23	0.366	-0.54
1427273_at	D130054N24Rik	RIKEN cDNA D130054N24 gene	-1.26	0.036	-1.13	0.248	1.39	0.01	-1.12	0.434	-0.53
1460106_at	Hydin	hydrocephalus inducing	-1.07	0.913	-1.89	0.134	1.6	0.16	-2.13	0.336	-0.87
1450111_a_at	Nudt8	nudix (nucleoside diphosphate linked moiety X)-type motif 8	-1.03	0.89	-1.1	0.297	1.2	0.465	-1.09	0.686	-0.51
1443452_at	Elp3	Elongation protein 3 homolog (S. cerevisiae)	-1.09	0.745	1.22	0.552	-1.08	0.57	-1.19	0.522	-0.53
1445465_at	N28178	expressed sequence N28178	1.37	0.623	-1	0.996	-1.42	0.459	-1.45	0.383	-0.63
1438458_a_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associat	-1.04	0.881	-1	0.984	1.11	0.518	-1.05	0.715	-0.49
1416390_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	-1.16	0.487	1.21	0.269	-1	0.999	-1.05	0.858	-0.5
1415779_s_at	Actg1	actin, gamma, cytoplasmic 1	-1.13	0.264	1.26	0.272	-1.08	0.435	-1.27	0.06	-0.56
1439382_x_at	Ddr1	discoidin domain receptor family, member 1	-1.3	0.198	1.31	0.637	-1	0.989	-3.25	0.189	-1.06
1456329_at	Prtg	protogenin homolog (Gallus gallus)	-2.18	0.242	2.14	0.152	-2.13	0.057	-1.81	0.266	-0.99
1416381_a_at	Prdx5	peroxiredoxin 5	-1.11	0.301	-1.14	0.068	1.3	0.292	-1.14	0.528	-0.52
1453651_a_at	Brp44l	brain protein 44-like	-1.1	0.019	-1.27	0.029	1.37	0.143	-1.29	0.298	-0.57
1416364_at	Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	-1.02	0.733	-1.03	0.822	1.13	0.122	-1.1	0.374	-0.51
1452893_s_at	1110065P19Rik ///	RIKEN cDNA 1110065P19 gene /// RIKEN cDNA 2310040A07 gene	-1.05	0.728	1.72	0.379	-2.48	0.028	-1.05	0.808	-0.71
1436722_a_at	Actb	actin, beta, cytoplasmic	1.29	0.61	-1.09	0.774	-1.16	0.267	-1.17	0.214	-0.53
1426931_s_at	D19Bwg1357e /// S	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed /// SWI/SN	-1.06	0.787	-1.15	0.09	1.26	0.179	-1.09	0.61	-0.51
1424919_at	Erbb2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma d	-1.03	0.851	1.17	0.593	-1.07	0.543	-1.21	0.744	-0.54
1422950_at	Hes7	hairy and enhancer of split 7 (Drosophila)	1.76	0.012	-2.67	0.107	-1.07	0.803	-3.8	0.132	-1.44
1455339_at	C430014M02Rik	RIKEN cDNA C430014M02 gene	-1.14	0.376	-1.05	0.542	1.24	0.273	-1.45	0.079	-0.6
1415713_a_at	Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-1.09	0.594	-1.03	0.667	1.19	0.275	-1.05	0.4	-0.5
1417696_at	Soat1	sterol O-acyltransferase 1	-1.28	0.393	1.4	0.039	-1.11	0.548	-1	0.988	-0.5
1423837_at	2400003C14Rik	RIKEN cDNA 2400003C14 gene	-1.07	0.783	1.24	0.124	-1.11	0.518	-1.06	0.672	-0.5
1460120_at	Ablim1	actin-binding LIM protein 1	1.76	0.53	-1.35	0.529	-1.73	0.334	-2.59	0.024	-0.98
1420987_at	Kif3b	kinesin family member 3B	-1.3	0.591	-1.05	0.887	1.35	0.441	-1	0.99	-0.5
1418625_s_at	LOC14433 /// LOC2	similar to glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyd	-1.05	0.067	-1.13	0.4	1.23	0.025	-1.03	0.573	-0.49
1459101_at	C78760	expressed sequence C78760	-1.49	0.129	1.58	0.061	-1.22	0.673	-1.04	0.888	-0.54
1441952_x_at	Lynx1	Ly6/neurotoxin 1	-1.01	0.937	-1.07	0.59	1.15	0.076	-2.71	0.036	-0.91
1441646_at	1110059P08Rik	RIKEN cDNA 1110059P08 gene	1.23	0.134	-1.1	0.773	-1.07	0.763	-1.02	0.905	-0.49
1448865_at	Hsd17b7	hydroxysteroid (17-beta) dehydrogenase 7	-1.33	0.133	-1.01	0.91	1.33	0.002	-1.03	0.949	-0.51
1440279_at	---	---	-1.08	0.589	1.33	0.064	-1.23	0.046	-1.39	0.061	-0.59
1442793_s_at	Tbrg4	transforming growth factor beta regulated gene 4	-1.08	0.171	-1.15	0.239	1.28	0.05	-1.12	0.61	-0.52
1424438_a_at	Leprot	leptin receptor overlapping transcript	-1.14	0.191	1.38	0.005	-1.22	0.047	-1.06	0.694	-0.51
1427947_at	BC028440	cDNA sequence BC028440	-1.13	0.545	-1.01	0.978	1.2	0.318	-1.21	0.303	-0.54
1450062_a_at	Maged1	melanoma antigen, family D, 1	-1.12	0.09	-1.09	0.623	1.27	0.266	-1.05	0.831	-0.5
1421142_s_at	Foxp1	forkhead box P1	1.27	0.671	-1.21	0.417	-1.02	0.954	-1.49	0.325	-0.61
1440412_at	Igsf4d	Immunoglobulin superfamily, member 4	-1.23	0.637	-1.14	0.696	1.38	0.233	-1.34	0.373	-0.58
1430658_a_at	Gsdm2	gasdermin 2	-1.98	0.134	2.03	0.13	-1.84	0.273	-1.69	0.613	-0.87
1441676_at	Zfp406	zinc finger protein 406	-1.09	0.124	1.23	0.746	-1.07	0.776	-1.01	0.942	-0.49
1424242_at	Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antig	-1.12	0.207	-1.24	0.12	1.37	0.143	-1.4	0.245	-0.6
1421749_at	---	---	1.27	0.576	-1.21	0.802	-1.02	0.971	-1.04	0.944	-0.5
1438813_at	1700003O08Rik	RIKEN cDNA 1700003O08 gene	-1.29	0.531	-1.01	0.929	1.31	0.331	-1.52	0.322	-0.63
1425463_at	Gata6	GATA binding protein 6	-1.42	0.361	1.46	0.176	-1.1	0.544	-1.16	0.487	-0.55

1435538_at	0610030E20Rik	RIKEN cDNA 0610030E20 gene	-1.08	0.359	-1.1	0.097	1.25	0.182	-1.19	0.445	-0.53
1453070_at	Pcdh17	protocadherin 17	-1.08	0.458	1.64	0.056	-1.95	0.044	-1.68	0.027	-0.77
1428958_at	Paqr8	progestin and adipoQ receptor family member VIII	1.46	0.114	-1.17	0.372	-1.31	0.167	-1.28	0.312	-0.57
1450738_at	Kif21a	kinesin family member 21A	-1.09	0.409	-1.18	0.256	1.31	0.382	-1.76	0.058	-0.68
1428835_at	Myh14 /// LOC6728	myosin, heavy polypeptide 14 /// similar to nonmuscle myosin heavy chain	-1.18	0.223	-1.01	0.944	1.24	0.076	-1.53	0.505	-0.62
1446217_at	LOC433202	hypothetical gene supported by AK036329	-1.02	0.969	-1.26	0.62	1.3	0.619	-1.72	0.459	-0.67
1442848_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	-1.03	0.977	-1.22	0.6	1.28	0.648	-1.51	0.559	-0.62
1424259_at	2400010G15Rik	RIKEN cDNA 2400010G15 gene	-1.1	0.639	-1.11	0.075	1.27	0.166	-1.36	0.182	-0.57
1444350_at	LOC672855	similar to schlafen 10	-1.52	0.274	-1.92	0.377	1.9	0.243	-1.49	0.223	-0.76
1424533_a_at	3110023B02Rik	RIKEN cDNA 3110023B02 gene	-1.11	0.39	-1.04	0.827	1.21	0.133	-1.06	0.534	-0.5
1418546_a_at	Stambpl1	Stam binding protein like 1	-1.14	0.26	1.22	0.357	-1.01	0.946	-1.62	0.061	-0.64
1440786_x_at	Sfxn2	Sideroflexin 2	-1.02	0.945	1.1	0.586	-1	0.997	-1.52	0.158	-0.61
1449847_a_at	Col4a3bp	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-1.35	0.161	-1.14	0.39	1.46	0.187	-1.07	0.718	-0.52
1430610_at	Mrpl38	mitochondrial ribosomal protein L38	-1.01	0.88	1.16	0.408	-1.08	0.592	-1.15	0.566	-0.52
1458534_at	D13Bwg1146e	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	-1.78	0.477	-1.11	0.87	1.62	0.332	-1.1	0.893	-0.59
1459127_at	---	Transcribed locus	-1.01	0.971	-1.31	0.444	1.33	0.499	-2.98	0.243	-0.99
1433374_at	Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	1.56	0.448	-1.63	0.622	-1.11	0.792	-1.03	0.954	-0.55
1435193_at	A230050P20Rik	RIKEN cDNA A230050P20 gene	-1.03	0.92	1.22	0.124	-1.14	0.639	-1.37	0.268	-0.58
1440362_at	A330068P14Rik	RIKEN cDNA A330068P14 gene	-1.23	0.697	-1.15	0.727	1.4	0.424	-1.41	0.084	-0.6
1434228_at	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	-1.27	0.383	1.31	0.5	-1.02	0.876	-1.08	0.528	-0.51
1415844_at	Syt4	synaptotagmin IV	-1.06	0.863	1.47	0.616	-1.51	0.011	-1.12	0.852	-0.55
1425865_a_at	Lig3	ligase III, DNA, ATP-dependent	-1.18	0.448	-1.25	0.354	1.43	0.359	-1.13	0.759	-0.53
1419591_at	Mlze	melanoma-derived leucine zipper, extra-nuclear factor	-1.01	0.973	1.14	0.444	-1.05	0.934	-2.31	0.166	-0.81
1425552_at	Hip1r	huntingtin interacting protein 1 related	-1.26	0.072	-1.42	0.527	1.58	0.205	-2.98	0.067	-1.02
1431495_at	6030440G07Rik	RIKEN cDNA 6030440G07 gene	1.46	0.095	-1.37	0.289	-1.13	0.752	-1.68	0.32	-0.68
1427534_at	4930535I16Rik	RIKEN cDNA 4930535I16 gene	-1.18	0.706	-1.61	0.346	1.61	0.032	-2.48	0.016	-0.92
1417735_at	1810030J14Rik /// I	RIKEN cDNA 1810030J14 gene /// similar to Serum amyloid P-component precur	-1.83	0.371	-1.41	0.54	1.82	0.13	-1.71	0.406	-0.78
1428497_at	Secisbp2	SECIS binding protein 2	-1.18	0.142	-1.03	0.845	1.26	0.039	-1.04	0.808	-0.5
1417224_a_at	Cd2bp2	CD2 antigen (cytoplasmic tail) binding protein 2	-1.04	0.68	-1.29	0.162	1.34	0.295	-1.2	0.025	-0.55
1436832_at	1110067B18Rik	RIKEN cDNA 1110067B18 gene	-1.28	0.204	1.47	0.335	-1.2	0.607	-1.3	0.432	-0.58
1447017_at	---	Transcribed locus	-1.3	0.633	1.4	0.589	-1.1	0.774	-1.28	0.554	-0.57
1446349_at	Zfp78	zinc finger protein 78	-1.43	0.75	1.85	0.132	-1.89	0.155	-2.67	0.182	-1.03
1423570_at	Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	-1.21	0.239	1.27	0.084	-1.02	0.924	-1.15	0.536	-0.53
1438264_a_at	Tpp2	tripeptidyl peptidase II	-1.1	0.509	-1.24	0.429	1.36	0.403	-1.03	0.907	-0.5
1456878_at	AI646023	expressed sequence AI646023	1.48	0.375	-1.31	0.355	-1.2	0.354	-2.17	0.143	-0.8
1459164_at	AU014678	expressed sequence AU014678	1.91	0.501	-2.56	0.283	-1.28	0.697	-1.27	0.748	-0.8
1423663_at	Flcn	folliculin	-1.18	0.353	-1.02	0.875	1.26	0.305	-1.23	0.265	-0.55
1455918_at	Adrb3	adrenergic receptor, beta 3	-2.26	0.338	-1.05	0.882	1.69	0.241	-1.78	0.144	-0.85
1417665_a_at	Cpsf1	cleavage and polyadenylation specific factor 1	-1.15	0.121	-1.17	0.006	1.36	0.044	-1.04	0.662	-0.5
1424238_at	Sirt7	sirtuin 7 (silent mating type information regulation 2, homolog) 7 (S. cerevisiae)	-1.01	0.866	-1.07	0.448	1.16	0.017	-1.34	0.168	-0.57
1448696_at	Heph	hephaestin	-1.51	0.121	1.89	0.054	-1.88	0.064	-1.13	0.739	-0.66
1437106_at	Jarid1a	jumonji, AT rich interactive domain 1A (Rbp2 like)	1.41	0.235	-1.03	0.895	-1.41	0.312	-1.21	0.656	-0.56
1450225_at	Insr	insulin receptor	-1	0.98	-1.13	0.639	1.2	0.511	-1.38	0.284	-0.58
1440588_at	---	---	1.68	0.026	-1.45	0.187	-1.39	0.078	-1.38	0.336	-0.64
1449855_s_at	Uchl3 /// Uchl4	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) /// ubiquitin carbo	-1.13	0.342	-1.08	0.036	1.28	0.399	-1.49	0.092	-0.61
1446295_at	Trim24	tripartite motif protein 24	-1.09	0.79	1.46	0.265	-1.43	0.118	-1.02	0.902	-0.52
1423222_at	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	-3.12	0.465	1.84	0.258	-1.08	0.771	-1.09	0.88	-0.86
1421646_a_at	Pias3	protein inhibitor of activated STAT 3	-1.03	0.918	-1.18	0.051	1.26	0.371	-1.02	0.944	-0.49
1425954_a_at	Apex2	apurinic/apyrimidinic endonuclease 2	-1.22	0.426	-1.29	0.61	1.49	0.411	-1.02	0.978	-0.51
1417728_at	Mbd3	methyl-CpG binding domain protein 3	1.18	0.327	-1.01	0.941	-1.09	0.462	-1.14	0.499	-0.52
1417420_at	Ccnd1	cyclin D1	1.55	0.139	-1.57	0.042	-1.11	0.389	-1.76	0.321	-0.72
1425527_at	Prrx1	paired related homeobox 1	1.18	0.57	-1.09	0.718	-1.02	0.912	-1.13	0.56	-0.51
1453344_at	1810032O08Rik	RIKEN cDNA 1810032O08 gene	-1.13	0.643	-1.12	0.497	1.31	0.102	-1.18	0.286	-0.53

1450661_x_at	Nfic	nuclear factor I/C	-1.14	0.656	-1.22	0.725	1.39	0.322	-1.03	0.904	-0.5
1453822_at	1700010H15Rik	RIKEN cDNA 1700010H15 gene	-1.04	0.966	-1.09	0.892	1.21	0.424	-1.77	0.043	-0.67
1438178_x_at	Atad3a	ATPase family, AAA domain containing 3A	-1.21	0.108	-1.09	0.295	1.34	0.039	-1.22	0.181	-0.55
1434355_at	Zfp617	zinc finger protein 617	1.25	0.357	-1.04	0.767	-1.14	0.327	-1.02	0.535	-0.49
1435454_a_at	BC006779	cDNA sequence BC006779	-1.26	0.293	-1.01	0.95	1.3	0.242	-2.34	0.048	-0.83
1421743_a_at	Pcbp2	poly(rC) binding protein 2	-1.01	0.794	-1.11	0.377	1.2	0.173	-1.08	0.592	-0.5
1441819_x_at	Timm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	-1.3	0.336	-1.35	0.381	1.58	0.4	-1.2	0.787	-0.57
1455001_x_at	Rpl13a	ribosomal protein L13a	-1.04	0.209	1.18	0.535	-1.07	0.779	-1.22	0.036	-0.53
1442673_at	Stam2	Signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	2.06	0.238	-1.95	0.044	-1.93	0.078	-1.79	0.353	-0.91
1457576_at	---	---	1.38	0.266	-1.05	0.797	-1.32	0.176	-1.31	0.567	-0.58
1438773_at	Steap2	six transmembrane epithelial antigen of prostate 2	-1.19	0.243	1.55	0.42	-1.44	0.152	-1.25	0.355	-0.58
1453721_a_at	Slc31a2	solute carrier family 31, member 2	-1.08	0.795	-1.06	0.892	1.22	0.624	-1.52	0.195	-0.61
1423921_at	Ints3	integrator complex subunit 3	-1.12	0.621	-1.06	0.591	1.25	0.199	-1.23	0.254	-0.54
1421058_at	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	1.4	0.524	-1.23	0.413	-1.15	0.617	-1.61	0.609	-0.65
1441623_at	---	---	1.56	0.576	-1.74	0.46	-1.06	0.908	-1.4	0.355	-0.66
1457194_at	---	---	1.72	0.596	-2.04	0.082	-1.14	0.81	-1.05	0.882	-0.63
1430848_a_at	2410017P07Rik	RIKEN cDNA 2410017P07 gene	1.32	0.279	-1.28	0.691	-1.01	0.972	-1.14	0.463	-0.53
1422025_at	Mitf	microphthalmia-associated transcription factor	-1.23	0.593	-2.23	0.181	1.82	0.033	-1.08	0.91	-0.68
1456615_a_at	Falz	fetal Alzheimer antigen	-1.01	0.977	1.1	0.351	-1.01	0.931	-1.61	0.089	-0.63
1451354_at	Foxred1	FAD-dependent oxidoreductase domain containing 1	-1.02	0.766	-1.01	0.659	1.12	0.591	-1.09	0.61	-0.5
1432543_a_at	Klf13	Kruppel-like factor 13	-1.11	0.851	-1.02	0.93	1.2	0.467	-1.67	0.105	-0.65
1430939_at	4930528D03Rik	RIKEN cDNA 4930528D03 gene	-1.65	0.186	1.49	0.452	-1	0.987	-1.16	0.771	-0.58
1444894_at	Ptpn18	Protein tyrosine phosphatase, non-receptor type 18	1.15	0.743	-1.05	0.918	-1.02	0.971	-1.56	0.482	-0.62
1429217_at	Zfp655	zinc finger protein 655	-1.07	0.541	1.16	0.351	-1	0.986	-1.15	0.18	-0.52
1450577_at	Sstr3	somatostatin receptor 3	-1.18	0.256	1.82	0.328	-2.38	0.201	-3.86	0.316	-1.4
1437142_a_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	-1.07	0.439	-1.1	0.501	1.25	0.14	-1.09	0.059	-0.5
1441407_at	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	-1.13	0.871	1.3	0.321	-1.11	0.289	-1.06	0.677	-0.5
1452966_at	9130430L19Rik	RIKEN cDNA 9130430L19 gene	-1.04	0.712	1.21	0.694	-1.09	0.607	-2.36	0.033	-0.82
1443143_at	Flrt1	fibronectin leucine rich transmembrane protein 3	1.37	0.283	-1.04	0.943	-1.33	0.582	-1.07	0.854	-0.52
1441132_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730010N	-1.14	0.728	1.34	0.031	-1.15	0.199	-1.21	0.481	-0.54
1450787_at	Clcn5	chloride channel 5	-1.13	0.431	-1.3	0.665	1.43	0.405	-1.27	0.557	-0.57
1431484_at	2010007L08Rik	RIKEN cDNA 2010007L08 gene	-1.57	0.185	1.85	0.325	-1.65	0.324	-1.97	0.339	-0.84
1424770_at	Cald1	caldesmon 1	1.39	0.144	-1.06	0.452	-1.33	0.012	-1.27	0.328	-0.57
1453898_at	Itgb1bp3	integrin beta 1 binding protein 3	-1.4	0.515	-2.24	0.352	1.93	0.37	-1.08	0.629	-0.7
1460708_s_at	Cdc42	cell division cycle 42 homolog (S. cerevisiae)	-1.02	0.795	1.13	0.106	-1.03	0.535	-1.17	0.149	-0.52
1459340_at	---	---	1.69	0.238	-1.08	0.849	-2.07	0.09	-1.09	0.662	-0.64
1454603_a_at	Cnot2	CCR4-NOT transcription complex, subunit 2	-1.02	0.945	-1.16	0.267	1.25	0.181	-1.02	0.812	-0.49
1460517_at	9130409J20Rik	RIKEN cDNA 9130409J20 gene	-1.02	0.961	1.11	0.75	-1	0.998	-1.27	0.023	-0.54
1418942_at	Ift74	intraflagellar transport 74 homolog (Chlamydomonas)	1.19	0.122	-1.08	0.549	-1.03	0.9	-1.27	0.02	-0.55
1442010_at	Casz1 /// LOC5473	castor homolog 1, zinc finger (Drosophila) /// similar to castor homolog 1, zinc fing	-1.61	0.52	1.73	0.132	-1.36	0.63	-1	0.995	-0.56
1418572_x_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	1.62	0.092	-1.51	0.175	-1.23	0.362	-2.43	0.133	-0.89
1431213_a_at	1300007C21Rik ///	RIKEN cDNA 1300007C21 gene /// similar to RIKEN cDNA 1300007C21 gene ///	1.62	0.277	-1.69	0.433	-1.13	0.513	-1.9	0.204	-0.78
1445403_at	---	Transcribed locus	1.67	0.413	-1.35	0.342	-1.48	0.427	-1.35	0.362	-0.63
1434648_a_at	Ccm2	cerebral cavernous malformation 2 homolog (human)	1.16	0.08	-1.08	0.198	-1	0.999	-1.84	0.095	-0.69
1451143_at	1110006G06Rik	RIKEN cDNA 1110006G06 gene	-1.08	0.77	-1.1	0.482	1.26	0.033	-1.07	0.387	-0.5
1416351_at	Map2k1	mitogen activated protein kinase kinase 1	-1.01	0.804	-1.05	0.533	1.15	0.101	-1.58	0.029	-0.62
1449338_at	D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	-1.01	0.933	-1.04	0.662	1.14	0.313	-1.22	0.196	-0.53
1430682_at	4930555I21Rik	RIKEN cDNA 4930555I21 gene	-1	0.959	-2.06	0.215	1.61	0.168	-2.2	0.47	-0.91
1440031_at	Dact3	dact 3	-1.1	0.591	1.35	0.608	-1.2	0.757	-1.8	0.276	-0.69
1454738_x_at	Pex6	peroxisomal biogenesis factor 6	-1.06	0.703	-1.06	0.707	1.2	0.038	-1.39	0.159	-0.58
1452643_at	Grhl2	grainyhead-like 2 (Drosophila)	-2.27	0.402	1.86	0.096	-1.26	0.53	-3.42	0.029	-1.27
1437334_x_at	Parn	poly(A)-specific ribonuclease (deadenylation nuclease)	1.17	0.151	-1.04	0.371	-1.04	0.696	-1.28	0.267	-0.55
1428693_at	2610044O15Rik	RIKEN cDNA 2610044O15 gene	-1.09	0.731	1.28	0.475	-1.12	0.703	-1.42	0.166	-0.59

1437151_at	Usp22	ubiquitin specific peptidase 22	-1.07	0.276	-1.01	0.944	1.17	0.224	-1.21	0.251	-0.53
1433577_at	A730017C20Rik	RIKEN cDNA A730017C20 gene	-1.34	0.497	1.39	0.518	-1.05	0.707	-1.33	0.425	-0.58
1425628_a_at	LOC669007	similar to General transcription factor II-I (GTFII-I) (TFII-I) (Bruton tyrosine kinase	-1.03	0.769	-1.15	0.084	1.25	0.162	-1.25	0.33	-0.54
1423601_s_at	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	-1.31	0.282	-1.51	0.195	1.67	0.168	-1.64	0.06	-0.7
1432934_at	4930429N05Rik	RIKEN cDNA 4930429N05 gene	-1.35	0.669	1.46	0.264	-1.12	0.78	-2.63	0.293	-0.91
1437481_at	LOC623451	hypothetical LOC623451	-1.01	0.953	-1.08	0.396	1.18	0.336	-1.19	0.257	-0.53
1428603_at	Glcci1	glucocorticoid induced transcript 1	-1.03	0.731	-1.14	0.225	1.25	0.19	-1	0.994	-0.48
1456728_x_at	Aco1	aconitase 1	-1.24	0.173	-1.07	0.32	1.35	0.14	-1.11	0.221	-0.52
1432025_at	4933430A20Rik	RIKEN cDNA 4933430A20 gene	1.38	0.476	-1.03	0.937	-1.35	0.602	-1.16	0.683	-0.54
1447292_at	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	-2.03	0.573	1.76	0.449	-1.18	0.752	-1.92	0.295	-0.84
1425934_a_at	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	-1.25	0.321	1.49	0.423	-1.24	0.284	-1.11	0.154	-0.53
1438168_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-1.05	0.249	1.15	0.353	-1.01	0.902	-1.08	0.781	-0.5
1447198_at	Recql	RecQ protein-like	1.34	0.578	-1.26	0.204	-1.04	0.848	-1.86	0.026	-0.7
1446408_at	Hoxa10	Homeo box A10	-1.81	0.113	2.07	0.064	-2.12	0.011	-1.55	0.404	-0.85
1428398_at	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	-1.09	0.788	-1.02	0.946	1.2	0.77	-1.19	0.5	-0.53
1453758_at	2810027O19Rik	RIKEN cDNA 2810027O19 gene	1.64	0.478	-1.32	0.763	-1.44	0.023	-1.33	0.635	-0.61
1446000_at	Zfp291	Zinc finger protein 291	1.31	0.017	-1.07	0.851	-1.18	0	-1.29	0.44	-0.56
1448319_at	Akr1b3 /// LOC235	aldo-keto reductase family 1, member B3 (aldose reductase) /// similar to Aldose	-1.41	0.404	1.4	0.022	-1.02	0.822	-1.44	0.285	-0.62
1459331_at	Surf6	surfeit gene 6	-1.05	0.947	-1.18	0.824	1.29	0.422	-1.78	0.035	-0.68
1439739_at	1700112C13Rik ///	RIKEN cDNA 1700112C13 gene /// testes-specific protease 50	-1.2	0.433	1.35	0.482	-1.09	0.747	-1.27	0.326	-0.55
1420754_at	Ttf1	transcription termination factor 1	1.23	0.206	-1.03	0.812	-1.11	0.473	-1.25	0.019	-0.54
1423141_at	Lip1	Lysosomal acid lipase 1	1.21	0.321	-1.05	0.685	-1.07	0.739	-1.15	0.302	-0.51
1457747_at	9330109K16Rik	RIKEN cDNA 9330109K16 gene	-1.27	0.691	1.4	0.496	-1.1	0.671	-1.66	0.565	-0.66
1444674_at	AU015680	expressed sequence AU015680	-2.12	0.184	1.76	0.349	-1.16	0.803	-2.41	0.312	-0.98
1447033_at	Gm829	gene model 829, (NCBI)	-4.16	0.004	-1.16	0.461	2	0.262	-1.37	0.074	-1.17
1428807_at	4932702K14Rik	RIKEN cDNA 4932702K14 gene	1.53	0.284	-1.1	0.872	-1.52	0.457	-1.92	0.583	-0.75
1456186_at	8030443D09Rik	RIKEN cDNA 8030443D09 gene	-1.33	0.588	-1.01	0.955	1.36	0.082	-1.09	0.445	-0.52
1424602_s_at	Xrcc4	X-ray repair complementing defective repair in Chinese hamster cells 4	-1.03	0.864	1.25	0.247	-1.14	0.481	-1.48	0.154	-0.6
1440128_s_at	Sez6l	seizure related 6 homolog like	-1.93	0.339	2.32	0.082	-3.79	0.087	-2.02	0.096	-1.36
1426268_at	C130090K23Rik	RIKEN cDNA C130090K23 gene	1.28	0.377	-1.04	0.941	-1.17	0.696	-3.26	0.142	-1.05
1442831_at	2900026A02Rik	RIKEN cDNA 2900026A02 gene	-1.19	0.643	1.66	0.534	-1.68	0.384	-1.33	0.164	-0.63
1448976_at	Tfip11	tuftelin interacting protein 11	-1.14	0.141	-1.08	0.269	1.3	0.041	-1.01	0.865	-0.48
1421907_at	Pparbp	peroxisome proliferator activated receptor binding protein	1.19	0.562	-1.02	0.87	-1.07	0.806	-1.2	0.2	-0.53
1420854_at	Eln	elastin	-1.06	0.89	1.27	0.215	-1.13	0.741	-1.27	0.319	-0.55
1422545_at	---	---	-1.1	0.551	1.3	0.436	-1.12	0.557	-1.15	0.652	-0.52
1428683_at	A930016P21Rik	RIKEN cDNA A930016P21 gene	-1	0.994	-1.13	0.418	1.21	0.149	-1.11	0.284	-0.51
1435387_at	Slc2a13	solute carrier family 2 (facilitated glucose transporter), member 13	-1.25	0.288	1.78	0.03	-1.94	0.026	-1.62	0.34	-0.76
1437019_at	2200001I15Rik	RIKEN cDNA 2200001I15 gene	-1.13	0.584	1.26	0.521	-1.05	0.81	-1.52	0.445	-0.61
1454706_at	Uvrag	UV radiation resistance associated gene	-1.01	0.904	-1.02	0.707	1.13	0.27	-1.49	0.139	-0.6
1448423_at	Tmed4	transmembrane emp24 protein transport domain containing 4	-1.28	0.486	1.37	0.483	-1.05	0.9	-1.12	0.531	-0.52
1431696_at	4632413K17Rik	RIKEN cDNA 4632413K17 gene	1.56	0.505	-1.73	0.217	-1.04	0.831	-1.66	0.079	-0.72
1437099_x_at	Hnrpf /// LOC63700	heterogeneous nuclear ribonucleoprotein F /// similar to heterogeneous nuclear ri	-1.1	0.72	1.27	0.154	-1.09	0.488	-1.06	0.684	-0.49
1456367_at	Fut8	fucosyltransferase 8	1.8	0.06	-1.3	0.72	-1.88	0.022	-1.23	0.353	-0.65
1432251_at	4930403O15Rik	RIKEN cDNA 4930403O15 gene	1.38	0.71	-1.08	0.865	-1.26	0.69	-2.12	0.239	-0.77
1416187_s_at	Pnrc2	proline-rich nuclear receptor coactivator 2	-1.07	0.351	1.26	0.224	-1.11	0.338	-1.15	0.329	-0.52
1424769_s_at	Cald1	caldesmon 1	1.24	0.313	-1	0.994	-1.17	0.132	-1.3	0.236	-0.56
1455343_at	Plekha7	pleckstrin homology domain containing, family A member 7	-1.01	0.932	-1.17	0.478	1.25	0.294	-1.1	0.645	-0.51
1451043_at	Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	-1.04	0.918	1.35	0.249	-1.27	0.26	-1.32	0.273	-0.57
1419992_x_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	-1.28	0.053	2.1	0.469	-4.53	0.075	-1.54	0.055	-1.31
1446930_at	Runx1	Runt related transcription factor 1	1.75	0.243	-1.37	0.366	-1.62	0.109	-1.15	0.674	-0.6
1453445_at	9030601B04Rik	RIKEN cDNA 9030601B04 gene	-1.18	0.717	1.57	0.35	-1.46	0.308	-1.32	0.41	-0.6
1433629_s_at	AI316787	expressed sequence AI316787	-1	0.982	-1.07	0.352	1.17	0.044	-1.19	0.34	-0.52
1424555_at	9430015G10Rik	RIKEN cDNA 9430015G10 gene	1.16	0.586	-1.04	0.886	-1.02	0.943	-1.26	0.53	-0.54

1457377_at	L3mbtl3	L(3)mbt-like 3 (Drosophila)	1.52	0.375	-1.25	0.327	-1.28	0.097	-1.94	0.156	-0.74
1439554_at	Scmh1	sex comb on midleg homolog 1	1.42	0.537	-1.02	0.947	-1.42	0.273	-1.09	0.774	-0.53
1433564_at	Dgkd	diacylglycerol kinase, delta	-1.08	0.631	-1	0.992	1.18	0.225	-1.81	0.087	-0.68
1427583_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	-1.51	0.423	-1.84	0.163	1.9	0.358	-1.01	0.981	-0.62
1444078_at	Cd8a /// LOC63614	CD8 antigen, alpha chain /// similar to T-cell surface glycoprotein CD8 alpha chai	-1.03	0.935	-1.17	0.677	1.28	0.569	-1.87	0.23	-0.7
1445101_at	---	---	1.59	0.09	-1.24	0.461	-1.42	0.344	-1.13	0.718	-0.55
1424019_at	Nol1	nucleolar protein 1	-1.27	0.155	-1.08	0.528	1.39	0.19	-1.06	0.652	-0.51
1421999_at	Tshr	thyroid stimulating hormone receptor	-1.84	0.179	-1.07	0.859	1.62	0.346	-1.94	0.435	-0.81
1424687_at	2700008B19Rik	RIKEN cDNA 2700008B19 gene	-1.06	0.798	-1.14	0.685	1.28	0.152	-1.34	0.404	-0.56
1453648_at	Susd3	sushi domain containing 3	-1.19	0.377	-1.63	0.325	1.65	0.193	-1.2	0.392	-0.59
1431228_s_at	4930526I15Rik	RIKEN cDNA 4930526I15 gene	1.25	0.003	-1.15	0.316	-1.02	0.888	-1.55	0.035	-0.62
1445488_at	---	Transcribed locus	-1.15	0.753	1.26	0.768	-1.02	0.966	-1.24	0.226	-0.54
1451232_at	Cd151	CD151 antigen	-1.03	0.907	1.26	0.003	-1.15	0.301	-1.11	0.444	-0.51
1434904_at	Hivep2	human immunodeficiency virus type I enhancer binding protein 2	1.17	0.613	-1.01	0.98	-1.06	0.777	-1.78	0.058	-0.67
1428381_a_at	2700038C09Rik	RIKEN cDNA 2700038C09 gene	-1.07	0.663	-1.07	0.368	1.24	0.161	-1.99	0.064	-0.72
1460556_at	---	---	-1.15	0.533	-1.06	0.702	1.29	0.207	-1.23	0.426	-0.54
1438874_at	Nme7	non-metastatic cells 7, protein expressed in	-1.36	0.486	1.66	0.242	-1.42	0.128	-2.29	0.361	-0.85
1427080_at	2610036D13Rik	RIKEN cDNA 2610036D13 gene	-1.05	0.826	-1.05	0.584	1.2	0.024	-1.04	0.763	-0.49
1429375_at	Anapc10	anaphase promoting complex subunit 10	-1.02	0.927	1.2	0.416	-1.08	0.528	-1.09	0.644	-0.5
1451961_a_at	Mbp	myelin basic protein	1.43	0.575	-1.3	0.325	-1.11	0.671	-1.17	0.466	-0.54
1427355_at	Calca	calcitonin/calcitonin-related polypeptide, alpha	1.64	0.506	-1.89	0.426	-1.07	0.833	-1.45	0.491	-0.69
1418571_at	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	1.47	0.033	-1.53	0.1	-1.02	0.839	-1.34	0.719	-0.61
1426940_at	Sidt2	SID1 transmembrane family, member 2	-1.01	0.874	-1.04	0.567	1.15	0.21	-1.38	0.243	-0.57
1430784_a_at	4932417H02Rik	RIKEN cDNA 4932417H02 gene	-1.04	0.938	-1.73	0.59	1.57	0.558	-2.16	0.088	-0.84
1428185_at	Kctd18	potassium channel tetramerisation domain containing 18	-1.06	0.647	1.31	0.21	-1.17	0.205	-1.27	0.331	-0.55
1449211_at	Bpnt1	bisphosphate 3'-nucleotidase 1	-1.13	0.109	-1.05	0.496	1.27	0.152	-1.35	0.284	-0.57
1432180_at	4933403G17Rik	RIKEN cDNA 4933403G17 gene	1.27	0.655	-1.14	0.772	-1.05	0.84	-1.23	0.67	-0.54
1450307_x_at	H2afy3	H2A histone family, member Y3	-1.18	0.723	1.34	0.644	-1.09	0.802	-1.06	0.737	-0.5
1419225_at	Cacna2d3	calcium channel, voltage-dependent, alpha2/delta subunit 3	1.48	0.39	-1.48	0.539	-1.05	0.917	-1.65	0.304	-0.68
1420528_at	Gpatc2	G patch domain containing 2	-1.14	0.452	-1.02	0.923	1.25	0.233	-1.17	0.562	-0.52
1423731_at	Aldh16a1	aldehyde dehydrogenase 16 family, member A1	-1.06	0.484	-1.1	0.202	1.25	0.151	-1.05	0.675	-0.49
1438134_at	Pcdh10	protocadherin 10	-2.08	0.412	-1.14	0.824	1.75	0.177	-1.03	0.95	-0.63
1452473_at	E130201N16Rik	RIKEN cDNA E130201N16 gene	-1.02	0.93	1.28	0.634	-1.19	0.662	-1.42	0.566	-0.59
1453695_at	B430211C08Rik	RIKEN cDNA B430211C08 gene	-1.12	0.686	-1.21	0.682	1.38	0.283	-3.75	0.185	-1.17
1446021_at	AU018466	expressed sequence AU018466	-1.16	0.671	1.58	0.211	-1.5	0.264	-1.25	0.245	-0.58
1436542_at	Ptger1	Prostaglandin E receptor 1 (subtype EP1)	-1.03	0.912	-1.03	0.703	1.16	0.402	-1.2	0.44	-0.52
1418793_at	Idua	iduronidase, alpha-L-	-1.04	0.334	-1.08	0.702	1.22	0.36	-1.07	0.742	-0.49
1438268_at	Mnab	membrane associated DNA binding protein	1.71	0.341	-1.25	0.477	-1.67	0.183	-1.01	0.984	-0.56
1446939_at	Trim34	Tripartite motif protein 34	-1.37	0.224	1.49	0.059	-1.12	0.636	-1.6	0.277	-0.65
1444451_at	Pappa2	pappalysin 2	1.71	0.231	-1.49	0.495	-1.38	0.331	-1.13	0.494	-0.57
1422085_at	Tbx19	T-box 19	-1.18	0.759	1.34	0.209	-1.09	0.774	-1.11	0.645	-0.51
1438393_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420416P1	-1.12	0.833	1.62	0.379	-1.69	0.215	-1.43	0.343	-0.65
1431394_a_at	Lrrk2	leucine-rich repeat kinase 2	-1.14	0.591	1.36	0.391	-1.15	0.582	-2.65	0.04	-0.9
1435778_at	Ankrd11	ankyrin repeat domain 11	-1.01	0.945	-1.05	0.431	1.16	0.546	-1.33	0.226	-0.56
1428040_at	Onecut3	one cut domain, family member 3	-1.18	0.12	1.4	0.472	-1.17	0.518	-1.29	0.23	-0.56
1457445_at	Trps1	trichorhinophalangeal syndrome I (human)	-1.21	0.396	1.56	0.161	-1.39	0.015	-1.83	0.08	-0.72
1445081_at	A930041I02Rik	RIKEN cDNA A930041I02 gene	1.26	0.532	-1.07	0.846	-1.09	0.784	-1.38	0.492	-0.57
1428407_at	Hnrpa0	heterogeneous nuclear ribonucleoprotein A0	-1.04	0.825	-1.04	0.681	1.18	0.037	-1.29	0.074	-0.55
1433682_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	-1.13	0.49	-1.23	0.592	1.41	0.205	-1.28	0.264	-0.56
1440544_at	Slc14a2	Solute carrier family 14 (urea transporter), member 2	-1.06	0.828	-1.1	0.763	1.26	0.527	-1.3	0.715	-0.55
1436478_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	-1.27	0.048	1.53	0.173	-1.27	0.329	-1.44	0.029	-0.61
1434477_at	Heca	headcase homolog (Drosophila)	-1.06	0.752	-1.02	0.769	1.18	0.356	-1.54	0.063	-0.61
1456565_s_at	Map3k12	mitogen activated protein kinase kinase kinase 12	1.79	0.331	-1.6	0.494	-1.45	0.364	-1.31	0.332	-0.64

1439946_at	Mef2c	Myocyte enhancer factor 2C	1.72	0.398	-1.65	0.048	-1.28	0.29	-2.56	0.094	-0.94
1455293_at	Leo1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.15	0.271	-1.1	0.456	1.33	0.134	-1.09	0.766	-0.5
1448401_at	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.1	0.628	-1.05	0.655	1.25	0.13	-1.13	0.136	-0.51
1454878_at	2310047C04Rik	RIKEN cDNA 2310047C04 gene	-1.07	0.705	1.43	0.233	-1.35	0.054	-1.18	0.268	-0.54
1455305_x_at	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	-1.1	0.302	-1.05	0.606	1.25	0.241	-1.01	0.962	-0.48
1453502_at	2210408I21Rik	RIKEN cDNA 2210408I21 gene	-1.53	0.094	1.65	0.41	-1.23	0.388	-1.04	0.829	-0.54
1443013_at	Adamts16	A disintegrin-like and metallopetidase (reprolysin type) with thrombospondin type	-2.39	0.014	1.74	0.323	-1.05	0.946	-2.28	0.067	-1
1419058_at	Polr1e	polymerase (RNA) I polypeptide E	-1.08	0.553	-1.06	0.804	1.24	0.317	-1.85	0.168	-0.69
1432213_at	9530047P18Rik	RIKEN cDNA 9530047P18 gene	-1.19	0.642	-1.34	0.698	1.52	0.458	-1.28	0.274	-0.57
1439858_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	1.26	0.432	-1.16	0.525	-1.01	0.964	-1.42	0.44	-0.58
1427948_a_at	Zfp99	zinc finger protein 99	-1.05	0.533	-1.08	0.84	1.23	0.607	-1.3	0.203	-0.55
1455786_at	2610036F08Rik	RIKEN cDNA 2610036F08 gene	-1.46	0.125	1.43	0.232	-1	0.993	-1.25	0.634	-0.57
1422393_at	Foxe3	forkhead box E3	-1.26	0.494	1.44	0.06	-1.13	0.399	-1.93	0.265	-0.72
1435168_at	Zfp710	zinc finger protein 710	-1.13	0.078	1.27	0.12	-1.04	0.8	-1.01	0.944	-0.48
1458511_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	-1.42	0.245	-1.06	0.759	1.47	0.098	-1.15	0.1	-0.54
1443254_at	D030011O10Rik	RIKEN cDNA D030011O10 gene	-1.03	0.91	-1.37	0.103	1.41	0.39	-1.46	0.33	-0.61
1419384_at	Pick1	protein interacting with C kinase 1	-1.02	0.885	1.22	0.11	-1.11	0.674	-1.31	0.121	-0.55
1440496_at	Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	1.76	0.256	-1.76	0.431	-1.27	0.667	-2.76	0.019	-1.01
1424790_at	2900084M01Rik	RIKEN cDNA 2900084M01 gene	-1.03	0.951	-1.22	0.306	1.32	0.406	-1.04	0.746	-0.49
1432547_at	C030005H24Rik	RIKEN cDNA C030005H24 gene	-2.12	0.343	1.65	0.229	-1	0.992	-1.17	0.776	-0.66
1460029_at	Gtpbp5	GTP binding protein 5	-1.24	0.763	1.31	0.207	-1	0.996	-1.36	0.233	-0.57
1436377_at	Gpr137	G protein-coupled receptor 137	1.22	0.108	-1.02	0.758	-1.09	0.585	-1.09	0.377	-0.5
1451003_at	Map3k7ip2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-1.06	0.716	1.2	0.462	-1.03	0.851	-1.06	0.593	-0.49
1457810_at	Zbtb37	zinc finger and BTB domain containing 37	1.42	0.479	-1.19	0.54	-1.17	0.446	-1.56	0.16	-0.62
1444306_at	Msi1	Musashi homolog 1(Drosophila)	-1.73	0.586	-1.41	0.414	1.83	0.217	-1.02	0.968	-0.58
1443319_at	Pag1	phosphoprotein associated with glycosphingolipid microdomains 1	-1.09	0.781	-1.08	0.89	1.27	0.525	-1.26	0.524	-0.54
1459079_at	---	---	-1.22	0.781	-1.06	0.795	1.36	0.349	-1.21	0.642	-0.54
1417872_at	Fhl1	four and a half LIM domains 1	-1.14	0.211	1.43	0.007	-1.23	0.028	-1.01	0.932	-0.49
1421928_at	Epha4	Eph receptor A4	-1.35	0.316	-1.18	0.558	1.53	0.1	-1.13	0.781	-0.53
1441443_at	Tex2	Testis expressed gene 2	-1.54	0.473	-1.41	0.644	1.76	0.258	-1.93	0.42	-0.78
1430690_at	5430411C19Rik	RIKEN cDNA 5430411C19 gene	-1.14	0.236	1.48	0.493	-1.31	0.355	-2.09	0.191	-0.77
1444951_at	4930467M19Rik	RIKEN cDNA 4930467M19 gene	1.38	0.142	-1.22	0.539	-1.1	0.787	-1.72	0.108	-0.66
1435185_at	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	-1.09	0.629	1.23	0.534	-1.02	0.908	-1.21	0.069	-0.52
1442825_at	Gorasp2	Golgi reassembly stacking protein 2	1.45	0.47	-1.46	0.589	-1.02	0.955	-1.13	0.801	-0.54
1448588_at	Cd320	CD320 antigen	1.31	0.458	-1.2	0.647	-1.03	0.967	-2.53	0.117	-0.86
1459785_at	Zfp383	Zinc finger protein 383	-1.08	0.92	1.39	0.355	-1.26	0.603	-2.9	0.187	-0.96
1417225_at	Arl6ip5	ADP-ribosylation factor-like 6 interacting protein 5	-1.68	0.397	-1.28	0.386	1.74	0.087	-2.17	0.283	-0.85
1429433_at	Bat2d	BAT2 domain containing 1	1.24	0.636	-1.08	0.673	-1.05	0.87	-1.51	0.422	-0.6
1439750_at	---	Transcribed locus	-1.46	0.563	1.78	0.221	-1.53	0.341	-1.07	0.769	-0.57
1452623_at	Zfp759	zinc finger protein 759	-1.1	0.76	1.26	0.343	-1.05	0.624	-1.19	0.541	-0.52
1443724_at	Jph3	junctophilin 3	-1.75	0.245	-1.64	0.37	1.94	0.315	-1.19	0.773	-0.66
1459175_at	---	Transcribed locus	-1.04	0.963	1.2	0.724	-1.05	0.923	-1.37	0.583	-0.56
1415749_a_at	Rragc	Ras-related GTP binding C	-1.02	0.848	-1.01	0.945	1.14	0.048	-1.08	0.152	-0.49
1436337_at	Dmtf1 /// 4930420K	cyclin D binding myb-like transcription factor 1 /// RIKEN cDNA 4930420K17 gene	1.15	0.438	-1.03	0.771	-1.01	0.968	-1.9	0.159	-0.7
1437597_at	---	Transcribed locus	-1.3	0.695	1.98	0.183	-2.69	0.169	-1.59	0.485	-0.9
1457740_at	Arntl	Aryl hydrocarbon receptor nuclear translocator-like	1.46	0.463	-1.1	0.759	-1.34	0.172	-1.16	0.578	-0.53
1430607_at	4930505D03Rik	RIKEN cDNA 4930505D03 gene	-1.15	0.807	-1.02	0.973	1.27	0.617	-1.71	0.319	-0.65
1445248_at	Ttc18	Tetratricopeptide repeat domain 18	1.56	0.502	-1.3	0.666	-1.26	0.323	-1.05	0.826	-0.51
1453351_at	Tbx20	T-box 20	-1.17	0.869	-1.01	0.97	1.28	0.596	-2.62	0.144	-0.88
1419749_at	Dnmt2	DNA methyltransferase 2	-1.15	0.276	1.25	0.106	-1	0.989	-1.17	0.12	-0.52
1448143_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	-1.18	0.362	-1.25	0.231	1.47	0.158	-1.46	0.114	-0.6
1419300_at	Flt1	FMS-like tyrosine kinase 1	1.14	0.384	-1.01	0.959	-1.01	0.916	-1.28	0.188	-0.54
1447356_at	LOC554292	UbiE-YGHL1 fusion protein	1.56	0.157	-1.62	0.425	-1.06	0.907	-1.05	0.887	-0.54

1447843_at	Psmd13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	-1.44	0.011	-1.76	0.15	1.85	0.019	-1.81	0.116	-0.79
1422107_at	2410066E13Rik	RIKEN cDNA 2410066E13 gene	-1.04	0.725	1.2	0.748	-1.05	0.83	-1.31	0.335	-0.55
1418904_at	---	---	-1.41	0.559	1.46	0.517	-1.06	0.927	-1.21	0.834	-0.55
1445672_at	---	Transcribed locus	-1.13	0.774	-2.49	0.073	1.84	0.149	-1.16	0.727	-0.74
1426524_at	Gnpda2	glucosamine-6-phosphate deaminase 2	-1.1	0.175	1.35	0.164	-1.17	0.029	-1.25	0.278	-0.54
1418562_at	Sf3b1	splicing factor 3b, subunit 1	1.19	0.574	-1.05	0.717	-1.02	0.94	-1.6	0.206	-0.62
1428678_s_at	Wdr73	WD repeat domain 73	-1.04	0.656	1.19	0.24	-1.03	0.864	-1.27	0.252	-0.54
1418406_at	Pde8a	phosphodiesterase 8A	-1.26	0.009	-1.23	0.199	1.51	0.017	-1.07	0.814	-0.51
1460447_at	Pus7l	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	-1.08	0.786	-1.23	0.214	1.39	0.127	-1.05	0.761	-0.49
1446671_at	Ppp1r14c	Protein phosphatase 1, regulatory (inhibitor) subunit 14c	-1.1	0.8	1.31	0.587	-1.1	0.656	-1.93	0.125	-0.71
1419884_at	Etnk1	Ethanolamine kinase 1	-1.1	0.066	-1.11	0.652	1.31	0.395	-1.4	0.209	-0.57
1422777_at	C1ql1	complement component 1, q subcomponent-like 1	-1.32	0.661	-1.15	0.722	1.5	0.228	-1.04	0.922	-0.5
1427390_at	Bloc1s3	biogenesis of lysosome-related organelles complex-1, subunit 3	-1.29	0.301	-1.12	0.515	1.45	0.142	-1.14	0.416	-0.52
1456864_at	---	---	1.47	0.176	-1.03	0.937	-1.45	0.188	-1.69	0.162	-0.68
1436180_at	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	-1.01	0.932	-1.01	0.864	1.14	0.297	-1.25	0.08	-0.53
1439815_at	A230048G03Rik ///	RIKEN cDNA A230048G03 gene /// similar to CG2747-PB, isoform B	-1.04	0.303	-1.03	0.84	1.2	0.431	-1.19	0.153	-0.52
1451303_at	BC002230	cDNA sequence BC002230	-1.01	0.958	-1.06	0.652	1.19	0.291	-1.29	0.099	-0.54
1445000_at	---	---	-1.92	0.45	1.61	0.547	-1.01	0.988	-1.55	0.404	-0.72
1423797_at	Aacs	acetoacetyl-CoA synthetase	-1.39	0.113	-1.17	0.767	1.55	0.123	-1.18	0.081	-0.55
1451998_at	Tasp1	taspase, threonine aspartase 1	-1.16	0.518	-1.08	0.645	1.34	0.137	-1.05	0.734	-0.49
1433938_at	Trp53bp2	transformation related protein 53 binding protein 2	-1.59	0.073	-1.12	0.456	1.6	0.238	-1.17	0.282	-0.57
1430279_at	3110038A09Rik	RIKEN cDNA 3110038A09 gene	1.72	0.111	-1.97	0.093	-1.11	0.818	-1.98	0.079	-0.84
1449190_a_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	-1.16	0.379	-1.02	0.711	1.29	0.124	-1.36	0.158	-0.57
1447321_at	Als2cr19	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (hum	-1.53	0.462	1.77	0.32	-1.42	0.166	-1.04	0.861	-0.56
1454708_at	Ablim1	actin-binding LIM protein 1	-1.11	0.587	1.41	0.041	-1.22	0.326	-2.72	0.082	-0.91
1455140_at	A330068P14Rik	RIKEN cDNA A330068P14 gene	-1.21	0.129	1.45	0.361	-1.17	0.605	-1.66	0.272	-0.65
1434505_a_at	---	---	-1.54	0.343	-1.15	0.708	1.61	0.14	-1.14	0.562	-0.56
1448350_at	Asl	argininosuccinate lyase	-1.36	0.048	-1.06	0.474	1.45	0.098	-1.17	0.356	-0.54
1442408_at	2010305B15Rik	RIKEN cDNA 2010305B15 gene	-1.03	0.896	-1.01	0.955	1.16	0.333	-1.92	0.126	-0.7
1429662_at	Spata1	spermatogenesis associated 1	-1.02	0.973	1.2	0.629	-1.06	0.778	-1.26	0.513	-0.53
1444969_at	5033414K04Rik	RIKEN cDNA 5033414K04 gene	1.43	0.649	-1.02	0.96	-1.39	0.267	-1.16	0.13	-0.54
1418836_at	Qprt	quinolinate phosphoribosyltransferase	-1.21	0.215	-1.03	0.846	1.33	0.618	-1.18	0.447	-0.52
1457184_at	Frmd6	FERM domain containing 6	-1.12	0.898	1.91	0.225	-3.11	0.004	-1.27	0.382	-0.9
1433128_at	4930423C22Rik	RIKEN cDNA 4930423C22 gene	-1.54	0.284	1.62	0.651	-1.18	0.069	-1.08	0.105	-0.54
1451201_s_at	Rnh1	ribonuclease/angiogenin inhibitor 1	-1.04	0.675	-1.05	0.416	1.21	0.167	-1.28	0.168	-0.54
1440895_at	---	---	-1.16	0.018	-1.17	0.658	1.41	0.045	-1.12	0.704	-0.51
1443963_at	---	Transcribed locus	1.41	0.625	-1.29	0.568	-1.06	0.861	-1.44	0.673	-0.6
1447470_at	Hdhd2	haloacid dehalogenase-like hydrolase domain containing 2	1.52	0.436	-1.18	0.543	-1.32	0.454	-2.84	0.168	-0.95
1451822_a_at	Scrn2	secernin 2	1.21	0.569	-1.07	0.625	-1.01	0.946	-1.31	0.669	-0.55
1442222_at	Ifnar1	interferon (alpha and beta) receptor 1	1.36	0.444	-1.16	0.479	-1.11	0.396	-1.85	0.15	-0.69
1435942_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	1.27	0.583	-1.07	0.887	-1.09	0.872	-1.85	0.434	-0.68
1436866_at	Efna5	ephrin A5	-1.01	0.879	1.18	0.271	-1.05	0.869	-1.1	0.696	-0.49
1454538_at	D730048A03Rik	RIKEN cDNA D730048A03 gene	1.51	0.143	-1.32	0.411	-1.16	0.54	-1.27	0.664	-0.56
1423824_at	Gpr177	G protein-coupled receptor 177	-1.15	0.328	1.42	0.004	-1.2	0.136	-1.1	0.764	-0.51
1451879_a_at	Slc6a18	solute carrier family 6 (neurotransmitter transporter), member 18	1.27	0.131	-1.05	0.881	-1.11	0.807	-1.37	0.326	-0.56
1444889_at	Rassf2	Ras association (RalGDS/AF-6) domain family 2	1.73	0.121	-1.43	0.625	-1.44	0.426	-1.87	0.268	-0.75
1430481_at	4930545L23Rik	RIKEN cDNA 4930545L23 gene	-2.3	0.282	1.69	0.115	-1	0.997	-1.13	0.344	-0.68
1442506_at	---	Transcribed locus	-1.16	0.597	1.39	0.588	-1.15	0.486	-1	0.997	-0.48
1429680_at	Tra2a	transformer 2 alpha homolog (Drosophila)	1.64	0.408	-1.11	0.756	-1.7	0.034	-1.09	0.747	-0.57
1444155_at	Nin	Ninein	-1.15	0.649	-1.31	0.658	1.49	0.425	-1.29	0.411	-0.56
1421962_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	-1.05	0.868	1.24	0.383	-1.07	0.491	-1.24	0.111	-0.53
1458891_at	Garnl3	GTPase activating RANGAP domain-like 3	1.45	0.27	-1.35	0.458	-1.07	0.759	-1.26	0.501	-0.56
1421203_at	Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4	-1.33	0.528	1.51	0.506	-1.15	0.456	-1.01	0.972	-0.5

1446736_at	Tbl1x	Transducin (beta)-like 1 X-linked	1.67	0.473	-1.01	0.973	-2.16	0	-1.19	0.292	-0.67
1436025_at	A430106J12Rik	RIKEN cDNA A430106J12 gene	-1.17	0.269	1.46	0.305	-1.23	0.376	-1.05	0.89	-0.5
1455199_at	AI429214	expressed sequence AI429214	-1.08	0.346	1.26	0.182	-1.06	0.758	-1.49	0.257	-0.59
1451778_at	Crtc3	CREB regulated transcription coactivator 3	-1.43	0.024	-1.04	0.904	1.47	0.052	-1.54	0.473	-0.63
1459965_at	Dyx1c1	Dyslexia susceptibility 1 candidate 1 homolog (human)	-1.1	0.874	1.3	0.146	-1.09	0.623	-1.67	0.052	-0.64
1418839_at	Glmn	glomulin, FKBP associated protein	-1.01	0.977	-1.15	0.255	1.27	0.29	-1.18	0.091	-0.52
1454323_at	5830433D23Rik	RIKEN cDNA 5830433D23 gene	1.99	0.51	-1.75	0.15	-1.74	0.084	-1.38	0.776	-0.72
1417242_at	Ddx48	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	-1.03	0.836	-1.12	0.275	1.27	0.007	-1.02	0.634	-0.48
1459684_at	2810449C10Rik	RIKEN cDNA 2810449C10 gene	1.62	0.58	-1.04	0.952	-1.8	0.354	-2.52	0.203	-0.94
1444210_at	---	---	-1.39	0.045	1.56	0.355	-1.17	0.589	-2.33	0.396	-0.83
1460643_at	Ell	elongation factor RNA polymerase II	-1.05	0.833	1.32	0.126	-1.16	0.535	-1.21	0.448	-0.53
1446256_at	---	---	-1.1	0.304	-1.08	0.684	1.29	0.204	-2.2	0.446	-0.77
1427244_at	Ttc15	tetratricopeptide repeat domain 15	-1.46	0.32	-1.11	0.498	1.54	0.014	-1.07	0.62	-0.52
1440104_at	Ranbp2	RAN binding protein 2	1.42	0.24	-1.09	0.621	-1.25	0.487	-1.14	0.651	-0.52
1451173_at	Lrrc49	leucine rich repeat containing 49	-1.34	0.43	1.51	0.357	-1.14	0.383	-1.53	0.555	-0.62
1427847_at	Runx1	runt related transcription factor 1	-1.47	0.012	1.49	0.403	-1.04	0.819	-1.32	0.374	-0.58
1457900_at	Ascc3	activating signal cointegrator 1 complex subunit 3	1.19	0.169	-1.01	0.94	-1.05	0.872	-1.12	0.493	-0.5
1415896_x_at	Snrpn	small nuclear ribonucleoprotein N	-1.06	0.855	-1.31	0.312	1.43	0.314	-1.88	0.289	-0.71
1428865_at	Bcl2l12	BCL2-like 12 (proline rich)	-1.07	0.627	-1.28	0.378	1.42	0.085	-1.15	0.361	-0.52
1423382_a_at	Hnrpf /// LOC63700	heterogeneous nuclear ribonucleoprotein F /// similar to heterogeneous nuclear ri	-1.22	0.065	-1.02	0.397	1.33	0.101	-1.26	0.058	-0.54
1435777_at	E030018N11Rik	RIKEN cDNA E030018N11 gene	-1.15	0.117	1.52	0.021	-1.33	0.099	-1.2	0.544	-0.54
1430102_at	Rnf148	ring finger protein 148	1.61	0.591	-1.38	0.466	-1.25	0.6	-2.53	0.032	-0.89
1421931_at	Icos	inducible T-cell co-stimulator	1.57	0.572	-1.71	0.122	-1.03	0.896	-1.52	0.38	-0.67
1431230_a_at	Btbd9	BTB (POZ) domain containing 9	-1.15	0.198	-1.06	0.62	1.32	0.077	-1.36	0.086	-0.56
1418339_at	Recql	RecQ protein-like	-1.2	0.274	1.34	0.2	-1.04	0.759	-1.09	0.605	-0.5
1444227_at	---	Transcribed locus	2.06	0.014	-1.49	0.556	-2.52	0.047	-1.25	0.696	-0.8
1430956_at	Prss23	Protease, serine, 23	-1.69	0.078	-1.39	0.37	1.83	0.341	-1.18	0.747	-0.61
1420350_at	Sprrl2	small proline rich-like 2	-1.02	0.93	1.34	0.565	-1.23	0.677	-1.14	0.551	-0.51
1416252_at	Stk38	serine/threonine kinase 38	-1.21	0.414	-1.03	0.796	1.34	0.09	-1.81	0.106	-0.68
1452190_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	-1.18	0.485	1.53	0.16	-1.33	0.03	-1.14	0.319	-0.53
1423126_at	Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide	-1.01	0.902	1.22	0.055	-1.08	0.629	-1.45	0.271	-0.58
1452135_at	Gpx6	glutathione peroxidase 6	-1.15	0.467	-1.13	0.832	1.38	0.366	-1.39	0.591	-0.57
1429617_at	Cyld	cylindromatosis (turban tumor syndrome)	-1.11	0.078	-1.06	0.486	1.29	0.188	-1.17	0.251	-0.51
1457052_at	AW536275	expressed sequence AW536275	-1.44	0.686	-1.27	0.656	1.66	0.301	-1.57	0.399	-0.66
1427482_a_at	Car8 /// LOC67679	carbonic anhydrase 8 /// similar to Carbonic anhydrase-related protein (CARP) (C	1.44	0.069	-1.22	0.12	-1.14	0.109	-1.24	0.766	-0.54
1418170_a_at	Zcchc14	zinc finger, CCHC domain containing 14	1.41	0.278	-1.23	0.179	-1.09	0.554	-1.18	0.416	-0.52
1455489_at	Lrrtm2	leucine rich repeat transmembrane neuronal 2	-1.1	0.808	1.42	0.467	-1.24	0.26	-2.05	0.017	-0.74
1416503_at	Lxn	latexin	-1.06	0.51	1.36	0.16	-1.2	0.046	-1.02	0.879	-0.48
1457964_at	1810044D09Rik	RIKEN cDNA 1810044D09 gene	-1.16	0.116	-1.22	0.058	1.46	0.184	-1.01	0.888	-0.48
1443246_at	Fastkd2	FAST kinase domains 2	1.64	0.39	-1.61	0.57	-1.14	0.848	-2.22	0.35	-0.83
1448208_at	Smad1	MAD homolog 1 (Drosophila)	-1.03	0.818	1.19	0.131	-1.03	0.852	-1.15	0.601	-0.5
1455822_x_at	Surf4	surfeit gene 4	-1.05	0.874	1.27	0.054	-1.09	0.139	-1.48	0.29	-0.59
1449408_at	Jam2	junction adhesion molecule 2	1.2	0.469	-1.04	0.902	-1.02	0.934	-1.4	0.001	-0.57
1438108_at	9430067K14Rik	RIKEN cDNA 9430067K14 gene	-1.58	0.209	-1.02	0.954	1.52	0.02	-1.26	0.005	-0.58
1422687_at	---	---	1.4	0.247	-1	0.989	-1.35	0.002	-1.06	0.727	-0.5
1441227_at	---	CDNA clone IMAGE:6815954	-1.82	0.114	-1.06	0.912	1.65	0.182	-2.99	0.013	-1.06
1428416_at	3110050N22Rik	RIKEN cDNA 3110050N22 gene	-1.04	0.352	1.44	0.344	-1.35	0.008	-1.6	0.117	-0.64
1450049_a_at	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	-1.17	0.862	1.3	0.256	-1.02	0.94	-1.24	0.457	-0.53
1455426_at	---	---	1.74	0.067	-1.29	0.144	-1.59	0.164	-1.13	0.667	-0.57
1429281_at	2610008E11Rik	RIKEN cDNA 2610008E11 gene	-1.02	0.815	1.47	0.251	-1.43	0.046	-1.82	0.072	-0.7
1437567_at	BC023179	CDNA sequence BC023179	-1.21	0.461	1.37	0.395	-1.06	0.886	-1.4	0.304	-0.57
1448440_x_at	D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	-1	0.991	1.22	0.25	-1.09	0.306	-1.06	0.799	-0.48
1456423_at	Mbd5	methyl-CpG binding domain protein 5	-1.23	0.463	1.5	0.219	-1.21	0.242	-1.38	0.123	-0.58

1444929_at	---	---	2.22	0.125	-2.41	0.178	-1.98	0.245	-1.01	0.994	-0.79
1423086_at	Npc1	Niemann Pick type C1	1.27	0.149	-1.09	0.684	-1.05	0.574	-1.14	0.739	-0.5
1435771_at	Plcb4	phospholipase C, beta 4	-1.03	0.863	1.38	0.135	-1.26	0.322	-1.54	0.114	-0.61
1419879_s_at	Trim25	tripartite motif protein 25	1.2	0.118	-1.06	0.417	-1	0.948	-1.35	0.155	-0.55
1418453_a_at	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	-1.06	0.57	-1.29	0.056	1.42	0.162	-2.81	0.016	-0.94
1419733_at	Glipr1l2	GLI pathogenesis-related 1 like 2	1.48	0.603	-1.13	0.618	-1.28	0.133	-1.35	0.534	-0.57
1441751_at	AW493563	expressed sequence AW493563	1.39	0.098	-1.15	0.198	-1.13	0.327	-1.14	0.354	-0.51
1428688_at	Pdcd11	programmed cell death protein 11	-1.09	0.004	-1.26	0.014	1.43	0.059	-1.17	0.213	-0.52
1434417_at	---	---	-1.06	0.167	-1.03	0.646	1.23	0.383	-1.08	0.66	-0.49
1430695_at	Tlr4	toll-like receptor 4	1.66	0.338	-1.43	0.598	-1.28	0.597	-1.88	0.372	-0.73
1422052_at	Cdh8	cadherin 8	-1.04	0.945	-1.47	0.287	1.5	0.079	-1.25	0.606	-0.56
1445723_at	Plcl1	phospholipase C-like 1	-1.1	0.45	1.26	0.365	-1.03	0.931	-1.28	0.437	-0.54
1416599_at	Glis2	GLIS family zinc finger 2	1.33	0.643	-1.17	0.524	-1.05	0.843	-1.02	0.953	-0.48
1437910_at	Tmem39b	transmembrane protein 39b	-1.17	0.315	-1.11	0.423	1.39	0.078	-1.12	0.631	-0.5
1443747_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	1.85	0.291	-1.43	0.586	-1.7	0.058	-2.74	0.021	-1
1443083_at	Cpsf2	Cleavage and polyadenylation specific factor 2	1.4	0.243	-1.16	0.64	-1.14	0.726	-1.08	0.673	-0.49
1453363_at	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	1.41	0.52	-1.13	0.455	-1.18	0.373	-1.4	0.295	-0.58
1447959_at	Zfp398	zinc finger protein 398	-1.21	0.46	-1.09	0.501	1.4	0.172	-2.3	0.054	-0.8
1459111_at	4831440E17Rik	RIKEN cDNA 4831440E17 gene	2.11	0.103	-2.33	0.018	-1.65	0.172	-1.13	0.763	-0.75
1431263_at	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-1.17	0.807	1.59	0.455	-1.42	0.268	-1.21	0.679	-0.56
1437790_at	Eml5	echinoderm microtubule associated protein like 5	-1.17	0.744	-1.17	0.711	1.43	0.345	-1.19	0.528	-0.52
1446622_at	A330068G13Rik	RIKEN cDNA A330068G13 gene	1.69	0.554	-1.5	0.55	-1.27	0.509	-1.81	0.56	-0.72
1438689_at	C730049F21Rik	RIKEN cDNA C730049F21 gene	-1.63	0.163	1.57	0.063	-1.04	0.804	-1.18	0.362	-0.57
1455056_at	Lmo7	LIM domain only 7	-1.04	0.883	1.3	0.098	-1.14	0.38	-1.04	0.885	-0.48
1450915_at	Ap3b1	adaptor-related protein complex 3, beta 1 subunit	-1.04	0.629	-1.05	0.893	1.24	0.509	-1.09	0.804	-0.49
1421709_a_at	Fmo5	flavin containing monooxygenase 5	-1.14	0.647	-1.02	0.87	1.29	0.29	-1.36	0.112	-0.56
1437873_at	6030490I01Rik	RIKEN cDNA 6030490I01 gene	-1.03	0.742	1.25	0.138	-1.08	0.455	-1.28	0.575	-0.54
1451414_at	D13Wsu177e	DNA segment, Chr 13, Wayne State University 177, expressed	-1.12	0.219	1.27	0.45	-1.02	0.941	-1.45	0.256	-0.58
1457959_at	---	Transcribed locus	-2.39	0.007	1.85	0.158	-1.14	0.727	-1.64	0.425	-0.83
1433178_at	4933427C19Rik	RIKEN cDNA 4933427C19 gene	-1.15	0.61	-1.72	0.118	1.69	0.238	-1.25	0.636	-0.61
1445473_at	Azi2 /// Diras2	5-azacytidine induced gene 2 /// DIRAS family, GTP-binding RAS-like 2	-1.05	0.953	-2.39	0.23	1.77	0.267	-1.26	0.73	-0.73
1431617_at	4933405E24Rik	RIKEN cDNA 4933405E24 gene	1.45	0.648	-1.13	0.835	-1.23	0.675	-1.32	0.587	-0.56
1416186_at	Pnrc2	proline-rich nuclear receptor coactivator 2	-1.07	0.625	1.25	0.096	-1.04	0.522	-1.32	0.172	-0.54
1433588_at	D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-1.05	0.602	1.29	0.008	-1.11	0.414	-1.38	0.236	-0.56
1456174_x_at	Ndrg1	N-myc downstream regulated gene 1	-1.26	0.206	-1.18	0.593	1.5	0.023	-1.53	0.05	-0.62
1417629_at	Prodh /// LOC6711(	proline dehydrogenase /// similar to Proline oxidase, mitochondrial precursor (Pro	-1.03	0.863	-1.04	0.878	1.21	0.196	-1.01	0.94	-0.47
1449304_at	2310061J03Rik	RIKEN cDNA 2310061J03 gene	-1.13	0.059	-1.15	0.41	1.39	0.073	-1.2	0.44	-0.52
AFFX-r2-Bs-phe-M_	---	---	1.34	0.572	-1.19	0.027	-1.03	0.919	-1.66	0.442	-0.63
1454510_at	2900034C19Rik	RIKEN cDNA 2900034C19 gene	-1.89	0.089	1.88	0.087	-1.36	0.143	-1.05	0.82	-0.6
1430945_at	A930028C08Rik	RIKEN cDNA A930028C08 gene	-1.54	0.11	1.74	0.233	-1.32	0.32	-1.08	0.733	-0.55
1445144_at	Sntb1	Syntrophin, basic 1	1.55	0.228	-1.03	0.895	-1.6	0.024	-1.41	0.247	-0.62
1449247_at	Actrt2	actin-related protein T2	1.45	0.749	-1.25	0.751	-1.12	0.729	-2.38	0.262	-0.82
1454203_at	1700061J05Rik	RIKEN cDNA 1700061J05 gene	2.15	0.175	-1.69	0.406	-2.43	0.004	-1.44	0.309	-0.85
1451788_at	F11	coagulation factor XI	-1.01	0.983	-1.23	0.31	1.35	0.454	-1.4	0.307	-0.57
1453862_at	4930465K10Rik	RIKEN cDNA 4930465K10 gene	-1.68	0.3	1.82	0.47	-1.37	0.374	-1.09	0.896	-0.58
1433808_at	D330001F17Rik	RIKEN cDNA D330001F17 gene	-1.15	0.013	-1.09	0.307	1.37	0.085	-1.05	0.775	-0.48
1441245_a_at	Gm632	gene model 632, (NCBI)	1.18	0.83	-1.01	0.961	-1.02	0.97	-1.27	0.739	-0.53
1433945_at	5730507A09Rik	RIKEN cDNA 5730507A09 gene	-1.73	0.349	-2.03	0.227	2.08	0.123	-1.62	0.248	-0.82
1454901_at	6430570G24	Hypothetical protein 6430570G24	-1.17	0.34	1.31	0.384	-1.02	0.919	-1.23	0.644	-0.53
1421526_at	Tll2	tolloid-like 2	1.83	0.561	-1.48	0.16	-1.55	0.505	-1.01	0.964	-0.55
1420457_at	Dvl3	dishevelled 3, dsh homolog (Drosophila)	1.27	0.261	-1.14	0.818	-1	0.996	-1.71	0.101	-0.64
1418873_at	Sfxn4	sideroflexin 4	-1.05	0.725	1.25	0.64	-1.06	0.76	-1.21	0.368	-0.52
1436002_at	---	Transcribed locus	1.44	0.152	-1.12	0.843	-1.22	0.643	-3.65	0.137	-1.14

1419692_a_at	Ltc4s	leukotriene C4 synthase	-1.08	0.727	-1.28	0.639	1.44	0.224	-1.92	0.053	-0.71
1436687_x_at	Zfp706	zinc finger protein 706	-1.26	0.439	1.37	0.583	-1.01	0.981	-1.36	0.284	-0.56
1431664_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	-1.01	0.993	1.24	0.458	-1.09	0.837	-1.27	0.695	-0.53
1435288_at	Coro1a	coronin, actin binding protein 1A	-1.05	0.913	-2.39	0.14	1.78	0.104	-2.02	0.136	-0.92
1427294_a_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	-1.13	0.497	-1.17	0.322	1.41	0.229	-1.01	0.972	-0.47
1439248_at	Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	1.54	0.376	-1.19	0.699	-1.29	0.301	-1.13	0.707	-0.52
1421107_at	Stk4	serine/threonine kinase 4	1.46	0.309	-1.29	0.339	-1.1	0.729	-1.58	0.341	-0.63
1444089_at	Spnb2	spectrin beta 2	-1.03	0.869	1.55	0.177	-1.57	0.004	-1.46	0.136	-0.63
1440027_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	1.25	0.252	-1.1	0.295	-1.01	0.925	-1.17	0.439	-0.51
1433239_at	4930448E06Rik	RIKEN cDNA 4930448E06 gene	-2.39	0.136	2.04	0.389	-1.45	0.511	-1.48	0.044	-0.82
1458816_at	---	---	1.99	0.091	-1.65	0.079	-1.8	0.011	-1.04	0.926	-0.63
1432524_at	4930550G17Rik	RIKEN cDNA 4930550G17 gene	1.54	0.017	-1.34	0.31	-1.15	0.515	-1.25	0.175	-0.55
1457299_at	Grm4	glutamate receptor, metabotropic 4	-1.58	0.335	-1.22	0.662	1.7	0.007	-1.14	0.591	-0.56
1457348_at	Arf4	ADP-ribosylation factor 4	-1.21	0.111	1.47	0.256	-1.17	0.435	-1.08	0.186	-0.5
1424567_at	Tspan2	tetraspanin 2	1.44	0.016	-1.13	0.678	-1.21	0.256	-1.82	0.087	-0.68
1454067_a_at	4931406C07Rik	RIKEN cDNA 4931406C07 gene	-1.01	0.93	-1.12	0.533	1.27	0.346	-1.01	0.969	-0.47
1457582_at	Uty	Ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	-1.17	0.142	-2.45	0.215	1.89	0.26	-1.12	0.665	-0.71
1417433_at	Lypla2	lysophospholipase 2	-1.02	0.92	-1.12	0.467	1.28	0.357	-1.07	0.664	-0.48
1458917_at	Depdc5	DEP domain containing 5	-1.09	0.913	1.56	0.245	-1.47	0.481	-1.31	0.292	-0.58
1427391_a_at	Col12a1	procollagen, type XII, alpha 1	1.44	0.136	-1.31	0.412	-1.06	0.609	-1.45	0.437	-0.59
1423805_at	Dab2	disabled homolog 2 (Drosophila)	-1.13	0.52	1.35	0.302	-1.09	0.801	-1.3	0.189	-0.54
1437572_at	Dcp1b	DCP1 decapping enzyme homolog b (S. cerevisiae)	-1.16	0.417	-1.5	0.272	1.63	0.011	-1.79	0.345	-0.71
1422737_at	Ncoa3	nuclear receptor coactivator 3	-1.21	0.089	-1.14	0.571	1.45	0.136	-1.75	0.094	-0.66
1435914_at	Ncor1	nuclear receptor co-repressor 1	-1.04	0.906	1.24	0.261	-1.06	0.715	-1.34	0.436	-0.55
1434902_at	Rnf157	ring finger protein 157	-1.89	0.056	-1.07	0.804	1.69	0.307	-1.22	0.483	-0.62
1451052_at	Cog8	component of oligomeric golgi complex 8	1.22	0.125	-1.07	0.6	-1.01	0.925	-1.03	0.922	-0.47
1444174_at	Adamts8	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.2	0.701	1.44	0.47	-1.13	0.504	-1.35	0.743	-0.56
1430165_at	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	1.36	0.601	-1.07	0.789	-1.15	0.498	-2.55	0.111	-0.85
1434622_at	Iqce	IQ motif containing E	-1.25	0.215	-1.14	0.496	1.48	0.039	-1.3	0.276	-0.55
1435060_at	Tmod2	tropomodulin 2	-1.45	0.47	1.68	0.141	-1.27	0.128	-1.39	0.084	-0.61
1452440_at	Tnfsf12 /// Tnfsf12-t	tumor necrosis factor (ligand) superfamily, member 12 /// tumor necrosis factor (li	-1.02	0.913	1.18	0.429	-1.01	0.98	-1.01	0.979	-0.46
1447909_s_at	Selk	selenoprotein K	-1.12	0.528	1.27	0.269	-1.01	0.951	-1.02	0.891	-0.47
1435517_x_at	Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	-1.03	0.766	1.41	0.006	-1.28	0.174	-1.25	0.136	-0.54
1431829_a_at	Rgl3	ral guanine nucleotide dissociation stimulator-like 3	-1.13	0.355	-1.03	0.685	1.3	0.133	-1.14	0.776	-0.5
1422374_s_at	Olfr65 /// Olfr66	olfactory receptor 64 /// olfactory receptor 66	-1.33	0.438	-1.28	0.454	1.62	0.08	-1.42	0.296	-0.6
1451248_at	Prmt7	protein arginine N-methyltransferase 7	-1.19	0.496	-1.03	0.777	1.35	0.081	-1.46	0.049	-0.59
1427696_at	Fech	ferrochelatase	-1.6	0.464	1.71	0.343	-1.22	0.191	-1.02	0.933	-0.53
1431454_at	4930523O13Rik	RIKEN cDNA 4930523O13 gene	1.29	0.702	-1.11	0.832	-1.03	0.956	-1.07	0.722	-0.48
1425723_at	Nr1i2	nuclear receptor subfamily 1, group I, member 2	-1.21	0.071	-1.26	0.253	1.54	0.269	-1.16	0.693	-0.52
1415721_a_at	1200013P24Rik	RIKEN cDNA 1200013P24 gene	-1.01	0.959	-1.26	0.098	1.37	0.046	-1.22	0.379	-0.53
1423730_at	Clptm1l	CLPTM1-like	-1.01	0.247	1.17	0.203	-1.01	0.892	-1.13	0.656	-0.49
AFFX-PheX-M_at	---	---	1.31	0.655	-1.15	0.096	-1.02	0.959	-1.79	0.453	-0.66
1458536_at	Ccni	Cyclin I	-1.14	0.845	-1.5	0.095	1.61	0.058	-1.15	0.516	-0.54
1435920_x_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	1.91	0.165	-1.75	0.187	-1.48	0.503	-2.43	0.06	-0.94
1422536_at	Tnni3	troponin I, cardiac	-1.02	0.97	1.39	0.493	-1.28	0.246	-1.57	0.253	-0.62
1423887_a_at	1200003M09Rik	RIKEN cDNA 1200003M09 gene	-1.13	0.416	-1.24	0.505	1.47	0.203	-1.37	0.365	-0.57
1438897_at	Zdhhc3	Zinc finger, DHHC domain containing 3	-1.07	0.728	1.41	0.078	-1.22	0.39	-1.05	0.799	-0.48
1428808_at	Prickle2	prickle-like 2 (Drosophila)	-1	0.984	1.44	0.17	-1.38	0.002	-1.15	0.577	-0.52
1441386_at	Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1	-1.61	0.306	1.81	0.145	-1.36	0.448	-1.99	0.046	-0.79
1421345_at	Lrat	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)	-1.02	0.975	1.41	0.02	-1.29	0.322	-2.52	0.115	-0.86
1451492_at	Sla2	Src-like-adaptor 2	-1.15	0.625	1.45	0.099	-1.18	0.292	-5.62	0.013	-1.63
1424215_at	Fundc1	FUN14 domain containing 1	-1.06	0.419	1.25	0.008	-1.03	0.629	-1.06	0.798	-0.48
1440136_at	Zfp509	Zinc finger protein 509	1.86	0.205	-1.79	0.435	-1.34	0.511	-1.49	0.187	-0.69

1457195_at	Plekhm1	pleckstrin homology domain containing, family M (with RUN domain) member 1	-1.1	0.765	-1.14	0.763	1.38	0.13	-1.86	0.109	-0.68
1419737_a_at	Ldha	lactate dehydrogenase A	-1	0.985	-1.05	0.771	1.21	0.01	-1.09	0.467	-0.48
1442276_at	Lphn3	Latrophilin 3	-1.4	0.502	2.08	0.385	-2.74	0.035	-2.05	0.227	-1.03
1457686_at	B230333C21Rik	RIKEN cDNA B230333C21 gene	-1.66	0.175	1.63	0.107	-1.08	0.751	-1.07	0.818	-0.54
1456264_at	Commd7 /// LOC63	COMM domain containing 7 /// similar to COMM domain containing protein 7 /// si	1.33	0.392	-1.05	0.804	-1.14	0.119	-1.36	0.306	-0.56
1437036_at	AL033314	Expressed sequence AL033314	1.74	0.296	-1.58	0.47	-1.27	0.331	-1.13	0.727	-0.56
1454645_at	Mgrn1	mahogunin, ring finger 1	-1.16	0.268	-1.22	0.015	1.48	0.045	-1.22	0.42	-0.53
1448093_s_at	C77405	expressed sequence C77405	2.08	0.331	-1.47	0.455	-2.5	0.011	-1.22	0.284	-0.78
1429384_at	Csnk1g3	casein kinase 1, gamma 3	-1.03	0.921	-1.05	0.624	1.24	0.195	-1.52	0.155	-0.59
1444581_at	Rangap1	RAN GTPase activating protein 1	-1.21	0.558	1.41	0.16	-1.08	0.728	-1.13	0.706	-0.5
1428158_at	Akt1s1	AKT1 substrate 1 (proline-rich)	-1.01	0.948	-1.12	0.501	1.29	0.357	-1.12	0.114	-0.49
1425099_a_at	Arntl	aryl hydrocarbon receptor nuclear translocator-like	-1.34	0.551	1.48	0.352	-1.06	0.827	-1.32	0.201	-0.56
1451474_a_at	Parp8	poly (ADP-ribose) polymerase family, member 8	-1.01	0.967	1.23	0.335	-1.06	0.738	-1.99	0.112	-0.71
1437495_at	Mbtps2	membrane-bound transcription factor peptidase, site 2	-1.28	0.194	1.53	0.244	-1.17	0.123	-1.46	0.118	-0.59
1434965_at	D19Ertd386e	DNA segment, Chr 19, ERATO Doi 386, expressed	1.46	0.147	-1.14	0.562	-1.21	0.428	-1.03	0.814	-0.48
1449853_at	Sfxn2 /// LOC67714	sideroflexin 2 /// similar to Sideroflexin-2	1.39	0.035	-1.06	0.624	-1.21	0.313	-1.12	0.581	-0.5
1433406_at	LOC668408 /// LOC	hypothetical protein LOC668408 /// hypothetical protein LOC670057	-1.55	0.463	1.62	0.422	-1.11	0.791	-1.32	0.436	-0.59
1439937_at	---	---	1.33	0.409	-1.01	0.974	-1.18	0.53	-1.09	0.696	-0.49
1459881_at	AI595406	expressed sequence AI595406	1.68	0.399	-1.57	0.497	-1.18	0.685	-1.16	0.759	-0.56
1422371_at	Olfr1507	olfactory receptor 1507	2.04	0.01	-1.49	0.631	-2.21	0.262	-1.13	0.855	-0.7
1452302_at	Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	-1.07	0.503	1.38	0.221	-1.17	0.434	-1.56	0.114	-0.61
1442127_at	---	Transcribed locus	-1.11	0.774	-1.13	0.52	1.39	0.25	-2.13	0.148	-0.75
1454972_at	Atcay	ataxia, cerebellar, Cayman type homolog (human)	1.82	0.519	-1.33	0.195	-1.68	0.039	-1.71	0.376	-0.72
1454583_at	2810034D10Rik	RIKEN cDNA 2810034D10 gene	-1.34	0.711	-1.29	0.646	1.65	0.185	-1.28	0.736	-0.57
1429232_at	2610528B01Rik	RIKEN cDNA 2610528B01 gene	-1.04	0.8	1.35	0.616	-1.17	0.167	-1.16	0.438	-0.5
1423264_at	Bop1	block of proliferation 1	-1.06	0.369	-1.16	0.002	1.36	0.069	-1.1	0.337	-0.49
1442773_at	---	Transcribed locus	1.5	0.056	-1.01	0.98	-1.46	0.136	-1.48	0.33	-0.61
1446150_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130070I2	1.39	0.356	-1.08	0.632	-1.18	0.514	-1.29	0.382	-0.54
1457533_at	---	---	-1.27	0.079	1.49	0.022	-1.12	0.859	-1.58	0.39	-0.62
1445278_at	Ggn	gametogenetin	-1.62	0.078	1.74	0.221	-1.23	0.095	-1.06	0.847	-0.54
1439065_x_at	MGC117846	Similar to zinc finger protein 665	-1.13	0.851	-1.2	0.047	1.45	0.37	-1.94	0.126	-0.7
1448637_at	Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	-1.12	0.731	-1.03	0.764	1.31	0.075	-1.15	0.517	-0.5
1443294_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	-1.17	0.818	1.32	0.409	-1.01	0.957	-1.15	0.664	-0.5
1416307_at	Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	-1.19	0.331	-1.08	0.24	1.41	0.048	-1.08	0.43	-0.49
1416562_at	Gad1	glutamic acid decarboxylase 1	-2.18	0.458	1.77	0.24	-1.06	0.915	-5.52	0.066	-1.75
1457581_at	Ubxd3	UBX domain containing 3	-1.4	0.139	1.97	0.044	-2.08	0.281	-1.39	0.65	-0.72
1425066_a_at	1110061O04Rik	RIKEN cDNA 1110061O04 gene	-1.12	0.372	-1.11	0.357	1.38	0.244	-1.27	0.002	-0.53
1435403_at	1700007L15Rik	RIKEN cDNA 1700007L15 gene	-1.06	0.631	-1.04	0.737	1.27	0.31	-1.3	0.074	-0.53
1443102_at	Zfp597	zinc finger protein 597	1.91	0.516	-1.34	0.05	-1.95	0.116	-2.27	0.352	-0.91
1432207_a_at	Toe1	target of EGR1, member 1 (nuclear)	-1.01	0.955	-1.16	0.569	1.32	0.146	-1.23	0.466	-0.52
1454458_at	6230426I18Rik	RIKEN cDNA 6230426I18 gene	-1.13	0.632	-1.23	0.283	1.47	0.456	-1.35	0.208	-0.56
1454053_at	5730527A11Rik	RIKEN cDNA 5730527A11 gene	-1.64	0.495	1.63	0.402	-1.07	0.86	-1.5	0.222	-0.65
1457556_at	---	PREDICTED: Mus musculus hypothetical LOC433662 (LOC433662), mRNA	1.87	0.309	-1.63	0.414	-1.45	0.116	-3.49	0.058	-1.18
1444871_at	AU022697	expressed sequence AU022697	1.5	0.115	-1.29	0.724	-1.11	0.602	-1.23	0.703	-0.53
1451126_at	Maf1	MAF1 homolog (S. cerevisiae)	-1.06	0.707	-1.01	0.94	1.24	0.196	-1.06	0.036	-0.47
1422019_at	Tgfbr2	transforming growth factor, beta receptor II	1.53	0.404	-1.26	0.594	-1.18	0.756	-1.03	0.953	-0.49
1448739_x_at	Rps18	ribosomal protein S18	1.32	0.051	-1.02	0.842	-1.14	0.105	-1.14	0.007	-0.5
1438155_x_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	-1.18	0.158	-1.02	0.893	1.34	0.184	-1.1	0.559	-0.49
1440181_at	Gm1568	gene model 1568, (NCBI)	-1.4	0.456	1.66	0.398	-1.25	0.721	-1.09	0.837	-0.52
1435254_at	Plxnb1	plexin B1	-1.09	0.648	1.29	0.265	-1.04	0.824	-1.23	0.473	-0.52
1448177_at	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.34	0.239	-1.39	0.708	1.71	0.365	-1.44	0.707	-0.62
1438331_at	Ypel2	Yippee-like 2 (Drosophila)	-1.11	0.72	1.44	0.344	-1.2	0.487	-1.35	0.347	-0.55
1446660_at	Ccdc46	Coiled-coil domain containing 46	1.72	0.413	-1.44	0.243	-1.31	0.307	-1	0.984	-0.51

1445717_at	E130108L08Rik	RIKEN cDNA E130108L08 gene	1.98	0.586	-1.74	0.228	-1.6	0.064	-1.19	0.724	-0.64
1427985_at	9630042H07Rik	RIKEN cDNA 9630042H07 gene	1.29	0.556	-1.08	0.853	-1.05	0.876	-1.21	0.333	-0.51
1421243_at	Rnf144	ring finger protein 144	-1.03	0.972	-1.25	0.745	1.4	0.484	-1.71	0.41	-0.65
1457919_at	D030054H15Rik	RIKEN cDNA D030054H15 gene	-1.18	0.75	-1.48	0.536	1.65	0.212	-1.02	0.94	-0.51
1459549_at	Dph5	DPH5 homolog (S. cerevisiae)	-1.45	0.217	1.55	0.431	-1.06	0.922	-1.64	0.435	-0.65
1456126_at	Malt1	mucosa associated lymphoid tissue lymphoma translocation gene 1	-1.18	0.329	-1.03	0.893	1.36	0.256	-2.17	0.085	-0.76
1424850_at	Map3k1 /// LOC670	mitogen activated protein kinase kinase kinase 1 /// similar to Mitogen-activated p	-1.03	0.653	1.25	0.415	-1.04	0.86	-1.18	0.351	-0.5
1428162_at	4933421E11Rik	RIKEN cDNA 4933421E11 gene	-1.01	0.927	1.24	0.185	-1.05	0.614	-1.53	0.106	-0.59
1425968_s_at	Speg	SPEG complex locus	-1.15	0.459	-1.11	0.624	1.41	0.225	-1.14	0.491	-0.5
1422394_at	V1rc4	vomeronasal 1 receptor, C4	-1.48	0.348	1.53	0.251	-1.03	0.964	-1.13	0.832	-0.53
1456100_at	BC089491	cDNA sequence BC089491	2.05	0.524	-2.93	0.064	-1.27	0.358	-2.84	0.212	-1.25
1438056_x_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.14	0.606	1.44	0.305	-1.16	0.032	-1.14	0.512	-0.5
1441575_at	---	---	2.01	0.457	-1.54	0.457	-1.92	0.028	-1.57	0.404	-0.76
1455651_at	Terf2	telomeric repeat binding factor 2	-1	0.983	1.19	0.18	-1.01	0.857	-1.13	0.027	-0.49
1445839_at	---	---	-1.2	0.447	-1.08	0.796	1.41	0.402	-1.3	0.317	-0.54
1431125_a_at	Tarsl1	threonyl-tRNA synthetase-like 1	-1.13	0.567	-1.27	0.12	1.51	0.007	-1.4	0.065	-0.57
1433904_at	Ggnbp1	gametogenetin binding protein 1	-1.3	0.049	-1.12	0.725	1.52	0.242	-1.22	0.622	-0.53
1443875_at	Gm603	gene model 603, (NCBI)	-1.43	0.345	1.68	0.159	-1.25	0.565	-2.36	0.055	-0.84
1447047_at	2610203C20Rik	RIKEN cDNA 2610203C20 gene	-1.16	0.594	1.87	0.102	-2.24	0.01	-1.22	0.742	-0.69
1432455_a_at	Prlpc4	prolactin-like protein C 4	-1.24	0.579	-1.05	0.932	1.42	0.463	-1	1	-0.47
1443224_at	Enpp2	ectonucleotide pyrophosphatase/phosphodiesterase 2	-1.35	0.46	1.7	0.454	-1.35	0.549	-1.9	0.328	-0.73
1457724_at	Ctsl	cathepsin L	-1.21	0.223	1.7	0.167	-1.55	0.077	-1.85	0.412	-0.73
1446691_at	Pdgfd	Platelet-derived growth factor, D polypeptide	-1.07	0.786	1.31	0.635	-1.07	0.709	-1.92	0.11	-0.69
1445271_at	9230105E10Rik	RIKEN cDNA 9230105E10 gene	-1.19	0.831	-1.42	0.336	1.63	0.138	-1.82	0.101	-0.7
1448709_at	Arid1a /// LOC6694	AT rich interactive domain 1A (Swi1 like) /// similar to AT rich interactive domain 1	-1.06	0.603	-1.13	0.164	1.35	0.245	-1.19	0.484	-0.51
1440316_at	6430526N21Rik	RIKEN cDNA 6430526N21 gene	-1.05	0.846	-1.05	0.837	1.28	0.144	-2.15	0.164	-0.74
1416380_at	Mov10	Moloney leukemia virus 10	-1.2	0.508	-1.07	0.71	1.41	0.175	-1.09	0.551	-0.49
1459031_at	Ttll4	tubulin tyrosine ligase-like family, member 4	1.62	0.422	-1.05	0.957	-1.65	0.071	-1.18	0.735	-0.57
1448733_at	Bmi1	B lymphoma Mo-MLV insertion region 1	-1.02	0.895	1.29	0.254	-1.1	0.338	-1.59	0.219	-0.61
1444716_at	---	---	-1.01	0.95	1.26	0.061	-1.09	0.621	-1.36	0.143	-0.55
1445180_at	Srd5a2l	steroid 5 alpha-reductase 2-like	1.5	0.442	-1.19	0.774	-1.19	0.39	-1.81	0.091	-0.67
1420440_at	Ppy	pancreatic polypeptide	-1.13	0.81	1.92	0.003	-2.65	0.033	-1.09	0.87	-0.74
1448400_a_at	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.01	0.975	-1.11	0.464	1.28	0.048	-1.41	0.07	-0.56
1433386_at	4933428C20Rik	RIKEN cDNA 4933428C20 gene	-1.19	0.343	1.69	0.146	-1.53	0.386	-1.22	0.298	-0.56
1447547_at	Ltbp1	latent transforming growth factor beta binding protein 1	1.37	0.623	-1.09	0.786	-1.13	0.342	-1.06	0.678	-0.48
1433878_at	Mrps26	mitochondrial ribosomal protein S26	-1.03	0.76	-1.06	0.357	1.27	0.047	-1.19	0.324	-0.5
1420533_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	1.47	0.453	-1.11	0.736	-1.24	0.551	-1	1	-0.47
1431225_at	Sox11	SRY-box containing gene 11	-1.08	0.815	1.36	0.596	-1.12	0.78	-1.91	0.105	-0.69
1450093_s_at	Zbtb7a	zinc finger and BTB domain containing 7a	-1.29	0.38	-1.6	0.014	1.78	0.064	-1.25	0.438	-0.59
1416692_at	Coil	coilin	-1.07	0.163	-1.02	0.795	1.27	0.127	-1.04	0.62	-0.47
1429279_at	Wars2	tryptophanyl tRNA synthetase 2 (mitochondrial)	-1.02	0.837	-1.11	0.626	1.3	0.228	-1.41	0.222	-0.56
1459407_at	Nbeal1	Neurobeachin like 1	1.46	0.112	-1.3	0.665	-1.05	0.939	-1.61	0.525	-0.63
1427621_at	Lrp2	Low density lipoprotein receptor-related protein 2	-1.38	0.624	1.55	0.256	-1.1	0.856	-1.39	0.091	-0.58
1456000_at	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	-1.07	0.842	1.37	0.574	-1.13	0.481	-1.16	0.395	-0.5
1431848_at	Angptl2	angiopoietin-like 2	1.65	0.326	-1.48	0.455	-1.18	0.726	-1.47	0.029	-0.62
1438111_at	Pvrl1	Poliovirus receptor-related 1	-1.01	0.979	-1.09	0.9	1.27	0.226	-3.05	0.237	-0.97
1453455_at	1810059M14Rik	RIKEN cDNA 1810059M14 gene	-1.19	0.059	1.43	0.361	-1.1	0.565	-1.62	0.034	-0.62
1452478_at	Alpk2	alpha-kinase 2	-2.92	0.209	-2.34	0.34	2.41	0.141	-2.04	0.091	-1.22
1450498_at	Mthfr	5,10-methylenetetrahydrofolate reductase	-1.33	0.681	-1.12	0.847	1.54	0.058	-1.11	0.856	-0.5
1422736_at	Ranbp9	RAN binding protein 9	-1.05	0.621	-1.09	0.137	1.31	0.046	-1.02	0.92	-0.46
1452407_at	Spag4	sperm associated antigen 4	-1.44	0.707	1.61	0.17	-1.14	0.819	-3.01	0.202	-0.99
1419625_at	Hspa1l	heat shock protein 1-like	-2.15	0.462	-1.08	0.833	1.79	0.274	-1.21	0.79	-0.66
1459776_x_at	Pdpk1	3-phosphoinositide dependent protein kinase-1	-2.26	0.171	1.75	0.356	-1.01	0.952	-1.3	0.356	-0.7

1430456_at	5830406C21Rik	RIKEN cDNA 5830406C21 gene	1.55	0.592	-1.1	0.576	-1.37	0.412	-1.19	0.76	-0.53
1454021_a_at	Exosc10	exosome component 10	-1.04	0.606	-1.09	0.424	1.3	0.211	-1.25	0.025	-0.52
1456501_at	2610528E23Rik	RIKEN cDNA 2610528E23 gene	1.56	0.519	-1.32	0.413	-1.15	0.552	-1.03	0.856	-0.49
1434873_a_at	Centb1	centaurin, beta 1	-1.36	0.31	-1.05	0.809	1.5	0.203	-2.58	0.057	-0.87
1416335_at	Mif	macrophage migration inhibitory factor	-1.03	0.907	-1.05	0.827	1.26	0.25	-1.02	0.869	-0.46
1422942_at	Galr2	galanin receptor 2	2.18	0.042	-1.65	0.195	-2.54	0.004	-1	0.995	-0.75
1435763_at	Tbc1d16	TBC1 domain family, member 16	1.35	0.125	-1.18	0.405	-1.01	0.924	-1.17	0.466	-0.5
1456078_x_at	Tubb2c	tubulin, beta 2c	-1	0.994	-1	0.99	1.19	0.333	-1.24	0.609	-0.51
1441314_at	Incenp	inner centromere protein	1.52	0.093	-1.38	0.355	-1.07	0.037	-1.34	0.637	-0.57
1452065_at	BC027127	cDNA sequence BC027127	1.93	0.018	-2.6	0.084	-1.15	0.549	-1.45	0.242	-0.82
1443679_at	2510003B16Rik	RIKEN cDNA 2510003B16 gene	-1.19	0.198	-1.13	0.773	1.46	0.109	-1.17	0.605	-0.51
1437670_x_at	Cd151	CD151 antigen	-1.12	0.011	1.48	0.005	-1.23	0.005	-1.14	0.3	-0.5
1456196_x_at	Fkbp1a	FK506 binding protein 1a	-1.06	0.394	1.27	0.084	-1.02	0.784	-1.45	0.172	-0.57
1426988_at	Klhdc5	kelch domain containing 5	1.33	0.296	-1.1	0.758	-1.05	0.863	-1.58	0.153	-0.6
1418410_at	Jrk	jerky	-1.1	0.218	1.37	0.044	-1.11	0.607	-1.04	0.654	-0.47
1434444_s_at	---	---	-1	0.95	1.26	0.245	-1.08	0.705	-1.03	0.495	-0.46
1447361_at	Mtx1	Metaxin 1	-1	0.994	1.56	0.363	-1.59	0.033	-1.32	0.492	-0.59
1418224_at	Sec11l1	Sec11-like 1 (S. cerevisiae)	-1.19	0.832	-1.04	0.716	1.38	0.481	-1.27	0.393	-0.53
1447992_s_at	Pcsk2	proprotein convertase subtilisin/kexin type 2	-1.15	0.801	-1.24	0.636	1.51	0.312	-1.63	0.439	-0.63
1440619_at	Mapk8ip1	mitogen activated protein kinase 8 interacting protein 1	-1.2	0.529	-1.09	0.763	1.43	0.345	-2.6	0.111	-0.86
1426586_at	Slc25a11	solute carrier family 25 (mitochondrial carrier oxoglutarate carrier), member 11	-1.13	0.545	-1.09	0.541	1.39	0.054	-1.39	0.207	-0.56
1434769_at	Btbd9	BTB (POZ) domain containing 9	-1.15	0.656	-1.03	0.749	1.35	0.208	-1.03	0.882	-0.47
1432825_at	2900018N21Rik	RIKEN cDNA 2900018N21 gene	1.69	0.452	-1.18	0.723	-1.53	0.15	-1.2	0.359	-0.56
1454729_at	Tmem108	transmembrane protein 108	-1.11	0.517	1.52	0.037	-1.29	0.178	-4.44	0.011	-1.33
1443522_s_at	Phip	pleckstrin homology domain interacting protein	-1.09	0.674	-1.26	0.719	1.48	0.247	-1.16	0.738	-0.51
1426280_at	AV249152	expressed sequence AV249152	-1.3	0.124	-1.25	0.365	1.62	0.219	-1.01	0.949	-0.48
1443127_at	9630021D06Rik	RIKEN cDNA 9630021D06 gene	-1.64	0.254	1.73	0.372	-1.17	0.577	-2.89	0.119	-1
1426109_a_at	Slc14a2	solute carrier family 14 (urea transporter), member 2	-1.27	0.262	1.48	0.118	-1.09	0.836	-1.27	0.51	-0.54
1423304_a_at	Rnf111	ring finger 111	-1.07	0.495	-1.09	0.35	1.34	0.056	-1.4	0.169	-0.56
1452187_at	Rbm5	RNA binding motif protein 5	-1.04	0.941	-1.03	0.915	1.26	0.566	-1.26	0.579	-0.52
1422243_at	Fgf7	fibroblast growth factor 7	1.36	0.528	-1.01	0.979	-1.19	0.319	-1.63	0.045	-0.62
1450021_at	Ubqln2	ubiquilin 2	-1.07	0.686	-1	0.995	1.26	0.065	-1.21	0.458	-0.51
1447946_at	Adam23	a disintegrin and metallopeptidase domain 23	-1.14	0.729	1.6	0.233	-1.4	0.232	-2.03	0.126	-0.74
1431789_s_at	Tmed5	transmembrane emp24 protein transport domain containing 5	-1.04	0.864	-1.29	0.318	1.45	0.419	-1.04	0.941	-0.48
1438174_x_at	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	-1.12	0.387	-1	0.944	1.3	0.381	-1.07	0.453	-0.47
1425689_at	Dpys	dihydropyrimidinase	-1.04	0.923	-1.5	0.158	1.57	0.151	-1.22	0.457	-0.55
1422818_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-1.14	0.181	1.45	0.172	-1.16	0.436	-2.08	0.06	-0.73
1420159_at	Myo1e	myosin IE	1.52	0.178	-1.18	0.672	-1.21	0.707	-1.14	0.636	-0.5
1419662_at	Ogn	osteoglycin	1.62	0.199	-1.65	0.205	-1.03	0.923	-1.8	0.082	-0.72
1432385_a_at	Agtpbp1	ATP/GTP binding protein 1	-1.16	0.724	-1.08	0.802	1.4	0.635	-1.33	0.651	-0.54
1456312_x_at	Gsn	gelsolin	-1.12	0.394	1.48	0.064	-1.22	0.053	-1.37	0.143	-0.56
1437516_at	---	Transcribed locus	-1.21	0.35	1.45	0.1	-1.08	0.779	-1.04	0.832	-0.47
1459827_x_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	-1.22	0.403	-1.13	0.255	1.49	0.106	-1.09	0.647	-0.49
1436734_at	E130309F12Rik	RIKEN cDNA E130309F12 gene	-1.83	0.042	1.98	0.295	-1.51	0.434	-1.62	0.55	-0.74
1425222_x_at	D630002G06Rik ///	RIKEN cDNA D630002G06 gene /// RIKEN cDNA C730048C13 gene /// similar to	-1.02	0.674	1.22	0.459	-1.01	0.975	-1.45	0.478	-0.56
1457438_at	---	---	-1.32	0.215	1.57	0.137	-1.15	0.792	-1	0.998	-0.48
1419495_at	Immp2l	IMP2 inner mitochondrial membrane peptidase-like (S. cerevisiae)	-1.31	0.269	-1.17	0.2	1.58	0.002	-1.59	0.14	-0.62
1454041_at	D14Ertd581e	DNA segment, Chr 14, ERATO Doi 581, expressed	-1.22	0.686	1.66	0.189	-1.4	0.222	-1.15	0.815	-0.53
1430343_at	Nup205	nucleoporin 205	-1.2	0.506	-1.36	0.24	1.63	0.11	-1.04	0.903	-0.49
1459782_x_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.29	0.836	1.5	0.49	-1.08	0.766	-1.25	0.668	-0.53
1453521_at	4933405L10Rik	RIKEN cDNA 4933405L10 gene	1.68	0.377	-1.44	0.443	-1.21	0.784	-1.74	0.509	-0.68
1438165_x_at	Vat1	vesicle amine transport protein 1 homolog (T californica)	-1.13	0.705	1.4	0.348	-1.1	0.726	-1.07	0.784	-0.47
1417262_at	Ptgs2	prostaglandin-endoperoxide synthase 2	-1.18	0.778	1.83	0.427	-1.94	0.015	-1.33	0.593	-0.66

1441566_at	---	Transcribed locus	-1.15	0.801	1.58	0.511	-1.34	0.215	-1.52	0.491	-0.61
1454761_at	BC005764	cDNA sequence BC005764	-1.04	0.858	-1.08	0.523	1.3	0.325	-1.44	0.511	-0.56
1417048_at	Prom2	prominin 2	-1.02	0.935	-1.71	0.372	1.64	0.403	-1.02	0.976	-0.53
1416598_at	Glis2	GLIS family zinc finger 2	-1.03	0.753	-1.18	0.66	1.38	0.202	-1.3	0.149	-0.53
1428506_at	Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydr	-1.24	0.554	-1.32	0.23	1.63	0.163	-1.31	0.421	-0.56
1455685_at	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2	1.44	0.149	-1.12	0.522	-1.17	0.214	-1.15	0.601	-0.5
1443841_x_at	---	---	-1.51	0.389	1.59	0.231	-1.06	0.867	-1.52	0.334	-0.63
1425822_a_at	Dtx1	deltex 1 homolog (Drosophila)	-1.27	0.264	-1.18	0.331	1.56	0.226	-2.52	0.075	-0.85
1435056_x_at	Pofut2	protein O-fucosyltransferase 2	-1.02	0.5	-1.02	0.884	1.24	0.088	-1.14	0.316	-0.49
1460037_at	2610510H03Rik	RIKEN cDNA 2610510H03 gene	-1.03	0.363	-1.17	0.194	1.37	0.046	-1.26	0.036	-0.52
1439906_at	---	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130004J	-1.32	0.258	1.56	0.084	-1.14	0.568	-1.01	0.984	-0.48
1442029_at	Kcnq1	Potassium voltage-gated channel, subfamily Q, member 1	-1.36	0.611	1.78	0.182	-1.45	0.098	-1.57	0.179	-0.65
1426510_at	Sccpdh	saccharopine dehydrogenase (putative)	-1.15	0.333	1.4	0.178	-1.07	0.624	-1.26	0.357	-0.52
1446634_at	D830036C21Rik	RIKEN cDNA D830036C21 gene	1.93	0.204	-1.11	0.847	-2.71	0.033	-1.77	0.294	-0.92
1451566_at	BC005471	cDNA sequence BC005471	-1.18	0.367	1.53	0.059	-1.23	0.209	-1.29	0.407	-0.54
1451812_at	Adam22	a disintegrin and metallopeptidase domain 22	-1.47	0.033	1.68	0.294	-1.19	0.534	-1.42	0.13	-0.6
1440779_s_at	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	1.39	0.293	-1.12	0.831	-1.09	0.565	-1.71	0.425	-0.63
1449762_at	---	Transcribed locus	-1.26	0.682	1.46	0.248	-1.06	0.655	-1.34	0.023	-0.55
1443441_x_at	LOC380850	similar to hypothetical protein FLJ14345	-1.35	0.618	1.63	0.583	-1.21	0.287	-1.66	0.244	-0.65
1423687_a_at	Man2c1	mannosidase, alpha, class 2C, member 1	-1.04	0.634	-1	0.961	1.24	0.125	-1.45	0.175	-0.56
1427492_at	Pof1b	premature ovarian failure 1B	-1.03	0.866	1.58	0.373	-1.55	0.019	-1.32	0.251	-0.58
1432728_at	5830433D23Rik	RIKEN cDNA 5830433D23 gene	-1.12	0.657	-1.78	0.159	1.74	0.038	-1.24	0.243	-0.6
1445756_at	---	Transcribed locus	1.48	0.142	-1.27	0.364	-1.08	0.903	-1.44	0.576	-0.58
1455670_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930003N	-1.33	0.045	1.56	0.43	-1.12	0.239	-1.21	0.44	-0.53
1433053_at	Itgb2l	integrin beta 2-like	-1.47	0.525	-1.05	0.945	1.56	0.348	-1.04	0.949	-0.5
1449876_at	Prkg1	protein kinase, cGMP-dependent, type I	2.34	0.057	-2.32	0.143	-2.35	0.091	-1.15	0.709	-0.87
1448316_at	Cmtm3	CKLF-like MARVEL transmembrane domain containing 3	-1.07	0.68	1.33	0.013	-1.08	0.646	-1.06	0.682	-0.47
1419487_at	Mybph	myosin binding protein H	-1.31	0.426	1.62	0.552	-1.23	0.113	-1.73	0.129	-0.66
1425981_a_at	Rbl2 /// LOC635075	retinoblastoma-like 2 /// similar to retinoblastoma-like 2	-1	0.942	-1.03	0.711	1.24	0.055	-1.19	0.448	-0.5
1451471_at	3230401I01Rik	RIKEN cDNA 3230401I01 gene	-1.23	0.191	-1.05	0.734	1.44	0.08	-1.5	0	-0.59
1433920_at	Sema4c	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	-1.16	0.302	1.34	0.103	-1	0.992	-1.08	0.661	-0.47
1459413_at	Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	-1.49	0.46	1.56	0.222	-1.03	0.925	-1.09	0.676	-0.51
1451809_s_at	Rwdd3	RWD domain containing 3	-1.11	0.744	-1.09	0.623	1.38	0	-1.23	0.59	-0.51
1444832_at	Hip1r	Huntingtin interacting protein 1 related	1.56	0.441	-1.16	0.776	-1.27	0.679	-2.57	0.427	-0.86
1449791_x_at	9130023D20Rik	RIKEN cDNA 9130023D20 gene	-1.06	0.9	1.45	0.373	-1.24	0.32	-1.23	0.544	-0.52
1430370_at	Eprs	glutamyl-prolyl-tRNA synthetase	1.85	0.286	-1.39	0.566	-1.58	0.089	-1.12	0.356	-0.56
1444411_at	---	---	1.51	0.118	-1.08	0.694	-1.3	0.193	-1.33	0.42	-0.55
1427012_at	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1	1.25	0.697	-1.01	0.976	-1.04	0.69	-1.15	0.649	-0.49
1456677_at	Herc4	Hect domain and RLD 4	1.72	0.186	-1.42	0.268	-1.28	0.181	-1.31	0.487	-0.57
1446152_at	Lass6	Longevity assurance homolog 6 (S. cerevisiae)	-1.58	0.54	1.59	0.339	-1.02	0.962	-1.76	0.126	-0.69
1433445_x_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-1.12	0.547	1.39	0.182	-1.08	0.652	-1.91	0.103	-0.68
1440197_at	BC032203	cDNA sequence BC032203	-1.3	0.205	-1.36	0.424	1.7	0.026	-1.47	0.318	-0.61
1460652_at	Esrra	estrogen related receptor, alpha	-1.25	0.318	-1.07	0.656	1.47	0.131	-1.37	0.264	-0.55
1449912_at	Ssxb1 /// LOC6310	synovial sarcoma, X member B, breakpoint 1 /// similar to SSXB1 protein	-1.55	0.331	1.89	0.424	-1.5	0.512	-1.12	0.82	-0.57
1451298_at	Plekhh3	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	-1.05	0.42	-1.21	0.539	1.43	0.495	-1.15	0.84	-0.5
1455186_a_at	1190003J15Rik	RIKEN cDNA 1190003J15 gene	1.29	0.283	-1.07	0.173	-1.02	0.914	-1.23	0.65	-0.51
1428649_at	Cand1	cullin associated and neddylation disassociated 1	-1.1	0.469	-1.14	0.317	1.42	0.285	-1.3	0.524	-0.53
1431041_at	Gtpbp8	GTP-binding protein 8 (putative)	-1.1	0.739	1.31	0.588	-1.01	0.985	-1.15	0.855	-0.49
1431806_at	4931408D14Rik	RIKEN cDNA 4931408D14 gene	-1.03	0.768	-1.04	0.917	1.27	0.306	-1.03	0.929	-0.46
1451426_at	D11Lgp2e	DNA segment, Chr 11, Lothar Hennighausen 2, expressed	-1.24	0.291	-1.21	0.129	1.58	0.015	-1.38	0.166	-0.57
1450786_x_at	LOC669660	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ an	-1.02	0.933	-1.58	0.163	1.59	0.493	-1.72	0.023	-0.68
1460441_at	LOC668166	similar to Zinc finger X-linked protein ZXDB	-1.12	0.23	-1.14	0.174	1.44	0.001	-1.15	0.652	-0.49
1430885_at	1110012N22Rik	RIKEN cDNA 1110012N22 gene	-1.14	0.709	1.4	0.179	-1.07	0.558	-1.1	0.523	-0.48

1449058_at	Gli1	GLI-Kruppel family member GLI1	-1.08	0.889	1.52	0.18	-1.31	0.462	-1.6	0.295	-0.62
1443058_at	2900006F19Rik	RIKEN cDNA 2900006F19 gene	-1.13	0.774	1.58	0.258	-1.35	0.193	-1.67	0.137	-0.64
1417668_at	Rtn4ip1	reticulon 4 interacting protein 1	-1.34	0.483	-1.23	0.225	1.65	0.04	-1.07	0.549	-0.5
1450458_at	Ncoa2	nuclear receptor coactivator 2	-1.15	0.634	-1.29	0.513	1.56	0.488	-1.67	0.471	-0.64
1433117_at	2300004M11Rik	RIKEN cDNA 2300004M11 gene	1.76	0.352	-1.54	0.152	-1.25	0.631	-2.52	0.154	-0.89
1460121_at	9630010G10Rik	RIKEN cDNA 9630010G10 gene	-1.03	0.929	1.54	0.371	-1.43	0.158	-1.43	0.34	-0.59
1447474_at	Ramp1	Receptor (calcitonin) activity modifying protein 1	-1.18	0.742	1.63	0.185	-1.37	0.548	-1.78	0.029	-0.67
1440102_at	Slc36a3	solute carrier family 36 (proton/amino acid symporter), member 3	-1.96	0.486	2.06	0.227	-1.55	0.422	-1.37	0.173	-0.71
1441977_at	9630023C09Rik	RIKEN cDNA 9630023C09 gene	-1.06	0.851	1.67	0.276	-1.68	0.189	-3.41	0.056	-1.12
1454291_at	4933428P19Rik	RIKEN cDNA 4933428P19 gene	1.54	0.4	-1.11	0.866	-1.3	0.681	-1.88	0.162	-0.69
1460490_at	Mrpl15	mitochondrial ribosomal protein L15	1.47	0.348	-1.07	0.893	-1.25	0.747	-1.68	0.158	-0.63
1455809_x_at	Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	-1.01	0.961	1.28	0.183	-1.06	0.614	-2.52	0.015	-0.83
1444575_at	1500002O20Rik	RIKEN cDNA 1500002O20 gene	-1.02	0.827	1.27	0.36	-1.04	0.861	-1.17	0.34	-0.49
1458810_at	---	---	-1.3	0.761	-1.24	0.685	1.64	0.258	-1.21	0.683	-0.53
1447382_at	Pigt	phosphatidylinositol glycan anchor biosynthesis, class T	-1.23	0.735	1.67	0.373	-1.37	0.071	-1.16	0.58	-0.52
1456060_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	-1.04	0.875	1.3	0.074	-1.06	0.536	-1.11	0.774	-0.47
1430085_at	4933412A08Rik	RIKEN cDNA 4933412A08 gene	-1.39	0.063	1.59	0.346	-1.1	0.787	-1.31	0.525	-0.55
1445069_at	---	---	2.14	0.171	-1.83	0.129	-1.9	0.1	-1.07	0.92	-0.66
1452201_at	2310047B19Rik	RIKEN cDNA 2310047B19 gene	-1.58	0.124	-1.05	0.92	1.63	0.271	-1.94	0.273	-0.73
1445246_at	Gfm2	G elongation factor, mitochondrial 2	-1.13	0.868	-1.22	0.28	1.52	0.217	-1.72	0.063	-0.64
1431632_at	4930526L06Rik	RIKEN cDNA 4930526L06 gene	-1.19	0.821	1.76	0.357	-1.63	0.36	-1.81	0.387	-0.72
1455279_at	Gm1060	gene model 1060, (NCBI)	-1.15	0.839	-1.15	0.685	1.47	0.172	-1.62	0.359	-0.61
1434624_x_at	Rps9	ribosomal protein S9	-1.01	0.974	1.27	0.062	-1.05	0.766	-1.51	0.042	-0.57
1443217_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230118O	-1.3	0.753	1.73	0.163	-1.4	0.512	-1.69	0.204	-0.66
1438272_at	Csmd3	CUB and Sushi multiple domains 3	-1.11	0.858	-1.18	0.538	1.46	0.396	-1.54	0.086	-0.59
1448572_at	Prlpa	prolactin-like protein A	1.36	0.078	-1.05	0.717	-1.11	0.79	-1.12	0.763	-0.48
1449139_at	2310008M10Rik	RIKEN cDNA 2310008M10 gene	-1.02	0.882	1.3	0.222	-1.07	0.562	-1.08	0.441	-0.47
1443381_at	Etv4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	1.71	0.355	-1.5	0.479	-1.2	0.723	-1.23	0.751	-0.55
1438323_at	Lim2	lens intrinsic membrane protein 2	1.51	0.294	-1.24	0.168	-1.1	0.652	-1.13	0.527	-0.49
1445926_at	---	---	1.49	0.351	-1.1	0.441	-1.23	0.662	-1.1	0.259	-0.48
1428744_s_at	Bri3bp	Bri3 binding protein	-1.12	0.242	-1.59	0.005	1.7	0.164	-1.39	0.122	-0.6
1459466_at	---	---	-1.25	0.605	1.47	0.132	-1.06	0.815	-1.39	0.28	-0.56
1433013_at	4930485G23Rik	RIKEN cDNA 4930485G23 gene	-2.14	0.472	2.28	0.025	-2.14	0.092	-1.76	0.331	-0.94
1450962_at	Pdha2	pyruvate dehydrogenase E1 alpha 2	1.9	0.436	-1.46	0.213	-1.59	0.105	-1.55	0.36	-0.67
1446716_at	---	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hy	1.8	0.268	-1.02	0.961	-2.3	0.078	-1.86	0.263	-0.84
1434155_a_at	2310061I04Rik	RIKEN cDNA 2310061I04 gene	-1	0.993	-1.27	0.044	1.43	0.041	-1	0.999	-0.46
1460031_at	Gpr45	G protein-coupled receptor 45	1.7	0.123	-1.24	0.554	-1.41	0.269	-1.13	0.838	-0.52
1445339_at	Cnga4	cyclic nucleotide gated channel alpha 4	-1.29	0.201	1.81	0.173	-1.58	0.427	-1.4	0.58	-0.61
1454523_at	C530007A02Rik	RIKEN cDNA C530007A02 gene	1.54	0.074	-1.32	0.514	-1.09	0.732	-1.02	0.968	-0.47
1459497_at	Fdft1	Farnesyl diphosphate farnesyl transferase 1	-1.01	0.954	1.56	0.288	-1.49	0.04	-1.16	0.354	-0.52
1438728_at	Nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)	-1.03	0.902	1.34	0.098	-1.1	0.352	-1.12	0.753	-0.48
1435918_at	BC055107	cDNA sequence BC055107	1.58	0.119	-1.46	0.531	-1.05	0.911	-2.85	0.15	-0.94
1433461_at	Sf3b2	splicing factor 3b, subunit 2	-1.06	0.692	-1.02	0.785	1.29	0.006	-1.12	0.202	-0.48
AFFX-GapdhMur/M	LOC14433	similar to glyceraldehyde-3-phosphate dehydrogenase	-1.1	0.347	-1.03	0.772	1.34	0.02	-1.01	0.856	-0.45
1458009_at	---	Transcribed locus	1.29	0.141	-1	0.995	-1.07	0.877	-1.49	0.411	-0.57
1435540_at	Irgq	immunity-related GTPase family, Q	-1.13	0.336	-1.06	0.686	1.39	0.143	-1.38	0.111	-0.54
1457570_at	A230001M10Rik	RIKEN cDNA A230001M10 gene	-1.8	0.618	-1.03	0.943	1.69	0.181	-1.33	0.663	-0.62
1432920_at	5330421C15Rik	RIKEN cDNA 5330421C15 gene	-2.95	0.075	-1.46	0.257	2.2	0.12	-2.96	0.002	-1.29
1430762_at	4833427G06Rik	RIKEN cDNA 4833427G06 gene	-1.41	0.42	1.56	0.377	-1.06	0.786	-1.98	0.345	-0.72
1428873_a_at	4121402D02Rik	RIKEN cDNA 4121402D02 gene	-1.47	0.134	-1.29	0.146	1.77	0.076	-1.53	0.195	-0.63
1419248_at	Rgs2	regulator of G-protein signaling 2	-1.15	0.568	1.58	0.013	-1.3	0.075	-1.92	0.133	-0.7
1431344_at	Grm2	G protein-coupled receptor, family C, group 1, member B	1.35	0.32	-1.1	0.672	-1.04	0.89	-1.69	0.312	-0.62
1456447_at	---	---	-1.19	0.755	1.43	0.241	-1.05	0.803	-1.06	0.689	-0.47

1442256_at	Prkcd	protein kinase C, delta	-1.13	0.769	1.37	0.278	-1.04	0.771	-1.75	0.029	-0.63
1450930_at	Hpca	hippocalcin	-1.68	0.25	1.98	0.366	-1.54	0.224	-1.44	0.556	-0.67
1426503_a_at	Rnf121	ring finger protein 121	1.25	0.35	-1.01	0.971	-1.01	0.971	-1.33	0.52	-0.53
1440482_at	Vps13a	vacuolar protein sorting 13A (yeast)	-1.74	0.141	1.75	0.401	-1.11	0.614	-1.23	0.592	-0.58
1438932_at	Rasgrp2	RAS, guanyl releasing protein 2	-1.07	0.298	1.38	0.049	-1.1	0.772	-1.31	0.143	-0.52
1459613_at	---	Transcribed locus	-1.09	0.467	-1.92	0.205	1.79	0.129	-1.15	0.819	-0.59
1437607_at	Gcnt2	Glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.6	0.357	-1.17	0.372	-1.3	0.151	-1.05	0.896	-0.48
1433771_at	5730446C15Rik	RIKEN cDNA 5730446C15 gene	1.35	0.017	-1.12	0.334	-1.02	0.944	-1.58	0.234	-0.59
1419750_at	Dnmt2	DNA methyltransferase 2	-1.4	0.277	-1.37	0.563	1.78	0.297	-2	0.378	-0.75
1441438_at	Gpc6	glypican 6	-1.13	0.478	1.58	0.012	-1.31	0.354	-1.11	0.84	-0.49
1438576_x_at	2900056M20Rik	RIKEN cDNA 2900056M20 gene	-1.02	0.957	1.35	0.271	-1.12	0.567	-1.23	0.529	-0.51
1421925_at	Mapk11	mitogen-activated protein kinase 11	1.7	0.24	-1.25	0.787	-1.39	0.575	-1.3	0.713	-0.56
1426436_at	Tmem159	transmembrane protein 159	-1	0.988	1.38	0.518	-1.18	0.093	-1.47	0.127	-0.57
1447766_x_at	Limd2 /// LOC6323	LIM domain containing 2 /// similar to epithelial protein lost in neoplasm	-1.23	0.778	1.68	0.086	-1.37	0.227	-2.56	0.196	-0.87
1440602_at	Grik2	Glutamate receptor, ionotropic, kainate 2 (beta 2)	1.84	0.345	-1.32	0.532	-1.61	0.339	-2.52	0.031	-0.9
1445284_at	---	---	-1.02	0.987	1.67	0.327	-1.75	0.087	-1.01	0.989	-0.53
1424248_at	Arpp21	cyclic AMP-regulated phosphoprotein, 21	-1.07	0.799	1.7	0.447	-1.69	0.208	-1.57	0.463	-0.66
1445120_at	AU021977	expressed sequence AU021977	1.61	0.235	-1.27	0.532	-1.21	0.755	-1.22	0.611	-0.52
1454409_at	4833408G04Rik	RIKEN cDNA 4833408G04 gene	1.79	0.292	-1.54	0.203	-1.27	0.77	-1.18	0.638	-0.55
1440629_at	Etf1	eukaryotic translation termination factor 1	-1.72	0.184	-1.54	0.379	1.99	0.094	-2.5	0.141	-0.94
1438846_x_at	Ihpk1	inositol hexaphosphate kinase 1	1.58	0.483	-1.1	0.908	-1.37	0.362	-1.71	0.304	-0.65
1430752_at	C330006D17Rik	RIKEN cDNA C330006D17 gene	1.33	0.631	-1.01	0.976	-1.11	0.778	-1.3	0.643	-0.52
1424303_at	Depdc7	DEP domain containing 7	-1.3	0.127	-1.02	0.899	1.48	0.372	-2.09	0.178	-0.73
1445293_at	2610002D18Rik	RIKEN cDNA 2610002D18 gene	1.31	0.525	-1.08	0.72	-1.01	0.974	-1.26	0.574	-0.51
1455867_at	Sox4	SRY-box containing gene 4	1.7	0.154	-1.56	0.226	-1.12	0.821	-1.32	0.158	-0.58
1424395_at	Asrgl1	asparaginase like 1	-1.01	0.955	1.34	0.065	-1.11	0.698	-1.16	0.14	-0.49
1420760_s_at	Ndrl	N-myc downstream regulated-like	-1.3	0.011	-1.24	0.434	1.65	0.036	-1.36	0.25	-0.56
1431553_at	---	---	-1.29	0.208	1.63	0.021	-1.21	0.396	-1.04	0.89	-0.48
1449380_at	Pacsin1	protein kinase C and casein kinase substrate in neurons 1	-1.5	0.484	1.8	0.304	-1.32	0.584	-1.59	0.101	-0.65
1416209_at	Glud1	glutamate dehydrogenase 1	-1.13	0.035	-1.11	0.486	1.45	0.023	-1.34	0.233	-0.53
1453659_at	Cenpo	centromere protein O	-1.2	0.712	-1.03	0.971	1.42	0.255	-1.8	0.492	-0.65
1440395_at	Rbm21	RNA binding motif protein 21	-1.85	0.206	1.72	0.378	-1.03	0.849	-1.25	0.324	-0.6
1415809_at	Tpbpa	trophoblast specific protein alpha	-1.19	0.776	1.89	0.224	-1.99	0.146	-1.34	0.469	-0.66
1460242_at	Cd55	CD55 antigen	-1.16	0.655	1.45	0.254	-1.09	0.657	-2.62	0.105	-0.86
1442782_at	Klhl8	Kelch-like 8 (Drosophila)	-1.56	0.42	1.73	0.346	-1.17	0.603	-1.85	0.218	-0.71
1454579_at	4930474A20Rik	RIKEN cDNA 4930474A20 gene	1.52	0.561	-1.32	0.486	-1.04	0.925	-1.39	0.204	-0.56
1451533_at	BC022687	cDNA sequence BC022687	-1.01	0.948	-1.07	0.682	1.31	0.443	-1.18	0.66	-0.49
1429097_at	C030044C12Rik	RIKEN cDNA C030044C12 gene	-1.27	0.187	1.62	0.013	-1.2	0.255	-1.05	0.753	-0.48
1429815_at	Armc3	armadillo repeat containing 3	-1.02	0.977	-1.1	0.907	1.34	0.504	-1.37	0.412	-0.54
1426255_at	Nefl	neurofilament, light polypeptide	-2.07	0.202	2.12	0.067	-1.59	0.486	-2.29	0.283	-0.96
1442912_at	Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	-1.3	0.681	-1.64	0.459	1.85	0.091	-1.07	0.937	-0.54
1418258_s_at	Dynll2	dynein light chain LC8-type 2	-1.43	0.455	-1.29	0.294	1.76	0.268	-1.11	0.769	-0.52
1437908_a_at	1200007D18Rik	RIKEN cDNA 1200007D18 gene	-1.32	0.526	-1.06	0.72	1.53	0.174	-1.5	0.289	-0.59
1431050_at	Rps6ka5	ribosomal protein S6 kinase, polypeptide 5	-1.01	0.984	1.5	0.407	-1.35	0.185	-1.41	0.081	-0.57
1446968_at	Picalm	phosphatidylinositol binding clathrin assembly protein	-1.15	0.176	1.73	0.221	-1.56	0.028	-1.18	0.597	-0.54
1456770_at	Zfp14	zinc finger protein 14	1.63	0.542	-1.3	0.485	-1.2	0.457	-2.2	0.08	-0.77
1430384_at	Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	1.87	0.31	-1.3	0.312	-1.68	0.018	-1.09	0.721	-0.55
1455437_at	BC033915	cDNA sequence BC033915	-1.02	0.929	-1.08	0.345	1.33	0.086	-1.25	0.354	-0.5
1438267_x_at	Rnps1	ribonucleic acid binding protein S1	-1.02	0.802	-1.01	0.901	1.26	0.031	-1.15	0.454	-0.48
1428905_at	Rraga	Ras-related GTP binding A	-1.29	0.111	-1.35	0.202	1.72	0.102	-1.33	0.344	-0.56
1429987_at	9930013L23Rik	RIKEN cDNA 9930013L23 gene	-1.14	0.767	1.54	0.34	-1.22	0.344	-1.72	0.019	-0.63
1433340_at	4930480K02Rik	RIKEN cDNA 4930480K02 gene	-1.48	0.079	1.76	0.571	-1.25	0.373	-1.17	0.54	-0.54
1432953_at	4921520E09Rik	RIKEN cDNA 4921520E09 gene	-1.14	0.429	-1.22	0.614	1.54	0.325	-1.11	0.741	-0.48

1425088_at	Scnn1a	sodium channel, nonvoltage-gated, type I, alpha	-1.05	0.626	-1.16	0.349	1.42	0	-1.17	0.85	-0.49
1440494_at	Mif4gd	MIF4G domain containing	-1.11	0.767	1.36	0.127	-1.03	0.897	-1.69	0.036	-0.62
1453838_at	4930471G03Rik	RIKEN cDNA 4930471G03 gene	-1.1	0.602	1.51	0.179	-1.22	0.587	-1.39	0.424	-0.55
1424114_s_at	Lamb1-1	laminin B1 subunit 1	-1.01	0.926	1.59	0.029	-1.5	0.161	-1.42	0.171	-0.59
1436880_at	Afp	Alpha fetoprotein	-1.65	0.105	1.88	0.235	-1.33	0.157	-1.39	0.418	-0.62
1434709_at	C130076O07Rik	RIKEN cDNA C130076O07 gene	1.82	0.266	-1.11	0.885	-1.94	0.032	-1.49	0.561	-0.68
1437596_at	Lypd4	Ly6/Plaur domain containing 4	2.03	0.154	-3.05	0.209	-1.14	0.823	-1.11	0.696	-0.82
1458770_at	D11Ertd4e	DNA segment, Chr 11, ERATO Doi 4, expressed	2.44	0.458	-1.88	0.099	-3.75	0.01	-1.43	0.442	-1.16
1444644_x_at	Tatdn1	TatD DNase domain containing 1	-1.21	0.138	1.61	0.022	-1.25	0.244	-1.35	0.269	-0.55
1422902_s_at	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	-1.13	0.27	-1.07	0.585	1.42	0.057	-1.07	0.47	-0.46
1453530_at	---	---	-1.02	0.941	1.68	0.271	-1.73	0.05	-1.36	0.145	-0.61
1455793_at	BC035537	cDNA sequence BC035537	-1.14	0.023	-1.2	0.138	1.53	0.023	-1.29	0.508	-0.52
1435090_at	Tubgcp6	tubulin, gamma complex associated protein 6	1.54	0.216	-1.34	0.395	-1.05	0.884	-1.2	0.172	-0.51
1432667_at	2210411G17Rik	RIKEN cDNA 2210411G17 gene	-1.07	0.857	1.44	0.21	-1.15	0.322	-1.57	0.054	-0.59
1457886_at	LOC552873	hypothetical LOC552873	-1.51	0.637	2.21	0.351	-2.69	0.018	-1.69	0.276	-0.92
1435013_at	Heatr2	HEAT repeat containing 2	-1.16	0.583	-1.25	0.206	1.58	0.097	-1	0.996	-0.46
1429196_at	Rabgap1l	RAB GTPase activating protein 1-like	1.43	0.236	-1.05	0.738	-1.17	0.444	-1.37	0.248	-0.54
1422309_a_at	Lenep	lens epithelial protein	-1.1	0.488	1.46	0.147	-1.14	0.359	-1.1	0.53	-0.47
1438013_x_at	Dhx32	DEAH (Asp-Glu-Ala-His) box polypeptide 32	-1.08	0.945	1.35	0.667	-1.04	0.932	-3.46	0.007	-1.06
1425588_at	Ptprj	protein tyrosine phosphatase, receptor type, J	-1.32	0.48	-1.01	0.986	1.5	0.203	-1.2	0.433	-0.51
1455307_at	BC037112	cDNA sequence BC037112	-1.16	0.005	-1.06	0.635	1.44	0.124	-1.43	0.392	-0.55
1457974_at	---	---	-1.37	0.168	1.86	0.154	-1.52	0.351	-1.09	0.817	-0.53
1451947_at	Igh-V7183	immunoglobulin heavy chain (V7183 family)	-1.28	0.363	1.67	0.263	-1.25	0.624	-1.67	0.452	-0.64
1440539_at	---	---	1.6	0.45	-1.2	0.485	-1.23	0.56	-1.02	0.975	-0.46
1436197_at	Cdc42bpg	CDC42 binding protein kinase gamma (DMPK-like)	-1.09	0.223	-1.04	0.782	1.37	0.372	-1.13	0.608	-0.47
1421705_at	Scn3a	sodium channel, voltage-gated, type III, alpha	1.77	0.635	-1.36	0.334	-1.36	0.358	-1.18	0.759	-0.53
1449150_at	A930040G15Rik	RIKEN cDNA A930040G15 gene	-1.01	0.977	-1.06	0.811	1.31	0.085	-2.06	0.012	-0.7
1442272_at	---	Transcribed locus	-1.76	0.083	1.73	0.357	-1.06	0.918	-1.31	0.351	-0.6
1428451_at	Lrrc47	leucine rich repeat containing 47	-1.06	0.203	-1.08	0.474	1.37	0.008	-1.02	0.683	-0.44
1416712_at	Pepd	peptidase D	-1.17	0.114	-1.04	0.777	1.43	0.044	-1.04	0.869	-0.45
1436719_at	Slc35f1	solute carrier family 35, member F1	-1.14	0.543	1.4	0.659	-1.02	0.962	-1.01	0.988	-0.45
1432335_at	4930551O13Rik	RIKEN cDNA 4930551O13 gene	1.38	0.553	-1.05	0.918	-1.09	0.21	-1.34	0.339	-0.53
1445635_at	Epha7	Eph receptor A7	-1.13	0.727	-1.09	0.878	1.45	0.338	-1.6	0.237	-0.59
1430863_at	4933411B09Rik	RIKEN cDNA 4933411B09 gene	1.71	0.474	-1.11	0.511	-1.57	0.351	-1.01	0.975	-0.5
1433720_s_at	Ndg2	Nur77 downstream gene 2	-1.08	0.718	-1.34	0.098	1.57	0.044	-1.03	0.886	-0.47
1418782_at	Rxrg	retinoid X receptor gamma	-1.08	0.907	-1.11	0.77	1.42	0.24	-3.96	0.03	-1.18
1419083_at	Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11	1.4	0.591	-1.09	0.825	-1.08	0.905	-1.82	0.138	-0.65
1419989_at	Commd5	COMM domain containing 5	-1.64	0.42	-1.47	0.617	1.96	0.069	-1.63	0.503	-0.7
1448893_at	Ncor2	nuclear receptor co-repressor 2	-1.06	0.122	-1.05	0.741	1.36	0.222	-1.14	0.711	-0.47
1449959_x_at	Sprrl9	small proline rich-like 9	-1.41	0.75	-2.54	0.26	2.15	0.06	-1.04	0.92	-0.71
1444259_at	Dmgdh	Dimethylglycine dehydrogenase precursor	1.55	0.507	-1.22	0.45	-1.13	0.424	-1.31	0.594	-0.53
1435799_at	Sfrs14	splicing factor, arginine/serine-rich 14	-1.16	0.237	1.46	0.038	-1.08	0.671	-1.18	0.311	-0.49
1417951_at	Eno3	enolase 3, beta muscle	-1.1	0.72	-1.27	0.296	1.56	0.302	-1.66	0.037	-0.62
1442661_at	C80113	expressed sequence C80113	-1.07	0.833	1.5	0.407	-1.22	0.501	-2.82	0.066	-0.9
1424505_at	0610042C05Rik	RIKEN cDNA 0610042C05 gene	-1.29	0.1	-1.03	0.864	1.51	0.214	-1.26	0.459	-0.52
1430588_at	Mro	Maestro	-1.06	0.943	1.72	0.115	-1.72	0.209	-1.74	0.225	-0.7
1443788_at	Runx1t1	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1.64	0.619	-1.45	0.359	-1.08	0.879	-1.41	0.558	-0.57
1433019_at	4833419G08Rik	RIKEN cDNA 4833419G08 gene	-1.28	0.687	1.77	0.239	-1.42	0.221	-1.29	0.674	-0.56
1443161_at	Trps1	Trichorhinophalangeal syndrome I (human)	-1.13	0.551	1.63	0.08	-1.35	0.015	-1.49	0.335	-0.59
1427295_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	-1.03	0.884	-1	0.989	1.28	0.32	-1.31	0.199	-0.51
1422958_at	Krtap5-4	keratin associated protein 5-4	-3.59	0.29	-1.04	0.955	2.02	0.13	-3.24	0.148	-1.46
1447462_at	D7Wsu130e	DNA segment, Chr 7, Wayne State University 130, expressed	1.68	0.529	-1.63	0.269	-1.04	0.88	-1.4	0.474	-0.6
1430296_at	4733401H21Rik	RIKEN cDNA 4733401H21 gene	-1.55	0.157	1.63	0.06	-1.02	0.962	-1.97	0.36	-0.73

1415709_s_at	Gbf1	golgi-specific brefeldin A-resistance factor 1	-1.05	0.571	-1.04	0.772	1.34	0.027	-1.18	0.361	-0.48
1427936_at	Thnsl1	threonine synthase-like 1 (bacterial)	-1.09	0.813	1.41	0.201	-1.08	0.626	-1.33	0.433	-0.52
1443728_at	---	Transcribed locus	2.02	0.153	-1.34	0.488	-2.03	0.008	-1.3	0.457	-0.66
1454828_at	AI790205	expressed sequence AI790205	-1.03	0.868	-1.02	0.824	1.3	0.118	-1.07	0.253	-0.45
1453196_a_at	Oasl2	2'-5' oligoadenylate synthetase-like 2	-1.22	0.158	-1.05	0.777	1.49	0.109	-1.06	0.754	-0.46
1441792_at	A630033E08Rik	RIKEN cDNA A630033E08 gene	-1.15	0.222	1.4	0.099	-1.01	0.973	-1.2	0.569	-0.49
1447266_at	Utp18	UTP18, small subunit (SSU) processome component, homolog (yeast)	-1.2	0.29	-1.15	0.682	1.55	0.263	-1.46	0.354	-0.56
1428799_at	4930431B11Rik	RIKEN cDNA 4930431B11 gene	-1.12	0.745	-1.19	0.706	1.53	0.141	-1.67	0.18	-0.61
1434143_at	BC060631	cDNA sequence BC060631	-1.06	0.598	-1.05	0.868	1.37	0.142	-1.36	0.261	-0.53
1431487_at	Klc2	kinesin light chain 2	-1.03	0.956	1.57	0.092	-1.4	0.302	-1.51	0.22	-0.59
1437494_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	-1.07	0.055	-1.01	0.951	1.34	0.06	-1.17	0.211	-0.48
1428404_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	-1.04	0.794	-1.11	0.515	1.4	0.006	-1	0.998	-0.44
1436486_x_at	Whrn	Whirlin	-1.13	0.747	-1.01	0.985	1.39	0.574	-2.74	0.018	-0.87
1457523_at	9530056K15Rik	RIKEN cDNA 9530056K15 gene	-1.02	0.981	-1.15	0.683	1.42	0.468	-1.92	0.191	-0.67
1459184_at	---	---	1.55	0.5	-1.08	0.867	-1.28	0.171	-1.36	0.418	-0.54
1459316_at	2900026A02Rik	RIKEN cDNA 2900026A02 gene	1.92	0.117	-1.84	0.103	-1.24	0.607	-3.75	0.077	-1.23
1415800_at	Gja1	gap junction membrane channel protein alpha 1	-1.18	0.596	1.69	0.11	-1.38	0.271	-1.54	0.053	-0.6
1458072_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.14	0.785	1.46	0.532	-1.08	0.861	-2.77	0.069	-0.88
1436125_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	1.55	0.159	-1.19	0.272	-1.14	0.121	-1.18	0.548	-0.49
1428984_a_at	1700012B09Rik	RIKEN cDNA 1700012B09 gene	-1.09	0.906	1.53	0.577	-1.22	0.384	-1.33	0.488	-0.53
1460427_a_at	Adam28	a disintegrin and metallopeptidase domain 28	1.74	0.622	-1.31	0.149	-1.31	0.235	-1.49	0.445	-0.59
1459866_x_at	Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	-1.05	0.615	1.41	0.261	-1.1	0.449	-1.05	0.862	-0.45
1418257_at	Slc12a7	solute carrier family 12, member 7	-1.02	0.858	-1.03	0.805	1.31	0.11	-1.3	0.307	-0.51
1418707_at	Bag4	BCL2-associated athanogene 4	-1.01	0.947	-1	0.992	1.28	0.287	-1.13	0.611	-0.47
1427862_at	Arl6ip3	ADP-ribosylation factor-like 6 interacting protein 3	-1.07	0.308	1.51	0.063	-1.22	0.339	-1.11	0.756	-0.47
1457376_at	Itga4	Integrin alpha 4	1.33	0.621	-1.06	0.847	-1	0.988	-1.27	0.485	-0.5
1435951_at	Grip1	glutamate receptor interacting protein 1	-1.29	0.186	1.69	0.395	-1.25	0.279	-1.95	0.345	-0.7
1439111_at	---	---	-1.1	0.643	1.49	0.451	-1.15	0.562	-1.01	0.986	-0.44
1444542_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	1.63	0.097	-1.3	0.26	-1.15	0.709	-1.21	0.362	-0.51
1421541_a_at	Mef2b	myocyte enhancer factor 2B	-1.35	0.755	-2.16	0.391	2.06	0.475	-3	0.241	-1.11
1428630_x_at	Haghl	hydroxyacylglutathione hydrolase-like	-1.14	0.609	-1.02	0.943	1.41	0.183	-1.07	0.68	-0.46
1460677_at	---	---	-1.23	0.411	1.77	0.108	-1.46	0.144	-1.55	0.257	-0.62
1420481_at	Cnnm3	cyclin M3	-1.09	0.406	-1.05	0.447	1.4	0.027	-1.26	0.294	-0.5
1450589_at	Olfr749	olfactory receptor 749	-1.37	0.623	1.87	0.482	-1.48	0.215	-1.88	0.448	-0.72
1431692_a_at	Cblc	Casitas B-lineage lymphoma c	-1.02	0.915	-1.03	0.904	1.32	0.204	-1.24	0.351	-0.49
1458011_s_at	D4Ertd117e	DNA segment, Chr 4, ERATO Doi 117, expressed	-1.07	0.886	-1.05	0.643	1.38	0.38	-1.4	0.576	-0.53
1457142_at	Efcbp1	EF hand calcium binding protein 1	1.48	0.196	-1.26	0.573	-1	0.997	-1.7	0.29	-0.62
1430967_at	3110080O07Rik	RIKEN cDNA 3110080O07 gene	1.91	0.099	-1.12	0.692	-2.12	0.143	-1.78	0.41	-0.78
1443844_at	1700123J19Rik	RIKEN cDNA 1700123J19 gene	1.38	0.543	-1.06	0.883	-1.05	0.93	-1.21	0.493	-0.49
1453868_at	Ccdc11	coiled-coil domain containing 11	-2.37	0.307	1.85	0.354	-1	0.997	-1.36	0.211	-0.72
1445620_at	---	Transcribed locus	-1.02	0.97	-1.66	0.536	1.69	0.342	-1.91	0.398	-0.73
1438367_x_at	Ddr1	discoidin domain receptor family, member 1	-1.82	0.152	-1.15	0.721	1.85	0.198	-1.74	0.066	-0.71
1419247_at	Rgs2	regulator of G-protein signaling 2	-1.11	0.687	1.55	0.001	-1.23	0.234	-1.67	0.18	-0.61
1443906_at	Cd55	CD55 antigen	-1.47	0.241	1.73	0.019	-1.16	0.305	-2.17	0.074	-0.77
1421357_at	Gtf2a1	general transcription factor II A, 1	-1.12	0.685	-1.15	0.459	1.51	0.04	-1.31	0.398	-0.52
1420620_a_at	Rnf13	ring finger protein 13	-1.04	0.88	-1.1	0.695	1.41	0.46	-1.05	0.904	-0.45
1456541_x_at	Atad3a	ATPase family, AAA domain containing 3A	-1.29	0.205	-1.12	0.48	1.6	0.088	-1.26	0.023	-0.51
1433071_at	6430605C03Rik	RIKEN cDNA 6430605C03 gene	1.53	0.485	-1.01	0.96	-1.32	0.646	-1.42	0.032	-0.56
1415952_at	Mark2	MAP/microtubule affinity-regulating kinase 2	-1.02	0.947	-1.11	0.029	1.39	0.066	-1.41	0.048	-0.54
1436831_at	4932408B21Rik	RIKEN cDNA 4932408B21 gene	-1.32	0.577	-1.08	0.894	1.59	0.342	-1.84	0.03	-0.66
1422799_at	Bat2	HLA-B associated transcript 2	-1.47	0.024	-1.27	0.061	1.81	0.19	-1.45	0.237	-0.6
1448215_a_at	Dpp3	dipeptidylpeptidase 3	-1.06	0.834	-1.15	0.15	1.46	0.047	-1.83	0.098	-0.65
1435337_at	Tshz3	teashirt zinc finger family member 3	-1.23	0.719	1.72	0.1	-1.34	0.173	-1.12	0.308	-0.49

1454753_at	Rnpepl1	arginyl aminopeptidase (aminopeptidase B)-like 1	-1.01	0.903	-1.13	0.106	1.4	0.109	-1.03	0.899	-0.44
1433444_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-1.07	0.674	1.4	0.235	-1.06	0.671	-1.86	0.105	-0.65
1435856_x_at	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.52	0.37	1.95	0.171	-1.48	0.172	-1.03	0.921	-0.52
1434897_a_at	Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.26	0.128	1.52	0.036	-1.03	0.699	-1.55	0.222	-0.58
1460651_at	Lat	linker for activation of T cells	-1.32	0.331	-1.03	0.955	1.55	0.031	-1.94	0.017	-0.69
1425357_a_at	Grem1	gremlin 1	1.48	0.311	-1.04	0.914	-1.2	0.175	-1.63	0.064	-0.6
1446564_at	D18Ertd169e	DNA segment, Chr 18, ERATO Doi 169, expressed	-1.49	0.461	1.61	0.393	-1.01	0.989	-1.15	0.72	-0.51
1432541_at	4930408O17Rik	RIKEN cDNA 4930408O17 gene	-1.12	0.906	-1.21	0.735	1.56	0.28	-1.35	0.398	-0.53
1425538_x_at	Ceacam1	CEA-related cell adhesion molecule 1	1.41	0.2	-1.14	0.528	-1.01	0.974	-1.57	0.422	-0.58
1442562_at	D630040G17Rik ///	RIKEN cDNA D630040G17 gene /// similar to zinc finger protein 64 (predicted)	1.62	0.13	-1.2	0.371	-1.21	0.308	-2.02	0.322	-0.7
1424165_a_at	Sharpin	SHANK-associated RH domain interacting protein	-1.13	0.536	-1.05	0.722	1.43	0.227	-1.51	0.142	-0.56
1456800_a_at	D130029J02Rik	RIKEN cDNA D130029J02 gene	-1.48	0.378	-1.33	0.552	1.85	0.337	-1.18	0.218	-0.53
1438700_at	Fnbp4	formin binding protein 4	1.7	0.163	-1.37	0.422	-1.18	0.513	-1.32	0.329	-0.54
1425808_a_at	Myocd	myocardin	-1.5	0.168	1.78	0.208	-1.21	0.704	-1.53	0.074	-0.61
1420047_at	Maf1	MAF1 homolog (S. cerevisiae)	1.51	0.486	-1.27	0.421	-1.02	0.964	-1.2	0.786	-0.49
1444026_at	AI593442	expressed sequence AI593442	-1.31	0.273	1.68	0.224	-1.2	0.426	-1.05	0.702	-0.47
1457135_at	Fath2	fat tumor suppressor homolog 2 (Drosophila)	1.89	0.51	-1.29	0.46	-1.63	0.293	-1.25	0.687	-0.57
1427557_at	Alg12	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransfera	-1.17	0.75	-1.57	0.168	1.79	0.306	-1.09	0.881	-0.51
1458730_at	Bach2	BTB and CNC homology 2	1.78	0.197	-1.24	0.704	-1.45	0.279	-1.42	0.224	-0.58
1435572_at	2310014L17Rik	RIKEN cDNA 2310014L17 gene	-1.29	0.593	1.67	0.219	-1.2	0.153	-1	0.989	-0.45
1432298_at	4921508M14Rik	RIKEN cDNA 4921508M14 gene	1.31	0.484	-1.01	0.983	-1.01	0.98	-1.43	0.471	-0.54
1445343_at	Tmed5	transmembrane emp24 protein transport domain containing 5	2.22	0.348	-2.23	0.223	-1.62	0.352	-2.43	0.137	-1.02
1439295_x_at	LOC434179	hypothetical LOC434179	1.66	0.005	-1.2	0.346	-1.27	0.392	-1.13	0.377	-0.48
1423583_at	Fem1a	feminization 1 homolog a (C. elegans)	-1.04	0.53	-1.05	0.658	1.37	0.053	-1.08	0.869	-0.45
1420696_at	Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	-1.27	0.048	-1.42	0.096	1.79	0.339	-1	0.992	-0.48
1434239_at	AA408556	expressed sequence AA408556	-1.02	0.921	-1.35	0.222	1.56	0.298	-1.12	0.485	-0.48
1452636_x_at	Gtpbp5	GTP binding protein 5	-1.16	0.879	1.77	0.229	-1.53	0.178	-1.03	0.882	-0.49
1456372_at	Itm2b	Integral membrane protein 2B	1.57	0.18	-1.12	0.857	-1.22	0.513	-1.3	0.022	-0.52
1442847_at	---	---	-1.04	0.962	1.76	0.275	-1.77	0.046	-1.22	0.703	-0.57
1439988_at	---	---	1.67	0.135	-1.04	0.835	-1.52	0.328	-1.45	0.261	-0.58
1432047_at	Depdc2	DEP domain containing 2	1.58	0.473	-1.06	0.877	-1.3	0.326	-2.98	0.053	-0.94
1430590_at	D3Ertd751e	DNA segment, Chr 3, ERATO Doi 751, expressed	-1.16	0.444	-1.46	0.143	1.74	0.21	-1.1	0.825	-0.5
1423413_at	Ndrg1	N-myc downstream regulated gene 1	-1.16	0.577	-1.26	0.57	1.64	0.176	-1.06	0.779	-0.46
1442787_at	---	---	1.59	0.19	-1.35	0.375	-1.05	0.694	-1.32	0.584	-0.53
1447744_s_at	---	---	-1.18	0.357	1.74	0.516	-1.43	0.316	-1.49	0.391	-0.59
1454501_at	6330419E04Rik	RIKEN cDNA 6330419E04 gene	-1.52	0.341	-1.07	0.829	1.7	0.079	-1.45	0.493	-0.59
1447885_x_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-1.31	0.619	1.54	0.421	-1.01	0.922	-1.69	0.092	-0.62
1428627_at	Zfp509	zinc finger protein 509	-1.01	0.981	-1.29	0.23	1.52	0.372	-2.66	0.235	-0.86
1437171_x_at	Gsn	gelsolin	-1.01	0.839	1.51	0.073	-1.26	0.01	-1.22	0.47	-0.5
1453775_at	4921505C17Rik	RIKEN cDNA 4921505C17 gene	-1.22	0.169	-1.02	0.958	1.49	0.238	-1.08	0.74	-0.46
1418058_at	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	-1.01	0.809	1.34	0.079	-1.04	0.853	-1.13	0.469	-0.46
1437616_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	-1.47	0.393	-1.07	0.742	1.68	0.057	-1.27	0.7	-0.53
1430496_at	6720408I04Rik	RIKEN cDNA 6720408I04 gene	-1.13	0.604	-1.03	0.905	1.44	0.37	-1.56	0.345	-0.57
1438878_at	6430537K16Rik	RIKEN cDNA 6430537K16 gene	-1.32	0.042	1.95	0.065	-1.69	0.069	-1.21	0.51	-0.57
1441489_at	LOC552878	hypothetical LOC552878	-1.15	0.272	1.88	0.014	-1.83	0.032	-1.95	0.066	-0.76
1441638_at	A630014C17Rik	RIKEN cDNA A630014C17 gene	-1	0.992	1.67	0.203	-1.59	0.229	-1.05	0.905	-0.49
1419050_at	1110002H13Rik	RIKEN cDNA 1110002H13 gene	1.71	0.187	-1.56	0.334	-1.06	0.891	-1.48	0.581	-0.6
1441418_at	Scap1	Src family associated phosphoprotein 1	-1.01	0.986	1.55	0.152	-1.33	0.16	-2.37	0.133	-0.79
1457117_at	Nfe2l2	nuclear factor, erythroid derived 2, like 2	1.69	0.307	-1.11	0.783	-1.41	0.052	-1.41	0.705	-0.56
1425304_s_at	Prima1	proline rich membrane anchor 1	-1.4	0.229	-1.21	0.728	1.76	0.113	-1.58	0.155	-0.61
1440325_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	1.89	0.221	-1.43	0.406	-1.43	0.234	-1.07	0.845	-0.51
1430975_at	8430416G17Rik	RIKEN cDNA 8430416G17 gene	-1.05	0.845	-1.54	0.032	1.69	0.135	-1.16	0.74	-0.51
1451629_at	Lbh	limb-bud and heart	-1.07	0.105	1.47	0.184	-1.12	0.328	-1.28	0.313	-0.5

1442994_at	Sod2	Superoxide dismutase 2, mitochondrial	-1.13	0.69	1.73	0.198	-1.49	0.493	-1.78	0.543	-0.66
1427291_at	Sycp1	synaptonemal complex protein 1	-2.19	0.137	1.96	0.232	-1.13	0.562	-1.17	0.718	-0.63
1435687_at	Sv2b	synaptic vesicle glycoprotein 2 b	-1.06	0.857	1.5	0.241	-1.17	0.402	-1.07	0.895	-0.45
1457759_at	A630081D01Rik	RIKEN cDNA A630081D01 gene	1.81	0.005	-1.54	0.596	-1.2	0.61	-1.5	0.318	-0.61
1451361_a_at	Pnpla7	patatin-like phospholipase domain containing 7	-1.09	0.54	-1.13	0.282	1.49	0.044	-1.23	0.338	-0.49
1422193_at	Gucy2e	guanylate cyclase 2e	-1.02	0.829	1.49	0.673	-1.2	0.305	-1.09	0.632	-0.46
1428097_at	2510009E07Rik	RIKEN cDNA 2510009E07 gene	-1.15	0.135	1.59	0.062	-1.19	0.078	-1.42	0.051	-0.54
1423872_a_at	Dag1	dystroglycan 1	-1.04	0.281	-1.01	0.956	1.34	0.266	-1.3	0.212	-0.5
1460181_at	Stmn3	stathmin-like 3	-1.35	0.21	1.73	0.134	-1.21	0.508	-1.35	0.41	-0.54
1446630_at	---	---	2.13	0.491	-1.37	0.235	-2.28	0.027	-1.15	0.391	-0.67
AFFX-r2-Bs-thr-5_s_	---	---	1.46	0.596	-1.2	0.602	-1	0.998	-2	0.552	-0.68
1447637_at	2410018C17Rik	RIKEN cDNA 2410018C17 gene	1.79	0.154	-1.03	0.947	-1.86	0.089	-1.27	0.699	-0.59
1425947_at	Ifng	interferon gamma	-1.03	0.953	-1.09	0.89	1.41	0.074	-1.01	0.808	-0.43
1430990_s_at	Mrpl44	mitochondrial ribosomal protein L44	-1.24	0.46	-1.03	0.875	1.52	0.036	-1.01	0.915	-0.44
1458659_at	Plac9	placenta specific 9	1.72	0.029	-1.03	0.959	-1.64	0.008	-1.72	0.092	-0.67
1452106_at	Npnt	nephronectin	-1.06	0.727	1.54	0.171	-1.22	0.528	-1.9	0.314	-0.66
1425030_at	Zfp622	zinc finger protein 622	-1.03	0.741	-1.2	0.216	1.49	0.057	-1.52	0.104	-0.56
1437930_at	Glt25d2	glycosyltransferase 25 domain containing 2	-1.31	0.005	2.02	0.149	-1.93	0.071	-1.27	0.813	-0.62
1451482_at	BC027344	cDNA sequence BC027344	-1.08	0.868	1.47	0.034	-1.1	0.652	-1.17	0.417	-0.47
1432944_at	2900046L07Rik	RIKEN cDNA 2900046L07 gene	-1.25	0.389	1.94	0.252	-1.78	0.025	-1.33	0.556	-0.61
1438970_x_at	1700034F02Rik	RIKEN cDNA 1700034F02 gene	1.64	0.247	-1.3	0.635	-1.11	0.86	-1.21	0.781	-0.5
1422456_at	Nsf	N-ethylmaleimide sensitive fusion protein	-1.02	0.566	-1.06	0.462	1.38	0	-1.07	0.422	-0.44
1459642_at	Adam23	A disintegrin and metallopeptidase domain 23	-1.07	0.783	1.44	0.143	-1.07	0.864	-1.59	0.145	-0.57
1420289_at	T25656	expressed sequence T25656	-1.52	0.291	1.83	0.012	-1.22	0.51	-1.69	0.542	-0.65
1458796_at	---	---	-1.31	0.005	2.17	0.083	-2.72	0.091	-1.03	0.97	-0.72
1436395_at	Card6	caspase recruitment domain family, member 6	-1.06	0.55	-1.1	0.586	1.46	0.358	-2.02	0.11	-0.68
1415773_at	Ncl	nucleolin	-1.09	0.543	-1.03	0.849	1.42	0.224	-1.1	0.762	-0.45
1445578_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	-1.04	0.656	-1.19	0.607	1.51	0.135	-1.47	0.307	-0.55
1435650_at	Hapln4	hyaluronan and proteoglycan link protein 4	-1.14	0.751	1.78	0.078	-1.53	0.175	-1.31	0.687	-0.55
1427709_at	Grik3	glutamate receptor, ionotropic, kainate 3	-1.08	0.399	-1.12	0.528	1.49	0.527	-1.48	0.345	-0.55
1452538_at	Igh-1a	Immunoglobulin heavy chain 1a (serum IgG2a)	-1.28	0.375	1.65	0.328	-1.14	0.586	-2.25	0.141	-0.75
1447830_s_at	Rgs2	regulator of G-protein signaling 2	-1.14	0.671	1.72	0.014	-1.41	0.094	-1.94	0.092	-0.69
1432488_a_at	Sf3a3 /// LOC62683	splicing factor 3a, subunit 3 /// similar to splicing factor 3a, subunit 3 (predicted)	-1.02	0.912	-1.12	0.65	1.43	0.233	-1.39	0.358	-0.52
1450002_at	Gsh1	genomic screened homeo box 1	-1.38	0.181	-1.36	0.326	1.85	0.147	-1.39	0.722	-0.57
1420674_at	Pla2g2e	phospholipase A2, group IIE	-1.52	0.29	1.89	0.413	-1.31	0.524	-1.51	0.32	-0.61
1454336_at	Ccnc	Cyclin C	-1.05	0.944	1.42	0.406	-1.06	0.858	-1.05	0.904	-0.44
1422896_at	---	---	-1.08	0.681	1.48	0.064	-1.11	0.509	-2.24	0.016	-0.74
1441202_at	Rabgap1l	RAB GTPase activating protein 1-like	-1.26	0.404	1.69	0.341	-1.21	0.299	-4.7	0.065	-1.37
1456012_x_at	Rnaset2	ribonuclease T2	-1.02	0.844	1.35	0.003	-1.02	0.793	-1.47	0.208	-0.54
1429888_a_at	Hspb2	heat shock protein 2	-1.07	0.558	1.51	0.151	-1.15	0.212	-1.24	0.584	-0.49
1449656_at	D930048N14Rik	RIKEN cDNA D930048N14 gene	1.83	0.541	-1.18	0.728	-1.58	0.042	-1.19	0.8	-0.53
1454178_at	2610027F03Rik	RIKEN cDNA 2610027F03 gene	-1.13	0.698	1.53	0.194	-1.12	0.416	-1.08	0.816	-0.45
1452523_a_at	4930527D15Rik	RIKEN cDNA 4930527D15 gene	-1.4	0.38	1.8	0.3	-1.25	0.481	-1.98	0.183	-0.71
1445826_at	Ankrd17	ankyrin repeat domain 17	1.81	0.139	-1.45	0.29	-1.23	0.163	-1.02	0.977	-0.47
1420599_at	2300006N05Rik ///	RIKEN cDNA 2300006N05 gene /// hypothetical protein LOC670472 /// hypothetic	-1.06	0.819	1.37	0.357	-1	0.997	-2.53	0.298	-0.81
1459463_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330073N	1.78	0.125	-1.2	0.645	-1.43	0.124	-1.08	0.831	-0.48
1435874_at	---	---	-1.06	0.605	1.59	0.066	-1.28	0.237	-1.37	0.195	-0.53
1443924_at	Wnk3	WNK lysine deficient protein kinase 3	-1.08	0.88	-1.04	0.527	1.43	0.326	-2.02	0.39	-0.68
1445650_at	---	---	-1.09	0.868	-1.44	0.084	1.7	0.216	-1.2	0.764	-0.51
1420502_at	Sat1	spermidine/spermine N1-acetyl transferase 1	-1.05	0.063	1.44	0.001	-1.08	0.544	-1.31	0.498	-0.5
1445061_at	Pcdh9	Protocadherin 9	1.75	0.352	-1.06	0.794	-1.62	0.377	-1.71	0.42	-0.66
1449960_at	Nptx2	neuronal pentraxin 2	-1.33	0.504	1.67	0.256	-1.11	0.824	-1.01	0.984	-0.45
1449772_at	Tbc1d14	TBC1 domain family, member 14	-1.01	0.838	1.53	0.082	-1.26	0.425	-1.1	0.788	-0.46

1459001_at	Vps33a	Vacuolar protein sorting 33A (yeast)	1.7	0.365	-1.19	0.595	-1.29	0.283	-1.81	0.163	-0.65
1452558_at	---	T-cell receptor gamma-chain mRNA V4-J1 region, 3' end	-1.27	0.669	-1.65	0.405	1.93	0.005	-1.48	0.49	-0.62
1433715_at	Cpne7	copine VII	1.7	0.396	-1.23	0.702	-1.24	0.437	-1.33	0.535	-0.53
1440184_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	1.46	0.212	-1.01	0.99	-1.15	0.16	-1.85	0.029	-0.64
1458289_at	Galntl4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.66	0.129	2.08	0.439	-1.57	0.413	-1.05	0.883	-0.55
1433428_x_at	Tgm2	transglutaminase 2, C polypeptide	-1.17	0.303	1.48	0.069	-1.01	0.933	-1.2	0.395	-0.48
1425530_a_at	Stx3	syntaxin 3	-1.17	0.294	1.76	0.223	-1.41	0.356	-1.09	0.851	-0.48
1426465_at	Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	-1.06	0.657	-1.05	0.771	1.42	0.062	-1.54	0.116	-0.56
1436420_a_at	Ipo4	importin 4	-1.07	0.222	-1.01	0.874	1.4	0.018	-1.26	0.234	-0.49
1442391_at	4930519H02Rik	RIKEN cDNA 4930519H02 gene	-1.09	0.721	-1.15	0.8	1.54	0.318	-1.3	0.604	-0.5
1441061_at	---	Visual cortex cDNA, RIKEN full-length enriched library, clone:K530018N01 produ	-1.07	0.51	-1.06	0.598	1.45	0.038	-1.34	0.228	-0.51
1454080_at	4933428M03Rik	RIKEN cDNA 4933428M03 gene	1.53	0.007	-1.14	0.771	-1.09	0.689	-1.61	0.535	-0.58
1424392_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	-1.31	0.429	-1.07	0.215	1.62	0.299	-1.09	0.835	-0.46
1430726_at	Rassf8	Ras association (RalGDS/AF-6) domain family 8	-1.05	0.878	1.44	0.385	-1.07	0.785	-2.57	0.279	-0.81
1432151_at	2810409H07Rik	RIKEN cDNA 2810409H07 gene	1.83	0.328	-1.51	0.431	-1.21	0.685	-1.34	0.292	-0.55
1424186_at	Ccdc80	coiled-coil domain containing 80	-1.07	0.46	1.46	0.163	-1.08	0.899	-1.34	0.117	-0.51
1426608_at	LOC633640	similar to CG10866-PA	1.44	0.495	-1.09	0.868	-1.04	0.953	-1.34	0.65	-0.51
1422884_at	Snrpd3	small nuclear ribonucleoprotein D3	-1.09	0.703	-1.03	0.788	1.44	0.097	-1.06	0.815	-0.44
1442066_at	C530028O21Rik	RIKEN cDNA C530028O21 gene	1.46	0.225	-1.05	0.678	-1.11	0.495	-1.39	0.166	-0.52
1416808_at	Nid1	nidogen 1	-1.02	0.87	1.51	0.082	-1.2	0.357	-1.11	0.589	-0.45
1426369_at	Mlstd2	male sterility domain containing 2	-1.12	0.45	1.59	0.125	-1.19	0.004	-1.08	0.513	-0.45
1458193_at	Pmp2	peripheral myelin protein 2	-2.12	0.025	2.04	0.248	-1.23	0.321	-1.34	0.163	-0.66
1446658_at	---	Transcribed locus	1.91	0.154	-2.36	0.164	-1	0.99	-2.66	0.026	-1.03
1437249_at	Scap1	src family associated phosphoprotein 1	-1.27	0.574	-1.01	0.972	1.55	0.031	-1.7	0.297	-0.61
1449926_at	Tnfsf7	tumor necrosis factor (ligand) superfamily, member 7	-1.01	0.971	-1.07	0.818	1.41	0.079	-1.02	0.925	-0.43
1459159_a_at	Ccdc6	coiled-coil domain containing 6	-1.65	0.132	1.75	0.156	-1.03	0.827	-1.32	0.108	-0.56
1444791_at	Pcp4l1	Purkinje cell protein 4-like 1	1.54	0.389	-1.01	0.977	-1.26	0.142	-1.05	0.877	-0.44
1434989_at	BC042720	cDNA sequence BC042720	-1.01	0.956	1.44	0.376	-1.11	0.688	-1.1	0.773	-0.45
1455739_at	6430704N06	hypothetical protein 6430704N06	-1.1	0.549	-1.02	0.913	1.43	0.076	-1.02	0.963	-0.42
1445369_at	B230359F08Rik	RIKEN cDNA B230359F08 gene	-1.11	0.906	1.44	0.253	-1.01	0.985	-1.38	0.459	-0.51
1437372_at	Cpsf6	cleavage and polyadenylation specific factor 6	1.43	0.449	-1.06	0.869	-1.05	0.896	-1.8	0.28	-0.62
1423252_at	Hdgfrp3	hepatoma-derived growth factor, related protein 3	-1.12	0.45	1.57	0.268	-1.15	0.359	-1.22	0.555	-0.48
1460587_at	B230215L15Rik	RIKEN cDNA B230215L15 gene	-1.28	0.747	-2.09	0.22	2.07	0.291	-4.15	0.245	-1.36
1419940_at	C030018P15Rik	RIKEN cDNA C030018P15 gene	-1.52	0.539	2.07	0.05	-1.64	0.055	-1.31	0.59	-0.6
1438692_at	Gtf3c4	general transcription factor IIIC, polypeptide 4	-1.17	0.48	-1.06	0.696	1.54	0.377	-1.33	0.412	-0.51
1453827_at	1110035H17Rik	RIKEN cDNA 1110035H17 gene	1.38	0.129	-1.02	0.937	-1.03	0.904	-1.45	0.036	-0.53
1438941_x_at	Ampd2	adenosine monophosphate deaminase 2 (isoform L)	-1.03	0.8	-1.2	0.14	1.53	0.037	-1.24	0.19	-0.48
1425695_at	Tbx5	T-box 5	-2.24	0.468	2.23	0.149	-1.53	0.167	-2.5	0.107	-1.01
1419729_at	Tex11	testis expressed gene 11	1.73	0.546	-1.28	0.668	-1.21	0.647	-2.05	0.148	-0.7
1447128_at	LOC329575	Hypothetical LOC329575	-1.03	0.955	-1.16	0.854	1.5	0.441	-1.07	0.676	-0.44
1446747_at	C230086A09Rik	RIKEN cDNA C230086A09 gene	-1.44	0.463	-1.02	0.824	1.66	0.412	-1.17	0.176	-0.49
1425878_at	Cabp4	calcium binding protein 4	-1.02	0.962	-1.07	0.841	1.41	0.593	-1.16	0.727	-0.46
1423616_at	Tarbp2	TAR (HIV) RNA binding protein 2	-1.02	0.892	-1.08	0.723	1.43	0.116	-1.09	0.558	-0.44
1427740_a_at	---	Strain C3H/HeN mRNA preferentially expressed in LPS-normoresponsive macrop	1.57	0.032	-1.27	0.429	-1.02	0.878	-1.01	0.917	-0.43
1443989_at	Trim9	tripartite motif protein 9	-1.8	0.524	-1.45	0.485	2.09	0.189	-1.4	0.588	-0.64
1452835_a_at	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	-1.02	0.881	-1.11	0.348	1.45	0.039	-1.17	0.238	-0.46
1453803_at	Tia1	cytotoxic granule-associated RNA binding protein 1	2.16	0.363	-1.61	0.181	-1.8	0.151	-1.63	0.209	-0.72
1421798_at	Msgn1	mesogenin 1	-1.84	0.047	-1.17	0.037	1.94	0.296	-1.49	0.584	-0.64
1442441_at	D11Bwg0434e	DNA segment, Chr 11, Brigham & Women's Genetics 0434 expressed	-1.55	0.45	1.88	0.086	-1.23	0.354	-1.82	0.054	-0.68
1415892_at	Sgpl1	sphingosine phosphate lyase 1	-1.42	0.084	-1.1	0.7	1.72	0.071	-1.04	0.874	-0.46
1455424_at	Wnk2	WNK lysine deficient protein kinase 2	1.91	0.139	-1.02	0.948	-2.19	0.206	-1.05	0.93	-0.59
1425414_at	Ppp1r16b	protein phosphatase 1, regulatory (inhibitor) subunit 16B	-1.28	0.761	1.77	0.271	-1.27	0.671	-1.48	0.508	-0.57
1437782_at	Cntnap2	contactin associated protein-like 2	-1.12	0.897	-1.64	0.5	1.84	0.098	-1.76	0.457	-0.67

1450141_at	Abcg3	ATP-binding cassette, sub-family G (WHITE), member 3	-1.09	0.429	1.46	0.011	-1.04	0.82	-1.46	0.176	-0.53
1443766_x_at	Rab11fip4	RAB11 family interacting protein 4 (class II)	-1.81	0.185	1.98	0.172	-1.23	0.113	-1.3	0.643	-0.59
1450257_at	Cer1	cerberus 1 homolog (Xenopus laevis)	-1.45	0.344	1.74	0.446	-1.1	0.742	-1.84	0.367	-0.66
1420962_at	Hapln2	hyaluronan and proteoglycan link protein 2	1.88	0.366	-1.38	0.088	-1.37	0.436	-1.05	0.925	-0.48
1440409_at	2210401J11Rik	RIKEN cDNA 2210401J11 gene	-1.42	0.46	1.73	0.091	-1.1	0.76	-1.29	0.634	-0.52
1428070_at	Syvn1	synovial apoptosis inhibitor 1, synoviolin	-1.03	0.775	-1.14	0.55	1.5	0.25	-1.08	0.795	-0.44
1432973_at	4933421H12Rik	RIKEN cDNA 4933421H12 gene	-2.04	0.37	-1.2	0.357	2.01	0.224	-2.06	0.466	-0.82
1419446_at	Tbc1d1	TBC1 domain family, member 1	-1.14	0.543	-1.31	0.208	1.7	0.238	-1.14	0.382	-0.47
1456731_x_at	Polr3k	Polymerase (RNA) III (DNA directed) polypeptide K	1.51	0.044	-1.17	0.369	-1.02	0.909	-1.03	0.864	-0.43
1459040_at	Hmgn3	High mobility group nucleosomal binding domain 3	-1.54	0.126	1.97	0.074	-1.39	0.27	-3.13	0.238	-1.02
1431905_s_at	4933427G17Rik	RIKEN cDNA 4933427G17 gene	1.82	0.252	-1.55	0.454	-1.15	0.457	-1.12	0.504	-0.5
1425550_a_at	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	-1.05	0.576	-1.04	0.65	1.43	0.159	-1.16	0.501	-0.46
1442096_at	BC031901	cDNA sequence BC031901	-1.16	0.663	-1.03	0.849	1.51	0.316	-1.23	0.715	-0.48
1425881_at	Psg28	pregnancy-specific glycoprotein 28	-1.48	0.366	1.8	0.115	-1.15	0.663	-1.12	0.424	-0.49
1442260_at	Cdc42bpa	Cdc42 binding protein kinase alpha	2.17	0.119	-1.96	0.237	-1.51	0.215	-1.38	0.513	-0.67
1452653_at	Slc25a22	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	-1.09	0.376	-1.31	0.224	1.66	0.065	-1.16	0.651	-0.47
1423804_a_at	Idi1	isopentenyl-diphosphate delta isomerase	-1.1	0.541	1.64	0.137	-1.27	0.029	-1	0.993	-0.43
1426649_at	Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	1.74	0.263	-1.25	0.706	-1.24	0.02	-1.33	0.196	-0.52
1446067_at	Piwil2	Piwi-like homolog 2 (Drosophila)	-1.04	0.925	1.65	0.149	-1.37	0.325	-1.08	0.832	-0.46
1453499_at	Ddo	D-aspartate oxidase	-1.34	0.486	-1.35	0.558	1.86	0.074	-1.89	0.259	-0.68
1457164_at	Trpa1	transient receptor potential cation channel, subfamily A, member 1	-1.43	0.412	1.68	0.568	-1.04	0.941	-1.61	0.44	-0.6
1446027_at	---	---	1.66	0.459	-1.1	0.814	-1.29	0.447	-4.13	0.134	-1.21
1424733_at	P2ry14	purinergic receptor P2Y, G-protein coupled, 14	-1.07	0.735	1.47	0.023	-1.06	0.73	-1.5	0.18	-0.54
1419144_at	Cd163	CD163 antigen	-1.01	0.996	-1.06	0.902	1.41	0.45	-1.33	0.608	-0.5
1445289_at	---	---	-1.19	0.792	1.67	0.372	-1.2	0.69	-1.9	0.091	-0.65
1424382_at	Rcn3	reticulocalbin 3, EF-hand calcium binding domain	1.5	0.022	-1.14	0.626	-1.04	0.909	-1.08	0.71	-0.44
1457601_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730010C	1.7	0.235	-1.16	0.149	-1.27	0.629	-1.57	0.35	-0.58
1429138_at	Npas3	neuronal PAS domain protein 3	2.02	0.194	-1.86	0.148	-1.27	0.487	-1.41	0.264	-0.63
1437985_a_at	2310061I04Rik	RIKEN cDNA 2310061I04 gene	-1.2	0.112	-1.14	0.059	1.64	0.002	-1.13	0.071	-0.46
1439774_at	Prrx1	paired related homeobox 1	1.59	0.1	-1.14	0.873	-1.14	0.686	-1.23	0.407	-0.48
1434715_at	1600014C10Rik	RIKEN cDNA 1600014C10 gene	-1.06	0.936	-1.19	0.541	1.56	0.004	-2.03	0.137	-0.68
1441105_at	---	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library,	-1.75	0.138	1.93	0.141	-1.18	0.418	-1.75	0.251	-0.69
1452160_at	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	-1.25	0.065	1.59	0.099	-1.05	0.732	-1.32	0.344	-0.51
1455309_at	Tmem16f	transmembrane protein 16F	-1.03	0.763	1.45	0.006	-1.08	0.618	-1.23	0.397	-0.47
1440571_at	Eif4g3	Eukaryotic translation initiation factor 4 gamma, 3	-1.12	0.473	1.61	0.078	-1.19	0.383	-1.25	0.493	-0.48
1458692_at	Tomm20	Translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.69	0.376	2.25	0.038	-1.96	0.058	-1.35	0.664	-0.69
1453180_at	6530404N21Rik	RIKEN cDNA 6530404N21 gene	-1	0.993	1.56	0.298	-1.27	0.102	-1.28	0.108	-0.5
1423224_at	4432405B04Rik	RIKEN cDNA 4432405B04 gene	-1.04	0.751	-1.06	0.818	1.45	0.172	-1.17	0.609	-0.46
1427820_at	---	---	-1.04	0.901	-1.14	0.802	1.52	0.395	-1.16	0.669	-0.46
1429573_at	Dmrtc1a	DMRT-like family C1a	-1.22	0.755	1.69	0.491	-1.18	0.649	-1.17	0.575	-0.47
1444897_at	AU017263	expressed sequence AU017263	-1.16	0.842	1.58	0.344	-1.09	0.48	-1.97	0.314	-0.66
1446791_at	Pi15	Peptidase inhibitor 15	-1.59	0.095	2.17	0.004	-1.82	0.114	-1.78	0.356	-0.75
1437529_at	Mrgprb1	MAS-related GPR, member B1	-1.06	0.946	1.53	0.559	-1.14	0.796	-1.12	0.811	-0.45
1459861_s_at	Fbxl10	F-box and leucine-rich repeat protein 10	-1.18	0.258	-1.03	0.854	1.53	0.002	-1.21	0.057	-0.47
1439875_at	Zfp128	zinc finger protein 128	-1.28	0.185	1.57	0.007	-1	0.985	-1.31	0.327	-0.5
1427976_at	Oog1	oogenesin 1	-3.24	0.35	2.34	0.153	-1.41	0.316	-1.97	0.412	-1.07
1439113_at	2410018L13Rik /// (	RIKEN cDNA 2410018L13 gene /// RIKEN cDNA 6030426L16 gene /// similar to I	1.81	0.574	-1.22	0.767	-1.38	0.705	-1.11	0.855	-0.48
1451039_at	2610027L16Rik	RIKEN cDNA 2610027L16 gene	-1.1	0.258	-1.03	0.82	1.47	0.002	-1.15	0.324	-0.45
1459637_at	---	---	-1.03	0.95	-1.06	0.93	1.44	0.378	-1.15	0.807	-0.45
1441747_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330024P	-1.09	0.908	1.65	0.141	-1.29	0.398	-1.63	0.179	-0.59
1436044_at	Scn7a	sodium channel, voltage-gated, type VII, alpha	2.14	0.012	-1.3	0.464	-2.25	0.008	-1.05	0.789	-0.62
1444440_at	4121402D02Rik	RIKEN cDNA 4121402D02 gene	-1.03	0.96	-1.38	0.573	1.66	0.294	-3.02	0.298	-0.94
1446936_at	---	---	2.01	0.519	-1.24	0.478	-1.84	0.116	-1.37	0.31	-0.61

1443799_at	Ppp1r14c	Protein phosphatase 1, regulatory (inhibitor) subunit 14c	-1.79	0.224	2.45	0.089	-2.92	0.001	-1.2	0.503	-0.86
1421989_s_at	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-1.02	0.886	-1.66	0.159	1.77	0.075	-1.83	0.13	-0.68
1421394_a_at	Birc4	baculoviral IAP repeat-containing 4	-1.17	0.793	-1.07	0.882	1.57	0.321	-1.46	0.181	-0.53
1421200_at	Dlgh2	discs, large homolog 2 (Drosophila)	1.75	0.459	-1.1	0.774	-1.43	0.422	-1.61	0.329	-0.6
1453301_a_at	Alkbh4	alkB, alkylation repair homolog 4 (E. coli)	-1.09	0.087	-1.25	0.19	1.64	0.012	-1.26	0.045	-0.49
1428060_at	Cd247	CD247 antigen	-1.19	0.667	-1.4	0.453	1.8	0.122	-3.1	0.193	-0.97
1443928_at	AI462064	expressed sequence AI462064	-1.36	0.093	1.84	0.059	-1.28	0.192	-2.46	0.028	-0.81
1432595_at	---	---	1.83	0.425	-1.18	0.258	-1.47	0.094	-1.3	0.199	-0.53
1431060_at	Peli1	pellino 1	1.77	0.212	-1.01	0.963	-1.66	0.162	-1.18	0.561	-0.52
1440737_at	Inadl	InaD-like (Drosophila)	2.14	0.146	-1.41	0.547	-1.94	0.32	-2.39	0.413	-0.9
1445694_at	---	Transcribed locus	-1.22	0.093	-1.02	0.901	1.57	0.094	-1.2	0.61	-0.47
1424964_at	Rp1h	retinitis pigmentosa 1 homolog (human)	2.22	0.121	-2.19	0.207	-1.47	0.303	-1.34	0.553	-0.69
1443701_at	BC025575	cDNA sequence BC025575	-1.73	0.395	-1.49	0.145	2.11	0.173	-1.44	0.591	-0.64
1417302_at	Rcor2	REST corepressor 2	-1.51	0.477	-1.26	0.113	1.9	0.195	-1.2	0.774	-0.52
1431659_at	Tmem86b	transmembrane protein 86B	-1.4	0.38	1.81	0.255	-1.2	0.533	-1.36	0.546	-0.54
1450114_at	Ksr1	kinase suppressor of ras 1	-1.19	0.555	-1.64	0.252	1.91	0.251	-1.23	0.709	-0.54
1453870_at	1810018F18Rik	RIKEN cDNA 1810018F18 gene	-1.78	0.274	1.96	0.347	-1.2	0.413	-3.24	0.192	-1.06
1431703_at	2900027M19Rik	RIKEN cDNA 2900027M19 gene	1.89	0.26	-1.27	0.685	-1.45	0.34	-1.81	0.411	-0.66
1451894_a_at	Scn8a	sodium channel, voltage-gated, type VIII, alpha	-1.6	0.442	2.13	0.218	-1.66	0.19	-1.04	0.927	-0.54
1420247_at	Glb1l	galactosidase, beta 1-like	2.29	0.299	-1.96	0.013	-1.77	0.109	-2.28	0.096	-0.93
1434983_at	B230363K08Rik	RIKEN cDNA B230363K08 gene	1.76	0.235	-1.37	0.466	-1.14	0.261	-1.27	0.625	-0.51
1445660_at	2700094F01Rik	RIKEN cDNA 2700094F01 gene	2.17	0.085	-1.6	0.083	-1.76	0.174	-1.45	0.063	-0.66
1444354_at	Aff3	AF4/FMR2 family, member 3	-1	0.937	1.7	0.466	-1.5	0.351	-1.93	0.596	-0.68
1424003_at	4930444A02Rik	RIKEN cDNA 4930444A02 gene	-1.06	0.123	1.6	0.019	-1.23	0.072	-1.3	0.402	-0.49
1459771_x_at	Phca	phytoceramidase, alkaline	-1.05	0.893	-2.96	0.42	2.08	0.159	-1.13	0.674	-0.77
1425651_at	Nhej1	nonhomologous end-joining factor 1	-1.11	0.733	-1.21	0.571	1.64	0.147	-1.04	0.756	-0.43
1437986_x_at	Fuk	fucokinase	-1.41	0.135	-1.08	0.829	1.73	0.066	-1.88	0.015	-0.66
1445057_at	C81285	expressed sequence C81285	1.88	0.403	-1.27	0.634	-1.43	0.396	-2.1	0.16	-0.73
1451071_a_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	-1.36	0.235	-1.31	0.321	1.87	0.097	-1.82	0.306	-0.65
1421336_at	Prox1	prospero-related homeobox 1	1.66	0.452	-1.35	0.35	-1.04	0.955	-4.44	0.039	-1.29
1428718_at	Scrn1	secernin 1	-1.01	0.97	1.42	0.573	-1.05	0.816	-1.53	0.498	-0.54
1420972_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	-1.08	0.7	-1.03	0.901	1.47	0.49	-1.12	0.658	-0.44
1440778_x_at	Zfp712	Zinc finger protein 712	-1.01	0.949	1.49	0.091	-1.13	0.461	-1.14	0.338	-0.45
1446015_at	Trak1	Trafficking protein, kinesin binding 1	1.77	0.415	-1.23	0.509	-1.27	0.592	-1.5	0.313	-0.56
1444071_at	9630013A20Rik	RIKEN cDNA 9630013A20 gene	-1.81	0.638	-2.97	0.3	2.48	0.091	-1.13	0.543	-0.86
1454512_at	9430018C23Rik	RIKEN cDNA 9430018C23 gene	-1.19	#DIV/0!	1.56	0.333	-1.03	0.585	-1.08	0.859	-0.44
1437133_x_at	Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	-1.37	0.499	1.67	0.018	-1.03	0.726	-1.7	0.183	-0.61
1422482_at	Ruvbl2	RuvB-like protein 2	-1.15	0.339	-1.17	0.463	1.64	0.07	-1.03	0.909	-0.43
1450592_at	Olfr69	olfactory receptor 69	-1.51	0.052	1.88	0.225	-1.2	0.679	-1.22	0.707	-0.51
1435952_at	---	---	-1.17	0.372	1.57	0.05	-1.05	0.751	-1.36	0.25	-0.51
1450460_at	Aqp3	aquaporin 3	-1.25	0.218	-1.33	0.623	1.82	0.149	-1.2	0.417	-0.49
1437817_at	Snap91	synaptosomal-associated protein 91	-1.23	0.151	1.65	0.346	-1.1	0.395	-1.25	0.22	-0.48
1446214_at	D430018E03Rik	RIKEN cDNA D430018E03 gene	2.33	0.429	-1.44	0.552	-2.84	0.022	-1.45	0.173	-0.85
1422919_at	Hrasls	HRAS-like suppressor	-1.27	0.027	-1.06	0.91	1.64	0.218	-1.9	0.321	-0.65
1456836_at	Itk	IL2-inducible T-cell kinase	1.74	0.17	-1.06	0.923	-1.45	0.253	-2.52	0.094	-0.82
1425096_a_at	Ptcd1	pentatricopeptide repeat domain 1	-1	0.996	-1.09	0.752	1.46	0.443	-1.08	0.701	-0.43
1418489_a_at	Calcrl	calcitonin receptor-like	-1.13	0.433	-1.21	0.623	1.66	0.491	-1.77	0.482	-0.61
1424023_at	Atpbd3	ATP binding domain 3	-1.15	0.459	-1.05	0.761	1.55	0.135	-1.05	0.528	-0.42
1425027_s_at	Sft2d2	SFT2 domain containing 2	-1.17	0.084	-1.13	0.507	1.64	0.119	-1.03	0.833	-0.43
1429706_at	Iqcf5	IQ motif containing F5	2.38	0.153	-2.02	0.278	-2.01	0.017	-1.78	0.464	-0.86
1458255_at	Wdr33	WD repeat domain 33	-1.29	0.132	-1.01	0.985	1.61	0.214	-1.81	0.293	-0.63
1455872_at	BC065085	cDNA sequence BC065085	-1.25	0.705	1.59	0.028	-1.02	0.885	-1.63	0.344	-0.58
1452090_a_at	Olfm3	olfactomedin 3	-1.35	0.204	1.82	0.256	-1.22	0.759	-2.59	0.096	-0.84

1432356_at	1700056N10Rik	RIKEN cDNA 1700056N10 gene	1.79	0.356	-1.14	0.844	-1.41	0.066	-1.77	0.024	-0.63
1437524_x_at	Coro7	coronin 7	-1.01	0.92	-1.02	0.903	1.41	0.01	-1.57	0.023	-0.55
1431616_at	1700067C01Rik	RIKEN cDNA 1700067C01 gene	2.05	0.493	-1.39	0.464	-1.65	0.083	-1.51	0.384	-0.62
1435661_at	Als2cr4	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	-1.01	0.96	1.59	0.022	-1.25	0.134	-1.29	0.333	-0.49
1440560_at	Ypel2	Yippee-like 2 (Drosophila)	-1.12	0.645	1.86	0.169	-1.61	0.156	-1.09	0.77	-0.49
1431298_at	5930416I19Rik	RIKEN cDNA 5930416I19 gene	-1.03	0.903	1.68	0.406	-1.37	0.611	-2.46	0.409	-0.8
1431097_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.36	0.378	-1.07	0.861	1.71	0.317	-1.98	0.238	-0.67
1444757_at	Eef1e1	Eukaryotic translation elongation factor 1 epsilon 1	1.98	0.098	-1.38	0.509	-1.48	0.25	-1.09	0.62	-0.49
1450381_a_at	Bcl6	B-cell leukemia/lymphoma 6	-1.01	0.952	-2.58	0.078	2.01	0.179	-1.87	0.072	-0.86
1440722_at	D19Ertd386e	DNA segment, Chr 19, ERATO Doi 386, expressed	2.02	0.149	-1.21	0.462	-1.88	0.106	-1.89	0.166	-0.74
1454384_at	2900057C01Rik	RIKEN cDNA 2900057C01 gene	-1.15	0.457	1.91	0.058	-1.68	0.214	-1.01	0.947	-0.48
1427571_at	Shh	sonic hedgehog	-3.26	0.262	-1.95	0.299	2.56	0.073	-1.23	0.769	-0.97
1433367_at	8430401P03Rik	RIKEN cDNA 8430401P03 gene	-1.22	0.391	1.6	0.282	-1.04	0.843	-1.9	0.18	-0.64
1416072_at	Cd34	CD34 antigen	-1.14	0.343	1.95	0.056	-1.81	0.012	-1.49	0.092	-0.62
1439048_at	2900078E11Rik	RIKEN cDNA 2900078E11 gene	-1.27	0.435	1.79	0.008	-1.24	0.55	-1.59	0.143	-0.58
1421556_at	Serpina3a	serine (or cysteine) peptidase inhibitor, clade A, member 3A	1.72	0.357	-1.35	0.368	-1.08	0.774	-1.1	0.899	-0.45
1418422_at	Serpinb9g	serine (or cysteine) peptidase inhibitor, clade B, member 9g	2.08	0.364	-2.49	0.19	-1.11	0.861	-1.21	0.547	-0.68
1456650_at	---	6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030010B11	-1.39	0.489	1.84	0.393	-1.21	0.538	-1.58	0.368	-0.59
1459700_at	Lemd3	LEM domain containing 3	2	0.505	-1.17	0.588	-1.9	0.376	-1.39	0.541	-0.61
1441679_at	Cacna1c	Calcium channel, voltage-dependent, L type, alpha 1C subunit	-1.25	0.639	2.26	0.023	-3.04	0.156	-1.27	0.685	-0.83
1448682_at	Dynll1	dynein light chain LC8-type 1	-1	0.993	1.59	0.223	-1.27	0.035	-1.05	0.827	-0.43
1453176_a_at	4933404M02Rik	RIKEN cDNA 4933404M02 gene	-1.1	0.871	1.67	0.551	-1.24	0.363	-2.63	0.338	-0.83
1456125_a_at	Dynll1 /// LOC6277	dynein light chain LC8-type 1 /// similar to dynein, cytoplasmic, light peptide /// sin	-1.01	0.593	1.63	0.245	-1.31	0.001	-1.08	0.666	-0.44
1418692_at	Rab8a	RAB8A, member RAS oncogene family	-1.07	0.783	-1.02	0.891	1.47	0.16	-1.07	0.767	-0.42
1437874_s_at	Hexb	hexosaminidase B	-1.11	0.587	1.5	0.01	-1.01	0.923	-1.51	0.234	-0.53
1439736_at	5830453J16Rik	RIKEN cDNA 5830453J16 gene	2.22	0.224	-2.04	0.12	-1.47	0.183	-2.09	0.235	-0.85
1457784_at	---	---	-1.06	0.789	1.88	0.349	-1.75	0.05	-1.51	0.251	-0.61
1439306_at	Solh	Small optic lobes homolog (Drosophila)	1.89	0.56	-1.62	0.125	-1.13	0.767	-1.19	0.626	-0.51
1430030_at	5330426P16Rik	RIKEN cDNA 5330426P16 gene	-1.02	0.882	1.66	0.006	-1.34	0.141	-1.43	0.096	-0.53
1443545_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.93	0.258	-1.22	0.536	-1.56	0.401	-3.36	0.385	-1.05
1424348_at	1110007A13Rik	RIKEN cDNA 1110007A13 gene	-1.01	0.843	-1.05	0.31	1.44	0.002	-1.06	0.549	-0.42
1456040_at	Sf3b2	splicing factor 3b, subunit 2	-1.16	0.162	-1.11	0.041	1.63	0.016	-1.06	0.394	-0.43
1425269_at	Apbb1ip	amyloid beta (A4) precursor protein-binding, family B, member 1 interacting prote	-1.91	0.429	-1.1	0.752	1.96	0.142	-1.07	0.803	-0.53
1456584_x_at	Phgdh /// LOC3829	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.32	0.025	-1.02	0.966	1.66	0.074	-1.36	0.361	-0.51
1419140_at	Acvr2b	activin receptor IIB	-1.07	0.792	1.81	0.006	-1.56	0.127	-1.3	0.559	-0.53
1453216_at	Gpt1	glutamic pyruvic transaminase 1, soluble	1.99	0.392	-1.22	0.525	-1.71	0.045	-1.13	0.821	-0.52
1418350_at	Hbegf	heparin-binding EGF-like growth factor	-1.27	0.14	1.65	0.278	-1.05	0.85	-1.02	0.955	-0.42
1419335_at	4930441O14Rik	RIKEN cDNA 4930441O14 gene	-1.04	0.831	-1.2	0.457	1.59	0.338	-1.89	0.209	-0.63
1433402_at	4930451E06Rik	RIKEN cDNA 4930451E06 gene	-1.01	0.93	1.73	0.097	-1.47	0.011	-1.03	0.963	-0.45
1442756_at	Lnk	Linker of T-cell receptor pathways	-1.23	0.477	1.6	0.27	-1.03	0.877	-1.05	0.775	-0.42
1430099_at	4930509E16Rik	RIKEN cDNA 4930509E16 gene	1.64	0.364	-1.17	0.773	-1.11	0.778	-1.32	0.315	-0.49
1427826_a_at	Slco1b2	solute carrier organic anion transporter family, member 1b2	1.88	0.395	-1.27	0.631	-1.39	0.447	-2.65	0.214	-0.85
1456739_x_at	Armcx2	armadillo repeat containing, X-linked 2	-1.07	0.728	1.55	0.01	-1.11	0.498	-1.76	0.111	-0.6
1427439_s_at	Prmt5	protein arginine N-methyltransferase 5	-1	0.991	-1.1	0.493	1.49	0.087	-1.03	0.932	-0.41
1417333_at	Rasa4	RAS p21 protein activator 4	-1.36	0.404	-1.39	0.508	1.94	0	-1.31	0.509	-0.53
1422689_at	4930547C10Rik	RIKEN cDNA 4930547C10 gene	-2.13	0.127	2.58	0.145	-2.87	0	-1.08	0.879	-0.88
1439838_a_at	Tmie	transmembrane inner ear	-1.67	0.13	-1.77	0.331	2.23	0.458	-1.16	0.669	-0.59
1443030_at	L3mbtl3	l(3)mbt-like 3 (Drosophila)	-1.12	0.806	1.55	0.426	-1.05	0.729	-1.98	0.22	-0.65
1436790_a_at	Sox11	SRY-box containing gene 11	-1.43	0.575	1.94	0.447	-1.33	0.358	-2.01	0.401	-0.71
1418804_at	Sucnr1	succinate receptor 1	-1.19	0.068	-1.17	0.768	1.7	0.44	-1.5	0.241	-0.54
1425443_at	Tcfap2d	transcription factor AP-2, delta	-2.02	0.263	-1.33	0.57	2.15	0.193	-1.04	0.912	-0.56
1435830_a_at	5430435G22Rik	RIKEN cDNA 5430435G22 gene	-1.16	0.876	1.9	0.148	-1.56	0.151	-1.2	0.601	-0.51
1440190_at	Leng9	leukocyte receptor cluster (LRC) member 9	-1.56	0.113	1.79	0.047	-1.03	0.877	-1.68	0.156	-0.62

1454895_at	Cybasc3	cytochrome b, ascorbate dependent 3	-1.01	0.884	-1.01	0.974	1.41	0.355	-2	0.036	-0.65
1418062_at	Eef1a2	eukaryotic translation elongation factor 1 alpha 2	-1.2	0.509	-1.42	0.058	1.86	0.186	-1.14	0.556	-0.48
1449927_at	S100a5	S100 calcium binding protein A5	-1.53	0.212	-1.36	0.007	2.01	0.073	-1.08	0.766	-0.49
1459099_at	Tmc7	transmembrane channel-like gene family 7	-1.35	0.651	-1.04	0.876	1.69	0.167	-1.11	0.819	-0.45
1430475_at	---	---	2.24	0.121	-3.71	0.01	-1.13	0.837	-2.04	0.437	-1.16
1452025_a_at	Zfp2	zinc finger protein 2	1.44	0.03	-1.01	0.982	-1.04	0.935	-1.88	0.072	-0.62
1415939_at	Fmod	fibromodulin	-1.34	0.375	-1.1	0.811	1.75	0.351	-1.23	0.55	-0.48
1446457_at	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	1.7	0.393	-1.01	0.983	-1.41	0.197	-1.01	0.982	-0.43
1424089_a_at	Tcf4	transcription factor 4	-1.03	0.5	1.66	0.023	-1.3	0.114	-1.33	0.329	-0.5
1439336_at	Tcf4	Transcription factor 4	-1.15	0.754	1.98	0.078	-1.83	0.009	-1.23	0.427	-0.56
1436409_at	Cox8a	cytochrome c oxidase, subunit VIIIa	-2.43	0.013	-1.03	0.962	2.02	0.027	-1.27	0.626	-0.68
1428147_at	Coro7	coronin 7	-1.07	0.835	-1.08	0.526	1.54	0.071	-1.02	0.907	-0.41
1426730_a_at	Prlpk	prolactin-like protein K	1.91	0.44	-1.24	0.679	-1.46	0.489	-1.69	0.39	-0.62
1449667_at	LOC626391	Similar to Zinc finger protein 124 (HZF-16)	1.62	0.532	-1.03	0.934	-1.22	0.676	-2.4	0.14	-0.76
1425065_at	Oas2	2'-5' oligoadenylate synthetase 2	-1.02	0.903	-1.13	0.578	1.54	0.059	-1.65	0.197	-0.57
1456963_at	1110039B18Rik	RIKEN cDNA 1110039B18 gene	2.12	0.195	-2.29	0.247	-1.18	0.499	-1.75	0.543	-0.78
1450599_at	V1rb3	vomeronasal 1 receptor, B3	-1.06	0.822	1.68	0.042	-1.28	0.685	-1.26	0.623	-0.48
1446450_at	Ttn	Titin	1.66	0.329	-1.03	0.952	-1.3	0.511	-1.6	0.049	-0.57
1423895_a_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.63	0.186	-1.07	0.649	-1.19	0.36	-1.72	0.135	-0.59
1427281_at	Scn2a1	sodium channel, voltage-gated, type II, alpha 1	-1.05	0.95	-1.03	0.952	1.49	0.299	-2.11	0.223	-0.68
1447588_x_at	G630024C07Rik	RIKEN cDNA G630024C07 gene	1.93	0.471	-1.17	0.715	-1.6	0.412	-1.07	0.819	-0.48
1425960_s_at	Pax6	paired box gene 6	1.69	0.573	-1.1	0.822	-1.23	0.498	-1.51	0.442	-0.54
1417066_at	Cabc1	chaperone, ABC1 activity of bc1 complex like (S. pombe)	-1.24	0.422	-1.29	0.246	1.83	0.21	-2.01	0.058	-0.68
1445063_at	D1Ertd228e	DNA segment, Chr 1, ERATO Doi 228, expressed	-2.47	0.042	2.02	0.123	-1.01	0.975	-1.14	0.872	-0.65
1435998_at	Gm288	gene model 288, (NCBI)	1.51	0.124	-1.03	0.968	-1.08	0.782	-1.44	0.542	-0.51
1431025_at	Fuz	fuzzy homolog (Drosophila)	-2.1	0.029	2.05	0.017	-1.13	0.276	-1.51	0.232	-0.67
1429045_at	Smurf2	SMAD specific E3 ubiquitin protein ligase 2	1.59	0.27	-1.18	0.591	-1.03	0.935	-1.41	0.375	-0.51
1418833_at	Agxt	alanine-glyoxylate aminotransferase	1.67	0.651	-1.29	0.071	-1.03	0.948	-1.22	0.737	-0.47
1438566_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	-1.2	0.208	-1.34	0.195	1.83	0.274	-1.41	0.112	-0.53
1424938_at	Steap1	six transmembrane epithelial antigen of the prostate 1	-1.11	0.356	1.68	0.333	-1.21	0.49	-1.28	0.342	-0.48
1440117_at	Lrrc48	leucine rich repeat containing 48	-1.11	0.658	1.67	0.18	-1.2	0.603	-1.22	0.554	-0.46
1457498_at	Man2a2	mannosidase 2, alpha 2	-1.1	0.683	1.56	0.385	-1.07	0.817	-1.21	0.457	-0.45
1432632_at	9430063H18Rik	RIKEN cDNA 9430063H18 gene	1.74	0.454	-1.06	0.885	-1.37	0.225	-1.23	0.573	-0.48
1452638_s_at	Dnm1l	dynamin 1-like	-1.05	0.964	-1.14	0.885	1.58	0.691	-1.64	0.605	-0.56
1454051_at	2600011E07Rik	RIKEN cDNA 2600011E07 gene	2	0.451	-2.03	0.131	-1.09	0.833	-1.11	0.848	-0.56
1459490_at	1110032E23Rik	RIKEN cDNA 1110032E23 gene	-1.14	0.256	1.78	0.155	-1.33	0.11	-1.01	0.944	-0.42
1430858_at	4632433K11Rik	RIKEN cDNA 4632433K11 gene	-1.01	0.989	1.43	0.498	-1.01	0.974	-1.17	0.6	-0.44
1442008_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.25	0.003	-1.37	0.065	1.88	0.074	-1.52	0.025	-0.56
1440238_at	Gltscr1	glioma tumor suppressor candidate region gene 1	-1.07	0.571	-1.05	0.82	1.53	0.074	-1.63	0.159	-0.55
1422271_at	Ppyr1	pancreatic polypeptide receptor 1	-3.18	0.407	2.11	0.339	-1.01	0.983	-1.87	0.209	-0.99
1417815_a_at	Serinc3	serine incorporator 3	-1.08	0.45	1.52	0.027	-1.03	0.799	-1.01	0.917	-0.4
1446973_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	-2.31	0.438	2.3	0.197	-1.47	0.062	-1.65	0.589	-0.78
1447688_at	Tbc1d20	TBC1 domain family, member 20	1.84	0.043	-1.03	0.93	-1.64	0.538	-1.48	0.532	-0.58
1436283_at	D630042F21Rik	RIKEN cDNA D630042F21 gene	-1.04	0.695	-2.19	0.36	2	0.12	-1.11	0.576	-0.59
1420347_at	Plunc	palate, lung, and nasal epithelium carcinoma associated	-1.21	0.85	1.81	0.216	-1.28	0.517	-1.67	0.366	-0.59
1441180_at	C330024D21Rik	RIKEN cDNA C330024D21 gene	-1.48	0.628	1.75	0.105	-1.01	0.992	-1.4	0.442	-0.54
1442753_at	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	-1.05	0.842	-1.16	0.648	1.6	0.109	-1.06	0.766	-0.42
1453389_a_at	Sh2b2	SH2B adaptor protein 2	-1.09	0.923	1.66	0.2	-1.18	0.667	-1.05	0.885	-0.42
1429704_at	Lrp2bp	Lrp2 binding protein	1.9	0.259	-1.31	0.684	-1.32	0.208	-1.09	0.78	-0.46
1449814_at	Frat1	frequently rearranged in advanced T-cell lymphomas	-1.01	0.988	-1.92	0.48	1.91	0.454	-1.64	0.326	-0.66
1455803_at	Slco4a1	solute carrier organic anion transporter family, member 4a1	-1.28	0.34	-2.18	0.019	2.18	0.009	-1.53	0.106	-0.7
1449665_at	4833422M21Rik	RIKEN cDNA 4833422M21 gene	-1.71	0.166	-1.01	0.949	1.85	0.272	-1.19	0.34	-0.52
1443692_at	BC057022	cDNA sequence BC057022	-1.36	0.723	-1.4	0.59	1.97	0.064	-1.12	0.438	-0.48

1439957_at	AI843190	expressed sequence AI843190	-1.11	0.897	1.9	0.272	-1.61	0.316	-2.08	0.129	-0.73
1441309_at	Adamts10	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.66	0.606	-1.07	0.903	-1.21	0.714	-2.1	0.27	-0.68
1458223_at	Mdm4 /// LOC5463	transformed mouse 3T3 cell double minute 4 /// similar to transformed mouse 3T3	-1.15	0.735	-2.3	0.131	2.12	0.126	-2.38	0.055	-0.93
1425650_at	Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	-1.12	0.497	-1.04	0.922	1.56	0.101	-1.13	0.601	-0.43
1426284_at	Krt20	keratin 20	-1.11	0.804	1.56	0.132	-1.04	0.938	-1.51	0.357	-0.53
1416549_at	Slc35b4	solute carrier family 35, member B4	-1.02	0.821	-1.11	0.497	1.55	0.038	-1.09	0.153	-0.42
1420279_at	BC048599	CDNA sequence BC048599	1.6	0.61	-1.12	0.749	-1.07	0.874	-1.75	0.413	-0.59
1445412_at	Ccdc73	coiled-coil domain containing 73	1.61	0.434	-1.13	0.847	-1.07	0.895	-1.52	0.442	-0.53
1432912_at	---	---	1.84	0.119	-1.35	0.265	-1.18	0.74	-1.62	0.457	-0.58
1456352_a_at	Sf3b2	splicing factor 3b, subunit 2	-1.09	0.513	-1.07	0.171	1.57	0	-1.07	0.424	-0.42
1420550_at	1110055J05Rik	RIKEN cDNA 1110055J05 gene	1.75	0.494	-1.21	0.741	-1.18	0.767	-1.04	0.919	-0.42
1458382_a_at	Zhx1	zinc fingers and homeoboxes protein 1	1.6	0.411	-1.12	0.687	-1.07	0.856	-1.71	0.491	-0.58
1458312_at	Cacna1a	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.02	0.951	-1.52	0.26	1.79	0.064	-1.01	0.984	-0.44
1443214_at	Gpr155	G protein-coupled receptor 155	1.69	0.233	-1.19	0.594	-1.12	0.645	-1.19	0.727	-0.45
1447873_x_at	Bid	BH3 interacting domain death agonist	-1.31	0.104	-1.23	0.488	1.85	0.15	-1.24	0.239	-0.48
1425558_at	Klc3	kinesin light chain 3	-1.12	0.298	1.68	0.063	-1.17	0.245	-2.06	0.234	-0.67
1451706_a_at	Gabra6	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6	1.78	0.41	-1.05	0.928	-1.45	0.431	-1.36	0.656	-0.52
1441277_s_at	Ptprk	protein tyrosine phosphatase, receptor type, K	-1.04	0.908	-1.29	0.73	1.69	0.433	-2.05	0.372	-0.67
1418095_at	Smpx	small muscle protein, X-linked	-2.13	0.055	-1.17	0.71	2.11	0.086	-2.16	0.141	-0.84
1440492_at	Xpo6	Exportin 6	-1.07	0.907	1.77	0.137	-1.37	0.152	-1.58	0.255	-0.57
1454806_at	D12Ertd553e	DNA segment, Chr 12, ERATO Doi 553, expressed	-1.09	0.732	1.8	0.11	-1.41	0.008	-1.63	0.162	-0.58
1430722_at	4921515J06Rik	RIKEN cDNA 4921515J06 gene	-2.24	0.283	2.04	0.218	-1.06	0.863	-1.2	0.682	-0.61
1422444_at	Itga6	integrin alpha 6	-1.08	0.873	1.52	0.157	-1.01	0.952	-1.1	0.807	-0.42
1441206_at	Synpo2	synaptopodin 2	1.79	0.187	-1.05	0.929	-1.44	0.009	-1.02	0.853	-0.43
1441482_at	---	---	-1.24	0.616	2.07	0.477	-1.78	0.302	-2.08	0.092	-0.76
1439655_at	Ube2d2	Ubiquitin-conjugating enzyme E2D 2	1.62	0.491	-1.06	0.901	-1.15	0.525	-1.15	0.49	-0.43
1422405_at	H2-D4	histocompatibility 2, D region locus 4	-1.15	0.854	-1.44	0.218	1.87	0.173	-1.03	0.954	-0.44
1441118_at	BC017647	cDNA sequence BC017647	-1.6	0.041	2.17	0.215	-1.58	0.331	-1.1	0.849	-0.53
1444628_at	Adam33	a disintegrin and metallopeptidase domain 33	2.07	0.493	-2.19	0.105	-1.1	0.625	-2.4	0.065	-0.91
1425659_at	Tom1l2	target of myb1-like 2 (chicken)	-1.03	0.949	-1.09	0.841	1.54	0.566	-1.02	0.982	-0.4
1444797_at	8030474K03Rik	RIKEN cDNA 8030474K03 gene	-1.83	0.159	-1.19	0.444	2.05	0.145	-1.83	0.207	-0.7
1426980_s_at	E130012A19Rik	RIKEN cDNA E130012A19 gene	-1.11	0.85	1.65	0.282	-1.13	0.489	-1.09	0.839	-0.42
1436092_at	---	Transcribed locus, moderately similar to XP_574723.1 PREDICTED: similar to LF	-1.03	0.943	-1.07	0.878	1.53	0.328	-1.02	0.969	-0.4
1443791_at	4931406I20Rik	RIKEN cDNA 4931406I20 gene	-2.7	0.245	2.16	0.169	-1.1	0.469	-1.08	0.927	-0.68
1448971_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	-1.02	0.912	1.64	0.127	-1.23	0.353	-1.11	0.158	-0.43
1438605_at	Cdc26	Cell division cycle 26	1.57	0.075	-1.14	0.586	-1.01	0.967	-1.68	0.162	-0.57
1434154_at	Kctd13	potassium channel tetramerisation domain containing 13	-1.02	0.968	-1.12	0.315	1.57	0.116	-1.26	0.252	-0.46
1451777_at	BC013672	cDNA sequence BC013672	-1.01	0.947	-1.03	0.893	1.48	0.047	-1.76	0.048	-0.58
1416869_x_at	Lime1	Lck interacting transmembrane adaptor 1	-1.05	0.882	-1.04	0.918	1.53	0.067	-1.1	0.784	-0.42
1433381_at	4921509A06Rik	RIKEN cDNA 4921509A06 gene	-1.87	0.141	-1.19	0.739	2.07	0.126	-2.86	0.136	-0.96
1435960_at	LOC434128	Similar to KIAA1183 protein	-1.07	0.803	1.66	0.154	-1.17	0.163	-1.09	0.672	-0.42
1419857_at	---	Transcribed locus	-1.07	0.792	-1.15	0.248	1.64	0.233	-1.78	0.348	-0.59
1417767_at	Cyb5b	cytochrome b5 type B	-1.04	0.863	-1.01	0.977	1.49	0.355	-1.15	0.522	-0.43
1425571_at	Slamf1	signaling lymphocytic activation molecule family member 1	-1.18	0.153	-1.08	0.611	1.68	0.454	-1.65	0.192	-0.56
1456853_at	---	Inhibitor of four 1 (Mif1)	-1.13	0.645	-1.14	0.66	1.68	0.167	-1.05	0.867	-0.41
1440481_at	Stat1	signal transducer and activator of transcription 1	1.54	0.361	-1.07	0.79	-1.03	0.874	-1.63	0.074	-0.55
1424851_at	Chchd5	coiled-coil-helix-coiled-coil-helix domain containing 5	-1.05	0.889	-1.26	0.374	1.7	0.111	-1.57	0.153	-0.55
1435644_at	Sh3pxd2b	SH3 and PX domains 2B	1.49	0.051	-1.01	0.931	-1.03	0.882	-1.45	0.392	-0.5
1445304_at	Mgrn1	mahogunin, ring finger 1	-1.11	0.88	2.15	0.111	-2.51	0.028	-1.35	0.667	-0.7
1427658_at	Ctbs	chitobiase, di-N-acetyl-	-1.03	0.747	1.56	0.099	-1.09	0.776	-1.18	0.25	-0.44
1439443_x_at	Tkt	transketolase	-1.19	0.405	-1.04	0.791	1.65	0.06	-1.21	0.618	-0.45
1448675_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	1.59	0.198	-1.06	0.762	-1.08	0.796	-1.35	0.066	-0.48
1438872_at	BC050188	cDNA sequence BC050188	-2.6	0.134	2.1	0.137	-1.04	0.942	-1.96	0.418	-0.87

1451765_a_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	-1.01	0.936	-1.11	0.448	1.56	0.049	-1.56	0.025	-0.53
1437086_at	Ascl1	achaete-scute complex homolog-like 1 (Drosophila)	1.91	0.296	-1.4	0.258	-1.2	0.506	-3.18	0.017	-0.97
1459618_at	Trex1	Three prime repair exonuclease 1	-1.42	0.482	1.85	0.119	-1.11	0.724	-1.03	0.869	-0.43
1444117_at	Amigo1	adhesion molecule with Ig like domain 1	1.83	0.283	-1.16	0.809	-1.33	0.595	-1.68	0.249	-0.58
1429909_at	4833411O04Rik	RIKEN cDNA 4833411O04 gene	-1.14	0.617	1.73	0.155	-1.18	0.221	-1.12	0.597	-0.43
1458625_at	---	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830014	2.04	0.055	-1.6	0.644	-1.26	0.747	-3.28	0.016	-1.03
1455154_at	Gli3	GLI-Kruppel family member GLI3	-1.16	0.387	1.7	0.353	-1.11	0.587	-1.06	0.865	-0.41
1434997_at	Cdc2l6	cell division cycle 2-like 6 (CDK8-like)	-1.15	0.294	-1.05	0.804	1.64	0	-1.36	0.093	-0.48
1423950_at	Kcnab3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	2.06	0.073	-1.83	0.226	-1.17	0.632	-1.26	0.572	-0.55
1441336_at	Nut	nuclear protein in testis	1.61	0.102	-1.02	0.886	-1.15	0.771	-1	0.997	-0.39
1417809_at	Slc22a18	solute carrier family 22 (organic cation transporter), member 18	-1.08	0.523	-1.05	0.666	1.58	0.015	-1.38	0.348	-0.48
1452745_at	1810044A24Rik	RIKEN cDNA 1810044A24 gene	-1.03	0.911	-1.13	0.057	1.6	0.002	-1.02	0.92	-0.39
1436254_at	---	Transcribed locus	-1.37	0.587	1.92	0.155	-1.24	0.366	-1.07	0.82	-0.44
1458396_at	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	-1.67	0.086	-1.07	0.707	1.93	0.236	-1.46	0.254	-0.57
1458935_at	C79744	expressed sequence C79744	-1.27	0.58	-1.01	0.985	1.69	0.241	-1.04	0.929	-0.41
1440798_x_at	Lrrc6	Leucine rich repeat containing 6 (testis)	-1.38	0.563	1.91	0.383	-1.2	0.515	-1.15	0.725	-0.46
1450271_at	Ptk6	PTK6 protein tyrosine kinase 6	-1.13	0.858	1.61	0.138	-1.04	0.762	-2.19	0.077	-0.69
1425144_at	Klk1b11	kallikrein 1-related peptidase b11	-1.59	0.241	2.22	0.343	-1.62	0.486	-1.05	0.931	-0.51
1418878_at	Acrv1	acrosomal vesicle protein 1	-1.38	0.505	1.75	0.182	-1.01	0.974	-1.55	0.041	-0.55
1430631_at	Ppm1f	protein phosphatase 1F (PP2C domain containing)	-2.72	0.03	-3.47	0.069	2.81	0.404	-1.2	0.75	-1.14
1440768_x_at	1700052I22Rik	RIKEN cDNA 1700052I22 gene	2.07	0.103	-1.57	0.351	-1.31	0.495	-1.2	0.702	-0.5
1449271_a_at	Hebp2	heme binding protein 2	-1.25	0.266	1.75	0.303	-1.09	0.566	-1.03	0.961	-0.41
1436702_at	1110038O08Rik	RIKEN cDNA 1110038O08 gene	-1.78	0.087	-1.58	0.461	2.27	0.04	-1.72	0.139	-0.7
1430136_at	Grm3	glutamate receptor, metabotropic 3	1.65	0.015	-1.08	0.903	-1.12	0.315	-1.27	0.638	-0.45
1447037_at	---	---	-1.07	0.923	1.69	0.232	-1.18	0.08	-1.44	0.333	-0.5
1458037_at	Ncald	Neurocalcin delta	-2.63	0.07	2.68	0.009	-2.47	0.004	-1.02	0.977	-0.86
1431218_at	Zdhhc20	zinc finger, DHHC domain containing 20	1.83	0.027	-1.12	0.787	-1.33	0.239	-1.59	0.237	-0.55
1441199_at	Ptprm	Protein tyrosine phosphatase, receptor type, M	1.93	0.147	-1.07	0.79	-1.67	0.25	-2.93	0.3	-0.93
1424685_at	Exosc4	exosome component 4	-1.02	0.912	-1.03	0.743	1.52	0.038	-1	0.999	-0.38
1422325_at	Magea5	melanoma antigen, family A, 5	1.83	0.038	-1.29	0.016	-1.16	0.413	-1.4	0.19	-0.5
1430049_at	4932701A20Rik	RIKEN cDNA 4932701A20 gene	1.74	0.47	-1.12	0.888	-1.19	0.743	-2.07	0.391	-0.66
1419780_at	---	---	-1.08	0.173	1.56	0.222	-1.01	0.851	-1.32	0.314	-0.46
1425633_at	BC026782	cDNA sequence BC026782	1.97	0.036	-1.58	0.006	-1.15	0.369	-1.28	0.767	-0.51
1438132_at	C030005G22Rik	RIKEN cDNA C030005G22 gene	-1.32	0.597	-1.4	0.578	2	0.02	-1.36	0.777	-0.52
1453763_at	Txndc11	thioredoxin domain containing 11	-1.25	0.35	-1.04	0.929	1.71	0.205	-1.03	0.833	-0.4
1443998_at	---	Transcribed locus	1.78	0.085	-1.12	0.771	-1.25	0.493	-2.68	0.114	-0.82
1441514_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	-1.07	0.89	-1.57	0.279	1.9	0.077	-1.3	0.505	-0.51
1420757_at	Myf5	myogenic factor 5	1.92	0.467	-1.67	0.427	-1.05	0.942	-1.66	0.313	-0.61
1429447_at	Evc2	Ellis van Creveld syndrome 2 homolog (human)	-1.06	0.042	1.53	0.424	-1	0.998	-1.43	0.485	-0.49
1430630_at	---	---	-1.06	0.812	1.57	0.326	-1.04	0.835	-1.12	0.717	-0.41
1432681_at	9130009M17Rik	RIKEN cDNA 9130009M17 gene	2.25	0.473	-1.4	0.595	-1.94	0.386	-1.61	0.532	-0.67
1457019_s_at	Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	-1.44	0.515	2	0.093	-1.28	0.207	-1.24	0.373	-0.49
1449473_s_at	Cd40	CD40 antigen	-1.15	0.758	1.75	0.191	-1.17	0.451	-2.6	0.076	-0.79
AFFX-GapdhMur/M	LOC14433	similar to glyceraldehyde-3-phosphate dehydrogenase	-1.01	0.938	-1.18	0.408	1.65	0.089	-1.1	0.639	-0.41
1443358_at	Rpp14	Ribonuclease P 14 subunit (human)	-2.02	0.219	-1.16	0.247	2.12	0.002	-1.47	0.339	-0.63
1437588_at	Pou4f2	POU domain, class 4, transcription factor 2	-1.43	0.496	2.26	0.193	-1.92	0.438	-2.43	0.298	-0.88
1457850_at	Slc7a14	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	-1.57	0.567	2.12	0.207	-1.38	0.41	-1.16	0.577	-0.5
1432921_at	---	---	-1.11	0.445	1.89	0.259	-1.45	0.091	-1.26	0.562	-0.48
1436527_at	---	---	-1.01	0.989	-1.09	0.656	1.57	0.487	-1.03	0.877	-0.39
1453903_at	4930503B20Rik	RIKEN cDNA 4930503B20 gene	-1.36	0.558	1.99	0.125	-1.31	0.303	-1.25	0.529	-0.48
1450971_at	Gadd45b	growth arrest and DNA-damage-inducible 45 beta	1.61	0.11	-1.11	0.74	-1.03	0.853	-1.49	0.316	-0.5
1458698_at	AB041803	CDNA sequence AB041803	-1.88	0.308	-1.02	0.969	1.97	0.055	-1.18	0.594	-0.53
1423354_at	Snap29	synaptosomal-associated protein	-1.03	0.795	-1.13	0.634	1.62	0.135	-1.29	0.463	-0.46

1454057_at	4930470B04Rik	RIKEN cDNA 4930470B04 gene	1.91	0.298	-1.15	0.865	-1.42	0.643	-1.86	0.333	-0.63
1419842_at	---	Transcribed locus	-1.48	0.73	1.9	0.315	-1.09	0.907	-3.14	0.067	-0.95
1423334_at	1200007D18Rik	RIKEN cDNA 1200007D18 gene	-1.43	0.557	-1.31	0.315	2.02	0.168	-1.3	0.503	-0.5
1419392_at	Pclo	piccolo (presynaptic cytomatrix protein)	-1.19	0.247	1.74	0.023	-1.1	0.508	-2.28	0.172	-0.71
1445918_at	Tmem2	Transmembrane protein 2	2.16	0.073	-1.24	0.477	-1.93	0.095	-1.54	0.228	-0.64
1421005_at	Cep110	centrosomal protein 110	1.75	0.241	-1.33	0.695	-1.02	0.955	-1.48	0.375	-0.52
1451527_at	Pcolce2	procollagen C-endopeptidase enhancer 2	-1.27	0.143	2.02	0.001	-1.48	0.101	-1.38	0.205	-0.53
1444519_at	Lgr5	leucine rich repeat containing G protein coupled receptor 5	-1.04	0.918	-1.21	0.646	1.7	0.317	-1.3	0.62	-0.46
1445351_at	---	---	2.35	0.237	-1.57	0.244	-1.98	0.095	-1.1	0.506	-0.58
1435825_at	Acvrl1	activin A receptor, type II-like 1	-1.13	0.73	-1.02	0.915	1.62	0.155	-1.37	0.189	-0.48
1443609_s_at	Syvn1	synovial apoptosis inhibitor 1, synoviolin	-1	0.999	-1.19	0.437	1.65	0.099	-1.24	0.467	-0.45
1457621_at	Rpain	RPA interacting protein	1.74	0.037	-1.17	0.761	-1.12	0.419	-1.58	0.342	-0.53
1444061_at	A030004J04Rik	RIKEN cDNA A030004J04 gene	1.69	0.176	-1.25	0.596	-1	0.991	-1.25	0.726	-0.45
1421138_a_at	Pkib	protein kinase inhibitor beta, cAMP dependent, testis specific	1.62	0.383	-1.03	0.958	-1.11	0.856	-2.42	0.073	-0.74
1419926_at	Txndc10	Thioredoxin domain containing 10	-1.19	0.612	1.76	0.082	-1.12	0.352	-1.31	0.151	-0.47
1459541_at	---	---	2.13	0.058	-1.6	0.393	-1.35	0.242	-1.38	0.561	-0.55
1454677_at	Timp2	tissue inhibitor of metalloproteinase 2	-1.03	0.757	1.62	0.156	-1.1	0.769	-1.18	0.688	-0.42
1441535_at	Mllt3	Myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosopl	-1.07	0.832	2.03	0.204	-1.89	0.019	-1.1	0.776	-0.51
1443598_at	LOC626854	Similar to zinc finger protein 709	-1.23	0.548	1.73	0.082	-1.05	0.881	-1.3	0.384	-0.46
1453661_at	9130403I23Rik	RIKEN cDNA 9130403I23 gene	-1.36	0.06	2.45	0.028	-3.18	0.012	-3.16	0.06	-1.32
1450814_a_at	Ipo4	importin 4	-1.09	0.634	-1.08	0.222	1.65	0.015	-1	0.961	-0.38
1443600_at	AA414992	expressed sequence AA414992	-1.67	0.305	1.95	0.031	-1.06	0.86	-1.69	0.456	-0.62
1447138_at	AI853502	expressed sequence AI853502	1.87	0.161	-1.59	0.16	-1	0.977	-1.16	0.746	-0.47
1427859_at	---	Immunoglobulin kappa chain complex	2.3	0.462	-3.71	0.117	-1.08	0.896	-3.14	0.031	-1.41
1437134_at	Uqcrq	Ubiquinol-cytochrome c reductase, complex III subunit VII	1.99	0.151	-1.32	0.729	-1.34	0.307	-1.2	0.759	-0.47
1447327_at	---	---	-1.46	0.509	1.85	0.317	-1.03	0.941	-1.8	0.472	-0.61
1431418_at	C030026M15Rik	RIKEN cDNA C030026M15 gene	1.98	0.464	-1.14	0.746	-1.56	0.27	-1.53	0.508	-0.56
1415931_at	Igf2	insulin-like growth factor 2	1.63	0.384	-1.11	0.741	-1.02	0.948	-1.01	0.984	-0.38
1417497_at	Cp	ceruloplasmin	1.73	0.22	-1.06	0.849	-1.22	0.207	-1.24	0.341	-0.45
1427893_a_at	Pmvk	phosphomevalonate kinase	-1.03	0.689	1.63	0.01	-1.11	0.757	-1.04	0.725	-0.39
1447291_at	Nphs1as	nephrosis 1 homolog, nephrin antisense	-1.3	0.056	-1.41	0.44	2.02	0.034	-1.55	0.14	-0.56
1446776_at	C77581	expressed sequence C77581	2.11	0.274	-1.71	0.369	-1.23	0.436	-1.23	0.431	-0.52
1438426_at	Tmem58	transmembrane protein 58	-1.34	0.268	1.95	0.357	-1.24	0.118	-1.68	0.259	-0.58
1457273_at	LOC669490	similar to odd Oz/ten-m homolog 2	-1.03	0.898	-1.13	0.744	1.64	0.153	-1.6	0.421	-0.53
1443091_at	---	---	-2.59	0.051	2.21	0.074	-1.1	0.593	-1.41	0.431	-0.72
1451286_s_at	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	-1.24	0.088	-1.2	0.139	1.86	0.008	-1.28	0.189	-0.46
1430409_at	Nsf	N-ethylmaleimide sensitive fusion protein	1.83	0.458	-1.32	0.349	-1.09	0.565	-1.02	0.919	-0.4
1421942_s_at	Tgfa	transforming growth factor alpha	1.83	0.285	-1.25	0.61	-1.15	0.775	-1.79	0.065	-0.59
1421275_s_at	Socs4	suppressor of cytokine signaling 4	1.79	0.175	-1.02	0.871	-1.36	0.291	-1.1	0.631	-0.42
1456590_x_at	Akr1b3	aldo-keto reductase family 1, member B3 (aldose reductase)	-1.58	0.271	1.95	0.01	-1.08	0.413	-1.7	0.162	-0.6
1442915_at	Slc9a4	solute carrier family 9 (sodium/hydrogen exchanger), member 4	2.03	0.357	-1.29	0.455	-1.42	0.448	-1.12	0.566	-0.45
1453346_at	1700011L22Rik	RIKEN cDNA 1700011L22 gene	2.32	0.316	-1.29	0.655	-2.43	0.231	-1.05	0.918	-0.61
1453719_at	4930506C21Rik	RIKEN cDNA 4930506C21 gene	1.89	0.347	-1.06	0.911	-1.48	0.178	-1.32	0.134	-0.49
1422291_at	Ccr8	chemokine (C-C motif) receptor 8	-1.25	0.8	-1.89	0.147	2.18	0.107	-1.4	0.625	-0.59
1455132_at	A430107D22Rik	RIKEN cDNA A430107D22 gene	-1.56	0.677	-2.11	0.488	2.4	0.005	-2.23	0.111	-0.88
1431702_at	---	---	-1.07	0.915	1.63	0.414	-1.05	0.907	-1.34	0.482	-0.46
1441695_at	LOC240444	Similar to Potassium voltage-gated channel subfamily G member 2 (Voltage-gate	-1.3	0.786	2.07	0.1	-1.48	0.425	-1.91	0.383	-0.66
1459190_at	D3Ertd258e	DNA segment, Chr 3, ERATO Doi 258, expressed	-1.08	0.507	1.83	0.462	-1.32	0.457	-1.15	0.756	-0.43
1443602_at	Ifngr1	Interferon gamma receptor 1	1.85	0.285	-1.46	0.34	-1.02	0.969	-1.05	0.882	-0.42
1458205_at	---	---	-1.05	0.822	-1.35	0.152	1.83	0.451	-1.31	0.38	-0.47
1455460_at	6430547I21Rik	RIKEN cDNA 6430547I21 gene	-1.2	0.805	1.94	0.217	-1.36	0.514	-1.15	0.792	-0.44
1450684_at	Etv1	ets variant gene 1	-1.32	0.276	1.79	0.12	-1.03	0.917	-1.1	0.679	-0.42
1417529_at	Rab33a	RAB33A, member of RAS oncogene family	-1.17	0.683	1.93	0.049	-1.37	0.077	-1.79	0.106	-0.6

1430930_at	0610038B21Rik	RIKEN cDNA 0610038B21 gene	2.06	0.248	-1.49	0.447	-1.27	0.67	-1.47	0.635	-0.54
1440593_at	Bnc2	Basonuclin 2	-1.12	0.446	1.92	0.075	-1.41	0.093	-1.37	0.185	-0.5
1450421_at	Tgfa	transforming growth factor alpha	-1.12	0.872	1.69	0.051	-1.07	0.665	-1.74	0.011	-0.56
1441472_at	Clk3	CDC-like kinase 3	-1.11	0.9	1.64	0.354	-1.02	0.943	-1.11	0.659	-0.4
1428054_at	Slc8a2	solute carrier family 8 (sodium/calcium exchanger), member 2	2.07	0.528	-1.63	0.227	-1.19	0.203	-1.07	0.698	-0.46
1451877_at	Eda	ectodysplasin-A	1.85	0.181	-1.24	0.645	-1.15	0.802	-1.05	0.952	-0.4
1445173_at	AK129341	cDNA sequence AK129341	-1.36	0.253	1.86	0.144	-1.08	0.641	-1.58	0.279	-0.54
1447274_at	Waspip	Wiskott-Aldrich syndrome protein interacting protein	-1.16	0.378	2.01	0.178	-1.54	0.092	-1.52	0.075	-0.55
1441958_s_at	Ager	advanced glycosylation end product-specific receptor	1.81	0.111	-1.04	0.337	-1.32	0.032	-3.22	0.034	-0.94
1449152_at	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	-1.26	0.15	1.91	0.32	-1.21	0.041	-2.9	0.047	-0.87
1429905_at	3110009O07Rik	RIKEN cDNA 3110009O07 gene	1.92	0.351	-1.14	0.784	-1.36	0.517	-1.5	0.561	-0.52
1425365_a_at	Cyp2d13	cytochrome P450, family 2, subfamily d, polypeptide 13	-1.03	0.967	-1.7	0.001	1.97	0.219	-1.69	0.351	-0.61
1456648_at	Man1a	Mannosidase 1, alpha	-1.15	0.566	-1.15	0.19	1.79	0.43	-1.7	0.05	-0.55
1417222_a_at	Tmem123	transmembrane protein 123	-1.08	0.351	1.65	0.021	-1.05	0.746	-1.45	0.197	-0.48
1419777_at	Stk25	Serine/threonine kinase 25 (yeast)	-1.17	0.839	1.97	0.146	-1.41	0.49	-1.51	0.009	-0.53
1437383_at	Ccnl1	Cyclin L1	-1.03	0.926	1.77	0.098	-1.27	0.423	-1.04	0.768	-0.39
1445013_at	C86098	expressed sequence C86098	-1.18	0.793	1.72	0.362	-1.05	0.937	-1.1	0.887	-0.4
1429958_x_at	Haghl	hydroxyacylglutathione hydrolase-like	-1.12	0.35	-1.11	0.639	1.73	0.004	-1.18	0.485	-0.42
1451190_a_at	Sbk1	SH3-binding kinase 1	-1	0.981	-1.02	0.923	1.56	0.029	-2.76	0.067	-0.81
1454192_at	4930579C15Rik	RIKEN cDNA 4930579C15 gene	-1.03	0.907	1.79	0.364	-1.3	0.636	-1.01	0.981	-0.39
1438103_at	Pcdhgc4	protocadherin gamma subfamily C, 4	2.39	0.141	-2.45	0.1	-1.36	0.281	-1.11	0.64	-0.63
1425171_at	Rho	rhodopsin	1.77	0.21	-1.23	0.674	-1.05	0.903	-1.01	0.988	-0.38
1443098_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.22	0.343	2.2	0.202	-1.94	0.088	-1.24	0.411	-0.55
1432490_a_at	Pde10a	phosphodiesterase 10A	2.14	0.045	-1.55	0.422	-1.34	0.383	-1.91	0.059	-0.66
1440844_at	Tob1	transducer of ErbB-2.1	2.53	0.469	-3.05	0.306	-1.47	0.019	-1.16	0.389	-0.79
1422989_a_at	Dmpk	dystrophia myotonica-protein kinase	-1	0.997	-1.39	0.16	1.82	0.366	-1.34	0.163	-0.48
1443409_at	C76434	expressed sequence C76434	-1.06	0.797	1.92	0.053	-1.48	0.401	-1.09	0.84	-0.43
1457038_at	Frem2	Fras1 related extracellular matrix protein 2	-1.15	0.247	1.81	0.326	-1.16	0.786	-1.9	0.356	-0.6
1446024_at	---	---	2.01	0.4	-1.32	0.683	-1.3	0.59	-2.38	0.36	-0.75
1433378_at	9430019H13Rik	RIKEN cDNA 9430019H13 gene	-1.62	0.078	1.99	0.057	-1.08	0.661	-1.43	0.637	-0.53
1427435_at	---	---	-1.09	0.921	-1.07	0.91	1.68	0.18	-1.11	0.542	-0.4
1430980_a_at	Eif4a1	eukaryotic translation initiation factor 4A1	-1.13	0.733	-1.2	0.604	1.82	0.237	-1.12	0.807	-0.41
1436972_at	Gpr61	G protein-coupled receptor 61	1.97	0.11	-1.29	0.59	-1.26	0.175	-1.13	0.787	-0.43
1439890_at	Fbxl7	F-box and leucine-rich repeat protein 7	-1.31	0.514	1.96	0.106	-1.22	0.659	-1.58	0.239	-0.54
1440292_at	D13Ertd666e	DNA segment, Chr 13, ERATO Doi 666, expressed	2.15	0.151	-1.83	0.039	-1.18	0.646	-2.97	0.469	-0.96
1419770_at	---	---	2.13	0.184	-1.04	0.948	-2.23	0.171	-1.71	0.589	-0.71
1443449_at	---	---	1.87	0.432	-1.15	0.834	-1.24	0.591	-1.63	0.53	-0.54
1434802_s_at	Ntf3	neurotrophin 3	-1.02	0.824	1.66	0.329	-1.09	0.526	-2.97	0.018	-0.86
1420403_at	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	1.96	0.111	-1.19	0.767	-1.33	0.508	-1.45	0.495	-0.5
1443878_at	Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	2.24	0.478	-2.37	0.213	-1.13	0.817	-2.07	0.231	-0.83
1432121_a_at	Lrrc44	leucine rich repeat containing 44	-1.03	0.653	-1.08	0.864	1.66	0.189	-2.42	0.303	-0.72
1452936_at	Crtac1	cartilage acidic protein 1	-1.03	0.939	1.89	0.125	-1.43	0.489	-1.22	0.769	-0.45
1421384_at	Lyst	lysosomal trafficking regulator	-1.27	0.692	-1.2	0.659	1.94	0.092	-1.51	0.369	-0.51
1459140_at	---	---	-1.55	0.207	1.97	0.137	-1.07	0.599	-1.22	0.67	-0.46
1422333_at	Cyp21a1	cytochrome P450, family 21, subfamily a, polypeptide 1	1.73	0.196	-1.15	0.759	-1.04	0.963	-1.24	0.218	-0.43
1446662_at	4930562C15Rik	RIKEN cDNA 4930562C15 gene	-1.5	0.291	-1.27	0.633	2.1	0.112	-1.02	0.944	-0.42
1447353_at	Gpr161	G protein-coupled receptor 161	2.06	0.492	-1.43	0.586	-1.25	0.631	-1.79	0.221	-0.6
1445386_at	---	Transcribed locus	-1.14	0.665	2.06	0.205	-1.63	0.096	-1.39	0.59	-0.52
1421839_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	-1.04	0.881	-1.01	0.99	1.6	0.41	-1.54	0.407	-0.5
1446314_at	A330041C17Rik	RIKEN cDNA A330041C17 gene	-2.14	0.386	2.27	0.144	-1.21	0.56	-1.07	0.921	-0.54
1424298_at	Zfp282	zinc finger protein 282	1.91	0.14	-1.17	0.748	-1.27	0.243	-1.77	0.053	-0.57
1416839_at	Mut	methylmalonyl-Coenzyme A mutase	-1.15	0.842	1.99	0.349	-1.43	0.283	-1.49	0.586	-0.52
1425970_a_at	Ros1	Ros1 proto-oncogene	-1.49	0.738	-1.74	0.103	2.32	0.008	-1.46	0.532	-0.59

1443855_at	Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	-2.16	0.338	-1.17	0.807	2.24	0.041	-1.6	0.385	-0.67
1425441_at	---	---	-2.01	0.224	2.29	0.213	-1.28	0.672	-2.03	0.139	-0.76
1443517_at	6030443O07Rik	RIKEN cDNA 6030443O07 gene	1.85	0.127	-1.25	0.594	-1.09	0.848	-1.39	0.551	-0.47
1458949_at	5330434G04Rik	RIKEN cDNA 5330434G04 gene	-1.82	0.238	2.15	0.289	-1.16	0.673	-1.82	0.038	-0.66
1417695_a_at	Soat1	sterol O-acyltransferase 1	-1.09	0.568	1.77	0.013	-1.15	0.167	-1.26	0.458	-0.43
1430086_at	Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	-1.07	0.752	1.7	0.374	-1.08	0.774	-1.93	0.41	-0.59
1440758_at	---	---	2.26	0.003	-1.44	0.19	-1.65	0.405	-1.73	0.408	-0.64
1445894_at	---	---	2.04	0.322	-1.6	0.202	-1.11	0.599	-1.12	0.678	-0.45
1453395_at	5330403D14Rik	RIKEN cDNA 5330403D14 gene	2.56	0.015	-2.69	0.303	-1.57	0.258	-2.63	0.064	-1.08
1440073_at	Rrm1	ribonucleotide reductase M1	-1.05	0.946	-1.09	0.904	1.7	0.399	-1.02	0.957	-0.37
1457010_at	3010001F23Rik	RIKEN cDNA 3010001F23 gene	2.27	0.115	-2.17	0.01	-1.2	0.242	-2.54	0.094	-0.91
1459410_at	LOC493582	hypothetical LOC493582	-2.95	0.447	2.62	0.376	-1.63	0.384	-1.17	0.463	-0.79
1445388_at	Cd226	CD226 antigen	-1.22	0.767	-1.05	0.931	1.8	0.023	-1.33	0.546	-0.45
1442975_at	---	Transcribed locus	2.3	0.392	-2.25	0.27	-1.21	0.539	-1.25	0.663	-0.6
1449990_at	Il2 /// LOC630222	interleukin 2 /// similar to Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCG	1.77	0.61	-1.18	0.688	-1.05	0.919	-1.18	0.614	-0.41
1442420_at	Large	Like-glycosyltransferase	2.25	0.224	-1.02	0.968	-2.93	0	-1.3	0.601	-0.75
1445782_at	---	---	-1.1	0.758	-1.06	0.734	1.72	0.051	-1.06	0.778	-0.37
1423145_a_at	Tcap	titin-cap	-1.04	0.95	-1.39	0.362	1.89	0.31	-1.31	0.191	-0.46
1456509_at	1110032F04Rik	RIKEN cDNA 1110032F04 gene	-1.35	0.524	2.09	0.066	-1.35	0.631	-1.68	0.173	-0.57
1434714_at	Ero1lb	ERO1-like beta (S. cerevisiae)	-1.03	0.892	-1.16	0.473	1.74	0.316	-1.46	0.317	-0.48
1450010_at	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	-1.43	0.411	-1.5	0.212	2.21	0.069	-1.91	0.141	-0.66
1420404_at	Cd86	CD86 antigen	-1.02	0.933	1.72	0.04	-1.13	0.485	-1.74	0.153	-0.54
1459353_at	Kctd3	potassium channel tetramerisation domain containing 3	-1.55	0.203	2.04	0.467	-1.12	0.834	-1.23	0.491	-0.46
1433429_at	Pigs	phosphatidylinositol glycan anchor biosynthesis, class S	-1.01	0.8	-1.06	0.477	1.64	0.006	-1.03	0.861	-0.36
1447677_x_at	Hars2	histidyl tRNA synthetase 2	-1.81	0.024	-1.17	0.761	2.17	0.047	-2.4	0.146	-0.8
1425999_at	LOC214403	complement factor H-related protein	1.87	0.585	-1.04	0.748	-1.34	0.081	-1.15	0.455	-0.42
1433124_at	4930534I15Rik	RIKEN cDNA 4930534I15 gene	2.57	0.205	-1.69	0.29	-2.42	0.183	-1.74	0.578	-0.82
1444745_at	Diap2	Diaphanous homolog 2 (Drosophila)	2.47	0.06	-2.06	0.203	-1.6	0.094	-4.25	0.229	-1.36
1441138_at	Foxn2	forkhead box N2	1.88	0.356	-1.14	0.694	-1.21	0.429	-1.26	0.062	-0.43
1416333_at	Dok2	docking protein 2	-1.1	0.774	1.88	0.007	-1.27	0.41	-1.48	0.051	-0.49
1420179_at	Ddost	dolichyl-di-phosphooligosaccharide-protein glycotransferase	1.96	0.356	-1.07	0.915	-1.45	0.175	-1.44	0.458	-0.5
1458589_at	---	---	-1.16	0.623	1.74	0.077	-1.02	0.955	-1.14	0.688	-0.4
1429873_at	1700125H20Rik	RIKEN cDNA 1700125H20 gene	-1.81	0.468	-1.04	0.88	2.07	0.234	-1.27	0.519	-0.51
1446243_at	5830404H04Rik	RIKEN cDNA 5830404H04 gene	-1.12	0.587	-1.08	0.406	1.77	0.165	-1.65	0.357	-0.52
1428758_at	Tmem86a	transmembrane protein 86A	-1.16	0.731	1.8	0.009	-1.08	0.603	-1.24	0.494	-0.42
1429154_at	Slc35f2	solute carrier family 35, member F2	-1.04	0.623	-1.58	0.314	1.99	0.053	-1.21	0.247	-0.46
1417868_a_at	Ctsz	cathepsin Z	-1.03	0.502	-1.02	0.794	1.64	0.008	-1.84	0.02	-0.56
1427398_at	Muc4	mucin 4	-1.02	0.94	1.61	0.462	-1.01	0.914	-1.54	0.201	-0.49
1419440_at	Trim54	tripartite motif-containing 54	-1.55	0.352	-1.18	0.359	2.1	0.063	-1.72	0.436	-0.59
1427431_at	---	---	1.95	0.271	-1.07	0.812	-1.41	0.353	-1.21	0.741	-0.44
1417382_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	-1	0.985	-1.03	0.78	1.63	0.18	-1.42	0.101	-0.46
1438175_x_at	Myom2	myomesin 2	-1.36	0.111	-1.7	0.141	2.27	0.075	-2.5	0.213	-0.82
1454783_at	Il13ra1	interleukin 13 receptor, alpha 1	-1.39	0.182	1.95	0.07	-1.08	0.662	-1.19	0.663	-0.43
1437601_at	Otx1	orthodenticle homolog 1 (Drosophila)	-1.79	0.449	-1	0.997	2.04	0.04	-1.29	0.758	-0.51
1446347_at	4631405J19Rik	RIKEN cDNA 4631405J19 gene	2.35	0.031	-2.35	0.084	-1.21	0.55	-1.43	0.126	-0.66
1438639_x_at	4933417E01Rik	RIKEN cDNA 4933417E01 gene	-3.73	0.027	2.61	0.131	-1.38	0.427	-1.46	0.582	-0.99
1444730_at	Tlk1	tousled-like kinase 1	-1.18	0.126	1.97	0.161	-1.28	0.416	-1.52	0.18	-0.5
1441147_at	D3Ertd229e	DNA segment, Chr 3, ERATO Doi 229, expressed	-3.06	0.162	2.82	0.371	-2.21	0.051	-2.49	0.038	-1.24
1418729_at	Star	steroidogenic acute regulatory protein	-1.07	0.764	-1.07	0.878	1.73	0.018	-1.57	0.188	-0.49
1443879_at	---	---	-1.03	0.91	1.74	0.133	-1.12	0.799	-1.25	0.643	-0.41
1435940_at	AI836758	expressed sequence AI836758	2.08	0.116	-1	0.993	-1.92	0.097	-2.2	0.172	-0.76
1432420_a_at	2310002L09Rik	RIKEN cDNA 2310002L09 gene	-1.02	0.985	-2.43	0.179	2.21	0.02	-2.32	0.286	-0.89
1453910_at	4930500A05Rik	RIKEN cDNA 4930500A05 gene	-1.16	0.275	-1.54	0.617	2.09	0.309	-1.38	0.33	-0.5

1459380_at	Tada1l	transcriptional adaptor 1 (HFI1 homolog, yeast) like	-1.05	0.953	1.89	0.304	-1.31	0.38	-1.25	0.366	-0.43
1426672_at	Tmem16k	transmembrane protein 16K	-1.04	0.659	1.77	0.171	-1.15	0.253	-1.33	0.027	-0.44
1437117_at	Centb1	centaurin, beta 1	-1.07	0.672	-1.62	0.117	2.05	0.005	-1.89	0.13	-0.63
1435831_at	Upk1b	uroplakin 1B	-1.94	0.332	2.49	0.011	-1.66	0.118	-1.39	0.622	-0.63
1423422_at	Asb4	ankyrin repeat and SOCS box-containing protein 4	2.08	0.417	-1.56	0.144	-1.12	0.801	-1.14	0.687	-0.44
1456860_at	Cdc26	cell division cycle 26	-1.17	0.661	2.08	0.465	-1.48	0.399	-1.04	0.929	-0.4
1441838_at	Ercc1	excision repair cross-complementing rodent repair deficiency, complementation g	1.69	0.46	-1.01	0.939	-1.07	0.745	-1.14	0.149	-0.38
1421301_at	Zic2	Zic finger protein of the cerebellum 2	-1.84	0.493	-1.37	0.536	2.34	0.189	-1.5	0.368	-0.59
1453537_a_at	Wdr17	WD repeat domain 17	-1.05	0.88	-1.38	0.417	1.93	0.302	-1.1	0.815	-0.4
1429075_a_at	1700018B08Rik	RIKEN cDNA 1700018B08 gene	-1.67	0.513	2.06	0.202	-1.05	0.916	-1.39	0.475	-0.51
1446238_at	4930431P03Rik	RIKEN cDNA 4930431P03 gene	1.75	0.304	-1.15	0.678	-1.01	0.983	-1.02	0.933	-0.36
1431384_at	1700095G12Rik	RIKEN cDNA 1700095G12 gene	-1.09	0.879	-2.2	0.174	2.24	0.141	-1.2	0.731	-0.56
1449729_at	Fgf4	fibroblast growth factor 4	-1.34	0.285	2.42	0.348	-2.22	0.103	-1.78	0.426	-0.73
1447446_at	Rerg	RAS-like, estrogen-regulated, growth-inhibitor	2.7	0.1	-1.72	0.497	-3.02	0.136	-1.81	0.416	-0.96
1441903_x_at	Metrnl	meteorin, glial cell differentiation regulator-like	-1.6	0.674	2.29	0.04	-1.41	0.234	-1.08	0.819	-0.45
1420443_at	Pcdhb19	protocadherin beta 19	-1.16	0.667	1.82	0.289	-1.06	0.849	-1.44	0.141	-0.46
1449231_at	Zfp296	zinc finger protein 296	-1.07	0.898	-1.18	0.783	1.84	0.302	-1.42	0.209	-0.46
1431192_at	2010203O03Rik	RIKEN cDNA 2010203O03 gene	2.16	0.024	-1.91	0.067	-1.06	0.883	-1.48	0.581	-0.57
1421502_at	Usp26	ubiquitin specific peptidase 26	1.98	0.526	-1.02	0.981	-1.51	0.391	-1.79	0.283	-0.59
1426121_at	Mrgpra3	MAS-related GPR, member A3	-1.78	0.116	2.16	0.16	-1.11	0.673	-1.62	0.618	-0.59
1450832_at	Hoxc5	homeo box C5	2.07	0.243	-1.04	0.871	-1.7	0.394	-1.25	0.448	-0.48
1441553_at	Aprin	androgen-induced proliferation inhibitor	-1.43	0.592	1.98	0.442	-1.05	0.828	-1.26	0.486	-0.44
1419849_at	Ankrd44	Ankyrin repeat domain 44	-1.11	0.879	1.87	0.123	-1.17	0.632	-2.11	0.167	-0.63
1421419_at	Kcnk4	potassium channel, subfamily K, member 4	-1.36	0.555	2.22	0.241	-1.47	0.32	-1.68	0.407	-0.58
1434740_at	Scarf2	scavenger receptor class F, member 2	1.91	0.005	-1.12	0.644	-1.2	0.464	-1.06	0.818	-0.37
1429994_s_at	Cyp2c65	cytochrome P450, family 2, subfamily c, polypeptide 65	-1.07	0.931	-1.06	0.889	1.75	0.093	-1.74	0.315	-0.53
1439761_x_at	D830026I12Rik	RIKEN cDNA D830026I12 gene	-1.41	0.404	2.09	0.324	-1.2	0.489	-2.05	0.396	-0.64
1459983_at	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	-1.34	0.169	2	0.11	-1.12	0.589	-1.26	0.339	-0.43
1443925_at	Gats	opposite strand transcription unit to Stag3	-1.56	0.523	-1.01	0.981	2	0.025	-1.75	0.553	-0.58
1445888_x_at	Parp3	poly (ADP-ribose) polymerase family, member 3	-1.08	0.539	1.79	0.013	-1.1	0.678	-1.43	0.251	-0.45
1453602_at	2810002I04Rik	RIKEN cDNA 2810002I04 gene	-1	0.994	-1.38	0.444	1.92	0.332	-1.93	0.472	-0.6
1450126_at	Gata5	GATA binding protein 5	2.02	0.322	-1.25	0.788	-1.23	0.542	-1.3	0.707	-0.44
1457663_at	1700006F04Rik	RIKEN cDNA 1700006F04 gene	-2.54	0.105	2.38	0.158	-1.15	0.832	-1.42	0.428	-0.69
1449870_a_at	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	-1.02	0.932	-1.13	0.609	1.78	0.142	-1.06	0.803	-0.36
1420472_at	Mtpn	myotrophin	-1.08	0.834	-1.27	0.516	1.93	0.334	-1.18	0.689	-0.4
1435292_at	Tbc1d4	TBC1 domain family, member 4	-1.15	0.554	1.86	0.101	-1.1	0.692	-1.97	0.142	-0.59
1456801_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13003	-1.1	0.268	1.91	0.185	-1.22	0.658	-1.62	0.411	-0.51
1435645_at	Mmd /// LOC67654	monocyte to macrophage differentiation-associated /// similar to monocyte to mac	-1.04	0.683	-1.39	0.142	1.96	0.143	-1.44	0.345	-0.48
1437091_at	Accn4	amiloride-sensitive cation channel 4, pituitary	-1.2	0.323	-1.26	0.337	2.02	0.161	-1.48	0.371	-0.48
1453647_at	9530059J11Rik	RIKEN cDNA 9530059J11 gene	2.08	0.263	-1.22	0.466	-1.35	0.314	-1.36	0.222	-0.46
1440231_at	Mtap9	microtubule-associated protein 9	-1.33	0.107	2.14	0.08	-1.34	0.121	-1.27	0.486	-0.45
1460084_at	---	---	1.92	0.072	-1.2	0.361	-1.12	0.526	-1.66	0.169	-0.52
1447814_x_at	Il16	interleukin 16	-1.63	0.086	2.2	0.299	-1.21	0.58	-1.57	0.499	-0.55
1447583_x_at	Gpr30	G protein-coupled receptor 30	-1.19	0.253	-1.64	0.398	2.19	0.031	-2.34	0.312	-0.74
1444713_at	---	---	-1.17	0.686	-1.87	0.195	2.26	0.027	-2.39	0.231	-0.79
1422326_at	G6pd2	glucose-6-phosphate dehydrogenase 2	-1.01	0.98	2.02	0.431	-1.58	0.027	-1.42	0.087	-0.5
1442438_at	---	---	1.95	0.296	-1.01	0.989	-1.41	0.32	-1.11	0.543	-0.4
1429272_a_at	9130022K13Rik ///	RIKEN cDNA 9130022K13 gene /// RIKEN cDNA 2210421G13 gene /// hypotheti	1.9	0.392	-1.22	0.51	-1.08	0.805	-2.91	0.035	-0.83
1420415_at	AY026312	cDNA sequence AY026312	-1.66	0.414	2.58	0.231	-2.12	0.013	-1.63	0.408	-0.71
1420658_at	Ucp3	uncoupling protein 3 (mitochondrial, proton carrier)	-1.21	0.661	-1.29	0.738	2.05	0.165	-1.57	0.181	-0.5
1451228_a_at	Sycn	syncollin	2.09	0.08	-1.25	0.726	-1.32	0.706	-1.79	0.564	-0.57
1436362_x_at	2700079J08Rik	RIKEN cDNA 2700079J08 gene	1.95	0.028	-1.04	0.746	-1.34	0.326	-1.17	0.556	-0.4
1420288_at	T25656	expressed sequence T25656	-1.12	0.879	2.16	0.354	-1.69	0.379	-2.14	0.354	-0.69

1453633_a_at	Rnf41	ring finger protein 41	-1.19	0.788	-1.09	0.84	1.89	0.314	-1.86	0.072	-0.56
1429211_at	2900078E11Rik	RIKEN cDNA 2900078E11 gene	2.49	0.239	-4.11	0	-1.09	0.797	-2.58	0.064	-1.32
1424551_at	Zfyve27	zinc finger, FYVE domain containing 27	-1.4	0.595	2.23	0.105	-1.4	0.391	-1.79	0.422	-0.59
1421130_at	Zfp111	zinc finger protein 111	-2.72	0.121	-2.39	0.037	2.87	0.013	-1.74	0.333	-1
1458752_at	---	PREDICTED: Mus musculus similar to otogelin (LOC627748), mRNA	-1.48	0.349	-1.15	0.704	2.12	0.153	-2.76	0.008	-0.82
1459760_at	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	-1.09	0.393	1.92	0.24	-1.21	0.381	-1.52	0.272	-0.48
1422067_at	Klrb1d	killer cell lectin-like receptor subfamily B member 1D	2.25	0.433	-1.06	0.921	-2.12	0.016	-1.02	0.727	-0.49
1445685_at	Gas7	growth arrest specific 7	1.9	0.301	-1.01	0.978	-1.3	0.418	-1.81	0.573	-0.55
1454225_s_at	D3Ertd751e	DNA segment, Chr 3, ERATO Doi 751, expressed	-1.02	0.955	-1.44	0.442	1.98	0.221	-1	0.996	-0.37
1424980_s_at	Aph1a	anterior pharynx defective 1a homolog (C. elegans)	-1.38	0.3	-1.08	0.626	2.01	0.047	-1.21	0.632	-0.41
1447309_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930539H17 pr	-1.29	0.57	2.16	0.276	-1.37	0.242	-1.41	0.617	-0.48
1425501_at	---	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library,	2.1	0.177	-1.11	0.688	-1.5	0.238	-1.1	0.882	-0.4
1442970_at	---	---	2.27	0.491	-1.94	0.297	-1.14	0.636	-2.08	0.46	-0.72
1430876_at	2610312I10Rik	RIKEN cDNA 2610312I10 gene	2.43	0.033	-1.61	0.568	-1.63	0.368	-2.63	0.255	-0.86
1449688_at	D10Ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed	-1.14	0.759	2.31	0.123	-2.05	0.29	-1.03	0.914	-0.48
1458777_at	Slc18a1	solute carrier family 18 (vesicular monoamine), member 1	-1.26	0.784	2.44	0.158	-2.27	0.227	-1.68	0.268	-0.7
AFFX-PyruCarbMur	Pcx	pyruvate carboxylase	-1.02	0.952	-1.31	0.717	1.93	0.347	-1.52	0.084	-0.48
1431164_at	Rragd	Ras-related GTP binding D	-1.22	0.514	-1.32	0.538	2.1	0.122	-1.17	0.836	-0.4
1432554_at	2310040G07Rik	RIKEN cDNA 2310040G07 gene	-1.28	0.155	1.92	0.235	-1.03	0.652	-1.12	0.805	-0.38
1452323_at	Spryd3	SPRY domain containing 3	-2	0.081	-1.06	0.887	2.22	0.231	-1.29	0.599	-0.53
1427728_at	Chrng	cholinergic receptor, nicotinic, gamma polypeptide	2.03	0.255	-1.17	0.826	-1.26	0.411	-1.65	0.022	-0.52
1460486_at	Rabgap1	RAB GTPase activating protein 1	1.85	0.136	-1.2	0.723	-1.01	0.986	-1.08	0.844	-0.36
1444920_at	D19Ertd386e	DNA segment, Chr 19, ERATO Doi 386, expressed	2.26	0.249	-1.25	0.469	-1.62	0.094	-1.1	0.648	-0.43
1456776_at	Spata2	spermatogenesis associated 2	-1.2	0.809	-1.95	0.121	2.33	0.386	-1.48	0.668	-0.58
1422878_at	Syt12	synaptotagmin XII	-1.34	0.446	1.97	0.381	-1.05	0.875	-1.99	0.349	-0.6
1427231_at	Robo1	roundabout homolog 1 (Drosophila)	-1	0.996	1.82	0.022	-1.16	0.473	-1.05	0.902	-0.35
1432338_at	4833419O12Rik	RIKEN cDNA 4833419O12 gene	-1.14	0.794	1.91	0.064	-1.12	0.79	-1.02	0.966	-0.34
1459823_at	Ehd2 /// LOC67325	EH-domain containing 2 /// similar to EH-domain containing 2	-1.29	0.095	2.09	0.059	-1.22	0.23	-1.44	0.331	-0.47
1432380_s_at	4933426G20Rik ///	RIKEN cDNA 4933426G20 gene /// similar to gasdermin 1	-2.13	0.065	2.25	0.212	-1.05	0.896	-2.54	0.407	-0.86
1426600_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	-1.03	0.588	-1.05	0.705	1.76	0.107	-1.59	0.156	-0.48
1424744_at	Sds	serine dehydratase	2.01	0.56	-1.03	0.869	-1.44	0.525	-1.07	0.936	-0.38
1459729_at	Slc13a5	solute carrier family 13 (sodium-dependent citrate transporter), member 5	-1.74	0.113	2.21	0.209	-1.11	0.767	-2.84	0.276	-0.87
1443170_at	---	---	-1.07	0.209	-1.05	0.873	1.79	0.119	-2.12	0.028	-0.61
1429855_at	1700023I07Rik	RIKEN cDNA 1700023I07 gene	2.04	0.429	-1.32	0.735	-1.13	0.81	-1.04	0.961	-0.36
1422758_at	Chst2	carbohydrate sulfotransferase 2	-1.06	0.618	1.89	0.115	-1.16	0.699	-1.18	0.513	-0.38
1426140_x_at	Klra19	killer cell lectin-like receptor, subfamily A, member 19	-1.27	0.718	2.31	0.183	-1.7	0.348	-4.02	0.047	-1.17
1460378_a_at	Tes	testis derived transcript	-1.18	0.286	1.98	0.09	-1.18	0.296	-2.03	0.129	-0.6
1427596_at	Tsix	X (inactive)-specific transcript, antisense	-1.71	0.166	-1.02	0.951	2.12	0.123	-1.76	0.253	-0.59
1442840_at	D4Ertd669e	DNA segment, Chr 4, ERATO Doi 669, expressed	-2.54	0.194	-1.43	0.485	2.59	0.062	-1.26	0.679	-0.66
1422428_at	Acsbg1	acyl-CoA synthetase bubblegum family member 1	2.17	0.125	-1.05	0.922	-1.77	0.328	-1.26	0.644	-0.48
1428538_s_at	Rarres2	retinoic acid receptor responder (tazarotene induced) 2	1.98	0.002	-1.16	0.314	-1.18	0.589	-1.6	0.179	-0.49
1446642_at	Phf14	PHD finger protein 14	1.88	0.254	-1.08	0.84	-1.13	0.765	-1.89	0.412	-0.55
1434246_at	L3mbtl3	l(3)mbt-like 3 (Drosophila)	-1.11	0.653	-1.07	0.775	1.86	0.146	-2.13	0.102	-0.61
1458051_at	A230048O21Rik	RIKEN cDNA A230048O21 gene	1.79	0.37	-1.08	0.862	-1.01	0.982	-1.86	0.365	-0.54
1443427_at	---	---	-1.27	0.141	-1.03	0.96	1.94	0.146	-1.04	0.932	-0.35
1438870_at	---	---	2.09	0.402	-1.65	0.38	-1	1	-1.78	0.469	-0.59
1444536_at	AI462171	expressed sequence AI462171	2.07	0.325	-1.18	0.63	-1.29	0.442	-2.45	0.496	-0.71
1446125_at	---	---	-2.1	0.176	2.75	0.138	-2.13	0.259	-2.16	0.036	-0.91
1457109_x_at	---	Transcribed locus	-2.54	0.063	2.36	0.198	-1.06	0.727	-1.38	0.169	-0.65
1458795_at	---	Transcribed locus	-1.63	0.027	2.47	0.005	-1.63	0.093	-1.14	0.861	-0.48
1437034_x_at	Marcks	myristoylated alanine rich protein kinase C substrate	-1.45	0.076	2.05	0.104	-1.04	0.931	-1.05	0.871	-0.37
1456044_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	-1.53	0.058	2.09	0.147	-1.05	0.832	-1.64	0.295	-0.53
1430445_at	Akap13	A kinase (PRKA) anchor protein 13	2.04	0.253	-1.11	0.299	-1.33	0.389	-1.54	0.427	-0.48

1416066_at	Cd9	CD9 antigen	-1.06	0.69	1.82	0.31	-1.06	0.562	-1.01	0.958	-0.33
1455679_at	5830411E10Rik	RIKEN cDNA 5830411E10 gene	-1.39	0.236	-1.07	0.888	2.05	0.014	-1.25	0.54	-0.42
1441394_at	C76554	expressed sequence C76554	2.66	0.087	-3.79	0.053	-1.28	0.406	-1.42	0.23	-0.96
1457692_at	---	---	2.13	0.04	-1.19	0.296	-1.37	0.042	-1.77	0.122	-0.55
1440806_x_at	5730526G10Rik	RIKEN cDNA 5730526G10 gene	2.62	0.434	-5.35	0.095	-1.11	0.791	-1.12	0.644	-1.24
1419430_at	Cyp26a1	cytochrome P450, family 26, subfamily a, polypeptide 1	-2.38	0.151	2.45	0.158	-1.19	0.739	-1.18	0.858	-0.58
1444814_at	D15Ertd180e	DNA segment, Chr 15, ERATO Doi 180, expressed	2.2	0.156	-1.29	0.634	-1.37	0.071	-1.04	0.873	-0.37
1432986_at	5430402M21Rik	RIKEN cDNA 5430402M21 gene	-1.37	0.37	2.17	0.123	-1.23	0.16	-1.36	0.392	-0.45
1425091_at	Rarres2	retinoic acid receptor responder (tazarotene induced) 2	2.04	0.037	-1.02	0.931	-1.43	0.281	-1.32	0.398	-0.43
1437183_at	Lrrc4b	leucine rich repeat containing 4B	1.98	0.203	-1.33	0.147	-1.02	0.931	-3.44	0.002	-0.95
1431608_at	Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	-1.1	0.868	1.97	0.217	-1.19	0.703	-2.37	0.074	-0.67
1438388_at	Nxph1	Neurexophilin 1	2.46	0.419	-1.12	0.833	-2.76	0.126	-1.17	0.869	-0.65
1430011_at	2610317O13Rik	RIKEN cDNA 2610317O13 gene	2.12	0.53	-1.03	0.937	-1.61	0.503	-1.73	0.585	-0.56
1420099_at	D13Ertd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	-1.64	0.313	-1.04	0.929	2.15	0.078	-1.14	0.455	-0.42
1431578_at	Wbp2nl	WBP2 N-terminal like	1.99	0.099	-1.31	0.616	-1.04	0.853	-1.14	0.757	-0.38
1458558_at	---	---	-1.14	0.657	-1.3	0.64	2.07	0.163	-1.24	0.505	-0.4
1420966_at	Slc25a15	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	-1.01	0.985	-1.12	0.765	1.84	0.324	-1.07	0.931	-0.34
1455650_at	---	Transcribed locus	2.22	0.22	-1.18	0.435	-1.52	0.181	-1.09	0.885	-0.39
1431542_at	Psen2	presenilin 2	-1.16	0.577	-1.11	0.776	1.96	0.119	-1.2	0.635	-0.38
1415856_at	Emb	embigin	-1.17	0.306	2.02	0.166	-1.17	0.434	-1.41	0.062	-0.43
1445338_at	Rnf144	Ring finger protein 144	-1.24	0.55	2.3	0.215	-1.61	0.04	-2.87	0.007	-0.86
1424911_a_at	Lyzl4	lysozyme-like 4	-2.04	0.328	2.83	0.115	-2.46	0.29	-1.2	0.619	-0.72
1457797_at	AI605517	expressed sequence AI605517	-1.22	0.217	2.26	0.138	-1.55	0.015	-1.4	0.192	-0.48
1422001_at	Inhbc	inhibin beta-C	2.02	0.483	-1.39	0.167	-1.01	0.981	-1.01	0.977	-0.35
1440170_at	Ankrd10	ankyrin repeat domain 10	2.09	0.512	-1.29	0.755	-1.15	0.677	-1.79	0.326	-0.54
1449398_at	Rpl3l	ribosomal protein L3-like	-1.08	0.842	-2.71	0.283	2.44	0.327	-1.8	0.276	-0.79
1431490_at	A930033C23Rik	RIKEN cDNA A930033C23 gene	-1.26	0.145	2.03	0.163	-1.1	0.819	-1.47	0.472	-0.45
1455209_at	Pck1	Phosphoenolpyruvate carboxykinase 1, cytosolic	-1.07	0.811	-1.27	0.38	2.02	0.037	-1.45	0.491	-0.44
1446707_at	---	---	1.97	0.27	-1.09	0.838	-1.18	0.564	-1.06	0.886	-0.34
1442512_at	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	2.31	0.044	-1.31	0.667	-1.51	0.444	-1.09	0.825	-0.4
1421485_at	Ttbk2	tau tubulin kinase 2	2.17	0.502	-1.21	0.56	-1.35	0.571	-2.16	0.171	-0.64
1449770_x_at	D16Bwg1494e	DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed	-1.18	0.267	-1.01	0.946	1.89	0.096	-1.57	0.201	-0.46
1430477_s_at	---	---	-1.03	0.935	-1.29	0.545	1.99	0.017	-2.36	0.35	-0.67
1427429_at	Csf2	colony stimulating factor 2 (granulocyte-macrophage)	-2.5	0.019	2.7	0.109	-1.56	0.223	-1.22	0.458	-0.65
1422020_at	Spry4	sprouty homolog 4 (Drosophila)	-1.03	0.913	-1.99	0.41	2.27	0.372	-2.78	0.137	-0.89
1459649_at	---	Transcribed locus	-1.1	0.871	2.02	0.098	-1.24	0.503	-1.53	0.361	-0.46
1445783_at	---	---	-1.08	0.931	-2.57	0.047	2.43	0.009	-2.06	0.199	-0.82
1440014_at	Pacs1	Phosphofurin acidic cluster sorting protein 1	-1.2	0.064	2.28	0.053	-1.6	0.125	-1.24	0.299	-0.44
1459097_at	Il17rd	Interleukin 17 receptor D	-1.15	0.272	2.11	0.257	-1.31	0.466	-1.18	0.492	-0.38
1444360_at	BC038822	CDNA sequence BC038822	-1.03	0.929	-1.01	0.983	1.78	0.091	-1.18	0.727	-0.36
1442227_at	Ap2m1	Adaptor protein complex AP-2, mu1	2.69	0.3	-2.5	0.2	-1.52	0.112	-1.56	0.463	-0.72
1422105_at	Cd3e	CD3 antigen, epsilon polypeptide	-1.5	0.197	-1.28	0.571	2.3	0.118	-1.26	0.627	-0.44
1416012_at	Ehd1	EH-domain containing 1	-1.01	0.983	1.82	0.026	-1.07	0.631	-1.21	0.589	-0.37
1459724_at	Zdhhc20	zinc finger, DHHC domain containing 20	-1.15	0.83	-1.47	0.232	2.2	0.084	-1.07	0.649	-0.37
1458153_at	Pex14	Peroxisomal biogenesis factor 14	-1.07	0.933	-1.21	0.686	1.99	0.076	-1.96	0.265	-0.56
1454431_at	9030613N10Rik	RIKEN cDNA 9030613N10 gene	-2.42	0.005	-1.19	0.74	2.5	0.166	-2.03	0.208	-0.78
1443383_at	Mbnl3	Muscleblind-like 3 (Drosophila)	2.43	0.047	-1.29	0.638	-1.83	0.026	-1.18	0.628	-0.47
1415687_a_at	Psap	prosaposin	-1.41	0.246	-1.03	0.884	2.08	0.015	-1.6	0.139	-0.49
1451285_at	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	-1.36	0.464	-1.12	0.674	2.12	0.09	-1.18	0.557	-0.38
1439356_at	Fliih	flightless I homolog (Drosophila)	-1.06	0.86	1.82	0.101	-1	0.993	-1.55	0.525	-0.45
1446255_at	Kcnq1	Potassium voltage-gated channel, subfamily Q, member 1	-1.26	0.371	2.46	0.114	-1.99	0.176	-1.15	0.677	-0.48
1425796_a_at	Fgfr3	fibroblast growth factor receptor 3	-1.05	0.942	-1.54	0.573	2.16	0.498	-4.47	0.272	-1.22
1441713_at	Anapc7	anaphase promoting complex subunit 7	1.84	0.311	-1.03	0.947	-1.06	0.919	-1.84	0.164	-0.52

1441941_x_at	Serpinb5	serine (or cysteine) peptidase inhibitor, clade B, member 5	2.05	0.45	-1.06	0.931	-1.29	0.645	-1.9	0.346	-0.55
1449130_at	Cd1d1	CD1d1 antigen	2	0.104	-1.13	0.144	-1.14	0.654	-1.47	0.427	-0.43
1457835_at	C920025J10	hypothetical protein C920025J10	-2.46	0.013	2.41	0.125	-1.05	0.915	-1.46	0.398	-0.64
1444805_at	4930473A06Rik	RIKEN cDNA 4930473A06 gene	-1.16	0.858	2.37	0.072	-1.86	0.057	-1.26	0.475	-0.48
1450342_at	Bmp8b	bone morphogenetic protein 8b	-1.08	0.814	1.88	0.181	-1.03	0.805	-1.71	0.34	-0.49
1416895_at	Efna1	ephrin A1	-1.01	0.962	2.01	0.147	-1.3	0.086	-1.36	0.219	-0.41
1432478_a_at	Ibrdc3	IBR domain containing 3	-1.03	0.509	-1.07	0.691	1.87	0.113	-1.01	0.88	-0.31
1449570_at	Klrb1c	killer cell lectin-like receptor subfamily B member 1C	2.27	0.416	-1.14	0.801	-1.58	0.093	-1.02	0.977	-0.37
1420069_at	---	PREDICTED: Mus musculus hypothetical protein LOC628408 (LOC628408), mR	2.4	0.449	-1.19	0.746	-1.88	0.013	-3.23	0.35	-0.98
1420742_at	Adam7	a disintegrin and metallopeptidase domain 7	-1.15	0.861	-1.33	0.655	2.15	0.053	-1.41	0.561	-0.43
1450703_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	2.23	0.287	-1.22	0.753	-1.38	0.53	-2.13	0.235	-0.62
1437377_a_at	Polrmt	polymerase (RNA) mitochondrial (DNA directed)	-1.01	0.828	-1.11	0.186	1.88	0.047	-1.29	0.255	-0.38
1423836_at	Zfp503	zinc finger protein 503	-1.06	0.333	1.85	0.002	-1.02	0.966	-1.14	0.75	-0.34
1449937_at	Pp11r	placental protein 11 related	-1.09	0.727	2.14	0.086	-1.38	0.15	-1.03	0.914	-0.34
1431021_at	Cyb561d1	cytochrome b-561 domain containing 1	-1.29	0.379	-1.65	0.43	2.4	0.157	-1.28	0.641	-0.46
1458306_at	Pigz	phosphatidylinositol glycan anchor biosynthesis, class Z	-1.13	0.131	-1.6	0.181	2.28	0.185	-1.01	0.972	-0.37
1436003_at	Vcam1	vascular cell adhesion molecule 1	1.92	0.17	-1.03	0.958	-1.13	0.466	-1.4	0.427	-0.41
1440907_at	A130038H09Rik	RIKEN cDNA A130038H09 gene	-1.17	0.803	-1.03	0.956	1.96	0.417	-1.58	0.243	-0.45
1460158_at	---	---	-1.5	0.358	-1.12	0.779	2.22	0.035	-1.24	0.654	-0.41
1417649_at	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	2.34	0.019	-1.24	0.526	-1.56	0.036	-1.36	0.337	-0.46
1418415_at	Hoxb5	homeo box B5	-1.05	0.57	1.9	0.166	-1.06	0.709	-1.14	0.763	-0.34
1456385_x_at	Ubxd3	UBX domain containing 3	-1.17	0.796	-1.2	0.534	2.1	0.085	-1.34	0.614	-0.4
1437523_s_at	Sgcg	sarcoglycan, gamma (dystrophin-associated glycoprotein)	2.33	0.419	-1.26	0.677	-1.49	0.125	-1.43	0.285	-0.46
1457092_at	C630007B19Rik	RIKEN cDNA C630007B19 gene	2.89	0.007	-1.65	0.212	-3.36	0.012	-1.12	0.837	-0.81
1421484_at	Ugt2a1 /// Ugt2a2	UDP glucuronosyltransferase 2 family, polypeptide A1 /// UDP glucuronosyltransf	2.27	0.044	-1.85	0.336	-1.02	0.965	-1.09	0.883	-0.42
1442754_at	C030013G03Rik	RIKEN cDNA C030013G03 gene	-1.08	0.697	-1.13	0.871	1.99	0.121	-2.63	0.192	-0.71
1428673_at	Sympk	symplekin	-1.21	0.478	-1.23	0.452	2.16	0.111	-1.37	0.27	-0.41
1444263_at	Ezh2	Enhancer of zeste homolog 2 (Drosophila)	-1.12	0.841	2.08	0.176	-1.21	0.613	-1.04	0.918	-0.32
1445569_at	LOC546611	similar to kelch-like 9	-1.02	0.958	1.86	0.157	-1.04	0.938	-1.05	0.895	-0.31
1449988_at	Gimap1	GTPase, IMAP family member 1	-1.02	0.875	-1.06	0.742	1.87	0.118	-2.46	0.093	-0.67
1427392_at	Dscaml1	Down syndrome cell adhesion molecule-like 1	2.15	0.247	-1.09	0.844	-1.36	0.531	-1.71	0.135	-0.5
1441717_at	D9Ertd596e	DNA segment, Chr 9, ERATO Doi 596, expressed	-2.12	0.4	-1.62	0.506	2.71	0.02	-1.53	0.444	-0.64
1443968_at	Adarb1	adenosine deaminase, RNA-specific, B1	2.52	0.372	-1.13	0.771	-2.54	0.033	-1.19	0.563	-0.58
1433653_at	BC029169	cDNA sequence BC029169	2.17	0.071	-1.21	0.222	-1.24	0.51	-1.2	0.504	-0.37
1437620_x_at	Aldh18a1	Aldehyde dehydrogenase 18 family, member A1	-1.09	0.891	-1.11	0.638	1.99	0.106	-1.03	0.915	-0.31
1419515_at	Fgd2	FYVE, RhoGEF and PH domain containing 2	-1.17	0.639	-1.14	0.632	2.07	0.236	-1.99	0.11	-0.56
1443393_at	Smurf1	SMAD specific E3 ubiquitin protein ligase 1	-1.29	0.123	2.5	0.022	-1.9	0.011	-1.34	0.262	-0.51
1433099_at	4933428L12Rik	RIKEN cDNA 4933428L12 gene	-1.63	0.412	2.68	0.022	-1.95	0.096	-1.15	0.71	-0.51
1451958_at	LOC211331 /// LOC	similar to Ig heavy chain V region 93G7 precursor /// similar to Ig heavy chain V re	1.85	0.481	-1.03	0.811	-1.01	0.94	-1.46	0.34	-0.41
1432518_at	4930430J20Rik	RIKEN cDNA 4930430J20 gene	-1.58	0.639	2.67	0.179	-1.96	0.127	-1.89	0.456	-0.69
1450270_at	Pcdhb11	protocadherin beta 11	-1.04	0.817	1.93	0.188	-1.09	0.77	-1.03	0.953	-0.31
1443761_at	Nrm	nurim (nuclear envelope membrane protein)	-2.25	0.342	2.5	0.142	-1.15	0.767	-3.33	0.308	-1.06
1419491_at	Defb1	defensin beta 1	-1.2	0.097	-2.8	0.021	2.62	0.165	-1.41	0.547	-0.7
1432840_at	Galnt11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-2.01	0.369	-2.63	0.142	2.94	0.125	-1.51	0.353	-0.8
1431976_at	4930526F13Rik	RIKEN cDNA 4930526F13 gene	-1.15	0.086	2.13	0.114	-1.22	0.271	-1.38	0.533	-0.41
1439397_at	Fmn1	formin 1	-1.29	0.069	2.22	0.068	-1.21	0.26	-1.21	0.609	-0.37
1436676_at	Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	-1.81	0.527	2.6	0.014	-1.5	0.15	-1.29	0.122	-0.5
1460633_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	-1.9	0.387	-1.92	0.275	2.78	0.253	-1.9	0.447	-0.74
1422324_a_at	Pthlh	parathyroid hormone-like peptide	2.34	0.199	-1.31	0.684	-1.39	0.057	-1.42	0.48	-0.44
1432809_at	1700113P08Rik	RIKEN cDNA 1700113P08 gene	-1.08	0.898	2.09	0.492	-1.24	0.674	-3.08	0.154	-0.83
1418004_a_at	1810009M01Rik	RIKEN cDNA 1810009M01 gene	-1.04	0.743	1.9	0.085	-1.04	0.459	-1.33	0.421	-0.38
1420943_at	Zfp185	zinc finger protein 185	2.06	0.059	-1.1	0.466	-1.17	0.732	-1.06	0.715	-0.32
1447354_at	Cep164	Centrosomal protein 164	2.74	0.265	-3.39	0.113	-1.25	0.568	-2.26	0.192	-1.04

1427565_a_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.12	0.336	2.1	0.14	-1.19	0.348	-1.29	0.094	-0.37
1436017_at	Aarsl	alanyl-tRNA synthetase like	-1.02	0.939	-1.23	0.065	2.05	0.01	-1.5	0.416	-0.43
1445943_at	---	---	-1.83	0.337	2.79	0.012	-2.01	0.167	-1.36	0.576	-0.6
1447613_at	Gdi1	Guanosine diphosphate (GDP) dissociation inhibitor 1	-1.26	0.696	2.08	0.157	-1.04	0.911	-1.12	0.765	-0.33
1429030_at	C1qtnf7	C1q and tumor necrosis factor related protein 7	-1.06	0.531	2.27	0.151	-1.58	0.052	-1.97	0.179	-0.59
1437132_x_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-1.05	0.737	2.1	0.05	-1.26	0.174	-2.11	0.078	-0.58
1457037_at	Gm1103	gene model 1103, (NCBI)	2.42	0.109	-1.67	0.589	-1.2	0.47	-1.21	0.684	-0.42
1420006_at	Bmp15	Bone morphogenetic protein 15	2.28	0.102	-1.72	0.331	-1.02	0.955	-3.71	0.134	-1.04
1426834_s_at	D930015E06Rik	RIKEN cDNA D930015E06 gene	-1	0.972	-1.13	0.718	1.97	0.109	-1.2	0.324	-0.34
1459295_at	Lphn3	Latrophilin 3	-1.27	0.74	2.33	0.041	-1.36	0.487	-1.9	0.206	-0.55
1449298_a_at	Pde1a	phosphodiesterase 1A, calmodulin-dependent	-1.05	0.661	2.04	0.13	-1.16	0.624	-1.42	0.384	-0.4
1441304_at	Rpl31 /// LOC43548	ribosomal protein L31 /// similar to ribosomal protein L31 /// similar to ribosomal p	-1.06	0.929	2.19	0	-1.37	0.261	-1.17	0.539	-0.35
1444683_at	---	---	2.45	0.169	-2.19	0.236	-1.05	0.917	-1.3	0.261	-0.52
1440016_at	Dbt	Dihydrolipoamide branched chain transacylase E2	1.93	0.155	-1.01	0.989	-1.06	0.787	-1.25	0.346	-0.35
1415845_at	Syt4	synaptotagmin IV	2.4	0.073	-1.62	0.324	-1.18	0.337	-1.01	0.985	-0.35
1425915_at	Slc26a8	solute carrier family 26, member 8	-1.13	0.607	2.35	0.289	-1.6	0.292	-2.11	0.044	-0.62
1417111_at	Man1a	mannosidase 1, alpha	-1.08	0.55	-1.11	0.257	2.04	0.211	-1.31	0.422	-0.36
1442152_at	4930513N10Rik	RIKEN cDNA 4930513N10 gene	-1.43	0.093	2.45	0.198	-1.4	0.412	-1.23	0.7	-0.4
1431160_x_at	LOC628850 /// LOC	similar to gonadotropin inducible ovarian transcription factor 1 /// similar to Hippoc	-1.12	0.747	2.09	0.079	-1.13	0.651	-1.22	0.527	-0.34
1432943_at	2900046L07Rik	RIKEN cDNA 2900046L07 gene	2.54	0.019	-1.05	0.907	-2.72	0.116	-1.59	0.165	-0.7
1421387_at	Kremen1	kringle containing transmembrane protein 1	-1.67	0.239	-1	0.99	2.27	0.053	-1.77	0.294	-0.54
1443045_at	Ints7	Integrator complex subunit 7	2.16	0.144	-1.06	0.849	-1.29	0.142	-1.2	0.14	-0.35
1460191_at	Ykt6	YKT6 homolog (S. Cerevisiae)	-1	0.994	-1.12	0.779	1.99	0.375	-1.08	0.864	-0.3
1460143_at	---	---	-1.16	0.159	-1.06	0.923	2.07	0.029	-3.17	0.131	-0.83
1459863_x_at	Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	2.43	0.181	-1.82	0.441	-1.12	0.56	-1.02	0.876	-0.38
1423009_at	Sec1	secretory blood group 1	2.35	0.021	-1.72	0.459	-1.05	0.928	-1.67	0.201	-0.53
1451560_at	Prr12	proline rich 12	1.98	0.413	-1.02	0.955	-1.09	0.664	-1.45	0.141	-0.39
1448072_at	2010010I01Rik	RIKEN cDNA 2010010I01 gene	2.05	0.098	-1.04	0.907	-1.16	0.75	-1.48	0.147	-0.4
1429989_at	1700008A04Rik	RIKEN cDNA 1700008A04 gene	-1.11	0.381	-1.29	0.696	2.2	0.069	-1.05	0.929	-0.31
1440487_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	2.04	0.29	-1	0.999	-1.19	0.263	-1.14	0.077	-0.32
1443366_at	Napg	N-ethylmaleimide sensitive fusion protein attachment protein gamma	2.12	0.085	-1.01	0.967	-1.29	0.388	-1.19	0.582	-0.34
1417210_at	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	-1.89	0.475	2.85	0.044	-1.98	0.146	-1.45	0.126	-0.62
1427337_at	Aldh8a1	aldehyde dehydrogenase 8 family, member A1	-1.03	0.564	-1	0.887	1.92	0.309	-1.09	0.734	-0.3
1454903_at	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	-2.5	0.097	-1.27	0.609	2.7	0.109	-1.19	0.665	-0.56
1433093_at	2900092N22Rik	RIKEN cDNA 2900092N22 gene	-1.13	0.801	2.43	0.034	-1.74	0.292	-1.34	0.409	-0.45
1444501_at	AI462521	expressed sequence AI462521	-1.13	0.803	2.32	0.2	-1.45	0.512	-1.09	0.713	-0.34
1439903_at	BC028663	cDNA sequence BC028663	-1.33	0.684	2.15	0.056	-1.01	0.985	-1.9	0.191	-0.52
1452470_at	Cep350	centrosomal protein 350	2.26	0.321	-1.02	0.931	-1.52	0.014	-1.9	0.033	-0.55
1437418_at	---	---	-1.06	0.943	2.13	0.161	-1.23	0.491	-1.19	0.772	-0.33
1447113_at	---	---	-1.18	0.541	-1.89	0.105	2.53	0.119	-1.51	0.484	-0.51
1447715_x_at	Prdx6-rs1	peroxiredoxin 6, related sequence 1	-2.44	0.502	-2.02	0.353	3	0.056	-1.47	0.608	-0.73
1441690_at	Cdh8	cadherin 8	-1.01	0.98	1.96	0.281	-1.04	0.911	-1.29	0.623	-0.35
1420364_at	Gpr87	G protein-coupled receptor 87	-1.07	0.938	1.99	0.261	-1.01	0.973	-1.18	0.544	-0.32
1450976_at	Ndrg1	N-myc downstream regulated gene 1	-1.48	0.02	-1.42	0.302	2.53	0.001	-1.18	0.469	-0.39
1458626_at	Nos1	nitric oxide synthase 1, neuronal	-2.14	0.054	-1.16	0.73	2.59	0.015	-1.27	0.285	-0.5
1435351_at	2310026E23Rik	RIKEN cDNA 2310026E23 gene	-1.26	0.14	-1.78	0.166	2.56	0.283	-2.27	0.128	-0.69
1456237_x_at	BC053401	CDNA sequence BC053401	-1.86	0.523	-1	0.999	2.38	0.172	-1.3	0.415	-0.44
1445194_at	Cnksr2	connector enhancer of kinase suppressor of Ras 2	2.7	0.454	-2.14	0.384	-1.33	0.43	-2.3	0.204	-0.77
1458363_at	Zdhhc17	zinc finger, DHHC domain containing 17	2.19	0.39	-1.2	0.686	-1.12	0.803	-3.2	0.043	-0.83
1436417_at	---	---	-1.05	0.755	2.27	0.158	-1.43	0.195	-1.54	0.033	-0.44
1430436_at	3321401G04Rik	RIKEN cDNA 3321401G04 gene	2.47	0.118	-1.7	0.123	-1.15	0.758	-1.58	0.283	-0.49
1451627_a_at	Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	2.28	0.103	-1.2	0.127	-1.23	0.283	-2.2	0.181	-0.59
1441095_at	A430041B07Rik	RIKEN cDNA A430041B07 gene	2.84	0.027	-1.75	0.6	-1.97	0.265	-1.29	0.399	-0.54

1440246_at	Lass6	longevity assurance homolog 6 (S. cerevisiae)	-1.13	0.311	2.65	0.039	-2.54	0.022	-1.5	0.339	-0.63
1446637_at	LOC666539	hypothetical protein LOC666539	-1.34	0.255	-1.09	0.893	2.26	0.266	-1.37	0.554	-0.39
1425705_a_at	Ero1lb	ERO1-like beta (S. cerevisiae)	-1.11	0.516	-1.23	0.354	2.21	0.226	-1.13	0.53	-0.31
1457463_at	Dscaml1	Down syndrome cell adhesion molecule-like 1	-1.13	0.717	2.2	0.232	-1.19	0.422	-1.21	0.775	-0.33
1435044_at	Ebf4	early B-cell factor 4	-1.47	0.546	2.52	0.198	-1.37	0.182	-1.45	0.406	-0.44
1427975_at	2210403B10Rik	RIKEN cDNA 2210403B10 gene	-1.21	0.502	-1.12	0.631	2.22	0.049	-2.04	0.488	-0.54
1423653_at	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	-1.43	0.444	-1.27	0.344	2.45	0.094	-1.62	0.372	-0.47
1431631_at	2900057B20Rik	RIKEN cDNA 2900057B20 gene	2.02	0.449	-1.07	0.871	-1.01	0.977	-1.07	0.943	-0.28
1422995_at	Bmf	Bcl2 modifying factor	-1.26	0.247	-1.85	0.14	2.61	0.352	-3.19	0.213	-0.92
1437515_at	---	---	-1.16	0.836	-1.05	0.954	2.13	0.342	-1.79	0.429	-0.47
1452515_a_at	Xylt2	xylosyltransferase II	2.23	0.03	-1.3	0.073	-1.05	0.757	-1.4	0.456	-0.38
1437722_x_at	Pcbp3	Poly(rC) binding protein 3	-1.16	0.358	2.16	0.056	-1.07	0.82	-1.23	0.145	-0.33
1457703_at	BE686333	expressed sequence BE686333	2.26	0.239	-1.13	0.836	-1.24	0.156	-1.47	0.032	-0.39
1457905_at	D7Ertd59e	DNA segment, Chr 7, ERATO Doi 59, expressed	-1.27	0.742	2.37	0.04	-1.25	0.486	-1.02	0.927	-0.29
1431634_at	4930455C13Rik	RIKEN cDNA 4930455C13 gene	-2.5	0.162	2.9	0.02	-1.52	0.111	-1.32	0.672	-0.61
1448895_a_at	Ctnna2	catenin (cadherin associated protein), alpha 2	-1.07	0.879	-1.11	0.87	2.12	0.122	-1.2	0.551	-0.31
1425061_at	Wasf3	WAS protein family, member 3	-1.96	0.39	-1.7	0.38	2.86	0.082	-1.01	0.971	-0.45
1447390_at	---	---	2.49	0.034	-1.02	0.975	-2.06	0.051	-1.65	0.401	-0.56
1437671_x_at	Prss23	protease, serine, 23	-1.13	0.695	2.08	0.019	-1	0.966	-1.45	0.375	-0.38
1431907_at	4933404M02Rik	RIKEN cDNA 4933404M02 gene	2.42	0.052	-1	0.999	-1.84	0.389	-1.45	0.302	-0.47
1440583_at	D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-1.07	0.92	2.06	0.007	-1.03	0.836	-1.85	0.082	-0.47
1446834_at	Ctsc	Cathepsin C	-1.02	0.961	2.02	0.178	-1.03	0.885	-1.02	0.951	-0.26
1415805_at	Clps	colipase, pancreatic	-1.06	0.939	2.36	0.151	-1.48	0.434	-1.04	0.908	-0.31
1436492_x_at	6430514M23Rik	RIKEN cDNA 6430514M23 gene	2.12	0.205	-1.01	0.97	-1.15	0.695	-1.1	0.839	-0.29
1433287_at	4833417J16Rik	RIKEN cDNA 4833417J16 gene	2.64	0.3	-1.93	0.394	-1.22	0.736	-1.95	0.167	-0.62
1445039_at	---	---	3.13	0.429	-2.59	0.011	-2.17	0.405	-3.21	0.005	-1.21
1447082_at	C630004L07	hypothetical protein C630004L07	-1.76	0.491	-1.01	0.986	2.42	0.049	-1.35	0.6	-0.43
1437939_s_at	Ctsc	cathepsin C	-1.07	0.901	2.24	0.098	-1.25	0.019	-1.34	0.039	-0.35
1443261_at	E130307A14Rik	RIKEN cDNA E130307A14 gene	-1.3	0.594	2.6	0.058	-1.64	0.175	-1.81	0.18	-0.54
1451875_at	AF366264	cDNA sequence AF366264	2.8	0.043	-1.65	0.428	-1.73	0.208	-1.06	0.904	-0.41
1452421_at	Hoxa3	homeo box A3	-1.4	0.111	2.28	0.017	-1.01	0.976	-1.33	0.577	-0.37
1417997_at	Ngb	neuroglobin	2.64	0.038	-1.2	0.232	-1.95	0.018	-1.43	0.594	-0.49
1428676_at	Tmprss6	transmembrane serine protease 6	2.07	0.002	-1.05	0.177	-1.05	0.931	-1.18	0.285	-0.3
1441513_at	Tank	TRAF family member-associated Nf-kappa B activator	-1.06	0.913	-1.01	0.979	2.06	0.035	-1.13	0.673	-0.29
1443087_at	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	2.25	0.25	-1.15	0.658	-1.15	0.653	-1.39	0.446	-0.36
1431906_at	2700068H02Rik	RIKEN cDNA 2700068H02 gene	-1.11	0.907	2.32	0.157	-1.3	0.314	-1.98	0.319	-0.52
1422409_at	Hes3	hairy and enhancer of split 3 (Drosophila)	-1.26	0.557	2.43	0.053	-1.31	0.598	-1.79	0.362	-0.48
1453963_at	1600014C23Rik	RIKEN cDNA 1600014C23 gene	-1.44	0.357	2.67	0.27	-1.58	0.427	-1.58	0.515	-0.48
1447466_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	2.68	0.003	-1.44	0.495	-1.58	0.038	-1.25	0.272	-0.4
1439029_at	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	-1.12	0.667	-1.14	0.485	2.23	0.137	-1.31	0.207	-0.33
1448457_at	Krt71	keratin 71	-1.11	0.888	2.34	0.102	-1.31	0.722	-1.13	0.819	-0.3
1432780_at	---	---	2.22	0.267	-1.14	0.716	-1.09	0.86	-2.1	0.363	-0.53
1451584_at	Havcr2	hepatitis A virus cellular receptor 2	-1.09	0.786	2.47	0.105	-1.6	0.005	-1.18	0.764	-0.35
1421116_a_at	Rtn4	reticulon 4	-3.33	0.342	-1.78	0.292	3.16	0.203	-3	0.226	-1.24
1417045_at	Bid	BH3 interacting domain death agonist	-1.2	0.213	-1.16	0.313	2.32	0.187	-1.49	0.068	-0.38
1425165_at	Gzmn	granzyme N	2.45	0.341	-1.4	0.483	-1.17	0.634	-1.94	0.503	-0.52
1442190_at	---	---	2.2	0.183	-1.13	0.868	-1.07	0.827	-1.08	0.918	-0.27
1446959_at	AU021871	expressed sequence AU021871	-3.4	0.024	2.96	0.191	-1.31	0.574	-1.33	0.413	-0.77
1445498_at	Ryr2	Ryanodine receptor 2, cardiac	-1.35	0.618	2.59	0.135	-1.44	0.189	-1.28	0.638	-0.37
1456129_at	E030013G06Rik	RIKEN cDNA E030013G06 gene	-1.4	0.167	-1.56	0.369	2.67	0.413	-1.13	0.532	-0.35
1443460_at	---	---	2.43	0.085	-1.09	0.651	-1.47	0.363	-1.41	0.551	-0.38
1453627_at	2610020P09Rik	RIKEN cDNA 2610020P09 gene	2.66	0.053	-1.48	0.411	-1.42	0.013	-1.31	0.312	-0.39
1444267_at	Xpr1	Xenotropic and polytropic retrovirus receptor 1	2.81	0.472	-2.27	0.131	-1.27	0.597	-1.77	0.208	-0.63

1446052_at	---	---	2.37	0.066	-1.14	0.65	-1.27	0.46	-1.42	0.125	-0.36
1457963_at	---	Transcribed locus	2.6	0.029	-2.15	0.164	-1.03	0.955	-1.23	0.811	-0.45
1444606_at	Efna2	ephrin A2	2.3	0.227	-1.04	0.959	-1.27	0.34	-4.87	0.203	-1.22
1429276_at	Lba1	lupus brain antigen 1	-1.02	0.73	2.35	0.075	-1.38	0.403	-1.2	0.389	-0.31
1445997_at	Etv3	ets variant gene 3	-1.16	0.679	2.57	0.001	-1.59	0.105	-1.09	0.887	-0.32
1457763_at	Gabrd	Gamma-aminobutyric acid (GABA-A) receptor, subunit delta	-1.2	0.4	2.61	0.142	-1.6	0.405	-1.91	0.092	-0.52
1433195_at	9530006O14Rik	RIKEN cDNA 9530006O14 gene	-1.1	0.913	2.46	0.096	-1.42	0.449	-1.82	0.09	-0.47
1416239_at	Ass1	argininosuccinate synthetase 1	-1.35	0.218	-1.34	0.232	2.59	0.159	-1.77	0.363	-0.47
1458973_at	---	PREDICTED: Mus musculus similar to RAB5A, member RAS oncogene family (L	2.16	0.18	-1.09	0.831	-1	0.999	-2.24	0.085	-0.54
1427930_at	Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	-1.19	0.622	-1.64	0.196	2.63	0.082	-1.35	0.353	-0.39
1437902_s_at	Rarres2	retinoic acid receptor responder (tazarotene induced) 2	2.32	0.003	-1.01	0.902	-1.29	0.458	-1.49	0.185	-0.37
1426222_s_at	Loh11cr2a	loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human)	-1.09	0.844	2.21	0.077	-1.05	0.699	-1.47	0.11	-0.35
1442334_at	MGC118150	PRAME family member LOC545693	2.42	0.072	-1	0.995	-1.51	0.151	-1.24	0.741	-0.33
1420232_at	---	---	-1.3	0.563	2.45	0.177	-1.15	0.713	-1.22	0.753	-0.31
1437053_x_at	Api5	apoptosis inhibitor 5	2.65	0.029	-1.31	0.627	-1.5	0.414	-2.06	0.332	-0.55
1444209_at	D19Ertd737e	DNA segment, Chr 19, ERATO Doi 737, expressed	2.71	0.058	-1.06	0.9	-2.29	0.013	-1.52	0.248	-0.54
1438054_x_at	Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isofor	-1.89	0.388	-1.68	0.404	2.97	0.005	-1.5	0.355	-0.53
1436733_at	E130309F12Rik	RIKEN cDNA E130309F12 gene	-1.6	0.292	2.79	0.197	-1.44	0.366	-2.05	0.047	-0.58
1425256_a_at	Dixdc1	DIX domain containing 1	-1.28	0.744	2.56	0.156	-1.31	0.602	-2.43	0.266	-0.61
1432103_a_at	Sh3gl3	SH3-domain GRB2-like 3	2.51	0.486	-1.1	0.547	-1.45	0.342	-1.33	0.399	-0.34
1452544_x_at	H2-D1	histocompatibility 2, D region locus 1	2.5	0.377	-1.19	0.435	-1.3	0.634	-1.41	0.502	-0.35
1457725_at	Ms4a4b	Membrane-spanning 4-domains, subfamily A, member 4B	-1.03	0.95	-1.04	0.925	2.17	0.334	-1.63	0.015	-0.38
1431740_at	Slc7a13	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13	-1.84	0.111	2.92	0.005	-1.54	0.378	-3.24	0.279	-0.92
1445032_at	Dapk1	Death associated protein kinase 1	-1.01	0.991	2.72	0.043	-2.49	0.014	-1.56	0.434	-0.58
1444115_at	---	PREDICTED: Mus musculus similar to membrane-associated ring finger (C3HC4	2.88	0.433	-1.54	0.47	-1.67	0.06	-2.62	0.316	-0.74
1430331_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	-2.01	0.382	-1.12	0.691	2.73	0.022	-1.43	0.565	-0.45
1447073_at	Trip12	thyroid hormone receptor interactor 12	2.62	0.114	-1.36	0.536	-1.29	0.659	-1.05	0.952	-0.27
1431903_at	4930524C18Rik	RIKEN cDNA 4930524C18 gene	-1.11	0.744	2.84	0.004	-2.54	0.05	-1.27	0.507	-0.52
1418799_a_at	Col17a1	procollagen, type XVII, alpha 1	2.33	0.274	-1.23	0.567	-1.01	0.987	-1.91	0.062	-0.46
1457864_at	Rab11fip3	RAB11 family interacting protein 3 (class II)	2.61	0.03	-1.29	0.554	-1.33	0.559	-1.38	0.544	-0.35
1432652_at	1700008H02Rik	RIKEN cDNA 1700008H02 gene	2.78	0.007	-1.33	0.016	-1.65	0.268	-3.36	0.128	-0.89
1421595_at	9630031F12Rik	RIKEN cDNA 9630031F12 gene	-1.17	0.58	-1.81	0.318	2.74	0.069	-2.6	0.144	-0.71
1428962_at	1700013F07Rik	RIKEN cDNA 1700013F07 gene	2.54	0.366	-1.53	0.505	-1.05	0.871	-1.21	0.779	-0.31
1447413_at	1110001A07Rik	RIKEN cDNA 1110001A07 gene	2.72	0.122	-2.06	0.303	-1.07	0.811	-1.04	0.921	-0.36
1457222_at	Creb5	cAMP responsive element binding protein 5	-1.76	0.347	2.61	0.067	-1.04	0.93	-1.74	0.238	-0.48
1427481_a_at	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-1.06	0.849	-1.08	0.895	2.27	0.025	-1.06	0.881	-0.23
1460280_at	Grap2 /// LOC6740	GRB2-related adaptor protein 2 /// similar to GRB2-related adaptor protein 2 (GAI	2.64	0.178	-1.23	0.651	-1.44	0.412	-1.59	0.325	-0.41
1450917_at	Myom2	myomesin 2	-1.37	0.397	-1.27	0.406	2.64	0.312	-1.15	0.732	-0.29
1427721_at	---	---	-1.19	0.722	-1.48	0.466	2.64	0.007	-1.48	0.387	-0.38
1421570_at	Il9r	interleukin 9 receptor	-1.23	0.151	-1.05	0.664	2.39	0.242	-1.4	0.663	-0.32
1441478_at	9930013L23Rik	RIKEN cDNA 9930013L23 gene	2.76	0.008	-1.69	0.382	-1.24	0.539	-2.34	0.065	-0.63
1449400_at	Csl	citrate synthase like	-1.09	0.825	2.56	0.037	-1.46	0.129	-2.75	0.086	-0.68
1435842_at	1110038O08Rik	RIKEN cDNA 1110038O08 gene	-3.82	0.051	-1.84	0.24	3.36	0.009	-1.5	0.043	-0.95
1446381_at	BC030499	CDNA sequence BC030499	-1.07	0.625	-1.21	0.457	2.4	0.151	-1.17	0.554	-0.26
1456031_at	Tubb2c	Tubulin, beta 2c	-1.61	0.092	2.69	0.249	-1.16	0.732	-1.34	0.387	-0.35
1439318_at	Mast4	microtubule associated serine/threonine kinase family member 4	-1.07	0.915	2.39	0.155	-1.16	0.692	-1.05	0.885	-0.22
1423328_at	Gdap1	ganglioside-induced differentiation-associated-protein 1	-1.28	0.751	2.53	0.167	-1.16	0.617	-1.01	0.988	-0.23
1421036_at	Npas2	neuronal PAS domain protein 2	-1.15	0.672	-1.07	0.923	2.38	0.376	-2.16	0.251	-0.5
1443422_at	2410089E03Rik ///	RIKEN cDNA 2410089E03 gene /// hypothetical LOC546032 /// hypothetical prote	2.61	0.21	-1.03	0.929	-1.65	0.214	-1.66	0.059	-0.43
1443675_at	Epc1	Enhancer of polycomb homolog 1 (Drosophila)	2.77	0.169	-1.4	0.593	-1.42	0.058	-1.93	0.074	-0.5
1457967_at	A030003K21Rik	RIKEN cDNA A030003K21 gene	2.39	0.367	-1.06	0.909	-1.16	0.564	-3.82	0.044	-0.91
1433022_at	2310068G24Rik	RIKEN cDNA 2310068G24 gene	2.36	0.323	-1.09	0.85	-1.09	0.835	-1.02	0.97	-0.21
1439534_at	Zfp248	zinc finger protein 248	2.79	0.31	-1.06	0.937	-2.14	0.141	-2.46	0.054	-0.72

1421126_at	Ryr2	ryanodine receptor 2, cardiac	2.54	0.138	-1.28	0.622	-1.14	0.439	-1.01	0.974	-0.22
1421593_at	Ncam2	neural cell adhesion molecule 2	-1.08	0.877	2.29	0.177	-1.01	0.979	-1.14	0.791	-0.23
1449978_at	Zfy2	zinc finger protein 2, Y linked	2.95	0.214	-1.67	0.414	-1.52	0.182	-1.3	0.649	-0.39
1442130_at	Hsh2d	Hematopoietic SH2 domain containing	-1.11	0.743	-1.43	0.138	2.61	0.001	-2.28	0.089	-0.55
1438144_x_at	Atxn2	ataxin 2	-1.04	0.948	-1.22	0.679	2.43	0.233	-1.11	0.492	-0.24
1441068_at	A130001G05Rik	RIKEN cDNA A130001G05 gene	-1.06	0.785	2.47	0.155	-1.24	0.456	-1.37	0.202	-0.3
1458265_at	Kns2	Kinesin 2	2.68	0.447	-1.57	0.441	-1.12	0.851	-2.27	0.299	-0.57
1454782_at	Bai3	brain-specific angiogenesis inhibitor 3	2.83	0.327	-1.15	0.704	-1.96	0.193	-1.62	0.419	-0.47
1418086_at	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	-1.03	0.906	2.61	0.04	-1.56	0.01	-2.12	0.048	-0.53
1458681_at	Tm9sf3	Transmembrane 9 superfamily member 3	-1.82	0.298	-1.63	0.434	3.06	0.041	-2.29	0.386	-0.67
1428173_at	Eml2	echinoderm microtubule associated protein like 2	-2.09	0.436	-1.37	0.531	3.01	0.172	-1.72	0.423	-0.54
1420328_at	2210417D09Rik	RIKEN cDNA 2210417D09 gene	2.9	0.064	-1.44	0.281	-1.59	0.03	-1.59	0.058	-0.43
1452031_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	-1.11	0.868	2.33	0.218	-1	0.953	-1.07	0.725	-0.21
1427555_at	BC032281	cDNA sequence BC032281	-1.58	0.213	2.64	0.135	-1.05	0.913	-1.2	0.762	-0.3
1422347_at	Npy6r	neuropeptide Y receptor Y6	-2.42	0.026	3.06	0	-1.33	0.633	-1.83	0.202	-0.63
1427683_at	Egr2	early growth response 2	2.28	0.414	-1.01	0.987	-1.05	0.921	-1.85	0.082	-0.41
1416760_at	Galntl1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	2.5	0.21	-1.1	0.423	-1.21	0.549	-1.2	0.762	-0.25
1426079_at	Cd247	CD247 antigen	-1.36	0.744	2.66	0.027	-1.2	0.254	-1.51	0.366	-0.35
1418935_at	Trpm1	transient receptor potential cation channel, subfamily M, member 1	-1.02	0.985	2.53	0.118	-1.4	0.4	-1.54	0.479	-0.35
1455374_at	---	---	-1.17	0.713	2.4	0.006	-1.01	0.979	-2.01	0.357	-0.45
1423064_at	Dnmt3a	DNA methyltransferase 3A	-1.17	0.669	2.59	0.061	-1.25	0.156	-1.2	0.564	-0.26
1438201_at	Ppm2c	protein phosphatase 2C, magnesium dependent, catalytic subunit	-1.02	0.952	2.47	0.233	-1.25	0.268	-1.57	0.226	-0.34
1450673_at	Col9a2	procollagen, type IX, alpha 2	2.62	0.371	-1.22	0.23	-1.24	0.236	-1.61	0.392	-0.36
1444102_at	---	---	-1.11	0.848	-1.68	0.482	2.76	0.14	-2.21	0.011	-0.56
1430441_at	4933438K21Rik	RIKEN cDNA 4933438K21 gene	2.8	0.204	-1.72	0.485	-1.13	0.413	-1.81	0.466	-0.46
1456507_at	Zfp454	zinc finger protein 454	2.45	0.141	-1.04	0.929	-1.15	0.647	-1.33	0.421	-0.27
1459886_at	---	Transcribed locus	2.76	0.505	-1.13	0.863	-1.59	0.196	-1.49	0.475	-0.36
1431093_at	Nphp3	nephronophthisis 3 (adolescent)	-1.09	0.155	-4.34	0.008	3.14	0.001	-1.25	0.638	-0.89
1459116_at	Ncam2	Neural cell adhesion molecule 2	-1.01	0.979	2.76	0.001	-1.86	0.135	-1.85	0.268	-0.49
1450312_at	Cdh20	cadherin 20	-1.56	0.629	-1.13	0.792	2.76	0.05	-1.61	0.518	-0.39
1450003_at	Adra2b	adrenergic receptor, alpha 2b	-1.02	0.936	2.56	0.351	-1.35	0.501	-1.03	0.868	-0.21
1428250_at	Gpr30	G protein-coupled receptor 30	-1.31	0.413	2.74	0.233	-1.27	0.103	-1.72	0.485	-0.39
1455038_at	LOC632764	similar to melanoma antigen	2.59	0.092	-1.16	0.029	-1.19	0.672	-5.13	0.048	-1.22
1450110_at	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	-1.09	0.304	2.39	0.036	-1.01	0.961	-1.65	0.102	-0.34
1421306_a_at	Hdac9	histone deacetylase 9	-1.65	0.546	-1.69	0.512	3.1	0.003	-1.25	0.79	-0.37
1438325_at	Evi1	ecotropic viral integration site 1	-1.11	0.422	2.7	0.047	-1.43	0.008	-1.15	0.512	-0.25
1454473_at	4933433M23Rik	RIKEN cDNA 4933433M23 gene	-1.07	0.849	-1.27	0.194	2.58	0.385	-1.12	0.765	-0.22
1417143_at	Edg2	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	-1.03	0.748	2.53	0.26	-1.26	0.319	-1.48	0.322	-0.31
1458411_at	Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1	-1.38	0.567	-1	0.993	2.59	0.412	-2.12	0.089	-0.48
1445752_at	---	---	-1.73	0.432	3.08	0.205	-1.52	0.08	-1.08	0.92	-0.31
1439777_at	B230218O03	hypothetical protein B230218O03	2.82	0.486	-1.74	0.347	-1.09	0.526	-1.69	0.152	-0.42
1421551_s_at	Ifi202b	interferon activated gene 202B	-1.07	0.7	2.4	0.219	-1.01	0.972	-1.51	0.504	-0.3
1453495_at	Klk12	kallikrein 12	2.95	0.409	-2.09	0.277	-1.13	0.651	-1.68	0.192	-0.49
1431084_x_at	1810014B01Rik	RIKEN cDNA 1810014B01 gene	-1.04	0.934	-1.74	0.053	2.78	0.084	-1.1	0.89	-0.27
1426415_a_at	Trim25	tripartite motif protein 25	-1.27	0.503	-1.1	0.864	2.62	0.121	-1.07	0.854	-0.2
1458041_at	C80360	expressed sequence C80360	-1.7	0.322	3.17	0.045	-1.76	0.453	-1.24	0.551	-0.38
1438899_at	Klf17	Kruppel-like factor 17	2.63	0.24	-1.22	0.629	-1.14	0.435	-2.24	0.422	-0.49
1445537_at	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	-1.57	0.238	2.78	0.208	-1.1	0.855	-3.38	0.054	-0.82
1458107_at	---	---	2.75	0.028	-1.17	0.755	-1.37	0.525	-1.65	0.25	-0.36
1443550_at	Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	-1.01	0.876	-1.14	0.746	2.47	0.082	-2.01	0.217	-0.42
1459311_at	Pde4d	phosphodiesterase 4D, cAMP specific	3.27	0.06	-2.16	0.109	-1.63	0.528	-2.01	0.423	-0.63
1440215_at	C130086A10	hypothetical protein C130086A10	-1.31	0.098	2.79	0.346	-1.26	0.319	-1.4	0.167	-0.3
1446733_at	---	---	2.67	0.063	-1.03	0.941	-1.42	0.263	-1.3	0.585	-0.27

1435907_at	Nrxn2	neurexin II	2.55	0.128	-1.02	0.962	-1.21	0.525	-1.02	0.966	-0.17
1435359_at	BC060632	cDNA sequence BC060632	2.79	0.055	-1.02	0.981	-1.7	0.316	-1.22	0.688	-0.29
1427814_at	Ofa	oncofetal antigen	-1.84	0.526	3.22	0.261	-1.67	0.348	-1.39	0.174	-0.42
1433291_at	C030045M22Rik	RIKEN cDNA C030045M22 gene	2.86	0.404	-1.56	0.49	-1.15	0.795	-1.08	0.863	-0.23
1432766_at	E130112B07Rik	RIKEN cDNA E130112B07 gene	-1.87	0.394	-1	0.991	2.84	0.024	-1.61	0.111	-0.41
1434152_at	2210421G13Rik ///	RIKEN cDNA 2210421G13 gene /// hypothetical protein LOC193676 /// similar to	-1.15	0.852	2.61	0.061	-1.12	0.582	-3.66	0.057	-0.83
1432208_at	4930459C07Rik	RIKEN cDNA 4930459C07 gene	-1.09	0.336	2.66	0.125	-1.26	0.586	-1.58	0.327	-0.32
1442597_at	C79122	expressed sequence C79122	-1.15	0.122	-1.05	0.898	2.55	0.145	-2.27	0.047	-0.48
1445075_at	---	---	2.9	0.379	-1.59	0.396	-1.16	0.723	-3.47	0.08	-0.83
1451593_at	H2-K1	Histocompatibility 2, K1, K region	-1.94	0.214	-1.27	0.417	3.08	0.014	-1.94	0.064	-0.52
1457394_at	2900002K06Rik	RIKEN cDNA 2900002K06 gene	2.62	0.172	-1.28	0.651	-1.01	0.976	-1.25	0.688	-0.23
1441461_at	Frmd4a	FERM domain containing 4A	3.17	0	-1.43	0.502	-1.92	0.11	-1.66	0.338	-0.46
1439806_at	Tada1l	Transcriptional adaptor 1 (HFI1 homolog, yeast) like	-1.2	0.675	2.81	0.034	-1.32	0.234	-1.67	0.367	-0.35
1452569_at	Slco1b2	solute carrier organic anion transporter family, member 1b2	3.43	0.043	-2.34	0.242	-1.82	0.252	-1.3	0.356	-0.51
1452403_a_at	Oc90	otoconin 90	3.48	0.001	-3.77	0.031	-1.5	0.452	-1.44	0.418	-0.81
1441795_at	Snapc4	small nuclear RNA activating complex, polypeptide 4	3	0.343	-1.94	0.529	-1.11	0.85	-1.1	0.861	-0.29
1430063_at	4930571K23Rik	RIKEN cDNA 4930571K23 gene	-1.44	0.251	-1.05	0.911	2.78	0.005	-1.8	0.147	-0.38
1456093_at	Zfp536	zinc finger protein 536	2.87	0.043	-1.5	0.532	-1.13	0.673	-2.5	0.309	-0.57
1432550_at	4930572D21Rik	RIKEN cDNA 4930572D21 gene	-1.4	0.339	3.16	0.053	-1.83	0.202	-1.17	0.762	-0.31
1433166_at	4930485E13Rik	RIKEN cDNA 4930485E13 gene	-3.49	0.03	3.3	0.234	-1.2	0.655	-2.07	0.073	-0.86
1416899_at	Utf1	undifferentiated embryonic cell transcription factor 1	-2.48	0	-1.09	0.843	3.12	0.375	-1.28	0.675	-0.43
1443351_at	Glra2	Glycine receptor, alpha 2 subunit	2.72	0.419	-1.23	0.43	-1.11	0.804	-1.02	0.948	-0.16
1440919_at	Mobkl2c	MOB1, Mps One Binder kinase activator-like 2C (yeast)	2.83	0.045	-1.32	0.354	-1.18	0.515	-2.05	0.176	-0.43
1431652_at	Umps	uridine monophosphate synthetase	-1.21	0.257	2.67	0.153	-1.04	0.926	-1.36	0.478	-0.23
1440018_at	A330043J11Rik	RIKEN cDNA A330043J11 gene	3.04	0.441	-1.44	0.498	-1.36	0.271	-1.08	0.723	-0.21
1430840_at	4930449C09Rik	RIKEN cDNA 4930449C09 gene	-1.32	0.197	-1.32	0.629	2.95	0.135	-1.03	0.955	-0.18
1421739_a_at	Matk	megakaryocyte-associated tyrosine kinase	-1.28	0.472	-1.05	0.749	2.75	0.423	-1.01	0.913	-0.15
1449266_at	Mecp2	methyl CpG binding protein 2	-1.15	0.684	-1.11	0.787	2.72	0.008	-1.1	0.287	-0.16
1427306_at	Ryr1	ryanodine receptor 1, skeletal muscle	-1.1	0.115	-1.59	0.164	2.95	0.092	-1.41	0.354	-0.29
1449798_at	---	Transcribed locus	2.76	0.305	-1.25	0.76	-1.08	0.82	-1.44	0.499	-0.25
1432500_at	2410006F04Rik	RIKEN cDNA 2410006F04 gene	-1.01	0.988	-1.06	0.91	2.56	0.016	-1.04	0.913	-0.14
1453080_at	9130022K13Rik ///	RIKEN cDNA 9130022K13 gene /// similar to apolipoprotein L, 3 (predicted)	2.75	0.499	-1.18	0.577	-1.1	0.831	-1.22	0.694	-0.19
1444708_at	Tmem29	transmembrane protein 29	2.99	0.005	-1.06	0.939	-1.77	0.427	-1.41	0.67	-0.31
1447890_at	Rcn1	reticulocalbin 1	2.6	0.099	-1.09	0.856	-1.01	0.987	-1.79	0.305	-0.32
1457655_x_at	Arhgap27	Rho GTPase activating protein 27	-1.07	0.733	2.92	0.013	-1.53	0.028	-1.68	0.386	-0.34
1438770_at	Gm266	gene model 266, (NCBI)	-1.26	0.514	-1.06	0.932	2.78	0.057	-1.69	0.39	-0.31
1438455_at	C330050A14Rik	RIKEN cDNA C330050A14 gene	3.05	0.004	-1.1	0.817	-1.79	0.062	-1.41	0.419	-0.31
1443458_at	D630033O11Rik	RIKEN cDNA D630033O11 gene	-1.38	0.426	2.88	0.129	-1.09	0.848	-1.33	0.588	-0.23
1427667_s_at	Tcrb-J	T-cell receptor beta, joining region	-1.15	0.636	-1.17	0.8	2.8	0.182	-4.16	0.149	-0.92
1421838_at	Rps18	ribosomal protein S18	3.15	0.004	-1.35	0.413	-1.56	0.055	-1.94	0.038	-0.43
1422600_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	2.77	0.379	-1.05	0.946	-1.23	0.542	-1.12	0.682	-0.16
1443437_at	LOC633285	similar to apobec-1 complementation factor	-1.26	0.232	2.79	0.043	-1.05	0.836	-1.29	0.489	-0.2
1433320_at	4930519N06Rik	RIKEN cDNA 4930519N06 gene	-7.05	0.009	3.55	0.16	-1.18	0.564	-1.19	0.714	-1.47
1449982_at	Il11	interleukin 11	2.93	0.098	-1.14	0.829	-1.36	0.189	-1.22	0.391	-0.2
1449179_at	Pdc	phosducin	2.71	0.099	-1.08	0.85	-1.09	0.677	-1.46	0.479	-0.23
1439114_at	BC013672	cDNA sequence BC013672	2.69	0.061	-1.08	0.83	-1.07	0.433	-2.36	0.167	-0.45
1437830_x_at	Zbed3	zinc finger, BED domain containing 3	-1.25	0.235	2.88	0.015	-1.13	0.707	-1.32	0.348	-0.2
1430455_at	Olfr701	olfactory receptor 701	-1.39	0.189	3	0.074	-1.17	0.171	-1.47	0.01	-0.26
1441495_at	Kctd8	potassium channel tetramerisation domain containing 8	3.37	0.04	-2	0.403	-1.41	0.465	-1.03	0.613	-0.27
1451033_a_at	Trpc4	transient receptor potential cation channel, subfamily C, member 4	3.74	0.017	-2.89	0.162	-2.04	0.182	-1.3	0.535	-0.62
1443502_at	Birc7	baculoviral IAP repeat-containing 7 (livin)	2.65	0.129	-1.05	0.939	-1.01	0.939	-1.03	0.891	-0.11
1458304_at	Smad2	MAD homolog 2 (Drosophila)	-1.13	0.716	3.05	0.044	-1.51	0.019	-2.27	0.371	-0.47
1429780_at	Ccdc39	coiled-coil domain containing 39	3.14	0.103	-1.75	0.516	-1.13	0.504	-1.8	0.54	-0.39

1458478_at	9230110F11Rik	RIKEN cDNA 9230110F11 gene	2.81	0.063	-1.21	0.796	-1.05	0.88	-1.47	0.641	-0.23
1435858_at	---	Transcribed locus	-1.32	0.626	-1.1	0.818	2.93	0.244	-1.68	0.222	-0.29
1452195_s_at	Sfi1 /// LOC673420	Sfi1 homolog, spindle assembly associated (yeast) /// similar to spindle assembly	3.09	0.035	-1.05	0.919	-1.81	0.034	-1.35	0.587	-0.28
1450977_s_at	Ndrg1 /// Ndrl	N-myc downstream regulated gene 1 /// N-myc downstream regulated-like	-1	0.994	-1.07	0.911	2.67	0.068	-1.1	0.862	-0.13
1425697_at	Sdccag1	serologically defined colon cancer antigen 1	2.89	0.38	-1.29	0.612	-1.05	0.882	-1.15	0.703	-0.15
1440326_at	Scap1	Src family associated phosphoprotein 1	2.92	0.122	-1.19	0.723	-1.16	0.744	-1.61	0.264	-0.26
1431675_a_at	Gtf2i	general transcription factor II I	-1.08	0.601	-1.8	0.168	3.16	0.184	-1.04	0.923	-0.19
1446979_at	Dcps	Decapping enzyme, scavenger	3.26	0.054	-1.44	0.528	-1.46	0.486	-1.64	0.285	-0.32
1427204_at	3322402L07Rik	RIKEN cDNA 3322402L07 gene	-1.4	0.356	3.56	0.079	-2.73	0.117	-1.09	0.836	-0.41
1422820_at	Lipe	lipase, hormone sensitive	-1.36	0.175	-1.05	0.85	2.97	0.12	-1.56	0.054	-0.25
1439149_s_at	LOC629141	hypothetical protein LOC629141	-3.06	0.256	3.37	0.002	-1.04	0.921	-1.18	0.588	-0.48
1458771_at	---	---	3.35	0.001	-1.36	0.604	-1.72	0.115	-1.26	0.542	-0.25
1445485_at	D7Ertd187e	DNA segment, Chr 7, ERATO Doi 187, expressed	3.19	0.187	-1.61	0.246	-1.17	0.527	-1.69	0.484	-0.32
1426197_at	---	Anti-human CD20 antibody 1F5 gamma heavy chain variable region	-1	0.996	2.95	0.363	-1.38	0.523	-3.4	0.341	-0.71
1452456_at	Nrip2	nuclear receptor interacting protein 2	-1.59	0.248	3.13	0.026	-1.07	0.293	-1.32	0.348	-0.21
1450211_at	Lrp1b	low density lipoprotein-related protein 1B (deleted in tumors)	-1.79	0.356	3.22	0.087	-1.09	0.64	-1.5	0.588	-0.29
1421011_at	Dhrs8	dehydrogenase/reductase (SDR family) member 8	-2.77	0.434	-2.25	0.2	3.9	0.135	-2.91	0.309	-1.01
1447615_at	Fmn1	Formin 1	-1.09	0.735	2.91	0.056	-1.13	0.545	-1.09	0.817	-0.1
1439997_at	Synj1	synaptojanin 1	-1.38	0.119	3.25	0.154	-1.33	0.261	-1.24	0.532	-0.17
1444656_at	BC030499	cDNA sequence BC030499	3.11	0.063	-1.27	0.655	-1.18	0.776	-1.37	0.633	-0.18
1458415_at	Clec2e	C-type lectin domain family 2, member e	3.49	0.003	-1.33	0.643	-1.96	0.121	-1.37	0.595	-0.29
1417330_at	Slc23a2	solute carrier family 23 (nucleobase transporters), member 2	-1.32	0.465	-1.21	0.728	3.17	0.358	-1.25	0.188	-0.15
1449794_x_at	Ctsf	Cathepsin F	-2.6	0.045	3.54	0.055	-1.21	0.588	-1.07	0.698	-0.33
1453751_at	Dhx38	DEAH (Asp-Glu-Ala-His) box polypeptide 38	-1.4	0.482	-1.37	0.602	3.31	0.238	-1.12	0.891	-0.14
1443940_at	Lrrc22	leucine rich repeat containing 22	2.9	0.199	-1.08	0.855	-1.07	0.882	-2.3	0.106	-0.39
1458171_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	3.26	0.419	-1.5	0.255	-1.18	0.8	-1.41	0.713	-0.21
1429293_at	Gpc2	glypican 2 (cerebroglycan)	3.77	0.027	-1.85	0.349	-2.06	0.018	-1.95	0.272	-0.52
1446854_at	Grm7	Glutamate receptor, metabotropic 7	3.89	0.117	-2.45	0.291	-1.91	0.323	-1.53	0.235	-0.5
1421590_at	Mrgprh	MAS-related GPR, member H	-1.71	0.248	3.33	0.099	-1.1	0.827	-1.27	0.616	-0.18
1441294_at	---	---	3.03	0.39	-1.01	0.987	-1.18	0.739	-1.34	0.7	-0.13
1458602_at	Bbx	bobby sox homolog (Drosophila)	-1.23	0.791	3.08	0.232	-1.02	0.924	-1.56	0.371	-0.18
1442923_at	Ptk6	PTK6 protein tyrosine kinase 6	-1.14	0.698	3.44	0.12	-1.79	0.163	-1.67	0.645	-0.29
1444162_at	Frs2	fibroblast growth factor receptor substrate 2	3.4	0.026	-1.28	0.6	-1.39	0.447	-2.29	0.313	-0.39
1436195_at	BC046404	cDNA sequence BC046404	-1.04	0.858	3.18	0.067	-1.31	0.057	-1.63	0.138	-0.2
1431512_at	4933437F24Rik	RIKEN cDNA 4933437F24 gene	3.4	0.002	-1.44	0.454	-1.23	0.176	-1.28	0.764	-0.14
1445297_at	---	Transcribed locus	-1.61	0.127	3.46	0.002	-1.18	0.659	-1	0.995	-0.08
1459278_at	Fgd1	FYVE, RhoGEF and PH domain containing 1	4.25	0.119	-2.63	0.06	-2.99	0.033	-1.1	0.8	-0.62
1420192_at	D16Bwg1494e	DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed	-1.66	0.04	3.47	0.192	-1.11	0.857	-2.34	0.171	-0.41
1458779_at	8030445P17Rik	RIKEN cDNA 8030445P17 gene	3.28	0.043	-1.32	0.647	-1.04	0.903	-1.92	0.054	-0.25
1450748_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	-1.1	0.808	3.49	0.015	-1.64	0.33	-1.03	0.586	-0.07
1459933_at	---	---	-1.16	0.763	3.19	0.203	-1.04	0.943	-3.22	0.154	-0.56
1435047_at	---	Transcribed locus	3.34	0.273	-1.15	0.646	-1.24	0.515	-1.43	0.59	-0.12
1425559_a_at	Acsm3	acyl-CoA synthetase medium-chain family member 3	-1.32	0.436	-1.52	0.122	3.64	0.098	-1.14	0.693	-0.08
1458815_at	AU021884	expressed sequence AU021884	4.14	0.09	-2.15	0.307	-2.17	0.073	-1.28	0.245	-0.37
1445551_at	Nfrkb	nuclear factor related to kappa B binding protein	-2.06	0.506	4	0.031	-1.57	0.212	-1.84	0.257	-0.37
1446552_at	Slc12a3	solute carrier family 12, member 3	3.54	0.194	-1.1	0.838	-1.47	0.333	-1.06	0.855	-0.02
1443188_at	Ube2w	ubiquitin-conjugating enzyme E2W (putative)	3.39	0.03	-1.27	0.666	-1.04	0.91	-2.41	0.224	-0.33
1428472_at	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	3.56	0.216	-1.54	0.448	-1.02	0.924	-1.11	0.73	-0.03
1447716_x_at	6330442E10Rik	RIKEN cDNA 6330442E10 gene	3.83	0.285	-1.16	0.859	-1.87	0.347	-1.76	0.24	-0.24
1454157_a_at	Pla2g2d	phospholipase A2, group IID	-1.91	0.015	-1.41	0.272	4.04	0.17	-2.16	0.22	-0.36
1422694_at	Ttyh1	tweety homolog 1 (Drosophila)	3.85	0.114	-1.41	0.614	-1.4	0.179	-1.42	0.419	-0.1
1447789_x_at	---	---	-2.5	0.174	4.08	0	-1.25	0.35	-2.56	0.051	-0.56
1419580_at	---	---	3.84	0.117	-1.47	0.517	-1.32	0.337	-1.21	0.397	-0.04

1421669_at	Sult3a1	sulfotransferase family 3A, member 1	4.2	0.453	-1.77	0.109	-1.68	0.374	-2.21	0.102	-0.37
1450611_at	Orm3	orosomucoid 3	-2.27	0.275	4.37	0.126	-1.81	0.246	-1.25	0.41	-0.24
1438861_at	Bnc2	basonuclin 2	-1.38	0.205	3.66	0.007	-1.01	0.968	-1.3	0.461	-0.01
1438380_at	Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	4.13	0.335	-1.21	0.743	-2.31	0.047	-1.52	0.433	-0.23
1430669_at	Krtap4-7	keratin associated protein 4-7	3.96	0.141	-1.4	0.508	-1.34	0.417	-1.91	0.522	-0.17
1447682_x_at	Traf5 /// LOC62260	Tnf receptor-associated factor 5 /// similar to TNF receptor-associated factor 5	3.64	0.162	-1.23	0.71	-1.01	0.97	-1.27	0.218	0.03
1431511_at	9230110F15Rik	RIKEN cDNA 9230110F15 gene	-1	0.997	3.88	0.003	-1.67	0.458	-1.06	0.89	0.04
1417653_at	Pvalb	parvalbumin	-1.27	0.341	-1.31	0.576	3.96	0.235	-1.97	0.341	-0.15
1419709_at	Stfa3	stefin A3	-1.96	0.052	-1.97	0.148	4.57	0.23	-1.26	0.749	-0.16
1432424_at	4930505H01Rik	RIKEN cDNA 4930505H01 gene	-1.08	0.814	-1.36	0.434	3.95	0.001	-1.01	0.983	0.12
1459092_at	Slco6c1	solute carrier organic anion transporter family, member 6c1	4.29	0.233	-1.08	0.918	-1.94	0.079	-1.53	0.525	-0.07
1417956_at	Cidea	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	-1.61	0.398	-1.57	0.455	4.49	0.101	-1.07	0.864	0.06
1418769_at	Myoz2	myozenin 2	-1.57	0.461	4.28	0.013	-1.21	0.337	-1.57	0.469	-0.02
1440061_at	Rbx1	ring-box 1	4.61	0.078	-3.11	0.031	-1.21	0.288	-1.26	0.586	-0.24
1429273_at	Bmper	BMP-binding endothelial regulator	-1.23	0.734	4.26	0.195	-1.35	0.02	-1.48	0.349	0.05
1455537_at	6430547I21Rik	RIKEN cDNA 6430547I21 gene	4.93	0.4	-2.89	0.025	-1.56	0.208	-1.09	0.927	-0.15
1453531_at	Zfp248	zinc finger protein 248	-1.2	0.37	4.14	0.01	-1.04	0.805	-1.35	0.319	0.14
1439351_at	A930031D07Rik	RIKEN cDNA A930031D07 gene	-1.03	0.942	4.36	0	-1.43	0.316	-1.06	0.909	0.21
1448207_at	Lasp1	LIM and SH3 protein 1	-1	0.999	-1.16	0.807	4.32	0.363	-1.43	0.682	0.18
1457413_at	Ror1	Receptor tyrosine kinase-like orphan receptor 1	4.62	0.006	-1.09	0.836	-1.34	0.607	-2.09	0.366	0.02
1433028_at	4833411I10Rik	RIKEN cDNA 4833411I10 gene	4.85	0.114	-1.09	0.727	-1.45	0.165	-2.58	0.143	-0.07
1455370_at	A630023P12Rik	RIKEN cDNA A630023P12 gene	-1.71	0.32	-2.05	0.214	5.8	0.206	-1.99	0.206	0.01
1440772_x_at	9530077C05Rik	RIKEN cDNA 9530077C05 gene	-1.33	0.523	5.52	0.152	-1.04	0.908	-1.41	0.562	0.44
1420097_at	D13Ertd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	-3.45	0.243	6.1	0.083	-1.15	0.78	-1.23	0.713	0.07
1434140_at	Mcf2l	mcf.2 transforming sequence-like	-1.01	0.969	5.62	0.085	-1.03	0.939	-1.19	0.695	0.6
1448789_at	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	-2.42	0.151	6.72	0.079	-1.28	0.503	-1.83	0.107	0.3
1446706_at	C79123	expressed sequence C79123	6.45	0.069	-1.17	0.594	-1.42	0.278	-1.06	0.926	0.7
1449280_at	Esm1 /// LOC63267	endothelial cell-specific molecule 1 /// similar to Endothelial cell-specific molecule	-1.23	0.604	6.81	0.014	-1.58	0.099	-1.62	0.303	0.59
1436260_at	---	Transcribed locus	-1.06	0.956	-1.5	0.237	7.14	0.214	-1.05	0.868	0.88
1416889_at	Tnni2	troponin I, skeletal, fast 2	-1.3	0.635	-1.14	0.584	10.63	0.236	-1.63	0.313	1.64
1419312_at	Atp2a1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	-2.19	0.11	-1.47	0.113	11.2	0.26	-1.1	0.81	1.61
1442263_at	Rgs13	regulator of G-protein signaling 13	-2.16	0.332	-1.4	0.567	13.23	0.272	-2.59	0.152	1.77
1418197_at	Ucp1	uncoupling protein 1 (mitochondrial, proton carrier)	-1.97	0.378	-1.14	0.67	20.67	0.37	-1.26	0.576	4.07
1439182_at	D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	-3.09	0.096	-4.16	0	1.02	0.96	1.06	0.894	-1.29
1425418_at	Wfdc5	WAP four-disulfide core domain 5	-5.15	0.061	1.07	0.913	-2.29	0.113	1.11	0.735	-1.32
1441691_at	---	Transcribed locus	-2.52	0.052	-3.52	0.095	1.04	0.932	1.61	0.256	-0.85
1456901_at	Adamts20	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-5.11	0.004	-3.27	0.134	1.22	0.38	1.01	0.988	-1.54
1457610_at	AL033326	Expressed sequence AL033326	-8.1	0.023	-2.49	0.214	1.2	0.767	1.84	0.381	-1.89
1437960_at	Capn13	calpain 13	-3.46	0.069	-3.06	0.036	1.17	0.428	1.21	0.696	-1.03
1460745_at	A630098A13Rik	RIKEN cDNA A630098A13 gene	-2.64	0.101	-2.66	0.343	1.04	0.924	1.51	0.435	-0.69
1457829_at	Clgn	calmegin	-2.69	0.167	-2.55	0.032	1.03	0.942	1.89	0.45	-0.58
1439987_at	Grik1	glutamate receptor, ionotropic, kainate 1	-2.47	0.131	-3.08	0.238	1.06	0.933	1.06	0.839	-0.86
1460340_at	Piwil1	piwi-like homolog 1 (Drosophila)	-2.8	0.226	-2.4	0.214	1.02	0.884	1.09	0.913	-0.77
1450580_at	Gpr45	G protein-coupled receptor 45	-2.91	0.121	1.03	0.895	-2.24	0.196	1.79	0.377	-0.58
1426099_at	Hrh4	histamine H4 receptor	1.03	0.975	-2.96	0.163	-2.16	0.349	1.44	0.441	-0.66
1431588_at	2900045O20Rik	RIKEN cDNA 2900045O20 gene	-1.73	0.11	-5.07	0.002	1.05	0.898	1.5	0.335	-1.06
1423180_at	Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1	1.03	0.902	-3.17	0.045	-1.95	0.261	1.21	0.765	-0.72
1430548_at	---	---	-4.44	0.005	1.02	0.944	-1.64	0.143	1.06	0.886	-1
1432991_at	4930519E07Rik	RIKEN cDNA 4930519E07 gene	-2.12	0.532	-2.8	0.216	1.03	0.941	1.82	0.305	-0.52
1456704_at	9530010C24Rik	RIKEN cDNA 9530010C24 gene	1.12	0.471	-2.17	0.392	-3.35	0.001	2.42	0.081	-0.49
1452465_at	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	-1.82	0.129	-3.58	0.001	1.05	0.82	1.23	0.758	-0.78
1419634_a_at	Ghrh	growth hormone releasing hormone	-3.82	0.204	-2.97	0.337	1.29	0.664	1.38	0.625	-1.03
1440633_at	Neil3	nei like 3 (E. coli)	-2.57	0.046	-3.61	0.065	1.22	0.677	5.74	0.148	0.2

1432703_at	5730405A17Rik	RIKEN cDNA 5730405A17 gene	-2.07	0.085	1.12	0.824	-3.55	0.003	1.1	0.722	-0.85
1433234_at	4930424E08Rik	RIKEN cDNA 4930424E08 gene	-1.99	0.203	1.09	0.913	-3.29	0.077	1.3	0.507	-0.72
1417686_at	Lgals12	lectin, galactose binding, soluble 12	-2.04	0.077	-2.57	0.114	1.02	0.952	1.43	0.549	-0.54
1446698_at	Morf4l1	Mortality factor 4 like 1	1.09	0.782	-2.55	0.38	-2.4	0.019	1.43	0.527	-0.61
1459580_at	G630055G22Rik	RIKEN cDNA G630055G22 gene	-2.51	0.467	1.04	0.943	-2.13	0.055	1.23	0.525	-0.59
1431987_at	4930510E17Rik	RIKEN cDNA 4930510E17 gene	-3.57	0.013	1.19	0.811	-2.27	0.079	1.35	0.598	-0.83
1457595_at	---	2 cells egg cDNA, RIKEN full-length enriched library, clone:B020028D20 product:	-3.09	0.163	1.02	0.965	-1.77	0.389	2.01	0.002	-0.46
1458832_at	Ghr	Growth hormone receptor	1.02	0.946	-2.37	0.069	-2.1	0.002	1.07	0.89	-0.6
1459336_at	Gucy1a2	Guanylate cyclase 1, soluble, alpha 2	-2.99	0.148	1.12	0.662	-2.07	0.134	1.31	0.615	-0.66
1423270_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	-2.43	0.224	1	1	-1.91	0.082	1.57	0.056	-0.44
1438628_x_at	Cntn3	contactin 3	1.04	0.454	-2.51	0.269	-2.01	0.146	1.2	0.696	-0.57
1449543_at	Zfp371	zinc finger protein 371	-4.96	0.031	-1.52	0.414	1.08	0.829	1.11	0.249	-1.07
1438450_at	Lin7a	lin-7 homolog A (C. elegans)	-3.76	0.102	-1.49	0.001	1	0.993	1.04	0.802	-0.8
1459604_at	Snurf	SNRPN upstream reading frame	1.12	0.893	-2.76	0.078	-2.2	0.254	1.17	0.828	-0.67
1443672_at	Lars2	leucyl-tRNA synthetase, mitochondrial	-2.49	0.408	1.06	0.861	-2.08	0.028	1.42	0.625	-0.52
1459865_x_at	Ces7	carboxylesterase 7	-2.23	0.19	-2.95	0.147	1.16	0.677	1.26	0.733	-0.69
1432357_at	4930566D17Rik	RIKEN cDNA 4930566D17 gene	-2.16	0.493	-2.09	0.128	1.01	0.978	1.17	0.483	-0.52
1441037_at	Sncaip	Synuclein, alpha interacting protein (synphilin)	-1.7	0.279	1.01	0.989	-2.8	0.012	2.43	0.011	-0.27
1444304_at	A330102K23Rik	RIKEN cDNA A330102K23 gene	-1.97	0.374	-2.26	0.221	1.01	0.99	1.3	0.556	-0.48
1448453_at	Hsd3b1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	1.08	0.799	-2.26	0.223	-2.29	0.144	1.52	0.166	-0.49
1436872_at	Tacc3	transforming, acidic coiled-coil containing protein 3	-3.25	0.361	-1.7	0.096	1.06	0.824	2.05	0.234	-0.46
1445968_at	Tmtc2	Transmembrane and tetratricopeptide repeat containing 2	1.14	0.604	-4.53	0.016	-1.66	0.141	1.01	0.961	-1.01
1421381_a_at	Col9a1	procollagen, type IX, alpha 1	-5.13	0.019	-1.74	0.365	1.2	0.673	1.67	0.433	-1
1453933_at	4933435E02Rik	RIKEN cDNA 4933435E02 gene	-1.92	0.137	-3.03	0.113	1.12	0.642	1.26	0.159	-0.64
1428981_at	2810007J24Rik	RIKEN cDNA 2810007J24 gene	1.09	0.77	-3.37	0.011	-1.71	0.157	1.04	0.911	-0.74
1416711_at	Tbr1	T-box brain gene 1	-3.94	0.09	1.06	0.93	-1.54	0.424	1.09	0.875	-0.83
1420272_at	---	---	-5.16	0.035	1.08	0.895	-1.44	0.254	1.28	0.722	-1.06
1452183_a_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	1.14	0.832	-4.16	0.128	-1.69	0.243	1.61	0.168	-0.77
1446016_at	---	---	-5.19	0.052	-3.02	0.019	1.45	0.393	1.75	0.083	-1.25
1446296_at	4631422O05Rik	RIKEN cDNA 4631422O05 gene	1.24	0.748	-3.38	0.085	-2.28	0.087	1.32	0.507	-0.77
1447154_at	Cacnb4	Calcium channel, voltage-dependent, beta 4 subunit	-2.17	0.08	-2.23	0.075	1.08	0.881	1.42	0.435	-0.47
1430443_at	Anxa10	annexin A10	-3.36	0.106	1.31	0.554	-2.56	0.218	3.33	0.023	-0.32
1458686_at	Ggnbp2	Gametogenetin binding protein 2	-1.78	0.313	-2.33	0.182	1.01	0.976	1.4	0.355	-0.43
1454486_at	9530002O20Rik	RIKEN cDNA 9530002O20 gene	-2.07	0.328	-5.03	0.309	1.32	0.454	1.16	0.713	-1.16
1436466_at	9130227C08Rik	RIKEN cDNA 9130227C08Rik gene	-2.06	0.328	-2.16	0.028	1.05	0.802	1.03	0.898	-0.54
1445899_at	AA409289	expressed sequence AA409289	-2.63	0.482	1.05	0.932	-1.75	0.157	1.18	0.778	-0.54
1444032_at	Keg1	Kidney expressed gene 1	1.08	0.875	-2.19	0.05	-2.14	0.187	1.67	0.376	-0.4
1426057_a_at	Epha3	Eph receptor A3	-1.69	0.586	-3.22	0.057	1.1	0.622	3.62	0.077	-0.05
1437534_at	---	PREDICTED: Mus musculus similar to Rap guanine nucleotide exchange factor 2	-1.59	0.324	-2.73	0.152	1.01	0.982	1.68	0.445	-0.41
1441094_at	Adh6b	alcohol dehydrogenase 6B (class V)	-1.51	0.026	1.02	0.965	-3.01	0.275	1.95	0.023	-0.39
1446056_at	---	---	-3.41	0.158	-1.46	0.432	1.04	0.762	1.16	0.48	-0.67
1445742_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	-2.24	0.092	-3.13	0.031	1.25	0.071	1.28	0.519	-0.71
1420204_at	---	---	1.12	0.877	-2.83	0.204	-1.84	0.325	1.29	0.538	-0.56
1459745_at	Ubap2	Ubiquitin-associated protein 2	1.17	0.275	-2.6	0.043	-2.11	0.029	1.23	0.43	-0.58
1455856_at	---	---	-3.17	0.088	-1.74	0.125	1.14	0.713	1.8	0.32	-0.49
1452010_at	Chrna3	cholinergic receptor, nicotinic, alpha polypeptide 3	1.01	0.991	-1.98	0.121	-1.93	0.232	1.26	0.373	-0.41
1455392_at	9630019K15Rik	RIKEN cDNA 9630019K15 gene	-3.11	0.013	-1.64	0.375	1.1	0.418	1.42	0.621	-0.56
1450590_at	Olfr159	olfactory receptor 159	1.05	0.88	-1.79	0.157	-2.35	0.33	2.98	0.313	-0.03
1415924_at	Tnp1	transition protein 1	1.01	0.99	-3.17	0.283	-1.41	0.469	1.02	0.975	-0.64
1447287_at	C77137	expressed sequence C77137	1.19	0.164	-3.61	0.005	-1.76	0.324	1.43	0.106	-0.69
1432324_at	4930432J09Rik	RIKEN cDNA 4930432J09 gene	-3.93	0.158	1.12	0.827	-1.53	0.22	1.33	0.491	-0.75
1452624_at	Lrrtm1	leucine rich repeat transmembrane neuronal 1	1	0.999	-2	0.131	-1.87	0.229	3.42	0.259	0.14
1446810_at	A730062M13Rik	RIKEN cDNA A730062M13 gene	-2.18	0.374	-2.59	0.177	1.19	0.769	1.34	0.309	-0.56

1419085_at	Pcp2	Purkinje cell protein 2 (L7)	-2.76	0.094	1	0.996	-1.49	0.456	2.3	0.106	-0.24
1422229_at	Dub2	deubiquitinating enzyme 2	-2.39	0.087	1.28	0.653	-2.88	0.019	1.18	0.453	-0.7
1450324_a_at	4930521E07Rik	RIKEN cDNA 4930521E07 gene	-2.04	0.448	-1.8	0.021	1	0.995	1.35	0.206	-0.37
1458427_at	Brip1	BRCA1 interacting protein C-terminal helicase 1	-2.37	0.016	-1.62	0.205	1.01	0.975	2.34	0.222	-0.16
1433509_s_at	Reep1	receptor accessory protein 1	-4.49	0.272	1.19	0.572	-1.58	0.134	1.16	0.707	-0.93
1427495_at	Scn7a	sodium channel, voltage-gated, type VII, alpha	1	0.996	-2.18	0.275	-1.69	0.163	1.44	0.396	-0.36
1433551_at	AI427515	expressed sequence AI427515	-3.38	0.031	-1.71	0.044	1.17	0.724	1.64	0.255	-0.57
1439592_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	-2.34	0.18	-1.74	0.423	1.05	0.921	1.25	0.676	-0.44
1431917_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	-2.41	0.115	-1.75	0.408	1.07	0.873	1.59	0.579	-0.37
1450763_x_at	Wnt3	wingless-related MMTV integration site 3	-3.48	0.066	1.18	0.391	-1.68	0.462	1.23	0.759	-0.69
1443101_at	Grid2	Glutamate receptor, ionotropic, delta 2	1.02	0.942	-2.12	0.395	-1.74	0.132	1.57	0.41	-0.32
1445335_at	C78888	expressed sequence C78888	-1.64	0.127	-2.75	0.076	1.1	0.838	1.22	0.567	-0.52
1420431_at	Rptn	repetin	-2.87	0.059	1.1	0.881	-1.61	0.221	1.36	0.611	-0.51
1459110_at	Myo9b	Myosin IXb	-2.37	0.073	-1.58	0.133	1.01	0.968	1.45	0.185	-0.37
1458749_at	Ssbp3	Single-stranded DNA binding protein 3	-2.16	0.321	-2.93	0.292	1.27	0.52	1.02	0.834	-0.7
1419795_at	AA517631	expressed sequence AA517631	-2.66	0.221	-1.45	0.485	1	0.995	2.16	0.254	-0.23
1456674_at	E130016E03Rik	RIKEN cDNA E130016E03 gene	-1.62	0.28	-2.46	0.108	1.05	0.905	2.54	0.249	-0.12
1439285_at	Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-2.34	0.004	-1.8	0.335	1.09	0.766	3.3	0.003	0.06
1421354_at	Prkg2	protein kinase, cGMP-dependent, type II	-2.84	0.062	-1.41	0.217	1.02	0.914	1.09	0.85	-0.54
1432406_at	Ces7	carboxylesterase 7	1.13	0.798	-1.92	0.349	-2.37	0.037	3.36	0.039	0.05
1430757_at	A330102H22Rik	RIKEN cDNA A330102H22 gene	-1.38	0.677	-2.86	0.029	1	0.986	1.42	0.451	-0.45
1434249_s_at	---	---	1.11	0.91	-2.91	0.149	-1.59	0.225	1.29	0.739	-0.53
1451615_at	BC026374	cDNA sequence BC026374	-2.49	0.179	-2.2	0.082	1.23	0.15	1.33	0.291	-0.53
1416169_at	Tpbpb	trophoblast specific protein beta	1.18	0.248	-3.22	0.24	-1.69	0.033	1.27	0.605	-0.61
1460070_at	Chst2	Carbohydrate sulfotransferase 2	-1.46	0.326	1.12	0.683	-3.67	0.14	1.06	0.714	-0.74
1435513_at	Htr2c	5-hydroxytryptamine (serotonin) receptor 2C	-1.59	0.276	-4.03	0.005	1.21	0.52	2.38	0.056	-0.51
1459364_at	C230094A16Rik	RIKEN cDNA C230094A16 gene	-1.98	0.171	-2.07	0.205	1.1	0.82	1.74	0.306	-0.3
1431504_at	2310061N02Rik	RIKEN cDNA 2310061N02 gene	1.36	0.409	-2.96	0.006	-2.58	0.188	1.35	0.307	-0.71
1442021_at	Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type	-4.37	0.087	-1.7	0.425	1.27	0.392	1.76	0.162	-0.76
1432479_at	---	Mus musculus, clone IMAGE:6772209, mRNA	-2.04	0.087	1.23	0.58	-2.71	0.132	1.41	0.31	-0.53
1452479_at	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2	-2.73	0.071	-1.53	0.123	1.07	0.844	1.49	0.553	-0.43
1441142_at	2700081L22Rik	RIKEN cDNA 2700081L22 gene	1.12	0.669	-2.55	0.29	-1.74	0.408	3.56	0.212	0.1
1460078_at	G630024C07Rik	RIKEN cDNA G630024C07 gene	-1.8	0.359	-2.34	0.121	1.11	0.802	1.64	0.281	-0.35
1442711_at	---	Transcribed locus	-1.72	0.255	-1.96	0.363	1	0.998	2.45	0.283	-0.06
1443606_at	---	Transcribed locus	-1.88	0.128	1.1	0.872	-2.17	0.103	1.08	0.914	-0.47
1443138_at	Sult5a1	Sulfotransferase family 5A, member 1	1.09	0.865	-2.43	0.004	-1.68	0.112	1.93	0.324	-0.27
1421262_at	Lipg	lipase, endothelial	1.17	0.518	-2.01	0.181	-2.33	0	2.66	0.303	-0.13
1454299_at	4833422B07Rik	RIKEN cDNA 4833422B07 gene	1.13	0.701	-2.98	0.027	-1.58	0.053	1.07	0.647	-0.59
1458175_at	Spon2	spondin 2, extracellular matrix protein	-1.98	0.183	-1.71	0.167	1.02	0.947	1.01	0.978	-0.42
1455799_at	Rorb	RAR-related orphan receptor beta	-2.71	0.378	-2.75	0.042	1.37	0.512	1.45	0.696	-0.66
1432470_at	1700016A09Rik	RIKEN cDNA 1700016A09 gene	-3.34	0.011	-1.54	0.24	1.16	0.734	1.09	0.789	-0.66
1445852_at	D19Ertd200e	DNA segment, Chr 19, ERATO Doi 200, expressed	-1.64	0.426	1.07	0.864	-2.32	0.065	1.47	0.628	-0.36
1459650_at	Terf2	telomeric repeat binding factor 2	-1.9	0.468	1.08	0.837	-2.01	0.073	1.37	0.417	-0.36
1457765_at	Psmd14	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	1.1	0.883	-4.22	0.048	-1.3	0.24	1.17	0.53	-0.81
1458522_at	---	---	1.04	0.916	-1.27	0.659	-3.53	0.001	1.46	0.423	-0.57
1441913_at	Luzp2	leucine zipper protein 2	-1.56	0.449	-2.2	0.183	1.02	0.924	1.29	0.711	-0.36
1457286_at	Hint1	Histidine triad nucleotide binding protein 1	-2.13	0.413	1.16	0.631	-2.05	0.271	1.56	0.306	-0.36
1431215_at	Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	-5.04	0.215	1.22	0.808	-1.44	0.283	1.1	0.878	-1.04
1426328_a_at	Scn3b	sodium channel, voltage-gated, type III, beta	-1.9	0.311	-1.78	0.304	1.03	0.952	1.68	0.063	-0.24
1452019_at	Cyyr1	cysteine and tyrosine-rich protein 1	-3.2	0.095	-1.55	0.369	1.16	0.74	2.35	0.14	-0.31
1427597_at	Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	1.01	0.981	-1.21	0.769	-3.57	0.004	1.5	0.591	-0.57
1449537_at	Msh5	mutS homolog 5 (E. coli)	-1.74	0.282	-2.18	0.255	1.08	0.853	2.67	0.137	-0.04
1431956_at	5830453K13Rik	RIKEN cDNA 5830453K13 gene	-2.78	0.183	1.05	0.83	-1.42	0.019	1.42	0.44	-0.43

1436105_at	2310015A05Rik	RIKEN cDNA 2310015A05 gene	-2.44	0.097	-1.52	0.499	1.05	0.861	2.93	0.094	0.01
1436671_at	A030011M19	hypothetical protein A030011M19	1.08	0.79	-2.76	0.09	-1.47	0.499	1.4	0.587	-0.44
1432545_at	Dcst1	DC-STAMP domain containing 1	-1.61	0.104	-2.06	0.165	1.01	0.982	1.22	0.422	-0.36
1449532_at	Chrng	cholinergic receptor, nicotinic, gamma polypeptide	-3	0.322	1.01	0.977	-1.28	0.377	1.19	0.502	-0.52
1422228_at	Wnt8a	wingless-related MMTV integration site 8A	-2.07	0.029	-2.08	0.187	1.16	0.467	1.28	0.588	-0.43
1432134_at	Spdya	speedy homolog A (Drosophila)	1.18	0.78	-2.07	0.348	-2.15	0.148	1.49	0.415	-0.39
1458911_at	C230086A09Rik	RIKEN cDNA C230086A09 gene	-3.19	0.422	-1.24	0.468	1	0.984	1.38	0.524	-0.51
1432075_a_at	Tekt1	tektin 1	-1.21	0.599	-4.16	0.013	1.06	0.78	1.81	0.284	-0.62
1418471_at	Pgf	placental growth factor	-1.97	0.011	-1.64	0.387	1.01	0.955	2.29	0.016	-0.08
1432576_at	1700084C06Rik	RIKEN cDNA 1700084C06 gene	-2.17	0.103	-1.56	0.156	1.03	0.91	1.5	0.481	-0.3
1442652_at	Gm410	gene model 410, (NCBI)	-1.53	0.106	-2.57	0.024	1.08	0.352	1.02	0.895	-0.5
1445584_at	---	---	-2.2	0.235	1.21	0.713	-2.14	0.169	2.09	0.001	-0.26
1444645_at	Sertad2	SERTA domain containing 2	1.02	0.979	-1.79	0.039	-1.81	0.237	1.35	0.719	-0.31
1432604_at	Rbl1	retinoblastoma-like 1 (p107)	1.01	0.945	-1.86	0.118	-1.73	0.138	1.82	0.094	-0.19
1453031_at	0610009B10Rik	RIKEN cDNA 0610009B10 gene	1.09	0.077	-4.41	0.1	-1.22	0.59	1.69	0.106	-0.72
1420799_at	Ntsr1	neurotensin receptor 1	-2.31	0.247	-1.53	0.628	1.05	0.852	1.74	0.176	-0.26
1453574_at	Hba-a1	hemoglobin alpha, adult chain 1	-3.34	0.144	-1.77	0.357	1.27	0.495	1.29	0.666	-0.64
1443343_at	---	---	-3.8	0.071	-2.11	0.174	1.4	0.545	2.81	0.315	-0.43
1447548_at	Abhd5	abhydrolase domain containing 5	-1.4	0.26	-3.16	0.144	1.1	0.802	1.35	0.231	-0.53
1446945_at	Cdc42bpa	Cdc42 binding protein kinase alpha	1.05	0.878	-1.66	0.1	-2.09	0.051	1.1	0.751	-0.4
1439290_at	Fxr1h	Fragile X mental retardation gene 1, autosomal homolog	1.02	0.963	-1.52	0.283	-2.18	0.039	1.01	0.984	-0.42
1449706_s_at	Nr5a2	nuclear receptor subfamily 5, group A, member 2	-1.8	0.435	1.04	0.669	-1.83	0.169	1.06	0.902	-0.39
1458471_at	Wac	WW domain containing adaptor with coiled-coil	-1.77	0.594	1.07	0.743	-1.99	0.127	1.75	0.293	-0.24
1447080_at	---	---	1.02	0.905	-2.22	0.037	-1.5	0.386	1.14	0.601	-0.39
1422131_at	Dcp1a	decapping enzyme	-2.35	0.166	-1.77	0.289	1.15	0.43	1.18	0.704	-0.45
1442223_at	Enah	Enabled homolog (Drosophila)	1.18	0.154	-1.98	0.063	-2.2	0.001	1.43	0.589	-0.39
1452332_at	Ccdc85a	coiled-coil domain containing 85A	1.01	0.965	-2.16	0.11	-1.51	0.234	1.1	0.877	-0.39
1428899_at	2310079P10Rik	RIKEN cDNA 2310079P10 gene	-1.9	0.005	-1.99	0.153	1.11	0.822	1.08	0.899	-0.43
1442467_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	1.27	0.823	-3.55	0.028	-1.71	0.163	1.02	0.978	-0.74
1431445_at	4921509A18Rik	RIKEN cDNA 4921509A18 gene	1.28	0.047	-2.66	0.269	-2.06	0.274	1.23	0.568	-0.55
1437018_at	Pnma2	paraneoplastic antigen MA2	-2.8	0.06	1.07	0.742	-1.41	0.35	1.84	0.317	-0.32
1444891_at	---	---	1.15	0.457	-1.7	0.219	-2.49	0.102	2.7	0.347	-0.09
1431595_at	2900064B16Rik	RIKEN cDNA 2900064B16 gene	-1.97	0.125	-1.61	0.095	1.01	0.969	1.23	0.544	-0.33
1445663_at	---	---	-2.65	0.13	-1.62	0.494	1.15	0.861	3.02	0.259	-0.03
1445528_at	Slc28a3	Solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	1.16	0.34	-1.69	0.495	-2.53	0.189	1.17	0.636	-0.47
1459221_at	---	---	-2.12	0.463	-2.33	0.337	1.24	0.295	1.43	0.324	-0.45
1449307_at	Dbndd1	dysbindin (dystrobrevin binding protein 1) domain containing 1	-2.56	0.01	-1.62	0.469	1.14	0.41	1.64	0.213	-0.35
1448051_at	---	---	-2.38	0.061	-1.51	0.208	1.07	0.705	1.54	0.424	-0.32
1425717_at	Lrba	LPS-responsive beige-like anchor	-1.78	0.248	-2.52	0.104	1.19	0.738	1.08	0.813	-0.51
1421430_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	-3.04	0.046	1.18	0.811	-1.57	0.005	1.68	0.327	-0.44
1453990_at	4930554G24Rik	RIKEN cDNA 4930554G24 gene	-2.5	0.109	1.09	0.899	-1.51	0.416	1.09	0.803	-0.46
1432891_at	5730564L20Rik	RIKEN cDNA 5730564L20 gene	1.14	0.322	-1.57	0.251	-2.66	0.01	1.31	0.506	-0.45
1443697_at	---	---	1.31	0.782	-2.32	0.051	-2.41	0.003	1	0.991	-0.61
1446677_at	A830029E22Rik	RIKEN cDNA A830029E22 gene	-1.77	0.371	1.05	0.819	-1.87	0.103	1.02	0.963	-0.39
1447015_at	---	---	-1.9	0.441	-2.6	0.209	1.24	0.587	1.15	0.798	-0.53
1445342_at	---	---	-3.8	0.034	-1.78	0.511	1.33	0.175	2.99	0.03	-0.32
1420060_s_at	AA675344	expressed sequence AA675344	-1.59	0.573	-2.34	0.233	1.1	0.85	1.86	0.078	-0.24
1416833_at	Keg1	kidney expressed gene 1	-1.3	0.047	-2.63	0.05	1.01	0.97	1.73	0.02	-0.3
1433030_at	5730406E14Rik	RIKEN cDNA 5730406E14 gene	-3.25	0.329	1.1	0.826	-1.33	0.42	1.02	0.976	-0.62
1441312_at	Cnnm1	Cyclin M1	-1.54	0.285	-2.76	0.07	1.14	0.683	2	0.148	-0.29
1418549_at	Cga	glycoprotein hormones, alpha subunit	-3.03	0.248	1.01	0.982	-1.22	0.501	1.09	0.562	-0.54
1436439_at	LOC666145 /// LOC	hypothetical protein LOC666145 /// hypothetical protein LOC672141 /// hypothetic	-4.84	0.28	-1.62	0.313	1.33	0.454	1.37	0.45	-0.94
1449761_at	AA589418	expressed sequence AA589418	-3.17	0.146	1.18	0.709	-1.51	0.49	1.61	0.18	-0.47

1443389_at	Egln1	EGL nine homolog 1 (C. elegans)	-1.53	0.616	1.02	0.971	-2.03	0.27	1.13	0.84	-0.35
1441569_at	E330009P21Rik	RIKEN cDNA E330009P21 gene	-4.34	0.392	1.32	0.023	-1.64	0.52	2.07	0.193	-0.65
1450303_at	Vax2	ventral anterior homeobox containing gene 2	-3.55	0.187	-1.4	0.52	1.16	0.578	1.7	0.191	-0.52
1431773_at	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	-1.36	0.312	-2.56	0.016	1.03	0.935	1.11	0.791	-0.44
1457157_at	Plch1	phospholipase C, eta 1	-1.55	0.098	-1.93	0.088	1	0.997	1.15	0.697	-0.33
1423227_at	Krt17	keratin 17	-1.97	0.409	1.02	0.968	-1.57	0.499	1.1	0.885	-0.36
1444477_at	Lrrtm3	Leucine rich repeat transmembrane neuronal 3	-2.57	0.127	1.09	0.897	-1.45	0.332	1.13	0.841	-0.45
1432644_at	6430711C07Rik	RIKEN cDNA 6430711C07 gene	-1.25	0.797	1.03	0.909	-2.95	0.031	1.61	0.425	-0.39
1446350_at	Itga4	Integrin alpha 4	1.07	0.704	-1.64	0.414	-2.05	0.079	2.11	0.402	-0.13
1447221_x_at	Fgf14	Fibroblast growth factor 14	1.34	0.683	-2.73	0.009	-2.16	0.256	2.2	0.053	-0.34
1458875_at	Sec24b	SEC24 related gene family, member B (S. cerevisiae)	1.03	0.91	-2.38	0.269	-1.4	0.368	1	0.996	-0.44
1441897_at	B230120H23Rik	RIKEN cDNA B230120H23 gene	-1.87	0.227	1.05	0.938	-1.72	0.052	1.56	0.568	-0.25
1454128_at	4930413E15Rik	RIKEN cDNA 4930413E15 gene	-1.98	0.341	1.07	0.446	-1.68	0.225	1.14	0.627	-0.36
1431927_at	5033417F24Rik	RIKEN cDNA 5033417F24 gene	-1.61	0.165	-2.13	0.223	1.08	0.827	1.03	0.965	-0.41
1419632_at	Tecta	tectorin alpha	-1.4	0.71	1.06	0.927	-2.52	0.015	1.16	0.695	-0.43
1456636_at	4930414L22Rik	RIKEN cDNA 4930414L22 gene	-2.34	0.243	-1.49	0.505	1.07	0.817	1.72	0.101	-0.26
1445714_at	B930042K01Rik	RIKEN cDNA B930042K01 gene	-2.85	0.314	1.22	0.647	-1.67	0.104	1.37	0.413	-0.48
1427750_at	Igk-V1	Immunoglobulin kappa chain variable 1 (V1)	-1.9	0.033	-1.84	0.27	1.11	0.846	1.43	0.532	-0.3
1449104_at	Upk3a	uroplakin 3A	-2.13	0.098	-2.35	0.081	1.28	0.408	1.34	0.621	-0.46
1425573_a_at	Ddef1	development and differentiation enhancing	-1.86	0.321	-1.76	0.273	1.07	0.852	1.35	0.529	-0.3
1429580_x_at	5133400G04Rik	RIKEN cDNA 5133400G04 gene	-2.59	0.067	-1.92	0.042	1.27	0.139	1.22	0.406	-0.5
1420242_at	---	---	1.11	0.564	-2.1	0.025	-1.69	0.106	1.14	0.578	-0.39
1434259_at	LOC666811	similar to H2A histone family, member J	-4.62	0.386	-1.16	0.101	1.1	0.852	1.9	0.042	-0.69
1445858_at	4933439G19Rik	RIKEN cDNA 4933439G19 gene	-1.69	0.012	-2.53	0.051	1.19	0.569	1.18	0.685	-0.46
1444698_at	Qk	Quaking	-1.68	0.185	1.04	0.937	-1.85	0.19	1.45	0.288	-0.26
1453791_at	2810449C10Rik	RIKEN cDNA 2810449C10 gene	-3.74	0.205	1	0.998	-1.1	0.756	1.03	0.944	-0.7
1457428_at	C230040D14	hypothetical protein C230040D14	-2.41	0.345	-1.6	0.174	1.14	0.796	1.35	0.681	-0.38
1456291_x_at	Scx	scleraxis	-1.92	0.287	1.11	0.869	-1.83	0.052	1.2	0.712	-0.36
1422242_at	Defcr-rs10	defensin related cryptdin, related sequence 10	-4.69	0.052	-1.48	0.403	1.29	0.694	1.73	0.271	-0.79
1440673_at	Exod1	Exonuclease domain containing 1	1.07	0.843	-1.51	0.401	-2.24	0.15	1.2	0.781	-0.37
1429258_at	1110025D03Rik	RIKEN cDNA 1110025D03 gene	1.12	0.891	-1.58	0.126	-2.36	0.15	1.24	0.282	-0.39
1432837_at	2700080J24Rik	RIKEN cDNA 2700080J24 gene	-2.36	0.032	-1.47	0.097	1.08	0.847	1.46	0.441	-0.32
1445713_at	9630041G16Rik	RIKEN cDNA 9630041G16 gene	1.04	0.921	-1.82	0.505	-1.67	0.318	1.41	0.574	-0.26
1454029_at	4930431F12Rik	RIKEN cDNA 4930431F12 gene	-1.68	0.176	-2.36	0.088	1.16	0.684	1.14	0.83	-0.43
1439939_at	E030042N06Rik	RIKEN cDNA E030042N06 gene	1.31	0.654	-1.96	0.214	-2.74	0.093	1.14	0.601	-0.56
1452077_at	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	1.3	0.356	-2.98	0.003	-1.8	0.098	1.75	0.575	-0.43
1445402_at	Adk	Adenosine kinase	1.05	0.964	-1.44	0.344	-2.28	0.046	1.81	0.097	-0.21
1439919_at	---	Transcribed locus	-2.04	0.472	-1.53	0.369	1.05	0.919	1.4	0.44	-0.28
1454415_at	Safb	scaffold attachment factor B	1.11	0.882	-1.61	0.449	-2.16	0.076	3.08	0.033	0.1
1434734_at	E130016E03Rik	RIKEN cDNA E130016E03 gene	1.02	0.683	-2.97	0.003	-1.2	0.811	2.6	0.144	-0.14
1446821_at	Pcdh17	Protocadherin 17	-2.08	0.298	-2.93	0.229	1.37	0.486	1.7	0.334	-0.48
1436190_at	Nedd10	neural precursor cell expressed, developmentally down-regulated gene 10	-1.37	0.174	-2.68	0.048	1.09	0.8	1.13	0.589	-0.46
1441302_at	---	---	1.01	0.99	-2.53	0.223	-1.27	0.505	1.3	0.488	-0.37
1427365_at	krt86	keratin 86	-1.56	0.325	-1.83	0.303	1.01	0.987	1.03	0.952	-0.34
1419735_at	Csn3	casein kappa	-2.27	0.233	-1.38	0.65	1.03	0.903	6.73	0.157	1.03
1421807_at	Defb6	defensin beta 6	-3	0.124	1.33	0.474	-1.88	0.314	1.58	0.367	-0.49
1443585_at	Zfp526	zinc finger protein 526	-2.15	0.189	1.02	0.969	-1.41	0.525	1.39	0.642	-0.29
1454340_at	9530025H10Rik	RIKEN cDNA 9530025H10 gene	1.08	0.896	-1.6	0.468	-2.02	0.076	1.06	0.837	-0.37
1440142_s_at	Gfap	glial fibrillary acidic protein	-1.94	0.061	-1.62	0.219	1.07	0.751	2.71	0.384	0.06
1446986_at	Scrt2	scratch homolog 2, zinc finger protein (Drosophila)	-2.38	0.42	-1.3	0.644	1.01	0.985	1.07	0.749	-0.4
1421514_a_at	Scml2	sex comb on midleg-like 2 (Drosophila)	-3.77	0.074	1.05	0.911	-1.13	0.573	1.21	0.774	-0.66
1440134_at	Cyp4a10 /// BC013	cytochrome P450, family 4, subfamily a, polypeptide 10 /// cDNA sequence BC01	1.03	0.838	-2.03	0.09	-1.46	0.378	1.28	0.614	-0.3
1460511_at	Pkp2	plakophilin 2	1.02	0.953	-1.43	0.406	-2.07	0.011	2.08	0.131	-0.1

1446749_at	Ktn1	kinectin 1	1.55	0.413	-3.62	0.11	-2.64	0.056	1.77	0.3	-0.73
1443787_x_at	Casp14	Caspase 14	-2.09	0.159	-1.68	0.022	1.14	0.624	1.41	0.111	-0.31
1437188_at	Gabbr1	gamma-aminobutyric acid (GABA-B) receptor, 1	1	0.994	-2.16	0.27	-1.34	0.036	1.04	0.904	-0.37
1430913_at	1810033M07Rik	RIKEN cDNA 1810033M07 gene	1.11	0.831	-1.77	0.117	-1.87	0.249	1.11	0.715	-0.35
1432361_a_at	Cenpp	centromere protein P	-1.58	0.411	-2.25	0.111	1.13	0.776	4.39	0.197	0.42
1443220_at	Rtn3	Reticulon 3	1.04	0.761	-1.86	0.186	-1.56	0.052	1.32	0.606	-0.27
1454395_at	4632404M16Rik	RIKEN cDNA 4632404M16 gene	-1.66	0.117	-2.09	0.205	1.13	0.597	1.06	0.687	-0.39
1440738_at	B020011L13Rik	RIKEN cDNA B020011L13 gene	-1.3	0.166	-2.63	0.177	1.06	0.632	1.19	0.509	-0.42
1441625_at	Rimbp2 /// LOC637	RIMS binding protein 2 /// similar to RIM binding protein 2 (RIM-BP2)	1.02	0.959	-1.83	0.392	-1.55	0.319	1.18	0.697	-0.3
1443483_at	Xlr5d	X-linked lymphocyte-regulated 5D	-1.98	0.435	-2.2	0.342	1.25	0.575	1.33	0.744	-0.4
1455560_at	Zfp653	Zinc finger protein 653	-1.22	0.641	-2.89	0.033	1.05	0.93	1.03	0.924	-0.51
1417537_at	Zmat2	zinc finger, matrin type 2	-2.53	0.033	-1.38	0.478	1.09	0.839	1.5	0.364	-0.33
1428399_a_at	Armc9	armadillo repeat containing 9	-1.75	0.064	-2.99	0.007	1.31	0.531	2.01	0.389	-0.36
1459891_at	C78444	expressed sequence C78444	-1.72	0.645	-1.76	0.351	1.07	0.888	1.66	0.4	-0.19
1456935_at	AI606473	expressed sequence AI606473	-2.58	0.26	1.07	0.773	-1.31	0.386	1.07	0.82	-0.44
1436721_x_at	Oog3	oogenesin 3	-1.82	0.375	-3.45	0.156	1.38	0.438	1.19	0.768	-0.67
1445319_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930509G02 pr	-2.93	0.096	-1.61	0.269	1.25	0.345	1.76	0.267	-0.38
1444394_at	Acad9	acyl-Coenzyme A dehydrogenase family, member 9	-2.17	0.101	-1.72	0.155	1.18	0.666	1.43	0.559	-0.32
1453673_at	Atp13a4	ATPase type 13A4	-2.41	0.034	1.12	0.717	-1.46	0.086	1.08	0.783	-0.42
1419136_at	Akr1c18	aldo-keto reductase family 1, member C18	-2.76	0.009	-3.42	0.005	1.56	0.274	3.97	0.059	-0.16
1454298_at	4932430A15Rik	RIKEN cDNA 4932430A15 gene	-1.86	0.014	1.04	0.938	-1.55	0.337	2.09	0.182	-0.07
1445655_at	---	Transcribed locus	-2.24	0.34	1.06	0.922	-1.4	0.427	1.04	0.954	-0.39
1421687_at	Msmb	beta-microseminoprotein	-2.49	0.144	-2.02	0.305	1.32	0.62	2.28	0.03	-0.23
1429098_s_at	Nhej1	nonhomologous end-joining factor 1	1.01	0.963	-1.62	0.077	-1.69	0.118	1.03	0.924	-0.32
1439279_at	3110007F17Rik	RIKEN cDNA 3110007F17 gene	-1.83	0.172	1.05	0.905	-1.61	0.009	2.07	0.184	-0.08
1445383_at	Tmem44	transmembrane protein 44	-2.44	0.292	-1.49	0.339	1.14	0.51	1.17	0.76	-0.4
1447076_at	Nell1	NEL-like 1 (chicken)	-2.66	0.249	-1.52	0.605	1.19	0.649	1.48	0.596	-0.38
1445520_at	Rab4a	RAB4A, member RAS oncogene family	-2.87	0.086	1.08	0.806	-1.26	0.483	3.17	0.037	0.03
1420026_at	Aak1	AP2 associated kinase 1	-3.58	0.043	1.15	0.788	-1.26	0.412	1.47	0.174	-0.56
1458543_at	---	---	1.07	0.915	-3.63	0.213	-1.14	0.755	1.22	0.78	-0.62
1432020_at	6330411D24Rik	RIKEN cDNA 6330411D24 gene	1.27	0.697	-1.78	0.341	-2.55	0.128	1.95	0.042	-0.28
1440110_at	B130019D13Rik	RIKEN cDNA B130019D13 gene	-2.39	0.209	-1.68	0.185	1.21	0.394	1.07	0.808	-0.45
1420194_at	---	---	-2.25	0.097	1.26	0.748	-1.9	0.155	1.17	0.83	-0.43
1420022_s_at	Suz12	Suppressor of zeste 12 homolog (Drosophila)	1.01	0.967	-1.75	0.058	-1.54	0.138	1.12	0.738	-0.29
1445060_at	D5Ertd470e	DNA segment, Chr 5, ERATO Doi 470, expressed	1.06	0.948	-2.21	0.327	-1.39	0.38	1.04	0.929	-0.38
1451268_at	Tram1l1	translocation associated membrane protein 1-like 1	1.25	0.498	-1.51	0.519	-3.16	0.006	1.89	0.343	-0.38
1425980_at	Wdr54	WD repeat domain 54	-1.69	0.518	-1.89	0.078	1.11	0.44	1.45	0.531	-0.26
1430482_at	---	---	-1.79	0.427	1	0.984	-1.5	0.424	1.11	0.772	-0.29
1452640_at	3110007F17Rik /// I	RIKEN cDNA 3110007F17 gene /// hypothetical LOC546368 /// hypothetical LOC	1.02	0.948	-1.77	0.218	-1.54	0.081	1.18	0.302	-0.28
1425103_at	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2	-1.06	0.832	-3.83	0.13	1.02	0.913	1.18	0.417	-0.67
1449825_at	Actrt1	actin-related protein T1	-1.28	0.716	1.05	0.904	-2.55	0.12	1.27	0.48	-0.37
1426340_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	1.02	0.942	-1.99	0.336	-1.41	0.118	1.11	0.622	-0.32
1436763_a_at	Klf9	Kruppel-like factor 9	-1.92	0.315	-1.52	0.064	1.05	0.867	1.07	0.905	-0.33
1443509_at	Cdh1	Cadherin 1	1.03	0.943	-1.38	0.412	-2.07	0.016	1.85	0.229	-0.14
1453398_at	A930009A15Rik	RIKEN cDNA A930009A15 gene	-1.69	0.135	-1.78	0.227	1.08	0.806	1.92	0.247	-0.12
1444997_at	Prdm1	PR domain containing 1, with ZNF domain	-1.62	0.594	-3.72	0.088	1.35	0.532	1.44	0.691	-0.64
1445579_at	Alox12e	arachidonate lipoxygenase, epidermal	-1.08	0.129	-3.31	0.252	1.01	0.987	1.09	0.754	-0.57
1458651_at	Map3k10	Mitogen activated protein kinase kinase kinase 10	-4.05	0.052	-1.87	0.376	1.45	0.148	3.81	0.073	-0.16
1432914_at	Lrrc52	leucine rich repeat containing 52	1.16	0.807	-3.31	0.055	-1.29	0.49	1.95	0.25	-0.37
1445715_at	A230001M10Rik	RIKEN cDNA A230001M10 gene	-1.79	0.219	-1.93	0.141	1.16	0.625	1.12	0.694	-0.36
1447808_s_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	1.16	0.327	-1.95	0.135	-1.78	0.044	1.13	0.685	-0.36
1447395_at	4930525K10Rik	RIKEN cDNA 4930525K10 gene	-7.05	0.074	1.11	0.506	-1.01	0.944	1.35	0.359	-1.4
1457803_at	Prkag1	Protein kinase, AMP-activated, gamma 1 non-catalytic subunit	-1.94	0.221	1.24	0.635	-2.08	0.091	1.29	0.14	-0.37

1458985_at	Fry	furry homolog (Drosophila)	-2.06	0.076	1.03	0.929	-1.39	0.086	1.27	0.491	-0.29
1447489_at	1110039B18Rik	RIKEN cDNA 1110039B18 gene	-1.66	0.275	1.08	0.876	-1.78	0.254	1.44	0.002	-0.23
1421584_at	Opn4	opsin 4 (melanopsin)	-2.02	0.136	-1.44	0.195	1.05	0.686	1.15	0.68	-0.31
1441057_at	Myh10	Myosin, heavy polypeptide 10, non-muscle	-2.86	0.046	1.29	0.263	-1.67	0.365	2.38	0.179	-0.21
1427400_at	Lbx1	ladybird homeobox homolog 1 (Drosophila)	-2.23	0.114	1.07	0.819	-1.38	0.214	1.39	0.363	-0.29
1459187_at	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	1.01	0.868	-1.28	0.461	-2.25	0.047	1.52	0.193	-0.25
1433183_at	6720477C19Rik	RIKEN cDNA 6720477C19 gene	-2.48	0.291	1.39	0.537	-2.21	0.072	1.11	0.906	-0.55
1441710_at	---	Transcribed locus	-1.26	0.525	-3.28	0.173	1.15	0.613	2.1	0.193	-0.33
1431307_at	4930589M24Rik	RIKEN cDNA 4930589M24 gene	-1.48	0.044	-2.22	0.272	1.12	0.763	1.33	0.625	-0.31
1436600_at	Tnrc9	trinucleotide repeat containing 9	1.02	0.907	-2.76	0.11	-1.16	0.435	4.04	0.016	0.29
1459892_at	AA408156	expressed sequence AA408156	-3.8	0.131	1.21	0.633	-1.3	0.359	1.02	0.962	-0.72
1449869_at	Vpreb1	pre-B lymphocyte gene 1	-1.19	0.276	1	0.993	-2.5	0.12	1.61	0.358	-0.27
1421400_at	Kcnmb1	potassium large conductance calcium-activated channel, subfamily M, beta meml	-1.7	0.317	-1.71	0.511	1.07	0.685	1.54	0.251	-0.2
1431643_at	Speer6-ps1	spermatogenesis associated glutamate (E)-rich protein 6, pseudogene 1	1.17	0.598	-2.17	0.07	-1.61	0.175	1.03	0.945	-0.4
1432959_at	4930447I22Rik	RIKEN cDNA 4930447I22 gene	-1.82	0.146	-1.77	0.21	1.14	0.71	1.38	0.224	-0.27
1446093_at	---	---	-1.86	0.354	1.02	0.914	-1.44	0.111	1.66	0.5	-0.16
1459761_x_at	Igsf4d	immunoglobulin superfamily, member 4	-4.03	0.018	-1.04	0.933	1.04	0.868	1.08	0.876	-0.74
1454237_at	Spata9	spermatogenesis associated 9	-1.75	0.01	-1.52	0.363	1.02	0.969	1.13	0.77	-0.28
1422383_at	V1rb6	vomeronasal 1 receptor, B6	1.14	0.336	-4.64	0	-1.12	0.551	1.17	0.37	-0.86
1420379_at	Slco1a1	solute carrier organic anion transporter family, member 1a1	1.21	0.714	-110.9	0.077	1.03	0.861	-1.65	0.493	-27.56
1416851_at	St13	Suppression of tumorigenicity 13	-2.03	0.267	1.06	0.897	-1.44	0.231	1.36	0.348	-0.26
1444080_at	---	---	1.11	0.893	-2.48	0.013	-1.36	0.64	1.01	0.93	-0.43
1436112_at	AI118078	expressed sequence AI118078	-2.34	0.17	1.35	0.558	-2.1	0.107	1.56	0.53	-0.38
1419931_at	Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	1.13	0.413	-1.7	0.151	-1.86	0.035	1.14	0.629	-0.33
1443309_at	Pdzrn3	PDZ domain containing RING finger 3	-1.85	0.441	1.25	0.676	-2.17	0.241	1.21	0.534	-0.39
1422337_at	Olfr156	olfactory receptor 156	-4.36	0.27	-1.21	0.829	1.2	0.675	1.21	0.444	-0.79
1455264_at	C1qdc2	C1q domain containing 2	-1.59	0.107	-1.66	0.425	1.02	0.927	2.85	0.123	0.16
1453305_at	Iqcd	IQ motif containing D	1.11	0.83	-2.68	0.083	-1.29	0.146	1.3	0.72	-0.39
1425029_a_at	Mboat2	membrane bound O-acyltransferase domain containing 2	-1.58	0.105	1.23	0.081	-2.57	0.008	3.32	0.198	0.1
1439674_at	Slc4a8	solute carrier family 4 (anion exchanger), member 8	-1.84	0.37	1.07	0.63	-1.56	0.14	1.43	0.202	-0.23
1425876_a_at	Glce	glucuronyl C5-epimerase	-2.13	0.095	-1.38	0.386	1.06	0.88	1.01	0.964	-0.36
1432024_at	2310015L07Rik	RIKEN cDNA 2310015L07 gene	-1.89	0.181	1.13	0.698	-1.67	0.056	1.61	0.332	-0.2
1453885_at	Slc24a2	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	-1.34	0.559	-3.86	0.089	1.25	0.659	1.25	0.371	-0.68
1456539_at	---	---	1.26	0.56	-4.57	0.115	-1.28	0.439	1.28	0.369	-0.83
1419000_at	Cpxm2	carboxypeptidase X 2 (M14 family)	-1.28	0.404	-3.24	0.001	1.17	0.608	1.21	0.443	-0.53
1456127_at	9630008K15Rik	RIKEN cDNA 9630008K15 gene	1	0.998	-1.46	0.241	-1.74	0.379	1.1	0.874	-0.27
1437065_at	Zbtb20	zinc finger and BTB domain containing 20	-1.43	0.035	1.01	0.895	-1.82	0.061	1.18	0.703	-0.26
1425212_a_at	Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	-2.05	0.235	-1.36	0.299	1.04	0.868	1.29	0.563	-0.27
1425499_at	LOC625794	Hypothetical protein LOC625794	-4.33	0.023	1.46	0.402	-1.74	0.515	1.35	0.698	-0.82
1427525_at	Cd151	CD151 antigen	-2.52	0.263	-1.49	0.037	1.2	0.199	1.51	0.298	-0.33
1450463_at	4833439L19Rik	RIKEN cDNA 4833439L19 gene	-1.53	0.108	-2.9	0.024	1.27	0.526	1.26	0.569	-0.48
1457403_at	9130409I23Rik	RIKEN cDNA 9130409I23 gene	-1.24	0.291	1.06	0.905	-2.51	0.157	1.26	0.552	-0.36
1432168_at	D730045A05Rik	RIKEN cDNA D730045A05 gene	-2.4	0.308	-1.53	0.45	1.19	0.708	1.07	0.845	-0.42
1443848_at	Rbm16	RNA binding motif protein 16	-1.94	0.156	1.14	0.712	-1.63	0.226	1.1	0.508	-0.33
1436807_x_at	Trim62	tripartite motif-containing 62	-1.64	0.618	-1.69	0.096	1.07	0.74	1.02	0.959	-0.31
1450827_at	Kif23	kinesin family member 23	-1.13	0.065	-6.5	0.015	1.23	0.591	2	0.34	-1.1
1453075_at	1600012P17Rik	RIKEN cDNA 1600012P17 gene	-2.44	0.047	-1.41	0.363	1.15	0.277	1.51	0.398	-0.3
1439829_at	Adcy5	Adenylate cyclase 5	-1.54	0.368	-1.69	0.214	1.03	0.945	1.48	0.024	-0.18
1442871_at	---	PREDICTED: Mus musculus similar to Nucleolar transcription factor 1 (Upstream	-1.49	0.308	1.08	0.902	-1.93	0.189	1.2	0.537	-0.29
1429230_at	Klk5	kallikrein 5	-1.64	0.274	-1.94	0.257	1.14	0.806	1.82	0.354	-0.15
1443368_at	---	2 cells egg cDNA, RIKEN full-length enriched library, clone:B020017L01 product:	-2.24	0.117	1.01	0.975	-1.23	0.676	1.19	0.372	-0.32
1415883_a_at	Ela3	elastase 3, pancreatic	-2.8	0.059	-2.05	0.316	1.43	0.529	2.37	0.272	-0.26
1422199_at	Omp	olfactory marker protein	1.12	0.608	-1.37	0.31	-2.34	0.264	1.08	0.871	-0.38

1433215_at	---	---	1.03	0.943	-2.51	0.001	-1.18	0.772	2.37	0.033	-0.07
1453394_at	2410017I17Rik	RIKEN cDNA 2410017I17 gene	-2.71	0.108	-1.24	0.485	1.1	0.733	1.18	0.812	-0.42
1450631_x_at	Defcr12 /// Defcr2 //	defensin related cryptdin 12 /// defensin related cryptdin 2 /// defensin related cryp	-1.46	0.549	1.17	0.723	-2.35	0.023	1.49	0.394	-0.29
1419533_at	Nhlh1	nescient helix loop helix 1	-3.55	0.077	1.62	0.535	-2.68	0.131	1.42	0.187	-0.8
1431790_at	4932412D23Rik	RIKEN cDNA 4932412D23 gene	-1.51	0.532	1.08	0.844	-1.87	0.097	1.01	0.982	-0.32
1437766_at	---	Transcribed locus	-4.57	0.244	-1.29	0.541	1.28	0.271	1.52	0.307	-0.76
1421970_a_at	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	1.17	0.509	-1.48	0.096	-2.31	0.121	1.37	0.203	-0.31
1427589_at	8430419L09Rik	RIKEN cDNA 8430419L09 gene	-2.35	0.331	-1.52	0.291	1.19	0.711	1.19	0.689	-0.37
1442115_at	9430028L06Rik	RIKEN cDNA 9430028L06 gene	-1.21	0.546	1.01	0.929	-2.28	0.014	1.78	0.478	-0.17
1440752_at	Sall4	Sal-like 4 (Drosophila)	-2.11	0.093	-1.28	0.544	1.03	0.961	1.09	0.831	-0.32
1456781_at	---	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830044	-1.27	0.765	1.06	0.902	-2.31	0.382	1.15	0.857	-0.34
1449177_at	Ccna1	cyclin A1	-2.03	0.447	1.2	0.672	-1.69	0.043	1.83	0.359	-0.18
1418298_s_at	Dpysl4	dihydropyrimidinase-like 4	-1.7	0.412	-1.86	0.101	1.16	0.492	1.13	0.604	-0.32
1446573_at	Edil3	EGF-like repeats and discoidin I-like domains 3	-1.25	0.696	1.02	0.964	-2.17	0.039	2.27	0.388	-0.03
1420837_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	1.03	0.942	-2.1	0.243	-1.3	0.628	1.28	0.005	-0.27
1432060_at	Iqca	IQ motif containing with AAA domain	-2.38	0.357	-1.47	0.358	1.18	0.625	1.23	0.576	-0.36
1459369_at	Epha6	Eph receptor A6	-3.23	0.433	1.17	0.856	-1.24	0.631	2.26	0.007	-0.26
1456371_a_at	Shroom1	shroom family member 1	-2.01	0.391	1.03	0.837	-1.33	0.574	1.34	0.424	-0.24
1427409_at	9-Mar	membrane-associated ring finger (C3HC4) 9	-2.09	0.016	-1.32	0.438	1.05	0.905	1.29	0.488	-0.27
1453831_at	Tmem138	transmembrane protein 138	-2.93	0.019	-2.7	0.151	1.57	0.446	1.35	0.566	-0.67
1458008_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.74	0.016	-1.48	0.437	1.04	0.921	1.31	0.384	-0.22
1445697_at	Itgb1bp1	Integrin beta 1 binding protein 1	-1.55	0.263	1.07	0.84	-1.75	0.122	1.49	0.16	-0.19
1459253_at	---	---	1.05	0.94	-2.16	0.229	-1.29	0.456	1.36	0.267	-0.26
1443432_at	AU022680	expressed sequence AU022680	1.02	0.981	-1.1	0.884	-2.8	0.069	1.03	0.919	-0.46
1440548_at	Btbd9	BTB (POZ) domain containing 9	-1.73	0.048	1.09	0.688	-1.63	0.047	1.5	0.32	-0.19
1449199_at	Muc1	mucin 1, transmembrane	1.12	0.04	-2.73	0.429	-1.25	0.105	1.42	0.462	-0.36
1443369_at	BC052055	cDNA sequence BC052055	1.06	0.727	-1.95	0.358	-1.4	0.062	1.19	0.584	-0.28
1420114_s_at	2410022L05Rik	RIKEN cDNA 2410022L05 gene	1.25	0.415	-1.62	0.341	-2.36	0.052	1.36	0.523	-0.34
1441485_at	Yipf6	Yip1 domain family, member 6	1.05	0.84	-1.72	0.114	-1.52	0.013	1.16	0.481	-0.26
1439198_at	Ptk2	PTK2 protein tyrosine kinase 2	1	0.987	-1.39	0.367	-1.78	0.192	1.09	0.579	-0.27
1444668_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930534N17 pr	-2.28	0.042	1.36	0.622	-2.02	0.061	1.23	0.303	-0.43
1447772_at	Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specif	-1.73	0.432	-1.91	0.105	1.19	0.653	1.78	0.276	-0.17
1441890_x_at	Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	1.08	0.73	-1.93	0.099	-1.45	0.101	1.69	0.404	-0.15
1438699_at	Srd5a1	steroid 5 alpha-reductase 1	-1.49	0.059	-1.75	0.072	1.05	0.745	1.72	0.138	-0.12
1431468_at	Crisp4	cysteine-rich secretory protein 4	-1.87	0.386	1.31	0.247	-2.25	0.299	1.43	0.064	-0.34
1416218_x_at	Rpl37a /// LOC629	ribosomal protein L37a /// similar to 60S ribosomal protein L37a /// similar to 60S	1.14	0.857	-2.13	0.052	-1.47	0.471	1.38	0.524	-0.27
1433301_at	4930478M09Rik	RIKEN cDNA 4930478M09 gene	-1.57	0.482	1.04	0.953	-1.62	0.264	1.32	0.442	-0.21
1418178_at	Ina	internexin neuronal intermediate filament protein, alpha	-1.46	0.38	1.05	0.812	-1.82	0.007	1.07	0.795	-0.29
1457044_at	4732474O15Rik	RIKEN cDNA 4732474O15 gene	1.2	0.373	-2.53	0.018	-1.44	0.015	1.17	0.709	-0.4
1453038_at	4930422G04Rik	RIKEN cDNA 4930422G04 gene	1.02	0.976	-2.35	0.302	-1.17	0.5	1.75	0.21	-0.19
1447377_at	Gm428 /// LOC623	gene model 428, (NCBI) /// hypothetical LOC623180 /// hypothetical LOC623197	-1.87	0.097	-1.75	0.123	1.19	0.177	1.31	0.53	-0.28
1430950_at	Osr2	odd-skipped related 2 (Drosophila)	-1.8	0.155	1.07	0.927	-1.5	0.509	1.25	0.527	-0.24
1459528_at	---	---	-2.76	0.014	-1.64	0.454	1.32	0.619	1.54	0.389	-0.38
1439402_at	---	---	-3.81	0.144	1.04	0.949	-1.01	0.967	2.12	0.17	-0.41
1452654_at	---	---	-1.43	0.478	-2.37	0.158	1.17	0.663	1.06	0.527	-0.39
1457868_at	Slc2a13	Solute carrier family 2 (facilitated glucose transporter), member 13	-1.48	0.165	1.18	0.851	-2.25	0.14	1.97	0.116	-0.14
1445600_at	Igf1r	Insulin-like growth factor I receptor	-1.43	0.094	1.1	0.599	-2.01	0.02	1.03	0.79	-0.33
1421629_at	Gabre	gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon	-3.28	0.072	1.08	0.88	-1.1	0.797	1.02	0.969	-0.57
1448716_at	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	-2.01	0.016	1.41	0.289	-2.57	0.135	1.08	0.765	-0.52
1447686_at	---	---	1.06	0.892	-1.66	0.453	-1.56	0.38	1.64	0.536	-0.13
1427782_a_at	Crhr1	corticotropin releasing hormone receptor 1	-2	0.465	-1.55	0.01	1.15	0.067	1.53	0.401	-0.22
1430262_at	5330411J11Rik	RIKEN cDNA 5330411J11 gene	-1.78	0.494	-2.15	0.034	1.27	0.589	1.11	0.903	-0.39
1458738_at	Gna14	Guanine nucleotide binding protein, alpha 14	-1.41	0.327	1.2	0.207	-2.56	0.005	1.36	0.405	-0.35

1422363_at	Olfr64	olfactory receptor 65	-2.19	0.477	-1.51	0.545	1.18	0.588	1.23	0.273	-0.32
1451682_at	Zfp142	zinc finger protein 142	-2.71	0.016	-1.28	0.664	1.15	0.771	1.11	0.721	-0.43
1445200_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	1.04	0.625	-1.22	0.458	-2.26	0.129	1.11	0.87	-0.33
1433584_at	Tuba1 /// LOC5448	tubulin, alpha 1 /// similar to tubulin, alpha 1	-1.93	0.12	-1.67	0.245	1.18	0.436	1.1	0.56	-0.33
1433233_at	5430425E15Rik	RIKEN cDNA 5430425E15 gene	1.24	0.257	-1.71	0.411	-2.1	0.171	1.39	0.466	-0.3
1447634_x_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	1.03	0.902	-2.03	0.022	-1.28	0.314	1.19	0.498	-0.27
1417415_at	Slc6a3	solute carrier family 6 (neurotransmitter transporter, dopamine), member 3	-2.32	0.463	-1.76	0.17	1.3	0.606	1.49	0.584	-0.32
1419294_at	1700011H14Rik	RIKEN cDNA 1700011H14 gene	1.08	0.357	-3.06	0.008	-1.12	0.602	1.79	0.229	-0.33
1445474_at	Prim2	DNA primase, p58 subunit	1.12	0.597	-1.65	0.294	-1.75	0.31	1.17	0.779	-0.28
1433127_at	4930513L20Rik	RIKEN cDNA 4930513L20 gene	-3.01	0.004	1.02	0.938	-1.05	0.77	1.2	0.605	-0.46
1451637_a_at	Muc10	mucin 10, submandibular gland salivary mucin	-1.3	0.278	1.07	0.749	-2.16	0.371	1.24	0.694	-0.29
1417860_a_at	Spon2	spondin 2, extracellular matrix protein	1.01	0.976	-1.33	0.537	-1.87	0.235	1.07	0.713	-0.28
1428044_at	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	-1.58	0.132	-1.73	0.175	1.09	0.788	1.09	0.675	-0.28
1438421_at	Pvrl1	poliovirus receptor-related 1	1.18	0.797	-1.4	0.313	-2.45	0.16	2.13	0.124	-0.13
1441756_at	Tcf7l2	Transcription factor 7-like 2, T-cell specific, HMG-box	1.15	0.447	-1.86	0.02	-1.63	0.095	1.09	0.495	-0.31
1440159_at	1700010B09Rik	RIKEN cDNA 1700010B09 gene	1.03	0.872	-1.4	0.239	-1.79	0.057	1.1	0.833	-0.26
1444583_at	D4Ertd767e	DNA segment, Chr 4, ERATO Doi 767, expressed	1	0.998	-1.08	0.656	-2.64	0.045	1.28	0.413	-0.36
1453265_at	4930579C15Rik	RIKEN cDNA 4930579C15 gene	-1.8	0.385	-1.43	0.642	1.05	0.921	1.12	0.653	-0.27
1444392_at	Leprel1	Leprecan-like 1	-1.19	0.808	1.12	0.829	-2.86	0.01	1.21	0.58	-0.43
1432006_at	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	-1.28	0.464	1.03	0.936	-2	0.005	1.17	0.583	-0.27
1441664_at	LOC433351	hypothetical gene supported by AK081809	-2.45	0.049	-1.41	0.502	1.19	0.522	1.1	0.747	-0.39
1427268_at	Flg /// LOC620355	filaggrin /// similar to Filaggrin /// similar to Filaggrin	1.1	0.922	-1.29	0.315	-2.31	0.063	1.64	0.134	-0.21
1446031_at	Thrap3	Thyroid hormone receptor associated protein 3	1.03	0.952	-1.25	0.174	-2.08	0.008	1.34	0.429	-0.24
1426589_at	Gab3	growth factor receptor bound protein 2-associated protein 3	-2.11	0.087	-1.42	0.515	1.13	0.544	1.24	0.343	-0.29
1425812_a_at	Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	-1.78	0.007	-1.41	0.326	1.04	0.814	1.32	0.208	-0.21
1453460_at	1700012I11Rik	RIKEN cDNA 1700012I11 gene	-2.04	0.461	1.11	0.732	-1.41	0.047	1.13	0.577	-0.3
1440301_at	---	---	-1.7	0.026	1.08	0.651	-1.57	0.119	1.89	0.232	-0.07
1443007_at	---	---	-1.17	0.499	-3.8	0.09	1.19	0.636	1.08	0.585	-0.67
1427242_at	Ddx4	DEAD (Asp-Glu-Ala-Asp) box polypeptide 4	-1.93	0.197	-1.77	0.158	1.23	0.546	1.68	0.05	-0.2
1442688_at	---	---	1.15	0.531	-2.11	0.326	-1.45	0.297	1.1	0.346	-0.33
1459394_at	D130052B06Rik	RIKEN cDNA D130052B06 gene	-1.04	0.893	-3.04	0.252	1.02	0.935	1.04	0.494	-0.5
1444258_at	Actn4	Actinin alpha 4	-1.21	0.281	1.03	0.928	-2.16	0.1	1.07	0.687	-0.32
1456560_at	Gm93	gene model 93, (NCBI)	-2.24	0.132	1.07	0.885	-1.26	0.689	1.41	0.113	-0.25
1417906_at	1700001F09Rik	RIKEN cDNA 1700001F09 gene	1.09	0.512	-1.52	0.474	-1.77	0.115	1.2	0.739	-0.25
1422917_at	Epha1	Eph receptor A1	-3.31	0.4	-1.77	0.294	1.45	0.545	1.97	0.448	-0.42
1420730_a_at	Tcp11	t-complex protein 11	-1.8	0.053	-1.62	0.246	1.14	0.331	1.46	0.559	-0.21
1457657_at	---	---	1.02	0.675	-1.51	0.558	-1.59	0.443	1.1	0.887	-0.25
1445622_at	---	---	-1.24	0.548	1.13	0.772	-2.6	0.054	1.14	0.739	-0.4
1444390_at	Prdm14 /// LOC637	PR domain containing 14 /// similar to PR domain containing 14	-1.91	0.371	1.14	0.701	-1.54	0.546	1.77	0.4	-0.13
1432510_at	4930512M02Rik	RIKEN cDNA 4930512M02 gene	-2.89	0.279	1.33	0.617	-1.56	0.412	1.45	0.338	-0.42
1457688_at	Zfp398	zinc finger protein 398	-1.55	0.207	-1.75	0.149	1.1	0.626	1.23	0.452	-0.24
1445344_at	Stac	Src homology three (SH3) and cysteine rich domain	-2.36	0.132	-2.48	0.154	1.49	0.518	1.6	0.544	-0.44
1444703_at	2810403D21Rik	RIKEN cDNA 2810403D21 gene	1.3	0.567	-2.46	0.044	-1.65	0.281	1	0.987	-0.45
1429462_at	Slc25a32	solute carrier family 25, member 32	-2.34	0.127	-1.16	0.673	1.02	0.903	1.39	0.296	-0.27
1432544_at	4930449E01Rik	RIKEN cDNA 4930449E01 gene	-3.38	0.408	-1.66	0.153	1.42	0.205	1.63	0.278	-0.5
1429167_at	Ccdc112	coiled-coil domain containing 112	1.18	0.558	-2.56	0.147	-1.35	0.076	1.01	0.972	-0.43
1444648_at	BC050210	cDNA sequence BC050210	-1.2	0.805	-2.08	0.422	1	0.996	1.3	0.525	-0.24
1441274_at	Casc3	Cancer susceptibility candidate 3	-1.28	0.446	1	0.984	-1.89	0.053	1.05	0.908	-0.28
1449816_at	Sult5a1	sulfotransferase family 5A, member 1	1.18	0.089	-2.36	0.001	-1.4	0.103	1.01	0.981	-0.39
1460160_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930520J05 prc	-3.07	0.008	1.21	0.645	-1.28	0.183	1.36	0.288	-0.45
1444669_at	Lrfn1	leucine rich repeat and fibronectin type III domain containing 1	-1.38	0.352	1.04	0.927	-1.83	0.217	1.07	0.891	-0.27
1442398_at	Ube2t	ubiquitin-conjugating enzyme E2T (putative)	-4.03	0.218	1.32	0.547	-1.33	0.584	1.45	0.656	-0.65
1422385_at	Olfr1264	olfactory receptor 1264	-2.03	0.061	1.07	0.849	-1.32	0.611	2.27	0.072	0

1432685_at	Mon1b	MON1 homolog b (yeast)	-1.9	0.081	1.09	0.882	-1.41	0.387	1.42	0.553	-0.2
1429531_at	Smpd4	sphingomyelin phosphodiesterase 4	-1.66	0.223	-1.41	0.126	1.01	0.966	2.17	0.191	0.03
1458316_at	---	Transcribed locus	-3.13	0.353	1.2	0.788	-1.25	0.031	2.15	0.193	-0.26
1443237_at	---	---	1.01	0.988	-2.28	0.181	-1.15	0.757	1.23	0.587	-0.3
1442418_at	B930096F20Rik	RIKEN cDNA B930096F20 gene	1.1	0.686	-1.62	0.158	-1.66	0.129	1.24	0.053	-0.23
1423693_at	Ela1	elastase 1, pancreatic	-1.3	0.092	-2.47	0.066	1.15	0.415	2.29	0.088	-0.09
1447439_at	---	---	-1.54	0.501	-1.57	0.19	1.03	0.906	1.18	0.805	-0.22
1445980_at	Aldh1a1	Aldehyde dehydrogenase family 1, subfamily A1	-1.39	0.562	1.13	0.752	-2.12	0.01	1.47	0.455	-0.23
1457342_at	Zfpn1a4	zinc finger protein, subfamily 1A, 4 (Eos)	-1.4	0.099	-1.75	0.514	1.04	0.877	1.01	0.932	-0.28
1446690_at	---	---	-2.42	0.143	1.02	0.979	-1.12	0.777	2.23	0.339	-0.07
1439230_at	4922505E12Rik	RIKEN cDNA 4922505E12 gene	-2.15	0.045	-1.77	0.431	1.29	0.622	1.26	0.699	-0.34
1420217_x_at	---	---	1.02	0.845	-2.2	0.01	-1.18	0.736	1.73	0.272	-0.16
1427028_at	Lgr6	leucine-rich repeat-containing G protein-coupled receptor 6	-2.25	0.076	-1.31	0.526	1.12	0.601	1.3	0.175	-0.29
1449145_a_at	Cav1	caveolin, caveolae protein 1	-1.72	0.077	1.04	0.6	-1.42	0.031	1.03	0.92	-0.27
1452522_at	Stom	stomatin	-2.51	0.336	-1.32	0.559	1.17	0.495	1.2	0.623	-0.37
1457557_at	A330076H08Rik	RIKEN cDNA A330076H08 gene	1.11	0.714	-1.72	0.059	-1.59	0.024	1.73	0.267	-0.12
1438751_at	Slc30a10	solute carrier family 30, member 10	-2.49	0.096	1.02	0.943	-1.1	0.805	2.26	0.195	-0.08
1432068_a_at	Entpd7	ectonucleoside triphosphate diphosphohydrolase 7	-1.7	0.036	1.05	0.769	-1.46	0.402	3.31	0.063	0.3
1420087_at	Fzd3	Frizzled homolog 3 (Drosophila)	-1.26	0.139	-1.98	0.152	1.03	0.904	1	0.992	-0.3
1427644_at	D0Kist4	DNA segment, KIST 4	1.05	0.504	-1.78	0.375	-1.4	0.195	1.17	0.345	-0.24
1416650_at	Rfpl4	ret finger protein-like 4	1.1	0.841	-2.39	0.255	-1.24	0.697	1.47	0.393	-0.27
1420294_at	Aytl2	Acyltransferase like 2	1.1	0.654	-1.71	0.244	-1.56	0.348	1.17	0.771	-0.25
1445133_at	Tcf12	Transcription factor 12	1.35	0.49	-1.63	0.481	-2.78	0.037	1.2	0.674	-0.46
1420568_at	Stra8	stimulated by retinoic acid gene 8	-1.96	0.165	-1.81	0.027	1.26	0.35	1.24	0.266	-0.32
1450319_at	Gabrb2	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 2	-2.23	0.232	1.09	0.816	-1.27	0.225	1.6	0.067	-0.2
1455005_s_at	Slc5a2	solute carrier family 5 (sodium/glucose cotransporter), member 2	-1.26	0.019	-2.32	0.113	1.1	0.644	1	0.978	-0.37
1457257_x_at	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030046E07	1.07	0.821	-1.41	0.411	-1.84	0.039	1.09	0.871	-0.27
1443792_at	Tsga14	testis specific gene A14	-1.2	0.453	-2.11	0.072	1.02	0.822	1.08	0.775	-0.3
1452511_at	Sox5	SRY-box containing gene 5	-2.85	0.102	-1.58	0.147	1.35	0.486	1.03	0.932	-0.51
1445114_at	Ctnnd2	Catenin (cadherin associated protein), delta 2	1.2	0.785	-1.74	0.475	-1.79	0.39	1.58	0.407	-0.19
1454598_at	4930425F17Rik	RIKEN cDNA 4930425F17 gene	-2.27	0.42	1.26	0.73	-1.58	0.248	1.93	0.212	-0.17
1459585_at	Gas6	growth arrest specific 6	1.23	0.004	-1.86	0.015	-1.76	0.135	1.07	0.91	-0.33
1435378_at	2210020M01Rik	RIKEN cDNA 2210020M01 gene	-1.23	0.215	-2.31	0.142	1.08	0.748	3.78	0.245	0.33
1443742_x_at	Ube2r2	Ubiquitin-conjugating enzyme E2R 2	-1.41	0.449	1.31	0.111	-3.22	0.015	1.42	0.536	-0.47
1458746_at	A430107O13Rik	RIKEN cDNA A430107O13 gene	1.12	0.481	-1.2	0.102	-2.69	0.007	1.18	0.239	-0.4
1447735_x_at	A2bp1	ataxin 2 binding protein 1	-1.32	0.497	1.05	0.827	-1.91	0.347	1.2	0.736	-0.25
1439220_at	Ank3	Ankyrin 3, epithelial	1.04	0.372	1.05	0.905	-4.17	0	-1.45	0.441	-0.88
1433009_at	9030607J07Rik	RIKEN cDNA 9030607J07 gene	-1.18	0.68	1	0.997	-2.07	0.332	1.27	0.541	-0.24
1432894_at	9130011L11Rik	RIKEN cDNA 9130011L11 gene	-2.61	0.134	-1.42	0.511	1.25	0.795	1.01	0.983	-0.45
1442872_at	BC021438	cDNA sequence BC021438	1.35	0.755	-3.7	0.011	-1.39	0.358	1.16	0.793	-0.65
1453509_at	Lypd2	Ly6/Plaur domain containing 2	1.11	0.113	-1.41	0.317	-1.97	0.06	1.16	0.543	-0.27
1421521_at	4930430A15Rik	RIKEN cDNA 4930430A15 gene	-2.72	0.062	-2	0.466	1.46	0.031	1.08	0.841	-0.54
1453506_at	4930500O09Rik	RIKEN cDNA 4930500O09 gene	-1.44	0.304	-2.26	0.335	1.19	0.106	1.53	0.303	-0.24
1430507_at	1700027J07Rik	RIKEN cDNA 1700027J07 gene	-2.41	0.153	1.06	0.896	-1.16	0.03	1.47	0.362	-0.26
1432531_at	9230104L09Rik	RIKEN cDNA 9230104L09 gene	-1.19	0.804	1.12	0.73	-2.68	0.001	1.72	0.458	-0.26
1451914_a_at	Add2	adducin 2 (beta)	-1.58	0.618	-1.52	0.471	1.05	0.713	12.27	0.177	2.55
1443732_at	Atp6v0a4	ATPase, H+ transporting, lysosomal V0 subunit A4	-1.31	0.567	-2.03	0.318	1.08	0.81	1.2	0.519	-0.27
1420575_at	Mt3	metallothionein 3	1.01	0.991	-1.54	0.585	-1.48	0.167	1.51	0.567	-0.12
1457616_at	---	PREDICTED: Mus musculus similar to gonadotropin inducible ovarian transcriptic	-3.28	0.021	1.33	0.363	-1.43	0.131	1.29	0.718	-0.52
1458931_at	6030427F01Rik	RIKEN cDNA 6030427F01 gene	-1.35	0.584	-1.86	0.062	1.06	0.707	1.03	0.94	-0.28
1439885_at	Hoxc5	homeo box C5	-1.55	0.239	-1.87	0.137	1.15	0.835	2.23	0.122	-0.01
1456649_at	Snx15	Sorting nexin 15	1.02	0.978	-1.26	0.561	-1.9	0.095	1.38	0.543	-0.19
1442580_at	A530020G20Rik	RIKEN cDNA A530020G20 gene	-1.2	0.804	-2.25	0.014	1.06	0.786	2.01	0.15	-0.1

1441070_at	Hoxa3	Homeo box A3	-1.65	0.127	1.1	0.843	-1.59	0.033	1.18	0.371	-0.24
1442976_at	C81072	expressed sequence C81072	-2.35	0.175	-1.15	0.676	1.04	0.913	1.34	0.582	-0.28
1440011_at	Ext1	Exostoses (multiple) 1	-1.3	0.054	1.1	0.645	-2.14	0.076	1.15	0.428	-0.29
1428765_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	-1.73	0.488	1.05	0.842	-1.4	0.517	1.23	0.358	-0.21
1428504_at	Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	1.2	0.479	-2.18	0.132	-1.46	0.477	1.23	0.695	-0.31
1437569_at	Tmem132e	transmembrane protein 132E	-1.71	0.415	1.34	0.244	-2.39	0.275	1.42	0.001	-0.34
1433064_at	Acot12	acyl-CoA thioesterase 12	-1.25	0.64	-2.97	0.182	1.2	0.67	1.16	0.858	-0.46
1441700_at	Slc4a8	solute carrier family 4 (anion exchanger), member 8	-1.17	0.705	-2.2	0.211	1.03	0.949	1.15	0.82	-0.3
1444007_at	A830082K12Rik	RIKEN cDNA A830082K12 gene	-2.65	0.09	-1.13	0.79	1.08	0.814	2.28	0.224	-0.11
1441097_at	---	Transcribed locus	1.04	0.91	-1.42	0.165	-1.69	0.009	1.94	0.244	-0.03
1444643_at	---	Transcribed locus	-2.27	0.051	-1.13	0.825	1.02	0.961	1.23	0.373	-0.29
1446725_at	A130094D17Rik	RIKEN cDNA A130094D17 gene	-1.7	0.136	1.07	0.754	-1.48	0.046	1.11	0.816	-0.25
1436894_at	D1Ertd471e	DNA segment, Chr 1, ERATO Doi 471, expressed	1.14	0.791	-1.36	0.142	-2.13	0.04	1.41	0.153	-0.23
1452562_at	Jarid1d	jumonji, AT rich interactive domain 1D (Rbp2 like)	-1.12	0.541	-3.19	0.155	1.14	0.615	1.69	0.338	-0.37
1445593_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930414J05 prc	-1.99	0.149	-1.28	0.353	1.06	0.863	2.29	0.207	0.02
1438382_x_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	-1.86	0.187	-1.41	0.114	1.1	0.745	1.07	0.741	-0.28
1419124_at	2210010L05Rik	RIKEN cDNA 2210010L05 gene	1.02	0.926	-1.95	0.146	-1.23	0.116	1.31	0.332	-0.21
1456680_at	B3gnt6	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 syntha	-1.96	0.376	1.11	0.785	-1.37	0.514	1.83	0.246	-0.1
1456578_x_at	Lasp1	LIM and SH3 protein 1	1.04	0.221	-1.56	0.127	-1.51	0.239	1.01	0.978	-0.26
1441523_at	Nf1	neurofibromatosis 1	1.07	0.874	-1.23	0.722	-2.18	0.028	1.94	0.157	-0.1
1453707_at	4930480G23Rik	RIKEN cDNA 4930480G23 gene	-1.43	0.527	-1.63	0.002	1.03	0.945	1.16	0.845	-0.22
1428485_at	Car12	carbonic anyhydrase 12	-1.81	0.06	-1.44	0.188	1.1	0.281	1.04	0.636	-0.28
1456295_at	B230114P17Rik	RIKEN cDNA B230114P17 gene	1.01	0.972	-1.52	0.143	-1.48	0.339	1.24	0.599	-0.19
1431157_at	1700025I17Rik	RIKEN cDNA 1700025I17 gene	-1.55	0.315	-1.53	0.444	1.05	0.863	1.19	0.699	-0.21
1457341_at	---	Transcribed locus, moderately similar to XP_579758.1 PREDICTED: hypothetical	1.02	0.847	-1.26	0.104	-1.88	0.154	1.08	0.484	-0.26
1453671_at	9430041J12Rik	RIKEN cDNA 9430041J12 gene	-3.59	0.05	1.42	0.468	-1.54	0.425	1.96	0.005	-0.44
1456665_at	Eya4	eyes absent 4 homolog (Drosophila)	-1.18	0.557	1.13	0.712	-2.7	0.203	1.45	0.163	-0.33
1437030_at	Plcd4	phospholipase C, delta 4	-1.61	0.285	-1.84	0.125	1.18	0.341	1.01	0.918	-0.32
1432746_at	6030442H21Rik	RIKEN cDNA 6030442H21 gene	1.41	0.008	-1.9	0.069	-2.43	0.012	1.54	0.228	-0.34
1460079_at	Ttc5	Tetratricopeptide repeat domain 5	-1.71	0.543	-2.7	0.269	1.39	0.44	2.06	0.258	-0.24
1443221_at	Wt1	Wilms tumor homolog	1.15	0.701	-2.73	0.132	-1.2	0.766	1.18	0.582	-0.4
1459492_at	---	---	-1.8	0.305	-1.36	0.462	1.06	0.835	1.38	0.342	-0.18
1459993_at	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030043J12	-2.19	0.087	-1.24	0.659	1.09	0.332	1.23	0.491	-0.28
1457211_at	Gls	Glutaminase	-1.96	0.055	1.02	0.963	-1.22	0.462	1.2	0.45	-0.24
1459789_at	---	---	-2.99	0.463	1.44	0.298	-1.74	0.351	1.23	0.616	-0.51
1445718_at	Wdfy3	WD repeat and FYVE domain containing 3	1.03	0.846	-1.25	0.167	-1.91	0.033	1.01	0.966	-0.28
1438145_at	Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	-2.11	0.094	-1.21	0.767	1.05	0.929	1.81	0.216	-0.11
1425450_at	Chi3l4	chitinase 3-like 4	-2	0.141	-1.48	0.202	1.18	0.583	1.02	0.982	-0.32
1457379_at	C78549	expressed sequence C78549	-1.84	0.285	1.04	0.958	-1.3	0.445	1.19	0.027	-0.23
1441171_at	Gm1614	gene model 1614, (NCBI)	-1.07	0.546	-2.41	0.242	1.01	0.967	1.26	0.549	-0.3
1433376_at	5830445D09Rik	RIKEN cDNA 5830445D09 gene	-2.75	0.023	-1.03	0.938	1.02	0.864	1.39	0.024	-0.34
1429147_at	Gas2	growth arrest specific 2	-2.03	0.042	1	0.996	-1.17	0.416	1.14	0.261	-0.26
1430743_at	4930412F12Rik	RIKEN cDNA 4930412F12 gene	-1.44	0.141	1.19	0.717	-2.12	0.034	1.19	0.718	-0.3
1440521_x_at	1700051A21Rik	RIKEN cDNA 1700051A21 gene	-4.49	0.33	-1.36	0.496	1.39	0.087	1.13	0.803	-0.83
1450466_at	B230310J22Rik	RIKEN cDNA B230310J22 gene	-1.63	0.144	1.01	0.982	-1.37	0.313	1.82	0.264	-0.04
1430965_at	9430064K01Rik	RIKEN cDNA 9430064K01 gene	-1.43	0.378	1.14	0.601	-1.95	0.105	1.48	0.569	-0.19
1453325_at	Saps2	SAPS domain family, member 2	-1.08	0.927	-2.94	0.001	1.09	0.852	1.37	0.329	-0.39
1450145_at	Dbpht1	DNA binding protein with his-thr domain	-1.4	0.658	1.08	0.901	-1.78	0.37	1.41	0.305	-0.17
1441701_at	Zfp148	Zinc finger protein 148	1	0.989	-1.13	0.73	-2.12	0.102	1.07	0.889	-0.3
1421477_at	Cplx2	complexin 2	-1.32	0.071	-4.02	0.046	1.35	0.212	1.14	0.562	-0.71
1442112_at	Vps18	vacuolar protein sorting 18 (yeast)	1	0.989	-1.39	0.015	-1.58	0.061	1.03	0.884	-0.24
1422852_at	Cib2	calcium and integrin binding family member 2	-1.43	0.18	-1.66	0.003	1.06	0.481	1.15	0.478	-0.22
1420038_at	Atp6v1e1	VATPase, H+ transporting, lysosomal V1 subunit E1	1.04	0.915	-1.48	0.16	-1.57	0.184	1.07	0.94	-0.23

1436904_at	Thrap1	thyroid hormone receptor associated protein 1	-1.8	0.083	-1.26	0.634	1.01	0.973	1.06	0.792	-0.25
1442727_at	---	---	1.05	0.867	-1.57	0.033	-1.49	0.468	1.34	0.524	-0.17
1432911_at	Safb	scaffold attachment factor B	-1.75	0.012	1.14	0.819	-1.55	0.137	1.45	0.4	-0.18
1428878_a_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.3	0.34	1.04	0.931	-1.81	0.116	1.43	0.421	-0.16
1431881_at	2410024F20Rik	RIKEN cDNA 2410024F20 gene	-1.97	0.027	1.33	0.21	-1.9	0.065	2.19	0.231	-0.09
1446532_at	---	---	-2.32	0.016	1.2	0.729	-1.37	0.126	1.14	0.778	-0.34
1430970_a_at	4930438O03Rik	RIKEN cDNA 4930438O03 gene	-1.77	0.175	-1.9	0.316	1.27	0.527	1.17	0.686	-0.31
1443685_at	6430526N21Rik	RIKEN cDNA 6430526N21 gene	-1.67	0.273	1.13	0.623	-1.57	0.364	1.52	0.474	-0.15
1422392_at	V1rc6	vomeronasal 1 receptor, C6	-2.04	0.236	1.2	0.727	-1.49	0.431	1.36	0.23	-0.24
1437803_at	Slbp /// LOC66697	stem-loop binding protein /// similar to stem-loop binding protein /// similar to stem	-3.9	0.056	-1.27	0.75	1.32	0.598	1.12	0.85	-0.68
1442572_at	Gabarapl1	Gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	1.02	0.977	-1.21	0.59	-1.92	0.305	1.22	0.607	-0.22
1452334_at	Cenpf	centromere protein F	-1.5	0.314	1.28	0.595	-2.42	0.009	2.9	0.255	0.07
1456837_at	A830007L07Rik	RIKEN cDNA A830007L07 gene	-1.65	0.513	1.25	0.522	-1.95	0.377	1.75	0.25	-0.15
1442520_at	5730509C05Rik	RIKEN cDNA 5730509C05 gene	-2.17	0.158	-1.15	0.858	1.03	0.847	1.05	0.839	-0.31
1440089_at	Creb5	cAMP responsive element binding protein 5	1.22	0.548	-2.26	0.041	-1.44	0.549	1.24	0.466	-0.31
1441719_at	---	Transcribed locus, weakly similar to XP_578477.1 PREDICTED: similar to hypoth	-2.81	0.013	1.39	0.547	-1.61	0.176	1.11	0.827	-0.48
1430022_at	Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A	1.14	0.415	-1.74	0.329	-1.54	0.226	1.84	0.259	-0.08
1430963_at	Gcnt3	glucosaminyl (N-acetyl) transferase 3, mucin type	1.36	0.751	-2.88	0.222	-1.51	0.398	2.41	0.069	-0.16
1444198_at	Dmt2	Dorso-medial telencephalon gene 2	-1.6	0.239	-1.69	0.358	1.15	0.563	1.21	0.62	-0.23
1440606_at	Tmem97	Transmembrane protein 97	1.02	0.95	-1.31	0.066	-1.71	0.069	1.27	0.324	-0.18
1434852_at	Pla2g2f	phospholipase A2, group IIF	1.05	0.904	-2.28	0.215	-1.14	0.555	2.11	0.118	-0.06
1442839_at	---	---	-1.6	0.422	1.14	0.796	-1.67	0.03	1.02	0.964	-0.28
1456529_at	---	---	1.11	0.282	-2.8	0.121	-1.12	0.491	1.17	0.431	-0.41
1432226_at	4930548G14Rik	RIKEN cDNA 4930548G14 gene	-2.02	0.089	-1.48	0.469	1.19	0.559	1.16	0.785	-0.28
1423497_at	Klhl10	kelch-like 10 (Drosophila)	-3.3	0.015	1.38	0.408	-1.46	0.317	1.45	0.547	-0.48
1439335_at	---	---	-1.79	0.568	-1.42	0.513	1.1	0.828	3.06	0.137	0.24
1441673_at	Pllp	plasma membrane proteolipid	1.11	0.79	-1.66	0.16	-1.52	0.12	1.24	0.573	-0.21
1459456_at	0610011L14Rik	RIKEN cDNA 0610011L14 gene	-1.4	0.588	-1.62	0.407	1.03	0.902	1.5	0.194	-0.12
1456546_at	1700097N02Rik	RIKEN cDNA 1700097N02 gene	-1.7	0.481	1.05	0.927	-1.37	0.59	2.04	0.215	0
1445310_at	Sytl3	synaptotagmin-like 3	-3.89	0.345	1.45	0.321	-1.51	0.482	1.01	0.975	-0.73
1437057_at	Megf6	multiple EGF-like-domains 6	-1.71	0.224	-1.35	0.39	1.04	0.76	1.02	0.9	-0.25
1417650_at	Lao1	L-amino acid oxidase 1	-1.94	0.165	1.25	0.643	-1.66	0.165	1.05	0.945	-0.32
1451729_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	1.06	0.806	-1.51	0.216	-1.54	0.144	1.31	0.117	-0.17
1440052_at	Efna5	Ephrin A5	-1.34	0.2	1.04	0.723	-1.71	0.053	1.33	0.364	-0.17
1459464_at	---	Transcribed locus	-1.32	0.365	1.12	0.699	-2.02	0.078	1.39	0.05	-0.21
1424563_at	Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-2.01	0.24	1.17	0.68	-1.43	0.301	1.19	0.746	-0.27
1440543_at	D930036F22Rik	RIKEN cDNA D930036F22 gene	-2.69	0.095	1.28	0.646	-1.39	0.103	1.43	0.354	-0.34
1423011_at	Evi1	ecotropic viral integration site 1	-1.42	0.592	1.1	0.862	-1.77	0.042	1.1	0.889	-0.25
1429866_at	Ahnak	AHNAK nucleoprotein (desmoyokin)	1.24	0.746	-1.5	0.292	-2.14	0.072	1.23	0.659	-0.29
1443123_at	Tanc2	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-1.43	0.599	1.06	0.911	-1.63	0.126	1.38	0.058	-0.16
1456192_x_at	Cypt3	cysteine-rich perinuclear theca 3	-2.91	0.142	-1.04	0.957	1.07	0.893	1.02	0.975	-0.47
1441686_at	---	---	-1.76	0.298	-1.59	0.363	1.17	0.683	1.34	0.545	-0.21
1459197_at	---	---	1.04	0.923	-1.96	0.025	-1.22	0.423	1.73	0.058	-0.1
1415938_at	Spink3	serine peptidase inhibitor, Kazal type 3	-1.12	0.325	-2.14	0.386	1.01	0.979	1.27	0.648	-0.24
1425748_at	Diras1	DIRAS family, GTP-binding RAS-like 1	-1.19	0.626	-2.25	0.177	1.09	0.831	2.46	0.019	0.03
1459162_at	Zfp644	Zinc finger protein 644	-2.1	0.168	1.57	0.536	-3.08	0.077	1.19	0.815	-0.6
1425918_at	Egln3	EGL nine homolog 3 (C. elegans)	1.18	0.06	-1.58	0.108	-1.79	0.12	1.03	0.909	-0.29
1419175_a_at	Btn1a1	butyrophilin, subfamily 1, member A1	-2.61	0.072	1.09	0.782	-1.11	0.644	1.66	0.173	-0.24
1441621_at	---	Transcribed locus	-1.28	0.589	-1.71	0.393	1.01	0.993	1.88	0.042	-0.02
1453560_at	Fem1a	feminization 1 homolog a (C. elegans)	-1.63	0.092	-1.54	0.019	1.11	0.676	2.14	0.415	0.02
1425376_at	Alox8	arachidonate 8-lipoxygenase	-3.59	0.39	-1.11	0.88	1.19	0.662	1.61	0.208	-0.47
1431476_at	4933407I05Rik	RIKEN cDNA 4933407I05 gene	-1.59	0.285	-1.56	0.171	1.11	0.658	1.26	0.442	-0.2
1430907_at	4930455J16Rik	RIKEN cDNA 4930455J16 gene	1.19	#DIV/0!	-1.4	0.262	-2.13	0.084	1.14	0.098	-0.3

1425046_at	BC018465	cDNA sequence BC018465	-1.49	0.712	1.14	0.763	-1.79	0.028	1.59	0.515	-0.14
1426000_at	Oxtr	oxytocin receptor	-1.92	0.544	1.08	0.881	-1.29	0.5	1.89	0.387	-0.06
1454546_at	4933403L11Rik	RIKEN cDNA 4933403L11 gene	1.23	0.41	-1.63	0.363	-1.89	0.316	1.19	0.708	-0.27
1443476_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630019	-1.3	0.669	1.08	0.865	-1.92	0.054	2.04	0.429	-0.02
1458373_at	5830483C08Rik	RIKEN cDNA 5830483C08 gene	1.01	0.99	-1.28	0.543	-1.7	0.414	2.24	0.188	0.07
1458014_at	Aff2	AF4/FMR2 family, member 2	-1.41	0.516	-2.6	0.029	1.28	0.627	1.59	0.396	-0.28
1454715_at	0710005M24Rik	RIKEN cDNA 0710005M24 gene	1.53	0.159	-3.47	0.29	-1.8	0.259	1.29	0.146	-0.61
1431556_at	4930435M08Rik	RIKEN cDNA 4930435M08 gene	-1.24	0.786	-1.8	0.296	1.01	0.971	3.33	0.038	0.33
1439904_at	Fstl5	follistatin-like 5	-1.01	0.982	1.09	0.888	-3.39	0	1.6	0.339	-0.43
1441464_at	A630035D09Rik	RIKEN cDNA A630035D09 gene	-1.87	0.276	1.28	0.629	-1.78	0.095	1.6	0.273	-0.19
1432981_at	Map3k9	mitogen-activated protein kinase kinase kinase 9	-1.31	0.37	-1.7	0.359	1.02	0.817	1.5	0.419	-0.12
1420083_at	AU016916	expressed sequence AU016916	-1.83	0.04	-1.75	0.078	1.26	0.412	1.82	0.187	-0.13
1419597_at	Eda	ectodysplasin-A	-2.33	0.035	1.05	0.913	-1.12	0.841	1.23	0.785	-0.29
1433369_at	8430401P03Rik	RIKEN cDNA 8430401P03 gene	1.06	0.873	-1.3	0.158	-1.81	0.003	1.15	0.591	-0.23
1421367_at	4930549C01Rik	RIKEN cDNA 4930549C01 gene	-1.74	0.321	-1.4	0.529	1.09	0.823	1.14	0.712	-0.23
1440577_at	Mkln1	Muskelin 1, intracellular mediator containing kelch motifs	1.12	0.671	-1.32	0.483	-2	0.11	1.09	0.847	-0.28
1438509_at	Psme3	Proteaseome (prosome, macropain) 28 subunit, 3	1.11	0.911	-2.89	0.022	-1.09	0.832	1.48	0.56	-0.35
1439037_at	Ddx17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	-1.38	0.647	-1.79	0.051	1.1	0.805	1.36	0.657	-0.18
1446682_at	---	Transcribed locus	-1.85	0.03	1.17	0.668	-1.49	0.156	1.1	0.633	-0.27
1444841_at	---	---	1.18	0.597	-1.56	0.447	-1.78	0.438	1.28	0.244	-0.22
1437222_x_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	1.1	0.688	-1.71	0.111	-1.44	0.151	1.04	0.93	-0.25
1416686_at	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	-1.29	0.157	1.06	0.904	-1.86	0.025	1	0.999	-0.27
1452987_at	Josd3	Josephin domain containing 3	1.13	0.535	-2.64	0.234	-1.15	0.593	1.31	0.023	-0.34
1457541_at	Akap14	A kinase (PRKA) anchor protein 14	-2.81	0.128	-1.18	0.05	1.18	0.586	1.59	0.379	-0.31
1431605_at	Rb1cc1	RB1-inducible coiled-coil 1	1.28	0.743	-2.66	0.172	-1.38	0.279	1.25	0.646	-0.38
1435046_at	Myo1d	Myosin ID	-1.18	0.15	1.05	0.908	-2.07	0.013	2.49	0.193	0.07
1457226_at	---	---	-1.14	0.888	1.06	0.911	-2.25	0.284	1.2	0.73	-0.28
1447845_s_at	Vnn1	vanin 1	1.25	0.208	-1.89	0.306	-1.65	0.015	1.53	0.471	-0.19
1432086_a_at	Ribc2	RIB43A domain with coiled-coils 2	-2.3	0.012	-1.27	0.511	1.16	0.628	1.28	0.046	-0.28
1422940_x_at	Serpinb3b	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	-1.17	0.839	1.15	0.65	-2.7	0.027	1.04	0.938	-0.42
1438892_at	Qk	Quaking	1	0.987	-1.56	0.286	-1.36	0.002	1.05	0.787	-0.22
1421133_at	Pvrl3	poliovirus receptor-related 3	1.2	0.099	-2.23	0.025	-1.37	0.093	1.11	0.809	-0.32
1460118_at	---	Transcribed locus	1.09	0.507	-1.37	0.555	-1.79	0.102	2.04	0.335	-0.01
1460529_at	4930455M05Rik	RIKEN cDNA 4930455M05 gene	-2.99	0.004	-1.14	0.827	1.17	0.692	1.45	0.591	-0.38
1429547_at	4930578I06Rik	RIKEN cDNA 4930578I06 gene	1.21	0.607	-2.46	0.39	-1.3	0.568	1.76	0.115	-0.2
1431543_at	9130001E16Rik	RIKEN cDNA 9130001E16 gene	-1.55	0.422	-1.73	0.149	1.16	0.656	1.16	0.76	-0.24
1432532_at	0610025J13Rik	RIKEN cDNA 0610025J13 gene	-1.01	0.964	-2.65	0.182	1.02	0.969	2.16	0.102	-0.12
1457643_x_at	2610316D01Rik	RIKEN cDNA 2610316D01 gene	1.35	0.394	-2.14	0.352	-1.76	0.422	1.67	0.542	-0.22
1434243_s_at	---	---	1.03	0.702	-1.32	0.182	-1.68	0.023	1.13	0.512	-0.21
1432673_at	2300010F08Rik	RIKEN cDNA 2300010F08 gene	1.02	0.968	-1.1	0.543	-2.17	0.307	1.37	0.569	-0.22
1460125_at	2610301F02Rik	RIKEN cDNA 2610301F02 gene	1.14	0.885	-1.75	0.193	-1.48	0.097	1.18	0.115	-0.23
1445070_at	---	Transcribed locus	1.05	0.949	-1.68	0.498	-1.34	0.547	1.18	0.703	-0.2
1419063_at	Ugt8a	UDP galactosyltransferase 8A	-1.24	0.2	1.09	0.86	-2.04	0.013	5.11	0.207	0.73
1431874_at	4931429L15Rik	RIKEN cDNA 4931429L15 gene	-2.12	0.063	-1.34	0.394	1.17	0.617	1.83	0.147	-0.12
1442362_at	Gm104	gene model 104, (NCBI)	1.21	0.697	-2.13	0.087	-1.41	0.162	2.08	0.333	-0.06
1433423_at	2210008N01Rik	RIKEN cDNA 2210008N01 gene	-2.35	0.167	-1.06	0.911	1.02	0.956	2.49	0.336	0.02
1435433_at	Centg2	centaurin, gamma 2	1.06	0.524	-3.16	0.044	1.01	0.967	-1.43	0.369	-0.63
1423510_at	Iapp	islet amyloid polypeptide	-1.24	0.144	1.25	0.693	-3.03	0.012	1.25	0.601	-0.44
1438807_at	Hnrpr	Heterogeneous nuclear ribonucleoprotein R	1.13	0.649	-1.27	0.341	-2.14	0.002	1.08	0.776	-0.3
1458745_at	D18Ertd201e	DNA segment, Chr 18, ERATO Doi 201, expressed	1.17	0.842	-2.12	0.181	-1.34	0.606	3.35	0.001	0.26
1432564_at	1700066C05Rik	RIKEN cDNA 1700066C05 gene	-1.98	0.084	1.14	0.7	-1.36	0.44	1.84	0.293	-0.09
1439128_at	Zbtb20	zinc finger and BTB domain containing 20	-1.28	0.011	1.02	0.855	-1.71	0.026	1.17	0.653	-0.2
1445224_at	Ap3b2	Adaptor-related protein complex 3, beta 2 subunit	1.21	0.55	-1.77	0.409	-1.62	0.097	1.14	0.707	-0.26

1453958_at	2610203C22Rik	RIKEN cDNA 2610203C22 gene	1.26	0.747	-1.21	0.54	-3.29	0.04	1.03	0.944	-0.55
1456882_at	Sox12	SRY-box containing gene 12	1.17	0.842	-1.34	0.431	-2.12	0.309	1.07	0.24	-0.3
1433242_at	5830415B17Rik	RIKEN cDNA 5830415B17 gene	1.16	0.538	-2.04	0.039	-1.35	0.506	1.52	0.027	-0.18
1446165_at	LOC621312	similar to fibrillarin	-1.86	0.148	1.04	0.91	-1.24	0.503	1.32	0.479	-0.18
1444193_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	-1.36	0.179	-3.41	0.166	1.36	0.336	1.73	0.199	-0.42
1431308_at	5730557B15Rik	RIKEN cDNA 5730557B15 gene	-1.37	0.141	-1.67	0.155	1.06	0.805	1.01	0.948	-0.24
1431876_at	4931429P17Rik	RIKEN cDNA 4931429P17 gene	1.16	0.702	-1.93	0.373	-1.4	0.39	1.17	0.776	-0.25
1431162_a_at	Enah	enabled homolog (Drosophila)	1.21	0.145	-2.93	0.09	-1.19	0.788	1.56	0.518	-0.34
1435199_at	---	---	-1.17	0.582	-2.63	0.109	1.16	0.805	1.2	0.42	-0.36
1419210_at	Hrh1	histamine receptor H 1	-1.47	0.142	1.11	0.853	-1.64	0.4	1.29	0.341	-0.18
1428424_at	Pcgf3	polycomb group ring finger 3	-1.72	0.465	1.26	0.687	-1.81	0.235	1.27	0.385	-0.25
1439514_at	Cks1b	CDC28 protein kinase 1b	1	0.996	-1.98	0.172	-1.13	0.429	1.15	0.662	-0.24
1442148_at	Psip1	PC4 and SFRS1 interacting protein 1	1.02	0.904	-1.57	0.294	-1.36	0.521	1.95	0.316	0.01
1444702_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230116A	-1.7	0.532	-1.68	0.374	1.21	0.643	1.2	0.669	-0.24
1429280_at	Col22a1	collagen, type XXII, alpha 1	1.07	0.936	-1.78	0.209	-1.31	0.568	1.49	0.593	-0.13
1444464_at	Ndufs4	NADH dehydrogenase (ubiquinone) Fe-S protein 4	-1.33	0.412	-1.79	0.166	1.09	0.81	1.09	0.732	-0.23
1454107_a_at	Kif2a	kinesin family member 2A	-1.59	0.028	-1.74	0.384	1.19	0.403	2.79	0.144	0.16
1417687_at	Lgals12	lectin, galactose binding, soluble 12	-1.46	0.096	-1.52	0.103	1.05	0.763	1.02	0.949	-0.23
1442989_at	Nars2	Asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	1.03	0.906	-1.44	0.068	-1.48	0.167	1.06	0.834	-0.21
1443514_at	---	---	-2.54	0.423	-2.79	0.189	1.65	0.288	1.51	0.529	-0.55
1443990_at	Ntrk1	neurotrophic tyrosine kinase, receptor, type 1	-1.88	0.129	-1.31	0.683	1.1	0.442	1.23	0.729	-0.21
1432740_at	4833420L08Rik	RIKEN cDNA 4833420L08 gene	-3.27	0.011	-2.58	0.099	1.71	0.258	1.07	0.928	-0.77
1430032_at	Rbm4b	RNA binding motif protein 4B	-1.41	0.16	1.03	0.869	-1.52	0.002	1.06	0.596	-0.21
1438443_at	Zbtb20	zinc finger and BTB domain containing 20	-1.16	0.325	1	0.931	-1.87	0.005	1.18	0.56	-0.21
1434464_at	Aqp12	aquaporin 12	-2.23	0.402	1.17	0.804	-1.29	0.643	2.07	0.146	-0.07
1453446_at	6430411K18Rik	RIKEN cDNA 6430411K18 gene	-1.64	0.351	1.15	0.596	-1.57	0.367	1.4	0.616	-0.16
1448690_at	Kcnk1	potassium channel, subfamily K, member 1	1.29	0.128	-2.49	0.115	-1.41	0.285	1.84	0.076	-0.19
1441244_at	---	Transcribed locus	-1.77	0.152	1.02	0.939	-1.23	0.468	1.2	0.2	-0.19
1430094_at	4931440L10Rik	RIKEN cDNA 4931440L10 gene	1.09	0.828	-1.73	0.082	-1.37	0.367	1.2	0.739	-0.2
1442708_at	---	0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630048D	-1.03	0.912	1.02	0.966	-2.42	0.338	1.01	0.973	-0.36
1449758_at	---	---	1.06	0.902	-1.68	0.112	-1.35	0.208	1.03	0.954	-0.23
1453436_at	4921516I12Rik	RIKEN cDNA 4921516I12 gene	-1.75	0.267	-1.39	0.579	1.11	0.59	1.6	0.433	-0.11
1422493_at	Cpox	coproporphyrinogen oxidase	-1.25	0.046	-1.69	0.004	1.01	0.865	7.57	0.133	1.41
1433218_at	4930566N20Rik	RIKEN cDNA 4930566N20 gene	-1.31	0.657	1.06	0.612	-1.72	0.398	1.35	0.37	-0.16
1450861_at	Fancc	Fanconi anemia, complementation group C	-1.33	0.441	1.02	0.968	-1.58	0.103	1.2	0.59	-0.17
1443933_at	Mtac2d1	membrane targeting (tandem) C2 domain containing 1	1.18	0.139	-1.57	0.157	-1.7	0	1.27	0.719	-0.21
1443078_at	6030439D06Rik	RIKEN cDNA 6030439D06 gene	-1.35	0.376	1	0.99	-1.52	0.335	1.6	0.47	-0.07
1447415_at	---	---	-1.76	0.194	1.13	0.677	-1.42	0.131	1.03	0.91	-0.26
1446783_at	Gadd45gip1	Growth arrest and DNA-damage-inducible, gamma interacting protein 1	1.06	0.721	-1.83	0.127	-1.25	0.27	1.28	0.375	-0.19
1440988_at	---	9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone	1.04	0.956	-1.3	0.527	-1.67	0.289	1.46	0.633	-0.12
1421561_at	Bhlhb4	basic helix-loop-helix domain containing, class B4	-2.17	0.325	1.14	0.766	-1.24	0.708	2.04	0.367	-0.06
1431110_at	5430431D22Rik	RIKEN cDNA 5430431D22 gene	-1.05	0.486	1.01	0.981	-2.25	0.004	1.35	0.482	-0.24
1423101_at	Paqr4	progestin and adipoQ receptor family member IV	1.19	0.601	-2.15	0.106	-1.34	0.049	1.88	0.215	-0.1
1445683_at	---	---	1.33	0.629	-1.67	0.417	-2.09	0.123	1.21	0.597	-0.31
1419269_at	Dut	deoxyuridine triphosphatase	1.03	0.943	-1.76	0.039	-1.24	0.42	1.99	0.261	0.01
1443440_at	---	---	-1.47	0.085	1.28	0.707	-2.24	0.219	1.51	0.242	-0.23
1420739_at	Cntn3	contactin 3	-2.11	0.345	1.2	0.721	-1.37	0.255	1.25	0.694	-0.26
1428328_at	Nup50	nucleoporin 50	-1.49	0.138	-1.39	0.042	1.02	0.849	1.24	0.441	-0.16
1431626_at	4933429K18Rik	RIKEN cDNA 4933429K18 gene	-1.88	0.281	1.07	0.652	-1.25	0.385	1.01	0.944	-0.26
1432212_at	1810073H04Rik	RIKEN cDNA 1810073H04 gene	1.04	0.911	-1.84	0.279	-1.21	0.56	1.24	0.427	-0.19
1434819_at	St6gal2	beta galactoside alpha 2,6 sialyltransferase 2	-1.6	0.564	1.15	0.788	-1.57	0.454	1.26	0.599	-0.19
1431258_at	Dido1	death inducer-obliterator 1	1.1	0.922	-1.54	0.382	-1.52	0.136	1.14	0.567	-0.21
1453571_at	Depdc6	DEP domain containing 6	1.1	0.581	-1.38	0.098	-1.71	0.036	1.11	0.762	-0.22

1456675_at	AA536749	expressed sequence AA536749	-2.24	0.018	-1.26	0.261	1.17	0.859	1.11	0.671	-0.31
1433086_at	5930427J20Rik	RIKEN cDNA 5930427J20 gene	-1.84	0.055	1.08	0.884	-1.29	0.562	1.52	0.571	-0.13
1443939_at	LOC230628 /// LOC	similar to C05G5.5 /// similar to C05G5.5 /// similar to C05G5.5	-1.13	0.39	-2.27	0.13	1.08	0.431	2.29	0.018	-0.01
1441515_at	---	---	-1.91	0.38	-1.24	0.421	1.08	0.874	1.01	0.967	-0.27
1451636_at	Ankrd33	ankyrin repeat domain 33	1.06	0.558	1.05	0.714	-3.31	0.029	-1	0.995	-0.55
1436599_at	AW493225	Expressed sequence AW493225	-1.53	0.657	-1.85	0.459	1.21	0.183	2.31	0.236	0.04
1440347_at	Arhgap10	Rho GTPase activating protein 10	-1.25	0.175	1.12	0.723	-2.05	0.033	1.03	0.761	-0.29
1429221_at	Wdr85	WD40 repeat domain 85	-1.97	0.408	-2.96	0.051	1.56	0.067	1.05	0.916	-0.58
1455397_at	Caskin1	CASK interacting protein 1	-1.53	0.642	1.15	0.673	-1.64	0.246	1.22	0.592	-0.2
1438281_x_at	1700023L04Rik	RIKEN cDNA 1700023L04 gene	-2.01	0.472	1.05	0.921	-1.16	0.545	1.94	0.17	-0.04
1442900_at	---	Transcribed locus	-1.34	0.276	1.04	0.952	-1.6	0.425	1.29	0.549	-0.15
1432850_at	5430434G16Rik	RIKEN cDNA 5430434G16 gene	1.02	0.917	-1.23	0.157	-1.73	0.006	1.82	0.243	-0.03
1433181_at	4930431N21Rik	RIKEN cDNA 4930431N21 gene	1.12	0.839	-1.23	0.147	-2.12	0.019	1.26	0.339	-0.24
1436587_at	1700123D08Rik	RIKEN cDNA 1700123D08 gene	-1.46	0.03	-1.39	0.23	1.01	0.956	1.12	0.684	-0.18
1427498_a_at	Spag5	sperm associated antigen 5	-1.36	0.081	1.02	0.902	-1.53	0.302	2.01	0.321	0.04
1422240_s_at	Sprr2h	small proline-rich protein 2H	-2.37	0.049	-1.98	0.439	1.48	0.244	1.42	0.312	-0.36
1439633_at	B230112P13Rik	RIKEN cDNA B230112P13 gene	-2.07	0.087	1.13	0.702	-1.25	0.215	1.01	0.964	-0.3
1446467_at	Atp9b	ATPas, class II, type 9B	-1.77	0.175	-1.34	0.582	1.1	0.84	1.76	0.425	-0.06
1454316_at	5830426C09Rik	RIKEN cDNA 5830426C09 gene	-1.53	0.204	-1.36	0.519	1.02	0.939	1.37	0.346	-0.12
1444620_at	Tcf12	Transcription factor 12	-1.22	0.664	1.01	0.936	-1.71	0.119	1.18	0.397	-0.19
1445668_at	Tbce	Tubulin-specific chaperone e	1.01	0.964	-1.94	0.135	-1.13	0.615	1.18	0.502	-0.22
1458731_at	---	Transcribed locus	-1.9	0.313	1.3	0.566	-1.7	0.217	1.31	0.633	-0.25
1442171_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	1.09	0.209	-1.29	0.246	-1.83	0.077	1.04	0.845	-0.25
1430823_at	2700029L08Rik	RIKEN cDNA 2700029L08 gene	1.23	0.695	-1.39	0.613	-2.19	0.036	1.9	0.123	-0.11
1429967_at	2600002B07Rik	RIKEN cDNA 2600002B07 gene	1.15	0.519	-1.53	0.076	-1.63	0.215	1.6	0.279	-0.1
1440006_at	BC026600	cDNA sequence BC026600	1.51	0.148	-2.65	0.111	-1.91	0.132	1.8	0.038	-0.31
1425041_at	Lhx3	LIM homeobox protein 3	-2.64	0.126	-1.25	0.582	1.24	0.68	1.02	0.969	-0.41
1455853_x_at	Tspan31	tetraspanin 31	-2.05	0.227	1.14	0.764	-1.28	0.438	1.37	0.064	-0.2
1444907_at	AU022138	expressed sequence AU022138	-2.73	0.012	-1.1	0.836	1.14	0.773	1.19	0.66	-0.38
1428001_at	Tshr	thyroid stimulating hormone receptor	1.57	0.405	-2.21	0.359	-2.55	0.223	2.87	0.056	-0.08
1448045_at	---	Adult male kidney cDNA, RIKEN full-length enriched library, clone:F530012N16 p	1.08	0.77	-1.49	0.027	-1.52	0.307	1.19	0.795	-0.18
1446111_at	D14Ertd611e	DNA segment, Chr 14, ERATO Doi 611, expressed	1.22	0.375	-1.76	0.32	-1.61	0.264	1.43	0.61	-0.18
1453125_at	Sox11	SRY-box containing gene 11	1.05	0.91	-1.03	0.933	-2.57	0.104	1.2	0.315	-0.34
1456368_at	Adam4b	a disintegrin and metalloprotease domain 4b	1.17	0.796	-1.47	0.334	-1.78	0.204	1.21	0.633	-0.22
1456457_at	Slc32a1	Solute carrier family 32 (GABA vesicular transporter), member 1	-1.32	0.772	-3.87	0.034	1.4	0.515	1.26	0.773	-0.63
1444705_at	App	Amyloid beta (A4) precursor protein	-1.43	0.129	1.2	0.344	-1.96	0.018	1.31	0.015	-0.22
1457866_at	C77717	expressed sequence C77717	-1.58	0.02	-1.71	0.438	1.2	0.184	1.25	0.402	-0.21
1430223_at	4930442P07Rik	RIKEN cDNA 4930442P07 gene	1.45	0.46	-2.76	0.16	-1.67	0.323	1.49	0.325	-0.37
1431984_at	1700007F19Rik	RIKEN cDNA 1700007F19 gene	-1.63	0.269	-1.59	0.023	1.17	0.69	1.07	0.859	-0.24
1446538_at	Kpna3	Karyopherin (importin) alpha 3	1.18	0.628	-1.69	0.124	-1.54	0.288	1.02	0.897	-0.26
1440491_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	-1.84	0.004	1.28	0.749	-1.7	0.098	2.29	0.106	0.01
1453821_at	Hemk2	HemK methyltransferase family member 2	-1.4	0.266	-1.46	0.144	1.02	0.933	1.1	0.632	-0.19
1447441_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	1.01	0.862	-1.65	0.432	-1.25	0.265	2.91	0.295	0.25
1445372_at	Mamdc1	MAM domain containing 1	-1.27	0.372	-2.02	0.042	1.13	0.771	1.03	0.886	-0.28
1440063_at	Farsla	phenylalanine-tRNA synthetase-like, alpha subunit	-1.65	0.595	1.08	0.892	-1.37	0.502	1.61	0.381	-0.08
1420669_at	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	-1.47	0.295	-2.09	0.068	1.26	0.117	1.28	0.343	-0.26
1446212_at	Ga17	Dendritic cell protein GA17	1.01	0.962	1.02	0.93	-2.62	0.009	-1.92	0.19	-0.63
1425856_at	Cib1	Calcium and integrin binding 1 (calmyrin)	-1.36	0.279	1.16	0.832	-1.92	0.346	1.15	0.624	-0.24
1427884_at	Col3a1	procollagen, type III, alpha 1	-1.04	0.926	1.12	0.538	-2.91	0.118	1.03	0.907	-0.45
1459071_at	---	Transcribed locus	-1.58	0.465	1	0.999	-1.28	0.57	1.35	0.326	-0.13
1443445_at	Diap3	Diaphanous homolog 3 (Drosophila)	1.2	0.542	-1.72	0.275	-1.56	0.254	4.64	0.32	0.64
1440148_at	Gpr6	G protein-coupled receptor 6	1.03	0.817	-1.22	0.756	-1.75	0.388	1.8	0.093	-0.03
1457238_at	---	Transcribed locus	1.13	0.708	-2.14	0.265	-1.21	0.483	2.14	0.198	-0.02

1451181_at	Tmem121	transmembrane protein 121	1.09	0.822	-1.03	0.933	-2.79	0.106	1.28	0.131	-0.36
1460473_at	6230400D17Rik	RIKEN cDNA 6230400D17 gene	1.33	0.721	-2.9	0.123	-1.33	0.241	1.18	0.745	-0.43
1422204_at	Avpr1b	arginine vasopressin receptor 1B	-2.17	0.453	1.55	0.359	-2.46	0.107	2.55	0.286	-0.13
1443248_at	Tmco3	transmembrane and coiled-coil domains 3	1.2	0.647	-1.49	0.315	-1.82	0.053	1.31	0.021	-0.2
1445601_at	---	6 days neonate spleen cDNA, RIKEN full-length enriched library, clone:F430214H	-1.23	0.486	-1.78	0.043	1.05	0.865	1.27	0.696	-0.17
1431140_at	Them4	thioesterase superfamily member 4	1.02	0.877	-1.61	0.158	-1.29	0.604	1.12	0.51	-0.19
1449720_at	---	---	-1.36	0.519	-1.72	0.057	1.1	0.765	1.68	0.226	-0.07
1438525_at	Mllt10	Myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosop	-1.34	0.368	-1.56	0.574	1.03	0.931	1.39	0.362	-0.12
1446962_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	-4.31	0.389	1.19	0.65	-1.01	0.99	1.3	0.637	-0.7
1422368_at	V1ra5	vomeronasal 1 receptor, A5	-3.53	0.008	-1.34	0.39	1.39	0.556	1.36	0.612	-0.53
1444830_at	---	Transcribed locus	1.03	0.9	-1.68	0.103	-1.26	0.57	1.27	0.325	-0.16
1442538_at	Rcor3	REST corepressor 3	1.01	0.969	-1.34	0.157	-1.51	0.053	1.06	0.87	-0.19
1439724_at	Ric8b	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	-1.05	0.438	-2.36	0.136	1.04	0.916	1.06	0.834	-0.33
1458646_at	Mms19l	MMS19 (MET18 S. cerevisiae)-like	1.08	0.815	-1.73	0.065	-1.3	0.31	1.14	0.773	-0.21
1420120_at	AU020177	expressed sequence AU020177	-2.29	0.195	1.1	0.791	-1.13	0.725	1.15	0.675	-0.29
1445964_at	---	---	-1.32	0.634	-1.99	0.021	1.16	0.538	1.1	0.639	-0.26
1460522_at	6030458E02Rik	RIKEN cDNA 6030458E02 gene	1.6	0.21	-2.18	0.096	-2.75	0.009	1.17	0.286	-0.54
1447282_at	---	---	-3.06	0.042	-1.06	0.834	1.15	0.562	1.2	0.545	-0.44
1417738_at	Rab25	RAB25, member RAS oncogene family	1.02	0.835	-1.78	0.269	-1.19	0.381	1.45	0.095	-0.12
1441509_at	A130009I22Rik	RIKEN cDNA A130009I22 gene	-1.3	0.461	1.16	0.539	-2.01	0.007	1.02	0.943	-0.28
1452471_at	Il17rd	interleukin 17 receptor D	-1.49	0.305	-1.44	0.503	1.06	0.63	1.53	0.199	-0.09
1454118_at	5830410O09Rik	RIKEN cDNA 5830410O09 gene	-2.27	0.189	-1.23	0.729	1.17	0.687	1.37	0.611	-0.24
1442326_at	Pcdh15	protocadherin 15	-1.05	0.942	-2.6	0.027	1.09	0.856	1.33	0.582	-0.31
1421444_at	Pgr	progesterone receptor	1.12	0.873	-1.3	0.486	-1.87	0.06	1.54	0.443	-0.13
1444799_at	AU022054	expressed sequence AU022054	1.02	0.928	-1.37	0.607	-1.49	0.192	1.42	0.713	-0.1
1431529_at	A930002H02Rik	RIKEN cDNA A930002H02 gene	-1.64	0.527	-1.34	0.658	1.07	0.911	1.18	0.737	-0.18
1437371_at	9930021J17Rik	RIKEN cDNA 9930021J17 gene	-1.06	0.782	-3.03	0.12	1.15	0.469	1.52	0.136	-0.35
1434583_at	Tmem26	transmembrane protein 26	1.22	0.633	-1.12	0.806	-3.18	0.013	1.28	0.14	-0.45
1433106_at	5830438M01Rik	RIKEN cDNA 5830438M01 gene	-1.6	0.474	-1.39	0.5	1.08	0.826	2.04	0.114	0.03
1449423_at	Mast1	microtubule associated serine/threonine kinase 1	-1.88	0.36	1.07	0.692	-1.22	0.694	1.46	0.208	-0.14
1430668_a_at	Ankra2	ankyrin repeat, family A (RFXANK-like), 2	-1.55	0.038	-1.46	0.019	1.1	0.559	1.06	0.55	-0.21
1441499_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-2.6	0.158	-1.04	0.925	1.08	0.867	1.29	0.628	-0.32
1443999_at	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	-2.06	0.261	-1.45	0.524	1.25	0.295	1.93	0.517	-0.08
1455184_at	Mobkl1a	MOB1, Mps One Binder kinase activator-like 1A (yeast)	1.01	0.936	-1.25	0.015	-1.62	0.002	1.49	0.209	-0.09
1446116_at	B230378P21Rik	RIKEN cDNA B230378P21 gene	-2.82	0.243	-1.32	0.577	1.31	0.388	1.29	0.217	-0.38
1422210_at	Foxd3	forkhead box D3	-1.13	0.8	-2.26	0.103	1.1	0.617	1.46	0.624	-0.21
1442367_at	Atp11c	Atpase, class VI, type 11C	-1.16	0.667	-1.85	0.2	1.03	0.956	1.15	0.596	-0.21
1447190_at	---	---	1.35	0.405	-2.61	0.387	-1.44	0.465	6	0.201	0.83
1454436_at	4921506L19Rik	RIKEN cDNA 4921506L19 gene	-1.94	0.051	1.16	0.616	-1.32	0.354	1.41	0.132	-0.18
1453582_at	Chka	choline kinase alpha	-1.02	0.889	1.01	0.97	-2.28	0.008	1.04	0.895	-0.31
1436962_at	Prdm6	PR domain containing 6	1.04	0.946	-1.4	0.477	-1.48	0.031	1.15	0.702	-0.17
1419117_at	Slc22a2	solute carrier family 22 (organic cation transporter), member 2	-1.23	0.321	-3.28	0.004	1.31	0.525	1.52	0.424	-0.42
1445628_at	Arhgap21	Rho GTPase activating protein 21	1.34	0.653	-2.76	0.258	-1.37	0.587	1.45	0.243	-0.33
1437000_at	Dgkq	diacylglycerol kinase, theta	-1.68	0.018	-1.41	0.039	1.13	0.55	1.2	0.242	-0.19
1454002_at	---	---	-1.6	0.204	-2.7	0.069	1.43	0.417	1.6	0.342	-0.32
1446331_at	Ptgfr	prostaglandin F receptor	1.02	0.953	-1.3	0.396	-1.56	0.192	1.15	0.758	-0.17
1439350_s_at	Cdc91l1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	-1.7	0.046	-1.21	0.398	1.01	0.953	1.14	0.09	-0.19
1454376_at	4833410I11Rik	RIKEN cDNA 4833410I11 gene	-1.37	0.773	-2.78	0.32	1.34	0.643	1.31	0.358	-0.37
1442882_at	---	---	1.07	0.543	-1.44	0.402	-1.51	0.083	1.94	0.075	0.02
1457397_at	Klf14	Kruppel-like factor 14	-1.19	0.631	-1.89	0.12	1.06	0.732	1.23	0.538	-0.2
1422345_s_at	Mageb1 /// Mageb2	melanoma antigen, family B, 1 /// melanoma antigen, family B, 2 /// melanoma ant	1.03	0.883	-1.54	0.089	-1.33	0.418	1.04	0.88	-0.2
1451215_at	---	---	-1.31	0.24	-2.11	0.007	1.19	0.736	1.59	0.163	-0.16
1447922_at	Stxbp5l	Syntaxin binding protein 5-like	1.27	0.556	-1.16	0.642	-3.37	0.058	1.75	0.361	-0.38

1440308_at	Cmpk	cytidylate kinase	1	0.995	-1.67	0.372	-1.21	0.322	1.34	0.335	-0.13
1440968_at	---	---	-1.35	0.63	1.09	0.76	-1.66	0.097	1.25	0.044	-0.17
1438778_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933018	-1.19	0.499	-1.96	0.162	1.08	0.705	1.56	0.327	-0.13
1445198_at	Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1	0.99	-1.38	0.118	-1.42	0.192	1.08	0.563	-0.18
1422935_x_at	Cbx1	chromobox homolog 1 (Drosophila HP1 beta)	-2.47	0.141	1.24	0.662	-1.27	0.329	1.28	0.515	-0.31
1459211_at	Gli2	GLI-Kruppel family member GLI2	-2.23	0.198	-1.13	0.772	1.1	0.732	1.26	0.057	-0.25
1446952_at	D11Ertd506e	DNA segment, Chr 11, ERATO Doi 506, expressed	-1.64	0.103	-1.36	0.27	1.09	0.705	1.17	0.718	-0.18
1430202_at	1700108F19Rik	RIKEN cDNA 1700108F19 gene	-2.15	0.096	1.23	0.744	-1.35	0.481	1.01	0.952	-0.31
1454700_at	Lrfn4	leucine rich repeat and fibronectin type III domain containing 4	1.06	0.935	-1.55	0.376	-1.37	0.397	1.08	0.679	-0.2
1456096_at	6430573F11Rik	RIKEN cDNA 6430573F11 gene	-1.02	0.958	-2.31	0.031	1.02	0.957	1	1	-0.33
1446921_at	Grb10	Growth factor receptor bound protein 10	-1.16	0.281	1.1	0.813	-2.12	0.039	1.04	0.846	-0.29
1437551_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.36	0.036	1	0.997	-1.44	0.051	1.18	0.146	-0.15
1436582_at	Zdhhc15	zinc finger, DHHC domain containing 15	-1.38	0.194	1.08	0.839	-1.59	0.001	1.18	0.248	-0.18
1439195_at	---	---	1.1	0.823	-1.75	0.501	-1.31	0.282	1.98	0.141	0
1430492_at	Phka2	phosphorylase kinase alpha 2	-1.39	0.118	1.04	0.894	-1.47	0.015	1.88	0.378	0.01
1458740_at	---	---	-1.94	0.004	-1.21	0.657	1.09	0.804	1.57	0.005	-0.12
1442534_at	Glt25d2	Glycosyltransferase 25 domain containing 2	-1.5	0.491	1.13	0.773	-1.55	0.032	1.88	0.147	-0.01
1445917_at	C81269	expressed sequence C81269	-2.46	0.012	1.08	0.876	-1.06	0.849	1.2	0.693	-0.31
1431194_at	6030468B19Rik	RIKEN cDNA 6030468B19 gene	-1.48	0.028	1.04	0.874	-1.38	0.017	12.08	0.258	2.56
1431167_at	Dgkg	diacylglycerol kinase, gamma	-1.19	0.289	-1.85	0.174	1.05	0.744	2.69	0.213	0.18
1445833_at	2400010G15Rik	RIKEN cDNA 2400010G15 gene	-1.22	0.75	1.3	0.583	-3.13	0.095	1.18	0.709	-0.47
1459452_at	---	Transcribed locus	1.16	0.368	-4.11	0.143	1.03	0.929	-1.37	0.495	-0.82
1416945_at	Ptov1	prostate tumor over expressed gene 1	1.02	0.901	-1.3	0.458	-1.53	0.118	1.1	0.88	-0.18
1448299_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, syst	1.14	0.051	-1.98	0.067	-1.27	0.284	1.09	0.835	-0.25
1420042_at	Thoc1	THO complex 1	-1.44	0.409	1.2	0.486	-1.85	0.251	1.13	0.653	-0.24
1419323_at	Padi1	peptidyl arginine deiminase, type I	-2	0.202	-1.53	0.084	1.28	0.432	1.2	0.388	-0.26
1459402_at	Oprm1	opioid receptor, mu 1	-1.41	0.642	1.2	0.777	-1.88	0.149	1.31	0.303	-0.2
1451960_a_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	-2.52	0.072	1.07	0.863	-1.03	0.936	1.04	0.941	-0.36
1460624_at	6330564D18Rik	RIKEN cDNA 6330564D18 gene	1.02	0.92	-1.55	0.152	-1.29	0.113	2.7	0.248	0.22
1433929_at	Nhlrc2	NHL repeat containing 2	-1.46	0.327	1.11	0.79	-1.55	0.084	1.08	0.822	-0.21
1443031_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930037E	1.3	0.661	-1.8	0.331	-1.72	0.33	1.15	0.777	-0.27
1454313_at	Egfr	epidermal growth factor receptor	-2.1	0.204	1.3	0.172	-1.5	0.094	1.29	0.635	-0.26
1432088_at	Veph1	ventricular zone expressed PH domain homolog 1 (zebrafish)	1.09	0.484	-1.17	0.79	-2.01	0.213	1.79	0.192	-0.08
1421105_at	Jag1	jagged 1	-1.73	0.316	-1.28	0.229	1.08	0.863	1.31	0.19	-0.16
1447449_at	---	---	-1.53	0.071	-1.54	0.121	1.13	0.374	1.49	0.161	-0.11
1460066_at	C80889	expressed sequence C80889	-1.18	0.105	-1.78	0.084	1.03	0.934	2.37	0.282	0.11
1447965_at	C80012	expressed sequence C80012	-1.53	0.049	1.1	0.593	-1.45	0.101	1.09	0.159	-0.2
1440078_at	Brd4	Bromodomain containing 4	1.06	0.674	-1.27	0.31	-1.7	0.015	1.05	0.689	-0.21
1438381_x_at	Ddx47	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	-1.91	0.168	-1.2	0.54	1.08	0.735	1.11	0.582	-0.23
1445048_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B	1.24	0.451	-1.78	0.022	-1.58	0.199	1	0.995	-0.28
1443377_at	Mapkapk5 /// Adam	MAP kinase-activated protein kinase 5 /// a disintegrin and metallopeptidase dom	-3.82	0.115	1.21	0.616	-1.04	0.957	1.3	0.087	-0.59
1438611_at	Tuba3	Tubulin, alpha 3	-1.57	0.311	-1.56	0.568	1.16	0.672	1.14	0.818	-0.21
1427792_at	LOC384413	Similar to immunoglobulin light chain variable region	1.28	0.611	-1.34	0.646	-2.41	0.196	1.36	0.137	-0.28
1457315_at	A230051G13Rik	RIKEN cDNA A230051G13 gene	-2.51	0.011	-1.02	0.951	1.06	0.926	3.01	0.219	0.13
1420779_at	Fhl3	four and a half LIM domains 3	1.01	0.918	-2.02	0.284	-1.07	0.744	1.77	0.414	-0.08
1427307_a_at	Dab1	disabled homolog 1 (Drosophila)	1.15	0.775	-1.6	0.334	-1.5	0.121	1.04	0.896	-0.23
1441521_at	Cacnb2	Calcium channel, voltage-dependent, beta 2 subunit	-2.23	0.403	-1.42	0.061	1.29	0.642	1.24	0.312	-0.28
1447436_at	AI451250	expressed sequence AI451250	1.03	0.921	-1.37	0.542	-1.47	0.36	2.03	0.25	0.06
1444000_at	B930059L03Rik	RIKEN cDNA B930059L03 gene	-1.52	0.438	-1.54	0.462	1.13	0.794	1.03	0.953	-0.22
1428567_at	Hspbap1	Hspb associated protein 1	-2.02	0.5	-1.07	0.922	1.01	0.976	1.06	0.878	-0.25
1443860_at	Ptprd	protein tyrosine phosphatase, receptor type, D	1.08	0.828	-1.33	0.145	-1.64	0.193	1.97	0.151	0.02
1432683_at	5530400K19Rik	RIKEN cDNA 5530400K19 gene	-1.29	0.765	-1.5	0.028	1	0.994	1.71	0.207	-0.02
1444292_at	D7Ertd143e	DNA segment, Chr 7, ERATO Doi 143, expressed	-1.83	0.359	1.23	0.438	-1.5	0.143	1.83	0.028	-0.07

1449718_s_at	4930453N24Rik	RIKEN cDNA 4930453N24 gene	-1.41	0.12	1.03	0.838	-1.43	0.074	1.03	0.904	-0.19
1445865_at	---	---	-1.26	0.706	-1.93	0.106	1.13	0.82	2.25	0.032	0.05
1439832_at	Wasl	Wiskott-Aldrich syndrome-like (human)	1.03	0.908	-1.15	0.286	-1.83	0.01	1.17	0.522	-0.19
1442850_at	---	---	-1.06	0.876	-2.67	0.057	1.12	0.787	1.25	0.611	-0.34
1419322_at	Fgd6	FYVE, RhoGEF and PH domain containing 6	-1.23	0.313	-1.66	0.056	1.03	0.91	1.34	0.31	-0.13
1440507_at	Cd151	CD151 antigen	1.03	0.919	-1.41	0.605	-1.41	0.275	1.79	0.301	0
1443577_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930422D11 pr	1.01	0.843	-1.18	0.614	-1.7	0.33	2.79	0.013	0.23
1431053_at	Mphosph9	M-phase phosphoprotein 9	-1.54	0.366	-1.43	0.325	1.1	0.776	1.13	0.651	-0.19
1430281_at	Glipr1l1	GLI pathogenesis-related 1 like 1	1.26	0.754	-2.07	0.36	-1.43	0.432	1.86	0.359	-0.1
1440086_at	Rnf182	ring finger protein 182	1.19	0.703	-2.55	0.09	-1.16	0.775	2.38	0.139	-0.04
1445109_at	Wdr4	WD repeat domain 4	-1.63	0.237	1.13	0.82	-1.42	0.551	1.11	0.88	-0.2
1425715_at	Il1f8	interleukin 1 family, member 8	-2.68	0.077	1.5	0.368	-1.75	0.347	1.35	0.413	-0.39
1450158_at	Rem1	rad and gem related GTP binding protein 1	1.05	0.901	-1.15	0.515	-1.92	0.054	1.7	0.554	-0.08
1422265_at	Brs3	bombesin-like receptor 3	-2.03	0.297	1.02	0.917	-1.07	0.743	1.4	0.128	-0.17
1454185_at	4933436E23Rik	RIKEN cDNA 4933436E23 gene	1.22	0.793	-1.56	0.216	-1.72	0.191	1.28	0.655	-0.2
1447767_at	Cdkl4	Cyclin-dependent kinase-like 4	-2.08	0.196	1.07	0.753	-1.12	0.521	1.53	0.516	-0.15
1443956_at	Zfp397	zinc finger protein 397	1.17	0.572	-1.46	0.381	-1.69	0.002	1.05	0.943	-0.23
1416223_at	Sh3bp5l	SH3 binding domain protein 5 like	-1.49	0.124	1	0.993	-1.3	0.112	1.36	0.14	-0.11
1436769_at	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	-1.69	0.428	1.01	0.966	-1.19	0.176	1.16	0.691	-0.18
1437066_at	Zbtb20	zinc finger and BTB domain containing 20	1.09	0.573	-1.11	0.561	-2.19	0.013	1.33	0.296	-0.22
1420947_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	1.24	0.615	-1.62	0.169	-1.7	0.18	1.03	0.922	-0.26
1443316_at	---	Transcribed locus	-1.71	0.3	-1.44	0.531	1.17	0.791	1.52	0.392	-0.12
1450923_at	Tgfb2	transforming growth factor, beta 2	1.31	0.144	-2.1	0.12	-1.51	0.36	1.1	0.239	-0.3
1446274_at	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	1.24	0.734	-1.93	0.198	-1.46	0.602	2.96	0.11	0.2
1451116_at	Aacs	acetoacetyl-CoA synthetase	-1.58	0.469	1.14	0.816	-1.48	0.379	1.68	0.256	-0.06
1453166_at	D130073L02Rik	RIKEN cDNA D130073L02 gene	-1.78	0.22	-1.36	0.16	1.15	0.49	1.03	0.9	-0.24
1443481_at	Tube1	epsilon-tubulin 1	-1.67	0.414	-1.28	0.587	1.07	0.908	1.77	0.273	-0.03
1444725_at	Mastl	microtubule associated serine/threonine kinase-like	1.21	0.806	-2.06	0.082	-1.34	0.588	1.11	0.861	-0.27
1447093_at	Col24a1	Procollagen, type XXIV, alpha 1	1.15	0.381	-2.05	0.005	-1.24	0.76	1.97	0.145	-0.04
1430001_at	Il31	interleukin 31	1.16	0.847	-1.2	0.502	-2.19	0.341	1.4	0.248	-0.21
1433188_at	B230112I24Rik	RIKEN cDNA B230112I24 gene	1.23	0.611	-1.1	0.806	-3.25	0.091	1.17	0.484	-0.49
1430677_at	4930442L01Rik	RIKEN cDNA 4930442L01 gene	-1.81	0.11	-1.15	0.175	1.03	0.886	1.06	0.837	-0.22
1431750_at	Ush2a	Usher syndrome 2A (autosomal recessive, mild) homolog (human)	1.03	0.907	-1.46	0.331	-1.37	0.091	1.04	0.83	-0.19
1445113_at	---	---	-1.48	0.271	1.02	0.972	-1.33	0.688	1.67	0.364	-0.03
1453249_a_at	Tex21	testis expressed gene 21	-1.91	0.007	-1.49	0.626	1.26	0.636	1.8	0.196	-0.09
1445708_x_at	3110021A11Rik	RIKEN cDNA 3110021A11 gene	-1.52	0.083	-1.37	0.298	1.06	0.771	1.17	0.319	-0.17
1426516_a_at	Lpin1	lipin 1	-1.47	0.519	-2.35	0.257	1.34	0.475	1.53	0.258	-0.24
1435579_at	Oprs1	Opioid receptor, sigma 1	-1.12	0.569	1.05	0.795	-1.99	0.108	1.24	0.342	-0.2
1431380_at	5730409L17Rik	RIKEN cDNA 5730409L17 gene	-1.2	0.145	1.1	0.871	-1.96	0.024	1.04	0.942	-0.25
1428770_at	Dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila)	-2.1	0.436	-1.06	0.854	1.03	0.882	1.06	0.91	-0.27
1449462_at	3110049J23Rik	RIKEN cDNA 3110049J23 gene	1.02	0.941	-1.24	0.411	-1.59	0.022	1.38	0.566	-0.11
1444985_at	Slc8a1	Solute carrier family 8 (sodium/calcium exchanger), member 1	-1.35	0.492	1.25	0.701	-2.18	0.328	1.31	0.648	-0.24
1453658_at	5830477G23Rik	RIKEN cDNA 5830477G23 gene	-1.6	0.323	-1.28	0.476	1.05	0.724	1.52	0.533	-0.08
1427995_at	Cpa5	carboxypeptidase A5	-2.74	0.139	1.26	0.54	-1.21	0.62	1.28	0.565	-0.35
1450030_at	Dctn4	dynactin 4	-1.62	0.068	-1.36	0.489	1.1	0.763	1.12	0.728	-0.19
1430906_at	2510016G02Rik	RIKEN cDNA 2510016G02 gene	1.45	0.4	-2.23	0.077	-1.81	0.3	3.55	0.008	0.24
1453764_at	3110021N24Rik	RIKEN cDNA 3110021N24 gene	1.07	0.563	-1.25	0.303	-1.71	0.015	1.57	0.088	-0.08
1445766_at	Ppfia2	Protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting p	1.01	0.978	-1.07	0.867	-1.96	0.354	1.22	0.714	-0.2
1428487_s_at	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	1.08	0.901	-1.27	0.588	-1.69	0.089	1.25	0.448	-0.16
1453546_at	1700029I08Rik	RIKEN cDNA 1700029I08 gene	-2.75	0.101	-1.37	0.561	1.36	0.65	1.24	0.679	-0.38
1440997_at	Tnrc6c	trinucleotide repeat containing 6C	-4.76	0.041	-1.08	0.86	1.32	0.584	1.78	0.51	-0.69
1427214_at	Agmat	agmatine ureohydrolase (agmatinase)	1.12	0.613	-1.31	0.114	-1.75	0.084	2.8	0.128	0.21
1428885_at	Afmid	arylformamidase	-1.39	0.098	-1.55	0.31	1.09	0.812	1.49	0.328	-0.09

1450704_at	Ihh	Indian hedgehog	1.13	0.771	-1.48	0.036	-1.54	0.033	1.1	0.807	-0.2
1417878_at	E2f1	E2F transcription factor 1	1.06	0.911	-1.69	0.23	-1.25	0.368	2.11	0.249	0.06
1438748_at	9830127L17Rik	RIKEN cDNA 9830127L17 gene	1.03	0.922	-1.13	0.538	-1.85	0.006	1.02	0.918	-0.23
1454524_at	2310075M01Rik	RIKEN cDNA 2310075M01 gene	1.02	0.972	-2.19	0.388	-1.03	0.95	1.35	0.617	-0.21
1454949_at	Usp7	Ubiquitin specific peptidase 7	1.02	0.958	-1.65	0.275	-1.2	0.353	1.15	0.744	-0.17
1458157_at	Nek8	NIMA (never in mitosis gene a)-related expressed kinase 8	-1.92	0.084	-1.8	0.062	1.38	0.53	1.17	0.751	-0.29
1432670_at	9030420N05Rik	RIKEN cDNA 9030420N05 gene	-1.22	0.342	-2.37	0.464	1.21	0.727	1.19	0.744	-0.3
1426193_at	Otos	otospiralin	-3.12	0.258	1.43	0.323	-1.42	0.333	1.34	0.329	-0.44
1439347_at	Tns4	tensin 4	-1.61	0.184	-1.42	0.659	1.13	0.753	1.15	0.656	-0.19
1433208_at	2210017G18Rik	RIKEN cDNA 2210017G18 gene	-2.47	0.308	-1.96	0.192	1.54	0.312	2.16	0.066	-0.18
1441200_at	Klf3	Kruppel-like factor 3 (basic)	1.02	0.884	-1.44	0.038	-1.34	0.29	1.1	0.682	-0.17
1421447_at	Onecut1	one cut domain, family member 1	1.19	0.721	-3.26	0.206	-1.04	0.9	1.09	0.776	-0.51
1453663_at	4932442E05Rik	RIKEN cDNA 4932442E05 gene	1.12	0.685	-1.09	0.879	-2.34	0.03	1.66	0.495	-0.17
1432257_at	Gsdmdc2	gasdermin domain containing 2	-1.08	0.935	-2.46	0.386	1.12	0.811	1.14	0.568	-0.32
1457313_at	Ocrl	oculocerebrorenal syndrome of Lowe	-1.31	0.005	1.11	0.738	-1.7	0.015	1.09	0.618	-0.2
1431497_at	C330022C24Rik	RIKEN cDNA C330022C24 gene	-1.73	0.049	-1.15	0.502	1.01	0.971	1.41	0.264	-0.11
1430742_a_at	Spata16	spermatogenesis associated 16	1.01	0.978	-1.41	0.677	-1.35	0.62	2.17	0.005	0.1
1459945_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.19	0.823	-1.25	0.563	-2.1	0.247	2.23	0.08	0.01
1430201_at	9130017K11Rik	RIKEN cDNA 9130017K11 gene	-1.64	0.43	-1.38	0.506	1.13	0.638	1.23	0.603	-0.17
1459251_at	A430088I17Rik	RIKEN cDNA A430088I17 gene	-1.13	0.854	-2.14	0.135	1.11	0.709	1.15	0.752	-0.25
1426021_a_at	Cdc7	cell division cycle 7 (S. cerevisiae)	-1.98	0.351	-1.19	0.659	1.12	0.482	1.4	0.277	-0.17
1450125_at	Gata5	GATA binding protein 5	-1.46	0.223	-1.84	0.08	1.23	0.357	1.21	0.123	-0.21
1420090_at	---	---	1.13	0.796	-1.89	0.121	-1.24	0.519	1.2	0.483	-0.2
1432756_at	2210409O19Rik	RIKEN cDNA 2210409O19 gene	-1.79	0.35	-1.3	0.612	1.13	0.737	1.49	0.469	-0.12
1460399_at	Ccdc117	coiled-coil domain containing 117	-1.31	0.022	-1.49	0.012	1.03	0.858	1.02	0.952	-0.19
1457333_at	Sdk2	sidekick homolog 2 (chicken)	-1.52	0.318	1.06	0.916	-1.35	0.236	1.18	0.424	-0.16
1449993_at	AF119384	cDNA sequence AF119384	-1.34	0.204	1.2	0.687	-1.94	0.039	1.13	0.439	-0.24
1428414_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	-2.83	0.456	1.04	0.93	1.07	0.763	-1.53	0.467	-0.56
1449424_at	Plek2	pleckstrin 2	1.13	0.586	-1.25	0.532	-1.89	0.097	11.86	0.214	2.46
1429945_at	2810406K13Rik	RIKEN cDNA 2810406K13 gene	-2.19	0.074	1.53	0.479	-2.11	0.038	1.01	0.97	-0.44
1454569_at	4930480K02Rik	RIKEN cDNA 4930480K02 gene	-1.95	0.279	1.33	0.635	-1.6	0.211	1.25	0.725	-0.24
1433045_at	4930535F04Rik	RIKEN cDNA 4930535F04 gene	-1.02	0.98	-2.95	0.138	1.14	0.783	1.66	0.18	-0.29
1447438_at	Whrn	Whirlin	-4.16	0.052	1.08	0.863	1.14	0.838	-1.6	0.254	-0.88
1455188_at	Ephb1	Eph receptor B1	-1.13	0.395	-2.26	0.214	1.13	0.744	1.24	0.254	-0.25
1458937_at	Nt5dc1	5'-nucleotidase domain containing 1	1.38	0.496	-1.84	0.479	-1.85	0.073	1.14	0.7	-0.29
1455715_at	2610044O15Rik	RIKEN cDNA 2610044O15 gene	-1.48	0.1	1.25	0.723	-1.84	0.026	1.1	0.793	-0.24
1426896_at	Zfp191	zinc finger protein 191	1.12	0.251	-1.42	0.003	-1.57	0.013	1.03	0.928	-0.21
1446344_at	Nyx	nyctalopin	-2.05	0.052	1.03	0.909	-1.05	0.761	1.01	0.962	-0.27
1450558_at	V1ra1	vomeronasal 1 receptor, A1	1.4	0.589	-1.44	0.618	-2.68	0.135	3.49	0.017	0.19
1458073_at	9330156P08Rik	RIKEN cDNA 9330156P08 gene	-1.7	0.181	-1.45	0.504	1.19	0.57	1.1	0.788	-0.22
1453500_at	Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	-1.26	0.009	-2.95	0.117	1.33	0.546	1.16	0.575	-0.43
1458828_at	AW146242	Expressed sequence AW146242	-2.13	0.221	1.11	0.859	-1.13	0.536	1.12	0.743	-0.26
1418486_at	Vnn1	vanin 1	1.26	0.08	-1.87	0.241	-1.49	0.026	1.49	0.38	-0.15
1431481_at	4930443O20Rik	RIKEN cDNA 4930443O20 gene	-2.17	0.14	1.23	0.627	-1.28	0.562	1.09	0.888	-0.29
1458140_at	Slit2	slit homolog 2 (Drosophila)	-1.11	0.639	1.06	0.918	-1.98	0.003	1.46	0.148	-0.14
1421831_at	---	---	-1.32	0.134	-1.99	0.196	1.21	0.805	1.35	0.678	-0.19
1456259_at	LOC674888	similar to integrator complex subunit 10	1.02	0.933	-1.98	0.476	-1.07	0.656	1.13	0.154	-0.22
1457960_at	---	Transcribed locus	1.29	0.328	-1.73	0.119	-1.67	0.449	1.92	0.184	-0.05
1456353_at	Supt4h1	suppressor of Ty 4 homolog 1 (S. cerevisiae)	-1.84	0.342	1.09	0.812	-1.2	0.445	1.24	0.376	-0.18
1431952_at	4930532I03Rik	RIKEN cDNA 4930532I03 gene	1.01	0.991	-3.61	0.03	1.18	0.727	-1.78	0.495	-0.8
1457352_x_at	9430071P14Rik	RIKEN cDNA 9430071P14 gene	-1.47	0.508	-1.95	0.262	1.27	0.72	1.22	0.796	-0.23
1452378_at	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	1.04	0.863	1.04	0.876	-2.58	0.039	-1.19	0.544	-0.42
1416761_at	---	---	-1.3	0.19	-1.75	0.39	1.12	0.596	1.39	0.306	-0.13

1447701_x_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	-1.48	0.133	-1.34	0.619	1.05	0.897	1.21	0.696	-0.14
1439611_at	Chrm1	cholinergic receptor, muscarinic 1, CNS	-2.34	0.121	1.19	0.507	-1.18	0.402	1.48	0.129	-0.21
1432326_at	1700042B14Rik	RIKEN cDNA 1700042B14 gene	-1.79	0.037	-1.25	0.726	1.11	0.846	2.56	0.007	0.16
1456572_x_at	Cct4	chaperonin subunit 4 (delta)	-1.82	0.072	1.16	0.554	-1.32	0.229	1.19	0.591	-0.2
1425579_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	-1.47	0.039	-1.41	0.164	1.08	0.798	1.05	0.803	-0.19
1421707_at	Tmc2	transmembrane channel-like gene family 2	-1.35	0.419	-1.49	0.65	1.06	0.89	1.28	0.655	-0.13
1450155_at	Itga4	integrin alpha 4	1.05	0.916	-2.06	0.105	-1.07	0.851	1.14	0.724	-0.23
1431604_a_at	Ccdc97	coiled-coil domain containing 97	-1.44	0.058	1.12	0.863	-1.52	0.464	1.02	0.955	-0.21
1454590_at	A930018O16Rik	RIKEN cDNA A930018O16 gene	-1.34	0.18	1.02	0.961	-1.42	0.554	1.16	0.677	-0.15
1439137_at	Slc4a9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	-1.8	0.084	1.33	0.713	-1.7	0.149	1.68	0.396	-0.12
1442938_at	D12Ertd247e	DNA segment, Chr 12, ERATO Doi 247, expressed	-1.29	0.442	-2.53	0.136	1.3	0.147	1.1	0.436	-0.35
1435985_at	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	-1.17	0.424	1.07	0.077	-1.84	0.045	1.15	0.521	-0.2
1447009_at	C79657	expressed sequence C79657	-1.32	0.171	1.01	0.97	-1.42	0.485	1.49	0.47	-0.06
1452609_at	1190005I06Rik	RIKEN cDNA 1190005I06 gene	-2.36	0.41	-1.11	0.343	1.15	0.755	1.12	0.871	-0.3
1445736_at	---	---	-2.04	0.11	-1.3	0.55	1.21	0.741	1.58	0.26	-0.14
1457308_at	Usp45	Ubiquitin specific petidase 45	1.19	0.342	-1.7	0.169	-1.44	0.324	1.1	0.868	-0.21
1459536_at	Calcrl	Calcitonin receptor-like	-1.39	0.586	1.3	0.51	-2.19	0.192	1.02	0.898	-0.32
1456602_at	4932417I16Rik	RIKEN cDNA 4932417I16 gene	-1.09	0.404	-2.28	0.042	1.12	0.258	1.43	0.1	-0.2
1451837_at	Ap3b2	adaptor-related protein complex 3, beta 2 subunit	-1.23	0.067	-2.84	0.054	1.31	0.615	1.32	0.581	-0.36
1440657_at	Cntn3	Contactin 3	-1.42	0.254	-1.41	0.491	1.05	0.839	1.93	0.329	0.04
1449557_at	1600012F09Rik /// I	RIKEN cDNA 1600012F09 gene /// hypothetical LOC624446	1.03	0.841	-1.37	0.08	-1.41	0.184	1.28	0.521	-0.12
1420707_a_at	Traip	TRAF-interacting protein	1.12	0.828	-2.22	0.063	-1.11	0.75	2.81	0.22	0.15
1425731_at	Ankrd24	ankyrin repeat domain 24	-2.08	0.068	-1.21	0.454	1.17	0.348	1.3	0.569	-0.21
1431720_at	2810404F17Rik	RIKEN cDNA 2810404F17 gene	-1.58	0.394	1.15	0.77	-1.45	0.548	1.74	0.069	-0.04
1446710_at	C76669	expressed sequence C76669	-1.75	0.007	1.19	0.52	-1.4	0.506	1.46	0.588	-0.13
1441984_at	Clspn	claspin homolog (Xenopus laevis)	1.09	0.733	-1.77	0.113	-1.22	0.694	2.13	0.354	0.06
1453275_at	2310002L13Rik	RIKEN cDNA 2310002L13 gene	-1.91	0.328	-1.15	0.827	1.08	0.576	1.45	0.419	-0.13
1427832_at	Tuba-rs1	tubulin alpha, related sequence 1	-1.42	0.51	-1.48	0.1	1.09	0.787	1.19	0.543	-0.15
1436249_at	Ttll4	tubulin tyrosine ligase-like family, member 4	-1.36	0.295	-1.39	0.009	1.02	0.732	1.35	0.445	-0.1
1438499_at	1700029I15Rik	RIKEN cDNA 1700029I15 gene	-1.36	0.688	-1.79	0.15	1.18	0.523	1.14	0.681	-0.21
1420130_s_at	D10Wsu52e	DNA segment, Chr 10, Wayne State University 52, expressed	1.02	0.964	-1.11	0.537	-1.8	0.035	1.12	0.766	-0.19
1430056_at	D130059P03Rik	RIKEN cDNA D130059P03 gene	-1.24	0.666	1.06	0.807	-1.64	0.058	1.05	0.781	-0.19
1433366_at	6030458A19Rik	RIKEN cDNA 6030458A19 gene	1.05	0.933	-1.26	0.133	-1.58	0.178	1.4	0.338	-0.1
1431571_at	4933437I04Rik	RIKEN cDNA 4933437I04 gene	-2	0.521	1.15	0.534	-1.21	0.624	1.04	0.779	-0.26
1454283_at	9130023D20Rik	RIKEN cDNA 9130023D20 gene	1	0.99	-1.19	0.435	-1.58	0.288	1.77	0.231	0
1428990_at	2310047K21Rik	RIKEN cDNA 2310047K21 gene	1.07	0.83	-1.73	0.131	-1.21	0.209	1.01	0.954	-0.21
1440547_at	---	---	-1.39	0.353	1.23	0.462	-1.88	0.222	1.15	0.552	-0.22
1459163_at	---	---	-3.17	0.167	1.07	0.611	1.09	0.767	-1.04	0.954	-0.51
1448878_at	Mxd3	Max dimerization protein 3	-1.52	0.427	1.03	0.958	-1.27	0.461	3.26	0.072	0.38
1441501_at	Serbp1	Serpine1 mRNA binding protein 1	1.05	0.798	-1.24	0.021	-1.62	0.047	1.18	0.622	-0.16
1444603_at	2810030D12Rik	RIKEN cDNA 2810030D12 gene	1.15	0.649	-1.4	0.33	-1.65	0.115	1.63	0.538	-0.07
1419921_s_at	Usp7	Ubiquitin specific peptidase 7	-1.3	0.589	1.04	0.939	-1.5	0.055	1.33	0.206	-0.11
1443054_at	Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	-1.37	0.307	1.15	0.758	-1.67	0	1.37	0.053	-0.13
1432870_at	4932429P19Rik	RIKEN cDNA 4932429P19 gene	1.16	0.479	-1.97	0.478	-1.24	0.778	1.88	0.144	-0.04
1439416_x_at	Tubb2c	tubulin, beta 2c	-2.41	0.484	1.2	0.851	-1.16	0.574	1.69	0.247	-0.17
1459358_at	Pkp2	Plakophilin 2	1.04	0.667	-1.27	0.257	-1.54	0.029	1.08	0.368	-0.17
1430356_at	2210402A03Rik	RIKEN cDNA 2210402A03 gene	1.37	0.23	-1.4	0.436	-2.54	0.009	1.06	0.814	-0.38
1429361_at	Pmch	pro-melanin-concentrating hormone	1.25	0.319	-1.56	0.307	-1.7	0.126	1.33	0.282	-0.17
1443492_at	Itpr1	Inositol 1,4,5-triphosphate receptor 1	1.17	0.81	-2.29	0.301	-1.15	0.861	1.53	0.396	-0.18
1432602_at	---	---	-3.27	0.039	1.41	0.466	-1.31	0.388	1.04	0.526	-0.53
1445423_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	1.06	0.851	-1.58	0.058	-1.27	0.113	1.37	0.395	-0.1
1420210_at	AV344025	Expressed sequence AV344025	-1.38	0.21	1.03	0.959	-1.37	0.587	2.23	0.017	0.13
1429445_at	4921510J17Rik	RIKEN cDNA 4921510J17 gene	-2.69	0.332	-1.31	0.537	1.35	0.298	1.19	0.832	-0.37

1430962_at	Ube2s	ubiquitin-conjugating enzyme E2S	-1.43	0.655	-3.21	0.139	1.47	0.04	1.95	0.195	-0.3
1460655_a_at	Ubp1	upstream binding protein 1	-1.45	0.081	-1.28	0.017	1.01	0.962	1.86	0.144	0.03
1443727_x_at	Smyd1	SET and MYND domain containing 1	-1.72	0.267	-1.23	0.48	1.08	0.848	2	0.031	0.03
1445170_at	2700012I20Rik	RIKEN cDNA 2700012I20 gene	-1.48	0.24	1.23	0.771	-1.73	0.049	1.01	0.987	-0.24
1446162_at	Pabpc5	poly A binding protein, cytoplasmic 5	1	0.997	-1.47	0.514	-1.25	0.621	1.87	0.135	0.04
1448294_at	Litaf /// LOC545182	LPS-induced TN factor /// hypothetical protein LOC545182	-1.39	0.312	-1.34	0.155	1.02	0.912	1.01	0.955	-0.18
1456527_at	Hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	-1.5	0.291	-1.61	0.425	1.2	0.393	1.04	0.923	-0.22
1431360_s_at	Dmrtc1a	DMRT-like family C1a	1.14	0.702	-1.88	0.107	-1.24	0.35	1.06	0.871	-0.23
1445992_at	---	Transcribed locus	-1.49	0.646	-1.49	0.461	1.14	0.787	1.37	0.626	-0.12
1443373_at	Map4k5	Mitogen-activated protein kinase kinase kinase kinase 5	-1.34	0.739	1.3	0.441	-2.31	0.053	1.02	0.933	-0.33
1442618_at	Ldhb	Lactate dehydrogenase B	1.11	0.231	-1.21	0.093	-1.83	0.023	1.82	0.079	-0.03
1459999_at	Sfrs15 /// LOC6703	splicing factor, arginine/serine-rich 15 /// similar to splicing factor, arginine/serine-	-3.17	0.078	-1.17	0.753	1.31	0.505	1.2	0.416	-0.46
1446941_at	C78505	expressed sequence C78505	1.02	0.925	-1.35	0.396	-1.39	0.148	1.24	0.294	-0.12
1459780_at	Trp53	transformation related protein 53	-2.25	0.474	1.57	0.408	-2.12	0.044	1.62	0.387	-0.29
1460306_at	Myoc	myocilin	-1.96	0.389	1.49	0.453	-2.06	0.254	1.36	0.391	-0.29
1447638_at	Afmid	Arylformamidase	-1.95	0.324	-1.15	0.726	1.1	0.86	1.83	0.158	-0.04
1459830_at	---	Transcribed locus	-1.59	0.076	-1.23	0.658	1.04	0.839	1.33	0.119	-0.11
1432649_at	3300002A11Rik	RIKEN cDNA 3300002A11 gene	1.03	0.753	-1.49	0.383	-1.27	0.449	1.1	0.687	-0.16
1432865_at	D730050C22Rik	RIKEN cDNA D730050C22 gene	-1.3	0.367	-1.42	0.495	1.01	0.982	2.03	0.236	0.08
1454515_at	5430425E15Rik	RIKEN cDNA 5430425E15 gene	1.5	0.378	-2.34	0.232	-1.8	0.209	1.11	0.861	-0.38
1422355_at	Taar1	trace amine-associated receptor 1	-1.39	0.491	-1.87	0.212	1.23	0.618	1.96	0.214	-0.02
1459660_at	---	---	1.04	0.882	-1.56	0.449	-1.25	0.16	1.45	0.378	-0.08
1446603_at	---	---	-2.22	0.049	1.04	0.95	-1.01	0.993	1.59	0.531	-0.15
1459520_at	---	---	-1.24	0.748	1.32	0.423	-2.76	0.039	1.1	0.864	-0.4
1443022_at	4930521E07Rik	RIKEN cDNA 4930521E07 gene	-1.14	0.864	-1.74	0.296	1.03	0.898	1.45	0.171	-0.1
1420692_at	Il2ra	interleukin 2 receptor, alpha chain	-2.34	0.112	1.01	0.975	1.04	0.874	-1.2	0.297	-0.37
1419701_s_at	Anks3	ankyrin repeat and sterile alpha motif domain containing 3	1.1	0.547	-2.8	0.015	1.03	0.854	-2.26	0.064	-0.73
1438829_at	Gm96	gene model 96, (NCBI)	-1.74	0.307	-1.31	0.663	1.15	0.535	1.24	0.061	-0.16
1436013_at	Gsg1l	GSG1-like	1.07	0.357	-2.03	0.354	-1.09	0.912	1.96	0.007	-0.02
1427364_a_at	Odc1 /// LOC63978	ornithine decarboxylase, structural 1 /// similar to Ornithine decarboxylase (ODC)	-1.48	0.024	-1.56	0.007	1.17	0.446	4.55	0.171	0.67
1456914_at	---	---	-1.41	0.106	-1.39	0.355	1.06	0.878	1.71	0.217	-0.01
1441182_at	Brwd3	bromodomain and WD repeat domain containing 3	-1.41	0.443	-1.47	0.355	1.1	0.874	1.39	0.644	-0.1
1443565_at	AI849538	expressed sequence AI849538	-1.41	0.653	-3.14	0.165	1.46	0.262	2.04	0.281	-0.26
1447435_at	---	---	1.13	0.884	-1.83	0.195	-1.24	0.621	1.84	0.022	-0.02
1454432_at	4933423N03Rik	RIKEN cDNA 4933423N03 gene	-1.62	0.276	1.28	0.517	-1.69	0.326	1.76	0.234	-0.07
1430253_at	2900006B11Rik	RIKEN cDNA 2900006B11 gene	-1.74	0.079	-2.09	0.09	1.43	0.499	1.28	0.378	-0.28
1442252_at	Kif13a	kinesin family member 13A	1.06	0.746	-1.37	0.143	-1.43	0.168	1.17	0.203	-0.14
1445353_at	---	---	1.46	0.626	-1.92	0.351	-1.99	0.21	1.41	0.456	-0.26
1421663_at	Dhrs2	dehydrogenase/reductase member 2	1.07	0.905	-1.29	0.543	-1.56	0.358	1.44	0.365	-0.08
1441399_at	---	---	-1.19	0.502	1.19	0.745	-2.17	0.173	1.65	0.204	-0.13
1455842_x_at	Usp15	ubiquitin specific peptidase 15	1.11	0.594	-1.37	0.058	-1.54	0.05	1.44	0.374	-0.09
1445642_at	Lemd1	LEM domain containing 1	-2.15	0.354	-1.47	0.396	1.34	0.257	1.3	0.642	-0.24
1456747_x_at	Cd99l2	Cd99 antigen-like 2	1.1	0.659	-1.15	0.652	-1.96	0.012	1.19	0.348	-0.2
1444811_at	Tloc1	translocation protein 1	1.23	0.582	-1.34	0.369	-1.97	0.028	1.53	0.261	-0.13
1429149_at	Gins3	GINS complex subunit 3 (Psf3 homolog)	-1.37	0.022	-1.44	0.145	1.06	0.799	1.67	0.388	-0.02
1441181_at	---	Transcribed locus	1.07	0.585	1.02	0.961	-2.51	0.054	-1.03	0.96	-0.36
1438295_at	Glcci1	Glucocorticoid induced transcript 1	-1.16	0.646	-1.76	0.149	1.06	0.783	1.34	0.281	-0.13
1427096_s_at	Ssr4	signal sequence receptor, delta	-2	0.236	1.15	0.477	-1.2	0.052	1.07	0.723	-0.24
1440074_at	LOC432988	hypothetical gene supported by AK082832	-1.88	0.004	-1.24	0.707	1.15	0.79	1.16	0.705	-0.2
1448872_at	Reg3g	regenerating islet-derived 3 gamma	1.1	0.602	-1.1	0.525	-2.08	0.087	1.19	0.686	-0.22
1456470_x_at	Tubb2c	tubulin, beta 2c	-2.32	0.049	-1.1	0.699	1.15	0.636	1.18	0.648	-0.27
1460515_at	8430419K02Rik	RIKEN cDNA 8430419K02 gene	1.03	0.962	-1.28	0.712	-1.47	0.302	1.88	0.209	0.04
1424895_at	Gpsm2	G-protein signalling modulator 2 (AGS3-like, C. elegans)	-1.36	0.011	1.07	0.591	-1.47	0.295	6.32	0.185	1.14

1422765_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	1.01	0.991	-1.28	0.648	-1.43	0.258	1.26	0.673	-0.11
1432818_at	1190002C06Rik	RIKEN cDNA 1190002C06 gene	1.12	0.745	-2.2	0.241	-1.09	0.78	1.01	0.988	-0.29
1437609_at	Ube2u	ubiquitin-conjugating enzyme E2U (putative)	-1.09	0.439	1.09	0.815	-2.08	0.205	1.14	0.835	-0.23
1436119_at	Aldh1l2	aldehyde dehydrogenase 1 family, member L2	-2.04	0.031	-1.1	0.622	1.09	0.792	1.02	0.968	-0.26
1458688_at	Arhgap28	Rho GTPase activating protein 28	-1.5	0.136	-1.23	0.364	1.01	0.904	1.02	0.947	-0.18
1436162_at	C730048C13Rik ///	RIKEN cDNA C730048C13 gene /// similar to integral membrane transport protei	-1.78	0.005	-1.52	0.01	1.27	0.775	1.29	0.47	-0.19
1458207_at	Zbed3	Zinc finger, BED domain containing 3	1.15	0.79	-1.36	0.695	-1.66	0.168	1.09	0.887	-0.19
1456908_at	BC023202	cDNA sequence BC023202	1.09	0.751	-1.32	0.586	-1.55	0.062	1.9	0.266	0.03
1447099_at	Grit	Rho GTPase-activating protein	-1.59	0.271	-2.05	0.171	1.37	0.601	1.15	0.768	-0.28
1454398_at	---	---	1.05	0.359	-2.62	0.389	1.06	0.888	-3.41	0.073	-0.98
1452359_at	AA536743	expressed sequence AA536743	1.14	0.451	-1.32	0.038	-1.68	0	1.26	0.335	-0.15
1449452_a_at	Gp2	glycoprotein 2 (zymogen granule membrane)	-1.62	0.168	-1.74	0.137	1.3	0.413	1.09	0.894	-0.24
1452546_x_at	Defb11	defensin beta 11	-1.51	0.153	1.03	0.95	-1.25	0.545	2.15	0.318	0.1
1431408_at	4930412B13Rik	RIKEN cDNA 4930412B13 gene	-2	0.139	1.37	0.535	-1.6	0.468	1.86	0.015	-0.09
1441730_at	Ppp1r12b	Protein phosphatase 1, regulatory (inhibitor) subunit 12B	1.21	0.72	-1.44	0.245	-1.7	0.044	1.03	0.44	-0.22
1427563_at	Dlx6as	distal-less homeobox 6, antisense	-1.65	0.093	-1.95	0.325	1.37	0.052	1.09	0.647	-0.29
1433298_at	5830461L22Rik	RIKEN cDNA 5830461L22 gene	1.08	0.857	-2.12	0.099	-1.07	0.896	2.28	0.292	0.04
1445391_at	Diap1 /// LOC6715	diaphanous homolog 1 (Drosophila) /// similar to Protein diaphanous homolog 1 (I	1.02	0.921	1.01	0.95	-2.18	0.016	-1.62	0.06	-0.44
1456414_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420414K2	-1.07	0.937	1.03	0.941	-1.91	0.049	1.67	0.267	-0.07
1460371_at	Hspa12b	heat shock protein 12B	-2.06	0.437	-1.09	0.672	1.09	0.754	1.18	0.729	-0.22
1438224_at	Zswim5	zinc finger, SWIM domain containing 5	-1.46	0.226	-1.27	0.364	1.02	0.743	1.43	0.322	-0.07
1449949_a_at	Cxadr	coxsackievirus and adenovirus receptor	-2.07	0.28	1.01	0.988	1	0.982	-1.15	0.302	-0.3
1418666_at	Ptx3	pentraxin related gene	-1.46	0.072	1.08	0.717	-1.38	0.195	1.18	0.627	-0.14
1416828_at	Snap25	synaptosomal-associated protein 25	-1.2	0.472	-1.58	0.429	1.03	0.929	2.63	0.002	0.22
1453690_at	Mpp7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	-1.51	0.359	1.3	0.566	-1.88	0.007	1.42	0.559	-0.17
1433647_s_at	Rhobtb3	Rho-related BTB domain containing 3	1.16	0.456	-1.45	0.097	-1.55	0.058	1.31	0.356	-0.13
1449034_at	Klkb1	kallikrein B, plasma 1	1.07	0.876	-1.48	0.036	-1.33	0.186	1.89	0.17	0.04
1448066_at	LOC552909	hypothetical LOC552909	-1.29	0.395	-2.27	0.385	1.28	0.636	1.33	0.51	-0.24
1448780_at	Slc12a2	solute carrier family 12, member 2	-1.16	0.546	1.01	0.937	-1.61	0.263	1.32	0.596	-0.11
1431898_at	4930403J07Rik	RIKEN cDNA 4930403J07 gene	-1.31	0.183	1.14	0.278	-1.7	0.296	1.79	0.299	-0.02
1444774_at	Det1	de-etiolated homolog 1 (Arabidopsis)	-2.55	0.407	-1.23	0.605	1.29	0.344	1.32	0.17	-0.29
1427717_at	Cd80	CD80 antigen	1.08	0.826	-3.65	0.004	1.14	0.622	-1.77	0.54	-0.8
1446569_at	Itga1	Integrin alpha 1	1.03	0.906	-1.07	0.546	-1.88	0.022	1.12	0.475	-0.2
1425830_a_at	2810452K22Rik ///	RIKEN cDNA 2810452K22 gene /// similar to cyclin-dependent kinase 2-interactir	1.05	0.769	-1.25	0.037	-1.54	0.004	1.7	0.217	-0.01
1442770_at	9530033F24Rik	RIKEN cDNA 9530033F24 gene	1.18	0.498	-1.59	0.44	-1.47	0.354	2.15	0.202	0.07
1439538_at	0610011N22Rik	RIKEN cDNA 0610011N22 gene	1.11	0.516	-1.58	0.098	-1.33	0.34	1.28	0.586	-0.13
1432451_at	4930445E18Rik	RIKEN cDNA 4930445E18 gene	-1.37	0.531	1.21	0.693	-1.8	0.468	1.18	0.777	-0.19
1450236_at	Foxo3a	forkhead box O3a	-1.21	0.668	-2.54	0.152	1.27	0.613	1.6	0.029	-0.22
1445657_at	AW111846	expressed sequence AW111846	-1.59	0.37	-1.17	0.311	1.01	0.948	1.56	0.124	-0.05
1450063_at	Fmn2	formin 2	-1.95	0.338	-1.12	0.861	1.09	0.839	1.14	0.807	-0.21
1432820_at	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.02	0.928	-1.35	0.217	-1.35	0.27	1.11	0.464	-0.15
1459371_at	Eif4e	Eukaryotic translation initiation factor 4E	1.23	0.786	-2.09	0.215	-1.27	0.397	1.3	0.57	-0.21
1437932_a_at	Cldn1	claudin 1	-1.08	0.621	1.06	0.846	-1.94	0.035	1.28	0.764	-0.17
1435767_at	Scn3b	sodium channel, voltage-gated, type III, beta	-1.1	0.864	1.05	0.805	-1.87	0.097	1.26	0.697	-0.16
1445869_at	Tmem28	Transmembrane protein 28	-1.36	0.663	1.01	0.99	-1.32	0.672	1.25	0.645	-0.11
1447341_at	D12Ertd551e	DNA segment, Chr 12, ERATO Doi 551, expressed	1.23	0.01	-3.45	0.022	-1.02	0.874	1.35	0.337	-0.47
1419264_at	1200014M14Rik	RIKEN cDNA 1200014M14 gene	1.15	0.662	-1.58	0.433	-1.4	0.021	1.02	0.941	-0.2
1454189_at	4930557J02Rik	RIKEN cDNA 4930557J02 gene	-1.05	0.772	-2.16	0.302	1.08	0.73	1.28	0.459	-0.21
1425446_at	---	---	1.12	0.729	-1.48	0.424	-1.42	0.253	1.31	0.25	-0.12
1428048_at	BC027582	cDNA sequence BC027582	-1.18	0.64	-1.7	0.175	1.06	0.741	1.19	0.38	-0.16
1445167_at	9630001P10Rik	RIKEN cDNA 9630001P10 gene	-1.23	0.656	-1.53	0.195	1.04	0.917	1.88	0.287	0.04
1443608_at	---	---	-5.86	0.256	-3.39	0.004	2.03	0.29	2.51	0.285	-1.18
1441641_at	D630032N06Rik	RIKEN cDNA D630032N06 gene	-1.13	0.352	1.06	0.863	-1.8	0.012	1.38	0.592	-0.12

1425411_at	Arl4a	ADP-ribosylation factor-like 4A	-1.4	0.294	-1.32	0.411	1.03	0.92	2.9	0.197	0.3
1439109_at	Ccdc68	coiled-coil domain containing 68	-1.2	0.264	1.03	0.935	-1.56	0.013	1.56	0.267	-0.04
1435147_x_at	Igsf4d	immunoglobulin superfamily, member 4	-1.46	0.551	-1.25	0.702	1.01	0.976	2.48	0.12	0.2
1422168_a_at	Bdnf	brain derived neurotrophic factor	-1.34	0.566	-1.45	0.391	1.06	0.757	1.39	0.359	-0.08
1432299_at	4921513I08Rik	RIKEN cDNA 4921513I08 gene	-2.72	0.057	1.32	0.652	-1.23	0.674	1	0.995	-0.41
1453828_at	4932422M17Rik	RIKEN cDNA 4932422M17 gene	1.36	0.695	-2.64	0.195	-1.32	0.646	1.28	0.517	-0.33
1431957_at	Lrrc44	leucine rich repeat containing 44	-1.38	0.356	-1.46	0.183	1.09	0.865	1.24	0.163	-0.13
1438660_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.02	0.934	-1.25	0.052	-1.48	0.13	1.01	0.945	-0.17
1438482_at	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	-1.32	0.203	-1.57	0.407	1.11	0.78	1.11	0.576	-0.17
1459846_x_at	Tmem4	transmembrane protein 4	-1.32	0.331	1.11	0.386	-1.58	0.05	1.03	0.877	-0.19
1431667_s_at	2610021K21Rik	RIKEN cDNA 2610021K21 gene	1.43	0.655	-3.34	0.13	-1.3	0.628	1.66	0.502	-0.39
1440556_at	---	---	-1.57	0.048	1.17	0.506	-1.44	0.168	1.36	0.154	-0.12
1432559_at	2210409D07Rik	RIKEN cDNA 2210409D07 gene	1.16	0.766	-1.32	0.592	-1.7	0.05	1.08	0.927	-0.2
1424021_at	LOC674449	similar to ADP-ribosylation-like factor 6-interacting protein 6	-1.46	0.035	-1.35	0.076	1.08	0.642	1.97	0.248	0.06
1424553_at	Gup1	Gup1, glycerol uptake/transporter homolog (yeast)	-1.11	0.721	-1.81	0.116	1.05	0.807	1.44	0.22	-0.11
1452397_at	2810474O19Rik	RIKEN cDNA 2810474O19 gene	-1.41	0.292	-1.7	0.068	1.21	0.607	1.45	0.45	-0.11
1452926_at	Ttc14	tetratricopeptide repeat domain 14	1.07	0.897	-1.79	0.147	-1.14	0.703	1.01	0.897	-0.21
1430139_at	Hells	helicase, lymphoid specific	-1.9	0.35	1.21	0.598	-1.3	0.317	1.37	0.268	-0.16
1422021_at	Spry4	sprouty homolog 4 (Drosophila)	1.19	0.388	-1.73	0.152	-1.37	0.248	1.51	0.519	-0.1
1445799_at	---	---	-1.32	0.664	1.19	0.679	-1.81	0.056	1.21	0.416	-0.18
1439759_x_at	2410078J06Rik	RIKEN cDNA 2410078J06 gene	-1.49	0.574	1.1	0.847	-1.36	0.466	1.16	0.321	-0.15
1442626_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	1.04	0.896	-1.16	0.482	-1.66	0.012	1.08	0.747	-0.18
1449831_at	Tctex1d1	Tctex1 domain containing 1	-1.35	0.432	-1.33	0.087	1.01	0.957	2.23	0.084	0.14
1438949_at	Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	-1.43	0.212	-1.45	0.417	1.12	0.644	1.25	0.584	-0.13
1457357_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	1.07	0.339	-1.22	0.293	-1.63	0.171	1.34	0.013	-0.11
1420199_at	Slc35a4	Solute carrier family 35, member A4	1.19	0.879	-2.21	0.295	-1.16	0.678	2.13	0.38	-0.01
1453986_at	Lig3	ligase III, DNA, ATP-dependent	-1.67	0.362	-1.28	0.444	1.13	0.87	2.25	0.115	0.11
1420325_at	Cramp1l	Crm, cramped-like (Drosophila)	-1.54	0.314	1.01	0.988	-1.18	0.518	1.2	0.142	-0.13
1446896_at	AU022186	expressed sequence AU022186	-1.73	0.289	-1.32	0.278	1.17	0.573	1.05	0.891	-0.21
1427252_at	Dmrtb1	DMRT-like family B with proline-rich C-terminal, 1	1.05	0.902	-2.61	0.346	1.07	0.846	-1.51	0.528	-0.5
1446266_at	Cts8	cathepsin 8	-1.72	0.281	1.48	0.557	-2.23	0.25	1.69	0.449	-0.19
1443800_at	Nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)	-1.36	0.745	-1.46	0.232	1.08	0.835	1.82	0.352	0.02
1439656_at	Pafah1b1	Platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	1.28	0.226	-1.27	0.349	-2.28	0	1.25	0.383	-0.26
1442587_at	---	---	-1.08	0.915	-1.96	0.168	1.07	0.734	1.03	0.957	-0.23
1418221_at	Csn1s2b	casein alpha s2-like B	-1.86	0.565	1.22	0.587	-1.33	0.616	1.01	0.959	-0.24
1426097_a_at	Ccdc106	coiled-coil domain containing 106	1.31	0.329	-2.23	0.213	-1.33	0.706	1.28	0.536	-0.24
1419699_at	Scgb3a1	secretoglobin, family 3A, member 1	-1.49	0.569	1.16	0.492	-1.48	0.179	1.11	0.809	-0.18
1425350_a_at	Myef2	myelin basic protein expression factor 2, repressor	1.1	0.38	-1.58	0.121	-1.29	0.063	1.9	0.326	0.03
1459489_at	---	---	-1.29	0.449	1.09	0.739	-1.56	0.358	1.11	0.887	-0.16
1453154_at	1700029M20Rik	RIKEN cDNA 1700029M20 gene	-1.39	0.398	-1.27	0.524	1.01	0.988	1.04	0.941	-0.16
1447942_x_at	Neu1	Neuraminidase 1	1.17	0.637	-1.65	0.162	-1.35	0.11	1.67	0.13	-0.04
1440630_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643051	-1.3	0.33	-2.63	0.179	1.36	0.676	1.34	0.677	-0.31
1441507_at	Spnb2	spectrin beta 2	-1.3	0.022	1.24	0.584	-1.98	0.039	1.19	0.446	-0.22
1419998_at	---	Transcribed locus	1.03	0.958	-1.56	0.263	-1.2	0.272	2.09	0.357	0.09
1446124_at	---	---	-1.27	0.486	1.07	0.919	-1.53	0.521	1.05	0.953	-0.17
1459236_at	AU022436	expressed sequence AU022436	1.02	0.938	-2.15	0.283	1.03	0.965	-2.55	0.299	-0.66
1442469_at	---	---	-2.76	0.116	1.14	0.624	1.01	0.918	-1.47	0.552	-0.52
1419161_a_at	Nox4	NADPH oxidase 4	-1.16	0.241	-1.65	0.098	1.04	0.928	1.77	0.237	0
1456985_at	Dnttip1	Deoxynucleotidyltransferase, terminal, interacting protein 1	1.04	0.887	-1.13	0.734	-1.71	0.073	1.11	0.48	-0.17
1435888_at	Egfr	epidermal growth factor receptor	-1.11	0.408	1.14	0.778	-2.1	0.042	1.09	0.756	-0.25
1443318_at	E130016E03Rik	RIKEN cDNA E130016E03 gene	1.15	0.804	-2.55	0.029	-1.03	0.95	1.07	0.856	-0.34
1421655_a_at	Ccr4	chemokine (C-C motif) receptor 4	-1.14	0.805	-2.08	0.092	1.15	0.649	1.4	0.558	-0.17
1442194_at	AU018552	expressed sequence AU018552	1.17	0.258	-1.31	0.132	-1.75	0.036	1.04	0.93	-0.21

1421438_at	---	---	-1.44	0.674	-2.22	0.101	1.37	0.439	1.34	0.646	-0.24
1432446_at	1700016K13Rik	RIKEN cDNA 1700016K13 gene	1.5	0.309	-2.28	0.384	-1.74	0.365	1.59	0.292	-0.23
1427279_at	---	---	-1.59	0.542	-1.15	0.594	1.01	0.974	1.14	0.442	-0.15
1447199_at	C80763	expressed sequence C80763	-1.18	0.157	1.23	0.562	-2.3	0.152	2.97	0.174	0.18
1443674_at	---	11 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:G63(	-2.9	0.033	1.5	0.336	-1.49	0.56	1.19	0.779	-0.43
1420202_at	---	---	-1.78	0.229	-1.16	0.866	1.09	0.06	2.01	0.317	0.04
1444984_at	C77649	expressed sequence C77649	-1.24	0.335	1.02	0.939	-1.45	0.266	1.31	0.152	-0.09
1455663_at	Olfml1	olfactomedin-like 1	1.02	0.905	-1.21	0.614	-1.49	0.22	1.22	0.431	-0.12
1426859_at	Inhbb	inhibin beta-B	-2.31	0.055	-1.44	0.173	1.39	0.087	2.18	0.156	-0.05
1440205_at	---	---	-1.16	0.633	-1.55	0.051	1	0.989	1.84	0.402	0.03
1445195_at	C77631	expressed sequence C77631	1.08	0.838	-1.86	0.053	-1.12	0.809	1.26	0.346	-0.16
1419386_at	Muc13	mucin 13, epithelial transmembrane	-1.12	0.798	-1.88	0.22	1.09	0.876	4.24	0.09	0.58
1445630_at	---	---	-2.46	0.149	1.08	0.766	1.03	0.916	-1.4	0.244	-0.44
1439667_at	---	---	-2.01	0.277	-1.51	0.256	1.35	0.109	1.79	0.218	-0.09
1428956_at	2300008B03Rik	RIKEN cDNA 2300008B03 gene	-1.39	0.429	-1.72	0.263	1.21	0.621	1.15	0.763	-0.19
1443218_at	Picalm	Phosphatidylinositol binding clathrin assembly protein	-2.29	0.024	1.36	0.465	-1.4	0.464	5.97	0.105	0.91
1433250_at	4931409D07Rik	RIKEN cDNA 4931409D07 gene	1.65	0.45	-2.15	0.03	-2.54	0.384	1.03	0.921	-0.5
1458288_at	4732475C15Rik	RIKEN cDNA 4732475C15 gene	1.52	0.522	-1.75	0.093	-2.4	0.273	1.7	0.47	-0.23
1450345_at	Ubqln1	ubiquilin 1	-1.32	0.754	-1.34	0.646	1.01	0.985	1.56	0.256	-0.02
1420301_at	AA414903	expressed sequence AA414903	-2.42	0.08	-1.08	0.762	1.18	0.213	2.17	0.012	-0.04
1441605_at	---	---	-2.02	0.201	1.06	0.881	-1.04	0.943	1.47	0.13	-0.13
1446068_at	Adk	adenosine kinase	1.09	0.767	-1.15	0.218	-1.78	0.012	1.26	0.37	-0.15
1430193_at	Casc5 /// LOC6772(	cancer susceptibility candidate 5 /// similar to cancer susceptibility candidate 5 isc	-1.12	0.736	-2.02	0.034	1.12	0.492	2.89	0.242	0.22
1446002_at	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	-1.68	0.16	1.16	0.776	-1.32	0.31	1	0.988	-0.21
1442330_at	Srrm1	Serine/arginine repetitive matrix 1	1.05	0.881	-1.13	0.775	-1.72	0.003	1.42	0.352	-0.1
1431523_at	4930564K09Rik	RIKEN cDNA 4930564K09 gene	-2.53	0.251	-1.5	0.356	1.45	0.347	1.02	0.958	-0.39
1445012_at	Nek11	NIMA (never in mitosis gene a)-related expressed kinase 11	-1.39	0.199	1.15	0.787	-1.56	0.038	1.13	0.624	-0.17
1426308_at	Mbd3l1	methyl-CpG binding domain protein 3-like 1	1	0.989	-2.14	0.111	1.04	0.838	-1.62	0.465	-0.43
1432555_at	Whrn	whirlin	-1.67	0.249	-1.31	0.29	1.15	0.469	1.33	0.53	-0.12
1426176_a_at	Prok2	prokineticin 2	-1.91	0.413	-1.59	0.196	1.36	0.592	1.27	0.083	-0.22
1417445_at	Kntc2	kinetochore associated 2	-1.38	0.626	-3.04	0.055	1.46	0.38	1.93	0.394	-0.26
1421576_at	4930524B15Rik	RIKEN cDNA 4930524B15 gene	-1.36	0.559	-1.36	0.477	1.05	0.915	2.15	0.136	0.12
1456219_at	LOC624168	similar to zinc finger protein of the cerebellum 5	-2.11	0.275	1.18	0.551	-1.16	0.512	1.08	0.878	-0.25
1453843_at	Thap6	THAP domain containing 6	-1.63	0.286	-1.35	0.308	1.16	0.829	1.3	0.692	-0.13
1430248_at	4930415O11Rik	RIKEN cDNA 4930415O11 gene	-2.14	0.532	1.35	0.649	-1.42	0.138	2.2	0.218	0
1457490_at	B230218L05Rik	RIKEN cDNA B230218L05 gene	-1.35	0.514	1.07	0.832	-1.42	0.466	1.06	0.777	-0.16
1454446_at	4930564B12Rik	RIKEN cDNA 4930564B12 gene	1.06	0.893	-1.19	0.766	-1.62	0.349	1.13	0.835	-0.16
1442323_at	2410193C02Rik	RIKEN cDNA 2410193C02 gene	-1.79	0.094	1.35	0.187	-1.66	0.111	1.6	0.326	-0.12
1445755_at	Eya2	Eyes absent 2 homolog (Drosophila)	1.2	0.072	-1.15	0.787	-2.25	0.026	1.45	0.368	-0.19
1453780_at	---	---	1.04	0.814	-1.73	0.065	-1.12	0.615	1.38	0.062	-0.11
1455367_at	Dnd1	dead end homolog 1 (zebrafish)	-1.45	0.43	-1.32	0.161	1.07	0.836	1.41	0.139	-0.07
1446139_at	AI661453	Expressed sequence AI661453	1.36	0.557	-1.47	0.072	-2.1	0.004	1.41	0.474	-0.2
1454636_at	Cbx5	chromobox homolog 5 (Drosophila HP1a)	-1.09	0.593	1	0.985	-1.68	0.04	2.27	0.122	0.13
1433185_at	2610019A05Rik	RIKEN cDNA 2610019A05 gene	-1.17	0.799	1.25	0.715	-2.43	0.012	1.53	0.206	-0.21
1422227_at	Klf12 /// D530033K(	Kruppel-like factor 12 /// RIKEN cDNA D530033K05 gene	1.19	0.827	-1.89	0.291	-1.25	0.684	2.09	0.356	0.03
1444245_at	B230118H07Rik	RIKEN cDNA B230118H07 gene	1.08	0.607	-1.19	0.705	-1.68	0.155	1.14	0.653	-0.16
1433787_at	Nell1	NEL-like 1 (chicken)	-2.34	0.35	-2.27	0.389	1.65	0.273	1.44	0.663	-0.38
1459301_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	-1.1	0.555	1.09	0.628	-1.93	0.087	1.26	0.234	-0.17
1419015_at	Wisp2	WNT1 inducible signaling pathway protein 2	-1.95	0.047	1.02	0.951	-1.01	0.96	1.29	0.27	-0.16
1439190_at	Fhad1	forkhead-associated (FHA) phosphopeptide binding domain 1	-1.79	0.487	1.08	0.811	-1.13	0.71	1.42	0.527	-0.11
1439747_at	Ptges	prostaglandin E synthase	-1.53	0.01	1.06	0.889	-1.24	0.335	1.15	0.061	-0.14
1445656_at	Mobp	Myelin-associated oligodendrocytic basic protein	-1.37	0.66	-1.38	0.469	1.06	0.884	3.32	0.158	0.41
1440746_at	Myst2	MYST histone acetyltransferase 2	-1.14	0.854	1.08	0.622	-1.78	0.09	1.08	0.839	-0.19

1425655_at	Krtap16-1	keratin associated protein 16-1	-1.08	0.906	-1.92	0.18	1.08	0.885	2.12	0.137	0.05
1430168_at	Cstad	CSA-conditional, T cell activation-dependent protein	-2	0.54	-1.25	0.263	1.22	0.658	1.02	0.962	-0.25
1435699_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	-1.41	0.369	1.15	0.714	-1.51	0.392	2.51	0.391	0.18
1430166_at	1700042D18Rik	RIKEN cDNA 1700042D18 gene	-1.37	0.323	-1.38	0.123	1.06	0.72	2.59	0.138	0.23
1458997_at	A230106M20Rik	RIKEN cDNA A230106M20 gene	-2.39	0.259	1.1	0.764	1	0.992	-2.03	0.235	-0.58
1456904_at	---	Transcribed locus	1.07	0.595	-1.37	0.05	-1.38	0.13	1.63	0.143	-0.01
1439521_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300(	-1.27	0.252	-1.47	0.225	1.06	0.791	1.16	0.827	-0.13
1450952_at	Pln	phospholamban	-1.62	0.278	-1.88	0.421	1.37	0.1	1.82	0.264	-0.08
1423366_at	Scd3	stearoyl-coenzyme A desaturase 3	-1.52	0.258	-1.32	0.565	1.1	0.807	1.18	0.77	-0.14
1436457_at	F830028O17Rik	RIKEN cDNA F830028O17 gene	1.3	0.327	-1.51	0.536	-1.79	0.25	1.02	0.864	-0.24
1447179_at	2210412D01Rik	RIKEN cDNA 2210412D01 gene	1.04	0.862	-1.27	0.131	-1.44	0.072	1.1	0.524	-0.14
1455758_at	Prkcc	protein kinase C, gamma	1.11	0.799	-2.07	0.023	-1.07	0.849	1.7	0.439	-0.08
1436268_at	Ddn	dendrin	1.05	0.831	-2.51	0.267	1.08	0.878	-1.96	0.253	-0.59
1458303_at	Gm96	gene model 96, (NCBI)	-1.74	0.001	-1.21	0.409	1.12	0.608	1.12	0.717	-0.18
1446611_at	Ate1	Arginine-tRNA-protein transferase 1	-1.26	0.523	1.07	0.888	-1.52	0.333	1.22	0.256	-0.12
1427807_at	LOC676582	hypothetical protein LOC676582	1.09	0.764	-2.58	0.058	1.05	0.812	-1.04	0.94	-0.37
1420566_at	---	---	1	0.936	-1.38	0.455	-1.26	0.303	2.61	0.236	0.24
1424676_s_at	Sec14l4	SEC14-like 4 (S. cerevisiae)	1.01	0.975	-1.41	0.096	-1.24	0.124	1.09	0.898	-0.14
1423257_at	Cyp4a14	cytochrome P450, family 4, subfamily a, polypeptide 14	-1.05	0.789	-2.09	0.091	1.1	0.709	1.41	0.607	-0.16
1425224_at	BC019561	cDNA sequence BC019561	-1.11	0.286	-2.15	0.105	1.16	0.569	1.08	0.771	-0.26
1422274_at	Gja8	gap junction membrane channel protein alpha 8	-1.87	0.464	-1.06	0.916	1.04	0.919	1.04	0.924	-0.21
1427588_a_at	Dtna	dystrobrevin alpha	-1.39	0.202	1.24	0.669	-1.76	0.1	2.24	0.263	0.08
1417575_at	Otub2	OTU domain, ubiquitin aldehyde binding 2	-1.15	0.396	-1.53	0.391	1	0.988	2.56	0.298	0.22
1432819_at	1190002C06Rik	RIKEN cDNA 1190002C06 gene	1.05	0.872	-1.51	0.116	-1.24	0.646	1.17	0.482	-0.13
1437160_at	Nlgn1	neuroligin 1	-3.47	0.392	1.38	0.543	-1.16	0.8	1.34	0.5	-0.48
1422617_at	Xmr /// LOC546272	Xmr protein /// similar to Xlr-related, meiosis regulated /// similar to Xlr-related, me	1.05	0.948	-1.62	0.469	-1.16	0.732	3.51	0.329	0.44
1455049_at	Igsf3	immunoglobulin superfamily, member 3	1.03	0.936	-1.04	0.953	-1.88	0.03	2.09	0.374	0.05
1423646_at	Zdhhc3	zinc finger, DHHC domain containing 3	-1.18	0.191	1.01	0.955	-1.49	0.009	1.13	0.478	-0.13
1454423_at	4930538D17Rik	RIKEN cDNA 4930538D17 gene	-1.53	0.05	-1.31	0.355	1.11	0.534	1.1	0.812	-0.16
1432050_at	4930571B16Rik	RIKEN cDNA 4930571B16 gene	-1.24	0.685	-1.45	0.087	1.03	0.965	1.06	0.858	-0.15
1458212_at	Pde4d	Phosphodiesterase 4D, cAMP specific	1.12	0.715	-1.34	0.45	-1.5	0.134	1.72	0.265	0
1438975_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	-1.21	0.413	1.03	0.851	-1.49	0.103	1.49	0.237	-0.04
1431353_at	C330050A14Rik	RIKEN cDNA C330050A14 gene	-2.56	0.386	1	0.985	1.13	0.591	-1.06	0.847	-0.37
1458945_at	AU015148	expressed sequence AU015148	-1	0.994	1.13	0.253	-2.47	0.004	1.03	0.943	-0.33
1419519_at	Igf1	insulin-like growth factor 1	1.01	0.963	-1.12	0.409	-1.6	0.044	1.31	0.43	-0.1
1449387_at	Krt33a	keratin 33A	1.05	0.169	-1.66	0.347	-1.14	0.143	1.08	0.813	-0.17
1415868_at	Cct4	chaperonin subunit 4 (delta)	1.42	0.563	-2.06	0.009	-1.6	0.066	1.27	0.615	-0.24
1437006_x_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	-1.25	0.04	-1.51	0.044	1.07	0.63	1.05	0.847	-0.16
1459120_at	Epb4.1l5	erythrocyte protein band 4.1-like 5	-1.41	0.083	-1.41	0.532	1.11	0.766	1.14	0.765	-0.14
1430707_s_at	1700081D17Rik	RIKEN cDNA 1700081D17 gene	1.26	0.508	-2.01	0.329	-1.3	0.319	1.27	0.689	-0.2
1418177_at	Gabrg2	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 2	-1	0.973	-2.74	0.006	1.17	0.817	1.11	0.617	-0.37
1458456_x_at	6430571L13Rik	RIKEN cDNA 6430571L13 gene	-1.64	0.054	-1.59	0.251	1.29	0.702	1.57	0.205	-0.09
1442781_at	Frrs1	Ferric-chelate reductase 1	-1.22	0.619	1.15	0.579	-1.78	0.178	1.08	0.843	-0.19
1430997_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	-1.34	0.666	-1.46	0.216	1.1	0.342	1.35	0.209	-0.09
1453902_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	1.02	0.937	-1.17	0.481	-1.51	0.218	4.68	0.213	0.75
1436940_at	Purb	Purine rich element binding protein B	-1.04	0.896	1.07	0.586	-2.01	0.096	1.19	0.704	-0.2
1432268_at	2310068J16Rik	RIKEN cDNA 2310068J16 gene	1.06	0.84	-1.39	0.081	-1.35	0.367	1.15	0.412	-0.13
1422069_at	Mc1r	melanocortin 1 receptor	-3.2	0.216	-1.33	0.369	1.47	0.531	2.07	0.397	-0.25
1433343_at	4930448K20Rik	RIKEN cDNA 4930448K20 gene	-1.41	0.569	-2.97	0.007	1.48	0.45	1.72	0.179	-0.29
1457325_at	Kcns2	K+ voltage-gated channel, subfamily S, 2	1	0.991	-1.52	0.325	-1.15	0.674	1.74	0.105	0.02
1422939_at	Serpinb3b	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3B	-2.01	0.454	-1.14	0.836	1.16	0.241	1.27	0.711	-0.18
1451710_at	Oscar	osteoclast associated receptor	-1.29	0.622	-1.5	0.239	1.09	0.659	1.1	0.825	-0.15
1418156_at	Kcne4	potassium voltage-gated channel, Isk-related subfamily, gene 4	1.14	0.604	-1.92	0.043	-1.16	0.501	1.64	0.368	-0.07

1452243_at	Kcnj14	potassium inwardly-rectifying channel, subfamily J, member 14	1.32	0.622	-2.64	0.101	-1.2	0.545	1.38	0.384	-0.28
1437263_at	A730089K16Rik	RIKEN cDNA A730089K16 gene	-1.81	0.418	1.27	0.509	-1.42	0.502	4.72	0.173	0.69
1417443_at	BC026682	cDNA sequence BC026682	-1.37	0.301	-1.42	0.444	1.1	0.803	1.24	0.134	-0.11
1443717_at	Dpyd	dihydropyrimidine dehydrogenase	1.52	0.47	-2.34	0.053	-1.72	0.388	1.4	0.397	-0.28
1446376_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	1.02	0.932	-1.68	0.237	-1.09	0.381	1.36	0.382	-0.1
1419012_at	Zfpm2	zinc finger protein, multitype 2	-1.33	0.343	-1.42	0.127	1.08	0.825	1.49	0.435	-0.05
1458678_at	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	-1.03	0.859	-1.96	0.1	1.05	0.798	1.17	0.69	-0.19
1432266_at	BC026657	cDNA sequence BC026657	-1.22	0.522	1.06	0.876	-1.54	0.08	2.67	0.123	0.24
1441375_at	Lrig1	Leucine-rich repeats and immunoglobulin-like domains 1	-1.1	0.596	1.19	0.64	-2.3	0.015	1.01	0.968	-0.3
1419389_at	Pde10a	phosphodiesterase 10A	-1.22	0.787	1.36	0.672	-2.8	0.064	1.11	0.797	-0.39
1434330_at	Lrrc35	leucine rich repeat containing 35	-1.2	0.241	-1.49	0.083	1.03	0.853	2.37	0.201	0.18
1443555_at	---	---	1.19	0.682	-1.31	0.751	-1.71	0.344	1.08	0.824	-0.19
1448820_a_at	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	-1.13	0.249	1.01	0.94	-1.57	0.038	1.02	0.909	-0.17
1426108_s_at	Cacnb1	calcium channel, voltage-dependent, beta 1 subunit	-1.29	0.672	-1.83	0.307	1.22	0.619	1.29	0.46	-0.15
1446297_at	Hibadh	3-hydroxyisobutyrate dehydrogenase	1.14	0.809	-1.5	0.235	-1.38	0.121	1.28	0.307	-0.11
1441076_at	---	Transcribed locus	1.28	0.737	-1.43	0.502	-1.8	0.457	1.3	0.603	-0.16
1434878_at	Slitrk4	SLIT and NTRK-like family, member 4	-1.16	0.808	-1.58	0.354	1.04	0.879	1.52	0.625	-0.04
1456356_at	B230217O12Rik	RIKEN cDNA B230217O12 gene	-1.32	0.413	-1.43	0.505	1.08	0.839	1.33	0.431	-0.09
1429674_at	1700113H08Rik	RIKEN cDNA 1700113H08 gene	-1.55	0.483	1.21	0.663	-1.47	0.364	2.44	0.123	0.16
1437727_at	Odz3	Odd Oz/ten-m homolog 3 (Drosophila)	-1.65	0.071	-1.26	0.071	1.14	0.798	1.3	0.287	-0.12
1450598_at	V1ra4	vomeronasal 1 receptor, A4	-2.09	0.44	-3.6	0.152	1.78	0.234	1.84	0.343	-0.52
1459024_at	---	Transcribed locus	1.02	0.934	-1.55	0.586	-1.16	0.813	1.58	0.452	-0.03
1452610_at	Zfp99	zinc finger protein 99	-2.29	0.082	1.03	0.869	1.07	0.815	-1.24	0.481	-0.36
1431447_at	4930432K09Rik	RIKEN cDNA 4930432K09 gene	-1.48	0.272	-2.06	0.15	1.37	0.482	1.4	0.449	-0.19
1421294_at	Hdgfl1	hepatoma derived growth factor-like 1	-1.24	0.23	1.07	0.889	-1.5	0.213	1.46	0.178	-0.06
1445371_at	Gm540	gene model 540, (NCBI)	1.18	0.066	-1.14	0.863	-2.1	0.046	1.47	0.641	-0.15
1432845_at	---	---	-1.88	0.046	1.16	0.671	-1.18	0.192	1.01	0.981	-0.22
1446257_at	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	1.16	0.783	-2.09	0.306	-1.11	0.845	1.66	0.079	-0.09
1417880_at	G6pc	glucose-6-phosphatase, catalytic	-1.2	0.155	-1.55	0.286	1.06	0.781	1.1	0.887	-0.15
1436901_at	Notch4	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library,	1.18	0.752	-1.72	0.262	-1.29	0.281	1.12	0.716	-0.18
1426188_s_at	BC005685	cDNA sequence BC005685	-1.63	0.336	-1.52	0.45	1.27	0.69	1.23	0.411	-0.16
1417257_at	Cel	carboxyl ester lipase	1.06	0.938	-1.52	0.28	-1.22	0.732	2.01	0.174	0.08
1421692_at	Cacna1e	calcium channel, voltage-dependent, R type, alpha 1E subunit	-1.44	0.619	-1.9	0.258	1.31	0.416	1.1	0.545	-0.23
1458666_at	D2Ertd391e	DNA segment, Chr 2, ERATO Doi 391, expressed	-1.21	0.556	1.26	0.593	-2.2	0.121	1.1	0.831	-0.26
1429854_at	2900092C05Rik	RIKEN cDNA 2900092C05 gene	-1.7	0.506	-1.42	0.537	1.25	0.493	1.01	0.99	-0.22
1442329_at	Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	-1.32	0.018	1	0.998	-1.28	0.368	2.53	0.144	0.23
1450999_a_at	1700029H14Rik	RIKEN cDNA 1700029H14 gene	-1.53	0.539	-1.48	0.312	1.21	0.722	1.17	0.406	-0.16
1449715_at	---	---	-1.36	0.581	1.13	0.731	-1.48	0.131	1.17	0.583	-0.14
1425593_at	Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	-1.25	0.631	-2.4	0.089	1.32	0.556	1.37	0.608	-0.24
1419424_at	Ptf1a	pancreas specific transcription factor, 1a	-2.41	0.171	-1.15	0.821	1.25	0.082	1.02	0.871	-0.32
1419804_at	1700051A21Rik	RIKEN cDNA 1700051A21 gene	-1.08	0.856	1.06	0.893	-1.81	0.218	1.07	0.683	-0.19
1436841_at	B230380D07Rik	RIKEN cDNA B230380D07 gene	-1.29	0.176	1.04	0.792	-1.38	0.198	1.17	0.427	-0.11
1458421_at	Kcnq3	potassium voltage-gated channel, subfamily Q, member 3	-1.3	0.41	1.11	0.751	-1.52	0.46	1.07	0.92	-0.16
1439083_at	Ahi1	Abelson helper integration site	1.12	0.876	-1.59	0.482	-1.27	0.746	2.07	0.441	0.09
1432055_at	Sash1	SAM and SH3 domain containing 1	-1.48	0.151	1.06	0.632	-1.25	0.623	2.36	0.024	0.17
1422625_at	Ly6h	lymphocyte antigen 6 complex, locus H	-1.32	0.659	1.23	0.278	-1.82	0.345	1.37	0.091	-0.13
1440139_at	Nedd4l	Neural precursor cell expressed, developmentally down-regulated gene 4-like	1.05	0.936	1.13	0.778	-2.76	0.055	-1.96	0.239	-0.64
1453323_at	2900079G21Rik	RIKEN cDNA 2900079G21 gene	-1.96	0.174	1.23	0.734	-1.24	0.66	1.88	0.256	-0.03
1443183_at	Huwe1	HECT, UBA and WWE domain containing 1	-1.32	0.073	-1.46	0.461	1.1	0.755	1.24	0.612	-0.11
1416063_x_at	Ceacam11	CEA-related cell adhesion molecule 11	-1.17	0.808	-2.39	0.384	1.27	0.72	1.42	0.008	-0.22
1431839_a_at	Ccdc81	coiled-coil domain containing 81	1.11	0.828	-3.91	0.168	1.18	0.327	-2.94	0.023	-1.14
1441868_x_at	Dcst2	DC-STAMP domain containing 2	1.26	0.722	-1.22	0.4	-2.19	0.076	1.24	0.523	-0.23
1455243_at	Brpf3	bromodomain and PHD finger containing, 3	-1.2	0.418	1.04	0.917	-1.49	0.074	2.63	0.128	0.25

1445209_at	AU021745	expressed sequence AU021745	-1.07	0.898	-1.74	0.052	1.03	0.897	1.01	0.992	-0.19
1438327_at	Zfp533	Zinc finger protein 533	-1.1	0.839	-1.58	0.205	1	0.999	1.03	0.97	-0.16
1447954_at	Lrrc49	leucine rich repeat containing 49	1.35	0.091	-2.1	0.397	-1.41	0.401	1.59	0.111	-0.14
1433978_at	4930430F08Rik	RIKEN cDNA 4930430F08 gene	-1.36	0.1	1.13	0.327	-1.48	0.1	2.22	0.224	0.13
1438826_x_at	Calm3	calmodulin 3	1.29	0.334	-2	0.108	-1.32	0.155	1.61	0.329	-0.11
1430783_at	4932416J16Rik	RIKEN cDNA 4932416J16 gene	-2.17	0.029	1.02	0.899	1.06	0.79	-1.1	0.858	-0.3
1420958_at	---	---	-1.48	0.036	-1.96	0.175	1.36	0.528	1.33	0.402	-0.19
1427843_at	AI840826	expressed sequence AI840826	-1.39	0.172	1.04	0.773	-1.27	0.295	1.2	0.35	-0.11
1447599_x_at	Epn2	epsin 2	-2.34	0.02	1.28	0.33	-1.2	0.202	1.26	0.505	-0.25
1420166_at	Dntt	Deoxynucleotidyltransferase, terminal	-1.68	0.1	-1.2	0.76	1.12	0.791	1.06	0.928	-0.18
1428088_at	2410002I01Rik	RIKEN cDNA 2410002I01 gene	-1.17	0.448	-1.56	0.476	1.05	0.916	1.07	0.875	-0.15
1441128_at	Rage	Renal tumor antigen	1.14	0.226	-2.88	0.006	1.05	0.892	-1.14	0.566	-0.46
1429136_at	1700052K11Rik	RIKEN cDNA 1700052K11 gene	-1.23	0.212	-1.41	0.185	1.02	0.75	1.21	0.404	-0.1
1430137_at	Map3k13	mitogen-activated protein kinase kinase kinase 13	-1.37	0.042	-1.24	0.282	1.01	0.967	1.04	0.785	-0.14
1444592_at	Osgep	O-sialoglycoprotein endopeptidase	-1.61	0.274	1.24	0.627	-1.47	0.121	1.3	0.362	-0.13
1443853_x_at	Sfmbt1	Scm-like with four mbt domains 1	1.26	0.702	-3.83	0.011	1.03	0.959	-1.06	0.873	-0.65
1434146_at	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2)	1.35	0.658	-2.12	0.306	-1.38	0.181	1.57	0.436	-0.14
1451407_at	Jam4	junction adhesion molecule 4	1.08	0.321	-1.22	0.04	-1.55	0.013	1.62	0.094	-0.02
1438466_at	Dnahc12 /// Dnahc7	dynein, axonemal, heavy chain 12 /// dynein, axonemal, heavy chain 7b /// dynein	-1.27	0.245	-1.45	0.314	1.07	0.714	1.85	0.091	0.05
1455167_at	Cox8c	cytochrome c oxidase, subunit VIIIc	-1.13	0.145	-1.63	0.054	1.05	0.837	1.12	0.163	-0.15
1421373_at	Cox4i2	cytochrome c oxidase subunit IV isoform 2	1.08	0.797	-1.09	0.873	-1.84	0.042	2.18	0.145	0.08
1422905_s_at	Fmo2	flavin containing monooxygenase 2	1.06	0.848	-1.67	0.124	-1.12	0.584	3.67	0.003	0.48
1441520_at	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	1.16	0.596	-2.41	0.076	-1.03	0.859	5.72	0.132	0.86
1458975_at	---	Transcribed locus	-1.74	0.003	-1.1	0.858	1.06	0.729	1.06	0.781	-0.18
1421110_at	Mtdh	Metadherin	1.27	0.426	-3.52	0.01	-1.01	0.97	1.1	0.792	-0.54
1445411_at	---	---	-1.06	0.473	1.2	0.609	-2.47	0.033	1.32	0.031	-0.25
1439463_x_at	Hmgb1 /// LOC434	high mobility group box 1 /// similar to High mobility group protein 1 (HMG-1) (Hig	1.01	0.539	-1.27	0.304	-1.34	0.225	1.06	0.484	-0.13
1438815_at	Hist2h2aa2	histone 2, H2aa2	-1.2	0.256	-1.58	0.385	1.08	0.579	3.19	0.058	0.37
1441848_at	Pmm2	Phosphomannomutase 2	1.01	0.955	-1	0.966	-1.84	0.013	1.06	0.686	-0.19
1416368_at	Gsta4	glutathione S-transferase, alpha 4	1.06	0.757	-1.31	0.504	-1.38	0.104	1.41	0.383	-0.06
1424991_s_at	Tyms /// Tyms-ps	thymidylate synthase /// thymidylate synthase, pseudogene	-1.4	0.241	-1.24	0.291	1.02	0.923	3.51	0.205	0.47
1438816_at	Ahctf1	AT hook containing transcription factor 1	1	0.978	-1.12	0.501	-1.54	0.062	1.02	0.935	-0.16
1446811_at	Mkx	Mohawk	1.06	0.74	-1.52	0.439	-1.21	0.701	1.27	0.522	-0.1
1436257_at	Ss18	synovial sarcoma translocation, Chromosome 18	1.18	0.6	-1.2	0.371	-1.85	0.016	1.12	0.674	-0.19
1458006_at	Cpm	Carboxypeptidase M	1.03	0.772	1.05	0.91	-2.16	0.058	-1.83	0.076	-0.48
1443740_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.27	0.066	1.38	0.605	-2.6	0.126	2.25	0.187	-0.06
1422315_x_at	Phkg1	phosphorylase kinase gamma 1	-1.44	0.705	-1.42	0.493	1.15	0.773	1.48	0.589	-0.06
1447696_x_at	Adcy5	adenylate cyclase 5	-1.39	0.325	-2.08	0.332	1.35	0.21	1.14	0.633	-0.25
1459243_at	---	PREDICTED: Mus musculus hypothetical protein LOC626097 (LOC626097), mR	1.06	0.471	-1.18	0.438	-1.55	0.137	1.17	0.416	-0.13
1442397_at	Nfx1	nuclear transcription factor, X-box binding 1	1	0.989	-1.91	0.085	1.02	0.927	-1.2	0.472	-0.27
1456625_at	---	---	-1.46	0.322	-1.2	0.169	1.03	0.805	1.15	0.239	-0.12
1430566_at	4733401A01Rik	RIKEN cDNA 4733401A01 gene	1.54	0.123	-2.12	0.042	-1.84	0.111	1.27	0.169	-0.29
1423631_at	Nr2e3	nuclear receptor subfamily 2, group E, member 3	-1.46	0.505	1.25	0.289	-1.63	0.25	2.16	0.434	0.08
1440447_at	Abhd2	abhydrolase domain containing 2	-1.41	0.168	-1.29	0.483	1.07	0.807	1.05	0.917	-0.15
1420132_s_at	Pttg1ip	Pituitary tumor-transforming 1 interacting protein	1.01	0.989	-1.18	0.253	-1.43	0.132	1.05	0.767	-0.14
1452606_at	Mnd1	meiotic nuclear divisions 1 homolog (S. cerevisiae)	1.18	0.739	-1.48	0.408	-1.44	0.327	2.73	0.273	0.25
1429297_at	Serpinb12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	-1.07	0.928	1.04	0.951	-1.73	0.201	1.27	0.566	-0.12
1451618_at	Rho	rhodopsin	-1.55	0.272	-1.25	0.452	1.11	0.559	1.19	0.546	-0.13
1435638_at	Gsk3a	glycogen synthase kinase 3 alpha	-1.46	0.113	-1.17	0.158	1.01	0.897	1.17	0.472	-0.11
1438468_at	Pramel4 /// Pramel5	preferentially expressed antigen in melanoma like 4 /// preferentially expressed ar	1.08	0.711	-1.14	0.773	-1.66	0.268	1.5	0.15	-0.06
1437598_at	Zbtb20	zinc finger and BTB domain containing 20	-1.08	0.009	1.04	0.605	-1.72	0.011	1.07	0.849	-0.17
1445963_at	Pde5a	Phosphodiesterase 5A, cGMP-specific	1.49	0.443	-1.42	0.064	-2.8	0.002	2.37	0.119	-0.09
1459487_at	4930554I06Rik	RIKEN cDNA 4930554I06 gene	-3.1	0.245	1.62	0.394	-1.65	0.131	2	0.23	-0.28

1434480_at	4930402E16Rik	RIKEN cDNA 4930402E16 gene	1.13	0.373	-1.36	0.209	-1.47	0.085	1.02	0.897	-0.17
1418323_at	Fem1b	feminization 1 homolog b (C. elegans)	-2.12	0.335	1.02	0.977	1.07	0.735	-1	0.996	-0.26
1424730_a_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	1.21	0.013	-1.46	0.128	-1.52	0.119	1.31	0.444	-0.12
1455851_at	Bmp5	bone morphogenetic protein 5	-1.3	0.419	1.19	0.095	-1.69	0.02	1.38	0.45	-0.1
1418348_a_at	Ascc2	activating signal cointegrator 1 complex subunit 2	-1.29	0.377	-1.33	0.052	1.03	0.888	1.15	0.338	-0.11
1425101_a_at	Fkbp6	FK506 binding protein 6	-1.54	0.044	-1.16	0.188	1.04	0.806	1.09	0.66	-0.14
1440515_at	LOC635529 /// LOC	similar to Doublecortin domain-containing protein 2 /// similar to Doublecortin dom	1	0.997	-2.52	0.019	1.16	0.144	-1.27	0.696	-0.41
1439363_at	1200014J11Rik	RIKEN cDNA 1200014J11 gene	-1.06	0.722	1.02	0.798	-1.7	0.034	1.11	0.146	-0.16
1427922_at	2310061C15Rik	RIKEN cDNA 2310061C15 gene	1.06	0.807	-1.59	0.021	-1.16	0.188	1.48	0.207	-0.05
1421104_at	Mpa2 /// Mpa2l /// L	macrophage activation 2 /// macrophage activation 2 like /// similar to macrophage	1.48	0.579	-1.75	0.164	-1.97	0.066	1.05	0.932	-0.3
1457429_s_at	Gm106	gene model 106, (NCBI)	1.03	0.745	-2.12	0.14	1.05	0.904	-1.03	0.941	-0.27
1440504_at	Ccdc39	Coiled-coil domain containing 39	-1.46	0.451	1.02	0.979	-1.18	0.701	1.16	0.674	-0.11
1437864_at	Adipor2	adiponectin receptor 2	-1.44	0.067	-1.35	0.167	1.12	0.627	1.39	0.071	-0.07
1428752_at	Slc5a11	solute carrier family 5 (sodium/glucose cotransporter), member 11	1.07	0.679	-1.67	0.157	-1.14	0.524	1.19	0.482	-0.13
1416592_at	Glrx	glutaredoxin	-1.29	0.053	-1.31	0.121	1.01	0.954	1.04	0.756	-0.14
1442300_at	---	---	-2.29	0.131	1.08	0.821	1.04	0.941	-2.92	0.102	-0.77
1427523_at	Six3 /// E130112M2	sine oculis-related homeobox 3 homolog (Drosophila) /// RIKEN cDNA E130112M	-1.81	0.192	-1	0.993	1.01	0.986	2.88	0.016	0.27
1437480_at	---	---	-1.13	0.601	1.02	0.642	-1.54	0.028	1.44	0.174	-0.05
1419143_at	Cypt5	cysteine-rich perinuclear theca 5	1.11	0.776	-3.89	0.013	1.19	0.563	-2.42	0.237	-1
1453430_at	2010315L10Rik	RIKEN cDNA 2010315L10 gene	1.04	0.73	-1.36	0.033	-1.28	0.335	1.45	0.211	-0.04
1448535_at	Elp4	elongation protein 4 homolog (S. cerevisiae)	1.06	0.548	-1.41	0.036	-1.27	0.012	1.15	0.73	-0.12
1440407_at	---	---	-1.37	0.275	-1.44	0.437	1.13	0.45	1.6	0.146	-0.02
1452655_at	Zdhhc2	zinc finger, DHHC domain containing 2	-1.01	0.853	-2.27	0.159	1.12	0.29	1.3	0.307	-0.21
1423553_at	Dnajb3	DnaJ (Hsp40) homolog, subfamily B, member 3	1.21	0.354	-1.3	0.72	-1.75	0.08	3.19	0.138	0.34
1427632_x_at	Daf2	decay accelerating factor 2	1.53	0.524	-2.16	0.119	-1.78	0.252	1.4	0.447	-0.25
1443594_at	AI043046	expressed sequence AI043046	-1.77	0.143	-1.21	0.574	1.16	0.647	1.14	0.675	-0.17
1442384_at	Gfm2	G elongation factor, mitochondrial 2	-1.34	0.586	1.07	0.74	-1.35	0.189	1.14	0.661	-0.12
1450115_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	-1.5	0.619	-1.55	0.455	1.25	0.465	1.24	0.626	-0.14
1428717_at	Scrn1	secernin 1	-1.06	0.597	-1.68	0.266	1.01	0.964	1.18	0.358	-0.14
1428482_at	Akap10	A kinase (PRKA) anchor protein 10	-1.35	0.021	-1.26	0.059	1.02	0.857	1.16	0.063	-0.11
1423487_at	Cript	cysteine-rich PDZ-binding protein	-1.35	0.134	1.03	0.897	-1.27	0.185	1.05	0.586	-0.13
1425989_a_at	Eya3	eyes absent 3 homolog (Drosophila)	-1.86	0.179	-1.24	0.4	1.21	0.629	1.07	0.767	-0.2
1442032_at	BC030500	cDNA sequence BC030500	-1.76	0.655	-1.4	0.501	1.28	0.483	1.61	0.257	-0.07
1456930_at	Camsap1	calmodulin regulated spectrin-associated protein 1	1.14	0.698	-1.43	0.221	-1.39	0.028	1.05	0.834	-0.16
1431767_at	4930442G15Rik	RIKEN cDNA 4930442G15 gene	-1.8	0.175	1.07	0.852	-1.07	0.837	1.73	0.2	-0.02
1432976_at	2310038E17Rik	RIKEN cDNA 2310038E17 gene	1.02	0.983	1.01	0.953	-1.88	0.213	-1.55	0.343	-0.35
1441347_at	Hrbl	HIV-1 Rev binding protein-like	-1.46	0.098	-1.21	0.231	1.05	0.945	1.96	0.291	0.08
1440692_at	Gm364	gene model 364, (NCBI)	-1.73	0.313	1.07	0.889	-1.1	0.651	1.17	0.682	-0.15
1420229_at	---	---	-1.34	0.303	1.02	0.925	-1.27	0.484	1.21	0.375	-0.09
1454242_at	2310079G19Rik	RIKEN cDNA 2310079G19 gene	-1.75	0.231	-1.13	0.691	1.1	0.634	1.27	0.398	-0.13
1457007_at	Ncor1	Nuclear receptor co-repressor 1	-1.18	0.259	1.05	0.665	-1.52	0.055	1.07	0.66	-0.14
1441310_at	Adamts15	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.07	0.778	-2.18	0.1	1.03	0.909	-1.16	0.603	-0.31
1458184_at	D030020J04Rik	RIKEN cDNA D030020J04 gene	-1.29	0.754	-1.63	0.279	1.17	0.635	1.56	0.271	-0.05
1436291_a_at	Dpys	dihydropyrimidinase	-1.36	0.501	-1.22	0.188	1	0.999	3.76	0.079	0.55
1430191_at	9130004J05Rik	RIKEN cDNA 9130004J05 gene	-1.51	0.006	1.16	0.518	-1.36	0.019	1.4	0.003	-0.08
1423860_at	Ptgds	prostaglandin D2 synthase (brain)	-1.24	0.541	-2.51	0.08	1.35	0.573	1.17	0.612	-0.31
1447872_at	---	Transcribed locus	-1.5	0.505	-1.72	0.323	1.31	0.387	2.86	0.211	0.24
1446601_at	---	---	-3.95	0.17	-1.1	0.565	1.4	0.112	2.12	0.065	-0.38
1419092_a_at	Slk	STE20-like kinase (yeast)	-1.4	0.214	-1.41	0.365	1.14	0.711	1.28	0.666	-0.1
1439740_s_at	Uck2	uridine-cytidine kinase 2	-1.29	0.298	-1.43	0.011	1.09	0.664	1.56	0.182	-0.02
1460289_at	Nrg3	neuregulin 3	-1.2	0.61	-2.49	0.01	1.33	0.541	1.24	0.759	-0.28
1441091_at	---	Transcribed locus	1.05	0.716	-1.65	0.283	-1.11	0.724	1.02	0.974	-0.17
1447699_at	Map3k13	Mitogen-activated protein kinase kinase kinase 13	-1.98	0.155	-1.2	0.584	1.23	0.579	1.53	0.1	-0.11

1443003_at	---	---	1.05	0.45	-1.12	0.562	-1.63	0.341	1.16	0.502	-0.13
1429490_at	LOC671598	similar to Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog) (	1.14	0.665	-1.41	0.119	-1.4	0.21	1.23	0.572	-0.11
1442649_at	1500009L16Rik	RIKEN cDNA 1500009L16 gene	-1.09	0.8	1.06	0.566	-1.7	0.16	1.11	0.875	-0.16
1425072_at	Skp2	S-phase kinase-associated protein 2 (p45)	-1.56	0.022	1.04	0.888	-1.14	0.423	1.89	0.016	0.06
1429660_s_at	Smc2	structural maintenance of chromosomes 2	-1.67	0.407	-1.68	0.154	1.37	0.385	5.25	0.234	0.82
1430609_at	Morn1	MORN repeat containing 1	-2.55	0.018	-1.98	0.018	1.66	0.088	2.3	0.189	-0.14
1457526_at	Grb14	growth factor receptor bound protein 14	1.19	0.833	-1.09	0.895	-2.19	0.15	1.14	0.848	-0.24
1416166_a_at	Prdx4	peroxiredoxin 4	-1.4	0.377	1.08	0.628	-1.3	0.109	1.29	0.128	-0.08
1447759_x_at	Ccdc22	coiled-coil domain containing 22	-1.47	0.079	-1.15	0.316	1.01	0.962	1.29	0.196	-0.08
1440981_at	Pak7	p21 (CDKN1A)-activated kinase 7	1.06	0.74	-1.84	0.312	-1.04	0.941	3.36	0.248	0.39
1433959_at	Zmat4	zinc finger, matrin type 4	-1.15	0.78	-1.51	0.442	1.03	0.895	1.03	0.95	-0.15
1425156_at	Gbp7	guanylate binding protein 7	1	0.994	-1.11	0.644	-1.52	0.021	1.03	0.824	-0.15
1450605_at	Tas2r108	taste receptor, type 2, member 108	1.02	0.974	-1.64	0.394	-1.08	0.727	1.3	0.508	-0.1
1423129_at	Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	1	0.993	-1.04	0.738	-1.68	0.032	1.35	0.182	-0.09
1419265_at	1200014M14Rik	RIKEN cDNA 1200014M14 gene	-1.05	0.416	-1.81	0.16	1.06	0.719	1.17	0.509	-0.16
1418691_at	Rgs9	regulator of G-protein signaling 9	-1.7	0.101	-1.1	0.597	1.06	0.609	1.16	0.453	-0.15
1457563_at	Egfr	epidermal growth factor receptor	-3.48	0.03	1.08	0.862	1.2	0.688	-1.5	0.584	-0.67
1419531_at	1700102P08Rik	RIKEN cDNA 1700102P08 gene	-1.88	0.344	-1.28	0.453	1.25	0.645	1.21	0.552	-0.17
1445417_at	Ephb2	Eph receptor B2	-1.9	0.465	1.02	0.969	1.02	0.97	-1.52	0.303	-0.35
1418824_at	Arf6	ADP-ribosylation factor 6	-1.49	0.525	1.19	0.753	-1.41	0.452	1.72	0.145	0
1423178_at	Abi1	abl-interactor 1	1.02	0.958	1.26	0.698	-3.44	0.011	-1.39	0.519	-0.64
1421064_at	Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	1.03	0.631	-1.13	0.526	-1.53	0.058	1.01	0.98	-0.16
1458005_at	---	---	1.63	0.046	-2.67	0.208	-1.8	0.264	1.53	0.243	-0.33
1434186_at	Gpr23	G protein-coupled receptor 23	-1.49	0.548	1.06	0.917	-1.2	0.413	2.02	0.124	0.1
1445253_at	Olfr1417	Olfactory receptor 1417	-1.69	0.095	1.28	0.474	-1.45	0.146	1.29	0.313	-0.14
1458914_at	---	---	1.15	0.736	-2.54	0.02	1.02	0.963	-1.12	0.693	-0.37
1441470_at	AV249152	expressed sequence AV249152	1.1	0.836	-1.47	0.447	-1.26	0.46	1.59	0.068	-0.01
1458909_at	---	---	-1.2	0.58	1.26	0.694	-2.14	0.361	1.46	0.484	-0.15
1458579_at	---	---	-1.97	0.433	1.66	0.232	-2.48	0.053	2.52	0.105	-0.07
1433211_at	Rptn	repetin	-1.41	0.331	1.19	0.681	-1.5	0.232	1.09	0.273	-0.16
1453279_x_at	Krt76	keratin 76	1.13	0.794	-1.78	0.329	-1.14	0.727	1.09	0.902	-0.18
1457754_at	4930430F08Rik	RIKEN cDNA 4930430F08 gene	1.03	0.95	-1.15	0.798	-1.5	0.223	1.78	0.197	0.04
1429464_at	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit	1.15	0.348	-1.49	0.27	-1.34	0.59	1.31	0.714	-0.09
1420304_x_at	---	Transcribed locus, strongly similar to XP_537399.1 PREDICTED: similar to 40S r	-1.51	0.078	1	0.981	-1.11	0.686	1.17	0.175	-0.11
1431622_at	4933406K04Rik	RIKEN cDNA 4933406K04 gene	-1.54	0.492	1.05	0.882	-1.15	0.797	1.68	0.077	0.01
1451610_at	BC024561	cDNA sequence BC024561	-1.63	0.236	1.11	0.84	-1.18	0.57	1.14	0.821	-0.14
1446696_at	Ift57	intraflagellar transport 57 homolog (Chlamydomonas)	-1.89	0.391	1.22	0.562	-1.22	0.29	1.07	0.917	-0.21
1431462_at	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-1.48	0.447	1.04	0.935	-1.18	0.22	1.32	0.247	-0.07
1440701_at	C530008M17Rik	RIKEN cDNA C530008M17 gene	1.21	0.851	-2.26	0.23	-1.09	0.82	4.48	0.316	0.59
1421498_a_at	2010204K13Rik	RIKEN cDNA 2010204K13 gene	-1	0.992	-2.17	0.082	1.11	0.632	1.25	0.488	-0.2
1430095_at	1500017I17Rik	RIKEN cDNA 1500017I17 gene	1.11	0.78	-1.26	0.373	-1.5	0.131	1.25	0.461	-0.1
1422416_s_at	Vpreb1 /// Vpreb2	pre-B lymphocyte gene 1 /// pre-B lymphocyte gene 2	1.23	0.437	-2.07	0.029	-1.17	0.637	1.17	0.601	-0.21
1433133_at	Edaradd	EDAR (ectodysplasin-A receptor)-associated death domain	1.07	0.844	1.12	0.694	-2.64	0.126	-2.73	0.008	-0.79
1452441_at	Phf3	PHD finger protein 3	-1.6	0.147	-1.21	0.275	1.11	0.659	1.13	0.763	-0.14
1451028_at	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	1	0.996	-1.71	0.071	-1.02	0.931	3.03	0.123	0.33
1453974_at	1700023A20Rik	RIKEN cDNA 1700023A20 gene	-1.36	0.719	-1.3	0.721	1.06	0.932	1.37	0.637	-0.06
1437460_x_at	Rin1	Ras and Rab interactor 1	-2.99	0.081	-2	0.148	1.73	0.226	1.2	0.702	-0.52
1440265_at	Jund1	Jun proto-oncogene related gene d1	-1.32	0.533	-1.43	0.559	1.11	0.563	1.02	0.965	-0.15
1448912_at	C1qtnf1	C1q and tumor necrosis factor related protein 1	-1.36	0.341	1.15	0.289	-1.48	0.036	1.79	0.184	0.03
1430716_at	5330421F07Rik	RIKEN cDNA 5330421F07 gene	-1.3	0.218	1.09	0.7	-1.42	0.283	1.11	0.659	-0.13
1419885_at	DXErtd223e	DNA segment, Chr X, ERATO Doi 223, expressed	-1.9	0.197	1.39	0.319	-1.53	0.003	1.85	0.03	-0.05
1436300_at	Ripk5	receptor interacting protein kinase 5	1.07	0.826	-1.15	0.351	-1.6	0.094	1.41	0.395	-0.07
1444134_at	Abl1	v-abl Abelson murine leukemia oncogene 1	-2.03	0.415	1.13	0.758	-1.06	0.79	1.07	0.791	-0.22

1447054_at	C85395	expressed sequence C85395	-1.77	0.425	-1.2	0.654	1.17	0.576	1.34	0.508	-0.11
1459793_s_at	---	---	1.05	0.726	-1.41	0.081	-1.24	0.164	1.08	0.755	-0.13
1447539_at	---	Transcribed locus	-1.98	0.481	1.14	0.761	-1.08	0.89	1.23	0.682	-0.17
1436749_at	Mesdc2	mesoderm development candiate 2	1.14	0.835	-1.18	0.613	-1.71	0.345	1.1	0.863	-0.16
1453952_at	4930572G02Rik	RIKEN cDNA 4930572G02 gene	1.11	0.822	-1.25	0.643	-1.52	0.295	1.09	0.497	-0.14
1458519_at	---	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833418G05	-1.9	0.474	-2.27	0.377	1.6	0.462	1.22	0.621	-0.34
1443671_x_at	2010001J22Rik	RIKEN cDNA 2010001J22 gene	-1.45	0.544	-1.44	0.004	1.19	0.503	1.29	0.613	-0.1
1449521_at	Cd93	CD93 antigen	-1.33	0.255	-2.75	0.018	1.45	0.2	1.03	0.936	-0.4
1437747_at	Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	-1.4	0.107	-1.37	0.007	1.13	0.422	1.17	0.396	-0.12
1418548_at	Svs6	seminal vesicle secretion 6	1.08	0.827	1.12	0.807	-2.69	0.133	-2.06	0.308	-0.64
1417028_a_at	Trim2	tripartite motif protein 2	-1.18	0.26	1	0.991	-1.38	0.027	1.31	0.245	-0.06
1459249_at	Tdrd3	Tudor domain containing 3	-1.17	0.715	1.17	0.728	-1.83	0.15	1.53	0.248	-0.07
1424719_a_at	Mapt	microtubule-associated protein tau	-1.14	0.676	-1.7	0.275	1.11	0.539	1.36	0.65	-0.09
1417795_at	Chl1	cell adhesion molecule with homology to L1CAM	1.44	0.458	-1.46	0.625	-2.21	0.24	1.31	0.658	-0.23
1421566_at	Pet2	plasmacytoma expressed transcript 2	-1.4	0.535	1.16	0.776	-1.44	0.503	1.52	0.172	-0.04
1440670_at	---	Transcribed locus	-1.21	0.477	-3.03	0.142	1.41	0.537	1	0.995	-0.45
1445350_at	Ppp4c	protein phosphatase 4, catalytic subunit	1.03	0.707	-1.08	0.708	-1.64	0.258	1.02	0.931	-0.16
1419139_at	Gdf5	growth differentiation factor 5	-1.5	0.584	-1.52	0.508	1.25	0.659	1.01	0.986	-0.19
1460161_at	D5Ertd422e	DNA segment, Chr 5, ERATO Doi 422, expressed	-1.24	0.661	1.37	0.613	-2.49	0.006	1.46	0.533	-0.23
1437614_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	-1.24	0.483	1.04	0.701	-1.38	0.232	1.33	0.428	-0.06
1444717_at	Zwint	ZW10 interactor	1.14	0.617	-1.32	0.31	-1.47	0.052	1.31	0.514	-0.09
1444118_at	---	---	-1.9	0.431	1.17	0.767	-1.14	0.819	1.12	0.49	-0.19
1425913_a_at	2810022L02Rik	RIKEN cDNA 2810022L02 gene	1.06	0.175	-1.37	0.183	-1.29	0.132	1.13	0.595	-0.12
1454907_at	---	---	-1.16	0.222	1.04	0.898	-1.48	0.323	1.21	0.66	-0.1
1437707_at	BC019561	cDNA sequence BC019561	1.19	0.422	-1.94	0.126	-1.14	0.448	1.26	0.698	-0.16
1458948_at	D630013N20Rik	RIKEN cDNA D630013N20 gene	-1.33	0.218	-2.74	0.061	1.46	0.488	1.05	0.92	-0.39
1416980_at	Mettl7b	methyltransferase like 7B	1.14	0.511	-1.07	0.665	-1.98	0.186	1.86	0.13	-0.01
1444499_at	---	Transcribed locus	1.2	0.393	-4.31	0.025	1.14	0.746	-2.11	0.398	-1.02
1436682_at	Tmsb10	thymosin, beta 10	-2.69	0.047	1.7	0.159	-2	0.019	1.16	0.791	-0.46
1433229_at	9430031J08Rik	RIKEN cDNA 9430031J08 gene	1.14	0.126	-1.22	0.468	-1.63	0.065	1.07	0.875	-0.16
1432641_at	5830490A12Rik	RIKEN cDNA 5830490A12 gene	-1.66	0.442	1.33	0.547	-1.56	0.43	1.37	0.661	-0.13
1432598_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	1.19	0.644	-1.31	0.625	-1.61	0.292	1.22	0.378	-0.13
1441025_at	3110047P20Rik	RIKEN cDNA 3110047P20 gene	-1.41	0.046	1.13	0.886	-1.36	0.473	1.28	0.337	-0.09
1445172_at	Lgtn	ligatin	1.02	0.934	-1.14	0.706	-1.49	0.229	1.82	0.377	0.05
1453048_at	Nhlrc2	NHL repeat containing 2	-1.2	0.44	1.05	0.798	-1.43	0.021	1.23	0.483	-0.09
1459502_at	D17Ertd589e	DNA segment, Chr 17, ERATO Doi 589, expressed	1.12	0.762	-1.72	0.306	-1.14	0.346	1.26	0.451	-0.12
1458583_at	1700123O12Rik	RIKEN cDNA 1700123O12 gene	-1.27	0.229	-1.54	0.314	1.14	0.59	1.15	0.588	-0.13
1455097_at	Wdr70	WD repeat domain 70	1.01	0.961	-1.13	0.403	-1.47	0.007	1.08	0.026	-0.13
1442999_at	B930036G03Rik	RIKEN cDNA B930036G03 gene	-1.62	0.005	1.01	0.979	-1.05	0.792	1.52	0.223	-0.04
1453139_at	Nudt12	nudix (nucleoside diphosphate linked moiety X)-type motif 12	-1.16	0.41	1.07	0.309	-1.56	0.17	2.4	0.052	0.19
1438234_at	Wdr26	WD repeat domain 26	-1.14	0.681	1.09	0.583	-1.64	0.004	1.51	0.179	-0.04
1445849_at	LOC665521 /// LOC	similar to PRAME family member 8 /// similar to PRAME family member 8 /// simil	-1.13	0.716	1.16	0.367	-1.87	0.253	2.92	0.342	0.27
1453668_at	3110052M02Rik	RIKEN cDNA 3110052M02 gene	1.01	0.994	-1.91	0.138	1.05	0.875	-1.62	0.409	-0.37
1428433_at	Hipk2	homeodomain interacting protein kinase 2	1.09	0.215	-1.36	0.114	-1.32	0.238	2.62	0.15	0.25
1460154_at	AI194348	expressed sequence AI194348	-3.32	0.015	1.38	0.666	-1.12	0.434	1.02	0.978	-0.51
1439196_at	Hook3	hook homolog 3 (Drosophila)	1.02	0.95	-1.16	0.404	-1.43	0.145	1.2	0.574	-0.09
1432562_at	1110006G14Rik	RIKEN cDNA 1110006G14 gene	-1.32	0.134	-1.64	0.002	1.21	0.57	1.37	0.47	-0.09
1456465_at	B430110G05Rik	RIKEN cDNA B430110G05 gene	-1.31	0.394	1.14	0.739	-1.48	0.019	1.23	0.556	-0.1
1431168_at	Six3os1	Six3 opposite strand transcript 1	-2.08	0.236	1.14	0.671	-1.04	0.856	1.99	0.132	0
1432666_at	---	---	-1.62	0.446	-2.42	0.121	1.55	0.338	1.3	0.073	-0.3
1446519_at	A730091E23Rik	RIKEN cDNA A730091E23 gene	-1.71	0.016	1.05	0.754	-1.06	0.705	1.38	0.191	-0.09
1445591_at	Sardh	Sarcosine dehydrogenase	-1.53	0.567	-1.65	0.085	1.32	0.638	1.92	0.081	0.02
1433057_at	4933411O13Rik	RIKEN cDNA 4933411O13 gene	-1.81	0.371	1.24	0.404	-1.26	0.222	3.83	0.118	0.5

1436976_a_at	9930028C20Rik	RIKEN cDNA 9930028C20 gene	1.22	0.248	-1.74	0.163	-1.27	0.052	3.64	0.186	0.46
1444958_at	C79017	expressed sequence C79017	-1.41	0.023	-1.18	0.419	1.02	0.919	1.58	0.041	0
1435512_at	AI836003	expressed sequence AI836003	-1.38	0.159	1.07	0.821	-1.27	0.387	1.23	0.34	-0.09
1458652_at	Cd8b1	CD8 antigen, beta chain 1	-1.78	0.322	-1.04	0.88	1.05	0.69	1.25	0.052	-0.13
1425303_at	Gck	glucokinase	-1.53	0.095	-1.45	0.477	1.24	0.461	1.08	0.824	-0.17
1441976_at	5430434G16Rik	RIKEN cDNA 5430434G16 gene	1.04	0.624	-1.07	0.709	-1.67	0.005	1.98	0.341	0.07
1437686_x_at	Cutl1	cut-like 1 (Drosophila)	1.14	0.825	-4.27	0.002	1.2	0.557	-1.01	0.982	-0.73
1442579_at	9330111N05Rik	RIKEN cDNA 9330111N05 gene	1.14	0.775	-1.35	0.391	-1.44	0.426	1.22	0.498	-0.11
1442092_at	Fancd2	Fanconi anemia, complementation group D2	-1.59	0.581	1.2	0.769	-1.34	0.207	2.55	0.094	0.21
1432283_at	4930417G10Rik	RIKEN cDNA 4930417G10 gene	-2.67	0.013	1.49	0.5	-1.39	0.192	1.05	0.934	-0.38
1459893_at	C76472	expressed sequence C76472	-1.45	0.403	-1.86	0.273	1.35	0.453	1.35	0.272	-0.15
1452550_a_at	Fmr1	fragile X mental retardation syndrome 1 homolog	-1.6	0.39	-1.63	0.136	1.34	0.407	1.01	0.971	-0.22
1431401_at	4930539J05Rik	RIKEN cDNA 4930539J05 gene	-1.04	0.888	-1.76	0.141	1.06	0.873	1.4	0.088	-0.09
1433704_s_at	Tloc1	translocation protein 1	1	1	-1.19	0.004	-1.35	0.063	1.24	0.126	-0.08
1458230_at	Gria4	Glutamate receptor, ionotropic, AMPA4 (alpha 4)	-1.72	0.335	-1.42	0.411	1.3	0.506	1.32	0.529	-0.13
1437399_at	Cldnd1	claudin domain containing 1	-1.21	0.51	1.09	0.826	-1.51	0.214	1.05	0.918	-0.15
1434504_at	Zfyve28	zinc finger, FYVE domain containing 28	1.01	0.968	-1.39	0.398	-1.18	0.105	1.44	0.131	-0.03
1449730_s_at	Fzd3	frizzled homolog 3 (Drosophila)	-1.78	0.079	1.14	0.824	-1.13	0.536	1.14	0.676	-0.16
1442020_at	Olfr1329	Olfactory receptor 1329	-2.18	0.112	1.44	0.441	-1.45	0.24	2.8	0.093	0.15
1437725_x_at	Tm2d2	TM2 domain containing 2	-1.12	0.501	1.12	0.532	-1.74	0.089	1.85	0.299	0.03
1447310_at	C630028N24Rik	RIKEN cDNA C630028N24 gene	1.04	0.894	-1.36	0.249	-1.23	0.28	1.03	0.895	-0.13
1429768_at	Dtna	dystrobrevin alpha	-1.11	0.444	1.16	0.804	-1.9	0.026	1.68	0.418	-0.04
1439584_at	Zfp526	zinc finger protein 526	-1.09	0.386	-1.54	0.09	1.02	0.854	1.16	0.246	-0.11
1439975_at	BC062109	cDNA sequence BC062109	-1.42	0.45	1.12	0.835	-1.31	0.392	1.01	0.975	-0.15
1437648_at	Pcyt1b	phosphate cytidylyltransferase 1, choline, beta isoform	1.02	0.922	-1.04	0.953	-1.68	0.29	1.8	0.518	0.03
1428606_at	Ccdc124	coiled-coil domain containing 124	1.43	0.64	-1.28	0.506	-2.71	0.102	1.12	0.787	-0.36
1445004_a_at	A330068P14Rik	RIKEN cDNA A330068P14 gene	-1.52	0.633	1.02	0.954	-1.1	0.655	1.5	0.209	-0.03
1426711_at	Tmco3	transmembrane and coiled-coil domains 3	-1.44	0.082	-1.18	0.236	1.04	0.798	1.1	0.297	-0.12
1424448_at	Trim6 /// LOC6334(	tripartite motif protein 6 /// similar to Tripartite motif protein 6	-1.25	0.279	-1.28	0.152	1	0.99	1.3	0.095	-0.06
1440177_at	9.63E+17	hypothetical protein 9630027E11	-2.26	0.084	-1.65	0.327	1.54	0.456	1.07	0.744	-0.33
1459387_at	Mast4	microtubule associated serine/threonine kinase family member 4	-1.91	0.209	-1.02	0.961	1.08	0.774	1.41	0.263	-0.11
1423559_at	Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	-2.21	0.293	-1.09	0.89	1.22	0.776	1.51	0.317	-0.15
1420581_at	Gpr143	G protein-coupled receptor 143	1.18	0.274	-1.21	0.695	-1.74	0.216	1.21	0.787	-0.14
1433813_at	Tmem48	transmembrane protein 48	-1.25	0.401	-1.28	0.076	1.01	0.952	1.57	0.281	0.01
1440095_at	---	---	1.18	0.262	-1.34	0.08	-1.52	0.053	1.01	0.969	-0.17
1440732_at	D030018L15Rik	RIKEN cDNA D030018L15 gene	-1.11	0.254	-1.47	0.342	1.01	0.989	1.16	0.814	-0.1
1458503_at	---	---	1.17	0.614	-1.56	0.083	-1.29	0.296	1.17	0.494	-0.13
1429574_at	Clic3	chloride intracellular channel 3	1.22	0.369	-3.25	0.024	1.06	0.548	-1.5	0.266	-0.62
1445517_at	---	---	-1.04	0.911	1.03	0.862	-1.68	0.014	1.45	0.34	-0.06
1418413_at	Cav3	caveolin 3	1.3	0.492	-1.8	0.457	-1.37	0.504	1.72	0.027	-0.04
1422867_at	Gzmg	granzyme G	1.17	0.584	-1.4	0.194	-1.42	0.528	1.03	0.919	-0.16
1429841_at	Megf10	multiple EGF-like-domains 10	-1.69	0.535	1.01	0.957	-1.02	0.975	1.76	0.281	0.02
1457090_at	---	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831433L12	-1.47	0.314	-2.09	0.091	1.43	0.257	1.02	0.879	-0.28
1422641_at	Dok5	docking protein 5	1.2	0.557	-1.56	0.133	-1.35	0.233	1.04	0.96	-0.17
1459267_at	2310033P09Rik	RIKEN cDNA 2310033P09 gene	-1.43	0.165	-1.28	0.362	1.11	0.742	1.28	0.325	-0.08
1428235_at	Sdhd	succinate dehydrogenase complex, subunit D, integral membrane protein	-1.24	0.197	-1.32	0.06	1.02	0.815	1.14	0.082	-0.1
1452500_at	Tmlhe	trimethyllysine hydroxylase, epsilon	1.09	0.766	1.03	0.876	-2.11	0.009	-1.22	0.493	-0.3
1444723_at	6530418L21Rik	RIKEN cDNA 6530418L21 gene	-1.83	0.05	1.04	0.944	1	0.991	-1.01	0.991	-0.2
1443615_at	1110057K04Rik	RIKEN cDNA 1110057K04 gene	-1.77	0.327	-1.03	0.937	1.05	0.943	1.19	0.786	-0.14
1418268_at	Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	1.37	0.172	-2.17	0.025	-1.31	0.525	1	0.992	-0.28
1422343_at	Olfr155	olfactory receptor 155	-2.47	0.157	1.65	0.466	-1.87	0.206	2.34	0.341	-0.09
1417188_s_at	Hip2	huntingtin interacting protein 2	-1.08	0.799	-1.59	0.021	1.04	0.758	1.19	0.6	-0.11
1445890_at	C230079E05Rik	RIKEN cDNA C230079E05 gene	-1.59	0.474	1.29	0.598	-1.49	0.473	3.65	0.017	0.46

1445325_at	Prkar2a	Protein kinase, cAMP dependent regulatory, type II alpha	1.06	0.323	-1.3	0.669	-1.32	0.505	1.47	0.486	-0.02
1459431_at	Nfia	Nuclear factor I/A	-1.54	0.622	1.04	0.902	-1.12	0.753	1.72	0.367	0.03
1459240_at	Tcf25	Transcription factor 25 (basic helix-loop-helix)	-1.3	0.008	1.02	0.942	-1.24	0.088	1.01	0.981	-0.13
1431026_at	Nat12	N-acetyltransferase 12	-1.34	0.224	-1.35	0.336	1.1	0.399	1.23	0.114	-0.09
1429404_at	2010317E24Rik	RIKEN cDNA 2010317E24 gene	-1.65	0.587	-1.33	0.198	1.23	0.739	3.57	0.078	0.46
1439193_at	Prrxl1	Paired related homeobox protein-like 1	1.24	0.724	-1.35	0.755	-1.65	0.314	1.09	0.805	-0.17
1456506_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1.18	0.734	-1.7	0.128	-1.21	0.604	1.2	0.583	-0.13
1426498_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	-1.21	0.672	-1.34	0.591	1.02	0.919	1.45	0.549	-0.02
1458736_at	---	---	1.04	0.872	-1.28	0.556	-1.31	0.392	2.79	0.007	0.31
1432634_at	4933429H19Rik	RIKEN cDNA 4933429H19 gene	1.23	0.691	-1.53	0.606	-1.41	0.402	1.38	0.697	-0.08
1443836_x_at	Wdr48	WD repeat domain 48	1.02	0.966	-1.65	0.161	-1.04	0.873	1.18	0.709	-0.12
1433225_at	6330403N20Rik	RIKEN cDNA 6330403N20 gene	1.24	0.291	1.01	0.987	-2.94	0.004	-1.04	0.745	-0.43
1459257_at	A230048G03Rik	RIKEN cDNA A230048G03 gene	-2.86	0.374	1.2	0.765	1.04	0.94	-2.77	0.059	-0.85
1456672_at	---	CDNA, clone:Y1G0143G21, strand:unspecified	-1.39	0.32	-1.15	0.644	1	0.995	1.55	0.408	0
1447365_at	---	Transcribed locus	-1.92	0.51	1.35	0.394	-1.39	0.553	1.01	0.969	-0.24
1449409_at	Sult1c2	sulfotransferase family, cytosolic, 1C, member 2	-1.14	0.372	-1.4	0.404	1	0.991	1.14	0.797	-0.1
1420184_at	---	---	-1.49	0.33	1.34	0.664	-1.73	0.059	1.29	0.366	-0.15
1445753_at	Aox3l1	Aldehyde oxidase 3-like 1	-1.6	0.292	1.16	0.765	-1.24	0.606	2.06	0.243	0.09
1425737_at	---	---	-1.29	0.728	-1.29	0.597	1.04	0.879	1.15	0.774	-0.1
1454314_at	1700031K17Rik	RIKEN cDNA 1700031K17 gene	1.35	0.689	-1.31	0.443	-2.07	0.32	1.03	0.963	-0.25
1455531_at	A930031D07Rik	RIKEN cDNA A930031D07 gene	1.19	0.031	-2.12	0.127	-1.07	0.785	1.52	0.072	-0.12
1458679_a_at	Tatdn1	TatD DNase domain containing 1	-1.15	0.513	1.11	0.577	-1.63	0.011	1.18	0.383	-0.12
1434198_at	Atpif1	ATPase inhibitory factor 1	1.05	0.673	-1.26	0.474	-1.35	0.181	1.69	0.226	0.04
1425429_s_at	Hif3a /// LOC64109	hypoxia inducible factor 3, alpha subunit /// similar to hypoxia inducible factor 3, a	-2.12	0.382	1.1	0.713	1.02	0.891	-1.38	0.245	-0.34
1430383_at	Ceacam20	CEA-related cell adhesion molecule 20	-1.68	0.255	1.18	0.798	-1.22	0.61	1.37	0.493	-0.09
1457026_at	Liph	lipase, member H	-2.07	0.188	1.2	0.317	-1.1	0.634	2.85	0.071	0.22
1437941_at	Phka2	phosphorylase kinase alpha 2	-1.41	0.255	1.06	0.779	-1.22	0.308	1.01	0.973	-0.14
1436389_at	---	Transcribed locus	1.06	0.658	-1.1	0.317	-1.6	0.004	1.11	0.113	-0.13
1416886_at	C1d	nuclear DNA binding protein	1.01	0.969	-1.18	0.296	-1.36	0.013	1.28	0.287	-0.06
1439272_at	Lcorl	ligand dependent nuclear receptor corepressor-like	1.01	0.952	-1.13	0.571	-1.43	0.188	1.28	0.098	-0.07
1449871_at	Tbx18	T-box18	-1.09	0.867	-1.78	0.31	1.11	0.815	1.8	0.296	0.01
1449505_at	Kpna1	karyopherin (importin) alpha 1	1.08	0.44	-1.08	0.138	-1.68	0.022	1.33	0.297	-0.09
1441413_at	Cat	Catalase	1.43	0.291	-1.66	0.147	-1.8	0.014	1.23	0.513	-0.2
1423161_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1.14	0.06	-1.33	0.046	-1.42	0.025	1.26	0.157	-0.09
1434151_at	Mettl7a	methyltransferase like 7A	-1.21	0.279	-1.42	0.052	1.06	0.726	1.4	0.408	-0.04
1456428_at	Cxcl15	Chemokine (C-X-C motif) ligand 15	1.14	0.616	-1.23	0.466	-1.57	0.006	2.22	0.32	0.14
1416879_at	Mrpl51	mitochondrial ribosomal protein L51	-1.22	0.007	-1.36	0.055	1.04	0.888	1.55	0.118	0
1432323_at	8430436N08Rik	RIKEN cDNA 8430436N08 gene	1.23	0.79	-1.61	0.27	-1.35	0.43	1.26	0.602	-0.12
1419258_at	Tcea1	transcription elongation factor A (SII) 1	1.01	0.942	-1.17	0.176	-1.37	0.059	1.14	0.427	-0.1
1454155_at	4930500H12Rik	RIKEN cDNA 4930500H12 gene	1.07	0.868	-1.35	0.463	-1.28	0.5	1.24	0.653	-0.08
1452816_at	Mlf1ip	myeloid leukemia factor 1 interacting protein	1.07	0.707	-1.19	0.456	-1.46	0.251	2.06	0.368	0.12
1449379_at	Kdr	kinase insert domain protein receptor	-1.11	0.122	1.12	0.553	-1.75	0.17	1.23	0.32	-0.13
1426311_s_at	Zdhhc5	zinc finger, DHHC domain containing 5	-1.24	0.295	1.02	0.888	-1.29	0.366	1.11	0.749	-0.1
1446844_at	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7	-1.18	0.37	-1.65	0.257	1.15	0.451	1.02	0.887	-0.17
1455601_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430079C	1.1	0.772	-1.28	0.434	-1.4	0.374	3.15	0.2	0.39
1419999_at	Igbp1	immunoglobulin (CD79A) binding protein 1	-1.62	0.189	-1.12	0.776	1.09	0.646	1.08	0.727	-0.14
1422739_at	Hs2st1	Heparan sulfate 2-O-sulfotransferase 1	-1.2	0.202	1.16	0.595	-1.65	0.01	1.05	0.805	-0.16
1419227_at	Cct6b	chaperonin subunit 6b (zeta)	1.23	0.42	-1.15	0.763	-1.98	0.071	1.77	0.36	-0.03
1415830_at	Orc5l	origin recognition complex, subunit 5-like (S. cerevisiae)	1.03	0.689	-1.23	0.225	-1.32	0.036	1.3	0.275	-0.06
1431277_at	---	---	-1.57	0.02	1.02	0.963	-1.06	0.753	1.07	0.706	-0.14
1449345_at	2810027O19Rik	RIKEN cDNA 2810027O19 gene	-1.25	0.229	-1.38	0.222	1.07	0.618	3.71	0.296	0.54
1429692_s_at	Gch1	GTP cyclohydrolase 1	-1.36	0.156	-1.27	0.145	1.08	0.404	2.85	0.155	0.32
1437012_x_at	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	-1.21	0.346	-1.54	0.282	1.12	0.736	1.01	0.963	-0.15

1447104_at	Arid1a	AT rich interactive domain 1A (Swi1 like)	-1.8	0.059	-2.65	0.027	1.67	0.088	1.38	0.459	-0.35
1450000_at	Nalp4c	NACHT, leucine rich repeat and PYD containing 4C	1.05	0.758	-1.02	0.923	-1.76	0.046	1.12	0.863	-0.15
1433073_at	4933425E08Rik	RIKEN cDNA 4933425E08 gene	-1.08	0.776	-1.57	0.189	1.04	0.914	1.38	0.655	-0.06
1425916_at	Capn8	calpain 8	-2.03	0.301	-1.03	0.96	1.13	0.534	1.02	0.919	-0.22
1444290_at	Steap2	six transmembrane epithelial antigen of prostate 2	-1.15	0.361	-1.39	0.084	1.01	0.962	1.6	0.631	0.02
1416271_at	Perp	PERP, TP53 apoptosis effector	1.05	0.565	-1.31	0.124	-1.27	0.197	1.13	0.172	-0.1
1445558_at	5930430L01Rik	RIKEN cDNA 5930430L01 gene	-1.08	0.895	1.18	0.781	-2.04	0.222	1.23	0.327	-0.18
1434979_at	4933403F05Rik	RIKEN cDNA 4933403F05 gene	-1.22	0.289	-1.29	0.364	1.01	0.968	1.28	0.333	-0.06
1442061_at	Btbd7	BTB (POZ) domain containing 7	1.12	0.537	-1.65	0.166	-1.15	0.566	1	0.994	-0.17
1446229_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130045L	-1.2	0.726	-2.68	0.041	1.39	0.091	2.02	0.338	-0.12
1444114_at	Mkln1	Muskelin 1, intracellular mediator containing kelch motifs	1.01	0.949	1.08	0.87	-1.98	0.006	-1.19	0.684	-0.27
1418324_at	Fem1b	feminization 1 homolog b (C. elegans)	1.04	0.641	-1.2	0.043	-1.38	0.001	1.07	0.691	-0.12
1440751_at	Ep400	E1A binding protein p400	-1.13	0.209	1.07	0.82	-1.55	0.126	1.08	0.607	-0.13
1433173_at	5430440L12Rik	RIKEN cDNA 5430440L12 gene	-1.17	0.16	-1.38	0.114	1.03	0.855	1.13	0.206	-0.1
1421995_at	Tcfap2a	transcription factor AP-2, alpha	-1.28	0.03	-1.48	0.256	1.14	0.644	1.31	0.558	-0.07
1457839_at	Dhx40	DEAH (Asp-Glu-Ala-His) box polypeptide 40	1.01	0.96	-1.26	0.105	-1.25	0.44	1.02	0.921	-0.12
1459482_at	Trpm2	transient receptor potential cation channel, subfamily M, member 2	-2	0.066	-1.15	0.147	1.23	0.467	1.05	0.696	-0.22
1442748_at	Btbd3	BTB (POZ) domain containing 3	-2.32	0.419	1.05	0.916	1.12	0.811	-1.14	0.684	-0.32
1454378_at	Ywhaq	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, thet	-1.66	0.121	-1.18	0.52	1.16	0.681	1.23	0.318	-0.12
1416334_at	Wwox	WW domain-containing oxidoreductase	-1.26	0.151	-1.77	0.076	1.25	0.155	1.14	0.368	-0.16
1456087_at	Nfia	nuclear factor I/A	1.11	0.29	-1.2	0.378	-1.52	0.162	1.49	0.115	-0.03
1458890_at	D030055H07Rik	RIKEN cDNA D030055H07 gene	-1.85	0.547	1.51	0.245	-1.81	0.188	1.48	0.542	-0.17
1420138_at	Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	-1.52	0.044	-1.33	0.162	1.2	0.261	1.12	0.576	-0.13
1446135_at	D030051J21Rik	RIKEN cDNA D030051J21 gene	-1.15	0.671	-1.41	0.313	1.02	0.952	1.1	0.861	-0.11
1441815_at	AI851453	expressed sequence AI851453	1.11	0.597	-2.13	0.297	1.02	0.927	-1.96	0.395	-0.49
1439101_at	D830007F02Rik	RIKEN cDNA D830007F02 gene	-2.03	0.196	-1.03	0.843	1.14	0.694	2.88	0.193	0.24
1448053_at	B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	1.04	0.955	-1.33	0.63	-1.24	0.362	1.58	0.159	0.01
1451873_a_at	Smad5	MAD homolog 5 (Drosophila)	-1.43	0.055	-1.24	0.548	1.1	0.74	1.09	0.563	-0.12
1428820_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	1.13	0.368	-1.51	0.219	-1.24	0.428	1.04	0.918	-0.14
1448065_at	Ppox	protoporphyrinogen oxidase	-1.25	0.579	1.06	0.942	-1.34	0.131	3.03	0.223	0.37
1452350_at	Brd8	bromodomain containing 8	-1.29	0.023	1.09	0.473	-1.37	0.068	1.13	0.596	-0.11
1452978_at	Tmem138	transmembrane protein 138	1.25	0.123	-2.17	0.238	-1.12	0.408	1.34	0.369	-0.18
1428211_at	4933406E20Rik	RIKEN cDNA 4933406E20 gene	1.07	0.674	-2.45	0.144	1.12	0.564	-2.81	0.141	-0.76
1444215_at	Pcdh9	Protocadherin 9	-1.71	0.388	1.11	0.86	-1.1	0.91	3.4	0.015	0.43
1459491_at	D12Ertd673e	DNA segment, Chr 12, ERATO Doi 673, expressed	-1.99	0.26	1.12	0.682	-1.02	0.912	1.08	0.841	-0.2
1434320_at	Gtf3c4	general transcription factor IIIC, polypeptide 4	1.01	0.738	-1.12	0.397	-1.42	0.131	1.11	0.334	-0.1
1425556_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	1.28	0.585	-1.31	0.279	-1.79	0.056	1.28	0.602	-0.14
1446310_at	C130053K05Rik	RIKEN cDNA C130053K05 gene	1.33	0.493	-1.45	0.497	-1.72	0.287	1.21	0.759	-0.16
1433408_a_at	Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	1.16	0.513	-1.58	0.303	-1.23	0.144	3.3	0.209	0.41
1438929_at	---	---	1.18	0.54	-1.22	0.457	-1.65	0.007	1.31	0.011	-0.09
1432209_at	1810010K12Rik	RIKEN cDNA 1810010K12 gene	-1.01	0.965	-1.7	0.169	1.03	0.956	2.45	0.006	0.19
1454351_at	4933435C09Rik	RIKEN cDNA 4933435C09 gene	-1.5	0.583	1.01	0.99	-1.07	0.843	1.9	0.319	0.08
1454344_at	Slc44a1	solute carrier family 44, member 1	1.14	0.832	-1.86	0.087	-1.07	0.883	1.32	0.592	-0.12
1434241_at	Wdr67	WD repeat domain 67	-1.57	0.116	-1.12	0.692	1.08	0.627	1.94	0.334	0.08
1459032_at	---	Transcribed locus	-1.23	0.735	1.26	0.718	-1.87	0.085	2.42	0.008	0.14
1429825_at	1700030E15Rik	RIKEN cDNA 1700030E15 gene	-1.11	0.86	1.37	0.308	-3.05	0.001	1.43	0.496	-0.34
1424429_s_at	Ccdc95	coiled-coil domain containing 95	-1.44	0.181	-1.36	0.294	1.18	0.258	1.02	0.879	-0.15
1451799_at	Ccdc25	coiled-coil domain containing 25	-1.31	0.026	1.14	0.809	-1.44	0.315	1.01	0.95	-0.15
1459777_at	Il1r1	interleukin 1 receptor, type I	1.26	0.499	-1.3	0.702	-1.72	0.429	1.09	0.822	-0.17
1453127_at	Ppm1j	protein phosphatase 1J	-1.54	0.641	-1.16	0.527	1.09	0.824	1.09	0.862	-0.13
1440934_at	AW742931	expressed sequence AW742931	-1.29	0.701	-1.32	0.208	1.08	0.765	1.07	0.835	-0.12
1430632_at	Asb1	ankyrin repeat and SOCS box-containing protein 1	-1.24	0.832	-1.56	0.132	1.16	0.723	3.23	0.285	0.4
1445993_at	---	---	1.08	0.597	-1.94	0.114	1.01	0.943	-1.65	0.268	-0.38

1437285_at	---	---	-1.32	0.449	-1.28	0.168	1.07	0.792	2.37	0.228	0.21
1457568_at	C230004L04	hypothetical protein C230004L04	1.03	0.735	-1.35	0.371	-1.2	0.138	1.12	0.546	-0.1
1418130_at	---	---	-1.28	0.285	-1.21	0.34	1	0.999	1.11	0.842	-0.1
1431896_at	Six6os1	Six6 opposite strand transcript 1	1.26	0.755	-1.65	0.465	-1.35	0.377	1.34	0.511	-0.1
1418288_at	Lpin1	lipin 1	-1.23	0.691	-1.88	0.354	1.26	0.559	1.72	0.243	-0.03
1430358_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	1.02	0.878	-1.24	0.537	-1.28	0.44	1.1	0.583	-0.1
1433048_at	4933428L01Rik	RIKEN cDNA 4933428L01 gene	-1.54	0.064	1.1	0.855	-1.16	0.627	1.56	0.349	-0.01
1446426_at	Enah	Enabled homolog (Drosophila)	-1.02	0.904	1.2	0.474	-2.36	0	1.72	0.019	-0.12
1418186_at	Gstt1	glutathione S-transferase, theta 1	1.01	0.954	-1.28	0.187	-1.22	0.016	1.33	0.009	-0.04
1415777_at	Pnliprp1	pancreatic lipase related protein 1	-1.59	0.552	1.11	0.531	-1.15	0.776	1.33	0.074	-0.08
1441804_at	---	---	1.06	0.798	1.02	0.89	-1.89	0.091	-2.46	0.029	-0.57
1457071_x_at	Prmt6	protein arginine N-methyltransferase 6	1.01	0.785	-1.39	0.474	-1.14	0.52	1.17	0.225	-0.09
1431624_a_at	2610206B13Rik	RIKEN cDNA 2610206B13 gene	1.23	0.64	-1.12	0.776	-2.07	0.019	1.55	0.274	-0.1
1438301_at	Ddef1	Development and differentiation enhancing	1.13	0.726	-1.24	0.359	-1.47	0.189	1.28	0.493	-0.08
1457799_at	Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	1.06	0.894	-2.36	0.219	1.13	0.238	-1.14	0.811	-0.33
1454455_at	6530413G14Rik	RIKEN cDNA 6530413G14 gene	1.03	0.95	-1.11	0.818	-1.48	0.143	1.19	0.699	-0.09
1444001_at	Strbp	Spermatid perinuclear RNA binding protein	1.06	0.945	-1.66	0.456	-1.05	0.862	1.02	0.954	-0.16
1454121_x_at	Ccdc18	coiled-coil domain containing 18	-1.66	0.033	-2.2	0.154	1.55	0.338	1.31	0.644	-0.25
1424958_at	Car8	carbonic anhydrase 8	1.17	0.384	-1.24	0.237	-1.59	0.089	1.06	0.809	-0.15
1459315_at	---	---	-1.08	0.445	1.02	0.91	-1.51	0.231	1.41	0.01	-0.04
1455514_at	Kcnd1	potassium voltage-gated channel, Shal-related family, member 1	-1.31	0.176	1.1	0.82	-1.34	0.568	1.02	0.953	-0.13
1433839_at	Nars2	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	-1.19	0.273	-1.38	0.064	1.05	0.822	1.64	0.03	0.03
1418950_at	Drd2	dopamine receptor 2	-1.72	0.477	-1.06	0.917	1.08	0.821	1.54	0.15	-0.04
1429034_at	Eme2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	-1.05	0.452	-1.83	0.197	1.11	0.587	1.01	0.927	-0.19
1428771_at	2410127E18Rik	RIKEN cDNA 2410127E18 gene	-1.34	0.084	-1.21	0.566	1.04	0.85	1.59	0.251	0.02
1434700_at	6030408C04Rik	RIKEN cDNA 6030408C04 gene	-1.21	0.344	1.02	0.839	-1.3	0.085	2.05	0.159	0.14
1440730_at	---	---	1.39	0.296	-2.47	0.11	-1.23	0.665	1.33	0.632	-0.24
1455368_at	Zdhhc3	zinc finger, DHHC domain containing 3	-1.02	0.906	1.04	0.838	-1.67	0.05	1.03	0.885	-0.16
1425744_a_at	Mgat5	mannoside acetylglucosaminyltransferase 5	1.09	0.671	-1.22	0.664	-1.43	0.294	1.16	0.716	-0.1
1444752_at	C230073G13Rik	RIKEN cDNA C230073G13 gene	-1.29	0.765	1.4	0.509	-2.29	0.095	1.59	0.466	-0.15
1432805_at	8030431A06Rik	RIKEN cDNA 8030431A06 gene	-1.08	0.316	1.01	0.941	-1.49	0.198	1.04	0.474	-0.13
1455412_at	---	---	-1.45	0.009	1.02	0.911	-1.11	0.735	1.1	0.636	-0.11
1445191_at	Exdl1	Vexonuclease 3'-5' domain-like 1	-1.19	0.375	1.02	0.9	-1.33	0.172	1.66	0.35	0.04
1440712_at	Pcbp3	Poly(rC) binding protein 3	-2.07	0.152	1.42	0.392	-1.42	0.022	1.5	0.219	-0.14
1445743_at	E330024J20Rik	RIKEN cDNA E330024J20 gene	1.42	0.088	-1.56	0.249	-1.82	0.063	1.17	0.747	-0.2
1457383_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	-1.06	0.685	1.14	0.796	-1.88	0.078	1.24	0.021	-0.14
1443916_at	2900026A02Rik	RIKEN cDNA 2900026A02 gene	-2.09	0.334	-1.13	0.435	1.25	0.565	1.09	0.827	-0.22
1458642_at	Klre1	killer cell lectin-like receptor family E member 1	-1.74	0.502	1.27	0.382	-1.3	0.567	1.06	0.905	-0.18
1459849_x_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	-1.21	0.762	1.22	0.607	-1.77	0.132	1.19	0.823	-0.14
1427386_at	Arhgef16	Rho guanine nucleotide exchange factor (GEF) 16	1.07	0.494	-2.4	0.054	1.13	0.516	-1.14	0.757	-0.34
1438396_at	Ocrl	oculocerebrorenal syndrome of Lowe	-1.31	0.276	1.11	0.515	-1.35	0.12	1.21	0.421	-0.09
1420012_at	Xbp1	X-box binding protein 1	-1.24	0.021	1.08	0.481	-1.38	0.215	1.07	0.735	-0.12
1444518_at	Acox1	Acyl-Coenzyme A oxidase 1, palmitoyl	1.02	0.942	-1.19	0.579	-1.32	0.072	1.46	0.184	-0.01
1440216_at	Ifitm5	interferon induced transmembrane protein 5	-1.72	0.045	-1.38	0.58	1.31	0.527	1.04	0.874	-0.19
1430374_at	Slc25a37	solute carrier family 25, member 37	-1.93	0.356	-1.06	0.858	1.15	0.695	1.66	0.467	-0.05
1447424_at	---	---	-1.14	0.909	1.17	0.63	-1.77	0.145	1.05	0.808	-0.17
1427302_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-1.05	0.786	1.13	0.536	-1.86	0.062	3.83	0.122	0.51
1457833_at	AI450241	expressed sequence AI450241	-1.65	0.149	1.07	0.921	-1.07	0.826	1.3	0.219	-0.09
1456854_at	Neurl	neuralized-like homolog (Drosophila)	-1.82	0.225	-1.33	0.503	1.31	0.385	1.64	0.025	-0.05
1425374_at	Oas3	2'-5' oligoadenylate synthetase 3	-1.92	0.23	-2.5	0.28	1.69	0.427	2.01	0.216	-0.18
1459045_at	Golph4	golgi phosphoprotein 4	-1.21	0.07	1.02	0.882	-1.31	0.241	2.67	0.134	0.29
1451565_s_at	Uroc1	urocanase domain containing 1	-1.18	0.247	1.14	0.422	-1.61	0.292	1.52	0.336	-0.03
1428255_at	Luc7l	Luc7 homolog (S. cerevisiae)-like	-1.25	0.165	-1.25	0.009	1.01	0.942	1.36	0.125	-0.03

1432036_at	4933436H12Rik	RIKEN cDNA 4933436H12 gene	-1.21	0.869	1.11	0.788	-1.48	0.225	2.32	0.246	0.18
1457506_at	Als2cr19	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (hum	-1.79	0.098	1.24	0.525	-1.23	0.344	1.06	0.832	-0.18
1439699_at	Pgr	Progesterone receptor	-1.05	0.868	1.02	0.954	-1.55	0.179	1.3	0.712	-0.07
1422011_s_at	Xlr /// 3830403N18I	X-linked lymphocyte-regulated complex /// RIKEN cDNA 3830403N18 gene	-1.16	0.509	1.08	0.876	-1.5	0.111	1.47	0.621	-0.03
1444401_at	C80913	Expressed sequence C80913	-1.36	0.461	1.2	0.606	-1.48	0.042	1.62	0.15	0
1454477_at	5530401A10Rik	RIKEN cDNA 5530401A10 gene	-1.19	0.708	-1.36	0.204	1.04	0.937	1.05	0.732	-0.11
1439519_at	Slc34a3	solute carrier family 34 (sodium phosphate), member 3	-1.63	0.152	1.17	0.569	-1.2	0.381	1.45	0.284	-0.05
1433901_at	Gpiap1	GPI-anchored membrane protein 1	-1.27	0.133	-1.22	0.306	1.01	0.842	1.03	0.854	-0.11
1456791_at	AA407452	EST AA407452	1.05	0.837	-1.16	0.309	-1.41	0.145	1.31	0.603	-0.05
1454872_at	B230308N11Rik	RIKEN cDNA B230308N11 gene	-1.1	0.71	1.02	0.874	-1.45	0.134	1.09	0.676	-0.11
1443570_at	Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	-2.08	0.126	1.28	0.682	-1.16	0.766	1.14	0.59	-0.21
1438276_at	Ncor1	Nuclear receptor co-repressor 1	-1.26	0.367	1.07	0.659	-1.32	0.368	1.04	0.86	-0.12
1454269_s_at	4930519L02Rik	RIKEN cDNA 4930519L02 gene	-1.08	0.834	-1.72	0.334	1.11	0.878	1.2	0.633	-0.12
1448439_at	D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	-1.29	0.566	1.15	0.216	-1.46	0.004	1.13	0.372	-0.11
1432328_at	4930516K23Rik	RIKEN cDNA 4930516K23 gene	-1.24	0.798	-1.65	0.212	1.2	0.703	1.3	0.557	-0.1
1432486_a_at	Tesp2	testicular serine protease 2	-1.65	0.371	-1.07	0.763	1.08	0.711	1.98	0.09	0.08
1446981_at	A830010M20Rik	RIKEN cDNA A830010M20 gene	-1.75	0.054	-3.56	0.048	1.76	0.204	1.14	0.803	-0.6
1416180_a_at	Rdx	radixin	1.05	0.616	-1.25	0.214	-1.31	0.361	1.75	0.087	0.06
1420957_at	Apc	adenomatosis polyposis coli	1.04	0.891	-2.28	0.037	1.14	0.831	-1.17	0.163	-0.32
1445051_at	---	---	-3.77	0.22	1.53	0.437	-1.22	0.705	1.76	0.232	-0.43
1453432_at	1700007G11Rik	RIKEN cDNA 1700007G11 gene	-1.44	0.124	-1.13	0.738	1.04	0.904	1.63	0.337	0.02
1442712_at	LOC627894	Similar to H3 histone, family 3B	1.29	0.68	-1.87	0.098	-1.26	0.225	1.33	0.063	-0.13
1430705_at	2410104I19Rik	RIKEN cDNA 2410104I19 gene	-1.72	0.11	1.19	0.526	-1.18	0.457	1.01	0.907	-0.18
1446322_at	C78568	expressed sequence C78568	-1.63	0.009	1.22	0.616	-1.28	0.204	1.02	0.969	-0.17
1436725_at	E130306D19Rik	RIKEN cDNA E130306D19 gene	1.13	0.715	-1.11	0.886	-1.69	0.158	3.31	0.273	0.41
1451684_a_at	Bicd1	bicaudal D homolog 1 (Drosophila)	1.02	0.933	-1.86	0.312	1.06	0.595	-1.06	0.677	-0.21
1443259_at	---	Transcribed locus	-1.38	0.463	1.5	0.338	-2.54	0.059	1.02	0.96	-0.35
1437618_x_at	Gpr85	G protein-coupled receptor 85	-1.41	0.002	-1.42	0.391	1.21	0.398	1.26	0.527	-0.09
1452251_at	Nbea	neurobeachin	1.02	0.949	-1.11	0.636	-1.42	0.06	1.22	0.393	-0.07
1442720_at	---	---	-1.26	0.628	1.26	0.629	-1.78	0.155	1.24	0.631	-0.13
1442454_at	Top2a	topoisomerase (DNA) II alpha	-1.52	0.289	1.03	0.893	-1.08	0.822	3.95	0.179	0.6
1419359_at	Hexim1	hexamethylene bis-acetamide inducible 1	1.03	0.879	-1.13	0.512	-1.41	0.022	1.16	0.492	-0.09
1446780_at	Ror2	Receptor tyrosine kinase-like orphan receptor 2	1.26	0.02	-2.03	0.217	-1.15	0.591	1.14	0.581	-0.19
1440774_x_at	BC052883	cDNA sequence BC052883	-1.72	0.51	-1.02	0.98	1.06	0.89	1.91	0.132	0.06
1428091_at	Klhl7	kelch-like 7 (Drosophila)	-1.52	0.021	1.13	0.289	-1.2	0.338	2.18	0.003	0.15
1429323_at	1700001E04Rik	RIKEN cDNA 1700001E04 gene	-1.89	0.184	-1.02	0.96	1.11	0.114	2.56	0.079	0.19
1456183_at	Oog4	oogenesin 4	-1.05	0.861	1.06	0.868	-1.66	0.324	1.41	0.393	-0.06
1445162_at	---	Transcribed locus	-2.34	0.036	1.14	0.763	1.05	0.9	-3.82	0.127	-0.99
1449359_at	Pax1	paired box gene 1	-1.27	0.549	-1.48	0.523	1.15	0.749	1.83	0.344	0.06
1445145_at	Stag1	Stromal antigen 1	1.12	0.71	-1.38	0.196	-1.29	0.569	1.66	0.251	0.03
1455275_at	E530001K10Rik	RIKEN cDNA E530001K10 gene	-1.46	0.036	-1.17	0.618	1.08	0.758	1.15	0.24	-0.1
1444147_at	Pcsk2	proprotein convertase subtilisin/kexin type 2	-1.47	0.459	1.24	0.594	-1.43	0.594	1.99	0.142	0.08
1439175_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	-1.03	0.913	1.17	0.62	-2.09	0.107	1.17	0.565	-0.19
1453463_at	1700019B03Rik	RIKEN cDNA 1700019B03 gene	-1.11	0.565	-1.78	0.486	1.16	0.704	1.88	0.043	0.04
1459775_at	Pdpk1	3-phosphoinositide dependent protein kinase-1	-1.92	0.052	1.18	0.532	-1.08	0.79	1.12	0.343	-0.18
1436641_at	AI415730	expressed sequence AI415730	-1.55	0.314	1.23	0.112	-1.34	0.184	1.03	0.908	-0.16
1437010_a_at	Oaz3	ornithine decarboxylase antizyme 3	-1.87	0.08	1.24	0.571	-1.18	0.534	1	0.991	-0.2
1442680_at	Ncam1	Neural cell adhesion molecule 1	1.39	0.358	-1.16	0.642	-2.7	0.164	1.47	0.382	-0.25
1428901_at	Dtwd2	DTW domain containing 2	-1.28	0.345	1.05	0.819	-1.27	0.298	1.12	0.673	-0.09
1433792_at	Nrip2	nuclear receptor interacting protein 2	-1.88	0.415	1.04	0.938	1.05	0.856	-1.27	0.306	-0.26
1439767_at	Dlgap2	discs, large (Drosophila) homolog-associated protein 2	1.26	0.663	-1.25	0.623	-1.79	0.352	1.38	0.717	-0.1
1456099_at	D930017J03Rik	RIKEN cDNA D930017J03 gene	-1.07	0.863	1.04	0.893	-1.53	0.064	1.14	0.674	-0.11
1437167_at	Tmod2	tropomodulin 2	-1.08	0.604	-1.82	0.18	1.15	0.704	1.77	0.046	0.01

1458137_at	---	Transcribed locus	-1.37	0.674	-1.18	0.82	1.05	0.916	1.79	0.298	0.07
1431011_at	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate comple	-1.38	0.324	-1.38	0.177	1.17	0.172	1.65	0.121	0.02
1457224_at	4631422O05Rik	RIKEN cDNA 4631422O05 gene	-1.32	0.257	1.39	0.674	-2.12	0.032	1.2	0.702	-0.21
1431761_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	1.01	0.863	-2.02	0.294	1.12	0.595	-1.49	0.156	-0.34
1432450_at	8030423J24Rik	RIKEN cDNA 8030423J24 gene	-1.7	0.578	1.08	0.846	-1.05	0.755	1.48	0.138	-0.05
1438701_at	Bicd1	bicaudal D homolog 1 (Drosophila)	-1.32	0.025	1.02	0.975	-1.18	0.383	1.17	0.68	-0.08
1435441_at	Ablim2	actin-binding LIM protein 2	-1.34	0.408	1.01	0.985	-1.15	0.434	1.1	0.397	-0.1
1456434_x_at	Hspb8	heat shock protein 8	1.05	0.94	-1.06	0.653	-1.6	0.234	1.29	0.699	-0.08
1444743_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	-1.52	0.522	1.13	0.765	-1.2	0.727	1.27	0.672	-0.08
1442909_at	Kcnq4	Potassium voltage-gated channel, subfamily Q, member 4	-1.16	0.755	-1.39	0.575	1.04	0.936	1.12	0.863	-0.1
1446411_at	9630020C08Rik	RIKEN cDNA 9630020C08 gene	-1.04	0.964	-1.75	0.59	1.09	0.906	1.18	0.519	-0.13
1432111_at	4930542D17Rik	RIKEN cDNA 4930542D17 gene	-1.59	0.076	-1.06	0.603	1.05	0.848	1.21	0.471	-0.1
1446793_at	---	Transcribed locus	1.03	0.947	-1.03	0.847	-1.62	0.113	1.08	0.887	-0.13
1453010_at	Iws1	IWS1 homolog (S. cerevisiae)	-1.24	0.225	1	0.994	-1.22	0.235	1.08	0.515	-0.1
1425729_at	Vmd2l1	vitelliform macular dystrophy 2-like protein 1	-1.01	0.945	1.17	0.747	-2.11	0.204	2.08	0.417	0.03
1447641_at	Dmwd	dystrophia myotonica-containing WD repeat motif	1.37	0.452	-1.17	0.224	-2.49	0.153	1	0.998	-0.32
1457324_at	Oprs1	Opioid receptor, sigma 1	1.32	0.314	-1.1	0.714	-2.52	0.082	1.26	0.181	-0.26
1440817_x_at	G630024C07Rik	RIKEN cDNA G630024C07 gene	1	0.999	-1.15	0.228	-1.33	0.199	1.05	0.777	-0.11
1419741_at	Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)	-1.11	0.517	1.09	0.315	-1.57	0.097	1.46	0.044	-0.03
1425720_at	---	---	-1.31	0.108	1.04	0.836	-1.21	0.688	1.65	0.165	0.04
1444241_at	Wac	WW domain containing adaptor with coiled-coil	-1.19	0.079	1.1	0.552	-1.48	0.029	1.14	0.565	-0.11
1434462_at	BC088983	cDNA sequence BC088983	-1.25	0.235	1.01	0.918	-1.23	0.129	1.3	0.417	-0.04
1428489_at	Zcrb1	zinc finger CCHC-type and RNA binding motif 1	1.05	0.646	-1.19	0.052	-1.36	0.001	1.22	0.364	-0.07
1439045_x_at	Mtac2d1	membrane targeting (tandem) C2 domain containing 1	1.18	0.749	-1.52	0.382	-1.27	0.276	1.12	0.692	-0.12
1436969_at	1700013E18Rik	RIKEN cDNA 1700013E18 gene	-1.82	0.323	1.15	0.543	-1.08	0.722	1.46	0.229	-0.07
1439239_at	Lin7b	lin-7 homolog B (C. elegans)	-1.46	0.433	-2.29	0.075	1.5	0.261	1.23	0.6	-0.25
1436785_a_at	1110069O07Rik	RIKEN cDNA 1110069O07 gene	-1.57	0.29	1.19	0.67	-1.26	0.012	1.93	0.219	0.08
1450369_at	Figla	folliculogenesis specific basic helix-loop-helix	-1.88	0.178	1.12	0.875	-1.03	0.933	1.12	0.686	-0.17
1446112_at	Usp34	Ubiquitin specific peptidase 34	1.11	0.238	-1.59	0.347	-1.12	0.76	1.92	0.157	0.08
1446769_at	2810439F02Rik	RIKEN cDNA 2810439F02 gene	1.26	0.79	-1.68	0.182	-1.29	0.625	1.45	0.309	-0.07
1449560_at	2310043L02Rik	RIKEN cDNA 2310043L02 gene	-1.06	0.912	1.08	0.861	-1.66	0.255	1.37	0.188	-0.07
1445501_at	---	12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530	-1.31	0.514	-1.89	0.262	1.33	0.489	2.2	0.395	0.08
1442731_at	9030416H16Rik	RIKEN cDNA 9030416H16 gene	1.05	0.817	-1.11	0.651	-1.48	0.109	1.01	0.9	-0.13
1449741_at	Dsg2	Desmoglein 2	1.3	0.452	-1.4	0.187	-1.63	0.047	1.54	0.453	-0.05
1444342_at	---	Transcribed locus	-1.24	0.438	-1.23	0.27	1.01	0.967	1.45	0.344	0
1432013_a_at	2610016C23Rik	RIKEN cDNA 2610016C23 gene	-2.59	0.106	1.45	0.208	-1.27	0.473	2.9	0.272	0.12
1435548_at	Mrs2l	MRS2-like, magnesium homeostasis factor (S. cerevisiae)	-1.3	0.116	-1.26	0.187	1.07	0.729	1.21	0.451	-0.07
1457910_at	Fmnl2	Formin-like 2	1.08	0.843	1.04	0.901	-1.96	0.057	-1.8	0.021	-0.41
1436932_at	Grhl3	grainyhead-like 3 (Drosophila)	-1.81	0.316	-1.05	0.925	1.12	0.817	2.04	0.313	0.08
1457039_at	Cecr2	cat eye syndrome chromosome region, candidate 2 homolog (human)	1.1	0.461	-1.62	0.099	-1.1	0.71	1.8	0.232	0.05
1456876_at	---	---	-1.2	0.611	-1.39	0.376	1.08	0.65	1.48	0.408	-0.01
1431224_at	Ube3a	ubiquitin protein ligase E3A	-1.79	0.035	-1.05	0.828	1.12	0.543	1.21	0.38	-0.13
1435610_at	C130034I18Rik	RIKEN cDNA C130034I18 gene	-1.16	0.72	1.08	0.874	-1.46	0.272	1.27	0.186	-0.07
1435339_at	Kctd15	potassium channel tetramerisation domain containing 15	1.02	0.842	-1.48	0.223	-1.07	0.264	1.06	0.604	-0.12
1419967_at	Seh1l	SEH1-like (S. cerevisiae	1.06	0.795	-1.16	0.761	-1.41	0.068	1.11	0.217	-0.1
1427266_at	Pb1	polybromo 1	1.13	0.542	-1.18	0.123	-1.52	0.006	1.51	0.222	-0.02
1445292_at	Cd300a	CD300A antigen	-2.02	0.355	-1.6	0.381	1.51	0.455	1.01	0.989	-0.28
1429053_at	1110012J17Rik	RIKEN cDNA 1110012J17 gene	-1.08	0.255	-1.51	0.287	1.04	0.798	1.38	0.377	-0.04
1434699_at	6030408C04Rik	RIKEN cDNA 6030408C04 gene	-1.36	0.001	1.05	0.751	-1.18	0.288	1.63	0.204	0.03
1440620_at	Rab8a	RAB8A, member RAS oncogene family	-1.46	0.008	-1.21	0.286	1.12	0.57	1.56	0.123	0
1438920_x_at	Crry	Complement receptor related protein	-1.03	0.839	-1.54	0.16	1.01	0.967	1.23	0.548	-0.08
1416419_s_at	Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	-1.25	0.006	-1.4	0.035	1.11	0.549	1.38	0.035	-0.04
1427745_x_at	MP4 /// MGC78233	proline rich protein MP4 /// similar to proline rich protein MP4 /// cDNA sequence I	-1.3	0.747	1.21	0.304	-1.54	0.141	1.09	0.838	-0.14

1445568_at	AI842396	Expressed sequence AI842396	-1.35	0.106	-1.48	0.092	1.21	0.374	1.37	0.42	-0.06
1454216_at	4930408F14Rik	RIKEN cDNA 4930408F14 gene	1.05	0.944	-2.16	0.428	1.12	0.818	-1.25	0.518	-0.31
1455089_at	Gng12	guanine nucleotide binding protein (G protein), gamma 12	-1.12	0.247	1.03	0.826	-1.4	0.065	1.12	0.192	-0.09
1447778_x_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	-1.21	0.008	1.04	0.723	-1.31	0.117	1.69	0.109	0.05
1425853_s_at	Prlr	prolactin receptor	-1.55	0.385	-1.03	0.892	1.02	0.946	1.68	0.047	0.03
1445880_at	Dcc	Deleted in colorectal carcinoma	1.01	0.961	-1.34	0.55	-1.14	0.79	1.44	0.644	-0.01
1420618_at	Cpeb4	cytoplasmic polyadenylation element binding protein 4	-1.13	0.45	1.04	0.725	-1.42	0.07	2.54	0.108	0.26
1434454_at	D16Wsu65e	DNA segment, Chr 16, Wayne State University 65, expressed	-1.02	0.933	-1.57	0.088	1.01	0.964	1.22	0.498	-0.09
1426865_a_at	Ncam1	neural cell adhesion molecule 1	1.19	0.683	-1.86	0.244	-1.1	0.834	1.32	0.641	-0.11
1447666_x_at	LOC628119 /// LOC	similar to Protein C11orf51 /// similar to Protein HSPC020	-2.06	0.09	-1.12	0.643	1.26	0.588	1.17	0.302	-0.19
1418013_at	Cml1	camello-like 1	-1.09	0.68	-1.58	0.061	1.08	0.599	1.25	0.506	-0.08
1451950_a_at	Cd80	CD80 antigen	-1.03	0.958	-1.81	0.05	1.11	0.841	1	0.998	-0.18
1454332_at	6030442H21Rik	RIKEN cDNA 6030442H21 gene	1.03	0.919	-1.13	0.661	-1.39	0.614	1.59	0.452	0.02
1452715_at	2310022K01Rik	RIKEN cDNA 2310022K01 gene	-1.11	0.336	-1.66	0.257	1.13	0.378	1.43	0.262	-0.05
1422920_at	Cldn13	claudin 13	-1.58	0.574	1.02	0.973	-1.02	0.969	9.1	0.164	1.88
1441587_at	Plcl4	phospholipase C-like 4	-1.4	0.393	-1.26	0.303	1.13	0.516	1.33	0.311	-0.05
1420258_at	1700073E17Rik	RIKEN cDNA 1700073E17 gene	1.03	0.94	-1.16	0.804	-1.36	0.588	1.65	0.333	0.04
1439364_a_at	Mmp2	matrix metallopeptidase 2	-1.07	0.704	1.16	0.523	-1.85	0.054	1.45	0.017	-0.08
1443447_at	2010110K16Rik	RIKEN cDNA 2010110K16 gene	-2.08	0.205	1.02	0.955	1.14	0.451	-1.42	0.34	-0.34
1451278_a_at	2610205E22Rik	RIKEN cDNA 2610205E22 gene	1.01	0.891	-1.46	0.178	-1.07	0.69	1.06	0.694	-0.11
1422213_s_at	Foxh1	forkhead box H1	1.18	0.754	-1.54	0.124	-1.25	0.488	1.14	0.714	-0.12
1431602_a_at	Ugcgl2	UDP-glucose ceramide glucosyltransferase-like 2	1.01	0.972	-1.14	0.715	-1.34	0.196	1	1	-0.12
1447006_at	Myo1d	Myosin ID	-1.24	0.06	1.22	0.49	-1.63	0.151	1.04	0.909	-0.16
1448046_at	Rabepk	Rab9 effector protein with kelch motifs	1.22	0.289	-1.27	0.037	-1.59	0.051	1.23	0.65	-0.1
1421054_at	Xpo4	exportin 4	-1.1	0.267	-1.39	0.457	1	0.989	1.47	0.438	0
1439857_at	Usp32	Ubiquitin specific peptidase 32	1.1	0.676	-1.08	0.489	-1.67	0.021	2.32	0.252	0.17
1454623_at	Cpa2	carboxypeptidase A2, pancreatic	1.03	0.871	-1.53	0.3	-1.05	0.913	2.58	0.032	0.26
1425884_at	Bxdc1	brix domain containing 1	1.25	0.284	-1.23	0.506	-1.75	0.074	1.13	0.683	-0.15
1438098_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	-1.02	0.971	1.22	0.366	-2.28	0.066	1.05	0.875	-0.26
1423351_at	Mrpl1	mitochondrial ribosomal protein L1	-1.25	0.155	-1.33	0.195	1.08	0.471	1.06	0.771	-0.11
1459531_at	Lmtk2	Lemur tyrosine kinase 2	1.03	0.922	1.24	0.71	-2.76	0.176	-1.45	0.345	-0.48
1457966_at	Fbxl7	F-box and leucine-rich repeat protein 7	1.05	0.662	1.1	0.465	-2.07	0.018	-1.14	0.393	-0.26
1421649_at	Tnfrsf8	tumor necrosis factor receptor superfamily, member 8	-2.58	0.115	1.04	0.948	1.21	0.396	-1.05	0.875	-0.35
1460414_at	AW822216	expressed sequence AW822216	1.02	0.98	-2.04	0.214	1.13	0.41	-1.39	0.324	-0.32
1436339_at	1810058I24Rik	RIKEN cDNA 1810058I24 gene	-1.63	0.23	-1.05	0.388	1.07	0.484	1.37	0.337	-0.06
1437729_at	Rpl27a	ribosomal protein L27a	1.02	0.932	-1.1	0.558	-1.41	0.253	1.1	0.42	-0.1
1427729_at	Ehd2	EH-domain containing 2	1.13	0.346	-1.28	0.576	-1.39	0.377	1.19	0.578	-0.09
1440093_at	Ednra	endothelin receptor type A	-1.35	0.557	1.48	0.257	-2.44	0.003	1.14	0.787	-0.29
1424386_at	Reep2	receptor accessory protein 2	-1.43	0.484	1.07	0.854	-1.16	0.133	1.24	0.044	-0.07
1446073_at	Yaf2	YY1 associated factor 2	1.11	0.552	-1.09	0.659	-1.64	0.02	1.09	0.798	-0.13
1431661_at	4930562A09Rik	RIKEN cDNA 4930562A09 gene	-2.3	0.014	-1.13	0.689	1.32	0.417	1.16	0.768	-0.24
1443412_s_at	Mmp16	matrix metallopeptidase 16	-2.08	0.533	-1.48	0.639	1.48	0.002	1.03	0.922	-0.26
1449998_at	Nkx3-1	NK-3 transcription factor, locus 1 (Drosophila)	1.11	0.737	1.02	0.969	-2	0.212	-1.12	0.723	-0.24
1456260_at	Rbbp4	retinoblastoma binding protein 4	1.2	0.466	-1.43	0.571	-1.36	0.244	1.07	0.801	-0.13
1455017_a_at	Zmym3	zinc finger, MYM-type 3	-1.34	0.337	1.06	0.852	-1.22	0.28	1.28	0.303	-0.05
1456041_at	Snx16	sorting nexin 16	1.32	0.332	-1.35	0.268	-1.74	0.002	1.46	0.128	-0.08
1435766_at	Pphln1	periphilin 1	-1.38	0.203	-1.17	0.72	1.05	0.793	1.08	0.712	-0.1
1445532_at	C230040D10Rik	RIKEN cDNA C230040D10 gene	-1.4	0.611	-1.27	0.527	1.13	0.675	1.2	0.681	-0.08
1460597_at	Asxl2	Additional sex combs like 2 (Drosophila)	-1.16	0.252	1.01	0.946	-1.3	0.002	1.14	0.375	-0.08
1440040_at	Cdk6	Cyclin-dependent kinase 6	-1.13	0.651	1.05	0.921	-1.42	0.225	1.14	0.635	-0.09
1459057_at	Tdrd3	Tudor domain containing 3	-1.04	0.835	1.08	0.879	-1.7	0.022	1.05	0.748	-0.15
1437917_at	D530037H12Rik	RIKEN cDNA D530037H12 gene	1.02	0.893	1.1	0.603	-1.93	0.069	-1.5	0.268	-0.33
1453340_at	1700057D03Rik	RIKEN cDNA 1700057D03 gene	-2.04	0.46	1.2	0.452	-1.06	0.902	1.89	0.296	0

1415898_at	Mgst1	microsomal glutathione S-transferase 1	-1.07	0.674	-1.9	0.048	1.18	0.557	1.02	0.948	-0.19
1428632_at	1810006K21Rik	RIKEN cDNA 1810006K21 gene	-1.34	0.085	1.09	0.739	-1.25	0.42	1.28	0.558	-0.06
1439021_at	Centb5	centaurin, beta 5	-2.34	0.368	-1.13	0.68	1.33	0.462	1.25	0.684	-0.22
1443215_at	Rims2	regulating synaptic membrane exocytosis 2	-1.55	0.66	1.53	0.578	-2.16	0.048	1.03	0.958	-0.29
1434564_at	E2f3	E2F transcription factor 3	-1.37	0.028	-1.14	0.384	1.03	0.895	1.35	0.472	-0.03
1456884_at	LOC67660	Hypothetical LOC67660	-1.52	0.039	-1.26	0.336	1.19	0.215	1.53	0.374	-0.01
1431440_at	Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	-1.24	0.342	1.08	0.877	-1.32	0.301	1.27	0.672	-0.06
1421673_s_at	Stx1b2 /// Stx1b1	syntaxin 1B2 /// syntaxin 1B1	-1.09	0.703	-1.39	0.202	1	0.994	1.22	0.064	-0.06
1420401_a_at	Ramp3	receptor (calcitonin) activity modifying protein 3	-1.13	0.327	-1.39	0.573	1.03	0.938	1.26	0.395	-0.06
1440475_at	AW011738	expressed sequence AW011738	1.36	0.501	-1.63	0.417	-1.51	0.086	1.29	0.675	-0.12
1444915_at	D1Ertd399e	DNA segment, Chr 1, ERATO Doi 399, expressed	1.05	0.946	-1.16	0.756	-1.37	0.184	1.26	0.73	-0.06
1428136_at	Sfrp1	secreted frizzled-related sequence protein 1	1.11	0.158	-1.17	0.625	-1.49	0.048	1.7	0.011	0.04
1428879_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.26	0.538	-1.78	0.07	1.28	0.441	1.1	0.817	-0.16
1432368_at	4930594M17Rik	RIKEN cDNA 4930594M17 gene	-1.6	0.476	1.49	0.428	-1.93	0.376	1.74	0.236	-0.07
1416748_a_at	Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	-1.26	0.019	-1.27	0.355	1.05	0.762	1.13	0.588	-0.09
1453792_at	A930003G23Rik	RIKEN cDNA A930003G23 gene	-1.25	0.718	1.09	0.874	-1.33	0.475	2.24	0.092	0.19
1441849_at	---	---	-1.09	0.751	1.22	0.219	-1.99	0.209	1.39	0.274	-0.12
1423110_at	Col1a2	procollagen, type I, alpha 2	1.05	0.408	1.15	0.687	-2.28	0.078	-1.37	0.089	-0.36
1440502_at	4930485B16Rik	RIKEN cDNA 4930485B16 gene	1.07	0.893	1.07	0.699	-2.03	0.416	-1.26	0.665	-0.29
1430775_at	Wdr44	WD repeat domain 44	-1.94	0.417	-1.3	0.313	1.35	0.144	1.41	0.066	-0.12
1429578_at	1700049K14Rik	RIKEN cDNA 1700049K14 gene	-1.36	0.004	-1.25	0.417	1.1	0.306	1.16	0.574	-0.09
1416147_at	Hspa4	heat shock protein 4	1.03	0.951	-1.25	0.363	-1.24	0.533	1.32	0.333	-0.03
1457551_at	Acvr1	Activin A receptor, type 1	1.07	0.786	1.04	0.749	-1.87	0.021	-1.09	0.871	-0.21
1439718_at	Pkig	Protein kinase inhibitor, gamma	-1.95	0.129	-1.1	0.872	1.21	0.758	1.19	0.616	-0.16
1420750_at	1110006O24Rik	RIKEN cDNA 1110006O24 gene	-1.07	0.921	-1.48	0.261	1.03	0.914	1.55	0.409	0.01
1455462_at	Adcy2	adenylate cyclase 2	1.02	0.941	-1.16	0.525	-1.32	0.123	1.29	0.411	-0.04
1447289_at	AA763521	expressed sequence AA763521	1.37	0.58	-1.62	0.388	-1.52	0.487	3.62	0	0.46
1445426_at	Map4k5	Mitogen-activated protein kinase kinase kinase kinase 5	-1.2	0.405	1.2	0.615	-1.64	0.035	1.71	0.292	0.02
1457015_at	A230070E04Rik	RIKEN cDNA A230070E04 gene	1.29	0.758	-1.31	0.638	-1.7	0.399	1.78	0.311	0.01
1458122_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.15	0.836	1.12	0.836	-1.53	0.412	1.97	0.294	0.1
1422406_at	Ifna9	interferon alpha 9	-1.07	0.745	-1.44	0.476	1.01	0.869	1.48	0.221	-0.01
1459043_at	Fntb	Farnesyltransferase, CAAX box, beta	-3.09	0.111	-1.56	0.565	1.68	0.215	10	0.16	1.76
1443690_at	---	Transcribed locus	1.09	0.884	-1.17	0.381	-1.43	0.549	1.38	0.637	-0.03
1447402_at	---	Transcribed locus	1.18	0.707	-2.81	0.006	1.1	0.842	-1.57	0.218	-0.52
1432187_at	Nup43	nucleoporin 43	1.15	0.502	-1.67	0.316	-1.12	0.5	1.36	0.363	-0.07
1444266_at	Hod	Homeobox only domain	1.44	0.482	-1.41	0.235	-2.04	0.051	1.25	0.395	-0.19
1433706_a_at	Ptplad1	protein tyrosine phosphatase-like A domain containing 1	1.01	0.674	-1.2	0.3	-1.26	0.091	1.32	0.044	-0.03
1435332_at	Htr7	5-hydroxytryptamine (serotonin) receptor 7	1.07	0.891	-1.21	0.576	-1.35	0.306	1.4	0.381	-0.02
1457031_at	Fsd2	fibronectin type III and SPRY domain containing 2	-1.45	0.36	-1.4	0.346	1.24	0.397	1.42	0.234	-0.05
1425458_a_at	Grb10	growth factor receptor bound protein 10	-1.17	0.294	1.04	0.786	-1.34	0.054	1.19	0.565	-0.07
1433014_at	6330436F06Rik	RIKEN cDNA 6330436F06 gene	-1.22	0.831	-1.31	0.631	1.06	0.905	1.69	0.27	0.06
1443322_at	---	Transcribed locus	-1.98	0.185	1.01	0.91	1.12	0.726	-1.18	0.703	-0.26
1455511_at	Sephs1	selenophosphate synthetase 1	1.04	0.552	-1.55	0.298	-1.04	0.712	1.17	0.413	-0.1
1441881_x_at	3110032G18Rik	RIKEN cDNA 3110032G18 gene	-1.72	0.246	-1.02	0.951	1.08	0.803	1.7	0.149	0.01
1429849_at	4632411B12Rik	RIKEN cDNA 4632411B12 gene	1.02	0.929	1.03	0.936	-1.66	0.051	-1.06	0.849	-0.17
1436787_x_at	1110069O07Rik	RIKEN cDNA 1110069O07 gene	-1.63	0.432	1.27	0.662	-1.32	0.009	1.92	0.369	0.06
1427277_at	Six1	sine oculis-related homeobox 1 homolog (Drosophila)	-1.71	0.624	-1.49	0.461	1.39	0.282	1.5	0.552	-0.08
1445840_at	---	Transcribed locus	-1.41	0.644	-1.44	0.459	1.24	0.524	1.16	0.804	-0.11
1437296_at	Pkn2	protein kinase N2	-1.1	0.067	-1.37	0.174	1	0.994	1.86	0.282	0.1
1456338_at	9130023D20Rik	RIKEN cDNA 9130023D20 gene	1.02	0.816	-1.43	0.308	-1.08	0.588	1.15	0.61	-0.08
1423115_at	St6galnac6	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	-1.3	0.092	1.06	0.545	-1.23	0.226	1.22	0.189	-0.06
1429402_at	Glt8d2	glycosyltransferase 8 domain containing 2	-1.41	0.527	-1.18	0.68	1.09	0.62	1.01	0.965	-0.12
1420538_at	Gprc5d	G protein-coupled receptor, family C, group 5, member D	-1.55	0.418	-1.4	0.462	1.28	0.541	1.11	0.9	-0.14

1429023_at	2900042E01Rik	RIKEN cDNA 2900042E01 gene	1.17	0.847	-2.23	0.085	1.03	0.946	-1.83	0.522	-0.47
1417093_a_at	Gtf2h4	general transcription factor II H, polypeptide 4	-1.24	0.165	-1.23	0.073	1.03	0.779	1.02	0.914	-0.11
1439551_at	BC006965	cDNA sequence BC006965	1.07	0.765	-2.41	0.155	1.16	0.644	-1.77	0.225	-0.49
1434947_at	Kif3c	kinesin family member 3C	1.39	0.097	-1.94	0.059	-1.35	0.091	1.24	0.311	-0.17
1445861_at	Usp25	Ubiquitin specific peptidase 25	-1.19	0.041	1.09	0.65	-1.4	0.166	1.4	0.454	-0.03
1439391_at	2810002I04Rik	RIKEN cDNA 2810002I04 gene	-1.19	0.052	-1.44	0.158	1.11	0.605	1.13	0.077	-0.1
1459767_x_at	Cspg2	chondroitin sulfate proteoglycan 2	-1.23	0.118	1.3	0.226	-1.88	0.433	2.35	0.185	0.14
1422413_at	---	---	-1.4	0.325	1.11	0.736	-1.22	0.103	1.65	0.129	0.03
1460413_s_at	Zdhhc1	zinc finger, DHHC domain containing 1	1.1	0.703	-2.82	0.267	1.19	0.491	-1.16	0.681	-0.42
1457393_at	2700008B19Rik	RIKEN cDNA 2700008B19 gene	-1.11	0.244	-1.43	0.321	1.04	0.747	1.03	0.831	-0.11
1445846_at	---	Adult male adrenal gland cDNA, RIKEN full-length enriched library, clone:733040	-1.51	0.493	-1.39	0.505	1.27	0.293	1.04	0.908	-0.15
1421504_at	Sp4	trans-acting transcription factor 4	1.06	0.859	-1.55	0.181	-1.07	0.861	2.22	0.275	0.17
1438881_at	Vezt	vezatin, adherens junctions transmembrane protein	1.55	0.539	-1.92	0.265	-1.75	0.072	1.02	0.949	-0.27
1430905_at	4921504E06Rik	RIKEN cDNA 4921504E06 gene	-1.68	0.001	1.18	0.714	-1.15	0.435	1.65	0.225	0
1429474_at	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	-1.02	0.966	1	0.988	-1.51	0.196	1.12	0.512	-0.1
1454816_at	Rp2h	retinitis pigmentosa 2 homolog (human)	-1.45	0.42	1.03	0.858	-1.08	0.717	1.17	0.624	-0.08
1426566_s_at	Il17re	interleukin 17 receptor E	1.02	0.882	-1.69	0.371	1.04	0.83	-1.22	0.232	-0.21
1417377_at	Igsf4a	immunoglobulin superfamily, member 4A	1.04	0.86	1.05	0.838	-1.78	0.025	-1.14	0.537	-0.21
1459333_at	---	Transcribed locus	-1.36	0.447	1.02	0.95	-1.12	0.718	1.6	0.283	0.03
1428400_at	2200002K05Rik	RIKEN cDNA 2200002K05 gene	1.21	0.36	-1.75	0.475	-1.16	0.82	1.56	0.271	-0.03
1431656_at	C630050I24Rik	RIKEN cDNA C630050I24 gene	-1.34	0.605	-1.36	0.131	1.16	0.649	1.01	0.971	-0.13
1420362_a_at	Bik	Bcl2-interacting killer	1.01	0.907	-1.06	0.785	-1.43	0.041	1.11	0.736	-0.09
1460364_at	Gtf2ird1	general transcription factor II I repeat domain-containing 1	1.35	0.492	-2.01	0.249	-1.26	0.591	1.53	0.5	-0.09
1440784_at	Eef2	Eukaryotic translation elongation factor 2	-1.01	0.991	1.02	0.98	-1.57	0.286	1.6	0.473	0.01
1453267_at	Atbf1	AT motif binding factor 1	1.05	0.865	-1.18	0.627	-1.34	0.042	1.55	0.409	0.02
1425442_at	Oscar	osteoclast associated receptor	-1.37	0.448	-1.74	0.49	1.34	0.435	2.01	0.034	0.06
1420117_at	---	Transcribed locus	1.18	0.118	-1.06	0.538	-1.9	0.095	1.32	0.15	-0.12
1454779_s_at	C230052I12Rik	RIKEN cDNA C230052I12 gene	-1.67	0.075	-1.11	0.199	1.15	0.457	1.09	0.617	-0.14
1443041_at	Zbtb17	zinc finger and BTB domain containing 17	1.25	0.097	-1.84	0.123	-1.18	0.692	1.27	0.532	-0.12
1448818_at	Wnt5a	wingless-related MMTV integration site 5A	1.02	0.952	-1.22	0.757	-1.24	0.334	1.65	0.167	0.05
1419184_a_at	Fhl2	four and a half LIM domains 2	1.16	0.109	-2.03	0.099	-1.01	0.968	1.16	0.591	-0.18
1443950_at	A630042L21Rik	RIKEN cDNA A630042L21 gene	1.04	0.731	-1.19	0.37	-1.31	0.098	1.1	0.398	-0.09
1435999_at	C630041L24Rik	RIKEN cDNA C630041L24 gene	-1.87	0.028	-1.22	0.505	1.29	0.442	1.17	0.796	-0.16
1430170_at	Bbs10	Bardet-Biedl syndrome 10 (human)	-1.18	0.7	1.05	0.78	-1.33	0.171	1.29	0.51	-0.04
1446164_at	Ncoa6ip	Nuclear receptor coactivator 6 interacting protein	1.07	0.843	-1.96	0.048	1.07	0.642	-1.18	0.379	-0.25
1441107_at	Dmrta2	doublesex and mab-3 related transcription factor like family A2	1.12	0.678	-1.01	0.987	-1.83	0.196	1.19	0.672	-0.14
1446288_at	C78692	expressed sequence C78692	1.06	0.58	-1.15	0.524	-1.38	0.269	1.18	0.404	-0.07
1446234_at	Utx	Ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1.16	0.51	-1.13	0.315	-1.64	0.03	1.14	0.373	-0.12
1422894_at	Sfmbt1	Scm-like with four mbt domains 1	-1.34	0.552	-1.19	0.209	1.06	0.76	1.41	0.401	-0.02
1433389_at	Cyp4f18	cytochrome P450, family 4, subfamily f, polypeptide 18	-1.01	0.987	-1.78	0.132	1.1	0.749	1.13	0.787	-0.14
1443391_at	Nt5c2	5'-nucleotidase, cytosolic II	1.01	0.99	1.05	0.893	-1.69	0.118	-1.4	0.009	-0.26
1449442_at	Pex11a	peroxisomal biogenesis factor 11a	1.1	0.425	-1.6	0.067	-1.08	0.607	1.08	0.736	-0.13
1443569_at	4930430E16Rik	RIKEN cDNA 4930430E16 gene	-1.69	0.183	1.17	0.718	-1.12	0.686	1.16	0.092	-0.12
1435468_at	C76566	expressed sequence C76566	1.2	0.549	-2.09	0.193	-1.03	0.926	1.21	0.112	-0.18
1436071_at	Ankrd26	Ankyrin repeat domain 26	-1.46	0.036	1.04	0.719	-1.08	0.63	1.32	0.375	-0.04
1447869_x_at	Rhobtb3	Rho-related BTB domain containing 3	1.18	0.851	-1.5	0.23	-1.25	0.637	1.02	0.97	-0.14
1457191_at	---	---	-1.07	0.738	1.07	0.796	-1.54	0.052	1.14	0.593	-0.1
1455313_at	Ablim2	actin-binding LIM protein 2	1.04	0.592	-1.21	0.446	-1.28	0.097	1.11	0.243	-0.08
1458827_at	Rab11fip4	RAB11 family interacting protein 4 (class II)	1.27	0.457	-1.22	0.581	-1.79	0.277	2.86	0.256	0.28
1449292_at	Rb1cc1	RB1-inducible coiled-coil 1	1.13	0.718	-1.05	0.844	-1.77	0.122	1.01	0.96	-0.17
1456528_x_at	Ncl	nucleolin	-1.22	0.732	1.19	0.485	-1.56	0.14	1.08	0.847	-0.13
1427305_at	Piga	phosphatidylinositol glycan anchor biosynthesis, class A	-1.24	0.59	1.09	0.612	-1.33	0.255	2.48	0.197	0.25
1423399_a_at	Yaf2	YY1 associated factor 2	-1.11	0.393	-1.34	0.034	1.01	0.939	1.26	0.306	-0.05

1423580_at	Ankrd48 /// LOC633	ankyrin repeat domain 48 /// similar to spermatogenic cell-specific gene 2	-2.5	0.384	-1.15	0.784	1.38	0.473	1.63	0.611	-0.16
1416363_at	Fkbp4	FK506 binding protein 4	1.26	0.674	-1.21	0.348	-1.77	0.027	1.07	0.854	-0.16
1425782_at	Plcb1	phospholipase C, beta 1	1.18	0.547	-1.49	0.263	-1.25	0.275	1.13	0.758	-0.11
1447170_at	---	---	1.19	0.813	-2.36	0.151	1.03	0.951	-1.03	0.915	-0.29
1428943_at	Nudt13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	-1.34	0.326	1.04	0.825	-1.15	0.476	1.11	0.8	-0.09
1435922_at	Fbxl19	F-box and leucine-rich repeat protein 19	-1.86	0.023	1.29	0.597	-1.21	0.635	1.52	0.372	-0.07
1434533_x_at	Ceacam11	CEA-related cell adhesion molecule 11	1.09	0.893	-1.83	0.49	1.01	0.98	-1.26	0.284	-0.25
1437459_x_at	Slc25a19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19	-1.74	0.019	1.28	0.429	-1.25	0.611	1.25	0.578	-0.12
1450815_s_at	Chchd2 /// 2410018	coiled-coil-helix-coiled-coil-helix domain containing 2 /// RIKEN cDNA 2410018M(	-1.21	0.052	-1.31	0.001	1.06	0.546	1.04	0.707	-0.1
1428647_at	LOC676870	region containing RIKEN cDNA 2310056B04 gene; pre B-cell leukemia transcripti	1.04	0.757	-1.14	0.608	-1.36	0.087	1.13	0.495	-0.08
1448649_at	Enpep	glutamyl aminopeptidase	-1.11	0.163	1.09	0.359	-1.51	0.04	1.13	0.559	-0.1
1423529_at	G6pc2	glucose-6-phosphatase, catalytic, 2	1.45	0.41	-1.48	0.453	-1.92	0.345	1.19	0.679	-0.19
1424863_a_at	Hipk2	homeodomain interacting protein kinase 2	1.14	0.513	-1.34	0.075	-1.3	0.411	1.52	0.283	0
1449251_at	Ndph	Norrie disease homolog	-2.14	0.043	1.54	0.495	-1.56	0.114	1.67	0.147	-0.12
1423998_at	Gtf3c5	general transcription factor IIIC, polypeptide 5	-1.06	0.56	-1.79	0.004	1.15	0.398	1.55	0.107	-0.04
1427562_a_at	Prkca	protein kinase C, alpha	1.04	0.799	-1.17	0.64	-1.33	0.597	1.62	0.383	0.04
1432149_at	Dph1	DPH1 homolog (S. cerevisiae)	1.14	0.892	-2.07	0.336	1.03	0.969	-1.68	0.413	-0.39
1431714_at	2310015D24Rik	RIKEN cDNA 2310015D24 gene	-1.08	0.566	1.23	0.571	-2.03	0.21	1.29	0.603	-0.15
1441272_at	---	---	-1.25	0.104	-1.47	0.474	1.18	0.275	1.47	0.46	-0.02
1449397_at	Hoxb2	homeo box B2	-1.21	0.251	-1.26	0.394	1.03	0.851	1.5	0.157	0.02
1430750_at	Dhfr	dihydrofolate reductase	-1.36	0.103	-1.36	0.214	1.18	0.246	1.78	0.243	0.06
1427362_x_at	Hoxc6	homeo box C6	-1.32	0.034	-1.34	0.086	1.15	0.585	1.51	0.37	0
1458582_at	AI461788	expressed sequence AI461788	-1.29	0.198	1.06	0.782	-1.23	0.374	1.28	0.595	-0.04
1421258_a_at	Pklr	pyruvate kinase liver and red blood cell	1.02	0.976	-1.22	0.599	-1.23	0.173	3.26	0.271	0.46
1433571_at	Serinc5	serine incorporator 5	-1.12	0.668	1.14	0.43	-1.61	0.046	1.73	0.012	0.04
1447370_at	Tmem16a	Transmembrane protein 16A	1.07	0.586	-1.24	0.616	-1.28	0.377	1.05	0.808	-0.1
1445256_at	Vcl	Vinculin	1.71	0.379	-2.2	0.172	-2.03	0.026	1.48	0.306	-0.26
1446168_at	---	---	-1.48	0.222	1.03	0.946	-1.06	0.842	1.1	0.814	-0.1
1455710_x_at	Mtcp1	mature T-cell proliferation 1	-1.32	0.139	-1.14	0.433	1.02	0.894	1.45	0.21	0
1457876_at	D9Ertd496e	DNA segment, Chr 9, ERATO Doi 496, expressed	-1.76	0.617	1.09	0.867	-1.01	0.974	1.36	0.535	-0.08
1421748_a_at	Tubd1	tubulin, delta 1	-1.24	0.324	-1.27	0.315	1.06	0.607	1.39	0.319	-0.02
1448714_at	Rngtt	RNA guanylyltransferase and 5'-phosphatase	-1.29	0.208	1.05	0.894	-1.21	0.533	1.48	0.352	0.01
1437528_x_at	A730017C20Rik	RIKEN cDNA A730017C20 gene	-1.76	0.307	1.57	0.459	-1.95	0.168	2.8	0.191	0.17
1431505_at	LOC629952 /// LOC	similar to Peptidyl-prolyl cis-trans isomerase H (PPIase H) (Rotamase H) /// simila	1.21	0.666	-1.18	0.55	-1.68	0.251	2.48	0.202	0.21
1422056_at	Ntn2l	netrin 2-like (chicken)	-1.18	0.696	-1.32	0.42	1.05	0.919	1.51	0.316	0.01
1422915_at	Gast	gastrin	-2.04	0.458	1.04	0.823	1.13	0.566	-1.05	0.294	-0.23
1416310_at	Nusap1	nucleolar and spindle associated protein 1	-2.1	0.478	-1.13	0.634	1.29	0.622	2.16	0.205	0.06
1429158_at	Fbxo28	F-box protein 28	1.11	0.215	-1.57	0.072	-1.1	0.636	1.34	0.403	-0.06
1432775_at	9430087J23Rik	RIKEN cDNA 9430087J23 gene	1.19	0.801	-1.52	0.64	-1.23	0.575	1.25	0.674	-0.08
1438004_at	Pols	polymerase (DNA directed) sigma	-1.26	0.176	-1.22	0.283	1.04	0.865	1.39	0.386	-0.01
1451949_at	Igh-4 /// Igh-6 /// Igh	immunoglobulin heavy chain 4 (serum IgG1) /// immunoglobulin heavy chain 6 (he	-1.07	0.681	1.23	0.631	-2.04	0.099	1.26	0.758	-0.16
1424314_at	Prpf3	PRP3 pre-mRNA processing factor 3 homolog (yeast)	1.09	0.501	-1.3	0.224	-1.27	0.204	1.16	0.522	-0.08
1456658_at	Acta2	actin, alpha 2, smooth muscle, aorta	-1.35	0.568	1.15	0.838	-1.31	0.571	1.2	0.669	-0.08
1440827_x_at	Sox5	SRY-box containing gene 5	-1.13	0.78	-1.37	0.163	1.04	0.822	1.25	0.673	-0.05
1435379_at	AK122209	cDNA sequence AK122209	1.05	0.672	-1.29	0.207	-1.2	0.177	1.14	0.543	-0.07
1459263_at	---	---	-1.47	0.245	1	0.991	-1.03	0.935	1.18	0.352	-0.08
1441530_at	Mbnl3	Muscleblind-like 3 (Drosophila)	-1.18	0.757	1.11	0.665	-1.42	0.083	1.12	0.383	-0.09
1416149_at	Olig1	oligodendrocyte transcription factor 1	-2.11	0.113	-1.23	0.708	1.37	0.57	2.94	0.141	0.24
1431234_at	1700041B20Rik	RIKEN cDNA 1700041B20 gene	-1.03	0.874	-2.09	0.128	1.21	0.13	1.68	0.101	-0.06
1426462_at	Gphn	gephyrin	-1.26	0.04	-1.18	0.159	1.01	0.915	1	0.95	-0.1
1455048_at	Igsf3	immunoglobulin superfamily, member 3	-1.11	0.602	1.11	0.771	-1.54	0.025	1.59	0.284	0.01
1448132_at	Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	-1.38	0.065	-1.44	0.204	1.24	0.179	1.44	0.463	-0.04
1439406_x_at	Fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)	-1.2	0.415	-1.32	0.096	1.06	0.718	1.28	0.603	-0.04

1422367_at	Olfr70	olfactory receptor 70	1.1	0.597	-1.18	0.497	-1.4	0.489	1.04	0.926	-0.11
1421601_at	Gsh2	genomic screened homeo box 2	-1.15	0.68	1.11	0.866	-1.48	0.413	1.05	0.879	-0.12
1431279_s_at	Ttll5	tubulin tyrosine ligase like family 5	-1.51	0.176	-1.01	0.968	1	0.994	1.18	0.318	-0.08
1448395_at	Sfrp1	secreted frizzled-related sequence protein 1	1.31	0.449	-1.92	0.263	-1.21	0.4	2.28	0.088	0.11
1449202_at	Sema4g	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	-1.13	0.593	1.03	0.808	-1.35	0.252	1.34	0.533	-0.03
1455686_at	---	---	-1.41	0.219	1.03	0.801	-1.08	0.527	1.06	0.756	-0.1
1429824_at	4930550C14Rik	RIKEN cDNA 4930550C14 gene	-1.06	0.68	-1.92	0.504	1.19	0.703	1.37	0.494	-0.1
1418120_at	Rbm8a	RNA binding motif protein 8a	-1.2	0.169	1.08	0.805	-1.34	0.183	1.31	0.257	-0.04
1428828_at	Rpain	RPA interacting protein	-1.3	0.099	1.09	0.387	-1.26	0.235	1.65	0.362	0.05
1431406_at	Agxt2l1	alanine-glyoxylate aminotransferase 2-like 1	1.5	0.468	-2.92	0.131	-1.22	0.54	1.46	0.375	-0.3
1434475_at	Ppig	peptidyl-prolyl isomerase G (cyclophilin G)	1.03	0.479	-1.02	0.928	-1.54	0.012	1.01	0.962	-0.13
1445507_at	1110054O05Rik	RIKEN cDNA 1110054O05 gene	-1.56	0.098	1	0.998	1.02	0.934	-1.13	0.612	-0.17
1423899_at	Trip12	thyroid hormone receptor interactor 12	1.01	0.956	1.03	0.851	-1.6	0.039	-1.09	0.62	-0.16
1427627_at	Slc34a1	Solute carrier family 34 (sodium phosphate), member 1	-1.12	0.434	-2.44	0.157	1.35	0.229	1.06	0.934	-0.29
1420030_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	-1.32	0.534	-1.2	0.719	1.07	0.853	1.63	0.311	0.04
1417027_at	Trim2	tripartite motif protein 2	-1.23	0.136	1.09	0.7	-1.33	0.032	1.52	0.08	0.01
1460133_at	---	---	-1.21	0.363	1.14	0.789	-1.44	0.228	2.02	0.114	0.13
1455461_at	A530017D24Rik	RIKEN cDNA A530017D24 gene	-1.62	0.05	1.03	0.928	1.01	0.931	-1.28	0.481	-0.22
1446872_at	AU021877	expressed sequence AU021877	1.06	0.907	-2.11	0.204	1.12	0.729	-1.17	0.796	-0.28
1423787_at	Nup133	nucleoporin 133	-1.16	0.331	-1.26	0.017	1.01	0.931	1.63	0.286	0.05
1453448_at	2310067E19Rik	RIKEN cDNA 2310067E19 gene	1.18	0.255	1.02	0.942	-2.18	0.004	-1	0.996	-0.25
1443586_at	Fip1l1	FIP1 like 1 (S. cerevisiae)	1.03	0.883	1	0.977	-1.6	0.026	-1.33	0.23	-0.22
1440561_at	C87259	expressed sequence C87259	1.05	0.959	-1.96	0.366	1.1	0.828	-1.47	0.201	-0.32
1457771_at	Ptpro	Protein tyrosine phosphatase, receptor type, O	-1.5	0.395	1.24	0.618	-1.32	0.179	1.68	0.365	0.02
1454664_a_at	Eif5	eukaryotic translation initiation factor 5	1.01	0.948	-1.34	0.001	-1.1	0.362	1.38	0.141	-0.01
1434744_at	Yrdc	yrdC domain containing (E.coli)	-1.08	0.748	-1.49	0.03	1.06	0.405	1.05	0.742	-0.11
1444690_at	Epha5	Eph receptor A5	1.11	0.49	-1.75	0.433	-1.03	0.752	1.26	0.724	-0.1
1456718_at	Tmem56	transmembrane protein 56	1.03	0.937	-1.21	0.288	-1.25	0.508	7.46	0.209	1.51
1453100_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	1.15	0.276	-1.73	0.071	-1.07	0.781	1.16	0.682	-0.12
1458375_at	6430524H05Rik	RIKEN cDNA 6430524H05 gene	1.04	0.899	-2.2	0.275	1.16	0.31	-2.97	0.193	-0.74
1427056_at	Adamts15	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.16	0.302	1.09	0.839	-1.41	0.291	1.51	0.313	0.01
1442662_at	0610041E09Rik	RIKEN cDNA 0610041E09 gene	-1.46	0.665	1	0.994	-1.03	0.952	3.08	0.014	0.4
1438287_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-1.47	0.652	1.15	0.635	-1.2	0.399	1.03	0.958	-0.12
1425257_at	Acot5	acyl-CoA thioesterase 5	-2	0.457	-1.08	0.742	1.24	0.748	1.19	0.684	-0.16
1424207_at	Smarca5 /// 923011	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.1	0.642	-1.38	0.139	1.03	0.875	1.42	0.383	-0.01
1422889_at	Pcdh18	protocadherin 18	1	0.99	1.22	0.666	-2.28	0.102	-2.26	0.215	-0.58
1426775_s_at	Scamp1	secretory carrier membrane protein 1	-1.21	0.171	1.06	0.578	-1.29	0.015	1.38	0.165	-0.01
1443388_at	1300018I05Rik	RIKEN cDNA 1300018I05 gene	-1.36	0.039	-1.09	0.784	1	0.984	1.07	0.809	-0.09
1448164_at	Klhdc3	kelch domain containing 3	-1.16	0.477	-1.25	0.063	1	0.986	1.06	0.666	-0.09
1460099_at	Atp9b	ATPas, class II, type 9B	1.34	0.513	-1.58	0.297	-1.46	0.324	1.06	0.913	-0.16
1432261_at	2310039D24Rik	RIKEN cDNA 2310039D24 gene	-1.64	0.019	1.02	0.862	1.03	0.821	-1.08	0.87	-0.17
1429442_at	Rpusd2	RNA pseudouridylate synthase domain containing 2	-1.83	0.211	-1.17	0.704	1.26	0.321	1.41	0.614	-0.08
1418247_s_at	Rbm9	RNA binding motif protein 9	-1.19	0.652	-1.35	0.581	1.08	0.611	1.13	0.854	-0.08
1428537_at	Csnk1a1	casein kinase 1, alpha 1	-1.16	0.052	1.06	0.056	-1.36	0.02	1.05	0.524	-0.1
1459422_at	---	---	-1.46	0.14	-1.04	0.853	1.01	0.96	1.13	0.672	-0.09
1442836_at	Xpo7	exportin 7	1.43	0.576	-1.42	0.599	-1.91	0.2	1.37	0.46	-0.13
1439970_at	Wnk1	WNK lysine deficient protein kinase 1	1.34	0.312	-1.22	0.366	-1.98	0	1.64	0.097	-0.06
1447200_at	Tbc1d5	TBC1 domain family, member 5	-1.17	0.215	-1.35	0.076	1.07	0.895	1.08	0.783	-0.09
1434270_at	Nptxr	neuronal pentraxin receptor	-1.44	0.345	-1.51	0.027	1.31	0.103	1.21	0.446	-0.11
1457888_at	Pcgf5	Polycomb group ring finger 5	-1.3	0.409	1.23	0.663	-1.5	0.112	1.13	0.41	-0.11
1430078_a_at	Ogg1	8-oxoguanine DNA-glycosylase 1	-1.26	0.561	-1.26	0.577	1.08	0.58	1.02	0.869	-0.11
1459544_at	---	---	1.16	0.831	-1.07	0.887	-1.74	0.115	1.21	0.348	-0.11
1435086_s_at	Klhdc2	kelch domain containing 2	-1.14	0.291	1.01	0.938	-1.28	0.075	1.4	0.531	0

1445010_at	---	Transcribed locus	-1.53	0.385	1.26	0.62	-1.33	0.512	1.21	0.599	-0.1
1459648_at	Rutbc3	RUN and TBC1 domain containing 3	1.01	0.985	-1.15	0.823	-1.28	0.069	1.22	0.3	-0.05
1417924_at	Pak3	p21 (CDKN1A)-activated kinase 3	1.47	0.411	-1.89	0.001	-1.5	0.615	1.69	0.364	-0.06
1422472_at	Pex13	peroxisomal biogenesis factor 13	-1.15	0.437	-1.34	0.058	1.05	0.803	1.04	0.884	-0.1
1456775_at	Ints8	integrator complex subunit 8	-1.33	0.098	1.08	0.82	-1.19	0.187	1.07	0.804	-0.09
1457312_at	Nhlrc2	NHL repeat containing 2	-1.16	0.349	1.04	0.852	-1.32	0.3	1.49	0.035	0.01
1438905_x_at	C030046I01Rik	RIKEN cDNA C030046I01 gene	-1.46	0.043	1.02	0.753	-1.04	0.821	1.08	0.809	-0.1
1449205_at	Ovol2	ovo-like 2 (Drosophila)	-1.36	0.263	-1.32	0.363	1.17	0.107	1.19	0.46	-0.08
1426336_at	Cacng7	calcium channel, voltage-dependent, gamma subunit 7	1.39	0.709	-1.51	0.434	-1.65	0.214	1.09	0.648	-0.17
1454452_at	4933428L01Rik	RIKEN cDNA 4933428L01 gene	1.52	0.68	-2.51	0.093	-1.33	0.472	1.22	0.186	-0.28
1431690_at	Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	1.38	0.27	-1.72	0.384	-1.43	0.133	1.27	0.774	-0.12
1449133_at	Sprr1a	small proline-rich protein 1A	1.2	0.747	-1.4	0.364	-1.32	0.116	1.38	0.404	-0.04
1449545_at	Fgf18	fibroblast growth factor 18	1.19	0.832	-1.9	0.392	-1.06	0.826	1.42	0.2	-0.09
1438889_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930025C	1.4	0.616	-1.83	0.453	-1.4	0.628	2.7	0.264	0.22
1429427_s_at	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	1.03	0.953	-1.16	0.377	-1.29	0.083	1.34	0.319	-0.02
1449627_at	Osbpl6	Oxysterol binding protein-like 6	-1.57	0.209	1.02	0.975	1.01	0.965	-1.92	0.268	-0.36
1435693_at	Mall	mal, T-cell differentiation protein-like	1.31	0.091	-1.62	0.335	-1.36	0.064	1.23	0.354	-0.11
1429120_at	Lnp	limb and neural patterns	1.16	0.75	-1.3	0.501	-1.36	0.378	1.69	0.214	0.05
1441643_at	3-Mar	membrane-associated ring finger (C3HC4) 3	-1.28	0.206	1.19	0.097	-1.44	0.198	4.44	0.107	0.73
1444865_at	---	---	-1.11	0.685	-1.41	0.607	1.06	0.906	1.82	0.341	0.09
1452909_at	2410127E18Rik	RIKEN cDNA 2410127E18 gene	-2.16	0.069	-1.29	0.297	1.43	0.177	1.4	0.334	-0.15
1425766_x_at	LOC622757 /// LOC	LOC622757 gene /// similar to transcription elongation factor B (SIII), polypeptide	-1.28	0.635	1.19	0.422	-1.43	0.418	1.02	0.93	-0.13
1438219_at	Pura	Purine rich element binding protein A	1.15	0.648	-1.26	0.48	-1.38	0.172	1.44	0.433	-0.01
1456947_at	Pafah1b1	Platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	1.15	0.605	-1.12	0.639	-1.59	0.028	1.3	0.197	-0.07
1454366_at	4833419A21Rik	RIKEN cDNA 4833419A21 gene	1.09	0.86	-1.93	0.029	1.06	0.754	-1.49	0.408	-0.32
1460075_x_at	Snrpn	Small nuclear ribonucleoprotein N	-1.38	0.252	1.01	0.984	-1.08	0.893	2.01	0.138	0.14
1442575_at	---	---	1.44	0.232	-2.22	0.038	-1.28	0.358	1.03	0.957	-0.26
1422802_at	Defcr3	defensin related cryptdin 3	-1.01	0.976	1.03	0.975	-1.54	0.514	1.14	0.853	-0.1
1457946_at	Og9x	OG9 homeobox gene	-1.63	0.055	1.19	0.281	-1.16	0.753	1.29	0.207	-0.08
1447465_at	4930558N01Rik	RIKEN cDNA 4930558N01 gene	-1.24	0.404	1.06	0.753	-1.26	0.404	1.34	0.432	-0.02
1417454_at	Cul4b	cullin 4B	1.05	0.578	-1.15	0.137	-1.33	0.042	1.04	0.675	-0.1
1460013_at	Nlgn2	neuroligin 2	-2.47	0.061	-1.2	0.769	1.43	0.155	1.39	0.502	-0.21
1418376_at	Fgf15	fibroblast growth factor 15	-1.02	0.894	-1.63	0.548	1.07	0.799	1.86	0.425	0.07
1422717_at	Acp1	acid phosphatase 1, soluble	-1.21	0.378	-1.25	0.068	1.04	0.51	2.9	0.227	0.37
1454755_at	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	-1.62	0.381	1.01	0.985	1.04	0.84	-1.48	0.143	-0.26
1460166_at	Rit2	Ras-like without CAAX 2	-1.22	0.531	1.02	0.976	-1.2	0.642	1.17	0.24	-0.06
1452317_at	Hoxb9	Homeo box B9	-1.26	0.307	-2.34	0.152	1.45	0.299	1.4	0.095	-0.19
1427251_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.33	0.216	-1.21	0.274	1.09	0.613	1.27	0.249	-0.04
1419557_a_at	Tmem9	transmembrane protein 9	-1.22	0.276	-1.23	0.058	1.03	0.832	1.65	0.328	0.06
1438534_x_at	BC004004	cDNA sequence BC004004	1.03	0.787	-1.08	0.554	-1.42	0.07	1.41	0.23	-0.01
1448556_at	Prlr	prolactin receptor	-1.67	0.041	-1.14	0.663	1.2	0.202	1.52	0.033	-0.02
1428762_at	Map3k7ip3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	1.12	0.441	-1.31	0.046	-1.27	0.214	2.75	0.186	0.32
1458722_at	1200015F23Rik	RIKEN cDNA 1200015F23 gene	-1.14	0.587	1.21	0.16	-1.71	0.307	2.59	0.377	0.24
1449818_at	Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	-1.11	0.67	-1.43	0.291	1.07	0.72	4.07	0.198	0.65
1419377_at	Med9	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)	-1.15	0.259	-1.3	0.054	1.04	0.697	1.04	0.668	-0.1
1430741_at	4933433G08Rik	RIKEN cDNA 4933433G08 gene	-1.21	0.501	1.07	0.743	-1.3	0.361	1.12	0.623	-0.08
1441708_at	Spag16	sperm associated antigen 16	-1.54	0.181	-1.16	0.714	1.16	0.586	1.26	0.446	-0.07
1458479_at	Smc2l1	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	-1.85	0.366	1.46	0.571	-1.5	0.426	2	0.309	0.03
1441547_at	Nfia	Nuclear factor I/A	-1.06	0.785	1.24	0.382	-2.08	0.026	1.42	0.247	-0.12
1426493_a_at	Kifc2	kinesin family member C2	-1.29	0.47	-1.19	0.349	1.05	0.887	1.01	0.954	-0.1
1416400_at	Pycrl	pyrroline-5-carboxylate reductase-like	1.03	0.873	-1.21	0.296	-1.22	0.294	1	0.97	-0.1
1432743_at	4930443G03Rik	RIKEN cDNA 4930443G03 gene	-4.89	0.237	1.16	0.805	1.31	0.568	-2.87	0.186	-1.32
1431548_at	4933424G05Rik	RIKEN cDNA 4933424G05 gene	-2.17	0.082	1.07	0.826	1.14	0.807	-1.14	0.799	-0.27

1439719_at	E430004N04Rik	RIKEN cDNA E430004N04 gene	1.13	0.706	-1.99	0.293	1.04	0.928	-3.24	0.194	-0.77
1440566_at	D330005C11Rik	RIKEN cDNA D330005C11 gene	-1.23	0.605	1.06	0.782	-1.25	0.72	1.3	0.544	-0.03
1430013_at	2210008F06Rik	RIKEN cDNA 2210008F06 gene	1.6	0.574	-2.09	0.278	-1.69	0.352	1.1	0.741	-0.27
1448954_at	Nrip3	nuclear receptor interacting protein 3	1.01	0.964	-1.36	0.648	-1.08	0.686	4.38	0.312	0.74
1430392_at	9530086O07Rik	RIKEN cDNA 9530086O07 gene	1.09	0.74	1	0.99	-1.73	0.091	-1.05	0.901	-0.17
1458130_at	1110001A07Rik	RIKEN cDNA 1110001A07 gene	-1.12	0.623	1.04	0.88	-1.37	0.272	1.53	0.38	0.02
1416730_at	Rcl1	RNA terminal phosphate cyclase-like 1	-1.27	0.094	-1.43	0.043	1.19	0.367	1.31	0.375	-0.05
1432824_at	2900018N21Rik	RIKEN cDNA 2900018N21 gene	-1.49	0.12	-1	0.951	1.01	0.984	1.38	0.332	-0.03
1445690_at	---	---	-1.02	0.935	-1.7	0.324	1.11	0.811	2.42	0.242	0.2
1421786_at	Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	1.1	0.586	1.06	0.566	-1.96	0.001	-1.43	0.178	-0.31
1434822_at	Pphln1	periphilin 1	-1.02	0.889	1.04	0.754	-1.53	0.055	1.01	0.959	-0.13
1437033_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	1.03	0.891	-1.35	0.029	-1.11	0.185	1.8	0.02	0.09
1431722_a_at	Afmid	arylformamidase	-1.61	0.025	-1.33	0.083	1.3	0.319	1.15	0.629	-0.12
1420395_a_at	Kif9	kinesin family member 9	-1.07	0.602	-2.35	0.09	1.31	0.362	1.29	0.409	-0.2
1428165_at	Vps24	vacuolar protein sorting 24 (yeast)	-1.13	0.345	1.03	0.68	-1.33	0.084	1.18	0.422	-0.06
1428369_s_at	Arhgap21	Rho GTPase activating protein 21	1	0.984	-1.19	0.138	-1.21	0.27	1.7	0.324	0.08
1459252_at	LOC245263	similar to double homeobox, 4	-1.09	0.682	1.01	0.937	-1.35	0.62	1.76	0.102	0.08
1436817_at	Exoc5	exocyst complex component 5	1	0.976	-1.06	0.34	-1.38	0.018	1.12	0.423	-0.08
1429489_at	Rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	1.03	0.915	-1.48	0.421	-1.04	0.868	1.59	0.046	0.02
1423710_at	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate comple	-1.19	0.136	-1.28	0.064	1.05	0.778	1.04	0.833	-0.1
1441656_at	B930068K11Rik	RIKEN cDNA B930068K11 gene	1.11	0.623	-1.1	0.689	-1.53	0.057	2.49	0.038	0.24
1445654_at	4930422I07Rik	RIKEN cDNA 4930422I07 gene	-1.64	0.094	1.34	0.392	-1.38	0.099	1.3	0.418	-0.09
1420050_at	---	Transcribed locus	-1.22	0.22	-1.2	0.592	1.02	0.963	1.18	0.491	-0.05
1418945_at	Mmp3	matrix metallopeptidase 3	1.46	0.305	-1.36	0.554	-2.08	0.063	2.42	0.029	0.11
1426011_a_at	Ggnbp2	gametogenetin binding protein 2	-1.13	0.474	1.01	0.955	-1.28	0.109	1.18	0.369	-0.06
1431963_at	4930556A20Rik	RIKEN cDNA 4930556A20 gene	-1.19	0.392	-1.24	0.711	1.03	0.952	1.64	0.142	0.06
1433985_at	Abi2	abl-interactor 2	-1.13	0.277	1.17	0.513	-1.6	0.034	1.07	0.701	-0.12
1454506_at	---	---	1.08	0.703	-1.29	0.416	-1.22	0.228	1.71	0.118	0.07
1434491_a_at	Cox6c	cytochrome c oxidase, subunit VIc	-1.2	0.467	1.06	0.683	-1.28	0.019	1.05	0.692	-0.09
1447417_at	Taf1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.6	0.437	1.04	0.956	1.01	0.993	-1.45	0.648	-0.25
1431328_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	-1.17	0.578	1.07	0.704	-1.33	0.376	1.21	0.494	-0.05
1459146_at	Mapk6	mitogen-activated protein kinase 6	1.02	0.987	-1.12	0.85	-1.31	0.593	1.72	0.2	0.08
1459378_at	Ppp3cb	Protein phosphatase 3, catalytic subunit, beta isoform	-1.09	0.651	1.12	0.553	-1.56	0.216	1.22	0.598	-0.08
1424266_s_at	AU018778	expressed sequence AU018778	-1.15	0.512	-1.71	0.181	1.22	0.326	1.44	0.271	-0.05
1444738_at	5730419I09Rik	RIKEN cDNA 5730419I09 gene	1.13	0.708	-1.3	0.671	-1.3	0.19	1.02	0.943	-0.11
1455938_x_at	Rad21	RAD21 homolog (S. pombe)	-1.3	0.255	1.01	0.954	-1.12	0.299	1.47	0.196	0.02
1418514_at	Mtf2	metal response element binding transcription factor 2	1.09	0.408	-1.17	0.33	-1.38	0.078	1.02	0.901	-0.11
1450955_s_at	Sort1	sortilin 1	-1.06	0.325	-3.15	0.025	1.42	0.322	1.28	0.033	-0.38
1436042_at	Tln1	talin 1	1.01	0.926	-1.43	0.114	-1.04	0.713	1.09	0.752	-0.09
1436167_at	Shf	Src homology 2 domain containing F	1.13	0.862	-1.05	0.719	-1.67	0.314	1.27	0.678	-0.08
1450736_a_at	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	-1.67	0.343	-1.18	0.027	1.23	0.656	2.73	0.324	0.28
1444573_at	Lmtk3	Lemur tyrosine kinase 3	1.26	0.467	-1.45	0.431	-1.37	0.531	1.26	0.697	-0.07
1440189_at	Ppp2r5a	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	-1.14	0.807	-1.54	0.541	1.15	0.797	1.4	0.446	-0.03
1415696_at	Sar1a	SAR1 gene homolog A (S. cerevisiae)	-1.1	0.267	1.01	0.801	-1.32	0.121	1.06	0.465	-0.09
1448980_at	Ghrl	ghrelin	1.14	0.886	-1.13	0.461	-1.53	0.027	1.2	0.628	-0.08
1452585_at	Mrps28	mitochondrial ribosomal protein S28	-1.14	0.228	1.06	0.473	-1.35	0.089	1.12	0.711	-0.08
1459860_x_at	Trim2	tripartite motif protein 2	-1.1	0.592	1.1	0.681	-1.49	0.001	1.35	0.163	-0.04
1426856_at	Hsdl2	hydroxysteroid dehydrogenase like 2	-1.07	0.754	-1.59	0.208	1.12	0.174	1.18	0.569	-0.09
1429944_at	Tchhl1	trichohyalin-like 1	-1.51	0.241	-1.14	0.834	1.14	0.821	1.25	0.826	-0.07
1447187_at	Ripk5	Receptor interacting protein kinase 5	1.02	0.89	-1.07	0.835	-1.38	0.085	1.31	0.371	-0.03
1432496_at	1700122O11Rik	RIKEN cDNA 1700122O11 gene	-1.2	0.692	-4.57	0.025	1.63	0.398	1.76	0.266	-0.59
1436415_at	---	Transcribed locus	-1.06	0.194	1	0.98	-1.36	0.075	1.03	0.927	-0.1
1450394_at	Golph3	golgi phosphoprotein 3	-1.25	0.165	1.01	0.934	-1.16	0.222	1.09	0.39	-0.07

1443397_at	Ncoa1	nuclear receptor coactivator 1	-1.56	0.052	-1.38	0.433	1.32	0.174	1.02	0.935	-0.15
1428766_at	Rnmtl1	RNA methyltransferase like 1	-1.4	0.062	-1.32	0.049	1.21	0.36	1.01	0.953	-0.13
1446294_at	---	Transcribed locus	-1.13	0.697	1.02	0.965	-1.28	0.125	1.33	0.128	-0.02
1424696_at	Gpr89	G protein-coupled receptor 89	1.02	0.911	-1.06	0.36	-1.39	0.01	1.12	0.46	-0.08
1437642_at	Hrbl	HIV-1 Rev binding protein-like	-1.27	0.302	-1.19	0.071	1.05	0.55	2.17	0.248	0.19
1444024_at	Ercc6l	excision repair cross-complementing rodent repair deficiency complementation gr	1.06	0.903	-1.18	0.683	-1.3	0.405	3.51	0.276	0.52
1454701_at	4930503L19Rik	RIKEN cDNA 4930503L19 gene	-1.23	0.421	1.01	0.981	-1.16	0.445	1.76	0.27	0.09
1441047_at	Slc45a4	solute carrier family 45, member 4	-1.21	0.08	-1.47	0.285	1.18	0.145	1.38	0.019	-0.03
1431663_a_at	Cntfr	ciliary neurotrophic factor receptor	-2.08	0.039	-1.88	0.352	1.67	0.288	1.44	0.479	-0.21
1438277_at	E130308A19Rik	RIKEN cDNA E130308A19 gene	-1.19	0.25	1.24	0.4	-1.68	0.094	1.02	0.918	-0.15
1417037_at	Orc6l	origin recognition complex, subunit 6-like (S. cerevisiae)	-1.44	0.138	1.19	0.371	-1.26	0.029	2.79	0.199	0.32
1423683_at	Cdca4	cell division cycle associated 4	1.18	0.798	-1.95	0.11	-1.01	0.896	1.44	0.253	-0.09
1452404_at	Phactr2	phosphatase and actin regulator 2	-1.09	0.709	1.01	0.986	-1.32	0.019	1.16	0.358	-0.06
1428014_at	Hist1h4h	histone 1, H4h	-1.75	0.022	1.11	0.745	-1	0.993	2.35	0.193	0.18
1457419_s_at	Speer1-ps1	Spermatogenesis associated glutamate (E)-rich protein 1, pseudogene 1	1.1	0.923	-2.98	0.129	1.25	0.49	-1.19	0.792	-0.46
1457521_at	---	---	-1.3	0.523	1.57	0.132	-2.92	0.171	1.31	0.516	-0.34
1434869_at	Tdrd3	tudor domain containing 3	-1.22	0.433	1.11	0.522	-1.32	0.177	1.15	0.559	-0.07
1426075_at	Klb	klotho beta	-2.54	0.323	-1.58	0.355	1.66	0.459	1.04	0.913	-0.36
1436674_at	Rap2ip	Rap2 interacting protein	1.13	0.777	-1.27	0.627	-1.31	0.61	1.22	0.65	-0.06
1416801_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	1.15	0.621	-1.74	0.325	-1.04	0.905	1.06	0.88	-0.14
1454842_a_at	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	-1.35	0.294	1.11	0.538	-1.21	0.363	1.05	0.824	-0.1
1442678_at	Ccdc28b	coiled coil domain containing 28B	-1.72	0.174	1.11	0.848	-1.01	0.981	3.11	0.292	0.37
1444942_at	Helz	helicase with zinc finger domain	1	0.999	-1.07	0.773	-1.34	0.298	1	1	-0.1
1441766_at	---	Transcribed locus	1.03	0.974	-1.04	0.945	-1.44	0.56	1.5	0.346	0.01
1426439_at	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	1.14	0.715	-1.54	0.045	-1.12	0.796	1.82	0.362	0.07
1432804_at	A230101C19Rik	RIKEN cDNA A230101C19 gene	1.29	0.34	-2.42	0.418	-1.02	0.955	1.08	0.927	-0.27
1457623_x_at	Trp53	transformation related protein 53	-1.08	0.838	-1.75	0.022	1.19	0.564	1.07	0.795	-0.15
1437928_at	Pcdh12	protocadherin 12	1.02	0.958	1.13	0.686	-1.88	0.195	-1.52	0.079	-0.31
1459450_at	Chd9	Chromodomain helicase DNA binding protein 9	-1.25	0.047	-1.33	0.388	1.13	0.492	1.16	0.747	-0.07
1437843_s_at	Nupl1	Nucleoporin like 1	-1.08	0.741	1.09	0.322	-1.52	0.011	1.13	0.558	-0.09
1431591_s_at	LOC677168	hypothetical protein LOC677168	-1.41	0.029	-1.24	0.079	1.17	0.32	2.34	0.277	0.21
1452784_at	Itgav	integrin alpha V	1.02	0.904	1.01	0.919	-1.54	0.003	-1.53	0.213	-0.26
1454986_at	Zfp668	zinc finger protein 668	-1.25	0.297	-1.2	0.6	1.04	0.772	1.07	0.797	-0.08
1441584_at	Fli1	Friend leukemia integration 1	1.06	0.729	1.05	0.852	-1.75	0.103	-2.19	0.068	-0.46
1438023_at	Spata6	spermatogenesis associated 6	1.09	0.728	-1.28	0.394	-1.24	0.673	1.03	0.97	-0.1
1417378_at	Igsf4a	immunoglobulin superfamily, member 4A	1.12	0.382	1.03	0.897	-1.87	0.031	-1.25	0.341	-0.24
1441845_at	Caps2	calcyphosphine 2	-1.05	0.906	-2.1	0.006	1.25	0.222	1.23	0.753	-0.17
1437552_at	2410127L17Rik /// I	RIKEN cDNA 2410127L17 gene /// similar to RIKEN cDNA 2410127L17 /// similar	-1.25	0.324	1.16	0.062	-1.39	0.034	1.75	0.166	0.07
1451213_at	Pex11b	peroxisomal biogenesis factor 11b	-1.19	0.345	1.01	0.803	-1.2	0.116	1.16	0.187	-0.06
1423347_at	Sec23a	SEC23A (S. cerevisiae)	1.06	0.386	-1.08	0.352	-1.44	0.008	1.38	0.165	-0.02
1447692_x_at	Map3k7ip1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	-1.57	0.647	-2.2	0.291	1.59	0.359	1.05	0.947	-0.28
1433419_at	4930405A07Rik	RIKEN cDNA 4930405A07 gene	-1	0.986	1.02	0.918	-1.5	0.2	1.5	0.54	0
1428072_a_at	Dolpp1	dolichyl pyrophosphate phosphatase 1	-1.33	0.067	1.03	0.716	-1.11	0.514	1.4	0.32	0
1426204_a_at	Oprl1	opioid receptor-like 1	-1.26	0.377	-1.2	0.659	1.05	0.877	1.5	0.636	0.02
1458465_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	-1.11	0.792	1.17	0.738	-1.63	0.277	1.34	0.396	-0.06
1445320_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-4.52	0.003	2.12	0.226	-2.94	0.016	1.37	0.353	-0.99
1450387_s_at	Ak3l1	adenylate kinase 3 alpha-like 1	1.16	0.737	-1.06	0.836	-1.72	0.111	1.88	0.26	0.06
1456968_at	Actn2	Actinin alpha 2	1.06	0.874	1.04	0.941	-1.72	0.446	-1.4	0.41	-0.25
1426263_at	Igsf4c	immunoglobulin superfamily, member 4C	-1.15	0.323	1.03	0.86	-1.27	0.132	1.01	0.983	-0.1
1441432_at	C820005J03Rik	RIKEN cDNA C820005J03 gene	-1.04	0.933	-1.39	0.6	1	0.995	1.15	0.747	-0.07
1433004_at	4833446E11Rik	RIKEN cDNA 4833446E11 gene	-2.72	0.002	1.01	0.98	1.31	0.471	-1.25	0.494	-0.41
1447627_at	Tmem132e	transmembrane protein 132E	-1.23	0.529	-1.22	0.603	1.05	0.732	1.11	0.857	-0.07
1442959_at	Birc6	baculoviral IAP repeat-containing 6	1.15	0.013	1.01	0.952	-1.89	0.01	-1.29	0.477	-0.26

1439570_at	Gm444	gene model 444, (NCBI)	-1.69	0.242	1.08	0.809	1.01	0.988	-1.82	0.045	-0.36
1439222_at	Morc2b	microrchidia 2B	1.03	0.948	1.04	0.945	-1.62	0.288	-2.07	0.283	-0.41
1422128_at	Rpl14	ribosomal protein L14	1.05	0.734	-1.23	0.39	-1.22	0.224	1.01	0.969	-0.1
1439116_at	Crsp2	Cofactor required for Sp1 transcriptional activation, subunit 2	-1.44	0.301	-1.08	0.383	1.06	0.845	1.08	0.705	-0.09
1440787_s_at	Bbs10	Bardet-Biedl syndrome 10 (human)	-1.24	0.353	-1.2	0.445	1.04	0.854	1.06	0.77	-0.08
1425317_x_at	Stk31	serine threonine kinase 31	-1.99	0.18	1.52	0.59	-1.51	0.262	1.05	0.941	-0.23
1419774_at	D2Ertd239e	DNA segment, Chr 2, ERATO Doi 239, expressed	1.05	0.809	-1.98	0.001	1.12	0.794	-2.37	0.13	-0.54
1449061_a_at	Prim1	DNA primase, p49 subunit	-1.34	0.284	-1.4	0.179	1.22	0.5	3.01	0.187	0.37
1449649_at	Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.48	0.553	1.32	0.457	-1.44	0.314	1.05	0.917	-0.14
1449017_at	Nutf2	nuclear transport factor 2	-1.14	0.481	1.01	0.928	-1.26	0.044	1.53	0.254	0.03
1449914_at	Ribc1	RIB43A domain with coiled-coils 1	-1.45	0.001	1.03	0.787	-1.04	0.881	1.27	0.351	-0.05
1430593_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	1.36	0.608	-1.24	0.696	-1.93	0.017	1.55	0.286	-0.07
1452121_at	Fbxo22	F-box only protein 22	-1.45	0.48	1.22	0.405	-1.3	0.517	1.06	0.915	-0.12
1439431_x_at	---	---	1.25	0.823	-1.08	0.933	-1.96	0.115	1.04	0.946	-0.19
1435452_at	Tmem20	transmembrane protein 20	-1.2	0.384	-1.52	0.085	1.19	0.431	1.53	0.32	0
1445875_at	A230057D06Rik	RIKEN cDNA A230057D06 gene	-1.52	0.547	-1.51	0.165	1.37	0.601	1.36	0.539	-0.08
1453866_a_at	Xkh	Kell blood group precursor (McLeod phenotype) homolog	-1.45	0.504	1.07	0.901	-1.08	0.738	2.02	0.4	0.14
1460088_at	6430531B16Rik	RIKEN cDNA 6430531B16 gene	-1.43	0.606	1.11	0.718	-1.14	0.587	1.55	0.286	0.02
1433407_at	Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	-2.75	0.085	-1.2	0.37	1.48	0.227	1.32	0.564	-0.28
1440038_at	B430007K19Rik	RIKEN cDNA B430007K19 gene	-1.11	0.44	1.11	0.356	-1.49	0.031	3.51	0.154	0.5
1440383_at	Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	1.1	0.871	-1.47	0.382	-1.1	0.473	1.95	0.33	0.12
1434717_at	Cul3	cullin 3	-1.23	0.164	1.05	0.665	-1.21	0.108	1.14	0.504	-0.07
1422916_at	Fgf21	fibroblast growth factor 21	1.01	0.994	-1.29	0.656	-1.11	0.833	1.3	0.459	-0.02
1451982_at	Map2k4	mitogen activated protein kinase kinase 4	-1.08	0.396	1.01	0.953	-1.33	0.034	1.32	0.052	-0.02
1432963_at	2410049M19Rik	RIKEN cDNA 2410049M19 gene	1.13	0.814	-1.07	0.676	-1.62	0.009	1.64	0.128	0.02
1416832_at	Slc39a8	solute carrier family 39 (metal ion transporter), member 8	1.11	0.406	-1.08	0.021	-1.54	0.1	4.77	0.219	0.81
1423965_at	Cd99l2	Cd99 antigen-like 2	1.05	0.802	-1.04	0.811	-1.48	0.011	1.37	0.245	-0.03
1432041_at	4930519A11Rik	RIKEN cDNA 4930519A11 gene	-1.77	0.452	1.14	0.505	-1.02	0.862	1.01	0.945	-0.16
1459855_x_at	Actr1a	ARP1 actin-related protein 1 homolog A (yeast)	-1.22	0.548	1.02	0.773	-1.19	0.525	1.05	0.898	-0.08
1441558_at	D230044B12Rik	RIKEN cDNA D230044B12 gene	1.05	0.763	1.02	0.933	-1.64	0.155	-1.28	0.155	-0.21
1422464_at	Mrpl3	mitochondrial ribosomal protein L3	-1.29	0.043	-1.19	0.265	1.07	0.406	1.03	0.805	-0.09
1422807_at	Arf5	ADP-ribosylation factor 5	1.06	0.628	-1.24	0.302	-1.22	0.367	2.78	0.191	0.35
1422424_at	Hpvc2	human papillomavirus 18 E5 central sequence motif gene 2	-1.17	0.12	-1.44	0.436	1.14	0.653	1.21	0.508	-0.07
1433628_at	Coq10a	coenzyme Q10 homolog A (yeast)	-1.26	0.312	-1.29	0.081	1.12	0.692	1.15	0.46	-0.07
1420559_a_at	Shox2	short stature homeobox 2	1.12	0.851	-1.14	0.657	-1.45	0.007	1.3	0.569	-0.04
1432051_at	Ccdc7	coiled-coil domain containing 7	1.09	0.736	-1.71	0.074	1.01	0.927	-2.64	0.207	-0.56
1431098_at	Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	1.15	0.522	-2.1	0.057	1.06	0.817	-1.18	0.212	-0.27
1421650_at	Mepe	matrix extracellular phosphoglycoprotein with ASARM motif (bone)	-1.52	0.443	1.1	0.549	-1.08	0.655	2.43	0.301	0.23
1422705_at	Tmepai	transmembrane, prostate androgen induced RNA	1.23	0.316	-1.72	0.104	-1.14	0.452	1.06	0.828	-0.14
1418315_at	Nr5a1	nuclear receptor subfamily 5, group A, member 1	-1.08	0.703	1.34	0.279	-2.39	0.255	1.09	0.766	-0.26
1439340_at	D630036G22Rik	RIKEN cDNA D630036G22 gene	-1.16	0.784	-1.22	0.382	1.01	0.987	1.33	0.257	-0.01
1445680_x_at	F2rl2	coagulation factor II (thrombin) receptor-like 2	-1.37	0.265	-2.28	0.302	1.52	0.374	1.92	0.336	-0.05
1457756_at	Zfp192	zinc finger protein 192	1.09	0.733	-1.43	0.264	-1.12	0.687	1.36	0.39	-0.02
1449895_at	Acr	preproacrosin	-2.11	0.024	1.17	0.546	1.04	0.845	-1.08	0.153	-0.24
1448528_at	Pdcd10	programmed cell death 10	-1.15	0.264	1.16	0.118	-1.52	0.066	1.02	0.844	-0.12
1422246_at	Dspp	dentin sialophosphoprotein	-1.21	0.57	-1.42	0.038	1.16	0.529	1.23	0.61	-0.06
1432101_a_at	Tssk4	testis-specific serine kinase 4	-1.13	0.635	-1.6	0.186	1.18	0.379	1.29	0.663	-0.07
1425002_at	BC010462	cDNA sequence BC010462	1.5	0.34	-1.59	0.173	-1.8	0.283	1.31	0.077	-0.14
1445129_at	---	---	1.51	0.027	-1.14	0.544	-3.28	0.237	1.3	0.429	-0.4
1456238_at	LOC668917	similar to Zinc finger protein 133	1.01	0.968	-2.22	0.006	1.23	0.625	-2.49	0.159	-0.62
1422943_a_at	Hspb1	heat shock protein 1	1.04	0.744	-1.25	0.203	-1.19	0.372	1.19	0.588	-0.05
1439115_at	Mcph1	microcephaly, primary autosomal recessive 1	1.2	0.67	-1.85	0.23	-1.05	0.84	1.9	0.205	0.05
1457929_at	Mdm2	transformed mouse 3T3 cell double minute 2	1.58	0.516	-1.54	0.201	-2.19	0.018	2.34	0.095	0.05

1445912_at	Ccdc60	coiled-coil domain containing 60	1.09	0.652	1	0.993	-1.67	0.189	-1.61	0.032	-0.3
1440681_at	Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	1.45	0.195	-1.59	0.455	-1.65	0.013	1.02	0.976	-0.19
1454300_at	4933424C09Rik	RIKEN cDNA 4933424C09 gene	-1.85	0.002	-1.18	0.731	1.3	0.56	1.02	0.982	-0.18
1431858_at	4930480K15Rik	RIKEN cDNA 4930480K15 gene	-1.61	0.349	-1.12	0.373	1.18	0.702	2.08	0.311	0.13
1443181_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.54	0.284	-1.53	0.342	1.39	0.139	1.17	0.696	-0.13
1439178_at	Adrbk2	adrenergic receptor kinase, beta 2	1.49	0.44	-2.05	0.321	-1.41	0.125	1.15	0.691	-0.2
1420285_at	---	---	1.67	0.593	-2.15	0.281	-1.81	0.219	1.12	0.599	-0.29
1429289_at	Letmd1	LETM1 domain containing 1	-1.2	0.794	1.15	0.83	-1.42	0.626	1.41	0.051	-0.01
1429839_a_at	Yaf2	YY1 associated factor 2	1.12	0.38	-1.46	0.069	-1.13	0.406	1.21	0.012	-0.07
1460400_at	Spast	spastin	1.04	0.813	-1.41	0.041	-1.07	0.637	1.15	0.396	-0.07
1443659_at	Zfp292	Zinc finger protein 292	1.26	0.491	-1.53	0.344	-1.28	0.546	2.1	0.198	0.14
1420598_x_at	Defcr-rs2	defensin related cryptdin, related sequence 2	-1.26	0.141	1.04	0.587	-1.17	0.199	1.41	0.182	0.01
1419349_a_at	Cyp2d9	cytochrome P450, family 2, subfamily d, polypeptide 9	1.78	0.027	-3.97	0.071	-1.52	0.227	1.13	0.871	-0.65
1459123_at	---	---	-1.05	0.858	1.21	0.4	-1.92	0.113	1.17	0.711	-0.15
1454871_at	Rbm15b	RNA binding motif protein 15B	-1.25	0.457	-1.23	0.298	1.08	0.775	1.8	0.141	0.1
1439125_at	Add1	Adducin 1 (alpha)	-1.69	0.024	1.42	0.335	-1.47	0.381	1.13	0.698	-0.15
1438014_at	Mrpl34	mitochondrial ribosomal protein L34	-1.14	0.422	-1.35	0.436	1.07	0.838	1.06	0.855	-0.09
1453878_at	Ubr2	ubiquitin protein ligase E3 component n-recognin 2	-1.45	0.365	1.08	0.87	-1.09	0.87	1	0.997	-0.11
1454363_at	9430099H24Rik	RIKEN cDNA 9430099H24 gene	-2.65	0.465	-1.37	0.635	1.58	0.4	1.01	0.991	-0.36
1432232_at	Rcor3	REST corepressor 3	1.03	0.954	-1.19	0.734	-1.22	0.275	1.3	0.5	-0.02
1460723_at	Mc5r	melanocortin 5 receptor	-1.02	0.833	-1.73	0.211	1.13	0.629	1.14	0.789	-0.12
1430498_at	9130009I01Rik	RIKEN cDNA 9130009I01 gene	1.14	0.78	1.01	0.964	-1.87	0.043	-1.72	0.381	-0.36
1456463_at	A230106M20Rik	RIKEN cDNA A230106M20 gene	-2.24	0.449	1.29	0.541	-1.04	0.904	1.27	0.727	-0.18
1444820_at	Tmem49	Transmembrane protein 49	1.24	0.683	-1.17	0.563	-1.67	0.186	1.3	0.587	-0.08
1419256_at	Spnb2	spectrin beta 2	1.08	0.806	-1.01	0.949	-1.6	0.293	1.03	0.882	-0.13
1427334_s_at	2810474O19Rik	RIKEN cDNA 2810474O19 gene	1.07	0.807	-1.34	0.21	-1.14	0.016	1.21	0.525	-0.05
1430485_at	3010009O07Rik	RIKEN cDNA 3010009O07 gene	1.09	0.34	-1.13	0.371	-1.4	0.137	1.1	0.64	-0.09
1439821_at	Lrp2bp	Lrp2 binding protein	-1.37	0.407	-1.07	0.645	1.03	0.809	2.1	0.068	0.17
1452685_at	0610009O20Rik	RIKEN cDNA 0610009O20 gene	-1.12	0.41	-1.26	0.164	1.01	0.937	1.27	0.331	-0.03
1433470_a_at	Immt	inner membrane protein, mitochondrial	-1.15	0.137	-1.32	0.032	1.06	0.619	1.17	0.181	-0.06
1452763_at	Nipa1	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	-1.11	0.698	1.01	0.986	-1.28	0.167	4.23	0.213	0.71
1435035_at	Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	-1.38	0.22	-1.09	0.362	1.05	0.675	1.13	0.567	-0.07
1443917_at	Tmbim4	transmembrane BAX inhibitor motif containing 4	-1.1	0.59	1.15	0.745	-1.58	0.076	1.13	0.626	-0.1
1453025_at	2900006F19Rik	RIKEN cDNA 2900006F19 gene	-1.03	0.332	-1.41	0.347	1.01	0.919	1.13	0.785	-0.07
1459415_at	---	---	-1.18	0.48	1.06	0.922	-1.27	0.328	2.18	0.147	0.2
1420973_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	1.04	0.893	-1.82	0.11	1.1	0.385	-1.36	0.488	-0.26
1459920_at	4933415E08Rik	RIKEN cDNA 4933415E08 gene	-1.2	0.385	-1.37	0.146	1.13	0.506	1.4	0.331	-0.01
1453001_at	Dleu8	deleted in lymphocytic leukemia 8	-1.09	0.274	-1.31	0.043	1.01	0.871	2.04	0.226	0.16
1457003_at	AW490526	expressed sequence AW490526	-1.75	0.471	-1.25	0.571	1.32	0.354	1.29	0.602	-0.1
1422630_at	Rad50	RAD50 homolog (S. cerevisiae)	-1.27	0.3	1	0.999	-1.1	0.395	1.07	0.612	-0.08
1429073_at	2210015D19Rik	RIKEN cDNA 2210015D19 gene	-1.22	0.389	-1.17	0.264	1.02	0.846	1.03	0.831	-0.08
1443997_at	C130040D06Rik	RIKEN cDNA C130040D06 gene	-1.95	0.395	1.49	0.402	-1.44	0.218	1.67	0.329	-0.06
1428518_at	Mlf1ip	myeloid leukemia factor 1 interacting protein	-1.71	0.106	1.25	0.416	-1.16	0.5	2.55	0.277	0.23
1438867_at	Gm1070	gene model 1070, (NCBI)	1.42	0.051	-1.32	0.518	-1.94	0.331	1.3	0.738	-0.13
1429432_at	Bat2d	BAT2 domain containing 1	1.02	0.975	1.14	0.806	-1.86	0.171	-1.04	0.904	-0.19
1430541_at	Fbxo44	: F-box protein 44	-1.7	0.086	1.46	0.284	-1.56	0.326	1.56	0.23	-0.06
1430333_at	Eftud1	elongation factor Tu GTP binding domain containing 1	-1.54	0.195	-1.42	0.015	1.34	0.639	1.54	0.384	-0.02
1432635_a_at	Tloc1	translocation protein 1	-1.1	0.46	1.08	0.819	-1.42	0.326	1.99	0.17	0.14
1451815_at	B3gnt4	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	1.04	0.857	-1.14	0.668	-1.29	0.62	1.18	0.683	-0.05
1422142_at	Nphs1	nephrosis 1 homolog, nephrin (human)	1.18	0.023	1	0.996	-1.95	0.188	-1.27	0.468	-0.26
1419056_at	Rtn2	reticulon 2 (Z-band associated protein)	1.31	0.69	-1.5	0.502	-1.38	0.169	1.11	0.852	-0.12
1447764_at	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	-1.1	0.657	-1.99	0.037	1.28	0.562	1.03	0.935	-0.19
1422904_at	Fmo2	flavin containing monooxygenase 2	-1.05	0.844	-1.59	0.091	1.12	0.675	1.18	0.748	-0.09

1420333_at	Txndc8	thioredoxin domain containing 8	-1.6	0.124	1.12	0.491	-1.06	0.9	1.8	0.193	0.07
1434534_at	---	---	1.06	0.932	1.1	0.852	-1.88	0.307	-2.31	0.121	-0.51
1428945_at	Ube1l2	ubiquitin-activating enzyme E1-like 2	-1.26	0.237	1.02	0.786	-1.13	0.417	1.02	0.93	-0.09
1438907_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630033	1.05	0.613	-1.39	0.352	-1.08	0.711	1.09	0.657	-0.08
1434985_a_at	Eif4a1	eukaryotic translation initiation factor 4A1	-1.22	0.028	1.01	0.921	-1.16	0.254	1.09	0.392	-0.07
1424532_at	Ylpm1	YLP motif containing 1	-1.33	0.08	-1.11	0.529	1.05	0.792	1.07	0.52	-0.08
1436166_at	Stox2	storkhead box 2	1.02	0.951	-1.05	0.929	-1.4	0.199	1.34	0.646	-0.02
1422930_at	Icam4	intercellular adhesion molecule 4, Landsteiner-Wiener blood group	-1.17	0.681	-1.48	0.226	1.16	0.519	8.21	0.209	1.68
1438500_at	Prrt3	proline-rich transmembrane protein 3	1.02	0.854	-1.49	0.246	1	0.988	-1.11	0.431	-0.14
1427920_at	Phf19	PHD finger protein 19	-1.53	0.088	1.01	0.981	1.03	0.869	-1.21	0.473	-0.17
1456757_at	G630024C07Rik	RIKEN cDNA G630024C07 gene	-2.41	0.302	1.1	0.832	1.18	0.613	-1.09	0.644	-0.3
1435620_at	1190002J23Rik	RIKEN cDNA 1190002J23 gene	-1.13	0.508	1.09	0.545	-1.38	0.026	1.07	0.686	-0.09
1444635_at	---	Transcribed locus	-1.38	0.047	-1.24	0.716	1.16	0.098	1.01	0.987	-0.11
1424414_at	Ogfrl1 /// LOC6738	opioid growth factor receptor-like 1 /// similar to opioid growth factor receptor-like	1.11	0.874	-1.31	0.342	-1.22	0.244	1.11	0.549	-0.08
1416242_at	Klhl13	kelch-like 13 (Drosophila)	-1.32	0.034	1.02	0.886	-1.09	0.573	1.27	0.044	-0.03
1442289_at	Josd3	Josephin domain containing 3	-1.4	0.587	1.07	0.915	-1.1	0.502	1.07	0.791	-0.09
1428705_at	1700007K13Rik	RIKEN cDNA 1700007K13 gene	-2.41	0.038	1.05	0.919	1.24	0.564	-1.11	0.874	-0.31
1427827_at	---	Murine retrovirus readthrough RNA sequence	1.27	0.247	-1.42	0.004	-1.38	0.058	1.13	0.563	-0.1
1454175_at	4930517N10Rik	RIKEN cDNA 4930517N10 gene	-1.36	0.557	-2.21	0.026	1.51	0.389	2.4	0.011	0.08
1444847_at	---	---	-1.66	0.249	1.03	0.904	1.06	0.884	-1.04	0.95	-0.15
1457930_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	1.14	0.258	-1.13	0.542	-1.49	0.178	1.12	0.569	-0.09
1458210_at	9130404H23Rik	RIKEN cDNA 9130404H23 gene	-1.27	0.635	-1.88	0.032	1.38	0.418	1.19	0.362	-0.14
1421155_at	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	-1.01	0.975	-1.69	0.07	1.11	0.538	1.27	0.118	-0.08
1452903_at	6230427J02Rik	RIKEN cDNA 6230427J02 gene	-1.18	0.649	-1.41	0.041	1.14	0.531	1.71	0.389	0.07
1417353_x_at	Snrpa1	small nuclear ribonucleoprotein polypeptide A'	-1.35	0.115	-1.1	0.344	1.05	0.557	1.01	0.944	-0.1
1423737_at	Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	-1.15	0.288	-1.31	0.043	1.06	0.29	1.13	0.131	-0.07
1444688_at	Pcqap	positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated protein	-1.47	0.308	1.56	0.552	-2.16	0.154	1.06	0.894	-0.26
1457661_at	B930036G03Rik	RIKEN cDNA B930036G03 gene	1.02	0.91	-1.08	0.747	-1.33	0.469	1.44	0.575	0.01
1445727_at	Ube3a	ubiquitin protein ligase E3A	1.16	0.493	-1.14	0.334	-1.52	0.114	1.14	0.333	-0.09
1443291_at	Ank1	Ankyrin 1, erythroid	1.51	0.581	-1.93	0.344	-1.48	0.328	2.26	0.219	0.09
1441510_at	Rhof	Ras homolog gene family, member f	-1.32	0.383	-1.14	0.326	1.06	0.882	2.42	0.23	0.26
1459762_x_at	Wdr12	WD repeat domain 12	1.07	0.919	-2.13	0.419	1.16	0.602	-1.54	0.559	-0.36
1424431_at	Galnact2	chondroitin sulfate GalNAcT-2	-1.09	0.767	1.09	0.339	-1.45	0.004	1.11	0.552	-0.08
1446281_at	C530008M07Rik	RIKEN cDNA C530008M07 gene	-1.38	0.017	1.06	0.858	-1.09	0.685	1.47	0.25	0.01
1432778_at	---	---	1.11	0.769	-1.49	0.584	-1.08	0.399	1.4	0.402	-0.02
1447797_x_at	Nop17	NOP17	-1.35	0.404	-1.05	0.91	1	0.986	1.21	0.578	-0.05
1421451_at	Crb1	crumbs homolog 1 (Drosophila)	-2.35	0.038	-1.4	0.427	1.56	0.037	1.06	0.751	-0.28
1458248_at	---	---	-1.49	0.042	1.03	0.906	-1	0.985	1.16	0.575	-0.08
1427581_at	Hic2	hypermethylated in cancer 2	-1.11	0.789	-1.47	0.136	1.12	0.81	1.39	0.604	-0.02
1441518_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930003C13 product	1.23	0.244	-1.08	0.916	-1.84	0.185	1.37	0.431	-0.08
1439574_at	2600015P10Rik	RIKEN cDNA 2600015P10 gene	1.02	0.948	-1.39	0.346	-1.05	0.82	2.3	0.271	0.22
1436458_at	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.24	0.295	1.25	0.547	-1.55	0.025	1.48	0.236	-0.01
1423566_a_at	Hsp110	heat shock protein 110	-1.15	0.498	-1.57	0.044	1.2	0.625	1.1	0.811	-0.11
1422843_at	---	---	-1.23	0.657	-1.43	0.294	1.19	0.463	1.23	0.504	-0.06
1451742_a_at	Ugp2	UDP-glucose pyrophosphorylase 2	-1.04	0.675	-1.37	0.161	1.01	0.945	1.03	0.865	-0.09
1453112_a_at	Lrrc18	leucine rich repeat containing 18	-2.29	0.42	1.05	0.906	1.21	0.532	-1.6	0.393	-0.41
1432066_at	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	-1.04	0.957	-1.8	0.122	1.19	0.623	1.76	0.245	0.03
1433041_at	Rabepk	Rab9 effector protein with kelch motifs	1.21	0.648	-1.14	0.67	-1.63	0.159	1.93	0.116	0.09
1457059_at	Zfp438	zinc finger protein 438	-1.13	0.321	-1.29	0.182	1.04	0.505	1.22	0.199	-0.04
1436874_x_at	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.17	0.008	-1.31	0.142	1.08	0.262	1.06	0.367	-0.09
1431965_at	4933411E08Rik	RIKEN cDNA 4933411E08 gene	-1.14	0.726	1.01	0.98	-1.24	0.421	1.14	0.771	-0.06
1417760_at	Nr0b1	nuclear receptor subfamily 0, group B, member 1	-2.78	0.096	1.18	0.575	1.16	0.624	-1.54	0.583	-0.5
1439741_x_at	Uck2	uridine-cytidine kinase 2	1.03	0.914	-1.21	0.259	-1.19	0.445	1.25	0.526	-0.03

1450508_at	Foxn1	forkhead box N1	1.04	0.969	-1.16	0.76	-1.25	0.541	1.15	0.698	-0.06
1448943_at	Nrp1	neuropilin 1	1.01	0.92	1.02	0.928	-1.48	0.053	-1.34	0.224	-0.2
1446624_at	Fcmd	Fukuyama type congenital muscular dystrophy homolog (human)	-1.32	0.477	-1.09	0.872	1.03	0.853	1.23	0.509	-0.04
1429817_at	Sohlh2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	-1.87	0.145	1.12	0.826	1.05	0.689	-1.04	0.838	-0.19
1459258_at	2610021K21Rik	RIKEN cDNA 2610021K21 gene	1.59	0.416	-3.72	0.113	-1.19	0.377	2.07	0.098	-0.31
1429496_x_at	2300002M23Rik	RIKEN cDNA 2300002M23 gene	-1.55	0.443	1.17	0.446	-1.14	0.451	1.09	0.789	-0.1
1417214_at	Rab27b	RAB27b, member RAS oncogene family	1.07	0.761	-1.31	0.197	-1.15	0.509	2.33	0.308	0.23
1459201_at	---	---	1.02	0.951	-1.14	0.674	-1.25	0.326	1.09	0.808	-0.07
1436107_at	Lsm8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.18	0.352	1.11	0.73	-1.33	0.314	1.28	0.201	-0.03
1418552_at	Opn1sw	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	-1.25	0.409	1.48	0.64	-2.37	0.078	1.11	0.579	-0.26
1418220_at	Foxf2	forkhead box F2	1.23	0.199	-1.4	0.351	-1.33	0.22	1.09	0.855	-0.1
1459233_at	Clasp1	CLIP associating protein 1	-2.15	0.004	1.28	0.257	-1.05	0.848	1.07	0.72	-0.21
1454661_at	Atp5g3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), i	-1.15	0.035	-1.24	0.214	1.03	0.536	1.11	0.334	-0.06
1451151_s_at	Zfp410	zinc finger protein 410	1.03	0.81	-1.14	0.31	-1.26	0.106	1.38	0.313	0
1457043_at	B3galtl	beta 1,3-galactosyltransferase-like	-1.19	0.355	1.04	0.716	-1.21	0.282	1.56	0.137	0.05
1415990_at	Vdac2	voltage-dependent anion channel 2	-1.28	0.173	-1.12	0.021	1.03	0.573	1.1	0.316	-0.07
1429895_at	2310010G23Rik	RIKEN cDNA 2310010G23 gene	-1.49	0.416	-1.43	0.629	1.34	0.164	1.61	0.367	0
1425910_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	1.28	0.591	-1.36	0.58	-1.46	0.253	1.93	0.447	0.1
1439908_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1.35	0.173	-1.33	0.555	-1.68	0.054	1.28	0.209	-0.09
1432117_at	4933422A05Rik	RIKEN cDNA 4933422A05 gene	-1.47	0.472	1.15	0.813	-1.15	0.807	1.08	0.831	-0.1
1450835_a_at	Gfra4	glial cell line derived neurotrophic factor family receptor alpha 4	-1.38	0.236	1.28	0.666	-1.44	0.302	1.11	0.805	-0.11
1422389_at	Tas2r105	taste receptor, type 2, member 105	1.08	0.851	-1.16	0.134	-1.32	0.597	1.87	0.467	0.12
1423926_at	Slc39a13	solute carrier family 39 (metal ion transporter), member 13	1.01	0.828	-1.1	0.543	-1.27	0.186	1.16	0.236	-0.05
1445728_at	---	---	-1.47	0.427	-1.29	0.629	1.25	0.695	1.51	0.396	0
1446147_at	C79248	expressed sequence C79248	1.07	0.818	1.04	0.558	-1.69	0.037	-1.09	0.678	-0.17
1427846_x_at	Fgfr4	fibroblast growth factor receptor 4	-1.07	0.604	1.06	0.778	-1.41	0.022	1.33	0.541	-0.02
1448946_at	Kif3c	kinesin family member 3C	-1.45	0.146	1.17	0.598	-1.19	0.22	1.28	0.166	-0.05
1450474_at	Serpinb9c	serine (or cysteine) peptidase inhibitor, clade B, member 9c	-1.51	0.02	-1.15	0.519	1.17	0.627	1.71	0.352	0.06
1448837_at	Vil1	villin 1	-1.07	0.217	-2.13	0.309	1.3	0.606	1.1	0.842	-0.2
1432946_at	5230400M06Rik	RIKEN cDNA 5230400M06 gene	1.11	0.282	1.03	0.899	-1.78	0.008	-1.17	0.374	-0.2
1432916_at	5730407I07Rik	RIKEN cDNA 5730407I07 gene	1.08	0.316	-1.22	0.544	-1.25	0.242	1.24	0.461	-0.04
1459327_at	4931406I20Rik	RIKEN cDNA 4931406I20 gene	-1.23	0.328	1.16	0.747	-1.36	0.282	1.21	0.182	-0.06
1439685_at	Rnf11	Ring finger protein 11	-1.42	0.228	1.08	0.897	-1.09	0.864	2.12	0.079	0.17
1459029_at	Pak1	P21 (CDKN1A)-activated kinase 1	1.1	0.743	-1.7	0.354	1.01	0.916	-1.09	0.503	-0.17
1419382_a_at	Dhrs4	dehydrogenase/reductase (SDR family) member 4	-1.16	0.787	-1.55	0.212	1.19	0.555	1.21	0.62	-0.07
1442359_at	Steap2	six transmembrane epithelial antigen of prostate 2	-1.1	0.185	1.06	0.825	-1.36	0.074	1.63	0.239	0.06
1445295_at	Epb4.1	Erythrocyte protein band 4.1	-2.09	0.08	1.59	0.27	-1.59	0.176	1.19	0.587	-0.22
1418254_at	Apip	APAF1 interacting protein	-1.23	0.019	-1.17	0.055	1.04	0.353	1.39	0.25	0.01
1450620_at	---	---	-2.4	0.253	-1.03	0.96	1.31	0.575	1.08	0.886	-0.26
1436060_at	0710005M24Rik	RIKEN cDNA 0710005M24 gene	-1.03	0.776	-1.5	0.137	1.07	0.734	1.06	0.75	-0.1
1460228_at	Usf2	upstream transcription factor 2	-1.32	0.137	-1.23	0.422	1.13	0.343	1.15	0.414	-0.07
1454956_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	1.01	0.97	-1.19	0.034	-1.16	0.057	1.07	0.533	-0.07
1446345_at	---	---	1.1	0.293	1.19	0.29	-2.4	0.007	-1.41	0.076	-0.38
1458227_at	---	---	1.01	0.988	1.01	0.857	-1.47	0.369	-1.38	0.589	-0.21
1441674_at	---	---	1.08	0.784	-1.49	0.553	-1.05	0.876	1.42	0.42	-0.01
1449707_at	Nr5a2	nuclear receptor subfamily 5, group A, member 2	1.2	0.839	-1.17	0.523	-1.54	0.165	1.75	0.044	0.06
1452814_at	Cpne3	copine III	1.08	0.664	-1.13	0.551	-1.36	0.221	1.38	0.232	-0.01
1431276_at	9130019P16Rik	RIKEN cDNA 9130019P16 gene	-1.21	0.745	1.13	0.756	-1.34	0.492	1.68	0.184	0.07
1435324_x_at	Hmgb1	high mobility group box 1	1.05	0.154	-1.18	0.315	-1.24	0.353	1.06	0.414	-0.08
1434824_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	-1.2	0.096	-1.17	0.022	1.02	0.837	1.21	0.041	-0.04
1422918_at	1810009J06Rik	RIKEN cDNA 1810009J06 gene	-1.46	0.476	1.13	0.599	-1.12	0.602	1.11	0.711	-0.09
1455626_at	Hoxa9	homeo box A9	-1.44	0.047	1.17	0.64	-1.19	0.685	2.34	0.251	0.22
1441213_at	---	---	-1.23	0.34	-1.21	0.582	1.07	0.877	1.35	0.672	-0.01

1453188_at	6230424C14Rik	RIKEN cDNA 6230424C14 gene	1.11	0.664	1.03	0.811	-1.77	0	-1.28	0.33	-0.23
1456070_at	5430405N12Rik	RIKEN cDNA 5430405N12 gene	1.07	0.793	1.07	0.808	-1.77	0.068	-1.37	0.308	-0.25
1417826_at	Akr1e1	aldo-keto reductase family 1, member E1	-1.2	0.195	-1.17	0.207	1.02	0.884	1.03	0.864	-0.08
1446692_at	Nufip2	Nuclear fragile X mental retardation protein interacting protein 2	1.05	0.874	1.16	0.455	-2.05	0.01	-1.53	0.202	-0.34
1419298_at	Pon3	paraoxonase 3	-1.29	0.481	1.01	0.93	-1.09	0.555	1.71	0.191	0.09
1443854_at	---	---	1.07	0.357	1.06	0.877	-1.76	0.388	-1.11	0.753	-0.18
1441191_at	2810454H06Rik	RIKEN cDNA 2810454H06 gene	-1.76	0.43	1.19	0.521	-1.05	0.83	1.09	0.747	-0.13
1455296_at	Adcy5	adenylate cyclase 5	-1.25	0.209	-1.44	0.093	1.21	0.245	1.15	0.406	-0.08
1417065_at	Egr1	early growth response 1	-1.67	0.174	1.07	0.85	1.03	0.95	-1.56	0.138	-0.28
1451429_at	Gfod2	glucose-fructose oxidoreductase domain containing 2	-1.55	0.041	-1.16	0.53	1.2	0.051	1.07	0.624	-0.11
1451890_at	Kif13a	kinesin family member 13A	-1.25	0.334	-1.36	0.025	1.17	0.67	1.26	0.52	-0.05
1438543_at	Spata13	Spermatogenesis associated 13	-1.09	0.732	1	0.999	-1.27	0.188	2.09	0.176	0.18
1447246_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430092C	-1.34	0.04	-1.35	0.377	1.21	0.226	1.09	0.772	-0.09
1424556_at	Pycr1	pyrroline-5-carboxylate reductase 1	-1.08	0.704	-1.52	0.115	1.13	0.616	1.96	0.064	0.12
1426337_a_at	Tead4	TEA domain family member 4	-1.86	0.61	-1.05	0.931	1.22	0.504	1.33	0.579	-0.09
1429762_a_at	Bbs5	Bardet-Biedl syndrome 5 (human)	1.02	0.931	-1.11	0.667	-1.28	0.235	2.21	0.046	0.21
1455528_at	---	Transcribed locus, weakly similar to NP_665733.1 Lipogenin [Rattus norvegicus]	-1.31	0.385	-1.39	0.19	1.23	0.205	2.21	0.245	0.18
1443880_at	Zbtb39	zinc finger and BTB domain containing 39	-1.43	0.172	-1.07	0.763	1.08	0.749	1.09	0.735	-0.08
1432877_at	4930544N03Rik	RIKEN cDNA 4930544N03 gene	-1.18	0.454	1.12	0.689	-1.34	0.121	1.18	0.757	-0.06
1436666_at	Flot2	Flotillin 2	-1.14	0.789	1.04	0.922	-1.26	0.321	1.03	0.909	-0.08
1440600_at	4930407I10Rik	RIKEN cDNA 4930407I10 gene	-1.04	0.936	-1.39	0.617	1.03	0.878	2.21	0.05	0.2
1439971_at	6330439K17Rik	RIKEN cDNA 6330439K17 gene	-1.08	0.796	-2.22	0.156	1.33	0.341	1.27	0.241	-0.17
1429354_at	Them5	thioesterase superfamily member 5	-1.25	0.493	-1.15	0.72	1.03	0.853	1.25	0.578	-0.03
1431073_at	Ptar1	protein prenyltransferase alpha subunit repeat containing 1	-1.22	0.321	-1.24	0.146	1.08	0.698	1.35	0.475	-0.01
1448098_at	AA517545	expressed sequence AA517545	1.4	0.745	-1.51	0.508	-1.55	0.252	1.94	0.244	0.07
1426877_a_at	Pb1	polybromo 1	-1.17	0.06	1.01	0.96	-1.18	0.05	1.13	0.598	-0.05
1427210_at	Baz2a	bromodomain adjacent to zinc finger domain, 2A	1.23	0.757	-1.53	0.203	-1.22	0.707	1.46	0.246	-0.01
1443923_at	Akap13	A kinase (PRKA) anchor protein 13	1.25	0.128	-1.52	0.309	-1.26	0.579	1.65	0.204	0.03
1433201_at	2310079F09Rik	RIKEN cDNA 2310079F09 gene	-2.52	0.1	-1.08	0.918	1.39	0.623	1.01	0.986	-0.3
1443281_at	C130076O07Rik	RIKEN cDNA C130076O07 gene	-1.41	0.536	1.07	0.829	-1.07	0.876	1.26	0.6	-0.04
1441928_x_at	Ell	elongation factor RNA polymerase II	-1.83	0.047	-1	0.998	1.16	0.479	1.2	0.425	-0.12
1416854_at	Slc34a2	solute carrier family 34 (sodium phosphate), member 2	-1.16	0.412	1.08	0.793	-1.32	0.049	1.46	0.555	0.02
1451411_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	1.33	0.317	-2.01	0.128	-1.14	0.59	1.73	0.109	-0.02
1459525_at	Cbara1	Calcium binding atopy-related autoantigen 1	-1.24	0.415	1.06	0.858	-1.18	0.409	1.65	0.126	0.07
1437068_at	Solt	SoxLZ/Sox6 leucine zipper binding protein in testis	1.21	0.196	-1.14	0.682	-1.61	0.09	4.53	0.234	0.75
1439918_at	Odf2	outer dense fiber of sperm tails 2	-1.05	0.925	1	0.983	-1.34	0.005	1.08	0.733	-0.07
1431958_at	Spag16	sperm associated antigen 16	1.11	0.816	-2.25	0.068	1.15	0.297	-1.49	0.401	-0.37
1439527_at	BB114106	Expressed sequence BB114106	-1.13	0.684	1.05	0.789	-1.29	0.441	1.32	0.234	-0.01
1449287_at	Srms	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylat	-1.74	0.103	1.06	0.613	1.07	0.712	-2.17	0.089	-0.44
1441395_at	---	---	-2.01	0.113	-1.17	0.758	1.35	0.381	1.37	0.62	-0.11
1416636_at	Rheb	RAS-homolog enriched in brain	-1.21	0.001	-1.16	0.018	1.02	0.895	1.21	0.284	-0.04
1456631_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	-1.1	0.75	-1.48	0.203	1.12	0.524	1.48	0.606	0.01
1418487_at	Ripk4	receptor-interacting serine-threonine kinase 4	-1.25	0.702	-1.14	0.753	1.03	0.856	1.21	0.716	-0.04
1431347_at	5730407M17Rik	RIKEN cDNA 5730407M17 gene	1.16	0.587	-1.28	0.304	-1.3	0.073	1.07	0.805	-0.09
1436642_x_at	Mef2d	Myocyte enhancer factor 2D	-1.74	0.151	1.02	0.981	1.12	0.747	-1.25	0.533	-0.21
1460345_at	2610208M17Rik	RIKEN cDNA 2610208M17 gene	1.04	0.809	1.01	0.971	-1.5	0.015	-1.23	0.186	-0.17
1438128_at	Gnat2	Guanine nucleotide binding protein, alpha transducing 2	1.07	0.719	-1.13	0.694	-1.33	0.486	1.24	0.632	-0.04
1447258_at	Myst4	MYST histone acetyltransferase monocytic leukemia 4	1.03	0.84	1.33	0.271	-2.82	0.012	-1	0.995	-0.37
1433033_at	2310007H11Rik	RIKEN cDNA 2310007H11 gene	1.08	0.553	-1.01	0.888	-1.55	0.312	1.62	0.324	0.03
1427462_at	E2f3	E2F transcription factor 3	-1.29	0.095	-1.44	0.371	1.24	0.449	1.08	0.514	-0.1
1432097_a_at	Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	-1.37	0.488	-1.26	0.581	1.19	0.493	1.74	0.488	0.07
1445467_at	---	Transcribed locus	-1.33	0.238	1.28	0.717	-1.47	0.401	1.02	0.974	-0.13
1423884_at	Cirh1a	cirrhosis, autosomal recessive 1A (human)	1.03	0.846	-1.22	0.071	-1.16	0.268	1.02	0.881	-0.08

1441906_x_at	Syap1	Synapse associated protein 1	-1.19	0.213	-1.19	0.2	1.03	0.696	1.09	0.5	-0.07
1444570_at	Cfdp1	Craniofacial development protein 1	1.1	0.585	1.13	0.684	-2.09	0.033	-1.38	0.379	-0.31
1452118_at	2600005C20Rik	RIKEN cDNA 2600005C20 gene	-1.24	0.184	-1.22	0.318	1.09	0.424	1.18	0.195	-0.05
1433142_at	4921504P05Rik	RIKEN cDNA 4921504P05 gene	-2.86	0.216	1.33	0.018	1.03	0.883	-1.1	0.632	-0.4
1459292_at	Map2k6	Mitogen activated protein kinase kinase 6	-2.23	0.19	1.08	0.879	1.18	0.638	-1.43	0.302	-0.35
1450689_at	Prss3 /// Prss1 /// L	protease, serine, 3 /// protease, serine, 1 (trypsin 1) /// trypsinogen 10 /// trypsinoc	-1.92	0.207	1.08	0.754	1.1	0.651	-2.87	0.084	-0.65
1447728_x_at	Hspa9a	heat shock protein 9A	-1.21	0.596	1.03	0.909	-1.17	0.42	1.23	0.357	-0.03
1449060_at	Kif2c /// LOC63165	kinesin family member 2C /// similar to Kinesin-like protein KIF2C (Mitotic centron	-1.41	0.105	-1.28	0.576	1.22	0.572	2.66	0.17	0.3
1456520_at	9530033F24Rik	RIKEN cDNA 9530033F24 gene	-1.2	0.231	-1.25	0.606	1.07	0.456	1.04	0.844	-0.08
1434689_at	Zfp637	zinc finger protein 637	-1.23	0.328	-1.13	0.095	1.01	0.885	1.02	0.902	-0.08
1459720_x_at	---	---	-1.21	0.54	1.05	0.786	-1.2	0.324	1.27	0.427	-0.02
1442478_at	---	---	-2.84	0.228	-1.12	0.885	1.46	0.512	1.07	0.796	-0.36
1426364_at	Mrrf	mitochondrial ribosome recycling factor	-1.32	0.133	-1.14	0.305	1.08	0.282	1	0.984	-0.09
1426525_at	Arid2	AT rich interactive domain 2 (Arid-rfx like)	1.03	0.864	-1.12	0.078	-1.27	0.122	1.04	0.764	-0.08
1447206_at	Arhgap21	Rho GTPase activating protein 21	1.37	0.398	-1.82	0.105	-1.26	0.298	1.48	0.482	-0.06
1460061_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643053	-1.51	0.215	1.13	0.436	-1.1	0.53	1.02	0.899	-0.11
1446613_at	1190005F20Rik	RIKEN cDNA 1190005F20 gene	-1.35	0.219	-1.07	0.767	1.04	0.911	1.08	0.802	-0.08
1423676_at	Atp5h	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	-1.26	0.015	-1.1	0.017	1.01	0.877	1.01	0.888	-0.08
1428813_a_at	Drd1ip	dopamine receptor D1 interacting protein	-1.48	0.179	-1.35	0.353	1.29	0.306	1.59	0.103	0.01
1447969_at	Mcmdc1	minichromosome maintenance deficient domain containing 1	1.09	0.539	-1.11	0.717	-1.39	0.345	1.8	0.439	0.1
1434850_at	Iqgap3	IQ motif containing GTPase activating protein 3	-2.13	0.064	1.4	0.373	-1.19	0.105	2.67	0.198	0.19
1454249_at	D530049N12Rik	RIKEN cDNA D530049N12 gene	1.3	0.396	-1.37	0.681	-1.46	0.521	2.07	0.224	0.13
1446404_at	---	---	1.21	0.607	-1.63	0.402	-1.12	0.856	1.48	0.031	-0.02
1455226_at	Spnb1	spectrin beta 1	-1.61	0.432	-1.12	0.648	1.2	0.582	1.27	0.562	-0.07
1442674_at	Fbxw4	F-box and WD-40 domain protein 4	1.04	0.866	-1.27	0.152	-1.13	0.463	1.06	0.792	-0.08
1416829_at	Atp5b	ATP synthase, H+ transporting mitochondrial F1 complex, beta subunit	-1.2	0.121	-1.22	0.201	1.06	0.384	1.13	0.383	-0.06
1416742_at	Cfdp1	craniofacial development protein 1	1.04	0.674	-1.09	0.497	-1.32	0.076	1.05	0.511	-0.08
1431004_at	Loxl2	lysyl oxidase-like 2	-1.23	0.626	-1.49	0.127	1.22	0.697	1.05	0.81	-0.11
1451509_at	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.09	0.204	-1.27	0.052	1	0.973	1.35	0.331	0
1445590_at	---	Transcribed locus	-1.1	0.834	-1.3	0.274	1.03	0.935	1.01	0.965	-0.09
1415763_a_at	---	---	1.03	0.801	-1.08	0.309	-1.31	0.044	1.01	0.913	-0.09
1417563_at	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	-1.56	0.347	1.31	0.486	-1.31	0.127	1.01	0.963	-0.14
1444099_at	---	PREDICTED: Mus musculus similar to apolipoprotein L, 3 (predicted), transcript v	-1.43	0.568	-1.02	0.877	1.04	0.934	1.06	0.899	-0.09
1422774_at	1700088E04Rik	RIKEN cDNA 1700088E04 gene	-1.14	0.516	-1.25	0.421	1.03	0.917	1.71	0.578	0.09
1454503_at	9030201C23Rik	RIKEN cDNA 9030201C23 gene	1.04	0.901	-1.42	0.559	-1.03	0.915	1.01	0.987	-0.1
1446803_at	Dock9	Dedicator of cytokinesis 9	1.08	0.708	1.06	0.887	-1.76	0.083	-1.38	0.146	-0.25
1422704_at	Gyk	glycerol kinase	1.05	0.75	-1.34	0.051	-1.09	0.671	1.29	0.487	-0.02
1418458_at	Anapc7	anaphase promoting complex subunit 7	-1.11	0.09	-1.24	0.143	1.01	0.944	1.04	0.506	-0.08
1424124_at	Mospd2	motile sperm domain containing 2	-1.17	0.177	1.03	0.304	-1.21	0.062	1.14	0.508	-0.05
1440668_at	Adamtsl3	ADAMTS-like 3	-1.69	0.2	1.42	0.228	-1.43	0.006	2.1	0.15	0.1
1454507_at	8430432A02Rik	RIKEN cDNA 8430432A02 gene	-1.21	0.731	1.01	0.984	-1.13	0.856	1.78	0.283	0.11
1447451_at	4930556M19Rik	RIKEN cDNA 4930556M19 gene	-1.25	0.566	1.24	0.249	-1.48	0.148	2.59	0	0.28
1426106_a_at	Syt6	synaptotagmin VI	-1.85	0.444	1.37	0.471	-1.24	0.467	1.36	0.322	-0.09
1418929_at	Ift57	intraflagellar transport 57 homolog (Chlamydomonas)	-1.12	0.348	-1.36	0.239	1.09	0.57	1.43	0.331	0.01
1454003_at	Afg3l2	AFG3(ATPase family gene 3)-like 2 (yeast)	-1.38	0.112	-1.22	0.596	1.17	0.513	1.12	0.757	-0.08
1448945_at	Pllp	plasma membrane proteolipid	-1.05	0.89	-1.4	0.006	1.04	0.875	1.26	0.666	-0.04
1450416_at	Cbx5	chromobox homolog 5 (Drosophila HP1a)	1	0.985	-1.12	0.521	-1.22	0.428	2.4	0.195	0.27
1444626_at	D930001B02	hypothetical protein D930001B02	1.03	0.95	-1.32	0.209	-1.07	0.504	1.05	0.875	-0.08
1427104_at	Zfp612	zinc finger protein 612	1.06	0.774	-1.24	0.372	-1.17	0.391	1.17	0.588	-0.05
1447723_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	1.04	0.95	-1.21	0.545	-1.18	0.417	1.1	0.865	-0.06
1452735_at	Pcnp	PEST proteolytic signal containing nuclear protein	1.08	0.494	-1.1	0.129	-1.37	0.023	1.16	0.387	-0.06
1445629_at	Slc35d1	Solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual tr	1.03	0.916	1.05	0.775	-1.57	0.012	-1.04	0.361	-0.13
1452000_s_at	Sars	seryl-aminoacyl-tRNA synthetase	1.04	0.417	-1.21	0.015	-1.17	0.072	1.07	0.668	-0.07

1437684_at	BC025546	CDNA sequence BC025546	-1.13	0.834	-1.51	0.511	1.17	0.662	1.42	0.344	-0.01
1447776_x_at	Rab6	RAB6, member RAS oncogene family	-1.34	0.208	1.17	0.338	-1.25	0.124	1.34	0.27	-0.02
1430621_at	Mmrn1	multimerin 1	-1.41	0.645	1.22	0.736	-1.28	0.728	1.34	0.453	-0.03
1456927_at	Mast2	microtubule associated serine/threonine kinase 2	-1.11	0.525	1.2	0.734	-1.63	0.035	1.26	0.274	-0.07
1418087_at	Ufd1l	ubiquitin fusion degradation 1 like	1.04	0.664	-1.21	0.014	-1.18	0.006	1.13	0.543	-0.05
1431811_a_at	Fbxo34	F-box only protein 34	-1.39	0.033	-1.01	0.95	1	0.988	2.56	0.153	0.29
1439339_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630050	-1.39	0.554	-1.16	0.821	1.13	0.751	1.4	0.379	0
1450509_at	Chst11	carbohydrate sulfotransferase 11	-1.53	0.419	-1.93	0.463	1.55	0.196	1.35	0.032	-0.14
1443974_at	Plcl1	phospholipase C-like 1	-1.99	0.156	1.37	0.48	-1.19	0.73	1.46	0.423	-0.09
1431312_at	5730577I03Rik	RIKEN cDNA 5730577I03 gene	-1.94	0.09	-1.4	0.426	1.49	0.615	1.19	0.732	-0.17
1459015_at	Kcnh8	Potassium voltage-gated channel, subfamily H (eag-related), member 8	-2.94	0.197	-1.45	0.504	1.69	0.23	1	0.994	-0.43
1438774_s_at	Pgm2l1	phosphoglucomutase 2-like 1	-1.83	0.134	-1.18	0.644	1.33	0.07	1.69	0.203	0
1449214_a_at	Opa1	optic atrophy 1 homolog (human)	-1.11	0.319	-1.4	0.04	1.1	0.697	1.48	0.256	0.02
1417170_at	Lztfl1	leucine zipper transcription factor-like 1	-1.27	0.132	-1.14	0.257	1.06	0.746	1.1	0.545	-0.06
1427394_at	Igf2as	insulin-like growth factor 2, antisense	-1.33	0.681	-1.08	0.791	1.04	0.94	1.23	0.628	-0.04
1428832_at	1600002H07Rik	RIKEN cDNA 1600002H07 gene	1.04	0.931	-1.44	0.049	-1.02	0.872	2.18	0.168	0.19
1418469_at	Nrip1	nuclear receptor interacting protein 1	1.06	0.9	-1.18	0.496	-1.24	0.444	1.32	0.586	-0.01
1438481_at	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	1.02	0.772	-1.3	0.178	-1.08	0.575	1.43	0.253	0.02
1445573_at	Ppp1r14b	Protein phosphatase 1, regulatory (inhibitor) subunit 14B	1.18	0.747	1.02	0.951	-1.94	0.022	-1.02	0.909	-0.19
1440255_at	Mizf	MBD2-interacting zinc finger	-1.43	0.199	-1.33	0.288	1.26	0.241	1.16	0.445	-0.08
1445291_at	Arsa	arylsulfatase A	-1.76	0.304	1.15	0.78	1	0.996	-1.25	0.313	-0.22
1434765_at	Ep300	E1A binding protein p300	-1.03	0.644	-1.42	0.017	1.04	0.756	1.02	0.872	-0.1
1436186_at	E2f8	E2F transcription factor 8	-1.31	0.709	-2.43	0.055	1.55	0.215	6.94	0.137	1.19
1434354_at	Maob	monoamine oxidase B	1.09	0.756	-1.33	0.032	-1.14	0.33	1.12	0.68	-0.07
1445981_at	---	---	-1.1	0.862	1.05	0.911	-1.31	0.633	1.58	0.32	0.05
1449977_at	Egr4	early growth response 4	-1	0.99	-2.44	0.29	1.31	0.575	1.02	0.957	-0.28
1429111_at	Tln2 /// LOC639214	talin 2 /// similar to talin 2	1.05	0.663	-1.28	0.194	-1.12	0.401	2.23	0.027	0.22
1447478_at	Ran	RAN, member RAS oncogene family	-1.36	0.649	-1.78	0.025	1.42	0.473	1.01	0.986	-0.18
1455142_at	Socs4	suppressor of cytokine signaling 4	-1.11	0.312	1.01	0.968	-1.23	0.061	1.24	0.342	-0.02
1431493_at	9530046B11Rik	RIKEN cDNA 9530046B11 gene	-1.63	0.13	-1.17	0.364	1.25	0.539	1.1	0.789	-0.11
1425677_a_at	Ank1	ankyrin 1, erythroid	-1.48	0.236	-2.12	0.012	1.57	0.179	9.21	0.156	1.8
1422483_a_at	Cycs /// LOC67219	cytochrome c, somatic /// similar to Cytochrome c, somatic	-1.27	0.123	-1.25	0.031	1.13	0.1	1.2	0.352	-0.05
1454295_at	Nrip1	nuclear receptor interacting protein 1	1.23	0.295	1.02	0.9	-2.12	0.128	-1.03	0.951	-0.22
1442503_at	---	---	-1.4	0.565	-2.12	0.284	1.54	0.08	1.2	0.693	-0.2
1459284_at	---	Transcribed locus	1.02	0.943	-1.54	0.523	1.05	0.772	-1.42	0.159	-0.22
1458282_at	---	---	1.13	0.407	-1.01	0.94	-1.67	0.129	1.1	0.741	-0.11
1427361_at	Hoxc6	homeo box C6	-1.51	0.237	1.03	0.862	1.03	0.912	-1.04	0.9	-0.12
1428343_at	Rcor3	REST corepressor 3	-1.03	0.742	-1.4	0.234	1.03	0.858	1.22	0.252	-0.04
1454500_at	6330419E04Rik	RIKEN cDNA 6330419E04 gene	-1.67	0.474	-1.64	0.193	1.51	0.088	1.91	0.314	0.03
1435248_a_at	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homol	1	0.993	-1.09	0.36	-1.24	0.055	1.09	0.505	-0.06
1445577_at	Ppfibp1	PTPRF interacting protein, binding protein 1 (liprin beta 1)	1.53	0.334	-1.98	0.016	-1.45	0.263	1.68	0.265	-0.06
1418716_at	Mrps25	mitochondrial ribosomal protein S25	-1	0.982	-1.73	0.129	1.14	0.31	1	0.996	-0.15
1434582_at	D14Ertd171e	DNA segment, Chr 14, ERATO Doi 171, expressed	1.06	0.819	-1.11	0.769	-1.32	0.45	1.08	0.912	-0.07
1420531_at	Hsd3b5	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 5	-1.11	0.659	-28.86	0.128	1.78	0.36	1.94	0.371	-6.56
1450336_at	Nsccn1	non-selective cation channel 1	1.13	0.134	-1.09	0.766	-1.48	0.166	1.02	0.881	-0.11
1433200_at	B230114A03Rik	RIKEN cDNA B230114A03 gene	-1.07	0.764	1.21	0.753	-1.74	0.091	1.99	0.38	0.1
1425394_at	BC023105	cDNA sequence BC023105	-1.06	0.657	1.12	0.367	-1.52	0.435	1.1	0.692	-0.09
1427340_at	Rgs6	regulator of G-protein signaling 6	1.11	0.897	-1.23	0.5	-1.25	0.626	1.06	0.867	-0.08
1445303_at	---	---	-1.02	0.977	-1.59	0.393	1.11	0.773	1.04	0.94	-0.11
1431597_a_at	Nrip3	nuclear receptor interacting protein 3	1.22	0.214	-1.6	0.394	-1.14	0.453	2.39	0.393	0.22
1460703_at	Ascc1	activating signal cointegrator 1 complex subunit 1	-1.21	0.395	-1.17	0.291	1.04	0.859	1.01	0.756	-0.08
1449992_at	Prss29	protease, serine, 29	1.23	0.503	-1.09	0.852	-1.72	0.468	1.71	0.422	0.03
1419373_at	Atp6v1b1	ATPase, H+ transporting, lysosomal V1 subunit B1	-3.79	0.284	-1.15	0.758	1.59	0.448	3.78	0.011	0.11

1450380_at	Epdr2	ependymin related protein 2 (zebrafish)	-1.4	0.241	-1.02	0.949	1.02	0.894	4.48	0.175	0.77
1449950_at	5830415L20Rik	RIKEN cDNA 5830415L20 gene	-1.07	0.832	-1.28	0.46	1.01	0.977	1.25	0.547	-0.02
1459794_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	1.03	0.963	1.16	0.836	-1.87	0.038	-1.2	0.65	-0.22
1439152_at	Mthfsd	methenyltetrahydrofolate synthetase domain containing	-1.22	0.233	-1.13	0.625	1.02	0.899	1.08	0.619	-0.06
1433821_at	1110012D08Rik	RIKEN cDNA 1110012D08 gene	-1.42	0.061	-1.07	0.61	1.08	0.745	1.04	0.549	-0.09
1441430_at	---	Transcribed locus	-1.13	0.755	-2.18	0.027	1.38	0.514	1.55	0.355	-0.1
1447862_x_at	Thbs2	thrombospondin 2	-1.04	0.909	-1.36	0.216	1.03	0.816	1.19	0.416	-0.05
1454628_at	A930037G23Rik	RIKEN cDNA A930037G23 gene	-1.09	0.51	-1.44	0.252	1.11	0.57	1.06	0.851	-0.09
1441833_at	Ngly1	N-glycanase 1	-1.14	0.643	-1.58	0.161	1.21	0.181	1.27	0.451	-0.06
1442783_x_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630030	-1.73	0.339	1.1	0.801	1.04	0.807	-1.31	0.116	-0.22
1457147_at	BC026657	cDNA sequence BC026657	-1.29	0.348	1.23	0.604	-1.39	0.164	1.08	0.625	-0.09
1426569_a_at	Frk	fyn-related kinase	-1.28	0.312	1.13	0.564	-1.23	0.303	1.26	0.728	-0.03
1430542_a_at	Slc25a5 /// LOC433	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.17	0.054	-1.28	0.073	1.09	0.367	1.08	0.523	-0.07
1454307_at	1810058N15Rik	RIKEN cDNA 1810058N15 gene	-2.58	0.032	-1.12	0.757	1.44	0.388	1.31	0.716	-0.24
1428842_a_at	Ngfrap1	nerve growth factor receptor (TNFRSF16) associated protein 1	-1.14	0.383	1.04	0.841	-1.24	0.087	1.55	0.195	0.05
1446211_at	Erbb4	V-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	-3.33	0.044	-1.78	0.228	1.86	0.216	1.31	0.39	-0.48
1436405_at	Dock4	dedicator of cytokinesis 4	-1.13	0.562	1.05	0.741	-1.27	0.092	1.06	0.799	-0.07
1443238_at	Phf14	PHD finger protein 14	1.01	0.949	1.19	0.721	-1.9	0.035	-1.33	0.193	-0.26
1440077_at	6330549D23Rik	RIKEN cDNA 6330549D23 gene	-1.16	0.014	1.23	0.621	-1.57	0.141	1.2	0.475	-0.08
1445506_at	1300007F04Rik	RIKEN cDNA 1300007F04 gene	-1.53	0.04	-1.11	0.724	1.17	0.545	1.44	0.39	-0.01
1423123_at	Rad54l	RAD54 like (S. cerevisiae)	-1.08	0.922	-1.29	0.462	1.02	0.952	2.68	0.246	0.33
1443164_at	Vps13d	Vacuolar protein sorting 13D (yeast)	-1.14	0.034	1.11	0.768	-1.36	0.212	1.32	0.128	-0.02
1429876_at	Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	-1.13	0.063	-1.42	0.097	1.14	0.323	1.19	0.104	-0.06
1421259_at	Pklr	pyruvate kinase liver and red blood cell	1.05	0.961	-1.45	0.577	-1.02	0.927	2.39	0.422	0.24
1442838_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930532C19 pr	1.14	0.724	-1.19	0.64	-1.33	0.224	1.22	0.671	-0.04
1431582_at	Itgb4bp	integrin beta 4 binding protein	1.03	0.946	-1.4	0.618	-1.02	0.941	1.05	0.847	-0.09
1439180_at	A430093A21Rik	RIKEN cDNA A430093A21 gene	1.14	0.711	-1.17	0.257	-1.35	0.42	1.18	0.279	-0.05
1441858_at	Uck2	Uridine-cytidine kinase 2	1.01	0.971	-1.24	0.602	-1.1	0.631	1.62	0.137	0.07
1435683_a_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.08	0.798	-1.27	0.147	1.01	0.95	1.14	0.692	-0.05
1419811_at	D16Wsu65e	DNA segment, Chr 16, Wayne State University 65, expressed	1.06	0.449	-1.2	0.279	-1.2	0.204	1.15	0.526	-0.05
1435021_at	Gabrb3	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 3	-1.37	0.091	1.5	0.189	-2.02	0.202	1.8	0.207	-0.02
1433334_at	1700024P12Rik	RIKEN cDNA 1700024P12 gene	-3.35	0.331	1.09	0.883	1.34	0.489	-1.02	0.983	-0.49
1436142_at	3526401B18Rik	RIKEN cDNA 3526401B18 gene	-1.09	0.851	1.15	0.68	-1.53	0.058	1.07	0.624	-0.1
1449248_at	Clcn2	chloride channel 2	1.06	0.765	-1.12	0.511	-1.28	0.633	10.44	0.181	2.27
1436159_at	Usp32	ubiquitin specific peptidase 32	-1.2	0.35	1.01	0.934	-1.13	0.132	2.58	0.169	0.31
1438847_at	Mxd3	Max dimerization protein 3	1.12	0.595	-1.31	0.337	-1.19	0.432	1.94	0.18	0.14
1423935_x_at	Krt14	keratin 14	-2.1	0.225	1.39	0.561	-1.16	0.472	1.4	0.328	-0.12
1427036_a_at	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	-1.16	0.564	1.03	0.747	-1.21	0.539	1.15	0.277	-0.05
1443198_at	---	1 cell embryo 1 cell cDNA, RIKEN full-length enriched library, clone:I0C0049K08	-1.43	0.01	-2.29	0.13	1.59	0.086	1.1	0.538	-0.26
1417531_at	Cyp2j5	cytochrome P450, family 2, subfamily j, polypeptide 5	-1.21	0.139	-1.19	0.003	1.06	0.571	1.2	0.275	-0.03
1428839_at	Wdr53	WD repeat domain 53	1.06	0.915	-1.39	0.154	-1.05	0.744	1.27	0.576	-0.03
1438803_s_at	Snx16	sorting nexin 16	1.22	0.456	-1.27	0.212	-1.39	0.048	1.07	0.707	-0.09
1456710_at	Pcdhb11	Protocadherin beta 11	-1.32	0.577	1.08	0.913	-1.13	0.76	2.02	0.15	0.16
1428703_at	1700012B07Rik	RIKEN cDNA 1700012B07 gene	-1.08	0.632	-1.43	0.331	1.1	0.472	1.33	0.472	-0.02
1456566_x_at	Rbm14	RNA binding motif protein 14	-1.17	0.308	-1.19	0.148	1.03	0.886	1.07	0.748	-0.06
1432847_at	2810457G06Rik	RIKEN cDNA 2810457G06 gene	1.72	0.074	-2.14	0.388	-1.85	0.026	1.77	0.097	-0.12
1453914_at	Hspb1	heat shock protein 1	-1.91	0.248	1.28	0.369	-1.08	0.859	1.02	0.98	-0.17
1456134_x_at	Yif1a	Yip1 interacting factor homolog A (S. cerevisiae)	-1.16	0.448	-1.25	0.107	1.07	0.706	1.23	0.241	-0.03
1449259_at	Rab3d	RAB3D, member RAS oncogene family	-1.31	0.374	-1.19	0.38	1.12	0.274	1.35	0.08	-0.01
1440277_at	AU041474	expressed sequence AU041474	-1.4	0.046	1.22	0.287	-1.26	0.45	1	0.991	-0.11
1456588_x_at	Cox5b	cytochrome c oxidase, subunit Vb	-1.09	0.27	-1.25	0.259	1.01	0.925	1.15	0.133	-0.04
1419035_s_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	1.18	0.528	-1.36	0.043	-1.24	0.32	1.11	0.653	-0.08
1421767_at	Adk	Adenosine kinase	-1.5	0.219	1.15	0.211	-1.1	0.787	1.18	0.719	-0.07

1423988_at	Ak1	adenylate kinase 1	-1.31	0.335	1.16	0.772	-1.24	0.213	1.89	0.459	0.13
1441086_at	4930451I11Rik	RIKEN cDNA 4930451I11 gene	1.05	0.945	1.15	0.803	-1.9	0.096	-1.55	0.228	-0.31
1456020_at	Sh3tc2	SH3 domain and tetratricopeptide repeats 2	1.08	0.47	-1.39	0.395	-1.08	0.88	13.79	0.124	3.1
1448386_a_at	Wap	whey acidic protein	1.23	0.162	-1.31	0.64	-1.36	0.15	1.28	0.68	-0.04
1429559_at	Gnaq	guanine nucleotide binding protein, alpha q polypeptide	1.02	0.868	-1.07	0.607	-1.29	0.323	1.16	0.489	-0.04
1417919_at	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	-1.15	0.111	-1.2	0.013	1.02	0.865	1.46	0.254	0.03
1437444_at	Pcdhgc3	protocadherin gamma subfamily C, 3	-1.15	0.886	1.31	0.474	-1.82	0.209	1.01	0.97	-0.16
1449848_at	Gna14	guanine nucleotide binding protein, alpha 14	-1.07	0.325	1.01	0.964	-1.28	0.284	1.38	0.317	0.01
1430194_at	1110018H23Rik	RIKEN cDNA 1110018H23 gene	1.11	0.621	-1.52	0.284	-1.04	0.948	1.15	0.719	-0.07
1436657_at	LOC629972	hypothetical protein LOC629972	-1.22	0.413	1.28	0.115	-1.59	0.146	1.29	0.454	-0.06
1430524_at	1700020N15Rik ///	RIKEN cDNA 1700020N15 gene /// hypothetical LOC627927	-1.42	0.377	-1.74	0.274	1.45	0.376	1.57	0.385	-0.04
1432515_at	2410124H12Rik	RIKEN cDNA 2410124H12 gene	-1.11	0.828	-1.32	0.617	1.07	0.878	1.36	0.592	0
1427003_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	-1.21	0.247	1.04	0.691	-1.17	0.218	1.04	0.873	-0.07
1439277_at	Frs3	fibroblast growth factor receptor substrate 3	-1.66	0.065	-1.36	0.642	1.39	0.31	1.46	0.387	-0.04
1447173_at	---	PREDICTED: Mus musculus hypothetical protein LOC624743 (LOC624743), mR	1.08	0.559	-2.18	0.216	1.19	0.619	-2.45	0.286	-0.59
1459857_at	Usp32	ubiquitin specific peptidase 32	1.01	0.971	-1.02	0.88	-1.35	0.232	1.9	0.259	0.14
1443132_at	LOC544809	hypothetical protein LOC544809	-1.29	0.474	1	0.999	-1.05	0.79	1.12	0.604	-0.05
1448370_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	-1.15	0.419	-1.19	0.48	1.01	0.948	2.14	0.115	0.21
1456262_at	Rbm5	RNA binding motif protein 5	1.35	0.456	-1.26	0.365	-1.69	0.207	1.13	0.441	-0.12
1441711_at	Unc45b	unc-45 homolog B (C. elegans)	1.18	0.368	-2.17	0.324	1.09	0.715	-1.32	0.278	-0.3
1437553_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	-1.34	0.445	1.14	0.592	-1.19	0.166	1.41	0.319	0.01
1433415_at	5430432H19Rik	RIKEN cDNA 5430432H19 gene	1.21	0.585	-1.12	0.671	-1.58	0.573	1.01	0.843	-0.12
1428653_x_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	-1.3	0.608	-1.06	0.936	1.02	0.899	1.27	0.386	-0.02
1417942_at	Lypd3	Ly6/Plaur domain containing 3	-1.25	0.656	-1.54	0.233	1.28	0.482	1.13	0.86	-0.09
1432032_a_at	Artn	artemin	1.12	0.638	-1.06	0.928	-1.5	0.316	4.95	0.1	0.88
1453018_at	Nvl	nuclear VCP-like	-1.13	0.494	1.04	0.723	-1.25	0.225	1.09	0.622	-0.06
1447896_s_at	2010109N14Rik	RIKEN cDNA 2010109N14 gene	1.05	0.176	1.03	0.75	-1.54	0.022	-1.32	0.182	-0.19
1456724_x_at	Wdr79	WD repeat domain 79	1.16	0.184	-1.33	0.251	-1.23	0.443	1.17	0.535	-0.05
1416073_a_at	Nup85	nucleoporin 85	-1.14	0.527	-1.18	0.081	1	0.961	1.73	0.219	0.11
1453496_at	9430073N08Rik	RIKEN cDNA 9430073N08 gene	1.75	0.556	-1.44	0.58	-3.54	0.002	2.23	0.04	-0.25
1435447_at	Mip	major intrinsic protein of eye lens fiber	-1.46	0.38	-1.26	0.587	1.25	0.594	1.2	0.738	-0.07
1429883_at	Actl6a	actin-like 6A	1.07	0.661	1.04	0.671	-1.62	0.045	-1.18	0.264	-0.17
1447562_at	Foxf2	forkhead box F2	1.49	0.427	-3	0.141	-1.1	0.574	1.74	0.344	-0.22
1425467_a_at	Plp1	proteolipid protein (myelin) 1	-1.32	0.183	-1.05	0.807	1.02	0.957	1.1	0.627	-0.06
1418912_at	Plxdc2	plexin domain containing 2	-1.22	0.091	1.09	0.842	-1.22	0.406	1.1	0.465	-0.06
1419207_at	Zfp37	zinc finger protein 37	1.02	0.844	1.01	0.966	-1.43	0.119	-1.24	0.559	-0.16
1417024_at	Hars	histidyl-tRNA synthetase	-1.35	0.033	-1.01	0.837	1	0.919	2.03	0.193	0.17
1424479_at	Cst8	cystatin 8 (cystatin-related epididymal spermatogenic)	-1.55	0.316	1.22	0.408	-1.15	0.516	1.05	0.835	-0.11
1425772_at	Col4a4	procollagen, type IV, alpha 4	-1.08	0.798	1.27	0.393	-1.88	0.001	1.5	0.606	-0.05
1439378_at	BC048671	cDNA sequence BC048671	1.36	0.314	-1.69	0.204	-1.29	0.184	1.27	0.362	-0.09
1441768_at	9430051O21Rik	RIKEN cDNA 9430051O21 gene	1.01	0.703	-1.05	0.415	-1.3	0.466	1.12	0.62	-0.05
1437612_at	Nup62	Nucleoporin 62	-2.84	0.202	1.15	0.442	1.23	0.467	-1.85	0.163	-0.58
1427477_at	Tmprss13	transmembrane protease, serine 13	1.39	0.015	-2.31	0.271	-1.1	0.754	1.28	0.479	-0.19
1433156_at	Kcnip1	Kv channel-interacting protein 1	1.62	0.462	-1.56	0.505	-2.1	0.123	1.08	0.904	-0.24
1443283_at	C330002D13Rik	RIKEN cDNA C330002D13 gene	-2.74	0.429	1.16	0.748	1.21	0.014	-2.66	0.443	-0.76
1425097_a_at	Zfp106	zinc finger protein 106	-1.15	0.543	-1.35	0.486	1.12	0.526	1.16	0.466	-0.05
1440203_at	Pcgf3	Polycomb group ring finger 3	-1.07	0.823	-1.26	0.508	1.01	0.956	1.42	0.489	0.02
1433385_at	4933428C20Rik	RIKEN cDNA 4933428C20 gene	-1.12	0.876	-1.55	0.335	1.19	0.641	1.56	0.343	0.02
1430474_a_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	-1.2	0.207	-1.18	0.137	1.05	0.628	1.15	0.582	-0.04
1458388_at	Gm172	gene model 172, (NCBI)	-1.69	0.078	1.07	0.888	1.07	0.908	-1.49	0.132	-0.26
1428886_at	Rbbp5	retinoblastoma binding protein 5	1.05	0.57	-1.11	0.216	-1.27	0.184	1.26	0.255	-0.02
1422856_at	Slc12a3	solute carrier family 12, member 3	1.26	0.065	-2.94	0.169	1.13	0.578	-1.38	0.097	-0.48
1418022_at	Narg1	NMDA receptor-regulated gene 1	1.12	0.496	-1.23	0.206	-1.25	0.357	1.14	0.185	-0.05

1427333_s_at	Sfrs15 /// LOC6703	splicing factor, arginine/serine-rich 15 /// similar to splicing factor, arginine/serine-	-1.2	0.27	-1.2	0.352	1.06	0.656	1.01	0.955	-0.08
1442165_at	Armc9	armadillo repeat containing 9	-1.35	0.244	-1.18	0.722	1.14	0.34	1.33	0.212	-0.01
1434161_at	5830457H20Rik	RIKEN cDNA 5830457H20 gene	-1.05	0.714	1.09	0.406	-1.43	0.06	1.02	0.94	-0.1
1458295_at	BC038331	cDNA sequence BC038331	1.16	0.297	-1.43	0.118	-1.14	0.309	1.06	0.851	-0.09
1422319_at	Galnt11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.03	0.97	1.18	0.701	-1.71	0.318	1.38	0.361	-0.05
1424986_s_at	Fbxw7	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	1.04	0.835	-1.09	0.399	-1.28	0.262	1.25	0.101	-0.02
1459480_at	D6Ertd90e	DNA segment, Chr 6, ERATO Doi 90, expressed	1.02	0.945	-1.26	0.256	-1.09	0.668	1.03	0.871	-0.07
1452396_at	Sfrs15 /// LOC6703	splicing factor, arginine/serine-rich 15 /// similar to splicing factor, arginine/serine-	1.16	0.263	-1.76	0.171	1.01	0.979	-1.1	0.473	-0.17
1441767_at	Zfp142	zinc finger protein 142	1.28	0.575	-1.36	0.256	-1.39	0.019	1.32	0.346	-0.04
1417124_at	Dstn	destrin	1.02	0.77	-1.07	0.685	-1.27	0.014	1	0.982	-0.08
1447640_s_at	Pbx3	pre B-cell leukemia transcription factor 3	1.14	0.435	-1.23	0.498	-1.28	0.181	1.56	0.073	0.05
1452571_at	Tuba-rs1	tubulin alpha, related sequence 1	-1.14	0.567	-1.25	0.689	1.06	0.885	1.24	0.557	-0.02
1452238_at	Hrb	HIV-1 Rev binding protein	1.03	0.685	-1.04	0.735	-1.34	0.09	1.14	0.621	-0.05
1438652_x_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.2	0.011	-1.15	0.287	1.03	0.71	2.55	0.19	0.31
1438360_x_at	Slc25a5 /// LOC433	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.46	0.08	-1.04	0.784	1.09	0.587	1.04	0.782	-0.09
1436181_at	Ddef2	development and differentiation enhancing factor 2	-1.16	0.146	1.06	0.832	-1.23	0.092	1.21	0.497	-0.03
1435325_at	Usp46	ubiquitin specific peptidase 46	1.05	0.331	-1.11	0.316	-1.29	0.058	2.72	0.263	0.35
1443531_at	A930005I04Rik	RIKEN cDNA A930005I04 gene	1.39	0.563	-1.13	0.811	-2.19	0.007	2.15	0.286	0.06
1433339_at	6030460B20Rik	RIKEN cDNA 6030460B20 gene	1.78	0.097	-4.25	0.196	-1.39	0.101	1.84	0.079	-0.5
1453932_at	4931433A01Rik	RIKEN cDNA 4931433A01 gene	-2.61	0.012	1.09	0.775	1.27	0.588	-1.33	0.653	-0.4
1419252_at	---	---	-1.16	0.107	1.06	0.659	-1.23	0.079	1.17	0.397	-0.04
1429382_at	Tomm40l	translocase of outer mitochondrial membrane 40 homolog-like (yeast)	-1.26	0.391	1.02	0.929	-1.08	0.221	1.01	0.946	-0.08
1458674_at	Pkn1	Protein kinase N1	-1.24	0.597	1.59	0.384	-2.94	0.005	1.06	0.91	-0.38
1425635_at	Tnk1	tyrosine kinase, non-receptor, 1	1.05	0.865	-1.17	0.688	-1.2	0.315	1.3	0.516	-0.01
1451394_at	Dpp6	dipeptidylpeptidase 6	1.25	0.75	-1.74	0.06	-1.1	0.772	1.07	0.453	-0.13
1452212_at	Lmna	lamin A	1.17	0.536	1.14	0.85	-2.36	0.023	-1.02	0.974	-0.27
1436554_at	Zfpn1a5	zinc finger protein, subfamily 1A, 5	-1.05	0.79	-1.38	0.213	1.06	0.706	1.3	0.468	-0.02
1453608_at	2310020J12Rik	RIKEN cDNA 2310020J12 gene	1.2	0.097	1.03	0.858	-1.98	0.019	-1.09	0.479	-0.21
1459591_at	---	---	-1.74	0.38	1.3	0.619	-1.17	0.629	1.08	0.863	-0.13
1434831_a_at	Foxo3a	forkhead box O3a	1.03	0.949	-1.05	0.867	-1.34	0.407	2.19	0.187	0.21
1424540_at	Hipk1	homeodomain interacting protein kinase 1	-1.24	0.462	-1.17	0.251	1.08	0.712	1.8	0.187	0.12
1417636_at	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-1.03	0.849	-1.5	0.008	1.1	0.364	4.59	0.149	0.79
1429292_a_at	2310046K01Rik	RIKEN cDNA 2310046K01 gene	-1.3	0.023	-1.12	0.558	1.08	0.339	1.01	0.924	-0.08
1453000_at	Camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	1	0.974	-1.08	0.599	-1.24	0.03	2.19	0.197	0.22
1435494_s_at	Dsp	desmoplakin	-1.3	0.201	-1.24	0.012	1.16	0.35	2.69	0.092	0.33
1440050_at	Hbs1l	Hbs1-like (S. cerevisiae)	-1.1	0.475	1.01	0.969	-1.21	0.089	1.05	0.817	-0.06
1457648_x_at	BC004044	cDNA sequence BC004044	-1.28	0.58	1.01	0.977	-1.06	0.878	1.1	0.811	-0.06
1437519_x_at	Hagh	hydroxyacyl glutathione hydrolase	1.02	0.915	-1.3	0.011	-1.05	0.657	4.11	0.207	0.69
1450025_at	Pard6g	par-6 partitioning defective 6 homolog gamma (C. elegans)	-1.6	0.489	-1.32	0.29	1.35	0.199	1.23	0.639	-0.08
1433872_at	2410042D21Rik	RIKEN cDNA 2410042D21 gene	-1.05	0.375	1.05	0.646	-1.37	0.135	1.25	0.418	-0.03
1424953_at	BC021614	cDNA sequence BC021614	-1.74	0.439	1.17	0.638	-1.01	0.898	1.39	0.066	-0.05
1438131_at	Fbxw2	F-box and WD-40 domain protein 2	1.05	0.871	-1.11	0.784	-1.27	0.094	1.22	0.581	-0.03
1449290_at	Dpysl5	dihydropyrimidinase-like 5	1.24	0.323	-1.51	0.352	-1.2	0.664	1.21	0.607	-0.06
1420237_at	---	Transcribed locus	-1.14	0.859	-1.23	0.593	1.05	0.947	1.06	0.928	-0.07
1438514_at	Npc1l1	NPC1-like 1	-2.26	0.233	1.38	0.242	-1.09	0.85	1.25	0.378	-0.18
1439126_at	1110007A13Rik	RIKEN cDNA 1110007A13 gene	1.09	0.124	1.03	0.905	-1.61	0.008	-1.68	0.045	-0.29
1430434_at	Tktl2	transketolase-like 2	-1.4	0.656	1.01	0.982	1.01	0.964	-1.79	0.491	-0.29
1451907_a_at	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specif	-1.41	0.035	-1.24	0.519	1.23	0.211	1.31	0.258	-0.03
1437255_at	Zbtb7a	Zinc finger and BTB domain containing 7a	1.26	0.426	-1.35	0.493	-1.36	0.321	1.89	0.16	0.11
1418143_at	Vps45	vacuolar protein sorting 45 (yeast)	1.01	0.89	-1.18	0.196	-1.13	0.308	1.03	0.828	-0.07
1460043_at	---	---	1.02	0.974	-1	1	-1.4	0.114	2.76	0.016	0.35
1451224_at	Scamp5	secretory carrier membrane protein 5	-1.31	0.147	-1.12	0.581	1.09	0.615	1.45	0.054	0.03
1429329_at	Cox10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransf	-1.65	0.015	-1.29	0.009	1.36	0.261	1.02	0.879	-0.14

1455760_at	Slc9a5	solute carrier family 9 (sodium/hydrogen exchanger), member 5	-1.31	0.403	-1.03	0.951	1	0.991	1.07	0.82	-0.07
1453654_at	Cnot10	CCR4-NOT transcription complex, subunit 10	1.01	0.987	1.05	0.936	-1.47	0.093	-1.25	0.551	-0.16
1451559_a_at	Dhrs4	dehydrogenase/reductase (SDR family) member 4	-1.08	0.864	-1.51	0.289	1.15	0.715	1	0.993	-0.11
1443352_at	C77614	EST C77614	1.08	0.788	-1.14	0.854	-1.28	0.444	2.3	0.115	0.24
1427991_s_at	Usp45	ubiquitin specific petidase 45	-1.12	0.454	1	0.988	-1.18	0.183	2.09	0.187	0.2
1438424_at	Tbc1d24	TBC1 domain family, member 24	1.13	0.645	-1.2	0.633	-1.29	0.012	1.47	0.308	0.03
1445116_at	Usp25	Ubiquitin specific peptidase 25	-1.02	0.955	1.12	0.261	-1.57	0.035	1.39	0.435	-0.02
1442319_at	Usp4	ubiquitin specific peptidase 4 (proto-oncogene)	1.23	0.175	-1.09	0.379	-1.7	0.055	1.23	0.614	-0.08
1453243_at	0610030E20Rik	RIKEN cDNA 0610030E20 gene	-1.31	0.181	-1.3	0.167	1.2	0.427	1.06	0.815	-0.08
1419338_at	ICRFP703B1614Q5	ICRFP703B1614Q5.5 gene	1.1	0.823	-1.53	0.36	-1.02	0.944	2.43	0.068	0.25
1431444_at	Spint4	serine protease inhibitor, Kunitz type 4	-1.62	0.159	-1.74	0.579	1.55	0.102	1.05	0.93	-0.19
1436753_at	Adck5	aarF domain containing kinase 5	-1.16	0.155	-1.57	0.002	1.24	0.087	1.06	0.664	-0.11
1437761_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	1.11	0.42	-1.08	0.025	-1.42	0.011	1.25	0.424	-0.03
1417689_a_at	Pdzk1ip1	PDZK1 interacting protein 1	-1.05	0.561	1.05	0.833	-1.36	0.276	6.59	0.189	1.31
1456427_at	Gp1bb	glycoprotein Ib, beta polypeptide	-1.78	0.01	1.02	0.913	1.16	0.663	-1.13	0.782	-0.18
1424118_a_at	Spbc25	spindle pole body component 25 homolog (S. cerevisiae)	-1.32	0.006	-1.14	0.47	1.1	0.674	3.88	0.21	0.63
1432603_at	Nrip1	nuclear receptor interacting protein 1	-1.6	0.066	-1.06	0.725	1.18	0.712	1.09	0.642	-0.1
1453476_at	1700060J05Rik	RIKEN cDNA 1700060J05 gene	-1.15	0.711	1.31	0.574	-1.79	0.47	1.76	0.516	0.03
1453689_at	Fance	Fanconi anemia, complementation group E	-1.07	0.581	1.07	0.876	-1.37	0.113	1.54	0.297	0.04
1429455_at	Gapvd1	GTPase activating protein and VPS9 domains 1	1.11	0.515	-1.09	0.491	-1.41	0.148	1.58	0.162	0.05
1431365_at	Rnf32	ring finger protein 32	1.17	0.633	-1.1	0.855	-1.52	0.217	1.09	0.743	-0.09
1426767_at	3230401M21Rik	RIKEN cDNA 3230401M21 gene	-1.3	0.099	-1.6	0.21	1.35	0.338	1.78	0.308	0.06
1430421_a_at	BC010787	cDNA sequence BC010787	1.05	0.744	-1.15	0.472	-1.23	0.237	1	0.996	-0.08
1439985_at	Abcc12	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	-1.47	0.598	1.42	0.389	-1.56	0.059	1.03	0.959	-0.14
1430643_at	Msh3	mutS homolog 3 (E. coli)	1.07	0.586	-1.08	0.848	-1.34	0.646	1.25	0.721	-0.03
1452184_at	Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	-1.1	0.123	-1.37	0.031	1.11	0.135	1.42	0.25	0.01
1446620_at	Myo1d	Myosin ID	-1.16	0.661	1.02	0.96	-1.16	0.272	2.2	0.004	0.22
1455430_at	3200001K10Rik	RIKEN cDNA 3200001K10 gene	-1.21	0.369	-1.33	0.136	1.16	0.097	1.7	0.149	0.08
1418510_s_at	Fbxo8	F-box only protein 8	-1.13	0.16	-1.19	0.011	1.02	0.865	1.28	0.222	-0.01
1422738_at	Ddr2	discoidin domain receptor family, member 2	1.15	0.621	1.02	0.952	-1.73	0.006	-1.01	0.955	-0.15
1455054_a_at	Tes3-ps /// Dcun1d	testis derived transcript 3, pseudogene /// DCUN1D1 DCN1, defective in cullin ne	-1.28	0.154	-1.06	0.489	1.01	0.932	1.8	0.227	0.12
1436345_at	5730559C18Rik	RIKEN cDNA 5730559C18 gene	-1.61	0.378	-1.06	0.899	1.18	0.098	1.25	0.345	-0.06
1441990_at	Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	1.07	0.862	-1.33	0.411	-1.09	0.753	1.16	0.428	-0.05
1443603_at	Pcmtd1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-1.14	0.554	-1.26	0.294	1.07	0.876	1.04	0.924	-0.07
1453168_at	1700029J07Rik	RIKEN cDNA 1700029J07 gene	-1.66	0.112	1.05	0.866	1.09	0.654	-1.83	0.204	-0.34
1432124_at	4921511I17Rik	RIKEN cDNA 4921511I17 gene	1.13	0.735	-1.28	0.372	-1.21	0.58	1.08	0.831	-0.07
1422524_at	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	-1.05	0.837	-1.35	0.094	1.05	0.773	4.57	0.166	0.8
1453107_s_at	Foxm1 /// Pebp1 ///	forkhead box M1 /// phosphatidylethanolamine binding protein 1 /// RIKEN cDNA	-1.16	0.715	1.15	0.842	-1.36	0.443	3.26	0.18	0.47
1430535_at	Tsc22d2	TSC22 domain family 2	-1.31	0.036	-1.08	0.558	1.05	0.601	1.12	0.513	-0.05
1426358_at	Taok1	TAO kinase 1	1.09	0.118	-1.08	0.627	-1.38	0.205	1.09	0.716	-0.07
1444952_a_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1.17	0.201	-1.01	0.974	-1.72	0.037	1.29	0.132	-0.07
1436912_at	Cacnb4	calcium channel, voltage-dependent, beta 4 subunit	-1.07	0.729	-1.46	0.27	1.12	0.72	1.32	0.671	-0.02
1450793_at	4930550L24Rik	RIKEN cDNA 4930550L24 gene	-1.26	0.055	-1.19	0.411	1.11	0.756	1.1	0.845	-0.06
1435008_at	Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	1.05	0.43	1.07	0.477	-1.59	0.015	-1.06	0.786	-0.13
1419806_at	Hdlbp	high density lipoprotein (HDL) binding protein	-1.46	0.543	-1	0.982	1.06	0.867	1.05	0.832	-0.09
1427989_at	Amhr2	anti-Mullerian hormone type 2 receptor	-1.35	0.413	1.58	0.192	-2.38	0.253	1.14	0.841	-0.25
1432104_a_at	Allc	allantoicase	1.35	0.258	-1.49	0.199	-1.38	0.12	1.39	0.009	-0.03
1430024_at	Yipf6	Yip1 domain family, member 6	-1.21	0.156	1.09	0.799	-1.22	0.357	1.1	0.448	-0.06
1459676_at	Ttc15	tetratricopeptide repeat domain 15	-1.58	0.31	-1.36	0.622	1.37	0.333	1.08	0.789	-0.12
1441291_at	Abl1	v-abl Abelson murine leukemia oncogene 1	1.17	0.626	-1.59	0.213	-1.06	0.882	1.1	0.22	-0.1
1420205_at	---	---	-1.01	0.986	-1.67	0.354	1.16	0.746	2.3	0.066	0.19
1443821_at	Lect2	leukocyte cell-derived chemotaxin 2	1.77	0.557	-1.48	0.43	-3.33	0.098	1.67	0.247	-0.34
1431255_at	Calr3	calreticulin 3	-1.1	0.275	1.02	0.965	-1.22	0.159	1.42	0.353	0.03

1436640_x_at	Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransf	-1.13	0.478	1.05	0.693	-1.24	0.305	1.75	0.136	0.11
1457125_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930515K13 pr	-1.35	0.762	1.56	0.376	-2.23	0.062	1.06	0.61	-0.24
1426889_at	4930566A11Rik	RIKEN cDNA 4930566A11 gene	-1.18	0.327	1.01	0.986	-1.12	0.259	1.17	0.507	-0.03
1417095_a_at	Hspa14	heat shock protein 14	-1.83	0.478	1.27	0.498	-1.07	0.768	1.28	0.563	-0.09
1417564_at	Crsp9	cofactor required for Sp1 transcriptional activation, subunit 9	-1.26	0.075	1.02	0.795	-1.07	0.175	1.32	0.318	0
1417427_at	1500026D16Rik	RIKEN cDNA 1500026D16 gene	1.01	0.971	-1.31	0.06	-1.03	0.872	1.34	0.362	0
1448631_a_at	Hipk2	homeodomain interacting protein kinase 2	-1.06	0.863	1.07	0.887	-1.36	0.057	3.67	0.217	0.58
1455352_at	AU023006	expressed sequence AU023006	-1.13	0.45	1	0.998	-1.16	0.322	1.13	0.532	-0.04
1432713_at	6430709C05Rik	RIKEN cDNA 6430709C05 gene	-1.92	0.548	-1.47	0.472	1.54	0.471	1.05	0.93	-0.2
1431892_a_at	Plcd3	phospholipase C, delta 3	1.13	0.389	-1.33	0.417	-1.17	0.481	1.76	0.035	0.1
1448298_at	Tnk2	tyrosine kinase, non-receptor, 2	-1.44	0.384	-1.09	0.648	1.13	0.646	1.07	0.491	-0.08
1450719_at	Mep1a	meprin 1 alpha	1.06	0.662	-2.12	0.323	1.21	0.298	-1.16	0.71	-0.25
1424554_at	Ppp1r8	protein phosphatase 1, regulatory (inhibitor) subunit 8	-1.08	0.589	1.04	0.79	-1.27	0.05	1.09	0.694	-0.06
1447024_at	---	---	1.27	0.346	-1.41	0.119	-1.31	0.228	1.28	0.454	-0.04
1425919_at	Ndufa12	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12	1.28	0.371	-1.23	0.634	-1.53	0.232	1	0.998	-0.12
1424373_at	Armcx3	armadillo repeat containing, X-linked 3	-1.18	0.407	1.07	0.81	-1.21	0.037	1.19	0.262	-0.03
1419689_at	Gpc6	glypican 6	-1.08	0.03	1.09	0.367	-1.38	0.074	1.05	0.786	-0.08
1427072_at	Stard8	START domain containing 8	-1.13	0.137	1.13	0.12	-1.37	0.224	1.17	0.507	-0.05
1449512_a_at	Zfx	zinc finger protein X-linked	1.15	0.028	-1.09	0.764	-1.48	0.294	1.07	0.83	-0.09
1451543_at	Fbxo21	F-box only protein 21	-1.17	0.566	-1.5	0.058	1.22	0.353	1.05	0.804	-0.1
1441029_at	Axin1	Axin 1	1.07	0.737	-1.76	0.476	1.11	0.831	-1.53	0.016	-0.28
1425992_at	Slc6a5	solute carrier family 6 (neurotransmitter transporter, glycine), member 5	1.08	0.814	-1.26	0.658	-1.15	0.79	2.76	0.025	0.36
1433796_at	Endod1	endonuclease domain containing 1	-1.25	0.189	1.08	0.352	-1.16	0.255	2.39	0.176	0.27
1440476_at	D6Ertd474e	DNA segment, Chr 6, ERATO Doi 474, expressed	-1.06	0.921	1.32	0.561	-2.07	0.14	1.21	0.633	-0.15
1438094_x_at	2810409H07Rik	RIKEN cDNA 2810409H07 gene	1	0.999	-1.17	0.188	-1.12	0.114	1.21	0.312	-0.02
1418385_at	Cuedc2	CUE domain containing 2	-3.18	0.114	1.42	0.326	1.02	0.945	-1.5	0.02	-0.56
1444517_at	---	---	-1.16	0.805	-1.28	0.627	1.1	0.594	1.75	0.372	0.1
1459453_at	Robo1	Roundabout homolog 1 (Drosophila)	-1.32	0.637	1.22	0.612	-1.31	0.235	1.52	0.122	0.03
1437883_s_at	---	---	1.02	0.95	1.13	0.572	-1.66	0.092	-1.2	0.547	-0.18
1446448_at	Pias1	protein inhibitor of activated STAT 1	1.13	0.682	1.11	0.377	-1.96	0.097	-1.33	0.299	-0.26
1448752_at	Car2	carbonic anhydrase 2	-1.45	0.019	-1	0.996	1.06	0.821	2.59	0.111	0.3
1450690_at	---	---	1.09	0.528	-1.06	0.322	-1.39	0.038	1.32	0.339	-0.01
1427182_s_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	1.21	0.51	-1.93	0.12	1.02	0.934	-1.72	0.096	-0.36
1435677_at	C85492	expressed sequence C85492	-1.23	0.131	-1.16	0.127	1.07	0.685	1.03	0.928	-0.07
1432885_at	4632432E15Rik	RIKEN cDNA 4632432E15 gene	1.01	0.966	-1.83	0.108	1.19	0.081	-1.37	0.027	-0.25
1459122_at	C230086A09Rik	RIKEN cDNA C230086A09 gene	1.12	0.883	-2.07	0.34	1.15	0.662	-1.45	0.538	-0.31
1428013_at	6030458C11Rik	RIKEN cDNA 6030458C11 gene	1.11	0.768	-1.57	0.263	-1	0.979	1.7	0.12	0.06
1453132_a_at	1810036H07Rik	RIKEN cDNA 1810036H07 gene	-1.28	0.102	1.03	0.967	-1.07	0.915	1.15	0.861	-0.04
1422872_at	Bmpr1b	bone morphogenetic protein receptor, type 1B	1.04	0.944	-1.57	0.114	1.07	0.869	-1.2	0.136	-0.17
1419499_at	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	-1.26	0.144	1.14	0.284	-1.23	0.299	1.07	0.721	-0.07
1423003_at	Setd7	SET domain containing (lysine methyltransferase) 7	-1.42	0.328	1.08	0.907	-1.04	0.904	1.37	0.581	0
1446373_at	Lrba	LPS-responsive beige-like anchor	-1.07	0.925	-1.41	0.534	1.1	0.841	1.23	0.726	-0.04
1441594_at	Aff1	AF4/FMR2 family, member 1	1.07	0.854	-1.11	0.778	-1.29	0.473	1.99	0.129	0.16
1442286_at	Wdr67	WD repeat domain 67	-1.22	0.568	1.12	0.758	-1.24	0.414	1.58	0.283	0.06
1424946_a_at	Mtfr1	mitochondrial fission regulator 1	-1.09	0.689	-1.26	0.129	1.04	0.82	3.43	0.249	0.53
1427974_s_at	Cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit	1.23	0.196	-1.11	0.611	-1.63	0.062	1.12	0.758	-0.1
1453749_at	2610507I01Rik	RIKEN cDNA 2610507I01 gene	1.06	0.412	-1.11	0.352	-1.27	0.189	1.02	0.939	-0.07
1431131_s_at	A630007B06Rik ///	RIKEN cDNA A630007B06 gene /// similar to oocyte-testis gene 1	-1.26	0.039	1.18	0.274	-1.29	0.166	1.43	0.019	0.02
1456703_at	D5Ertd301e	DNA segment, Chr 5, ERATO Doi 301, expressed	-1.06	0.943	1.25	0.545	-1.81	0.184	1.31	0.421	-0.08
1453954_a_at	Mrps5	mitochondrial ribosomal protein S5	1.04	0.92	-1.44	0.144	1.02	0.946	-1.06	0.851	-0.11
1424109_a_at	Glo1	glyoxalase 1	-1.11	0.087	-1.24	0.013	1.04	0.822	2.25	0.276	0.23
1419263_a_at	Adrm1	adhesion regulating molecule 1	-1.18	0.523	-1.25	0.014	1.1	0.624	1.17	0.505	-0.04
1446459_at	---	---	-4.91	0.185	-1.14	0.814	1.67	0.296	1.58	0.485	-0.7

1427107_at	Slc16a11	solute carrier family 16 (monocarboxylic acid transporters), member 11	-1.4	0.047	-1.19	0.188	1.19	0.2	1.21	0.666	-0.05
1442363_at	1110012J17Rik	RIKEN cDNA 1110012J17 gene	1.3	0.454	-2.06	0.161	-1.04	0.751	2.06	0.427	0.06
1426522_at	Hadhb /// LOC6230	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl	-1.08	0.177	-1.5	0.007	1.16	0.55	1.02	0.856	-0.1
1438515_at	Zfp207	zinc finger protein 207	1.33	0.288	-1.3	0.413	-1.55	0.128	1.15	0.401	-0.09
1459437_at	LOC640536 /// LOC	similar to kinesin-like motor protein C20orf23 /// similar to kinesin-like motor prote	1.31	0.299	-1.11	0.846	-1.86	0.169	1.15	0.46	-0.13
1434561_at	Asxl1	additional sex combs like 1 (Drosophila)	-1.12	0.278	1.06	0.394	-1.26	0.058	1.02	0.907	-0.07
1432755_at	2210409O19Rik	RIKEN cDNA 2210409O19 gene	-1.46	0.481	1.61	0.561	-2.2	0.172	1.06	0.929	-0.25
1421785_at	Uevld	UEV and lactate/malate dehyrogenase domains	-1.75	0.309	-1.28	0.503	1.4	0.275	2.07	0.403	0.11
1445730_at	Rab11fip2	RAB11 family interacting protein 2 (class I)	1.24	0.079	1.06	0.922	-2.27	0.042	-1.71	0.398	-0.42
1438262_at	Slc8a2	solute carrier family 8 (sodium/calcium exchanger), member 2	-1.12	0.693	-1.24	0.535	1.05	0.802	1.16	0.693	-0.04
1430082_at	4930511H01Rik	RIKEN cDNA 4930511H01 gene	1.01	0.992	1.12	0.702	-1.61	0.006	-1.24	0.703	-0.18
1445315_at	---	---	-1.23	0.715	-1.18	0.563	1.09	0.805	1.04	0.893	-0.07
1419670_at	Ftcd	formiminotransferase cyclodeaminase	1.29	0.424	-1.22	0.048	-1.55	0.23	1.63	0.191	0.04
1430134_a_at	Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)	-1.2	0.431	-1.16	0.128	1.06	0.656	1.21	0.564	-0.02
1437999_x_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.19	0.055	-1.29	0.146	1.13	0.166	3.66	0.187	0.58
1438062_at	4832420A03Rik	RIKEN cDNA 4832420A03 gene	1.09	0.646	1.07	0.699	-1.69	0.009	-1.15	0.348	-0.17
1423948_at	Bag2	Bcl2-associated athanogene 2	-1.26	0.061	-1.29	0.057	1.18	0.187	4.24	0.218	0.72
1445636_at	Fmnl1	Formin-like 1	-1.01	0.977	1.04	0.899	-1.38	0.324	1.28	0.161	-0.02
1450888_at	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	-1.29	0.375	1.06	0.598	-1.1	0.605	1.57	0.241	0.06
1454390_at	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	-1.09	0.745	1.03	0.95	-1.24	0.1	1.1	0.726	-0.05
1437467_at	Alcam	activated leukocyte cell adhesion molecule	1.06	0.748	1.17	0.1	-1.93	0	-1.72	0.147	-0.36
1425055_at	Saps2	SAPS domain family, member 2	-1.39	0.394	1.19	0.543	-1.19	0.503	1.51	0.31	0.03
1426306_a_at	Maged2	melanoma antigen, family D, 2	-1.02	0.861	1.14	0.601	-1.59	0.04	1.17	0.449	-0.08
1438090_x_at	Ankrd54	ankyrin repeat domain 54	-1.13	0.606	1.01	0.895	-1.18	0.253	1.71	0.194	0.1
1429411_a_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	-1.19	0.117	1.11	0.335	-1.26	0.081	1.28	0.307	-0.01
1439305_at	---	---	1.06	0.856	-1.06	0.663	-1.33	0.284	1.13	0.603	-0.05
1430215_at	2610020H08Rik	RIKEN cDNA 2610020H08 gene	-1.26	0.402	-1.11	0.8	1.06	0.779	1.04	0.878	-0.07
1433751_at	Slc39a10	solute carrier family 39 (zinc transporter), member 10	1.12	0.367	1.01	0.932	-1.61	0.011	-1.45	0.028	-0.23
1453173_at	2310005E10Rik	RIKEN cDNA 2310005E10 gene	-1.42	0.035	1.27	0.276	-1.29	0.068	1.01	0.99	-0.11
1441639_at	Zcchc8	zinc finger, CCHC domain containing 8	1.07	0.853	-1.03	0.945	-1.39	0.051	1.04	0.85	-0.08
1448746_at	Nbn	nibrin	1.1	0.637	-1.42	0.015	-1.05	0.751	1.15	0.629	-0.06
1458616_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	-1.28	0.007	1.38	0.35	-1.67	0.002	1.21	0.522	-0.09
1460687_at	Setd8	SET domain containing (lysine methyltransferase) 8	-1.26	0.037	-1.05	0.743	1	0.982	1.73	0.114	0.11
1417376_a_at	Igsf4a	immunoglobulin superfamily, member 4A	1.14	0.084	1.01	0.97	-1.64	0.045	-1.18	0.336	-0.17
1459274_at	Gpr135	G protein-coupled receptor 135	-1.14	0.255	1.05	0.773	-1.21	0.471	2.14	0.033	0.21
1432560_at	1700127D06Rik	RIKEN cDNA 1700127D06 gene	1.01	0.989	-1.77	0.479	1.18	0.592	-2.02	0.032	-0.4
1454172_at	Bcorl1	BCL6 co-repressor-like 1	-1.06	0.798	1.05	0.459	-1.31	0.366	1.91	0.157	0.15
1446359_at	Gnal	guanine nucleotide binding protein, alpha stimulating, olfactory type	-2.4	0.093	1.27	0.591	1.06	0.882	-1.7	0.235	-0.44
1416763_at	G431001I09Rik	RIKEN cDNA G431001I09 gene	-1.13	0.365	-1.16	0.059	1.01	0.968	1.03	0.904	-0.06
1438582_at	Actr5	ARP5 actin-related protein 5 homolog (yeast)	-1.08	0.786	-1.24	0.379	1.02	0.936	1.06	0.845	-0.06
1452850_s_at	Brms1l	breast cancer metastasis-suppressor 1-like	1.08	0.509	-1.1	0.613	-1.3	0.07	1.1	0.673	-0.06
1428974_s_at	Lztfl1	leucine zipper transcription factor-like 1	1.34	0.166	-1.52	0.077	-1.32	0.382	1.27	0.276	-0.06
1441297_at	Muc6	mucin 6, gastric	1.14	0.456	-1.3	0.228	-1.18	0.413	1.22	0.377	-0.03
1444467_at	C77534	expressed sequence C77534	-2.12	0.171	-1.07	0.844	1.34	0.358	1.41	0.446	-0.11
1443684_at	---	---	-1.44	0.681	-1.58	0.387	1.43	0.353	3.31	0.203	0.43
1424501_at	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	1	0.995	-1.1	0.162	-1.19	0.072	1.01	0.877	-0.07
1450160_at	Lif	leukemia inhibitory factor	-2.6	0.422	1.24	0.757	1.12	0.651	-1.64	0.289	-0.47
1460526_at	4833420L08Rik	RIKEN cDNA 4833420L08 gene	1.29	0.619	-1.24	0.512	-1.53	0.25	1.16	0.756	-0.08
1429313_at	Ror1	receptor tyrosine kinase-like orphan receptor 1	1.01	0.959	1.08	0.73	-1.5	0.144	-1.12	0.573	-0.13
1421567_at	Npas3	neuronal PAS domain protein 3	-1.37	0.386	-1.09	0.618	1.1	0.691	1.07	0.829	-0.07
1452488_at	---	---	1.47	0.099	-1.39	0.288	-1.78	0.015	1.04	0.886	-0.16
1439792_at	---	Transcribed locus, strongly similar to XP_579813.1 PREDICTED: hypothetical pr	-1.32	0.66	-1.23	0.445	1.19	0.452	1.17	0.603	-0.05
1457006_at	1700106J12Rik	RIKEN cDNA 1700106J12 gene	-1.34	0.459	-1.05	0.92	1.05	0.887	1.21	0.44	-0.03

1421729_a_at	Fert2	fer (fms/fps related) protein kinase, testis specific 2	-1.27	0.508	-1.04	0.843	1	0.985	1.55	0.073	0.06
1434150_a_at	Mettl7a /// Ubie	methyltransferase like 7A /// UbiE-YGHL1 fusion protein	1.09	0.763	-1.28	0.182	-1.13	0.5	1.56	0.108	0.06
1436443_a_at	Kdelc1	KDEL (Lys-Asp-Glu-Leu) containing 1	-1.15	0.26	1.04	0.84	-1.18	0.425	1.18	0.455	-0.03
1451148_at	Pink1	PTEN induced putative kinase 1	1.03	0.763	-1.18	0.347	-1.15	0.148	1	0.987	-0.07
1415881_at	Ghitm	growth hormone inducible transmembrane protein	-1.14	0.216	-1.18	0.103	1.03	0.513	1.39	0.363	0.02
1458622_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	1.08	0.921	-1.09	0.807	-1.31	0.47	2.23	0.08	0.23
1431589_at	Hydin	hydrocephalus inducing	1.23	0.654	-1.15	0.795	-1.52	0.265	1.59	0.443	0.04
1426091_a_at	Wnt10b	wingless related MMTV integration site 10b	-1.09	0.587	-1.29	0.109	1.06	0.927	1.04	0.834	-0.07
1435516_x_at	Rtel1	regulator of telomere elongation helicase 1	-1.39	0.447	1.33	0.082	-1.41	0.264	1.05	0.884	-0.11
1442083_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	1.02	0.925	1.02	0.728	-1.41	0.139	-1.32	0.164	-0.17
1450734_at	Lztr2	leucine zipper transcription regulator 2	1.07	0.88	1.06	0.373	-1.59	0.035	-1.27	0.578	-0.19
1428463_a_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	1.14	0.339	-1.22	0.3	-1.25	0.27	1.07	0.767	-0.07
1457486_at	D9Ucla1	DNA segment, Chr 9, University of California at Los Angeles 1	1.1	0.315	-1.34	0.205	-1.1	0.575	1.28	0.552	-0.01
1440182_at	Fzd10	frizzled homolog 10 (Drosophila)	-1.19	0.863	-1.26	0.204	1.12	0.567	2.27	0.141	0.24
1416984_at	Mrps18a	mitochondrial ribosomal protein S18A	1.05	0.852	-1.2	0.33	-1.15	0.127	1.1	0.607	-0.05
1421894_a_at	Tpp2	tripeptidyl peptidase II	-1.18	0.251	-1.11	0.458	1	0.979	1.1	0.519	-0.04
1421609_a_at	Cml3	camello-like 3	1.07	0.851	-1.72	0.27	1.1	0.837	-2.98	0.174	-0.63
1425795_a_at	Map3k7	mitogen activated protein kinase kinase kinase 7	-1.06	0.813	-1.27	0.13	1.02	0.894	1.18	0.413	-0.03
1450502_at	Dpysl2	dihydropyrimidinase-like 2	-1.17	0.824	1.07	0.819	-1.21	0.592	1.45	0.44	0.04
1437862_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	1.12	0.483	1.01	0.915	-1.61	0.115	-1.09	0.668	-0.14
1425937_a_at	Hexim1	hexamethylene bis-acetamide inducible 1	-1.14	0.177	-1.22	0.05	1.06	0.645	1.06	0.57	-0.06
1416800_at	Trpm7	transient receptor potential cation channel, subfamily M, member 7	-1.11	0.437	-1.23	0.169	1.04	0.819	1.12	0.663	-0.04
1422461_at	Atad3a	ATPase family, AAA domain containing 3A	-1.15	0.331	-1.14	0.466	1.01	0.972	1.13	0.24	-0.04
1431480_at	4833419E13Rik	RIKEN cDNA 4833419E13 gene	-1.18	0.726	-1.2	0.827	1.07	0.835	1.64	0.057	0.08
1434171_at	C330011K17Rik	RIKEN cDNA C330011K17 gene	-1.08	0.731	1	0.962	-1.22	0.157	1.28	0.156	0
1453769_at	Ckap2l	cytoskeleton associated protein 2-like	1.18	0.714	-1.47	0.344	-1.12	0.78	3	0.25	0.4
1449712_s_at	Atp6v1e1	VATPase, H+ transporting, lysosomal V1 subunit E1	-1.19	0.032	1	0.941	-1.1	0.441	1.29	0.279	0
1443633_at	1700086O06Rik	RIKEN cDNA 1700086O06 gene	1.08	0.875	-1.15	0.63	-1.24	0.55	2.23	0.356	0.23
1447993_a_at	1700026B20Rik	RIKEN cDNA 1700026B20 gene	1.15	0.526	-1.19	0.398	-1.31	0.132	1.19	0.607	-0.04
1424625_a_at	Dennd1a	DENN/MADD domain containing 1A	-1.08	0.692	-1.26	0.455	1.04	0.926	1.15	0.296	-0.04
1458129_at	Rora	RAR-related orphan receptor alpha	1.11	0.417	-1.15	0.648	-1.29	0.317	1.15	0.607	-0.04
1417053_at	Phb /// LOC665511	prohibitin /// similar to prohibitin /// similar to prohibitin /// similar to prohibitin	-1.05	0.685	-1.25	0.035	1.01	0.94	1.01	0.963	-0.07
1454303_at	Epn2	epsin 2	1.06	0.598	1.09	0.842	-1.65	0.413	-2.52	0.093	-0.51
1443201_at	Gpc6	Glypican 6	1.21	0.638	-1.55	0	-1.11	0.44	1.56	0.421	0.03
1451179_a_at	Qk	quaking	-1.05	0.027	1.04	0.572	-1.31	0.042	1.19	0.155	-0.03
1442861_at	Crtc1	CREB regulated transcription coactivator 1	-1.28	0.038	1	0.899	-1.03	0.833	1.42	0.453	0.03
1449801_at	---	---	-4.14	0.06	1.73	0.534	-1.28	0.076	1.17	0.532	-0.63
1416336_s_at	Snrpd1	small nuclear ribonucleoprotein D1	-1.21	0.184	1.04	0.261	-1.12	0.589	1.24	0.56	-0.01
1448005_at	Sash1	SAM and SH3 domain containing 1	-1.1	0.691	1	0.998	-1.18	0.147	1.07	0.838	-0.05
1455248_at	0610011N22Rik	RIKEN cDNA 0610011N22 gene	-1.01	0.919	1.02	0.854	-1.33	0.095	1.12	0.629	-0.05
1454831_at	Foxn2	forkhead box N2	-1.07	0.778	1.03	0.859	-1.27	0.158	1.02	0.737	-0.07
1437029_at	Tacr3	tachykinin receptor 3	1.44	0.554	-1.21	0.727	-2.03	0.154	1.85	0.383	0.01
1416292_at	Prdx3	peroxiredoxin 3	-1.25	0.071	1.05	0.416	-1.1	0.291	2.06	0.234	0.19
1422458_at	Tcl1	T-cell lymphoma breakpoint 1	-1.67	0.277	1.21	0.349	-1.05	0.887	1.21	0.232	-0.08
1429566_a_at	Hipk2	homeodomain interacting protein kinase 2	-1.33	0.462	-1.45	0.269	1.32	0.536	1.83	0.316	0.09
1454695_at	Wdr18	WD repeat domain 18	-1.14	0.016	-1.56	0.023	1.24	0.527	1.17	0.388	-0.07
AFFX-TrpnX-M_at	---	---	1.21	0.264	-1.2	0.44	-1.4	0.272	1.2	0.275	-0.05
1426291_at	Dimt1	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	-1.78	0.068	1.36	0.364	-1.19	0.421	1.07	0.847	-0.14
1452128_a_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	1.01	0.938	-1.12	0.186	-1.17	0.464	1.04	0.782	-0.06
1451230_a_at	Wbp5	WW domain binding protein 5	-1.04	0.294	1.07	0.675	-1.37	0.097	1.8	0.08	0.11
1428362_at	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	1.01	0.859	-1.09	0.096	-1.2	0.05	1.14	0.291	-0.04
1445373_at	Pde3a	Phosphodiesterase 3A, cGMP inhibited	-1.43	0.468	1.17	0.609	-1.13	0.785	1.82	0.149	0.11
1416398_at	Mesdc1	mesoderm development candidate 1	-1.73	0.403	1.16	0.597	1.02	0.941	-1.1	0.539	-0.16

1434096_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	-1.28	0.01	-1.08	0.586	1.05	0.579	2.29	0.123	0.25
1435451_at	Hel308	helicase, mus308-like (Drosophila)	-1.04	0.829	1.02	0.946	-1.28	0.274	1.23	0.629	-0.02
1418611_at	Gpr162	G protein-coupled receptor 162	-1.69	0.147	-1.47	0.019	1.49	0.111	1.01	0.947	-0.17
1445275_at	C130092O11Rik	RIKEN cDNA C130092O11 gene	-2.67	0.346	1.1	0.908	1.28	0.561	-1.02	0.961	-0.33
1429153_at	6530406A20Rik	RIKEN cDNA 6530406A20 gene	1.1	0.613	-1.42	0.251	-1.05	0.804	1.03	0.862	-0.08
1422857_at	Trip4	thyroid hormone receptor interactor 4	-1.18	0.024	-1.17	0.416	1.06	0.69	1.05	0.74	-0.06
1421404_at	Cxcl15	chemokine (C-X-C motif) ligand 15	-1.48	0.406	1.34	0.513	-1.34	0	1.2	0.749	-0.07
1444862_at	1700112E06Rik	RIKEN cDNA 1700112E06 gene	1.17	0.567	-1.25	0.726	-1.28	0.168	1.28	0.503	-0.02
1459687_x_at	Cpsf6	Cleavage and polyadenylation specific factor 6	1.01	0.865	1.09	0.559	-1.54	0.107	-1	0.994	-0.11
1435570_s_at	D630029K05Rik	RIKEN cDNA D630029K05 gene	-1.03	0.912	1.01	0.986	-1.29	0.068	1.22	0.329	-0.02
1455076_a_at	4933424B01Rik	RIKEN cDNA 4933424B01 gene	-1.2	0.077	-1.18	0.125	1.08	0.745	1.39	0.285	0.02
1452003_at	Rbm14	RNA binding motif protein 14	-1.03	0.935	-2.17	0.304	1.32	0.421	1.05	0.879	-0.2
1448309_at	Ap3m1	adaptor-related protein complex 3, mu 1 subunit	1	0.996	-1.34	0.331	1.01	0.972	-1.06	0.875	-0.1
1432952_at	4930448E22Rik	RIKEN cDNA 4930448E22 gene	1.15	0.841	-1.32	0.087	-1.18	0.427	1.24	0.499	-0.02
1439442_x_at	Yars2	tyrosyl-tRNA synthetase 2 (mitochondrial)	-1.27	0.376	-1.21	0.444	1.14	0.554	1.03	0.93	-0.08
1453669_at	4930578C19Rik	RIKEN cDNA 4930578C19 gene	1.33	0.434	-1.09	0.839	-1.95	0.365	1.36	0.477	-0.09
1459808_at	Fkbp4	FK506 binding protein 4	-2.56	0.358	1.59	0.195	-1.29	0.546	1.15	0.757	-0.28
1433209_at	2210017G18Rik	RIKEN cDNA 2210017G18 gene	-1.19	0.694	1.46	0.134	-2.18	0.088	1.03	0.921	-0.22
1424876_s_at	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	-1.4	0.136	-1.13	0.295	1.16	0.201	1.06	0.43	-0.08
1441965_at	Ccdc38	coiled-coil domain containing 38	-1.14	0.872	-1.65	0.04	1.27	0.57	1.28	0.766	-0.06
1426997_at	Thra	thyroid hormone receptor alpha	-1.03	0.908	1.05	0.745	-1.36	0.112	1.47	0.226	0.03
1450082_s_at	Etv5	ets variant gene 5	-1.1	0.888	-1.36	0.388	1.12	0.641	1.27	0.027	-0.02
1421986_at	Eif4e2	eukaryotic translation initiation factor 4E member 2	1.22	0.241	-1.73	0.081	-1.04	0.818	1.03	0.884	-0.13
1444999_at	C77651	expressed sequence C77651	1.04	0.898	1.05	0.918	-1.48	0.204	-1.11	0.647	-0.13
1432777_at	9430032J07Rik	RIKEN cDNA 9430032J07 gene	1.25	0.263	-1.11	0.878	-1.64	0.338	1.98	0.337	0.12
1421512_at	Cep250	centrosomal protein 250	1.09	0.613	-1.92	0.118	1.15	0.558	-1.01	0.968	-0.17
1415884_at	Ela3	elastase 3, pancreatic	1.35	0.621	-1.73	0.341	-1.21	0.661	1.27	0.706	-0.08
1446786_at	Aplp2	Amyloid beta (A4) precursor-like protein 2	1.25	0.066	-1.19	0.492	-1.49	0.025	1.68	0.203	0.06
1449439_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.03	0.122	1.06	0.58	-1.49	0.05	-1.13	0.469	-0.13
1458015_at	Megf11	multiple EGF-like-domains 11	-1.24	0.004	1.11	0.742	-1.17	0.532	1.03	0.803	-0.07
1424365_at	1810037I17Rik	RIKEN cDNA 1810037I17 gene	-1.03	0.567	1.03	0.814	-1.31	0.07	1.38	0.27	0.02
1437783_x_at	Tmem4	transmembrane protein 4	1.01	0.789	1.03	0.744	-1.4	0.037	-1.27	0.469	-0.15
1420933_a_at	Eya3	eyes absent 3 homolog (Drosophila)	-1.24	0.101	-1.09	0.433	1.04	0.853	1.08	0.65	-0.05
1425060_s_at	Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	1.08	0.695	-1.21	0.506	-1.17	0.561	1.2	0.603	-0.02
1426609_at	2810028N01Rik	RIKEN cDNA 2810028N01 gene	-1.11	0.393	-1.37	0.017	1.13	0.297	1.59	0.283	0.06
1433174_a_at	5430440L12Rik	RIKEN cDNA 5430440L12 gene	-1.22	0.345	-1.07	0.605	1.01	0.934	1.58	0.276	0.07
1423751_at	Sf1	splicing factor 1	-1.55	0.282	-1.01	0.96	1.13	0.616	1.4	0.321	-0.01
1438021_at	BC013481	cDNA sequence BC013481	1.01	0.972	-1.3	0.431	-1.02	0.941	1.62	0.101	0.08
1454917_at	AU045404	expressed sequence AU045404	1.01	0.862	-1.17	0.036	-1.11	0.518	1.12	0.148	-0.04
1420607_at	Rbm18	RNA binding motif protein 18	-1.07	0.651	-1.27	0.434	1.03	0.937	1.19	0.664	-0.03
1432443_at	1700021P22Rik	RIKEN cDNA 1700021P22 gene	1.05	0.437	1.05	0.741	-1.52	0.149	-1.37	0.604	-0.2
1426409_at	Lzts2	leucine zipper, putative tumor suppressor 2	-1.15	0.425	1.01	0.962	-1.13	0.569	1.14	0.384	-0.03
1418397_at	Zfp275	zinc finger protein 275	1.02	0.814	1.04	0.441	-1.43	0.036	-1.34	0.468	-0.18
1454573_at	4933412L11Rik	RIKEN cDNA 4933412L11 gene	1.7	0.321	-1.58	0.161	-2.33	0.188	2.35	0.234	0.04
1458969_at	AU019559	expressed sequence AU019559	1.03	0.619	1.12	0.174	-1.63	0.124	-1.37	0.282	-0.21
1420537_at	Kctd4	potassium channel tetramerisation domain containing 4	1.06	0.912	-1.85	0.442	1.17	0.326	-1.15	0.664	-0.19
1420640_at	Jmy	junction-mediating and regulatory protein	1	0.986	-1.22	0.055	-1.07	0.652	1.56	0.069	0.07
1445987_at	---	Transcribed locus	1.22	0.758	-1.3	0.567	-1.3	0.679	1.08	0.883	-0.07
1418384_at	9430083G14Rik	RIKEN cDNA 9430083G14 gene	-1.29	0.009	-1.29	0.001	1.21	0.226	1.01	0.941	-0.09
1421704_a_at	Pik3c2g	phosphatidylinositol 3-kinase, C2 domain containing, gamma polypeptide	-1.33	0.094	1.07	0.636	-1.06	0.744	1.58	0.184	0.06
1446860_at	Gab2	Growth factor receptor bound protein 2-associated protein 2	-1.14	0.627	1.31	0.09	-1.72	0.154	1.22	0.171	-0.08
1435238_x_at	2310009A05Rik	RIKEN cDNA 2310009A05 gene	1	0.985	1.03	0.559	-1.37	0.058	-1.29	0.206	-0.16
1449620_s_at	D16Wsu65e	DNA segment, Chr 16, Wayne State University 65, expressed	1.02	0.61	-1.17	0.178	-1.13	0.49	1.44	0.281	0.04

1437923_at	AI314760	expressed sequence AI314760	1.18	0.278	-1.01	0.957	-1.69	0.018	1.19	0.596	-0.08
1422552_at	Rprm	reprimo, TP53 dependent G2 arrest mediator candidate	1.67	0.132	-3.78	0.007	-1.21	0.371	1.26	0.39	-0.51
1418926_at	Zfhx1a	zinc finger homeobox 1a	1.14	0.197	-1.1	0.528	-1.41	0.06	1.13	0.461	-0.06
1417730_at	Ext1	exostoses (multiple) 1	-1.05	0.465	1.02	0.782	-1.27	0.052	1.68	0.073	0.09
1445251_at	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	1.1	0.761	-1.51	0.328	-1.01	0.98	1.05	0.501	-0.09
1424745_at	2900006B13Rik	RIKEN cDNA 2900006B13 gene	-1.17	0.138	-1.16	0.174	1.05	0.434	1.05	0.76	-0.06
1437189_x_at	Ga17	dendritic cell protein GA17	1.02	0.974	-1.34	0.508	-1.01	0.966	1.17	0.604	-0.04
1423910_at	Centg3	centaurin, gamma 3	-1.16	0.374	-1.2	0.548	1.07	0.827	1.28	0.314	0
1425754_a_at	Btn1a1	butyrophilin, subfamily 1, member A1	-1.69	0.606	-1.03	0.867	1.2	0.617	1.09	0.892	-0.11
1436842_at	B230380D07Rik	RIKEN cDNA B230380D07 gene	-1.16	0.459	1.01	0.965	-1.12	0.479	1.07	0.715	-0.05
1453962_at	Pfn3	profilin 3	-1.23	0.136	1.08	0.652	-1.15	0.116	1.17	0.607	-0.03
1417829_a_at	Rab15	RAB15, member RAS oncogene family	-1.39	0.197	1.28	0.642	-1.31	0.254	1.33	0.416	-0.02
1456476_at	Atxn2l	ataxin 2-like	-1.26	0.59	1.19	0.547	-1.29	0.211	1.42	0.202	0.02
1446143_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	1.06	0.918	1.04	0.895	-1.51	0.097	-1.16	0.653	-0.14
1444289_at	Yipf5	Yip1 domain family, member 5	1.05	0.773	-1.05	0.722	-1.31	0.102	1.11	0.489	-0.05
1426141_at	Mrgpra1	MAS-related GPR, member A1	1.21	0.829	-2.38	0.042	1.13	0.199	-1.19	0.493	-0.31
1458053_at	Abi2	abl-interactor 2	1.14	0.35	1.08	0.872	-1.84	0.166	-1.1	0.838	-0.18
1442173_at	Phf3	PHD finger protein 3	-1.14	0.847	-1.44	0.181	1.19	0.606	1.08	0.827	-0.08
1428375_at	4932415G12Rik	RIKEN cDNA 4932415G12 gene	-1.17	0.388	-1.11	0.793	1.01	0.955	1.06	0.626	-0.05
1436921_at	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	-1.27	0.155	1.3	0.016	-1.48	0.001	1.09	0.761	-0.09
1423374_at	Ncoa6	nuclear receptor coactivator 6	-1.26	0.22	1	0.966	-1.03	0.821	1.07	0.616	-0.06
1437179_at	Rif1 /// LOC671598	Rap1 interacting factor 1 homolog (yeast) /// similar to Telomere-associated prote	1.12	0.657	-1.18	0.314	-1.25	0.32	1.33	0.376	0
1440048_at	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.54	0.517	1.4	0.194	-1.4	0.404	1.15	0.683	-0.1
1449116_a_at	Dtymk	deoxythymidylate kinase	-1.11	0.494	-1.19	0.372	1.02	0.919	2.02	0.214	0.19
1434204_x_at	Shmt2	Serine hydroxymethyl transferase 2 (mitochondrial)	-1.49	0.44	-1.37	0.504	1.36	0.31	1.06	0.853	-0.11
1446779_at	Nploc4	Nuclear protein localization 4 homolog (S. cerevisiae)	-1.03	0.371	1.06	0.717	-1.37	0.067	1.13	0.511	-0.05
1418743_a_at	Tesc	tescalcin	1.04	0.55	-1.63	0.102	1.11	0.568	-2.65	0.046	-0.53
1415877_at	Dpysl3	dihydropyrimidinase-like 3	1.01	0.97	1.15	0.696	-1.65	0.047	-1.17	0.305	-0.16
1440007_at	Slc43a1	solute carrier family 43, member 1	1.22	0.663	-1.28	0.182	-1.31	0.337	2.08	0.217	0.18
1433241_at	9430013L17Rik	RIKEN cDNA 9430013L17 gene	1.08	0.28	-1.71	0.173	1.1	0.824	-1.16	0.101	-0.17
1431916_at	9030618K22Rik	RIKEN cDNA 9030618K22 gene	1.11	0.467	-2.34	0.036	1.22	0.644	-1.6	0.46	-0.4
1416590_a_at	Rab34	RAB34, member of RAS oncogene family	-1.32	0.058	1.09	0.215	-1.09	0.54	1.14	0.465	-0.05
1416029_at	Klf10	Kruppel-like factor 10	1.02	0.948	-1.22	0.547	-1.08	0.64	1.32	0.018	0.01
1433877_at	4732473B16Rik	RIKEN cDNA 4732473B16 gene	1.06	0.849	-2.43	0.053	1.29	0.52	-1.44	0.607	-0.38
1437220_x_at	Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	-1.06	0.611	1.02	0.832	-1.25	0.129	1.03	0.897	-0.06
1436018_at	2700083E18Rik	RIKEN cDNA 2700083E18 gene	1	0.995	-1.06	0.765	-1.22	0.33	1.55	0.122	0.07
1436677_at	1810032O08Rik	RIKEN cDNA 1810032O08 gene	-1.11	0.715	-1.21	0.638	1.03	0.913	1.16	0.751	-0.03
1452737_at	2810008M24Rik	RIKEN cDNA 2810008M24 gene	1	0.96	1.02	0.897	-1.34	0.022	-1.36	0.016	-0.17
1446970_at	Cnot8	CCR4-NOT transcription complex, subunit 8	-1.53	0.595	1.31	0.24	-1.25	0.38	1.01	0.967	-0.11
1416394_at	Bag1	Bcl2-associated athanogene 1	1.06	0.497	-1.12	0.418	-1.23	0.041	1.27	0.308	-0.01
1430244_at	4921509J17Rik	RIKEN cDNA 4921509J17 gene	-1.57	0.496	1.41	0.07	-1.39	0.156	1.07	0.884	-0.12
1452892_at	Stk33	serine/threonine kinase 33	1.09	0.929	-2.38	0.251	1.26	0.478	-1.1	0.524	-0.28
1416301_a_at	Ebf1	early B-cell factor 1	1.3	0.093	-3.13	0.144	1.14	0.717	-3.24	0.048	-0.98
1449562_at	1700001G17Rik	RIKEN cDNA 1700001G17 gene	-1.47	0.511	1.13	0.619	-1.05	0.816	1.42	0.591	0.01
1422500_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	-1.13	0.07	-1.32	0.171	1.13	0.632	1.44	0.251	0.03
1431975_at	4930521O11Rik	RIKEN cDNA 4930521O11 gene	-1.19	0.362	1.35	0.38	-1.72	0.086	1.27	0.619	-0.07
1425316_at	B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	-1.06	0.919	-1.69	0.394	1.23	0.641	1.03	0.929	-0.12
1435634_at	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-1.17	0.197	-1.2	0.078	1.08	0.545	1.01	0.969	-0.07
1430179_at	4921507G05Rik	RIKEN cDNA 4921507G05 gene	-1.17	0.873	-1.47	0.195	1.23	0.368	1.73	0.186	0.08
1425297_at	BC012278	cDNA sequence BC012278	-1.48	0.379	-1.06	0.652	1.15	0.465	1.01	0.966	-0.1
1451159_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	-1.07	0.592	-1.25	0.129	1.03	0.913	2.76	0.121	0.37
1445096_at	Ccdc51	Coiled-coil domain containing 51	1.35	0.208	-1.17	0.715	-1.77	0.112	1.12	0.748	-0.12
1427600_at	Tnfrsf19	Tumor necrosis factor receptor superfamily, member 19	-1.6	0.484	1.36	0.602	-1.28	0.365	1.07	0.89	-0.11

1427971_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	-1.29	0.264	-1.05	0.486	1.04	0.724	1.05	0.744	-0.06
1422064_a_at	Zbtb20	zinc finger and BTB domain containing 20	-1.07	0.495	1.08	0.33	-1.32	0.069	1.11	0.82	-0.05
1455399_at	Cnksr1 /// LOC6371	connector enhancer of kinase suppressor of Ras 1 /// similar to connector enhanc	1.09	0.566	-1.21	0.761	-1.18	0.27	1.4	0.376	0.03
1429534_a_at	Immt	inner membrane protein, mitochondrial	-1.18	0.124	-1.22	0.09	1.1	0.068	1.32	0.118	0
1436518_at	Usp46	Ubiquitin specific peptidase 46	1.23	0.142	-1.06	0.606	-1.69	0.023	2.95	0.245	0.36
1419984_s_at	Zfp644	zinc finger protein 644	1.03	0.895	1.11	0.204	-1.6	0.033	-1.19	0.273	-0.16
1455009_at	Cpd	carboxypeptidase D	-1.15	0.189	1.12	0.572	-1.28	0.036	2.34	0.249	0.26
1420064_s_at	Tktl1	transketolase-like 1	1.09	0.742	-1.17	0.412	-1.22	0.718	1.82	0.104	0.13
1451922_at	Lman1l	lectin, mannose-binding 1 like	1.05	0.951	-2.44	0.23	1.3	0.505	-1.43	0.383	-0.38
1453484_at	1700081D17Rik	RIKEN cDNA 1700081D17 gene	1.13	0.13	-2.46	0.126	1.23	0.156	-2.17	0.235	-0.57
1457935_at	Tshz2	Teashirt zinc finger family member 2	-1.35	0.383	1.5	0.3	-1.91	0.068	1.13	0.578	-0.16
1458590_at	Ints7	Integrator complex subunit 7	-1.11	0.738	-1.56	0.181	1.23	0.594	1.53	0.423	0.02
1456993_at	D2Ertd640e	DNA segment, Chr 2, ERATO Doi 640, expressed	1.43	0.291	-1.27	0.295	-1.81	0.021	1.48	0.012	-0.04
1429025_a_at	Hexim2	hexamthylene bis-acetamide inducible 2	1.12	0.123	-1.46	0.476	-1.04	0.917	1.79	0.117	0.1
1416450_at	Tbn	taube nuss	1.01	0.983	-1.41	0.384	1.05	0.878	-1.28	0.484	-0.16
1455706_at	Stxbp4	syntaxin binding protein 4	-1.27	0.569	-1.05	0.834	1.03	0.791	1.77	0.135	0.12
1433547_s_at	Nudcd1	NudC domain containing 1	1.08	0.611	-1.07	0.552	-1.33	0.168	1.41	0.157	0.02
1456503_at	Nup214	nucleoporin 214	1.15	0.809	-1.56	0.221	-1.02	0.802	1	1	-0.11
1436992_x_at	Vdac1	voltage-dependent anion channel 1	-1.13	0.387	-1.14	0.167	1	0.964	1.18	0.276	-0.02
1422501_s_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	-1.13	0.529	-1.71	0.016	1.3	0.274	1.62	0.227	0.02
1426922_s_at	Hrb	HIV-1 Rev binding protein	-1.03	0.855	1.03	0.726	-1.3	0.054	1.28	0.518	-0.01
1425415_a_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, syst	1.17	0.412	-1.75	0.113	1.02	0.882	-1.63	0.376	-0.3
1457437_at	C630035N08Rik	RIKEN cDNA C630035N08 gene	1.1	0.722	-1.33	0.253	-1.09	0.76	1.13	0.66	-0.05
1444255_at	D630045J12Rik	RIKEN cDNA D630045J12 gene	-1.37	0.426	-3.24	0.17	1.73	0.457	1.03	0.879	-0.46
1445582_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	1.27	0.66	-1.01	0.986	-1.97	0.236	1.59	0.33	-0.03
1452366_at	4732435N03Rik	RIKEN cDNA 4732435N03 gene	1.22	0.258	-1.27	0.628	-1.31	0.024	1.84	0.176	0.12
1449476_at	Rage	renal tumor antigen	-1.11	0.74	-1.48	0.188	1.19	0.572	1.03	0.817	-0.09
1427951_s_at	Ccdc28a	coiled-coil domain containing 28A	-1.19	0.371	1.05	0.493	-1.14	0.47	1.04	0.818	-0.06
1417208_at	Amacr	alpha-methylacyl-CoA racemase	-1.16	0.046	-1.18	0.077	1.06	0.373	1.1	0.644	-0.04
1441671_at	Glcci1	Glucocorticoid induced transcript 1	-1.5	0.572	-1.43	0.381	1.4	0.402	1.29	0.688	-0.06
1444905_at	D1Ertd705e	DNA segment, Chr 1, ERATO Doi 705, expressed	1.32	0.564	-1.37	0.379	-1.4	0.46	1.09	0.813	-0.09
1451548_at	---	---	-1.33	0.801	-1.23	0.653	1.2	0.749	1.44	0.722	0.02
1431897_at	Chst9	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9	1.28	0.113	-1.65	0.568	-1.13	0.82	1.23	0.165	-0.07
1454059_at	4930500F04Rik	RIKEN cDNA 4930500F04 gene	-4.34	0.003	1.21	0.745	1.33	0.629	-2.16	0.321	-0.99
1436088_at	0910001A06Rik	RIKEN cDNA 0910001A06 gene	1.04	0.897	-1.62	0.005	1.11	0.365	-1.38	0.335	-0.21
1456369_at	Pot1	protection of telomeres 1	-1.29	0.703	-2.2	0.201	1.54	0.373	1.74	0.151	-0.05
1438551_at	Neurog1	neurogenin 1	1.23	0.451	-1.6	0.018	-1.09	0.5	1.09	0.768	-0.09
1443120_at	Pdzd4	PDZ domain containing 4	-1.04	0.959	-1.71	0.386	1.23	0.674	2.1	0.021	0.14
1421736_at	V1rd3	vomeronasal 1 receptor, D3	1.5	0.312	-1.75	0.386	-1.43	0.416	2.14	0.169	0.12
1438493_at	4933433K01Rik	RIKEN cDNA 4933433K01 gene	-1.03	0.925	1.29	0.404	-1.97	0.221	1	0.991	-0.18
1419751_x_at	AB056442	cDNA sequence AB056442	-1.12	0.577	1.13	0.577	-1.34	0.621	1.68	0.486	0.09
1420853_at	Sdc3	syndecan 3	-1.17	0.197	-1.12	0.503	1.03	0.913	1.32	0.523	0.01
1428987_at	Dynlrb2	dynein light chain roadblock-type 2	-1.63	0.12	1.15	0.712	1.01	0.968	-1.44	0.005	-0.23
1457314_at	L1td1	LINE-1 type transposase domain containing 1	-1.12	0.217	-1.24	0.623	1.07	0.711	1.11	0.348	-0.04
1420956_at	Apc	adenomatosis polyposis coli	1	0.996	1.04	0.698	-1.36	0.071	-1.11	0.723	-0.11
1447761_x_at	Sod1 /// LOC54584	superoxide dismutase 1, soluble /// similar to Superoxide dismutase /// similar to S	-1.49	0.387	1.61	0.121	-2.06	0.025	1.47	0.429	-0.12
1419837_at	Treml2	triggering receptor expressed on myeloid cells-like 2	-1.67	0.486	1.02	0.965	1.16	0.645	-1.18	0.723	-0.17
1424020_at	Arl6ip6 /// LOC6744	ADP-ribosylation factor-like 6 interacting protein 6 /// similar to ADP-ribosylation-li	-1.23	0.136	-1.22	0.118	1.14	0.568	1.51	0.35	0.05
1449035_at	4930544G11Rik	RIKEN cDNA 4930544G11 gene	-1.57	0.047	1.6	0.337	-1.89	0.034	1.38	0.263	-0.12
1448904_at	D6Wsu176e	DNA segment, Chr 6, Wayne State University 176, expressed	-1.06	0.572	1.05	0.745	-1.28	0.14	1.11	0.712	-0.04
1446434_at	Galnact2	Chondroitin sulfate GalNAcT-2	1.49	0.47	-1.48	0.067	-1.66	0.003	1.16	0.238	-0.12
1442143_at	Tmem16d	transmembrane protein 16D (eight membrane-spanning domains)	1.31	0.549	1.09	0.895	-2.71	0.021	-1.36	0.672	-0.42
1419871_at	Ppp2r1b	Protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-1.13	0.213	1.18	0.363	-1.42	0.005	1.35	0.387	0

1453526_at	4930503E14Rik	RIKEN cDNA 4930503E14 gene	1.47	0.16	-2.14	0.245	-1.19	0.609	2.86	0.019	0.25
1447276_at	D13Ertd37e	DNA segment, Chr 13, ERATO Doi 37, expressed	-2.06	0.54	1.49	0.323	-1.25	0.273	6.85	0.281	1.26
1453126_at	Lrfn2	leucine rich repeat and fibronectin type III domain containing 2	1.43	0.434	-1.77	0.131	-1.29	0.652	1.24	0.621	-0.1
1436229_at	BC049806	CDNA sequence BC049806	1.19	0.218	-1.69	0.157	-1.01	0.986	1.23	0.184	-0.07
1449093_at	Ctf1	cardiotrophin 1	-1.14	0.539	1.02	0.895	-1.14	0.479	2.38	0.033	0.28
1424108_at	Glo1	glyoxalase 1	1.07	0.46	-1.21	0.003	-1.15	0.251	1.69	0.292	0.1
1422077_at	Acot4	acyl-CoA thioesterase 4	1.21	0.604	-1.17	0.735	-1.41	0.337	1.38	0.247	0
1420774_a_at	4930583H14Rik	RIKEN cDNA 4930583H14 gene	-1.79	0.326	-1.35	0.146	1.48	0.374	1.28	0.575	-0.1
1444497_at	BC059050	cDNA sequence BC059050	-1.94	0.614	1	0.997	1.26	0.433	-1.02	0.953	-0.18
1429548_at	Tex22	testis expressed gene 22	1.03	0.961	-1.75	0.366	1.17	0.769	-2.18	0.018	-0.43
1447159_at	Syne2	Synaptic nuclear envelope 2	-1.09	0.835	1.27	0.36	-1.7	0.048	1.25	0.213	-0.07
1447910_x_at	Selk	selenoprotein K	1.05	0.302	-1.09	0.336	-1.23	0.208	1.18	0.384	-0.02
1453567_s_at	2810441K11Rik	RIKEN cDNA 2810441K11 gene	-1.22	0.304	-1.26	0.044	1.16	0.535	1.54	0.344	0.06
1432699_at	2900024I21Rik	RIKEN cDNA 2900024I21 gene	-1.62	0.124	1.35	0.496	-1.24	0.038	1.21	0.641	-0.07
1449946_a_at	Zfp593	zinc finger protein 593	1.14	0.282	-2.39	0.081	1.21	0.625	-1.3	0.134	-0.33
1416112_at	Cox8a	cytochrome c oxidase, subunit VIIIa	-1.15	0.297	-1.12	0.352	1.01	0.951	1.03	0.82	-0.06
1449538_a_at	Gcnt1 /// LOC6359	glucosaminyl (N-acetyl) transferase 1, core 2 /// similar to glucosaminyl (N-acetyl)	-1.35	0.156	-2.63	0.076	1.65	0.29	1.55	0.427	-0.19
1441459_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130020A	1.26	0.8	-1.46	0.375	-1.2	0.492	1.59	0.499	0.05
1430794_at	4933426K07Rik	RIKEN cDNA 4933426K07 gene	-1.4	0.578	-1.95	0.146	1.54	0.36	1.02	0.912	-0.2
1433642_at	Arl15	ADP-ribosylation factor-like 15	-1.08	0.551	1.03	0.837	-1.22	0.197	1.27	0.408	0
1447386_at	Usp8	Ubiquitin specific peptidase 8	1.25	0.61	-1.16	0.452	-1.5	0.109	1.07	0.882	-0.09
1429344_at	Cttnbp2	cortactin binding protein 2	-1.21	0.23	1.28	0.425	-1.5	0.181	1.11	0.578	-0.08
1459472_at	---	---	-2.03	0.025	1.16	0.446	1.12	0.78	-1.19	0.761	-0.23
1429648_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), m	1.06	0.545	-1.22	0.045	-1.11	0.303	1.02	0.906	-0.06
1450035_a_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	1.11	0.8	-1.27	0.283	-1.14	0.657	1.44	0.463	0.04
1459374_at	Diap3	Diaphanous homolog 3 (Drosophila)	1.58	0.635	-1.89	0.411	-1.51	0.128	4.28	0.205	0.62
1434229_a_at	Polb	polymerase (DNA directed), beta	1.02	0.826	1.04	0.733	-1.39	0.052	-1.62	0.205	-0.24
1421985_a_at	Eif4e2	eukaryotic translation initiation factor 4E member 2	-1.14	0.457	-1.36	0.105	1.16	0.435	1.09	0.644	-0.06
1416114_at	Sparcl1	SPARC-like 1 (mast9, hevin)	1.09	0.551	-1.09	0.523	-1.3	0.226	1.11	0.623	-0.05
1459088_at	C79557	expressed sequence C79557	-1.95	0.345	-1.2	0.639	1.43	0.095	1.21	0.424	-0.13
1439395_at	9630025I21Rik	RIKEN cDNA 9630025I21 gene	1.01	0.99	1.19	0.804	-1.72	0.204	-1.01	0.961	-0.14
1424878_at	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	-1.29	0.225	-1.06	0.576	1.05	0.784	1.51	0.116	0.05
1440450_at	Hspa1l	Heat shock protein 1-like	1.36	0.065	-1.18	0.692	-1.76	0.014	1.22	0.668	-0.09
1455780_at	Ttll6	tubulin tyrosine ligase-like family, member 6	-1.34	0.276	-1.16	0.799	1.17	0.221	1.53	0.289	0.05
1456580_s_at	Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-1.06	0.499	-1.31	0.116	1.07	0.576	1.11	0.121	-0.05
1438985_x_at	Otud5	OTU domain containing 5	-1.14	0.602	-1.94	0.113	1.39	0.172	1.22	0.521	-0.12
1433150_at	4933415B22Rik	RIKEN cDNA 4933415B22 gene	-1.18	0.214	1.07	0.756	-1.16	0.188	1.26	0.055	0
1449938_at	Pp11r	placental protein 11 related	-1.19	0.716	-1.17	0.659	1.08	0.708	1.08	0.142	-0.05
1422961_at	Nat3	N-acetyltransferase 3	-1.99	0.23	-1.06	0.787	1.33	0.497	2.57	0.239	0.21
1424404_at	0610040J01Rik	RIKEN cDNA 0610040J01 gene	1.09	0.582	-1.18	0.115	-1.19	0.522	2.99	0.133	0.43
1442322_at	Slit2	Slit homolog 2 (Drosophila)	-1.01	0.979	1.23	0.359	-1.8	0.043	1.26	0.06	-0.08
1437565_a_at	LOC633966	similar to guanine nucleotide binding protein-like 2 (nucleolar)	-1.23	0.068	1.1	0.457	-1.16	0.213	1.02	0.888	-0.07
1418251_at	Tulp3	tubby-like protein 3	-1.25	0.367	-1.08	0.892	1.05	0.902	1.01	0.981	-0.07
1446646_at	Taf3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.31	0.318	-1.37	0.16	1.28	0.574	2.3	0.415	0.23
1429907_at	1700094D03Rik	RIKEN cDNA 1700094D03 gene	1.02	0.895	-1.39	0.141	1.04	0.881	-1.3	0.529	-0.16
1422860_at	Nts	neurotensin	1.7	0.452	-1.74	0.041	-2	0.04	1.37	0.139	-0.17
1432707_at	Phgdh /// LOC3829	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.45	0.467	-2.68	0.003	1.71	0.089	1.06	0.845	-0.34
1423109_s_at	Slc25a20	solute carrier family 25 (mitochondrial carnitine/acylcarnitine translocase), membe	1.07	0.768	-1.34	0.087	-1.05	0.646	1.05	0.734	-0.07
1448017_at	Ubap2l	ubiquitin associated protein 2-like	1.44	0.323	-2.92	0.196	-1.01	0.968	1.86	0.085	-0.16
1442191_at	AF397014	cDNA sequence AF397014	-1.17	0.365	-1.58	0.031	1.29	0.386	1.22	0.72	-0.06
1434783_at	Tmem106c	transmembrane protein 106C	-1.1	0.759	-1.31	0.136	1.11	0.74	1.03	0.918	-0.07
1443271_at	Tmem28	Transmembrane protein 28	1.14	0.836	-1.61	0.506	1.01	0.973	-1.47	0.278	-0.23
1434860_at	Narg3	NMDA receptor-regulated gene 3	-1.12	0.111	1.08	0.191	-1.24	0.009	1.09	0.47	-0.05

1455230_at	Cacng4	calcium channel, voltage-dependent, gamma subunit 4	-1.99	0.165	1.02	0.95	1.25	0.675	-1.13	0.816	-0.21
1427602_at	Dep1	diabetic embryopathy 1	-1.16	0.804	-1.15	0.37	1.05	0.889	1.33	0.47	0.02
1457141_at	Aqp11	Aquaporin 11	1.27	0.34	-1.1	0.582	-1.66	0.164	2.35	0.234	0.21
1454267_a_at	Prss32	protease, serine, 32	-1.67	0.296	1.14	0.744	1.03	0.914	-1.07	0.885	-0.14
1444931_at	Tek	Endothelial-specific receptor tyrosine kinase	-1.43	0.726	1.48	0.687	-1.68	0.259	1.02	0.957	-0.15
1433171_at	3110049I03Rik	RIKEN cDNA 3110049I03 gene	-1.25	0.075	-1.07	0.894	1.04	0.924	1.25	0.607	-0.01
1444474_at	C630028L02Rik	RIKEN cDNA C630028L02 gene	-2.24	0.097	-1.1	0.858	1.42	0.319	1.09	0.671	-0.21
1427232_at	Tshz1	teashirt zinc finger family member 1	-1.21	0.309	-1.32	0.072	1.19	0.267	1.24	0.074	-0.02
1417315_at	Gripap1	GRIP1 associated protein 1	-1.38	0.147	-1.16	0.449	1.19	0.317	1.12	0.437	-0.06
1459505_at	---	---	-2.51	0.318	-1.25	0.692	1.58	0.213	1.4	0.096	-0.19
1427465_at	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	1.01	0.987	-1.92	0.146	1.25	0.631	-1.2	0.431	-0.22
1432790_at	9030218A15Rik	RIKEN cDNA 9030218A15 gene	1	0.996	1.12	0.852	-1.52	0.341	-1.41	0.508	-0.2
1455124_at	Trim68	tripartite motif containing 68	1.02	0.853	-1.54	0.029	1.11	0.397	-1.62	0.314	-0.26
1436510_a_at	Lrrfip2	leucine rich repeat (in FLII) interacting protein 2	-1.02	0.775	1.01	0.916	-1.27	0.076	1.31	0.124	0.01
1443390_at	Dock1	Dedicator of cyto-kinesis 1	1.09	0.752	1.18	0.395	-1.97	0.05	-1.1	0.461	-0.2
1422716_a_at	Acp1	acid phosphatase 1, soluble	-1.18	0.712	1.06	0.747	-1.15	0.256	1.62	0.314	0.09
1418678_at	Has2	hyaluronan synthase 2	-1.34	0.322	1.14	0.377	-1.12	0.763	1.03	0.946	-0.07
1427698_at	Brca1	breast cancer 1	-1.19	0.485	-1.16	0.395	1.07	0.448	1.09	0.223	-0.05
1433623_at	Zfp367	zinc finger protein 367	-1.25	0.119	1.03	0.902	-1.05	0.488	2.32	0.132	0.26
1431340_a_at	2310002J21Rik	RIKEN cDNA 2310002J21 gene	-1.12	0.462	1.06	0.617	-1.21	0.179	2.06	0.188	0.2
1419880_x_at	---	Transcribed locus	-1.75	0.044	1.13	0.627	1.07	0.805	-1.03	0.829	-0.14
1423525_at	Mastl	microtubule associated serine/threonine kinase-like	-1.26	0.65	1.3	0.711	-1.46	0.216	3.13	0.306	0.43
1431757_s_at	5033417F24Rik	RIKEN cDNA 5033417F24 gene	-1.06	0.872	-1.37	0.021	1.1	0.828	1.03	0.952	-0.07
1429730_at	1810009N02Rik	RIKEN cDNA 1810009N02 gene	-1.26	0.161	-1.15	0.596	1.11	0.59	1.06	0.844	-0.06
1423908_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	-1.17	0.428	-1.11	0.065	1.02	0.876	1.02	0.922	-0.06
1455517_at	Rbm4	RNA binding motif protein 4	-1.29	0.212	-1.03	0.866	1.03	0.85	1.21	0.557	-0.02
1445892_at	Per2	Period homolog 2 (Drosophila)	1.04	0.93	1.08	0.809	-1.51	0.186	-1.45	0.008	-0.21
1451456_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	1.01	0.974	-1.23	0.636	-1.04	0.771	2.13	0.094	0.22
1430465_at	---	---	-1.02	0.954	1.45	0.447	-2.88	0.151	1.28	0.702	-0.29
1451476_at	Zdhhc8	zinc finger, DHHC domain containing 8	-1.46	0.228	1.09	0.498	-1	0.999	1.04	0.69	-0.08
1448671_at	Ube2e3	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	-1.14	0.369	-1.57	0.073	1.26	0.62	1.62	0.454	0.04
1452849_at	Sin3b	transcriptional regulator, SIN3B (yeast)	-1.08	0.636	-1.24	0.361	1.05	0.777	1.22	0.311	-0.01
1451044_at	Sip1	survivor of motor neuron protein interacting protein 1	1.02	0.951	-1.27	0.348	-1.02	0.892	1.45	0.334	0.04
1444556_at	Slfn1	Schlafen 1	-1.65	0.05	1.04	0.936	1.14	0.714	-1.24	0.315	-0.18
1445898_at	Ggcx	gamma-glutamyl carboxylase	-1.32	0.393	1.16	0.587	-1.16	0.184	1.11	0.797	-0.05
1445810_at	C85163	expressed sequence C85163	-1.1	0.562	1.21	0.708	-1.52	0.287	1.45	0.396	0.01
1436883_at	Mbtps2	membrane-bound transcription factor peptidase, site 2	-1.09	0.44	1.06	0.564	-1.24	0.151	1.04	0.877	-0.06
1425961_at	BC016548	cDNA sequence BC016548	-1.07	0.858	1.25	0.669	-1.69	0.069	1.29	0.284	-0.05
1424289_at	BC010311	cDNA sequence BC010311	1.05	0.73	-1.12	0.758	-1.19	0.227	1.2	0.267	-0.01
1447178_at	---	---	1.1	0.751	-1.14	0.549	-1.25	0.745	3	0.342	0.43
1451639_at	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	1.02	0.847	-1.06	0.743	-1.23	0.43	1.19	0.068	-0.02
1420875_at	Ptk9	protein tyrosine kinase 9	-1.08	0.232	1.05	0.611	-1.23	0.145	1.02	0.779	-0.06
1423239_at	Impdh1	inosine 5'-phosphate dehydrogenase 1	-1.35	0.572	-1.15	0.329	1.17	0.268	1.04	0.8	-0.07
1438680_at	Auts2	autism susceptibility candidate 2	-1.14	0.627	-1.21	0.664	1.08	0.667	1.34	0.312	0.02
1457782_at	Tln1	talin 1	-1.05	0.613	1.04	0.883	-1.27	0.391	1.03	0.609	-0.06
1447892_at	---	---	-1.76	0.13	1.18	0.188	1.03	0.86	-1.39	0.429	-0.24
1443901_at	---	---	-1.51	0.395	1	1	1.12	0.651	-1.08	0.852	-0.12
1426952_at	Arhgap18	Rho GTPase activating protein 18	-1.27	0.147	-1.15	0.475	1.12	0.352	1.23	0.313	-0.02
1434553_at	Tmem56	transmembrane protein 56	1.05	0.679	-1.29	0.109	-1.04	0.842	13.03	0.184	2.94
1458606_at	---	---	-1.1	0.568	1.07	0.563	-1.24	0.063	2.04	0.02	0.19
1440608_at	---	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732488M1	-1.6	0.185	-1.51	0.084	1.49	0.064	1.27	0.437	-0.09
1421032_a_at	Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12	-1.09	0.608	1.02	0.847	-1.18	0.224	1.46	0.137	0.05
1416202_at	Phb2	prohibitin 2	-1.1	0.427	-1.2	0.281	1.04	0.696	1.1	0.388	-0.04

1421578_at	Ccl4	chemokine (C-C motif) ligand 4	-1.94	0.003	1.29	0.553	-1.03	0.916	1.52	0.077	-0.04
1415728_at	Pabpn1	poly(A) binding protein, nuclear 1	-1.27	0.012	1.02	0.937	-1.02	0.939	1.1	0.779	-0.04
1456984_at	Scml2	sex comb on midleg-like 2 (Drosophila)	-1.16	0.117	1.23	0.447	-1.46	0.286	2.24	0.113	0.21
1440123_at	---	---	1.08	0.823	-1.28	0.577	-1.08	0.782	1.22	0.537	-0.02
1460012_at	Wfdc3	WAP four-disulfide core domain 3	-1.23	0.492	-1.98	0.241	1.46	0.521	1.58	0.334	-0.04
1416314_at	---	---	-1.51	0.665	-1.64	0.549	1.51	0.54	1.65	0.148	0
1416890_at	Wdr74	WD repeat domain 74	-1.14	0.39	-1.27	0.087	1.12	0.634	1.01	0.944	-0.07
1441469_at	Dock4	dedicator of cytokinesis 4	-1.22	0.057	1.18	0.483	-1.28	0.222	1.13	0.751	-0.05
1456942_x_at	LOC668339	hypothetical protein LOC668339	-1.83	0.578	-1.3	0.68	1.47	0.351	1.38	0.519	-0.07
1452433_at	---	---	-1.12	0.094	1.06	0.748	-1.21	0.335	1.19	0.447	-0.02
1433180_at	Morn1	MORN repeat containing 1	-1.38	0.458	1.33	0.069	-1.37	0.1	1.66	0.248	0.06
1430915_at	Fndc8	fibronectin type III domain containing 8	-1.44	0.274	1.18	0.658	-1.11	0.859	1.29	0.648	-0.02
1420032_at	Chek1	Checkpoint kinase 1 homolog (S. pombe)	1.08	0.862	-1.05	0.955	-1.34	0.634	1.23	0.671	-0.02
1441991_at	BC039632	cDNA sequence BC039632	1.26	0.065	-1.67	0.177	-1.08	0.754	1.13	0.64	-0.09
1427609_at	Sox14	SRY-box containing gene 14	-1.32	0.718	-1.31	0.286	1.26	0.2	1.04	0.597	-0.08
1416815_s_at	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	-1.07	0.459	1	0.985	-1.18	0.09	1.22	0.284	-0.01
1416428_at	Thap11	THAP domain containing 11	-1.17	0.154	-1.11	0.352	1.03	0.84	1.03	0.887	-0.05
1435219_x_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	-1.03	0.939	-1.34	0.457	1.07	0.928	1.32	0.685	0
1459954_at	---	---	1.22	0.776	-1.62	0.171	-1.06	0.873	1.08	0.798	-0.1
1456266_at	Rpl30	ribosomal protein L30	1.14	0.681	-1.65	0.287	1.04	0.855	-1.59	0.115	-0.27
1428125_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	-1.05	0.471	1.07	0.493	-1.33	0.126	1.15	0.186	-0.04
1442305_at	Gtpbp2	GTP binding protein 2	1.07	0.673	-1	0.948	-1.39	0.203	1.55	0.248	0.06
1421025_at	Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransf	1.02	0.896	-1.19	0.413	-1.09	0.615	1.31	0.053	0.02
1425184_at	2810433K01Rik	RIKEN cDNA 2810433K01 gene	-1.57	0.523	1.71	0.319	-2.33	0.011	1.37	0.36	-0.2
1443009_at	---	Transcribed locus	-1.08	0.785	-2.1	0.104	1.38	0.217	1.06	0.888	-0.18
1418444_a_at	Mir16	membrane interacting protein of RGS16	1	0.995	-1.01	0.964	-1.26	0.073	1.03	0.892	-0.06
1424723_s_at	Cstf3	cleavage stimulation factor, 3' pre-RNA, subunit 3	-1.22	0.19	-1.1	0.619	1.06	0.496	1.02	0.899	-0.06
1433070_at	5830433M15Rik	RIKEN cDNA 5830433M15 gene	-1.42	0.422	1.31	0.078	-1.3	0.191	1.07	0.728	-0.08
1450950_at	Smc3	structural maintenace of chromosomes 3	-1.1	0.557	1.03	0.824	-1.17	0.366	1.35	0.204	0.03
1420190_at	---	---	1.36	0.389	-1.37	0.531	-1.45	0.228	1.18	0.655	-0.07
1457144_at	Scn2b	sodium channel, voltage-gated, type II, beta	-1.67	0.341	-1.01	0.95	1.19	0.601	1.11	0.834	-0.09
1435616_at	Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	-1.14	0.58	1.03	0.453	-1.14	0.2	1.06	0.699	-0.05
1428452_at	2810025M15Rik	RIKEN cDNA 2810025M15 gene	-1.14	0.005	1.28	0.135	-1.59	0.054	1.08	0.632	-0.09
1455829_at	Usp14	ubiquitin specific peptidase 14	-1.04	0.804	-1.31	0.046	1.06	0.55	1.62	0.183	0.08
1436005_at	Sfrs14	splicing factor, arginine/serine-rich 14	-2.17	0.17	-1.71	0.359	1.74	0.402	1.22	0.226	-0.23
1423713_at	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-1.11	0.044	-1.15	0.257	1.01	0.929	1.3	0.454	0.01
1458751_at	---	---	-1.04	0.94	-1.27	0.272	1.04	0.92	1.31	0.42	0.01
1442235_at	Plagl2	Pleiomorphic adenoma gene-like 2	1.2	0.552	-1.29	0.668	-1.24	0.207	1.24	0.542	-0.02
1450304_at	Klrc2	killer cell lectin-like receptor subfamily C, member 2	1.08	0.897	-1.56	0.496	1.06	0.945	-1.81	0.39	-0.31
1420892_at	Wnt7b	wingless-related MMTV integration site 7B	1.07	0.854	-1.35	0.63	-1.03	0.889	1.36	0.279	0.01
1417516_at	Ddit3	DNA-damage inducible transcript 3	-1.19	0.402	-1.13	0.481	1.06	0.616	1.31	0.285	0.01
1454932_at	Rcor1	REST corepressor 1	-1.31	0.082	-1.03	0.833	1.06	0.808	1.5	0.201	0.05
1426824_at	Psme4	proteasome (prosome, macropain) activator subunit 4	-1.33	0.155	-1.13	0.509	1.15	0.434	1.41	0.442	0.02
1441797_at	---	---	1.27	0.5	-1.19	0.338	-1.49	0.054	1.25	0.45	-0.04
1445602_at	A630055G03Rik	RIKEN cDNA A630055G03 gene	1.07	0.719	-1.29	0.535	-1.07	0.835	1.64	0.145	0.09
1433736_at	Hcfc1	host cell factor C1	-1.27	0.027	-1.07	0.301	1.07	0.624	1.5	0.221	0.05
1435733_x_at	1500026D16Rik	RIKEN cDNA 1500026D16 gene	1.03	0.786	-1.27	0.071	-1.04	0.805	1.54	0.291	0.07
1440911_at	Col23a1	procollagen, type XXIII, alpha 1	-1.19	0.307	1.15	0.827	-1.26	0.305	1.05	0.887	-0.06
1423091_a_at	Gpm6b	glycoprotein m6b	1.2	0.333	1.02	0.963	-1.76	0.006	-1.77	0.183	-0.33
1436278_at	---	---	1.05	0.868	-1.05	0.88	-1.28	0.208	1.02	0.963	-0.07
1431580_at	4833421K07Rik	RIKEN cDNA 4833421K07 gene	-1.33	0.552	-1.01	0.962	1.05	0.877	1.46	0.502	0.04
1420984_at	Pctp	phosphatidylcholine transfer protein	-1.05	0.751	-1.51	0.107	1.17	0.202	1.21	0.505	-0.05
1458940_at	5730507A11Rik	RIKEN cDNA 5730507A11 gene	-1.59	0.435	1.34	0.313	-1.23	0.275	1.23	0.447	-0.06

1425111_at	Sorcs3	sortilin-related VPS10 domain containing receptor 3	-1.54	0.494	1.65	0.368	-2.07	0.006	1.15	0.803	-0.2
1432924_at	2810404I24Rik	RIKEN cDNA 2810404I24 gene	1.07	0.74	1.11	0.708	-1.64	0.024	-1.34	0.098	-0.2
1448086_at	D1Ertd164e	DNA segment, Chr 1, ERATO Doi 164, expressed	-2.71	0.359	1.06	0.886	1.35	0.348	-1.7	0.263	-0.5
1426356_at	6330578E17Rik	RIKEN cDNA 6330578E17 gene	-1.07	0.632	-1.24	0.27	1.05	0.879	1.06	0.836	-0.05
1430381_at	Ftsj1	Ftsj homolog 1 (E. coli)	-2.03	0.176	1.31	0.065	-1.01	0.965	1.22	0.333	-0.13
1451469_at	D530005L17Rik	RIKEN cDNA D530005L17 gene	-1.08	0.272	1.05	0.788	-1.24	0.108	1.36	0.22	0.02
1427858_at	Igk-V1	Immunoglobulin kappa chain variable 1 (V1)	1.01	0.971	1.09	0.763	-1.45	0.516	-1.9	0.074	-0.31
1459593_x_at	LOC669005	similar to NFkB interacting protein 1	-1.29	0.029	-1.21	0.354	1.19	0.251	1.58	0.127	0.07
1449865_at	Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	-1.38	0.721	1.06	0.92	-1	0.991	1.06	0.809	-0.07
1438194_at	2900019G14Rik	RIKEN cDNA 2900019G14 gene	1.07	0.751	-1.62	0.035	1.1	0.677	-7.03	0.008	-1.62
1431113_at	Rbm4b	RNA binding motif protein 4B	-1.57	0.39	1.41	0.247	-1.34	0.347	1.25	0.487	-0.07
1442331_at	Alas1	Aminolevulinic acid synthase 1	1.01	0.972	1	0.997	-1.29	0.088	-1.48	0.456	-0.19
1436938_at	Rbms3	RNA binding motif, single stranded interacting protein	1.23	0.258	1.02	0.897	-1.87	0.018	-1.77	0.145	-0.35
1428745_a_at	2310003L22Rik	RIKEN cDNA 2310003L22 gene	-1.4	0.06	1.01	0.937	1.06	0.461	-1.13	0.452	-0.11
1416846_a_at	Pdzrn3	PDZ domain containing RING finger 3	1.15	0.4	-1.21	0.528	-1.24	0.466	1.01	0.985	-0.07
1456281_at	Fbxl18	F-box and leucine-rich repeat protein 18	1.31	0.398	-1.48	0.455	-1.24	0.352	1.15	0.786	-0.07
1417478_a_at	4930511A21Rik	RIKEN cDNA 4930511A21 gene	-1.12	0.266	-1.17	0.081	1.03	0.821	1.03	0.877	-0.06
1436211_at	Thoc4	THO complex 4	-1.31	0.438	1.26	0.295	-1.31	0.301	1.03	0.883	-0.08
1416654_at	Slc31a2	solute carrier family 31, member 2	-1.04	0.729	-1.24	0.239	1.02	0.914	1.35	0.08	0.02
1438963_s_at	Tfpt	TCF3 (E2A) fusion partner	1.27	0.064	-1.51	0.14	-1.16	0.34	1.17	0.389	-0.06
1447754_x_at	Thap4	THAP domain containing 4	-1.09	0.145	-1.21	0.251	1.04	0.467	1.04	0.839	-0.06
1429550_at	Entpd8	ectonucleoside triphosphate diphosphohydrolase 8	-1.18	0.236	-1.21	0.138	1.11	0.723	1.12	0.656	-0.04
1429774_a_at	Ccdc98	coiled-coil domain containing 98	1.21	0.131	-1.48	0.265	-1.12	0.429	1.17	0.664	-0.05
1428591_at	Pnpla2	patatin-like phospholipase domain containing 2	1.2	0.532	-1.15	0.76	-1.38	0.222	1.74	0.336	0.1
1425779_a_at	Tbx1	T-box 1	-2.09	0.014	1.29	0.685	1.02	0.922	-1.54	0.058	-0.33
1442170_at	Ela3	Elastase 3, pancreatic	-1.23	0.436	-1.04	0.698	1.02	0.865	1.24	0.451	0
1442159_at	D2Ertd48e	DNA segment, Chr 2, ERATO Doi 48, expressed	1.22	0.652	-1.05	0.887	-1.62	0.237	1.26	0.659	-0.05
1448284_a_at	Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	-1.21	0.027	-1.06	0.215	1.02	0.868	1.05	0.729	-0.05
1456522_at	---	---	-1.12	0.916	-1.44	0.467	1.2	0.721	1.18	0.833	-0.05
1427124_at	4932416H05Rik	RIKEN cDNA 4932416H05 gene	-1.59	0.047	1.19	0.76	-1.03	0.894	1	0.998	-0.11
1434563_at	Rps6kc1	ribosomal protein S6 kinase polypeptide 1	1.18	0.378	-1.15	0.242	-1.35	0.16	1.14	0.673	-0.05
1447739_x_at	Klhdc4 /// LOC3843	kelch domain containing 4 /// hypothetical gene supported by NM_145605	1.03	0.672	-1.14	0.652	-1.14	0.505	1.25	0.234	0
1457711_at	Ranbp3	RAN binding protein 3	-1.16	0.165	1.13	0.546	-1.25	0.094	1.07	0.73	-0.05
1438902_a_at	Hsp90aa1	heat shock protein 90kDa alpha (cytosolic), class A member 1	-1.06	0.317	1.02	0.94	-1.21	0.121	1.14	0.476	-0.03
1434712_at	Smcr7l	Smith-Magenis syndrome chromosome region, candidate 7-like (human)	1.15	0.382	-1.18	0.052	-1.26	0.047	1.13	0.417	-0.04
1436704_x_at	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahy	-1.12	0.779	1.18	0.496	-1.39	0.096	1.8	0.415	0.12
1438795_x_at	Fkbp1a	FK506 binding protein 1a	1.31	0.727	-2.38	0.253	1.06	0.817	-1.3	0.511	-0.33
1416240_at	Psmb7	proteasome (prosome, macropain) subunit, beta type 7	-1.09	0.183	-1.16	0.041	1.01	0.932	1.15	0.488	-0.02
1455904_at	Gas5	growth arrest specific 5	-1.28	0.374	-1.19	0.304	1.17	0.55	1.09	0.549	-0.05
1422277_at	Glra1	glycine receptor, alpha 1 subunit	1.2	0.751	-1.13	0.77	-1.41	0.272	1.03	0.767	-0.08
1429726_at	Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), member 9	-1.06	0.858	1.21	0.262	-1.57	0.03	1.15	0.645	-0.07
1459645_at	Adk	Adenosine kinase	1.22	0.733	-1.79	0.134	1.01	0.986	-1.02	0.964	-0.14
1448703_at	Lsm8	LSM8 homolog, U6 small nuclear RNA associated (S. cerevisiae)	-1.12	0.13	1.07	0.234	-1.21	0.019	1.04	0.802	-0.05
1459538_at	BC050092	CDNA sequence BC050092	-1.57	0.368	1.87	0.183	-3.55	0.058	1.05	0.943	-0.55
1449027_at	Rhou	ras homolog gene family, member U	1.01	0.97	-1.06	0.669	-1.19	0.217	1.54	0.416	0.07
1424477_at	BC019731	cDNA sequence BC019731	1	0.995	-1.13	0.193	-1.11	0.388	1.37	0.593	0.03
1442356_at	Mga	MAX gene associated	1.21	0.468	-1.12	0.778	-1.45	0	1.15	0.602	-0.05
1422441_x_at	Cdk4	cyclin-dependent kinase 4	-1.17	0.643	-1.09	0.554	1.01	0.881	1.05	0.763	-0.05
1424731_at	Nle1	notchless homolog 1 (Drosophila)	-1.28	0.36	-1.5	0.304	1.34	0.496	1.11	0.637	-0.08
1458123_at	9630002A11Rik	RIKEN cDNA 9630002A11 gene	-1.74	0.3	-1.7	0.566	1.62	0.328	3.51	0.001	0.43
1449367_at	Trex2	three prime repair exonuclease 2	-1.52	0.391	-1.39	0.545	1.42	0.374	1.92	0.087	0.11
1418149_at	Chga	chromogranin A	-3.2	0.03	-1.39	0.535	1.76	0.065	1.97	0.496	-0.22
1434592_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	-1.46	0.033	-1.18	0.313	1.26	0.044	4.11	0.181	0.68

1457451_at	---	---	-1.06	0.868	1.39	0.27	-2.18	0.037	1.3	0.519	-0.14
1445230_at	Ncor1	Nuclear receptor co-repressor 1	1.16	0.709	-1.66	0.015	1.03	0.829	-1.64	0.313	-0.28
1422967_a_at	Tfrc	transferrin receptor	-1.42	0.337	-2.16	0.269	1.62	0.521	5.96	0.205	1
1426464_at	Nr1d1	nuclear receptor subfamily 1, group D, member 1	1.17	0.772	-1.55	0.36	-1.03	0.931	1.13	0.87	-0.07
1425872_at	Krtap6-1	keratin associated protein 6-1	-1.57	0.452	1	0.994	1.15	0.841	-1.25	0.651	-0.17
1437581_at	AA407452	EST AA407452	-1.63	0.031	-1.37	0.393	1.45	0.447	1.18	0.769	-0.09
1425912_at	Cep164	centrosomal protein 164	-1.84	0.147	1.09	0.763	1.15	0.459	-1.99	0.231	-0.39
1418779_at	Rce1	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)	-1.27	0.157	-1.21	0.182	1.18	0.192	1.14	0.559	-0.04
1419606_a_at	Tnnt1	troponin T1, skeletal, slow	-1.33	0.558	-1.37	0.399	1.31	0.63	1.41	0.407	0
1457081_at	D630038D15Rik	RIKEN cDNA D630038D15 gene	1.63	0.11	-1.62	0.027	-1.83	0.024	1.01	0.901	-0.2
1417052_at	Psmb3	proteasome (prosome, macropain) subunit, beta type 3	1.06	0.751	-1.07	0.429	-1.26	0.199	1.03	0.882	-0.06
1440905_at	Hs2st1	Heparan sulfate 2-O-sulfotransferase 1	1.14	0.39	1.15	0.348	-2.01	0.004	-1.41	0.102	-0.28
1447750_x_at	Nop17	NOP17	1.01	0.953	-1.21	0.12	-1.05	0.703	1.12	0.322	-0.03
1435401_at	Ttc26	tetratricopeptide repeat domain 26	-1.14	0.411	1	0.997	-1.09	0.248	1.09	0.529	-0.04
1456533_at	Dpy19l1	dpy-19-like 1 (C. elegans)	-1.1	0.286	-1.18	0.558	1.03	0.921	1.11	0.772	-0.03
1455390_at	1500005P14Rik ///	RIKEN cDNA 1500005P14 gene /// alkB, alkylation repair homolog 6 (E. coli)	1.04	0.872	-1.41	0.025	1.05	0.684	-1.91	0.027	-0.31
1449711_at	Atp6v1e1	VATPase, H+ transporting, lysosomal V1 subunit E1	-1.12	0.872	-1.21	0.551	1.07	0.863	1.35	0.653	0.02
1426345_at	Prepl	prolyl endopeptidase-like	-1.21	0.189	-1.27	0.15	1.17	0.221	1.13	0.162	-0.04
1445798_at	Dlgh1	discs, large homolog 1 (Drosophila)	1.21	0.267	-1.27	0.325	-1.27	0.293	1.04	0.855	-0.07
1418941_at	Pcdhb22	protocadherin beta 22	1.04	0.908	-1.15	0.55	-1.14	0.572	1.77	0.076	0.13
1453294_at	1700012B15Rik	RIKEN cDNA 1700012B15 gene	1.04	0.46	-1.27	0.276	-1.04	0.598	1.02	0.949	-0.06
1440431_at	Meis1	Myeloid ecotropic viral integration site 1	1.32	0.346	-1.18	0.466	-1.61	0.031	1.05	0.83	-0.1
1459202_at	---	---	-1.17	0.582	1.13	0.494	-1.23	0.399	1.14	0.656	-0.03
1442595_at	C77713	Expressed sequence C77713	-1.2	0.054	1.06	0.932	-1.11	0.845	1.45	0.542	0.05
1424889_at	Nupl2	nucleoporin like 2	-1.36	0.152	-1.24	0.332	1.25	0.136	1.13	0.476	-0.06
1430406_at	4930467M19Rik	RIKEN cDNA 4930467M19 gene	-1.74	0.045	1.24	0.174	-1.02	0.823	1.27	0.146	-0.06
1437964_at	Nxph2	neurexophilin 2	1.26	0.726	1.02	0.975	-1.97	0.194	-2.35	0.137	-0.51
1459246_at	D230021J17Rik	RIKEN cDNA D230021J17 gene	1.18	0.598	-1.45	0.294	-1.08	0.807	1.08	0.802	-0.07
1453278_a_at	Rsnl2	restin-like 2	-1.59	0.011	1.18	0.664	-1.02	0.745	1.07	0.912	-0.09
1418597_at	Top3a	topoisomerase (DNA) III alpha	-1.48	0.25	1.01	0.918	1.11	0.065	-1.2	0.058	-0.14
1441503_at	Dcdc2a	doublecortin domain containing 2a	-1.31	0.424	1.03	0.918	-1	0.999	1.09	0.059	-0.05
1416595_at	Mrps22	mitochondrial ribosomal protein S22	-1.12	0.21	-1.15	0.086	1.02	0.821	1.06	0.851	-0.05
1451100_a_at	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	-1.02	0.934	-1.41	0.092	1.11	0.567	1.2	0.562	-0.03
1437685_x_at	Fmod	fibromodulin	1.12	0.726	-1.9	0.068	1.15	0.681	-1.21	0.583	-0.21
1451745_a_at	Znhit1	zinc finger, HIT domain containing 1	-1.23	0.189	-1.07	0.05	1.05	0.74	1.07	0.532	-0.05
1453182_a_at	Smpd4	sphingomyelin phosphodiesterase 4	-1.11	0.096	-1.26	0.106	1.1	0.802	1.45	0.274	0.04
1430469_at	Ttll5	tubulin tyrosine ligase like family 5	-1.79	0.142	1.28	0.387	-1.04	0.798	1.22	0.612	-0.08
1439770_at	6430598A04Rik	RIKEN cDNA 6430598A04 gene	-1.18	0.724	-1.41	0.432	1.24	0.434	1.11	0.844	-0.06
1420885_a_at	Sez6	seizure related gene 6	-1.3	0.506	-1.07	0.866	1.09	0.728	1.47	0.281	0.05
1416919_a_at	Nphp1	nephronophthisis 1 (juvenile) homolog (human)	-1.17	0.251	-1.24	0.547	1.13	0.296	1.57	0.22	0.07
1444460_at	Ube2r2	ubiquitin-conjugating enzyme E2R 2	-1.07	0.809	-1.25	0.158	1.06	0.645	1.32	0.503	0.01
1458834_at	Mtus1	Mitochondrial tumor suppressor 1	-1.19	0.16	1.27	0.701	-1.47	0.34	1.91	0.376	0.13
1447164_at	Rlf	Rearranged L-myc fusion sequence	1.18	0.516	-1.16	0.442	-1.33	0.179	1.35	0.216	0.01
1446916_at	---	---	1.01	0.986	-1.1	0.896	-1.14	0.365	1.03	0.96	-0.05
1433165_at	4930570E01Rik	RIKEN cDNA 4930570E01 gene	-1.23	0.704	1.11	0.61	-1.15	0.288	1.75	0.14	0.12
1436102_at	Sec22c	SEC22 vesicle trafficking protein-like C (S. cerevisiae)	-1.32	0.378	-1.22	0.573	1.21	0.434	1.04	0.705	-0.07
1420624_a_at	Vamp8	vesicle-associated membrane protein 8	-1.03	0.686	1.02	0.721	-1.25	0.152	1.19	0.027	-0.02
1452938_at	Anks1b /// LOC544	ankyrin repeat and sterile alpha motif domain containing 1B /// similar to AIDA-1b	-1.91	0.007	-1.09	0.883	1.35	0.421	1.5	0.452	-0.04
1426344_at	Gle1l	GLE1 RNA export mediator-like (yeast	1	0.99	1.01	0.929	-1.27	0.274	-1.12	0.369	-0.1
1426164_a_at	Usf1	upstream transcription factor 1	-1.18	0.356	-1.28	0.521	1.16	0.447	1.03	0.786	-0.07
1455805_x_at	Ccdc22	coiled-coil domain containing 22	-1.1	0.35	1.1	0.139	-1.27	0.29	1.06	0.708	-0.05
1427275_at	Smc4	structural maintenance of chromosomes 4	-1.07	0.528	-1.21	0.229	1.03	0.877	2.03	0.216	0.2
1429599_a_at	C630010D07Rik ///	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofolate dehydro	-1.27	0.411	1.2	0.57	-1.23	0.393	1.13	0.222	-0.04

1448863_a_at	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	1.09	0.173	1.02	0.623	-1.47	0.015	-1.26	0.412	-0.15
1433870_at	Atad4	ATPase family, AAA domain containing 4	-1.12	0.645	1.01	0.983	-1.13	0.507	1.35	0.475	0.03
1429250_at	Dync2h1	dynein cytoplasmic 2 heavy chain 1	-1.26	0.194	-1.08	0.372	1.08	0.571	1.02	0.943	-0.06
1445068_at	Malt1	mucosa associated lymphoid tissue lymphoma translocation gene 1	1.08	0.904	-1.82	0.144	1.16	0.766	-1.51	0.423	-0.27
1416693_at	Foxc2	forkhead box C2	-1.1	0.686	1.09	0.51	-1.27	0.678	1.05	0.868	-0.06
1424512_a_at	Txndc9	thioredoxin domain containing 9	-1.22	0.029	-1.03	0.787	1.01	0.935	1.03	0.885	-0.05
1429336_at	2610301K12Rik	RIKEN cDNA 2610301K12 gene	1.03	0.866	-1.12	0.583	-1.15	0.465	1.02	0.821	-0.05
1443764_x_at	Rab27b	RAB27b, member RAS oncogene family	-1.37	0.511	1.06	0.767	-1	0.997	1.46	0.492	0.04
1423230_at	Inpp5e	inositol polyphosphate-5-phosphatase E	-1.05	0.838	-1.21	0.484	1.01	0.909	1.09	0.63	-0.04
1451717_s_at	Senp2	SUMO/sentrin specific peptidase 2	-1.21	0.183	-1.18	0.073	1.12	0.345	1.44	0.293	0.04
1418761_at	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	-1.02	0.958	-1.47	0.519	1.14	0.655	1.31	0.552	-0.01
1425582_a_at	Emcn	endomucin	1.01	0.945	1.2	0.583	-1.73	0.012	-1.41	0.249	-0.23
1452724_at	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	-1.35	0.275	-1.22	0.187	1.23	0.297	1.51	0.316	0.05
1422680_at	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	-1.09	0.61	-1.29	0.166	1.1	0.514	1.19	0.319	-0.02
1439218_at	Ust	Uronyl-2-sulfotransferase	-1.2	0.015	1.37	0.426	-1.69	0.035	1	0.999	-0.13
1430536_a_at	Erh	enhancer of rudimentary homolog (Drosophila)	-1.3	0.169	-1.04	0.747	1.07	0.556	1.21	0.514	-0.02
1435150_at	---	2 days neonate sympathetic ganglion cDNA, RIKEN full-length enriched library, c	-1.1	0.647	-1.23	0.544	1.07	0.783	1.31	0.114	0.01
1455753_at	C630035N08Rik	RIKEN cDNA C630035N08 gene	1.33	0.285	-1.82	0.076	-1.09	0.81	1.88	0.274	0.07
1442436_at	Fn3k	fructosamine 3 kinase	-1.56	0.053	-1.23	0.252	1.34	0.133	5.1	0.204	0.91
1452660_s_at	Klhl7	kelch-like 7 (Drosophila)	-1.13	0.068	1	0.993	-1.1	0.247	1.97	0.127	0.18
1437004_at	LOC547109	similar to tripartite motif-containing 43	-1.27	0.477	-1.06	0.909	1.06	0.932	3.56	0.063	0.57
1455970_at	Pde5a	Phosphodiesterase 5A, cGMP-specific	-1.16	0.444	1.42	0.362	-1.97	0.014	1.93	0.435	0.06
1453074_at	Dusp23	dual specificity phosphatase 23	-1.11	0.71	1.01	0.798	-1.13	0.538	1.19	0.376	-0.01
1423348_at	Fzd8	frizzled homolog 8 (Drosophila)	1	0.956	-1.83	0.152	1.24	0.496	-1.8	0.186	-0.35
1451205_at	Psmb4	proteasome (prosome, macropain) subunit, beta type 4	1	0.971	-1.31	0.013	1.03	0.71	-1.03	0.796	-0.08
1455285_at	Slc31a1	solute carrier family 31, member 1	-1.28	0.08	-1.15	0.192	1.14	0.725	1.18	0.152	-0.03
1430961_at	Zfp292	zinc finger protein 292	1.12	0.542	-1.43	0.452	-1.02	0.944	1.17	0.651	-0.04
1435502_a_at	Brdt	bromodomain, testis-specific	-2.45	0.266	1.5	0.442	-1.13	0.774	1.37	0.608	-0.18
1446535_at	Colec12	Collectin sub-family member 12	-1.63	0.393	1.11	0.859	1.07	0.698	-1.78	0.462	-0.31
1443596_at	---	PREDICTED: Mus musculus similar to SRY-box 13, transcript variant 2 (LOC621	1.13	0.764	-1.37	0.044	-1.07	0.766	1.07	0.291	-0.06
1445155_at	---	Transcribed locus	-1.44	0.401	-1.07	0.901	1.16	0.617	1.31	0.644	-0.01
1427674_a_at	Sez6	seizure related gene 6	-1.1	0.516	1.08	0.8	-1.23	0.024	1.09	0.747	-0.04
1431252_a_at	Zfp655	zinc finger protein 655	-1.3	0.351	-1.03	0.929	1.05	0.853	1.52	0.255	0.06
1431086_s_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.02	0.871	-1.05	0.624	-1.22	0.111	1.81	0.309	0.14
1442546_at	C730027H18Rik	RIKEN cDNA C730027H18 gene	-1.26	0.216	-1.03	0.898	1.04	0.923	1.2	0.707	-0.02
1450285_at	Ube1y1	ubiquitin-activating enzyme E1, Chr Y 1	1.02	0.973	1.01	0.99	-1.29	0.541	-1.84	0.007	-0.28
1434668_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1	0.987	-1.11	0.101	-1.12	0.247	1.22	0.269	0
1430041_at	6330548G22Rik	RIKEN cDNA 6330548G22 gene	-1.27	0.121	-1.13	0.125	1.13	0.439	1.64	0.186	0.09
1431013_at	Psmd11 /// LOC627	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 /// similar to 26S	1.08	0.859	-1.07	0.866	-1.27	0.374	1.06	0.9	-0.05
1426059_at	Gckr	glucokinase regulatory protein	-1.21	0.783	-1.09	0.395	1.05	0.921	1.09	0.852	-0.04
1456330_at	Pcgf2	polycomb group ring finger 2	-1.61	0.487	1.03	0.953	1.15	0.721	-3.77	0.223	-0.8
1446838_at	Atad1	ATPase family, AAA domain containing 1	1.39	0.19	-1.76	0.241	-1.2	0.46	1.16	0.569	-0.1
1455003_at	Thap1	THAP domain containing, apoptosis associated protein 1	-1.25	0.152	-1.33	0.074	1.24	0.228	1.1	0.543	-0.06
1423971_at	Thoc3	THO complex 3	-1.59	0.124	-1.25	0.176	1.37	0.269	1.05	0.877	-0.1
1430190_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	1.08	0.612	-2.02	0.001	1.22	0.309	-1.2	0.309	-0.23
1444491_at	---	Transcribed locus, strongly similar to XP_344663.2 PREDICTED: neuregulin 2 [R	-1.04	0.813	-2.13	0.13	1.37	0.116	1.19	0.447	-0.16
1444220_at	2410089E03Rik	RIKEN cDNA 2410089E03 gene	-1.04	0.876	1.02	0.92	-1.24	0.484	1.54	0.209	0.07
1429991_at	Fezf1	Fez family zinc finger 1	1.55	0.392	-1.57	0.367	-1.63	0.322	1.06	0.835	-0.15
1459844_at	Tnip2	TNFAIP3 interacting protein 2	1.05	0.865	1.1	0.728	-1.55	0.119	-1.17	0.7	-0.14
1457276_at	Snf1lk2	SNF1-like kinase 2	-1.47	0.14	-1.28	0.471	1.34	0.42	1.47	0.31	0.01
1426043_a_at	Capn3	calpain 3	-1.08	0.887	-1.56	0.223	1.23	0.423	1.31	0.509	-0.02
1426391_at	Arf1 /// LOC545267	ADP-ribosylation factor 1 /// similar to ADP-ribosylation factor 1	1.35	0.74	-1.79	0.178	-1.12	0.837	1.11	0.859	-0.11
1434072_at	Smcr7	Smith-Magenis syndrome chromosome region, candidate 7 homolog (human)	1.01	0.971	-1.38	0.139	1.06	0.772	-1.27	0.367	-0.14

1453855_at	1810057P16Rik	RIKEN cDNA 1810057P16 gene	1.41	0.452	-1.74	0.201	-1.24	0.375	1.07	0.779	-0.12
1438366_x_at	Clcn3	chloride channel 3	1.06	0.55	-1.16	0.144	-1.14	0.486	2.45	0.165	0.3
1441403_at	6430501K19Rik	RIKEN cDNA 6430501K19 gene	1.28	0.001	-1	0.981	-1.91	0.011	1.13	0.657	-0.13
1454929_s_at	Safb	scaffold attachment factor B	-1.56	0.002	-1.02	0.873	1.18	0.414	1.07	0.567	-0.08
1450596_at	Olfr66	olfactory receptor 66	1.06	0.912	1.13	0.756	-1.65	0.116	-2.19	0.369	-0.41
1451511_at	Hibch	3-hydroxyisobutyryl-Coenzyme A hydrolase	-1.61	0.353	-1.11	0.554	1.27	0.157	1.15	0.531	-0.07
1442899_at	---	Transcribed locus	-1.16	0.744	-1.73	0.189	1.36	0.279	1.02	0.981	-0.13
1437746_at	Lrrtm1	leucine rich repeat transmembrane neuronal 1	1.21	0.816	-1.76	0.083	1.02	0.971	-1.9	0.338	-0.36
1447479_at	---	---	1.16	0.581	1.01	0.977	-1.6	0.026	-1.13	0.673	-0.14
1430800_at	4930518F22Rik	RIKEN cDNA 4930518F22 gene	1.04	0.905	-1.94	0.308	1.24	0.777	-3.23	0.009	-0.72
1418759_at	Ptpn20	protein tyrosine phosphatase, non-receptor type 20	1.09	0.65	-1.17	0.793	-1.16	0.237	1.27	0.567	0.01
1417130_s_at	Angptl4	angiopoietin-like 4	1.26	0.675	-1.32	0.252	-1.29	0.425	1.1	0.7	-0.06
1445193_x_at	D8Ertd575e	DNA segment, Chr 8, ERATO Doi 575, expressed	-1.11	0.724	-2.33	0.236	1.47	0.412	1.43	0.148	-0.13
1455933_at	Tra2a	transformer 2 alpha homolog (Drosophila)	-1.04	0.925	1.06	0.853	-1.29	0.422	1.56	0.05	0.07
1447802_x_at	---	---	-1.26	0.611	-1.02	0.97	1.02	0.953	3.17	0.224	0.48
1458667_at	4930519N13Rik	RIKEN cDNA 4930519N13 gene	-1.27	0.523	-1.23	0.315	1.2	0.5	3.17	0.256	0.47
1440211_at	Cyp2j11	cytochrome P450, family 2, subfamily j, polypeptide 11	-1.08	0.557	-1.27	0.584	1.08	0.848	1.12	0.777	-0.04
1419507_at	Krtap15	keratin associated protein 15	-1.31	0.594	-1.2	0.664	1.2	0.667	1.06	0.922	-0.06
1447088_at	Ttyh2	Tweety homolog 2 (Drosophila)	-2.06	0.145	-1.07	0.772	1.38	0.326	1.21	0.493	-0.14
1438677_at	Pkp4	plakophilin 4	1.17	0.28	-1.13	0.451	-1.34	0.115	1.1	0.345	-0.05
1416866_at	Bet1	blocked early in transport 1 homolog (S. cerevisiae)	-1.08	0.61	1.13	0.211	-1.34	0.002	1.13	0.082	-0.04
1453259_at	3830422K02Rik	RIKEN cDNA 3830422K02 gene	-1.22	0.56	-1.02	0.896	1	0.997	1.26	0.663	0
1458946_at	---	---	1.45	0.616	-1.1	0.815	-2.24	0.093	1.17	0.691	-0.18
1420110_s_at	Zfp334	zinc finger protein 334	-1.3	0.372	1.13	0.656	-1.1	0.625	1.06	0.809	-0.06
1433610_at	AA986860	expressed sequence AA986860	-1.08	0.313	-1.15	0.749	1	0.963	3.11	0.164	0.47
1429567_at	4632411J06Rik	RIKEN cDNA 4632411J06 gene	-1.59	0.149	1.06	0.889	1.1	0.38	-1.84	0.462	-0.31
1434398_at	Nkrf	NF-kappaB repressing factor	-1.14	0.338	-1.15	0.281	1.06	0.711	1.12	0.557	-0.03
1436759_x_at	Cnn3	calponin 3, acidic	1.03	0.623	1.04	0.806	-1.37	0.009	-1.91	0.081	-0.3
1434288_at	Bivm	basic, immunoglobulin-like variable motif containing	1.01	0.954	-1.03	0.641	-1.23	0.295	1.06	0.866	-0.05
1432613_at	E130201N16Rik	RIKEN cDNA E130201N16 gene	-1.54	0.292	1.49	0.498	-1.52	0.463	1.32	0.665	-0.06
1455438_at	Pxmp4	peroxisomal membrane protein 4	1.26	0.442	-1.15	0.273	-1.49	0.091	1.29	0.297	-0.02
1431751_a_at	Mpped2	metallophosphoesterase domain containing 2	-1.53	0.053	1.35	0.351	-1.26	0.25	1.62	0.503	0.05
1456850_at	---	---	1.47	0.072	-1.79	0.112	-1.3	0.517	1.63	0.34	0
1423416_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.11	0.222	-1.17	0.01	1.04	0.616	1	0.998	-0.06
1426639_a_at	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	-1.43	0.506	-1.14	0.842	1.22	0.706	1.13	0.839	-0.05
1440596_at	Cabin1	calcineurin binding protein 1	-1.14	0.818	1.47	0.605	-2.21	0.207	1.23	0.576	-0.16
1425827_at	Nkx2-3	NK2 transcription factor related, locus 3 (Drosophila)	-1.83	0.202	1.05	0.922	1.21	0.287	-1.24	0.369	-0.2
1445237_at	---	---	-1.84	0.417	1.44	0.647	-1.23	0.236	1.16	0.805	-0.12
1434031_at	Zfp692	zinc finger protein 692	-1.07	0.72	1.03	0.703	-1.21	0.09	1.04	0.894	-0.05
1434711_at	BC030867	cDNA sequence BC030867	-1.65	0.247	-1.01	0.938	1.21	0.215	2.42	0.199	0.24
1430813_at	1810057I13Rik	RIKEN cDNA 1810057I13 gene	-1.09	0.034	-1.16	0.646	1.02	0.924	1.29	0.471	0.01
1428514_at	Cpne3	copine III	-1.21	0.544	-1.11	0.377	1.08	0.759	1.53	0.01	0.07
1451831_at	Osbpl6	oxysterol binding protein-like 6	-1.29	0.043	1.41	0.028	-1.62	0.432	1.1	0.322	-0.1
1438706_at	6430517E21Rik	RIKEN cDNA 6430517E21 gene	-1.03	0.968	1.09	0.773	-1.36	0.494	1.03	0.943	-0.07
1418429_at	Kif5b	kinesin family member 5B	1.1	0.501	-1.09	0.305	-1.27	0.142	1.01	0.982	-0.07
1431152_at	Hapln3	hyaluronan and proteoglycan link protein 3	1.32	0.583	-2.3	0.208	1.05	0.913	-1.25	0.237	-0.3
1425722_at	LOC435565	similar to interferon-inducible GTPase	-1.84	0.067	-1.52	0.29	1.6	0.155	1.14	0.731	-0.16
1440775_at	1700054K19Rik	RIKEN cDNA 1700054K19 gene	1.19	0.728	-1.48	0.371	-1.07	0.88	1.07	0.885	-0.07
1431354_a_at	Fars2	phenylalanine-tRNA synthetase 2 (mitochondrial)	-1.11	0.275	-1.27	0.094	1.12	0.512	1.68	0.173	0.1
1418624_at	Ybx1	Y box protein 1	1.04	0.488	-1.07	0.492	-1.22	0.06	1.04	0.604	-0.05
1443252_at	Ibrdc2	IBR domain containing 2	-1.02	0.932	1.31	0.155	-1.99	0.241	1.12	0.873	-0.14
1421808_at	Defb5	defensin beta 5	1.72	0.5	-1.66	0.449	-2.07	0.133	1.02	0.97	-0.25
1457329_at	Adcy1	adenylate cyclase 1	1.15	0.054	-1.17	0.571	-1.25	0.285	1.12	0.791	-0.04

1450388_s_at	Twsg1	twisted gastrulation homolog 1 (Drosophila)	1.01	0.822	-1.08	0.055	-1.15	0.557	1.18	0.502	-0.01
1429827_at	1700010B08Rik	RIKEN cDNA 1700010B08 gene	-1.54	0.418	-1.09	0.902	1.23	0.577	1.71	0.146	0.08
1444288_at	Pnpt1	polyribonucleotide nucleotidyltransferase 1	-1.33	0.267	1.02	0.954	1.03	0.921	-1.3	0.286	-0.14
1430353_at	Glis3	GLIS family zinc finger 3	-1.18	0.115	-1.21	0.517	1.13	0.229	1.07	0.83	-0.05
1445621_at	---	---	-1.24	0.726	-1.17	0.771	1.14	0.801	1.32	0.583	0.01
1457361_at	C630007C17Rik	RIKEN cDNA C630007C17 gene	1.3	0.361	-1.23	0.445	-1.46	0.382	1.91	0.224	0.13
1457236_at	Gpr62	G protein-coupled receptor 62	1.14	0.839	1.17	0.767	-2.04	0.323	-1.04	0.951	-0.19
1447957_at	---	---	1.44	0.555	-1.71	0.278	-1.28	0.63	3.15	0.041	0.4
1446567_at	Ccnd3	Cyclin D3	1.17	0.59	1.05	0.922	-1.71	0.114	-1.98	0.134	-0.37
1418609_at	Il1f6	interleukin 1 family, member 6	-1.07	0.384	-1.38	0.121	1.14	0.44	1.5	0.392	0.05
1460034_at	Samd4b	sterile alpha motif domain containing 4B	-1.23	0.091	-1.05	0.59	1.04	0.751	1.1	0.499	-0.04
1437363_at	Homer1	homer homolog 1 (Drosophila)	-1.13	0.21	1.05	0.75	-1.16	0.519	1.46	0.191	0.06
1457406_at	---	Adult male brain UNDEFINED_CELL_LINE cDNA, RIKEN full-length enriched libı	-1.34	0.753	-1.09	0.767	1.14	0.765	1.07	0.874	-0.05
1424504_at	Rab22a	RAB22A, member RAS oncogene family	1.06	0.871	-1.03	0.94	-1.3	0.28	1.53	0.062	0.07
1426521_at	D230025D16Rik	RIKEN cDNA D230025D16 gene	1.12	0.675	-1.27	0.049	-1.12	0.312	1.04	0.799	-0.06
1456485_at	Npat	nuclear protein in the AT region	-1.1	0.102	1.05	0.8	-1.18	0.186	1.37	0.319	0.03
1429962_at	Cebpz	CCAAT/enhancer binding protein zeta	-1.2	0.498	1.18	0.501	-1.26	0.204	1.36	0.051	0.02
1434775_at	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	-1.06	0.746	-1.22	0.242	1.04	0.596	1.02	0.841	-0.05
1443411_at	Spata9	Spermatogenesis associated 9	1.21	0.515	-1.64	0.424	-1.02	0.947	1.44	0.156	0
1456021_at	Atf6	activating transcription factor 6	-1.14	0.233	-1.42	0.016	1.23	0.26	1.27	0.061	-0.02
1420048_at	---	---	1.05	0.82	1.02	0.978	-1.36	0.329	-1.35	0.131	-0.16
1428095_a_at	Tmem24	transmembrane protein 24	1.01	0.899	-1.11	0.715	-1.12	0.276	1.47	0.153	0.06
1417867_at	Cfd	complement factor D (adipsin)	-3.06	0.118	-2.58	0.261	2.09	0.464	36.35	0.036	8.2
1457283_at	---	---	1.28	0.025	-1.54	0.129	-1.15	0.698	1.09	0.892	-0.08
1456679_at	Obfc1	Oligonucleotide/oligosaccharide-binding fold containing 1	1.29	0.606	-1.19	0.766	-1.49	0.458	1.32	0.184	-0.02
1458640_at	---	6 days neonate skin cDNA, RIKEN full-length enriched library, clone:A030007I19	-1.63	0.484	1.06	0.923	1.13	0.844	-1.58	0.191	-0.26
1418551_at	Mybpc3	myosin binding protein C, cardiac	-3.43	0.467	-1.29	0.477	1.74	0.04	1.23	0.475	-0.44
1452022_at	Baalc	brain and acute leukemia, cytoplasmic	1.15	0.846	-1.13	0.84	-1.29	0.387	2.07	0.131	0.2
1456256_at	Eif5	eukaryotic translation initiation factor 5	-1.01	0.893	-1.29	0.002	1.04	0.848	1.11	0.649	-0.04
1427046_at	Grhl2	grainyhead-like 2 (Drosophila)	1.1	0.663	-1.14	0.779	-1.21	0.164	1.11	0.857	-0.03
1433526_at	Klhl8	kelch-like 8 (Drosophila)	1.22	0.354	-1.87	0.14	1.04	0.903	-1.31	0.671	-0.23
1459354_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.06	0.736	1.19	0.174	-1.49	0.157	1.02	0.817	-0.09
1450751_at	Zpbp	zona pellucida binding protein	1.28	0.745	1.03	0.977	-2.02	0.02	-1.88	0.245	-0.4
1458138_at	Rnf190	Ring finger protein 190	-1.94	0.317	1.45	0.307	-1.2	0.594	1.56	0.441	-0.03
1426742_at	Atp5f1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	-1.17	0.038	-1.22	0.011	1.12	0.048	1.14	0.521	-0.03
1452982_at	Igf1r	insulin-like growth factor I receptor	-1.06	0.801	1	0.985	-1.17	0.242	1.08	0.771	-0.04
1437466_at	Alcam	activated leukocyte cell adhesion molecule	1.07	0.012	1.11	0.257	-1.6	0.038	-1.63	0.314	-0.26
1458391_at	---	---	-1.85	0.09	-1.09	0.686	1.35	0.404	1.05	0.595	-0.14
1446597_at	LOC67660	Hypothetical LOC67660	-1.08	0.841	1.07	0.882	-1.24	0.251	1.1	0.912	-0.04
1434202_a_at	BC055107	cDNA sequence BC055107	1.3	0.142	-2.29	0.032	1.07	0.896	-3.57	0.261	-0.87
1432256_at	1700111N16Rik	RIKEN cDNA 1700111N16 gene	-1.37	0.73	1.33	0.55	-1.34	0.656	2.04	0.085	0.16
1436609_a_at	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	-1.05	0.416	1.01	0.862	-1.19	0.025	1.03	0.801	-0.05
1442453_at	Fcho2	FCH domain only 2	1.18	0.285	-1.04	0.636	-1.51	0.016	1.47	0.151	0.03
1456891_at	Dennd2c	DENN/MADD domain containing 2C	-1.38	0.239	-1.11	0.645	1.18	0.368	4.63	0.245	0.83
1432772_at	1700081H04Rik	RIKEN cDNA 1700081H04 gene	1.53	0.532	-1.21	0.765	-2.24	0.025	1.21	0.576	-0.18
1442095_at	Asxl3	additional sex combs like 3 (Drosophila)	-1.43	0.215	-1.06	0.803	1.16	0.672	1.43	0.41	0.03
1432732_at	---	---	-1.69	0.002	-1.07	0.821	1.28	0.545	1.03	0.91	-0.11
1444202_at	Zfp703	zinc finger protein 703	-1.12	0.363	-1.19	0.204	1.07	0.383	1.05	0.8	-0.05
1417536_at	Zmat2	zinc finger, matrin type 2	1	0.994	-1.13	0.248	-1.08	0.61	1.16	0.437	-0.01
1458860_at	---	---	-1.42	0.504	-1.1	0.861	1.19	0.753	1.12	0.648	-0.05
1437879_at	AU045404	expressed sequence AU045404	-1.19	0.377	-1.28	0.454	1.18	0.376	1.34	0.167	0.01
1454916_s_at	Arfip1	ADP-ribosylation factor interacting protein 1	1.1	0.522	1.02	0.767	-1.47	0.035	-1.26	0.245	-0.15
1427672_a_at	Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1.21	0.08	-1.12	0.371	-1.43	0.047	1.41	0.173	0.02

1448862_at	Icam2	intercellular adhesion molecule 2	1.05	0.798	1.11	0.545	-1.55	0.011	-1.91	0.083	-0.32
1449041_a_at	Trip6	thyroid hormone receptor interactor 6	-1.02	0.886	1.06	0.684	-1.3	0.072	1.19	0.379	-0.02
1449579_at	Sh3yl1	Sh3 domain YSC-like 1	-1.35	0.145	1.17	0.255	-1.13	0.352	4.3	0.154	0.75
1453872_at	Dmrtc2	doublesex and mab-3 related transcription factor like family C2	-1.44	0.07	1.52	0.417	-1.69	0.496	1.1	0.79	-0.13
1441381_at	9430029E18Rik	RIKEN cDNA 9430029E18 gene	-1.74	0.048	1.41	0.199	-1.22	0.349	1.11	0.783	-0.11
1460542_s_at	Mdm4	transformed mouse 3T3 cell double minute 4	-1.44	0.162	1.07	0.611	1.04	0.856	-1.32	0.364	-0.16
1449612_x_at	Mphosph1	M-phase phosphoprotein 1	-1.1	0.886	-1.32	0.613	1.14	0.654	1.35	0.28	0.02
1423711_at	Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	-1.21	0.112	-1.11	0.17	1.08	0.459	1.21	0.369	-0.01
1434384_at	Nrip1	nuclear receptor interacting protein 1	1.08	0.626	-1.05	0.462	-1.29	0.257	1.58	0.176	0.08
1434741_at	Rreb1	ras responsive element binding protein 1	1.02	0.718	1.07	0.651	-1.4	0.034	-1.01	0.968	-0.08
1422658_at	Plcz1	phospholipase C, zeta 1	1.11	0.51	-1.53	0.096	1.05	0.705	-1.57	0.48	-0.24
1443921_at	C130037N17Rik	RIKEN cDNA C130037N17 gene	-1.05	0.818	-1.26	0.477	1.06	0.803	1.72	0.28	0.12
1418225_at	Orc2l	origin recognition complex, subunit 2-like (S. cerevisiae)	-1.02	0.92	1.04	0.808	-1.28	0.056	1.7	0.171	0.11
1425371_at	Polb	polymerase (DNA directed), beta	1.06	0.577	1.28	0.547	-2.15	0.044	-1.33	0.113	-0.28
1459951_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	1.17	0.04	-1.14	0.368	-1.32	0.165	1.1	0.506	-0.05
1426659_a_at	Rpl23a	ribosomal protein L23a	1.02	0.839	1.05	0.003	-1.35	0.003	-1.21	0.019	-0.12
1451652_a_at	5033428A16Rik	RIKEN cDNA 5033428A16 gene	-1.03	0.204	1.11	0.203	-1.37	0.001	1.07	0.684	-0.05
1437849_x_at	Armcx2	armadillo repeat containing, X-linked 2	-1.35	0.175	1.03	0.681	1.04	0.705	-1.07	0.626	-0.09
1417351_a_at	Snrpa1	small nuclear ribonucleoprotein polypeptide A'	-1.13	0.404	1.04	0.598	-1.13	0.197	1.04	0.781	-0.05
1417892_a_at	Sirt3	sirtuin 3 (silent mating type information regulation 2, homolog) 3 (S. cerevisiae)	-1.11	0.213	-1.12	0.521	1.02	0.923	1.01	0.951	-0.05
1422633_at	1700020D05Rik	RIKEN cDNA 1700020D05 gene	1.04	0.935	-2.47	0.167	1.36	0.322	-2.02	0.147	-0.52
1431324_at	Ecm2	extracellular matrix protein 2, female organ and adipocyte specific	1.29	0.282	-1.6	0.421	-1.12	0.817	1.24	0.675	-0.05
1446654_at	---	---	-1.1	0.52	-1.48	0.505	1.22	0.268	1.04	0.92	-0.08
1428562_at	2210403K04Rik	RIKEN cDNA 2210403K04 gene	1.11	0.824	-1.06	0.274	-1.32	0.183	1.29	0.505	0
1445448_at	---	---	1.18	0.516	-1.61	0.089	1.01	0.961	-1.24	0.227	-0.17
1428133_at	Snip1	Smad nuclear interacting protein 1	-1.07	0.672	-1.22	0.279	1.06	0.414	1.08	0.586	-0.04
1459828_at	Srrm1	Serine/arginine repetitive matrix 1	1.24	0.047	-1.08	0.524	-1.56	0.048	1.02	0.902	-0.09
1447628_x_at	Mrps5	mitochondrial ribosomal protein S5	-1.22	0.356	-1.32	0.128	1.23	0.524	1.12	0.387	-0.05
1421020_at	Ranbp17	RAN binding protein 17	-2.12	0.173	-1.36	0.435	1.6	0.483	1.4	0.58	-0.12
1454731_at	Myo10	myosin X	-1.3	0.327	-1.04	0.746	1.07	0.82	1.34	0.422	0.02
1448832_a_at	Cplx1	complexin 1	-1.02	0.904	1.11	0.713	-1.39	0.585	1.17	0.8	-0.03
1423081_a_at	Tomm20	translocase of outer mitochondrial membrane 20 homolog (yeast)	-1.13	0.276	1.01	0.909	-1.09	0.612	1.09	0.641	-0.03
1440748_at	---	---	1.27	0.447	1.1	0.879	-2.26	0.031	-1.27	0.701	-0.29
1442119_at	AI449212	expressed sequence AI449212	1.04	0.843	-1.81	0.062	1.21	0.493	-1.25	0.409	-0.2
1449106_at	Gpx3	glutathione peroxidase 3	-1.04	0.273	-1.2	0.765	1.02	0.758	1.01	0.968	-0.05
1433540_x_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	-1.07	0.637	1.06	0.497	-1.22	0.005	1.3	0.369	0.02
1459732_at	---	Transcribed locus	-1.68	0.333	1.24	0.614	-1.03	0.929	1.12	0.7	-0.09
1451196_at	Ypel5	yippee-like 5 (Drosophila)	1.01	0.843	-1.04	0.536	-1.19	0.187	1.39	0.293	0.04
1439142_at	Smarcal1	Swi/SNF related matrix associated, actin dependent regulator of chromatin, subfa	-1.06	0.77	1.07	0.858	-1.25	0.114	1.49	0.5	0.06
1434729_at	AK129302	cDNA sequence AK129302	1.03	0.661	1.16	0.693	-1.62	0	-1.67	0.161	-0.27
1424751_at	Abt1	activator of basal transcription	-1.14	0.055	1.02	0.912	-1.09	0.53	1.07	0.588	-0.04
1416224_at	Zbtb17	zinc finger and BTB domain containing 17	1.11	0.592	-1.21	0.154	-1.14	0.13	1.02	0.923	-0.06
1417773_at	Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	-1.1	0.613	1	0.988	-1.12	0.342	1.2	0.387	0
1451912_a_at	Fgfrl1	fibroblast growth factor receptor-like 1	1.01	0.959	-1.17	0.58	-1.06	0.762	2.76	0.142	0.39
1440120_at	Gnb2l1	Guanine nucleotide binding protein (G protein), beta polypeptide 2 like 1	1.05	0.846	-1.43	0.139	1.06	0.823	-1.05	0.775	-0.09
1427347_s_at	Tubb2a /// Tubb2b	tubulin, beta 2a /// tubulin, beta 2b /// similar to tubulin, beta 3 /// similar to tubulin,	1.05	0.81	-1.07	0.782	-1.22	0.29	1.39	0.355	0.04
1452753_at	Foxk2	forkhead box K2	-1.15	0.385	-1.11	0.443	1.04	0.597	1.33	0.093	0.03
1417506_at	Gmnn	geminin	-1.4	0.243	-1.05	0.708	1.15	0.403	2.6	0.219	0.32
1445029_at	A330019N05Rik	RIKEN cDNA A330019N05 gene	1.63	0.449	-1.27	0.628	-2.55	0.162	2.21	0.169	0.01
1438729_at	BB176347	Expressed sequence BB176347	1.06	0.599	-1.05	0.785	-1.25	0.446	1.31	0.465	0.02
1446078_at	Fkbp7	FK506 binding protein 7	-1.68	0.1	1.38	0.544	-1.2	0.733	1.27	0.641	-0.06
1445619_at	---	---	1.03	0.794	1.08	0.897	-1.42	0.587	-1	0.996	-0.08
1460192_at	Osbpl1a	oxysterol binding protein-like 1A	-1.15	0.017	-1.14	0.047	1.07	0.516	2.53	0.108	0.32

1430789_at	4930452B06Rik	RIKEN cDNA 4930452B06 gene	-1.84	0.217	-2.19	0.017	1.81	0.131	1.45	0.547	-0.19
1429785_at	5830458C19Rik	RIKEN cDNA 5830458C19 gene	-1.8	0.593	-1.32	0.502	1.5	0.506	1.4	0.315	-0.06
1426540_at	Endod1	endonuclease domain containing 1	-1.04	0.874	1	0.988	-1.19	0.221	3.3	0.136	0.52
1434847_at	---	---	-1.2	0.268	1.02	0.957	-1.05	0.899	1.04	0.747	-0.05
1458332_x_at	Sox4	SRY-box containing gene 4	-1.01	0.964	1.01	0.987	-1.23	0.681	1.23	0.651	0
1429259_a_at	1810014B01Rik	RIKEN cDNA 1810014B01 gene	-1.17	0.452	-1.23	0.014	1.14	0.433	1.19	0.306	-0.02
1433880_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.2	0.231	-1.03	0.779	1	0.994	1.44	0.398	0.05
1444930_at	Rabep1	Rabaptin, RAB GTPase binding effector protein 1	-1.32	0.256	1.02	0.83	1.03	0.861	-1.08	0.858	-0.09
1451674_at	Slc12a5	solute carrier family 12, member 5	1.03	0.84	1.11	0.719	-1.51	0.174	-1.81	0.174	-0.29
1444097_at	Metrnl	meteorin, glial cell differentiation regulator-like	1.09	0.788	-1.05	0.916	-1.3	0.075	1.65	0.221	0.1
1456466_x_at	Atxn10	ataxin 10	-1.27	0.099	-1.02	0.866	1.04	0.793	1.01	0.92	-0.06
1421223_a_at	Anxa4	annexin A4	1	0.925	1.01	0.856	-1.25	0.023	-1.18	0.617	-0.1
1418533_s_at	Fzd2	frizzled homolog 2 (Drosophila)	1.36	0.642	-2.11	0.168	-1.02	0.933	1.09	0.693	-0.17
1430153_at	Tmod2	tropomodulin 2	-1.81	0.215	1.23	0.563	1.03	0.839	-1.09	0.819	-0.16
1449616_s_at	Golga3	golgi autoantigen, golgin subfamily a, 3	-1.14	0.436	1.05	0.435	-1.13	0.431	1.1	0.674	-0.03
1424192_at	1500011H22Rik	RIKEN cDNA 1500011H22 gene	-1.17	0.297	-1.06	0.671	1.01	0.941	1.35	0.221	0.03
1431366_at	4930519G04Rik	RIKEN cDNA 4930519G04 gene	-2.15	0.23	1.71	0.467	-1.58	0.149	1.01	0.976	-0.25
1427626_at	Muc5b /// LOC6401	mucin 5, subtype B, tracheobronchial /// similar to mucin 5, subtype B, tracheobro	-1.24	0.747	-1.37	0.461	1.28	0.399	2.46	0.194	0.28
1459961_a_at	Stat3	Signal transducer and activator of transcription 3	1.02	0.753	1.25	0.445	-1.85	0.009	-1.29	0.291	-0.22
1428598_at	Tbc1d7	TBC1 domain family, member 7	-1.06	0.626	-1.16	0.176	1.01	0.964	1.56	0.096	0.09
1418202_a_at	Wiz	widely-interspaced zinc finger motifs	-1.41	0.082	-1.07	0.385	1.17	0.359	1.3	0.179	0
1446159_at	Pak7	p21 (CDKN1A)-activated kinase 7	-1.24	0.6	1.06	0.903	-1.06	0.883	1.31	0.584	0.02
1423255_at	Atp6v1g1	ATPase, H+ transporting, lysosomal V1 subunit G1	-1.19	0.053	1.01	0.851	-1.04	0.719	1.04	0.585	-0.04
1435784_at	Atg9a	autophagy-related 9A (yeast)	-1.17	0.006	-1.15	0.195	1.09	0.292	1.85	0.231	0.15
1450039_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	-1.07	0.576	-1.14	0.562	1	0.993	1.37	0.125	0.04
1443229_at	Atad2	ATPase family, AAA domain containing 2	-1.52	0.504	-2.12	0.379	1.68	0.403	1.94	0.273	0
1460525_at	2810047J09Rik	RIKEN cDNA 2810047J09 gene	1.17	0.738	-1.93	0.308	1.12	0.834	-2.31	0.267	-0.49
1425315_at	Dock7	dedicator of cytokinesis 7	-1.74	0.062	1.56	0.084	-1.48	0.258	1.12	0.679	-0.13
1420695_at	Dach1	dachshund 1 (Drosophila)	-1.45	0.165	1.17	0.824	-1.05	0.88	1.12	0.877	-0.05
1431269_at	Prdx4	peroxiredoxin 4	-1.39	0.523	1.24	0.481	-1.18	0.737	1.01	0.967	-0.08
1446070_at	Tyw1	tRNA-yW synthesizing protein 1 homolog (S. cerevisiae)	-1.12	0.689	1.11	0.785	-1.23	0.148	1.24	0.298	0
1442057_at	AA986695	expressed sequence AA986695	-1.3	0.548	-1.16	0.763	1.19	0.206	1.58	0.275	0.08
1438761_a_at	Odc1 /// LOC66623	ornithine decarboxylase, structural 1 /// similar to Ornithine decarboxylase (ODC)	-1.31	0.006	-1.17	0.348	1.19	0.396	2.45	0.11	0.29
1439260_a_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-1.08	0.729	1.28	0.316	-1.65	0.188	2.16	0.114	0.18
1442571_at	---	13 days embryo head cDNA, RIKEN full-length enriched library, clone:3110033I2	-1.04	0.649	1.33	0.565	-1.92	0.004	1.18	0.746	-0.11
1438233_at	6030443O07Rik	RIKEN cDNA 6030443O07 gene	1.04	0.519	1	0.998	-1.3	0.475	-1.08	0.708	-0.08
1421240_at	Ern1	endoplasmic reticulum (ER) to nucleus signalling 1	-1.38	0.012	-1.12	0.871	1.2	0.482	1.84	0.134	0.13
1453427_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	-1.33	0.278	-1.04	0.755	1.09	0.375	1.11	0.784	-0.04
1448829_at	Smc6	structural maintenance of chromosomes 6	1.11	0.525	-1.11	0.482	-1.25	0.17	1.07	0.81	-0.05
1426385_x_at	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsil	1	0.969	-1.05	0.27	-1.17	0.03	1.04	0.327	-0.04
1442533_at	Nr3c2	Nuclear receptor subfamily 3, group C, member 2	-1.3	0.561	-1.03	0.911	1.07	0.903	1.27	0.295	0
1434378_a_at	Mxd4	Max dimerization protein 4	1.07	0.377	1.07	0.62	-1.48	0.173	-1.89	0.054	-0.31
1449121_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	-1.17	0.278	-1.14	0.156	1.08	0.713	1.22	0.618	0
1435493_at	Dsp	desmoplakin	-1.26	0.343	-1.06	0.696	1.08	0.427	2.87	0.087	0.41
1417458_s_at	Cks2	CDC28 protein kinase regulatory subunit 2	-1.22	0.555	1.01	0.719	-1.02	0.952	3.14	0.136	0.48
1426175_a_at	Tpsab1	tryptase alpha/beta 1	1.52	0.49	-1.27	0.522	-1.97	0.07	1.11	0.808	-0.15
1434400_at	Tgif2	TGFB-induced factor 2	-1.52	0.159	1.15	0.786	1.01	0.965	-1.23	0.445	-0.15
1456829_at	Pnma3	paraneoplastic antigen MA3	-1.3	0.5	-1.54	0.543	1.39	0.356	1.13	0.696	-0.08
1442006_at	---	Transcribed locus	1.02	0.892	-1.18	0.249	-1.05	0.815	1.05	0.791	-0.04
1424202_at	Seh1l	SEH1-like (S. cerevisiae	-1.07	0.406	-1.19	0.109	1.04	0.843	1.53	0.258	0.08
1449406_at	Cyhr1	cysteine and histidine rich 1	-1.13	0.003	-1.11	0.571	1.03	0.881	1.24	0.352	0.01
1415692_s_at	Canx	calnexin	-1.07	0.643	1.04	0.614	-1.19	0.236	1.14	0.327	-0.02
1432769_at	Slc44a1	solute carrier family 44, member 1	-1.53	0.452	1.44	0.486	-1.38	0.181	1.35	0.369	-0.03

1456730_x_at	Actl6a	actin-like 6A	-1.34	0.132	1.09	0.443	-1.03	0.853	1.07	0.754	-0.05
1434846_at	1700065A05Rik	RIKEN cDNA 1700065A05 gene	-1.2	0.433	1.15	0.294	-1.2	0.109	1.12	0.538	-0.03
1426857_a_at	Hsdl2	hydroxysteroid dehydrogenase like 2	-1.05	0.706	-1.52	0.069	1.2	0.102	1.43	0.201	0.02
1442290_at	---	---	1.04	0.961	-1.3	0.564	1	0.99	-1.98	0.313	-0.31
1420641_a_at	Sqrdl	sulfide quinone reductase-like (yeast)	-1.05	0.626	1.03	0.83	-1.2	0.12	1.17	0.293	-0.01
1415963_at	Hnrph2	heterogeneous nuclear ribonucleoprotein H2	-1.14	0.392	1.03	0.762	-1.1	0.253	1.07	0.155	-0.04
1436206_at	Fbxo10	F-box protein 10	-1.32	0.248	-1.64	0.278	1.45	0.065	1.7	0.184	0.05
1423288_s_at	Cbln1	cerebellin 1 precursor protein	-1.3	0.347	1.09	0.83	-1.05	0.818	1.07	0.788	-0.05
1424450_at	Gprc5c	G protein-coupled receptor, family C, group 5, member C	-1.01	0.886	-1.22	0.464	1	0.981	1.77	0.068	0.14
1419912_s_at	Strap	Serine/threonine kinase receptor associated protein	-1.08	0.636	1.01	0.789	-1.14	0.273	1.3	0.294	0.02
1430587_at	4933425L03Rik	RIKEN cDNA 4933425L03 gene	-1.14	0.694	-1.31	0.677	1.17	0.608	1.36	0.386	0.02
1437143_a_at	Txndc1	thioredoxin domain containing 1	-1.16	0.117	1.1	0.373	-1.17	0.231	1.44	0.157	0.05
1425560_a_at	S100a16	S100 calcium binding protein A16	1.01	0.935	1.06	0.377	-1.34	0.026	-1.13	0.49	-0.1
1431457_at	7420700N18Rik	RIKEN cDNA 7420700N18 gene	1.32	0.445	1.04	0.955	-2.15	0.003	-2.09	0.165	-0.47
1428299_at	Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	1.16	0.515	-1.24	0.033	-1.18	0.446	1.06	0.704	-0.05
1441529_at	9130230N09Rik	RIKEN cDNA 9130230N09 gene	-1.49	0.02	-1.29	0.541	1.37	0.287	1.3	0.025	-0.03
1426809_at	C430004E15Rik	RIKEN cDNA C430004E15 gene	-1.2	0.034	-1.17	0.382	1.13	0.535	1.13	0.55	-0.03
1434338_at	1110029E03Rik	RIKEN cDNA 1110029E03 gene	-1.07	0.602	-1.28	0.231	1.1	0.637	1.1	0.5	-0.04
1422488_at	Nxt1	NTF2-related export protein 1	1.03	0.832	-1.16	0.124	-1.08	0.158	1.13	0.459	-0.02
1434661_at	Syngr1	synaptogyrin 1	-1.12	0.331	-1.12	0.553	1.02	0.889	2.08	0.185	0.22
1426847_at	Sirt4	sirtuin 4 (silent mating type information regulation 2 homolog) 4 (S. cerevisiae)	-1.44	0.415	-1.17	0.449	1.27	0.602	1.02	0.852	-0.08
1433958_at	Cntrob	centrobin, centrosomal BRCA2 interacting protein	-1.19	0.39	1.01	0.894	-1.04	0.819	1.09	0.202	-0.03
1420310_at	---	---	1.1	0.916	1.05	0.941	-1.49	0.54	-2.9	0.165	-0.56
1425712_at	BC025446	cDNA sequence BC025446	-1.1	0.543	-1.2	0.01	1.07	0.851	1.51	0.141	0.07
1442121_at	Arpp21	cyclic AMP-regulated phosphoprotein, 21	-2.89	0.037	1.8	0.542	-1.48	0.37	1.58	0.302	-0.25
1416258_at	Tk1	thymidine kinase 1	-1.37	0.037	-1.34	0.447	1.34	0.354	3.79	0.199	0.61
1443289_at	Pde4d	Phosphodiesterase 4D, cAMP specific	1.47	0.219	-1.03	0.94	-2.68	0.072	2.6	0.203	0.09
1436845_at	Axin2	axin2	-1.4	0.182	1.04	0.829	1.06	0.839	-1.83	0.107	-0.28
1420017_at	Tspan8	tetraspanin 8	-1.06	0.401	1.18	0.759	-1.44	0.086	2.7	0.263	0.34
1421638_at	Psg17	pregnancy specific glycoprotein 17	-1.33	0.561	-1.26	0.754	1.27	0.514	1.15	0.858	-0.04
1450667_a_at	Cs	citrate synthase	-1.1	0.224	-1.44	0.005	1.21	0.115	1.13	0.372	-0.05
1426912_at	Rfwd2 /// LOC6212	ring finger and WD repeat domain 2 /// similar to constitutive photomorphogenic p	1	0.984	-1.13	0.052	-1.07	0.505	1.12	0.599	-0.02
1418318_at	Rnf128	ring finger protein 128	-1.07	0.221	-1.15	0.146	1.01	0.958	3.32	0.094	0.53
1434570_at	AK122525	cDNA sequence AK122525	-1.23	0.45	-1.31	0.139	1.24	0.453	1.34	0.119	0.01
1418758_a_at	Pscd3	pleckstrin homology, Sec7 and coiled-coil domains 3	-1	0.959	1.02	0.898	-1.25	0.35	2.78	0.177	0.39
1427816_at	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	-1.33	0.206	-1.24	0.403	1.26	0.384	1.42	0.372	0.03
1454719_at	Rhbdd3	rhomboid domain containing 3	1.17	0.742	-1.03	0.837	-1.49	0.071	1.27	0.47	-0.02
1444003_at	Lincr	lung-inducible neuralized-related C3HC4 RING domain protein	1.07	0.726	-1.66	0.584	1.14	0.42	-2.21	0.19	-0.41
1453612_at	Nek1	NIMA (never in mitosis gene a)-related expressed kinase 1	-1.18	0.104	-1.31	0.641	1.2	0.655	1.37	0.564	0.02
1442197_at	AI480624	expressed sequence AI480624	1.41	0.187	-1.15	0.473	-1.85	0.15	1.06	0.668	-0.13
1420963_at	Hapln2	hyaluronan and proteoglycan link protein 2	-1.01	0.962	1.26	0.592	-1.75	0.029	1.01	0.989	-0.12
1434918_at	Sox6	SRY-box containing gene 6	-1.27	0.087	-1.18	0.162	1.18	0.414	11.2	0.219	2.48
1441697_at	Maml1	Mastermind like 1 (Drosophila)	1.25	0.246	-1.71	0.046	-1.01	0.973	1.43	0.426	-0.01
1448222_x_at	Cox8a	cytochrome c oxidase, subunit VIIIa	-1.15	0.336	-1.13	0.218	1.06	0.71	1.23	0.2	0
1427460_at	Taf4a	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.4	0.095	-1.12	0.463	1.21	0.417	1.17	0.522	-0.04
1431668_at	Capzb	capping protein (actin filament) muscle Z-line, beta	1.2	0.293	-1.69	0.28	1.02	0.96	-1.07	0.905	-0.13
1425964_x_at	Hspb1	heat shock protein 1	1.15	0.339	-1.31	0.369	-1.1	0.613	1.35	0.531	0.02
1437379_x_at	Trap1	TNF receptor-associated protein 1	-1.17	0.426	-1.1	0.49	1.05	0.373	1.22	0.014	0
1426301_at	Alcam	activated leukocyte cell adhesion molecule	1.11	0.836	1.11	0.429	-1.67	0.018	-1.45	0.145	-0.23
1428515_at	2410012H22Rik	RIKEN cDNA 2410012H22 gene	-1.16	0.251	-1.2	0.153	1.13	0.575	1.1	0.679	-0.04
1424075_at	9430016H08Rik	RIKEN cDNA 9430016H08 gene	-1.23	0.176	-1.07	0.347	1.07	0.644	1.05	0.662	-0.04
1428922_at	1200009O22Rik	RIKEN cDNA 1200009O22 gene	-1.31	0.212	1.31	0.467	-1.34	0.393	1.32	0.463	-0.01
1422208_a_at	Gnb5	guanine nucleotide binding protein, beta 5	-1.25	0.272	1.09	0.85	-1.07	0.624	1.06	0.785	-0.04

1430023_at	5133400G04Rik	RIKEN cDNA 5133400G04 gene	-1.03	0.672	1.01	0.983	-1.18	0.375	1.49	0.429	0.07
1416128_at	Tuba6 /// LOC6265	tubulin, alpha 6 /// similar to Tubulin alpha-6 chain (Alpha-tubulin 6)	-1.04	0.913	1.16	0.451	-1.42	0.413	1.26	0.59	-0.01
1424184_at	Acadvl	acyl-Coenzyme A dehydrogenase, very long chain	-1	0.983	-1.32	0.062	1.06	0.767	1.04	0.545	-0.05
1434142_at	Ppm1d	protein phosphatase 1D magnesium-dependent, delta isoform	-1.29	0.347	-1.15	0.628	1.17	0.218	1.72	0.247	0.11
1427218_at	Klhl11	kelch-like 11 (Drosophila)	-1.11	0.629	1.15	0.389	-1.31	0.413	1.16	0.546	-0.03
1426002_a_at	Cdc7	cell division cycle 7 (S. cerevisiae)	-1.36	0.253	1.21	0.703	-1.15	0.64	1.22	0.668	-0.02
1448720_at	Lrrc40	leucine rich repeat containing 40	1.05	0.761	-1.1	0.25	-1.17	0.17	1.09	0.504	-0.03
1446863_at	Kcnq1ot1	KCNQ1 overlapping transcript 1	1.09	0.876	-1	1	-1.37	0.326	1.3	0.234	0
1452214_at	Skil	SKI-like	1.02	0.926	1.07	0.733	-1.38	0.032	-1.47	0.238	-0.19
1420682_at	Chrnb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	1.01	0.773	-1.03	0.963	-1.2	0.339	1	0.991	-0.05
1437888_at	Wnk1	WNK lysine deficient protein kinase 1	-1.17	0.286	-1.13	0.617	1.08	0.827	2.01	0.224	0.2
1426584_a_at	Sord	sorbitol dehydrogenase	-1.08	0.518	-1.21	0.396	1.07	0.343	2.19	0.175	0.24
1429094_at	Ddi2	DNA-damage inducible protein 2	1.05	0.839	-1.2	0.018	-1.07	0.672	1.11	0.436	-0.03
1416346_at	Timm8a1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	-1.3	0.294	-1.04	0.773	1.09	0.528	1.34	0.477	0.02
1455801_x_at	Tbcd	tubulin-specific chaperone d	-1.24	0.042	-1.07	0.422	1.08	0.734	1.57	0.139	0.09
1434120_a_at	Metap2	methionine aminopeptidase 2	-1.11	0.069	1.05	0.586	-1.15	0.148	1.95	0.199	0.19
1428112_at	Armet	arginine-rich, mutated in early stage tumors	-1.11	0.312	1.12	0.744	-1.24	0.128	1.08	0.744	-0.04
1427385_s_at	Actn1	actinin, alpha 1	1	0.994	-1.17	0.661	-1.04	0.901	1	0.999	-0.05
1451731_at	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	-1.07	0.342	1.02	0.756	-1.16	0.218	1.46	0.038	0.06
1415778_at	Morf4l2	mortality factor 4 like 2	-1.18	0.027	1.11	0.409	-1.16	0.084	1.1	0.062	-0.03
1430126_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	-1.04	0.903	-1.23	0.462	1.05	0.776	1.09	0.259	-0.03
1420809_a_at	1500003O03Rik	RIKEN cDNA 1500003O03 gene	-1.11	0.669	-1.1	0.499	1.01	0.91	1.12	0.447	-0.02
1424814_a_at	Bcl2l14	Bcl2-like 14 (apoptosis facilitator)	-2	0.261	1.23	0.685	1.1	0.623	-1.47	0.141	-0.29
1417480_at	Fbxo9	f-box only protein 9	-1.05	0.679	-1.2	0.002	1.03	0.626	1.94	0.275	0.18
1416877_a_at	Mrpl51	mitochondrial ribosomal protein L51	-1.16	0.246	-1.09	0.419	1.04	0.476	1.22	0.224	0
1424891_a_at	Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	-1.17	0.444	-1.13	0.429	1.08	0.465	1.15	0.656	-0.02
1432594_at	4933413I22Rik	RIKEN cDNA 4933413I22 gene	-1.2	0.404	-1.17	0.648	1.13	0.791	2.5	0.248	0.31
1423025_a_at	Schip1	schwannomin interacting protein 1	-1.1	0.666	1.14	0.075	-1.29	0.28	1.47	0.348	0.05
1418311_at	Fn3k	fructosamine 3 kinase	-1.62	0.02	-1.2	0.313	1.37	0.396	6.48	0.162	1.26
1448986_x_at	Dnase2a	deoxyribonuclease II alpha	1.05	0.812	-1.48	0.45	1.09	0.337	-1.27	0.152	-0.15
1460660_x_at	Rer1	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	-1.03	0.85	1	0.967	-1.18	0.264	1.04	0.858	-0.04
1450947_at	2610528J11Rik	RIKEN cDNA 2610528J11 gene	-1.26	0.155	-1.13	0.402	1.14	0.568	2.84	0.277	0.4
1421770_a_at	Tlx2	T-cell leukemia, homeobox 2	-1.1	0.892	-1.4	0.359	1.19	0.31	1.36	0.552	0.02
1424059_at	Suv420h2	suppressor of variegation 4-20 homolog 2 (Drosophila)	-1.09	0.7	1.05	0.704	-1.16	0.037	1.84	0.257	0.16
1430547_s_at	Cryzl1	crystallin, zeta (quinone reductase)-like 1	-1.13	0.288	-1.31	0.11	1.17	0.528	1.16	0.641	-0.03
1458709_a_at	Atxn7l1	ataxin 7-like 1	-1.23	0.67	-1.51	0.494	1.35	0.411	1.42	0.374	0.01
1432738_at	2810026P18Rik	RIKEN cDNA 2810026P18 gene	1.01	0.981	-1.04	0.885	-1.18	0.602	1.08	0.85	-0.03
1454085_at	4933409D19Rik	RIKEN cDNA 4933409D19 gene	-1.02	0.966	1.02	0.97	-1.22	0.522	1.66	0.53	0.11
1448892_at	Dock7	dedicator of cytokinesis 7	-1.13	0.266	1.2	0.477	-1.35	0.035	1.05	0.847	-0.06
1424452_at	Sltm	SAFB-like, transcription modulator	1.01	0.944	-1.1	0.305	-1.11	0.513	1.06	0.717	-0.04
1423125_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	-1.25	0.18	-1.26	0.68	1.23	0.633	1.32	0.526	0.01
1417922_at	Kbtbd4	kelch repeat and BTB (POZ) domain containing 4	-1.39	0.003	-1.01	0.919	1.12	0.436	1.06	0.724	-0.06
1428342_at	Rcor3	REST corepressor 3	1.02	0.846	-1.1	0.399	-1.12	0.551	1.19	0.318	0
1436314_at	Scyl2	SCY1-like 2 (S. cerevisiae)	-1.32	0.175	-1.1	0.836	1.15	0.701	1.7	0.194	0.11
1455074_at	---	---	1.36	0.211	-3.3	0.007	1.16	0.642	-1.31	0.26	-0.52
1452673_at	Ranbp3	RAN binding protein 3	-1.09	0.672	-1.4	0.001	1.19	0.208	1.1	0.288	-0.05
1434580_at	Enpp4	ectonucleotide pyrophosphatase/phosphodiesterase 4	-1.15	0.319	1.1	0.688	-1.17	0.399	1.21	0.417	0
1454464_at	2700078F05Rik	RIKEN cDNA 2700078F05 gene	-1.93	0.535	1.6	0.467	-1.41	0.542	1.77	0.016	0.01
1442390_at	---	Transcribed locus	-1.86	0.453	-1.32	0.455	1.53	0.489	1.42	0.522	-0.06
1456394_at	Rint1	RAD50 interactor 1	1.02	0.932	-1.12	0.373	-1.09	0.47	1.31	0.546	0.03
1445298_at	---	---	-1.04	0.937	1.18	0.628	-1.47	0.165	1.28	0.46	-0.01
1460211_a_at	Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-1.13	0.026	1.03	0.814	-1.1	0.661	1.05	0.812	-0.04
1420639_at	Jmy	junction-mediating and regulatory protein	-1.29	0.189	1.18	0.439	-1.15	0.036	1.38	0.371	0.03

1433819_s_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	1.03	0.858	-1.29	0.254	1.02	0.868	-1.26	0.399	-0.12
1441828_at	Stard5	StAR-related lipid transfer (START) domain containing 5	1.38	0.182	-1.39	0.396	-1.37	0.189	1.53	0.485	0.03
1455455_at	Glt28d2	glycosyltransferase 28 domain containing 2	1.13	0.422	-1.03	0.844	-1.38	0.079	1.3	0.008	0
1430316_at	4930579E17Rik	RIKEN cDNA 4930579E17 gene	-1.12	0.438	1.11	0.294	-1.22	0.39	1.05	0.79	-0.05
1438619_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	-1.07	0.807	1.19	0.286	-1.43	0.127	1.47	0.373	0.04
1428775_at	1110008L16Rik	RIKEN cDNA 1110008L16 gene	1.1	0.645	-1.23	0.229	-1.09	0.716	1.2	0.668	-0.01
1432671_at	4933407A17Rik	RIKEN cDNA 4933407A17 gene	1.25	0.433	-1.2	0.635	-1.36	0.32	1.03	0.92	-0.07
1419477_at	Clec2d	C-type lectin domain family 2, member d	1.22	0.705	1.01	0.979	-1.69	0.213	-1.07	0.923	-0.13
1436795_at	9630058J23Rik	RIKEN cDNA 9630058J23 gene	-1.05	0.726	-1.33	0.073	1.12	0.079	1.25	0.482	0
1454684_at	Bbs7	Bardet-Biedl syndrome 7	-1.09	0.25	-1.12	0.507	1.01	0.926	1.44	0.097	0.06
1425613_at	Pcdha11	protocadherin alpha 11	-1.29	0.062	1.36	0.115	-1.47	0.282	1.52	0.163	0.03
1453246_at	Rab39b	RAB39B, member RAS oncogene family	-1.15	0.625	-1.12	0.883	1.06	0.895	1.04	0.931	-0.04
1418702_a_at	2810428I15Rik	RIKEN cDNA 2810428I15 gene	1.04	0.566	-1.11	0.264	-1.13	0.353	1.03	0.909	-0.04
1437844_x_at	Cog1	component of oligomeric golgi complex 1	-1.29	0.113	1.01	0.633	1.03	0.557	-1.02	0.804	-0.06
1428447_at	Tmem14a	transmembrane protein 14A	1.03	0.816	-1.3	0.418	1.03	0.837	-1.12	0.375	-0.09
1440510_at	C430002N11Rik	RIKEN cDNA C430002N11 gene	-1.1	0.602	-3.4	0.125	1.62	0.392	1.24	0.659	-0.41
1445732_at	---	---	1.06	0.929	1.08	0.896	-1.46	0.531	-1.16	0.724	-0.12
1417901_a_at	Ica1	islet cell autoantigen 1	-1.36	0.116	1.38	0.598	-1.42	0.105	1.33	0.416	-0.02
1437064_at	Ar	androgen receptor	-1.22	0.488	1.11	0.498	-1.13	0.776	1.5	0.065	0.07
1441743_at	Pax3	paired box gene 3	-1.14	0.814	-1.23	0.777	1.13	0.852	2.01	0.146	0.19
1447078_at	---	---	-1.5	0.6	-1.13	0.702	1.27	0.672	1.43	0.638	0.02
1447379_at	Sap30l	SAP30-like	1.56	0.235	-1.57	0.245	-1.6	0.112	1.25	0.452	-0.09
1418511_at	Dpt	dermatopontin	1.14	0.722	1.3	0.255	-2.61	0	-1.08	0.806	-0.31
1437780_at	Fancb	Fanconi anemia, complementation group B	1.3	0.384	-1.08	0.84	-1.67	0.004	1.39	0.182	-0.02
1441162_at	Rock1	Rho-associated coiled-coil forming kinase 1	1.05	0.788	1.1	0.778	-1.49	0.138	-1.09	0.639	-0.11
1457018_at	Kcnma1	Potassium large conductance calcium-activated channel, subfamily M, alpha mer	-1.31	0.151	1.26	0.751	-1.24	0.767	1.23	0.703	-0.02
1443566_at	Igf1r	Insulin-like growth factor I receptor	-1.26	0.38	1.54	0.237	-2.02	0.081	1.4	0.116	-0.09
1444898_at	---	---	-1.05	0.871	1.12	0.747	-1.33	0.141	1.2	0.662	-0.01
1418640_at	Sirt1	sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	-1.08	0.721	1.05	0.787	-1.18	0.068	1.18	0.409	-0.01
1420683_at	Bnipl	BCL2/adenovirus E1B 19kD interacting protein like	1.06	0.814	-1.01	0.927	-1.29	0.213	2.84	0.301	0.4
1436737_a_at	Sorbs1	sorbin and SH3 domain containing 1	-1.3	0.076	-1.14	0.322	1.18	0.47	1.66	0.273	0.1
1451117_a_at	Tom1l1	target of myb1-like 1 (chicken)	-1.24	0.146	-1.23	0.098	1.21	0.529	5.83	0.218	1.14
1423565_at	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoim	-1.02	0.58	1.1	0.371	-1.34	0.06	1.35	0.237	0.02
1437926_at	Xpnpep3	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	1.03	0.776	-1.26	0.094	1	0.994	-1.02	0.909	-0.06
1423369_at	Fmr1	fragile X mental retardation syndrome 1 homolog	-1.14	0.308	1.02	0.829	-1.08	0.448	1.4	0.124	0.05
1443890_at	---	Transcribed locus	1.5	0.503	-1.41	0.502	-1.62	0.144	1.61	0.146	0.02
1437584_at	Ccnd3	Cyclin D3	1.08	0.687	1.09	0.754	-1.54	0.143	-2.09	0.138	-0.36
1425700_at	Grm1	glutamate receptor, metabotropic 1	1.09	0.776	-1.21	0.077	-1.1	0.642	1.01	0.981	-0.05
1432608_at	Nnt	nicotinamide nucleotide transhydrogenase	1.28	0.402	-1.38	0.537	-1.22	0.687	1.39	0.58	0.02
1444559_at	Phtf2	Putative homeodomain transcription factor 2	1.1	0.684	-1.34	0.352	-1.02	0.943	1.2	0.414	-0.01
1452230_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	-1.03	0.88	1.01	0.967	-1.18	0.206	1.29	0.538	0.02
1446008_at	D3Ertd246e	DNA segment, Chr 3, ERATO Doi 246, expressed	1.06	0.846	-1.47	0.57	1.08	0.848	-3.79	0.054	-0.78
1426275_a_at	Uxs1	UDP-glucuronate decarboxylase 1	-1.02	0.863	1.07	0.697	-1.29	0.09	1.12	0.604	-0.03
1424397_at	Dhx36	DEAH (Asp-Glu-Ala-His) box polypeptide 36	1.05	0.808	-1.28	0.079	-1.01	0.969	1.06	0.739	-0.04
1420075_at	Atp8b1	ATPase, class I, type 8B, member 1	-1.16	0.322	1.11	0.397	-1.17	0.504	1.11	0.426	-0.03
1452331_s_at	Qser1	glutamine and serine rich 1	1.05	0.751	-1.02	0.892	-1.26	0.053	1.02	0.906	-0.05
1455523_at	Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	-1.14	0.803	-1.25	0.363	1.15	0.231	1.1	0.653	-0.04
1433154_at	B230204H03Rik	RIKEN cDNA B230204H03 gene	1.26	0.401	-1.38	0.436	-1.19	0.621	2.91	0.087	0.4
1422792_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	1.01	0.953	-1.05	0.659	-1.16	0.077	1.38	0.2	0.05
1420546_at	Th	tyrosine hydroxylase	1.35	0.527	-2.8	0.139	1.12	0.716	-1.07	0.898	-0.35
1432925_at	4933416A02Rik	RIKEN cDNA 4933416A02 gene	-1.15	0.717	1.08	0.864	-1.14	0.563	1.01	0.961	-0.05
1435259_s_at	Tmem141	transmembrane protein 141	-1.02	0.837	1.27	0.034	-1.74	0.018	1.31	0.198	-0.04
1437301_a_at	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	-1.09	0.288	1.02	0.879	-1.13	0.479	1.06	0.7	-0.03

1448079_at	Rnf166	ring finger protein 166	1.09	0.532	1.11	0.609	-1.59	0.129	-1.39	0.172	-0.19
1459104_at	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	1.17	0.611	-1.22	0.302	-1.2	0.243	1.47	0.322	0.06
1428575_at	Fcho1	FCH domain only 1	1.03	0.949	-1.21	0.443	-1.03	0.916	1.15	0.655	-0.02
1456477_at	Ccnt1	cyclin T1	1.12	0.062	-1.01	0.886	-1.38	0.123	1.07	0.239	-0.05
1445247_at	C530044C16Rik	RIKEN cDNA C530044C16 gene	1.13	0.85	-1.35	0.58	-1.04	0.811	1	0.993	-0.07
1456874_at	Flrt2	fibronectin leucine rich transmembrane protein 2	-1.48	0.234	1.02	0.926	1.13	0.489	-1.28	0.159	-0.15
1454674_at	Fez1	fasciculation and elongation protein zeta 1 (zygin I)	-1.26	0.746	-1.12	0.856	1.13	0.57	1.22	0.747	0
1457749_at	Cc2d1b	coiled-coil and C2 domain containing 1B	-1.43	0.265	-1.17	0.7	1.27	0.234	1.04	0.849	-0.07
1434111_at	Lphn2	latrophilin 2	1.02	0.596	-1.02	0.906	-1.22	0.27	1.2	0.218	0
1418573_a_at	Raly	hnRNP-associated with lethal yellow	1.1	0.848	-1.26	0.528	-1.07	0.84	1.86	0.415	0.16
1432394_a_at	Aatf	apoptosis antagonizing transcription factor	-1.07	0.687	-1.22	0.291	1.07	0.47	1.06	0.604	-0.04
1448961_at	Plscr2	phospholipid scramblase 2	-1.06	0.719	1.02	0.847	-1.16	0.555	1.09	0.21	-0.03
1443288_at	Traf6	Tnf receptor-associated factor 6	1.1	0.62	-1.21	0.328	-1.11	0.028	1.1	0.761	-0.03
1435488_at	C630010D07Rik ///	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofolate dehydro	1.2	0.447	-1.04	0.905	-1.49	0.122	1.15	0.061	-0.04
1421822_at	Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	-1.42	0.431	1.33	0.223	-1.26	0.168	1.23	0.457	-0.03
1437867_at	---	2 cells egg cDNA, RIKEN full-length enriched library, clone:B020014N01 product:	-1.06	0.766	-3.77	0.002	1.62	0.402	1.1	0.747	-0.53
1416591_at	Rab34	RAB34, member of RAS oncogene family	-1.23	0.473	1.08	0.526	-1.07	0.523	1.18	0.469	-0.01
1431064_at	Dpp8	dipeptidylpeptidase 8	-1.07	0.364	-1.19	0.414	1.05	0.886	1.19	0.655	0
1442790_at	---	---	-1.21	0.513	-1.49	0.232	1.33	0.245	1.12	0.747	-0.06
1444447_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	1.34	0.115	-1.12	0.618	-1.66	0.121	1.05	0.891	-0.1
1426453_at	Pitrm1	pitrilysin metallepetidase 1	-1.23	0.097	-1.05	0.736	1.06	0.569	2.3	0.279	0.27
1436828_a_at	Tpd52l2	tumor protein D52-like 2	-1.09	0.476	1.01	0.847	-1.12	0.463	1.15	0.521	-0.01
1458147_at	Mamdc1	MAM domain containing 1	1.28	0.702	-1.45	0.509	-1.17	0.647	1.48	0.232	0.04
1417417_a_at	Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	-1.15	0.074	-1.19	0.222	1.12	0.01	1.02	0.807	-0.05
1450044_at	Fzd7	frizzled homolog 7 (Drosophila)	-1.19	0.351	-1.16	0.433	1.12	0.777	1.65	0.039	0.11
1438073_at	Spry3	sprouty homolog 3 (Drosophila)	1.74	0.28	-2.17	0.47	-1.58	0.281	1.03	0.908	-0.25
1446917_at	---	---	-1.17	0.655	-1.04	0.929	1.02	0.969	1.42	0.569	0.06
1416700_at	Rnd3	Rho family GTPase 3	1.03	0.86	1.14	0.572	-1.51	0.255	-1.25	0.441	-0.15
1437103_at	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	-1.14	0.303	1.28	0.496	-1.49	0.053	1.3	0.555	-0.01
1445445_s_at	Ptger1	prostaglandin E receptor 1 (subtype EP1)	-1.13	0.748	1.27	0.662	-1.47	0.228	1.3	0.584	-0.01
1456211_at	Nalp10	NACHT, leucine rich repeat and PYD containing 10	-1.2	0.661	-1.2	0.817	1.16	0.775	1.39	0.327	0.04
1418039_at	Rabl3	RAB, member of RAS oncogene family-like 3	-1.05	0.56	1.04	0.183	-1.18	0.085	1.28	0.225	0.02
1444766_at	Atxn7l1	ataxin 7-like 1	-1.07	0.241	-1.65	0.357	1.28	0.46	1.5	0.28	0.02
1431847_at	5330439K02Rik	RIKEN cDNA 5330439K02 gene	1.3	0.524	-1.6	0.005	-1.11	0.51	1.94	0.368	0.13
1425356_at	Zfp142	zinc finger protein 142	-1.23	0.608	-1.21	0.14	1.19	0.185	1.1	0.647	-0.04
1430676_at	Col19a1	procollagen, type XIX, alpha 1	-1.31	0.705	1.33	0.301	-1.36	0.559	1.6	0.183	0.06
1426611_at	Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	-1.11	0.468	-1.13	0.141	1.04	0.646	1.26	0.154	0.02
1416968_a_at	Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	1.15	0.435	-1.33	0.041	-1.08	0.327	1.11	0.619	-0.04
1446029_at	Tanc1	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	1.19	0.546	1.22	0.461	-2.43	0.01	-1.09	0.653	-0.28
1445439_at	Epb4.9	erythrocyte protein band 4.9	-1.23	0.18	1.02	0.838	-1.01	0.947	3.23	0.207	0.5
1417948_s_at	Ilf2	interleukin enhancer binding factor 2	-1.03	0.537	1.01	0.76	-1.17	0.111	1.11	0.37	-0.02
1438181_x_at	Tm2d2	TM2 domain containing 2	1.03	0.773	1.09	0.518	-1.42	0.045	-1.12	0.626	-0.1
1436746_at	Wnk1	WNK lysine deficient protein kinase 1	1.05	0.801	-1.01	0.938	-1.28	0.247	1.45	0.018	0.05
1438623_x_at	Rbx1	ring-box 1	-2.33	0.341	1.54	0.234	-1.16	0.387	1.01	0.972	-0.24
1423677_at	Fkbp9	FK506 binding protein 9	-1.09	0.497	1.02	0.649	-1.13	0.595	1.02	0.923	-0.04
1427262_at	Xist	inactive X specific transcripts	1.12	0.708	-1.09	0.432	-1.26	0.46	1.11	0.443	-0.03
1425015_at	Ephb2	Eph receptor B2	1.03	0.918	-1.02	0.968	-1.22	0.691	1.48	0.213	0.07
1442518_at	C030044O21Rik	RIKEN cDNA C030044O21 gene	-1.05	0.943	1.25	0.6	-1.6	0.182	1.72	0.174	0.08
1445469_at	Auts2	Autism susceptibility candidate 2	-1.11	0.71	1.19	0.767	-1.36	0.624	1.38	0.629	0.03
1423982_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	-1.13	0.723	-1.09	0.486	1.03	0.75	1.16	0.392	-0.01
1460294_at	Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	1.24	0.123	1.2	0.799	-2.55	0.168	-1.13	0.865	-0.31
1421632_at	Kcnn3	potassium intermediate/small conductance calcium-activated channel, subfamily	1.07	0.601	1.02	0.946	-1.36	0.063	-1.12	0.716	-0.1
1442344_at	Ap1gbp1	AP1 gamma subunit binding protein 1	-2.2	0.414	1.32	0.709	1.06	0.914	-1.97	0.244	-0.45

1449028_at	Rhou	ras homolog gene family, member U	-1.23	0.732	1.03	0.748	-1.01	0.93	3.41	0.161	0.55
1426327_s_at	Cntf /// Zfp91	ciliary neurotrophic factor /// zinc finger protein 91	1.02	0.946	-1.05	0.773	-1.17	0.16	1.03	0.848	-0.04
1458842_at	---	---	-1.28	0.708	-1.19	0.676	1.21	0.772	1.63	0.524	0.09
1444332_at	9130019P16Rik	RIKEN cDNA 9130019P16 gene	-1.48	0.462	-1.04	0.918	1.2	0.65	1.26	0.61	-0.02
1447455_at	---	---	1.62	0.205	-3	0.049	-1.15	0.742	1.71	0.282	-0.2
1442614_at	Il1rap	interleukin 1 receptor accessory protein	1.04	0.951	-1.36	0.555	1.05	0.875	-2.61	0.227	-0.47
1458574_at	E2f2	E2F transcription factor 2	1.16	0.681	-1.05	0.909	-1.4	0.022	4.5	0.187	0.8
1437300_at	Mef2d	myocyte enhancer factor 2D	-1.09	0.631	-1.71	0.022	1.33	0.255	1.06	0.679	-0.1
1423783_at	Tor2a	torsin family 2, member A	-1.13	0.561	1	0.995	-1.06	0.485	1.05	0.163	-0.03
1444623_at	E530011L22Rik	RIKEN cDNA E530011L22 gene	-1.38	0.257	1.05	0.922	1.05	0.849	-1.2	0.454	-0.12
1430872_at	4930412O13Rik	RIKEN cDNA 4930412O13 gene	-1.27	0.608	-1.08	0.923	1.12	0.53	1.24	0.449	0
1456637_at	Lrrtm2	leucine rich repeat transmembrane neuronal 2	1.33	0.592	1.04	0.862	-2.18	0.139	-1.23	0.816	-0.26
1437622_x_at	Mrpl28	mitochondrial ribosomal protein L28	-1.1	0.489	-1.09	0.05	1.01	0.949	1.28	0.373	0.02
1433034_at	2310007H11Rik	RIKEN cDNA 2310007H11 gene	1.04	0.791	-1.03	0.901	-1.23	0.576	1.33	0.613	0.03
1416973_at	Nhp2l1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	1.06	0.79	-1.14	0.303	-1.12	0.526	1.09	0.713	-0.03
1425791_at	Pon2	paraoxonase 2	1.18	0.532	-1.15	0.777	-1.28	0.257	1.06	0.817	-0.05
1448884_at	Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)	1.03	0.755	-1.1	0.356	-1.13	0.353	1.57	0.365	0.09
1448349_at	Vapa	vesicle-associated membrane protein, associated protein A	1.23	0.833	-1.67	0.388	1.01	0.987	-1.08	0.856	-0.13
1417117_at	Cstf1	cleavage stimulation factor, 3' pre-RNA, subunit 1	-1.32	0.378	1.01	0.938	1.06	0.729	-1.17	0.46	-0.1
1417825_at	Esd	esterase D/formylglutathione hydrolase	-1.04	0.552	-1.22	0.047	1.05	0.678	1.05	0.78	-0.04
1418137_at	Mrp63	mitochondrial ribosomal protein 63	-1.04	0.695	-1.16	0.09	1.01	0.957	1.28	0.168	0.02
1443670_at	2010001J22Rik	RIKEN cDNA 2010001J22 gene	-1.12	0.75	-1.17	0.531	1.08	0.634	1.08	0.91	-0.03
1434195_at	Prss35	protease, serine, 35	-1.43	0.069	1.26	0.756	-1.15	0.801	1.01	0.985	-0.08
1433299_at	5830461L22Rik	RIKEN cDNA 5830461L22 gene	-1.3	0.557	1.02	0.93	1.04	0.921	-1.43	0.217	-0.17
1429071_at	Me3	malic enzyme 3, NADP(+)-dependent, mitochondrial	-1.09	0.325	-1.37	0.678	1.18	0.553	1.18	0.783	-0.02
1455567_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	1.05	0.902	-1.13	0.641	-1.12	0.722	1.1	0.717	-0.02
1419172_at	Dhfr	dihydrofolate reductase	-1.19	0.03	-1.03	0.621	1.02	0.888	2.28	0.18	0.27
1441580_at	Sgpp2	Sphingosine-1-phosphate phosphotase 2	-1.24	0.197	1.43	0.28	-1.7	0.152	1.06	0.627	-0.11
1439405_x_at	Becn1	Beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	-1.06	0.829	1.08	0.748	-1.23	0.128	1.01	0.914	-0.05
1455775_at	4932415D10Rik	RIKEN cDNA 4932415D10 gene	1.03	0.737	-1.54	0.002	1.15	0.577	-1.3	0.55	-0.17
1451413_at	Cast	calpastatin	1.15	0.45	-1.12	0.043	-1.27	0.114	1.21	0.417	-0.01
1436758_at	Hdac4	histone deacetylase 4	-1.23	0.304	-1.12	0.626	1.13	0.586	1.02	0.936	-0.05
1417191_at	Dnajb9	DnaJ (Hsp40) homolog, subfamily B, member 9	-1.09	0.738	1.01	0.945	-1.11	0.386	1.03	0.909	-0.04
1434658_at	3110056O03Rik	RIKEN cDNA 3110056O03 gene	-1.07	0.475	-1.2	0.244	1.06	0.736	1.74	0.205	0.13
1436586_x_at	Rps14	ribosomal protein S14	1.01	0.587	1.02	0.7	-1.25	0.037	-1.3	0.013	-0.13
1437784_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	-1.01	0.743	1.17	0.698	-1.48	0.03	1.07	0.881	-0.06
1450735_at	1810003N24Rik	RIKEN cDNA 1810003N24 gene	-1.18	0.11	-1.18	0.064	1.13	0.308	1.1	0.635	-0.03
1425716_s_at	Bak1	BCL2-antagonist/killer 1	-1.24	0.706	-1.18	0.779	1.18	0.349	1.48	0.422	0.06
1444093_at	4930557M11Rik	RIKEN cDNA 4930557M11 gene	1.21	0.748	-1.15	0.807	-1.33	0.507	1.64	0.377	0.09
1445264_at	Catsper2	cation channel, sperm associated 2	-1.61	0.169	1.3	0.467	-1.09	0.237	1.44	0.288	0.01
1440659_at	2610027L16Rik	RIKEN cDNA 2610027L16 gene	1.15	0.477	-1.16	0.442	-1.23	0.121	1.01	0.967	-0.06
1448876_at	Evc	Ellis van Creveld gene homolog (human)	-1.06	0.598	-1.42	0.155	1.19	0.596	1.12	0.675	-0.04
1440312_at	Elovl7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	1.02	0.76	-1.07	0.927	-1.15	0.596	1.32	0.482	0.03
1445117_at	Glt28d1	Glycosyltransferase 28 domain containing 1	-1.22	0.747	1.2	0.711	-1.23	0.692	1.61	0.161	0.09
1448842_at	Cdo1	cysteine dioxygenase 1, cytosolic	1.09	0.649	-1.3	0.215	-1.02	0.94	1.46	0.441	0.06
1439394_x_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	-1.18	0.318	-1.22	0.732	1.17	0.283	1.08	0.804	-0.04
1442716_at	---	Transcribed locus	-1.16	0.816	-3.19	0.173	1.66	0.107	1.33	0.392	-0.34
1450013_at	2900073G15Rik	RIKEN cDNA 2900073G15 gene	1.03	0.432	1.05	0.67	-1.34	0.01	-1.11	0.164	-0.09
1418423_s_at	Serpinb9f /// Serpin	serine (or cysteine) peptidase inhibitor, clade B, member 9f /// serine (or cysteine)	-1.87	0.317	1.01	0.917	1.28	0.652	-1.2	0.513	-0.19
1453657_at	2310065F04Rik	RIKEN cDNA 2310065F04 gene	-2.29	0.303	-1.13	0.743	1.51	0.271	1.16	0.719	-0.19
1422050_at	Nkx1-2	NK1 transcription factor related, locus 2 (Drosophila)	1.14	0.852	1.06	0.898	-1.57	0.131	-1.54	0.482	-0.23
1432249_a_at	Ercc8	excision repaiross-complementing rodent repair deficiency, complementation gro	-1.27	0.327	-1.26	0.333	1.25	0.278	1.88	0.372	0.15
1427736_a_at	Ccrl2	chemokine (C-C motif) receptor-like 2	1.13	0.563	-1.34	0.22	-1.04	0.607	3.4	0.214	0.53

1445574_at	---	Transcribed locus	1.08	0.806	-1.57	0.375	1.12	0.536	-1.11	0.776	-0.12
1419664_at	Srr	serine racemase	-1.01	0.953	-1.22	0.394	1.03	0.902	1.03	0.842	-0.04
1445575_at	Fbxl20	F-box and leucine-rich repeat protein 20	1.2	0.459	-1.2	0.73	-1.26	0.341	1.65	0.144	0.1
1455473_at	Usp13	ubiquitin specific peptidase 13 (isopeptidase T-3)	-1.04	0.946	1.06	0.877	-1.23	0.568	1.08	0.781	-0.03
1421545_a_at	Syne1	synaptic nuclear envelope 1	-1.53	0.477	-1.34	0.315	1.43	0.175	1.31	0.349	-0.03
1434463_at	Bfsp2	beaded filament structural protein 2, phakinin	-3.16	0.002	1.4	0.222	1.12	0.624	-4.29	0.092	-1.23
1428781_at	Dmkn	dermokine	-1.39	0.639	-1.04	0.929	1.15	0.678	2.07	0.474	0.2
1444200_at	D19Ertd386e	DNA segment, Chr 19, ERATO Doi 386, expressed	-2.07	0.218	1.32	0.408	1.03	0.919	-1.02	0.897	-0.19
1420781_at	Etos1	ectopic ossification 1	-1.82	0.096	1.67	0.101	-1.62	0.391	1.14	0.526	-0.16
1456090_at	Pdhx	pyruvate dehydrogenase complex, component X	-1.18	0.096	-1.19	0.183	1.15	0.535	1.13	0.592	-0.02
1443824_s_at	Car7	carbonic anhydrase 7	-1.46	0.3	-1.01	0.991	1.15	0.626	1.29	0.338	0
1433231_at	4933426I03Rik	RIKEN cDNA 4933426I03 gene	1.09	0.77	1.12	0.654	-1.6	0.297	-1.37	0.508	-0.19
1420617_at	Cpeb4	cytoplasmic polyadenylation element binding protein 4	-1.25	0.078	-1.03	0.886	1.06	0.63	3.53	0.149	0.58
1451300_a_at	Chmp7	CHMP family, member 7	1.04	0.617	-1.33	0.005	1.04	0.28	-1.42	0.026	-0.17
1439912_at	9430098F02Rik	RIKEN cDNA 9430098F02 gene	-1.25	0.631	-1.08	0.761	1.11	0.669	1.53	0.187	0.08
1433993_at	4931406P16Rik	RIKEN cDNA 4931406P16 gene	-1.12	0.013	1.06	0.665	-1.13	0.109	1.13	0.465	-0.02
1437209_at	Cep76	centrosomal protein 76	1.06	0.786	-1.18	0.195	-1.08	0.728	7.38	0.192	1.55
1439156_at	Gm962	gene model 962, (NCBI)	1	0.988	-1.28	0.03	1.05	0.733	-1.06	0.8	-0.07
1429603_at	2610110G12Rik	RIKEN cDNA 2610110G12 gene	1.05	0.857	-1.19	0.243	-1.05	0.72	1.06	0.788	-0.03
1424224_at	Asb8	ankyrin repeat and SOCS box-containing protein 8	-1.2	0.018	-1.05	0.551	1.05	0.203	1.11	0.549	-0.02
1459671_at	---	Transcribed locus	1.58	0.161	-1.89	0.076	-1.38	0.355	1.21	0.489	-0.12
1459817_at	---	---	-1.61	0.129	-1.21	0.476	1.39	0.546	1.64	0.376	0.05
1432967_at	4930456A14Rik	RIKEN cDNA 4930456A14 gene	1.03	0.972	-1.04	0.91	-1.18	0.671	1.17	0.567	-0.01
1437646_at	Znrf3 /// LOC63180	zinc and ring finger 3 /// similar to Goliath homolog precursor (Ring finger protein	1.93	0.2	-2.83	0.022	-1.83	0.262	1.04	0.953	-0.42
1416395_at	Guk1	guanylate kinase 1	1.12	0.251	-1.07	0.464	-1.28	0.133	1.07	0.653	-0.04
1436141_at	Zmat5	zinc finger, matrin type 5	-1.78	0.455	1.18	0.701	1.09	0.838	-1.67	0.383	-0.29
1459513_at	---	---	-1.73	0.32	1.5	0.442	-1.32	0.357	1.03	0.957	-0.13
1438058_s_at	Ptov1	prostate tumor over expressed gene 1	1.06	0.788	-1.22	0.162	-1.04	0.711	1.22	0.142	0
1449003_a_at	Vti1b	vesicle transport through interaction with t-SNAREs 1B homolog	1.02	0.86	1	0.981	-1.22	0.091	-1.46	0.157	-0.17
1437095_at	Tspan18	tetraspanin 18	-1.68	0.145	-2.33	0.035	1.81	0.29	1.19	0.693	-0.25
1450733_at	Bicd2	bicaudal D homolog 2 (Drosophila)	1.22	0.356	-1.13	0.513	-1.36	0.277	1.45	0.288	0.04
1423219_a_at	Mrpl49	mitochondrial ribosomal protein L49	1.07	0.241	-1.28	0.059	-1.01	0.846	1.32	0.412	0.02
1416756_at	Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	1.09	0.802	-1.23	0.223	-1.07	0.818	1.2	0.808	0
1421735_a_at	St8sia5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	-1.15	0.67	-1.23	0.611	1.15	0.318	1.22	0.192	0
1447895_x_at	Pan3	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	1.02	0.97	1.05	0.905	-1.3	0.512	-1.41	0.378	-0.16
1432181_s_at	Ecgf1	endothelial cell growth factor 1 (platelet-derived)	1.07	0.234	-1.3	0.004	1	0.995	-1.16	0.453	-0.1
1449894_at	Lrrc18	leucine rich repeat containing 18	-2.7	0.014	1.3	0.586	1.17	0.601	-2.07	0.066	-0.58
1417879_at	Nenf	neuron derived neurotrophic factor	1.26	0.199	-1.04	0.789	-1.62	0.003	1.28	0.054	-0.03
1454825_at	1110014N23Rik	RIKEN cDNA 1110014N23 gene	-1.26	0.236	-1.08	0.685	1.11	0.496	1.02	0.906	-0.05
1432384_a_at	Mettl6	methyltransferase like 6	-1.23	0.243	-1.05	0.659	1.07	0.716	1.22	0.297	0
1427087_at	Luc7l2	LUC7-like 2 (S. cerevisiae)	-1.17	0.512	1.01	0.903	-1.03	0.848	1.58	0.218	0.1
1432054_at	Golga1	golgi autoantigen, golgin subfamily a, 1	1.15	0.543	-1.3	0.191	-1.09	0.537	1.01	0.952	-0.06
1450899_at	Nedd1	neural precursor cell expressed, developmentally down-regulated gene 1	-1.04	0.633	1.01	0.866	-1.17	0.085	1.42	0.227	0.06
1431682_at	4930594C11Rik	RIKEN cDNA 4930594C11 gene	-1.67	0.411	1.04	0.888	1.2	0.726	-1.3	0.41	-0.18
1421047_at	Smad5	MAD homolog 5 (Drosophila)	1.12	0.74	-1.06	0.866	-1.29	0.41	1.32	0.126	0.02
1417457_at	Cks2	CDC28 protein kinase regulatory subunit 2	-1.24	0.313	-1.01	0.929	1.05	0.872	2.37	0.08	0.29
AFFX-BioB-5_at	---	---	1.17	0.131	1.03	0.804	-1.58	0.011	-1.08	0.759	-0.11
1440860_at	Mab21l1	mab-21-like 1 (C. elegans)	-1.16	0.759	-1.27	0.292	1.19	0.536	1.12	0.806	-0.03
1459131_at	Trp53bp1	Transformation related protein 53 binding protein 1	-1.03	0.911	1.39	0.463	-2.1	0.19	1	0.98	-0.18
1458528_at	C330002I19Rik	RIKEN cDNA C330002I19 gene	1.11	0.766	-1.02	0.956	-1.34	0.106	1.11	0.387	-0.03
1435125_at	BB120497	expressed sequence BB120497	1.12	0.693	-2.33	0.22	1.29	0.708	-1.44	0.619	-0.34
1446583_at	---	Transcribed locus	-1.11	0.758	1.08	0.841	-1.17	0.566	1.25	0.665	0.01
1448877_at	Dlx2	distal-less homeobox 2	-1.88	0.256	1.04	0.921	1.26	0.595	-1.01	0.975	-0.15

1421799_at	Uts2	urotensin 2	1.25	0.188	-3.02	0.336	1.26	0.576	-1.51	0.427	-0.51
1440980_at	Kcnh8	potassium voltage-gated channel, subfamily H (eag-related), member 8	1.11	0.839	-1.26	0.675	-1.07	0.888	1.3	0.684	0.02
1426666_a_at	Unc84a	unc-84 homolog A (C. elegans)	-1.14	0.116	1.12	0.367	-1.19	0.006	1.18	0.463	-0.01
1416445_at	2810405J04Rik	RIKEN cDNA 2810405J04 gene	1.07	0.499	-1.07	0.599	-1.2	0.183	1.01	0.95	-0.05
1427098_at	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	1.08	0.422	-1.2	0.121	-1.08	0.666	1.69	0.018	0.12
1453722_s_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	-1.16	0.244	-1.09	0.203	1.06	0.747	1.18	0.356	0
1428560_at	Xpo5	exportin 5	-1.11	0.196	-1.33	0.111	1.18	0.346	1.05	0.595	-0.05
1455697_at	---	PREDICTED: Mus musculus hypothetical protein LOC629064 (LOC629064), mR	-1.01	0.896	1.05	0.762	-1.25	0.22	1.24	0.644	0.01
1454165_at	1700025K04Rik	RIKEN cDNA 1700025K04 gene	-1.21	0.726	-1.04	0.937	1.05	0.885	2.53	0.01	0.33
1431776_at	Tob2	transducer of ERBB2, 2	1.01	0.992	-1.49	0.372	1.16	0.559	-1	0.998	-0.08
1437623_x_at	Xrcc3	X-ray repair complementing defective repair in Chinese hamster cells 3	-1.11	0.895	-1.62	0.341	1.32	0.649	2.26	0.141	0.21
1442826_at	Usp25	Ubiquitin specific peptidase 25	-1.07	0.81	1.08	0.881	-1.21	0.628	1.04	0.924	-0.04
1436937_at	Rbms3	RNA binding motif, single stranded interacting protein	1.21	0.456	1.1	0.629	-1.9	0.016	-1.43	0.24	-0.26
1420303_x_at	---	Transcribed locus, strongly similar to XP_537399.1 PREDICTED: similar to 40S r	-1.14	0.711	-1.45	0.555	1.27	0.007	1.11	0.663	-0.05
1424515_at	B230354K17Rik	RIKEN cDNA B230354K17 gene	-1	0.981	1.09	0.625	-1.33	0.352	2.13	0.207	0.22
1425173_s_at	Golph3l	golgi phosphoprotein 3-like	1.19	0.146	-1.21	0.474	-1.22	0.376	1.25	0.322	0
1453720_at	Rnf157	ring finger protein 157	-1.94	0.452	-1.05	0.931	1.37	0.057	1.29	0.523	-0.08
1427453_at	BC018473	cDNA sequence BC018473	1.18	0.723	-1.05	0.886	-1.43	0.209	2.02	0.071	0.18
1454035_at	3110009E22Rik	RIKEN cDNA 3110009E22 gene	1.46	0.544	-1.15	0.787	-1.96	0.313	3.83	0.009	0.55
1445774_at	Kcnma1	Potassium large conductance calcium-activated channel, subfamily M, alpha mer	1.01	0.968	1.08	0.753	-1.34	0.264	-1.86	0.265	-0.28
1435946_at	D5Ertd135e	DNA segment, Chr 5, ERATO Doi 135, expressed	-1.01	0.947	-1.29	0.377	1.07	0.749	1.55	0.366	0.08
1439164_at	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.01	0.965	1.05	0.793	-1.3	0.171	-1.23	0.638	-0.12
1448434_at	Rnf103	ring finger protein 103	-1.14	0.445	1.01	0.724	-1.05	0.538	1.06	0.9	-0.03
1432876_at	4632418H02Rik	RIKEN cDNA 4632418H02 gene	-1.31	0.085	1.08	0.702	-1.01	0.983	1.2	0.374	-0.01
1431899_at	Nkx6-3	NK6 transcription factor related, locus 3 (Drosophila)	1.39	0.715	-1.95	0.318	-1.06	0.863	1.12	0.757	-0.13
1445044_at	Ptgis	Prostaglandin I2 (prostacyclin) synthase	-1.16	0.564	-1.57	0.065	1.34	0.612	1.02	0.975	-0.09
1423349_at	Socs5	suppressor of cytokine signaling 5	1.01	0.711	1	0.977	-1.21	0.041	-1.09	0.498	-0.07
1428192_at	Kbtbd7	kelch repeat and BTB (POZ) domain containing 7	-1.13	0.364	-1.21	0.094	1.12	0.494	1.14	0.587	-0.02
1454857_at	Rnf122	ring finger protein 122	-1.32	0.342	1.06	0.752	1.02	0.956	-1.43	0.454	-0.17
1458992_at	Senp5	SUMO/sentrin specific peptidase 5	1.35	0.558	-1.78	0.417	-1.08	0.862	1.14	0.632	-0.09
1423698_at	D15Ertd785e	DNA segment, Chr 15, ERATO Doi 785, expressed	-1	0.982	-1.25	0.143	1.04	0.657	1.54	0.188	0.08
1437061_at	Mbd1	methyl-CpG binding domain protein 1	1.07	0.69	-1.01	0.981	-1.29	0.135	1.04	0.837	-0.05
1427923_at	Zmpste24	zinc metallopeptidase, STE24 homolog (S. cerevisiae)	1.11	0.082	1.08	0.059	-1.54	0.029	-1.02	0.889	-0.09
1427505_a_at	Cradd	CASP2 and RIPK1 domain containing adaptor with death domain	1.04	0.7	1.03	0.852	-1.29	0.1	-1.31	0.232	-0.13
1460646_at	Csnk2a2	casein kinase 2, alpha prime polypeptide	-1.11	0.636	-1.41	0.029	1.23	0.396	1.24	0.16	-0.01
1416341_at	Polr2c	polymerase (RNA) II (DNA directed) polypeptide C	-1.19	0.014	-1.14	0.118	1.12	0.385	1.18	0.462	-0.01
1453195_at	Sdccag3	serologically defined colon cancer antigen 3	1.02	0.864	1.01	0.936	-1.24	0.044	-1.25	0.017	-0.12
1437260_at	Mmrn1	multimerin 1	-1.11	0.096	-1.15	0.715	1.07	0.805	1.66	0.573	0.12
1422294_at	Xcr1	chemokine (C motif) receptor 1	1.69	0.048	-2.31	0.092	-1.39	0.562	1.01	0.977	-0.25
1421059_a_at	Alg2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferas	-1.07	0.618	-1.23	0.112	1.09	0.267	1.1	0.498	-0.03
1429127_at	Nradd	neurotrophin receptor associated death domain	-1.53	0.221	1.14	0.776	1.05	0.826	-1.73	0.009	-0.27
1433136_at	4930432H08Rik	RIKEN cDNA 4930432H08 gene	1.39	0.359	-1.46	0.554	-1.31	0.615	1.09	0.878	-0.07
1427433_s_at	Hoxa3	homeo box A3	-1.16	0.234	1.11	0.818	-1.16	0.597	1.62	0.03	0.1
1428462_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	-1.07	0.801	1.04	0.879	-1.15	0.296	1.2	0.079	0
1424882_a_at	Nt5dc2	5'-nucleotidase domain containing 2	-1.03	0.445	1.05	0.393	-1.21	0.547	3.53	0.178	0.58
1420710_at	Rel	reticuloendotheliosis oncogene	1.22	0.677	-1.77	0.019	1.06	0.872	-2.33	0.135	-0.46
1423387_at	Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	1.12	0.792	-1.13	0.714	-1.2	0.391	1.51	0.146	0.08
1428706_at	Prr6	proline-rich polypeptide 6	-1.01	0.917	-1.19	0.34	1.01	0.912	2.23	0.109	0.26
1427114_at	Ttc19	tetratricopeptide repeat domain 19	-1.1	0.702	-1.27	0.292	1.14	0.204	1.16	0.321	-0.02
1455173_at	Gspt1	G1 to S phase transition 1	-1.17	0.035	-1.09	0.649	1.07	0.772	1.24	0.555	0.01
1415831_at	Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	-1.07	0.269	-1.11	0.074	1.01	0.927	1.02	0.758	-0.04
1433203_at	6030400A10Rik	RIKEN cDNA 6030400A10 gene	1.12	0.092	-1.18	0.206	-1.15	0.187	1.41	0.321	0.05
1420986_s_at	---	---	-1.13	0.535	-1.17	0.293	1.1	0.498	1.07	0.147	-0.03

1430159_at	5830408C22Rik	RIKEN cDNA 5830408C22 gene	1.13	0.885	-1.64	0.205	1.1	0.615	-2.34	0.099	-0.44
1452722_a_at	Cul5	cullin 5	1.31	0.185	-1.32	0.232	-1.3	0.311	1.24	0.541	-0.02
1452131_at	---	---	1.24	0.277	-2.43	0.302	1.19	0.645	-1.11	0.853	-0.28
1415720_s_at	Mad2l1bp	MAD2L1 binding protein	-1.15	0.455	-1.15	0.118	1.1	0.537	1.52	0.353	0.08
1443404_s_at	D13Ertd94e	DNA segment, Chr 13, ERATO Doi 94, expressed	-2.71	0.231	1.74	0.066	-1.37	0.275	2.17	0.054	-0.04
1419911_at	Coro1c	Coronin, actin binding protein 1C	-1.5	0.223	-1.02	0.922	1.19	0.457	1.13	0.749	-0.05
1452059_at	Slc35f5	solute carrier family 35, member F5	-1.08	0.303	1.11	0.465	-1.24	0.098	1.14	0.51	-0.02
1436974_at	A230069A22Rik	RIKEN cDNA A230069A22 gene	-1.24	0.626	-1.23	0.44	1.22	0.56	1.37	0.52	0.03
1453235_at	1700012F11Rik	RIKEN cDNA 1700012F11 gene	-1.97	0.129	1.57	0.411	-1.32	0.403	1.26	0.717	-0.11
1446602_at	Frmd3	FERM domain containing 3	-1.29	0.729	1.4	0.483	-1.52	0.214	2.11	0.27	0.18
1455456_a_at	Timm50	translocase of inner mitochondrial membrane 50 homolog (yeast)	1.04	0.852	-1.04	0.68	-1.19	0.314	1.27	0.083	0.02
1431883_at	Tac1	tachykinin 1	-1.14	0.758	1.31	0.497	-1.54	0.293	1.22	0.697	-0.04
1432832_at	4933435G04Rik	RIKEN cDNA 4933435G04 gene	-1.08	0.559	-1.23	0.702	1.1	0.767	1.52	0.083	0.08
1443341_at	Anxa4	Annexin A4	1.12	0.65	1.21	0.375	-1.93	0.036	-1.7	0.047	-0.33
1437202_at	Mysm1	myb-like, SWIRM and MPN domains 1	1.02	0.853	1.04	0.268	-1.28	0.163	-1.44	0.064	-0.17
1458915_at	C77949	expressed sequence C77949	1.15	0.802	1.25	0.308	-2.25	0.109	-2.04	0.019	-0.47
1449813_at	Zfp30	zinc finger protein 30	1.34	0.725	1.08	0.77	-2.39	0.047	-1.35	0.58	-0.33
1430004_s_at	Wdr20	WD repeat domain 20	-1.32	0.575	1.21	0.227	-1.14	0.748	1.53	0.221	0.07
1428916_s_at	Sirt5	sirtuin 5 (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	-1.04	0.853	-1.32	0.045	1.12	0.351	1.09	0.751	-0.04
1442058_s_at	Psmc3ip	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	-1.15	0.56	-1.14	0.691	1.1	0.617	2.26	0.199	0.27
1442635_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.44	0.144	1.23	0.683	-1.08	0.875	2.92	0.006	0.41
1416156_at	Vcl	vinculin	1.06	0.346	-1.06	0.235	-1.18	0.386	1.52	0.342	0.08
1435870_at	Sycp3	Synaptonemal complex protein 3	1.01	0.903	1.05	0.584	-1.28	0.209	-1.22	0.375	-0.11
1452291_at	Centd1	centaurin, delta 1	1.08	0.706	1.06	0.504	-1.42	0.01	-1.49	0.428	-0.19
1438922_x_at	Slc25a5 /// LOC433	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.48	0.103	-1.14	0.548	1.29	0.036	1.08	0.665	-0.06
1417487_at	Fosl1	fos-like antigen 1	-2.36	0.35	1	0.997	1.42	0.379	-1.33	0.609	-0.32
1429092_at	Vkorc1l1	vitamin K epoxide reductase complex, subunit 1-like 1	-1.1	0.337	1.07	0.187	-1.16	0.372	1.92	0.262	0.18
1417368_s_at	Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	1.01	0.902	1.09	0.228	-1.36	0.03	-1.1	0.743	-0.09
1437610_x_at	Rps8	ribosomal protein S8	1.06	0.153	1.07	0.258	-1.4	0.004	-1.41	0.007	-0.17
1435847_at	Cdc42bpa	Cdc42 binding protein kinase alpha	-1.03	0.835	-1.16	0.284	1.01	0.887	1.76	0.115	0.14
1450968_at	Uqcrfs1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	-1.12	0.072	-1.14	0.032	1.07	0.2	1.13	0.604	-0.01
1431170_at	Efna3	ephrin A3	-1.15	0.567	-1.07	0.921	1.04	0.861	1.06	0.859	-0.03
1443873_at	---	---	1.06	0.894	-1.15	0.696	-1.1	0.78	1.02	0.956	-0.04
1419897_at	BB001228	expressed sequence BB001228	1.31	0.319	-1.96	0.09	1.02	0.973	-2.09	0.17	-0.43
1430976_a_at	Mrpl9	mitochondrial ribosomal protein L9	1.06	0.808	-1.35	0.227	1.04	0.818	-1.21	0.629	-0.11
1433084_at	4930402C16Rik	RIKEN cDNA 4930402C16 gene	1.18	0.189	-1.19	0.053	-1.22	0.648	1.11	0.547	-0.03
1458106_at	---	---	-1.14	0.905	-1.07	0.878	1.03	0.929	1.15	0.526	-0.01
1452129_at	Pthr2	parathyroid hormone receptor 2	-1.47	0.276	-1.27	0.811	1.38	0.381	1.2	0.7	-0.04
1423723_s_at	Tardbp	TAR DNA binding protein	-1.18	0.167	1.04	0.788	-1.05	0.637	1	0.992	-0.05
1416052_at	Prps1	phosphoribosyl pyrophosphate synthetase 1	-1.06	0.663	1.04	0.481	-1.16	0.069	1.54	0.196	0.09
1430227_at	1700007I08Rik	RIKEN cDNA 1700007I08 gene	1.37	0.047	-1.33	0.44	-1.39	0.454	1.15	0.81	-0.05
1425682_a_at	Tprkb	Tp53rk binding protein	-1.08	0.753	-1.14	0.349	1.04	0.638	1.18	0.242	0
1444340_at	C230066G23Rik	RIKEN cDNA C230066G23 gene	1.23	0.364	-1.27	0.113	-1.21	0.488	1.13	0.448	-0.03
1460452_at	Mospd3	motile sperm domain containing 3	-1.16	0.401	-1.08	0.656	1.06	0.555	1.56	0.055	0.09
1439811_at	Mtr	5-methyltetrahydrofolate-homocysteine methyltransferase	-1.24	0.149	1.05	0.838	-1.02	0.814	1.29	0.405	0.02
1426508_at	Gfap	glial fibrillary acidic protein	-1.47	0.727	1.18	0.412	-1.02	0.968	5.37	0.141	1.02
1432062_at	Mdga1	MAM domain containing glycosylphosphatidylinositol anchor 1	-1.72	0.56	-1.19	0.801	1.42	0.276	1.21	0.652	-0.07
1438191_a_at	Rnf40	ring finger protein 40	-1.2	0.529	-1.1	0.265	1.1	0.298	1.14	0.173	-0.02
1447602_x_at	Sulf2	sulfatase 2	1.09	0.588	-2.03	0.06	1.26	0.066	-1.16	0.671	-0.21
1452018_at	Nkx2-6	NK2 transcription factor related, locus 6 (Drosophila)	-1.1	0.808	-1.42	0.423	1.23	0.593	2	0.211	0.18
1452996_a_at	Aven	apoptosis, caspase activation inhibitor	1.1	0.596	-1.27	0.008	-1.05	0.703	1.13	0.379	-0.02
1443268_at	---	Transcribed locus	-3.35	0.032	1.91	0.203	-1.58	0.267	1.75	0.448	-0.32
1434367_s_at	Nutf2	nuclear transport factor 2	-1.03	0.587	1.03	0.746	-1.19	0.053	1.2	0.209	0

1426173_at	Cyp51	Cytochrome P450, family 51	1.31	0.727	-1.03	0.958	-1.78	0.245	1.53	0.534	0.01
1439680_at	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	-1.23	0.284	1.11	0.732	-1.09	0.68	1.22	0.408	0
1434391_at	Hnrpu	Heterogeneous nuclear ribonucleoprotein U	-1.12	0.023	-1.06	0.5	1	0.99	1.07	0.771	-0.03
1421082_s_at	Banf1	barrier to autointegration factor 1	-1.13	0.399	-1.11	0.172	1.06	0.72	1.05	0.786	-0.03
1448615_at	Ccs	copper chaperone for superoxide dismutase	-1.07	0.471	-1.3	0.004	1.14	0.274	1.19	0.417	-0.01
1445028_at	Prkca	Protein kinase C, alpha	-1.02	0.966	1.1	0.444	-1.31	0.269	2.43	0.085	0.3
1419708_at	Wnt6	wingless-related MMTV integration site 6	-1.11	0.865	-1.08	0.642	1.01	0.973	1.03	0.872	-0.04
1434440_at	Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	1.03	0.758	-1.08	0.757	-1.13	0.612	1.51	0.031	0.08
1456961_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	1.07	0.839	1.02	0.96	-1.33	0.207	-1.43	0.526	-0.17
1426419_at	Rbm26	RNA binding motif protein 26	-1.25	0.204	1.03	0.741	1.02	0.928	-1.58	0.055	-0.2
1448706_at	Ttrap	Traf and Tnf receptor associated protein	-1.11	0.07	1.08	0.675	-1.16	0.355	1.04	0.867	-0.04
1435526_at	Tor1aip2	torsin A interacting protein 2	-1.16	0.412	1.13	0.167	-1.18	0.334	1.47	0.254	0.07
1448685_at	2900010M23Rik	RIKEN cDNA 2900010M23 gene	1.11	0.059	-1.08	0.38	-1.24	0.163	1.06	0.73	-0.04
1441102_at	Prlr	prolactin receptor	-1.39	0.007	-1.1	0.739	1.21	0.627	2.18	0.019	0.23
1434603_at	Thrap2	thyroid hormone receptor associated protein 2	-1.05	0.756	-1.14	0.246	1.01	0.936	1.52	0.264	0.09
1446974_at	Pip5k3	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	1.1	0.418	1.02	0.958	-1.37	0.123	-1.17	0.63	-0.11
1438655_a_at	1100001I22Rik	RIKEN cDNA 1100001I22 gene	1	0.959	1.1	0.456	-1.33	0.019	-1.44	0.017	-0.17
1429638_at	Wrnip1	Werner helicase interacting protein 1	1.55	0.537	-3.11	0.002	-1.03	0.948	3.52	0.022	0.23
1449198_a_at	St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1.11	0.745	-1.26	0.487	-1.06	0.437	4.03	0.149	0.71
1454815_at	Sertad2	SERTA domain containing 2	-1.1	0.226	1.05	0.528	-1.13	0.537	2.34	0.178	0.29
1424640_at	Arl8a	ADP-ribosylation factor-like 8A	-1.15	0.417	-1.03	0.887	1	0.994	1.08	0.804	-0.02
1460615_at	Nt5dc1	5'-nucleotidase domain containing 1	-1.18	0.413	-1.07	0.45	1.07	0.617	1.01	0.931	-0.04
1422292_at	A030005K14Rik	RIKEN cDNA A030005K14 gene	1.01	0.971	-2.49	0.089	1.43	0.422	-1.39	0.615	-0.36
1427032_at	Herc4	hect domain and RLD 4	-1.34	0.112	1.01	0.84	1.09	0.372	-1.4	0.203	-0.16
1429676_at	---	Adult male stomach cDNA, RIKEN full-length enriched library, clone:2210408O09	-1.34	0.566	-2.26	0.05	1.66	0.057	1.94	0.195	0
1423218_a_at	Mrpl49	mitochondrial ribosomal protein L49	-1.1	0.625	1.01	0.913	-1.09	0.514	1.11	0.655	-0.02
1438146_x_at	Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	1.2	0.629	-1.36	0.469	-1.1	0.743	1.06	0.537	-0.05
1440446_at	LOC634379 /// LOC	similar to naked cuticle 1 homolog /// similar to naked cuticle 1 homolog	-1.6	0.1	1.36	0.566	-1.16	0.39	1.39	0.655	0
1449433_at	P2rx5	purinergic receptor P2X, ligand-gated ion channel, 5	1.12	0.537	-1.41	0.429	1.02	0.93	-2.26	0.103	-0.38
1441800_at	---	---	-1.03	0.977	1.05	0.829	-1.22	0.63	1.19	0.709	0
1446996_at	---	---	-1.56	0.665	-1.21	0.803	1.38	0.443	1.55	0.235	0.04
1453130_at	Ep400	E1A binding protein p400	1.03	0.874	-1.14	0.773	-1.07	0.34	1.01	0.973	-0.04
1417386_at	Npepps	aminopeptidase puromycin sensitive	1.05	0.547	-1.2	0.292	-1.04	0.836	1.42	0.314	0.06
1442425_at	A030014E15Rik	RIKEN cDNA A030014E15 gene	1.37	0.293	-1.99	0.01	-1.02	0.963	1.18	0.773	-0.12
1421083_x_at	Banf1	barrier to autointegration factor 1	-1.03	0.592	-1.15	0.131	1.01	0.946	1.16	0.467	0
1432142_at	Slc35f4	solute carrier family 35, member F4	-1.57	0.517	-1.42	0.467	1.51	0.102	1.21	0.68	-0.07
1444602_at	---	Transcribed locus, weakly similar to XP_343428.2 PREDICTED: neural precursor	-1.02	0.869	1.01	0.965	-1.17	0.229	2.32	0.044	0.28
1427025_at	Mtmr7	myotubularin related protein 7	-1.03	0.653	1.03	0.938	-1.18	0.085	1.15	0.689	-0.01
1456277_at	7530414M10Rik	RIKEN cDNA 7530414M10 gene	-1.14	0.523	1.04	0.64	-1.08	0.726	1.37	0.417	0.05
1424698_s_at	Gca	grancalcin	-1.11	0.701	-1.11	0.822	1.04	0.801	1.12	0.616	-0.01
1460560_at	Bahcc1	BAH domain and coiled-coil containing 1	-1.15	0.48	-1.1	0.682	1.07	0.732	1.12	0.645	-0.01
1430801_at	2310042E16Rik ///	RIKEN cDNA 2310042E16 gene /// vacuolar protein sorting 13B (yeast) /// similar	1.25	0.406	-1.54	0.447	-1.06	0.718	1.04	0.853	-0.07
1445425_at	LOC432958	hypothetical gene supported by AK040104	1.33	0.443	-1.82	0.002	-1.03	0.874	1.39	0.031	-0.03
1439634_at	4930505D03Rik	RIKEN cDNA 4930505D03 gene	1.04	0.938	1.12	0.478	-1.45	0.078	-2.02	0.223	-0.33
1432417_a_at	Tspan2	tetraspanin 2	1.18	0.8	-1.96	0.157	1.16	0.772	-1.11	0.737	-0.18
1418586_at	Adcy9	adenylate cyclase 9	-1.01	0.944	-1.2	0.242	1.02	0.903	1.42	0.072	0.06
1440168_x_at	Kctd7	potassium channel tetramerisation domain containing 7	-1.62	0.056	-1.07	0.71	1.29	0.086	2.05	0.209	0.17
1436726_s_at	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	-1.21	0.315	1	0.985	1.02	0.872	-1.24	0.285	-0.11
1449038_at	Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	1.32	0.343	-1.33	0.144	-1.29	0.115	1.09	0.374	-0.05
1445457_at	---	Adult male cecum cDNA, RIKEN full-length enriched library, clone:9130219A07 p	1.16	0.605	-2.45	0.016	1.28	0.444	-1.54	0.359	-0.39
1418009_at	1810007M14Rik	RIKEN cDNA 1810007M14 gene	-1.53	0.672	1.44	0.342	-1.33	0.58	1.16	0.827	-0.06
1433304_at	4930483C01Rik	RIKEN cDNA 4930483C01 gene	1.46	0.642	-1.06	0.754	-2.26	0.249	2.41	0.012	0.14
1439202_at	---	---	1.98	0.512	-2.07	0.305	-2.58	0.029	1.07	0.878	-0.4

1433081_at	4933407I18Rik	RIKEN cDNA 4933407I18 gene	-1.26	0.248	-1.13	0.142	1.17	0.706	1.28	0.516	0.02
1428823_at	Hddc2	HD domain containing 2	1.09	0.123	1.01	0.986	-1.34	0.122	-1.3	0.169	-0.14
1416843_at	Pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta	-1.02	0.861	1.04	0.726	-1.22	0.138	1.05	0.731	-0.03
1459403_at	Ldlr	low density lipoprotein receptor	1.1	0.486	1.1	0.628	-1.53	0.106	-1.11	0.612	-0.11
1449897_a_at	Mtcp1	mature T-cell proliferation 1	1.1	0.526	-1	0.999	-1.33	0.111	1.56	0.054	0.08
1458112_at	Adarb2	adenosine deaminase, RNA-specific, B2	-1.96	0.336	1.43	0.323	-1.1	0.568	1.53	0.2	-0.02
1458105_at	---	---	1.14	0.659	-1.58	0.514	1.08	0.375	-1.01	0.987	-0.09
1444199_at	---	---	1.16	0.477	-1.98	0.205	1.18	0.703	-1.56	0.518	-0.3
1446864_at	S100pbp	S100P binding protein	-1.09	0.899	1.12	0.878	-1.23	0.696	1.49	0.221	0.07
1424401_at	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	-1.15	0.454	1.22	0.243	-1.31	0.241	2.45	0.013	0.3
1426276_at	Ifih1	interferon induced with helicase C domain 1	1.12	0.462	-1.15	0.266	-1.16	0.197	1.07	0.351	-0.03
1417921_at	2610029G23Rik	RIKEN cDNA 2610029G23 gene	-1.16	0.414	1.04	0.83	-1.06	0.583	1.25	0.205	0.02
1457372_at	---	---	-1.05	0.947	-1.7	0.322	1.31	0.389	1.3	0.377	-0.03
1429213_at	2310030N02Rik	RIKEN cDNA 2310030N02 gene	-1.03	0.841	-1.37	0.071	1.15	0.386	1	0.993	-0.06
1427579_at	Rhbdl3	rhomboid, veinlet-like 3 (Drosophila)	1.54	0.11	-2.06	0.242	-1.22	0.603	2.19	0.091	0.11
1448300_at	Mgst3	microsomal glutathione S-transferase 3	1.02	0.951	-1.12	0.763	-1.07	0.765	6.07	0.173	1.23
1456245_x_at	Vamp3	vesicle-associated membrane protein 3	-1.1	0.493	1.13	0.232	-1.24	0.056	1.26	0.385	0.01
1432987_at	---	---	-1.2	0.55	1.18	0.635	-1.2	0.297	1.54	0.24	0.08
1434602_at	Thrap2	thyroid hormone receptor associated protein 2	1.19	0.156	-1.15	0.635	-1.26	0.34	1.61	0.24	0.09
1454285_at	2900042E19Rik	RIKEN cDNA 2900042E19 gene	-1.42	0.678	1.03	0.967	1.11	0.706	-1.31	0.389	-0.15
1451899_a_at	Gtf2ird1	general transcription factor II I repeat domain-containing 1	-1.11	0.142	-1.18	0.343	1.1	0.34	1.05	0.538	-0.03
1442868_at	C130026L21Rik	RIKEN cDNA C130026L21 gene	1.26	0.476	-1.75	0.003	1.02	0.926	-1.48	0.258	-0.24
1434221_at	BC030863	cDNA sequence BC030863	-1.12	0.395	-1.12	0.648	1.07	0.818	1.9	0.06	0.18
1449295_at	Sap30bp	SAP30 binding protein	-1.35	0.329	1.02	0.922	1.09	0.793	-1.12	0.303	-0.09
1436281_at	LOC245305	Similar to hypothetical protein FLJ38281	1.16	0.699	-1.53	0.012	1.03	0.805	-1.61	0.125	-0.24
1423897_at	Rnf187	ring finger protein 187	-1.15	0.609	1.06	0.274	-1.09	0.575	1.29	0.006	0.03
1458756_at	Grid2	Glutamate receptor, ionotropic, delta 2	-1.57	0.375	-1.08	0.887	1.29	0.531	1.24	0.655	-0.03
1442890_at	Socs5	Suppressor of cytokine signaling 5	1.02	0.834	1.14	0.782	-1.46	0.284	-1.24	0.554	-0.13
1452758_s_at	Eif4g2	eukaryotic translation initiation factor 4, gamma 2	1.06	0.509	1.01	0.861	-1.28	0.002	-1.11	0.072	-0.08
1418947_at	Nek3	NIMA (never in mitosis gene a)-related expressed kinase 3	-1.15	0.369	-1.03	0.866	1.01	0.932	1.07	0.752	-0.02
AFFX-LysX-3_at	---	---	1.04	0.937	-1.24	0.106	1	0.995	-1.4	0.43	-0.15
1460671_at	Gpx1	glutathione peroxidase 1	-1.09	0.123	-1.15	0.396	1.06	0.65	1.12	0.528	-0.01
1428488_at	Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	-1.09	0.761	1.04	0.559	-1.11	0.176	1.18	0.445	0
1450451_at	Spock2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	-1.99	0.089	-1.15	0.668	1.48	0.2	2.41	0.07	0.19
1423968_at	Ugt3a2	UDP glycosyltransferases 3 family, polypeptide A2	-1.03	0.745	1.02	0.757	-1.16	0.835	2.52	0.027	0.34
1444435_at	Vps13b /// LOC666	vacuolar protein sorting 13B (yeast) /// similar to vacuolar protein sorting 13B isof	-1.81	0.536	1.45	0.372	-1.18	0.681	1.39	0.646	-0.04
1433210_at	Rptn	repetin	-1.13	0.784	1.01	0.99	-1.04	0.857	1.08	0.761	-0.02
1430871_at	Plcb4	phospholipase C, beta 4	1.25	0.703	-1.2	0.73	-1.3	0.551	1.99	0.281	0.18
1419367_at	Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	1.15	0.017	-1.38	0.069	-1.02	0.792	1.01	0.894	-0.06
1416696_at	D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expressed	-1.03	0.765	1.06	0.615	-1.22	0.193	1.04	0.852	-0.04
1415766_at	Sec22b	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	1.02	0.729	1.09	0.331	-1.34	0.023	-1.05	0.643	-0.07
1421389_a_at	Eif2ak4	eukaryotic translation initiation factor 2 alpha kinase 4	1.02	0.936	-1.25	0.2	1.03	0.895	-2.12	0.069	-0.33
1442185_at	---	---	1.05	0.823	-1.29	0.183	1.03	0.888	-1.23	0.118	-0.11
1449552_at	Zfr	zinc finger RNA binding protein	-1.02	0.932	-1.2	0.457	1.04	0.875	1.16	0.396	-0.01
1428858_at	Wdr70	WD repeat domain 70	-1.31	0.065	1.11	0.266	-1.03	0.87	1.25	0.39	0.01
1456727_a_at	Csnk1d	casein kinase 1, delta	1.04	0.888	-1.13	0.469	-1.08	0.736	1.21	0.411	0.01
1441698_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	-1.04	0.889	1.02	0.917	-1.15	0.7	1.05	0.744	-0.03
1426050_at	Bcl2l1	Bcl2-like 1	-1.22	0.587	1.19	0.733	-1.18	0.659	2.09	0.142	0.22
1449173_at	Mpp2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	1.2	0.501	-1.02	0.969	-1.49	0.275	3.35	0.125	0.51
1436375_at	Srbd1	S1 RNA binding domain 1	-1.3	0.522	-1.27	0.361	1.29	0.192	1.24	0.326	-0.01
1448198_a_at	Ndufb8	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	-1.04	0.715	-1.13	0.363	1.01	0.932	1.16	0.264	0
1449595_at	C79490	expressed sequence C79490	-1.46	0.106	1.38	0.673	-1.27	0.348	1.09	0.606	-0.07
1418084_at	Nrp1	neuropilin 1	1.09	0.32	-1.06	0.268	-1.22	0.377	1.07	0.863	-0.03

1435882_at	Ubap2l	ubiquitin associated protein 2-like	-1.11	0.597	1.06	0.667	-1.12	0.135	1.09	0.669	-0.02
1418524_at	Pcm1	pericentriolar material 1	1.01	0.908	1.15	0.589	-1.45	0.06	-1.18	0.059	-0.12
1447655_x_at	Sox6	SRY-box containing gene 6	-1.33	0.001	-1.16	0.333	1.24	0.111	8.47	0.187	1.8
1458737_at	C77097	expressed sequence C77097	-1.06	0.511	1.27	0.512	-1.57	0.003	5.43	0.251	1.02
1424300_at	Gemin6	gem (nuclear organelle) associated protein 6	-1.09	0.325	-1.13	0.042	1.05	0.489	1.12	0.717	-0.01
1432477_at	4930412D23Rik	RIKEN cDNA 4930412D23 gene	-1.17	0.187	1.12	0.642	-1.14	0.66	1.23	0.454	0.01
1456263_at	Notch4	Notch gene homolog 4 (Drosophila)	-1.52	0.28	1.18	0.616	1.01	0.936	-1.38	0.414	-0.17
1459557_at	Zbtb16	Zinc finger and BTB domain containing 16	1.35	0.602	1.08	0.878	-2.35	0.107	-1.4	0.505	-0.33
1427924_at	Stx17	syntaxin 17	1.22	0.562	-1.42	0.031	-1.07	0.646	1.03	0.88	-0.06
1452705_at	2210010A19Rik	RIKEN cDNA 2210010A19 gene	-1.05	0.495	1.13	0.065	-1.3	0.012	1.02	0.905	-0.05
1438554_x_at	Wbscr1	Williams-Beuren syndrome chromosome region 1 homolog (human)	-1.14	0.232	-1.08	0.315	1.05	0.264	1.02	0.519	-0.04
1455133_s_at	AI848100	expressed sequence AI848100	-1.04	0.68	1.1	0.5	-1.26	0.266	1.22	0.26	0.01
1452780_at	Gtf3c2	general transcription factor IIIC, polypeptide 2, beta	-1.17	0.526	-1.15	0.121	1.13	0.353	1.18	0.337	0
1422031_a_at	Zfand6	zinc finger, AN1-type domain 6	-1.22	0.154	-1.41	0.027	1.33	0.129	1.84	0.223	0.13
1435679_at	Optn	optineurin	1.05	0.549	-1.16	0.417	-1.06	0.694	2.63	0.195	0.37
1424796_at	1700054N08Rik	RIKEN cDNA 1700054N08 gene	-1.41	0.252	-1.04	0.823	1.18	0.597	3.21	0.288	0.49
1430439_at	Mctp1	multiple C2 domains, transmembrane 1	-2.23	0.157	-1.06	0.789	1.46	0.374	1.16	0.498	-0.17
1451331_at	Ppp1r1b	protein phosphatase 1, regulatory (inhibitor) subunit 1B	1.31	0.462	-1.55	0.25	-1.11	0.539	1.03	0.938	-0.08
1415695_at	Psma1	proteasome (prosome, macropain) subunit, alpha type 1	-1.16	0.051	1.01	0.917	-1.02	0.824	1.06	0.687	-0.03
1422418_s_at	Supt4h1 /// Supt4h2	suppressor of Ty 4 homolog 1 (S. cerevisiae) /// suppressor of Ty 4 homolog 2 (S	-1.03	0.793	-1.25	0.015	1.09	0.633	1.01	0.959	-0.05
1423662_at	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	-1.07	0.557	1.01	0.777	-1.09	0.127	1.1	0.442	-0.02
1429661_at	Rhobtb3	Rho-related BTB domain containing 3	1.38	0.05	-1.24	0.457	-1.5	0.27	1.14	0.664	-0.05
1449777_at	Dus4l	Dihydrouridine synthase 4-like (S. cerevisiae)	1.21	0.771	-1.62	0.281	1.02	0.958	-1.29	0.704	-0.17
1451172_at	1200015A19Rik	RIKEN cDNA 1200015A19 gene	1.1	0.172	-1.06	0.401	-1.24	0.005	1.09	0.255	-0.03
1423120_at	Ide	insulin degrading enzyme	-1.07	0.347	-1.11	0.272	1.02	0.79	1.41	0.024	0.06
1436535_at	Trove2	TROVE domain family, member 2	1.21	0.576	-1.28	0.386	-1.16	0.609	1.26	0.416	0.01
1456042_s_at	Cramp1l	Crm, cramped-like (Drosophila)	-1.12	0.324	-1.07	0.564	1.02	0.934	1.45	0.083	0.07
1458324_x_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130051K	1.24	0.532	1.14	0.768	-2.1	0.138	-1.62	0.102	-0.33
1435249_at	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homol	1.02	0.916	-1.06	0.671	-1.12	0.371	1.57	0.218	0.1
1449836_x_at	Bik	Bcl2-interacting killer	-1.11	0.648	1.03	0.867	-1.08	0.647	3.28	0.04	0.53
1452896_at	Gtl3	gene trap locus 3	-1.07	0.452	-1.23	0.098	1.11	0.241	1.08	0.677	-0.03
1456948_at	Ap4e1	adaptor-related protein complex AP-4, epsilon 1	1.29	0.103	-1.12	0.258	-1.49	0.226	1	0.985	-0.08
1448151_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	-1.03	0.551	-1.19	0.051	1.05	0.691	1.11	0.271	-0.02
1447826_x_at	A930037G23Rik	RIKEN cDNA A930037G23 gene	-1.52	0.526	-1.3	0.084	1.43	0.448	1.33	0.481	-0.02
1419370_a_at	Mfap1	microfibrillar-associated protein 1	-1.14	0.377	-1.04	0.698	1.01	0.944	1.11	0.617	-0.01
1439646_at	---	Adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:533043	-1.7	0.448	1.6	0.338	-1.49	0.528	1.16	0.435	-0.11
1423234_at	Psmd5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	1.05	0.476	-1.04	0.419	-1.19	0.13	1.24	0.385	0.02
1425977_a_at	Slk	STE20-like kinase (yeast)	1	0.977	-1.1	0.621	-1.07	0.814	1.24	0.528	0.02
1458597_at	---	Transcribed locus	-1.38	0.419	-1.04	0.952	1.17	0.47	1.21	0.039	-0.01
1458253_at	---	Adult male bone cDNA, RIKEN full-length enriched library, clone:9830128M12 pr	-1.57	0.316	1.12	0.871	1.1	0.896	-3.49	0.161	-0.71
1439878_at	Ivl	involucrin	-1.76	0.485	1.48	0.355	-1.23	0.678	1.41	0.38	-0.03
1422058_at	---	---	-1.43	0.303	-1.16	0.561	1.29	0.294	1.18	0.538	-0.03
1455529_at	2700083E18Rik	RIKEN cDNA 2700083E18 gene	1.09	0.698	-1.49	0.473	1.09	0.789	-1.23	0.524	-0.13
1440070_at	Chat	choline acetyltransferase	1.3	0.449	-1.28	0.687	-1.3	0.439	1.41	0.27	0.04
1415821_at	Nptn	neuroplastin	-1.08	0.525	1.06	0.507	-1.15	0.147	1.19	0.107	0
1421930_at	Icos	inducible T-cell co-stimulator	-1.38	0.333	1.05	0.853	1.08	0.809	-1.23	0.639	-0.12
1448643_at	Ssna1	Sjogren's syndrome nuclear autoantigen 1	-1.01	0.689	1.02	0.798	-1.19	0.281	1.38	0.214	0.05
1429047_at	Rtf1	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	1.04	0.81	-1.23	0.333	1	0.974	-1.05	0.518	-0.06
1424738_at	4932432K03Rik	RIKEN cDNA 4932432K03 gene	-1.09	0.422	-1.15	0.027	1.07	0.771	1.24	0.171	0.02
1421720_a_at	Dtx2	deltex 2 homolog (Drosophila)	1.21	0.528	-2.07	0.305	1.17	0.244	-1.28	0.33	-0.24
1449047_at	Hacl1	2-hydroxyacyl-CoA lyase 1	-1.32	0.002	-1.21	0.319	1.27	0.39	1.28	0.274	0.01
1422520_at	Nef3	neurofilament 3, medium	1.54	0.36	-1.7	0.304	-1.38	0.648	3.13	0.018	0.4
1459917_at	AI451896	expressed sequence AI451896	1.3	0.326	-1.2	0.382	-1.38	0.25	1.29	0.519	0

1452800_a_at	0610008C08Rik ///	RIKEN cDNA 0610008C08 gene /// hypothetical LOC621156 /// hypothetical prote	-1.15	0.008	-1.2	0.092	1.16	0.306	1.99	0.171	0.2
1426068_at	Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	-1.2	0.327	-1.28	0.119	1.24	0.24	1.68	0.12	0.11
1439948_at	BC046401	cDNA sequence BC046401	-1.16	0.406	1.14	0.242	-1.17	0.472	1.09	0.709	-0.02
1425019_at	Ubxd4	UBX domain containing 4	1.18	0.572	-1.11	0.495	-1.28	0.106	1.76	0.13	0.14
1423636_at	Wdr31	WD repeat domain 31	-1.36	0.03	-1.16	0.743	1.25	0.513	1.13	0.246	-0.03
1416461_at	Gpiap1	GPI-anchored membrane protein 1	-1.08	0.065	-1.1	0.272	1.02	0.898	1.22	0.108	0.02
1437364_at	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)	1.01	0.969	-1.17	0.591	-1.01	0.947	1.05	0.876	-0.03
1426764_at	Oaz2	ornithine decarboxylase antizyme 2	-1.05	0.816	-1.19	0.288	1.06	0.84	1.01	0.967	-0.04
1458627_at	---	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030	-1.21	0.237	1.37	0.505	-1.52	0.153	1.87	0.223	0.13
1418460_at	Sh3d19	SH3 domain protein D19	-1.55	0.46	-1.16	0.618	1.35	0.527	1.06	0.788	-0.07
1425348_a_at	Srprb	signal recognition particle receptor, B subunit	1.03	0.897	-1.14	0.385	-1.05	0.731	1.16	0.187	0
1420406_at	Peg12	paternally expressed 12	1.16	0.574	-2.42	0.153	1.28	0.43	-1.02	0.947	-0.25
1456773_at	Nupl2	nucleoporin like 2	-1.37	0.142	-1.05	0.87	1.17	0.404	1.37	0.113	0.03
1437765_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	1.02	0.966	-1.05	0.669	-1.14	0.653	2.92	0.116	0.44
1440766_at	Gnl3	Guanine nucleotide binding protein-like 3 (nucleolar)	-1.03	0.864	1.21	0.465	-1.47	0.02	1.05	0.927	-0.06
1451816_at	Zfp451	zinc finger protein 451	1.13	0.881	1.06	0.894	-1.51	0.338	-1.49	0.053	-0.2
1417193_at	Sod2	superoxide dismutase 2, mitochondrial	-1.19	0.115	-1.13	0.061	1.13	0.198	1.17	0.334	-0.01
1431554_a_at	Anxa9	annexin A9	-1.4	0.44	-1.44	0.416	1.44	0.045	1.71	0.273	0.08
1423956_at	Smap1	stromal membrane-associated protein 1	-1.19	0.061	-1.11	0.088	1.12	0.334	2.13	0.175	0.24
1450335_at	---	---	-1.07	0.873	1.23	0.405	-1.43	0.032	1.01	0.988	-0.07
1416962_at	Rcc1	regulator of chromosome condensation 1	-1.14	0.209	-1.06	0.867	1.04	0.933	1.53	0.198	0.09
1445007_at	Lrrc50	Leucine rich repeat containing 50	-1.01	0.981	-1.24	0.097	1.06	0.905	1.12	0.743	-0.02
1444527_at	Runx1	Runt related transcription factor 1	1.38	0.575	-1.23	0.59	-1.49	0.415	1.15	0.636	-0.05
1454616_at	5730410I19Rik	RIKEN cDNA 5730410I19 gene	1.06	0.757	-1.14	0.367	-1.09	0.567	1.28	0.318	0.03
1450537_at	Mid2	midline 2	-1.07	0.81	1	0.997	-1.08	0.77	1.02	0.955	-0.03
1417373_a_at	Tuba4	tubulin, alpha 4	-1.16	0.143	-1.27	0.157	1.21	0.27	1.46	0.256	0.06
1460174_at	Dexi	dexamethasone-induced transcript	-1.36	0.011	1.08	0.326	1.05	0.673	-1.62	0.094	-0.21
1460696_at	BC026585	cDNA sequence BC026585	-1.09	0.622	-1.08	0.629	1.01	0.937	1.01	0.936	-0.04
1460293_at	Freq	frequenin homolog (Drosophila)	-1.44	0.497	1.12	0.585	1.04	0.814	-1.2	0.335	-0.12
1452268_at	2810485I05Rik	RIKEN cDNA 2810485I05 gene	-1.11	0.631	-1.22	0.353	1.14	0.334	1.25	0.46	0.01
1436823_x_at	Hbb-y	hemoglobin Y, beta-like embryonic chain	-1.07	0.87	1.28	0.62	-1.58	0.443	2.71	0.363	0.34
1433193_at	4930433M22Rik	RIKEN cDNA 4930433M22 gene	1.1	0.137	-1	0.995	-1.32	0.52	1.48	0.231	0.07
1431322_at	Igsf3	immunoglobulin superfamily, member 3	-1.02	0.895	1.31	0.38	-1.74	0.007	1.76	0.233	0.08
1423970_at	Thoc3	THO complex 3	-1.13	0.216	-1.31	0.02	1.21	0.039	1.19	0.397	-0.01
1429001_at	Pir	pirin	-1.11	0.739	-1.11	0.5	1.05	0.772	2.5	0.222	0.33
1433145_at	4933431C10Rik	RIKEN cDNA 4933431C10 gene	1.31	0.673	-1.29	0.713	-1.29	0.605	1.1	0.784	-0.04
1441904_x_at	9130005N14Rik	RIKEN cDNA 9130005N14 gene	-1.11	0.554	1.06	0.65	-1.12	0.652	1.41	0.196	0.06
1430773_a_at	Tcte2	t-complex-associated testis expressed 2	1.04	0.933	1.15	0.8	-1.51	0.565	-1.56	0.111	-0.22
1431769_at	2210406O10Rik	RIKEN cDNA 2210406O10 gene	-1.03	0.809	1.05	0.875	-1.2	0.492	1.01	0.98	-0.04
1456844_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	-1.74	0.497	1.01	0.984	1.27	0.641	-1.39	0.254	-0.21
1433214_x_at	2700008E08Rik	RIKEN cDNA 2700008E08 gene	1.13	0.355	-1.52	0.252	1.07	0.504	-1.5	0.377	-0.2
1433999_at	Slk	STE20-like kinase (yeast)	-1.22	0.018	1.1	0.192	-1.06	0.535	1.37	0.343	0.05
1425034_at	Slc17a2	solute carrier family 17 (sodium phosphate), member 2	1.3	0.383	-1.18	0.345	-1.4	0.51	1.48	0.497	0.05
1445240_at	AU019796	expressed sequence AU019796	-1.33	0.407	1.67	0.339	-2.29	0.089	1.28	0.629	-0.17
1423482_at	Uros	uroporphyrinogen III synthase	-1.16	0.21	-1.08	0.498	1.07	0.672	4.38	0.202	0.8
1418127_a_at	Pdcd8	programmed cell death 8	-1.12	0.373	-1.19	0.01	1.13	0.041	1.17	0.22	0
1435304_at	Sod1	superoxide dismutase 1, soluble	1.1	0.423	-1.03	0.819	-1.26	0.018	1.11	0.013	-0.02
1457858_at	LOC226957	similar to RNA and export factor binding protein 2	-1.31	0.12	-1.07	0.901	1.16	0.753	1.35	0.422	0.03
1441308_at	Mobp	myelin-associated oligodendrocytic basic protein	-1.11	0.138	-1.16	0.482	1.1	0.229	1	0.981	-0.04
1447152_at	Ulk2	Unc-51 like kinase 2 (C. elegans)	1.05	0.919	1.11	0.669	-1.43	0.528	-1.8	0.227	-0.27
1420513_at	Efcab2	EF-hand calcium binding domain 2	-1.43	0.078	1.13	0.599	1.03	0.916	-1.09	0.584	-0.09
1459285_at	---	---	1.11	0.603	1.15	0.169	-1.66	0.265	-1.64	0.418	-0.26
1434112_at	Lphn2	latrophilin 2	-1.03	0.859	1.01	0.949	-1.14	0.536	1.57	0.01	0.1

1425439_a_at	Slc41a3	solute carrier family 41, member 3	-1.15	0.127	1.1	0.644	-1.13	0.553	1.72	0.213	0.14
1438163_x_at	Rhbdd2	Rhomboid domain containing 2	1	0.994	-1.19	0.759	1.02	0.972	-4.49	0.209	-0.92
1416323_at	Kctd20	potassium channel tetramerisation domain containing 20	-1.19	0.408	1.05	0.72	-1.04	0.777	1.26	0.324	0.02
1452704_at	1200015F23Rik	RIKEN cDNA 1200015F23 gene	-1.17	0.26	-1.11	0.043	1.11	0.162	1.38	0.253	0.05
1437448_s_at	Ctnnd1	catenin (cadherin associated protein), delta 1	1.01	0.971	-1.02	0.825	-1.14	0.648	1.01	0.97	-0.04
1455174_at	Rps19bp1	ribosomal protein S19 binding protein 1	-1.03	0.854	-1.16	0.136	1.02	0.919	1.03	0.862	-0.03
1416873_a_at	Cdk2	cyclin-dependent kinase 2	-1.2	0.182	-1.07	0.526	1.09	0.496	1.4	0.317	0.06
1450986_at	Nol5	nucleolar protein 5	-1.05	0.717	-1.19	0.41	1.07	0.707	1.11	0.748	-0.02
1453019_at	Nvl	nuclear VCP-like	-1.3	0.135	-1.01	0.934	1.1	0.022	1.11	0.317	-0.02
1456642_x_at	S100a10	S100 calcium binding protein A10 (calpactin)	1.18	0.145	1.03	0.736	-1.53	0.005	-1.45	0.372	-0.19
1459454_at	Sap30bp	SAP30 binding protein	-1.19	0.778	1.24	0.659	-1.29	0.044	1.44	0.027	0.05
1428269_a_at	Glt8d1	glycosyltransferase 8 domain containing 1	1.02	0.85	1.06	0.708	-1.28	0.088	-1.09	0.365	-0.07
1423850_at	Nsun2	NOL1/NOP2/Sun domain family 2	-1.26	0.024	-1.04	0.336	1.1	0.369	1.14	0.559	-0.01
1437893_at	Plb1 /// BC033606 /	phospholipase B1 /// cDNA sequence BC033606 /// similar to phospholipase B	1.16	0.502	1	0.995	-1.43	0.046	-1.89	0.444	-0.29
1426190_at	Aym1	activator of yeast meiotic promoters 1	1.05	0.913	-1.24	0.573	1	0.993	-1.84	0.101	-0.26
1435789_x_at	---	Transcribed locus	-1.07	0.701	-1.39	0.222	1.21	0.666	1.35	0.184	0.02
1431392_at	Hoxa3 /// 5730596E	homeo box A3 /// RIKEN cDNA 5730596B20 gene	-1.21	0.552	1.29	0.436	-1.34	0.553	1.2	0.508	-0.02
1416429_a_at	Cat	catalase	-1.12	0.359	-1.06	0.392	1.02	0.809	1.16	0.485	0
1428220_at	5730419I09Rik	RIKEN cDNA 5730419I09 gene	-1.1	0.622	-1.09	0.707	1.03	0.878	1.36	0.213	0.05
1443524_x_at	Bcl10	B-cell leukemia/lymphoma 10	-1.31	0	-1.01	0.94	1.11	0.628	1.13	0.672	-0.02
1454136_a_at	4921524J17Rik	RIKEN cDNA 4921524J17 gene	1.05	0.492	1	0.964	-1.24	0	-1.03	0.425	-0.05
1426946_at	Ranbp5	RAN binding protein 5	-1.04	0.799	-1.13	0.347	1.02	0.897	1.44	0.104	0.07
1448450_at	Ak2	adenylate kinase 2	-1.21	0.178	-1.19	0.454	1.19	0.248	1.02	0.906	-0.05
1457721_at	AI118064	Expressed sequence AI118064	-1.13	0.626	-1.35	0.258	1.23	0.231	2.55	0.064	0.33
1456112_at	Tpr	translocated promoter region	1.22	0.498	-1.09	0.493	-1.39	0.2	1.05	0.772	-0.05
1450224_at	Col4a3	procollagen, type IV, alpha 3	-1.42	0.167	1.26	0.728	-1.11	0.786	1.08	0.87	-0.05
1426570_a_at	Frk	fyn-related kinase	-1.14	0.113	1.15	0.673	-1.2	0.372	1.15	0.699	-0.01
1427568_a_at	Ift80	intraflagellar transport 80 homolog (Chlamydomonas)	-1.08	0.666	1.17	0.552	-1.3	0.01	1.24	0.53	0.01
1426670_at	Agrin	agrin	1.15	0.124	-1.13	0.031	-1.21	0.508	1.29	0.491	0.02
1449834_at	Pdzx	PDZ domain containing, X chromosome	-1.04	0.767	-1.28	0.31	1.12	0.689	1.19	0.391	0
1456755_at	Trak1	trafficking protein, kinesin binding 1	1.11	0.701	-1.68	0.445	1.16	0.46	-1.24	0.414	-0.17
1418232_s_at	Lims1	LIM and senescent cell antigen-like domains 1	-1.28	0.061	1.32	0.047	-1.32	0.021	1.23	0.305	-0.01
1423564_a_at	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoim	-1.1	0.133	1.05	0.361	-1.1	0.13	1.2	0.418	0.01
1433868_at	Btbd3	BTB (POZ) domain containing 3	1.09	0.458	-1	0.986	-1.29	0.284	1.01	0.955	-0.05
1432070_at	4921511C10Rik	RIKEN cDNA 4921511C10 gene	1.11	0.838	1.28	0.654	-2.13	0.302	-3.76	0.21	-0.87
1437593_x_at	Api5	apoptosis inhibitor 5	-1.04	0.515	1.07	0.24	-1.21	0.005	1.03	0.409	-0.04
1456287_at	BB236558	expressed sequence BB236558	1.17	0.322	-1.52	0.381	1.04	0.907	-1.09	0.847	-0.1
1419951_at	Lman1	Lectin, mannose-binding, 1	-1.4	0.187	-1.25	0.118	1.35	0.142	1.03	0.926	-0.07
1436782_at	---	---	-1.33	0.716	-1.52	0.472	1.45	0.408	1.73	0.078	0.08
1435410_at	Tcam1	testicular cell adhesion molecule 1	1.14	0.84	-2.16	0.043	1.26	0.232	-1.01	0.966	-0.19
1434801_x_at	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.15	0.027	-1.19	0.009	1.15	0.134	1.06	0.567	-0.03
1425591_a_at	Chmp2a	chromatin modifying protein 2A	-1.08	0.363	-1.07	0.352	1.01	0.838	1.07	0.705	-0.02
1453566_at	3200001K10Rik	RIKEN cDNA 3200001K10 gene	-1.16	0.528	-1.27	0.768	1.21	0.647	3.8	0.112	0.65
1453793_at	1700026J12Rik	RIKEN cDNA 1700026J12 gene	-1.33	0.506	1.15	0.731	-1.04	0.913	1.37	0.101	0.04
1435642_at	9630019K15Rik	RIKEN cDNA 9630019K15 gene	-1.34	0.559	-1.34	0.33	1.37	0.154	1.17	0.477	-0.03
1424806_s_at	1110039B18Rik	RIKEN cDNA 1110039B18 gene	1.02	0.841	1.09	0.517	-1.33	0.003	-1.12	0.396	-0.08
1436709_at	C230096C10Rik	RIKEN cDNA C230096C10 gene	-1.1	0.697	-1.19	0.332	1.11	0.435	1.26	0.222	0.02
1430003_at	6330412A17Rik	RIKEN cDNA 6330412A17 gene	1.26	0.22	-1.01	0.954	-1.63	0.087	2.26	0.052	0.22
1425438_at	---	---	-1.37	0.518	1.03	0.95	1.1	0.684	-1.16	0.655	-0.1
1435338_at	Cdk6	cyclin-dependent kinase 6	-1.03	0.894	1.12	0.445	-1.31	0.313	1.44	0.088	0.06
1448504_a_at	Cbx3 /// LOC62957	chromobox homolog 3 (Drosophila HP1 gamma) /// similar to chromobox homolo	1.08	0.221	-1.05	0.622	-1.2	0.266	1.51	0.073	0.08
1431208_a_at	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	1.03	0.784	-1.22	0.432	1.02	0.873	-1.14	0.443	-0.08
1434657_at	Gls	glutaminase	-1.03	0.132	1.01	0.958	-1.13	0.478	1.24	0.228	0.02

1444380_at	AI844869	expressed sequence AI844869	1.22	0.798	-1.38	0.327	-1.09	0.667	1.45	0.486	0.05
1433721_x_at	Rps21	ribosomal protein S21	1.07	0.632	1.06	0.311	-1.35	0.002	-1.26	0.047	-0.12
1427639_a_at	Nek4	NIMA (never in mitosis gene a)-related expressed kinase 4	-1.12	0.376	-1.11	0.655	1.07	0.73	1.51	0.152	0.09
1418148_at	Abhd1	abhydrolase domain containing 1	1.02	0.922	-1.32	0.006	1.08	0.694	-1.27	0.358	-0.12
1430349_at	Zdhhc11	zinc finger, DHHC domain containing 11	-1.75	0.395	-1.13	0.779	1.41	0.271	1.13	0.8	-0.09
1427496_at	Cep152	centrosomal protein 152	-1.39	0.34	1.29	0.349	-1.17	0.466	1.38	0.49	0.03
1449364_at	Aurkc	aurora kinase C	1.01	0.965	1.32	0.697	-1.85	0.136	-1.34	0.478	-0.22
1430385_a_at	Glb1l	galactosidase, beta 1-like	-1.2	0.366	-1.06	0.808	1.09	0.49	1.25	0.06	0.02
1430164_a_at	Grb10	growth factor receptor bound protein 10	-1.9	0.017	1.75	0.161	-1.71	0.035	1.38	0.363	-0.12
1446633_at	Atg7	autophagy-related 7 (yeast)	1.1	0.668	1.09	0.707	-1.47	0.397	-1.33	0.556	-0.15
1457198_at	Nrp1	neuropilin 1	1.12	0.086	1.13	0.422	-1.63	0.159	-1.01	0.951	-0.1
1433573_x_at	Prss2	protease, serine, 2	-5.56	0.009	-1.04	0.929	1.73	0.158	1.2	0.7	-0.92
1451147_x_at	Csdc2	cold shock domain containing C2, RNA binding	-1.71	0.361	1.01	0.987	1.27	0.632	-1.53	0.585	-0.24
1416531_at	Gsto1	glutathione S-transferase omega 1	-1.17	0.322	-1.19	0.233	1.17	0.458	1.21	0.068	0
1444712_at	Gm739 /// LOC672	gene model 739, (NCBI) /// hypothetical protein LOC672930	1.41	0.531	-2.2	0.153	1	0.993	-1.02	0.89	-0.2
1418566_s_at	Nudcd2	NudC domain containing 2	-1	0.987	1.04	0.642	-1.21	0.053	1.4	0.36	0.06
1439134_s_at	4930524O07Rik	RIKEN cDNA 4930524O07 gene	1.29	0.415	-1.21	0.426	-1.35	0.41	1.11	0.863	-0.04
1422554_at	Ndnl2	necdin-like 2	-1.06	0.372	-1.27	0.002	1.13	0.434	1.03	0.73	-0.04
1447367_at	Scfd2	sec1 family domain containing 2	-1.12	0.878	1.18	0.808	-1.27	0.591	1.48	0.447	0.07
1448526_at	Kpnb1	karyopherin (importin) beta 1	-1.11	0.095	1.07	0.409	-1.11	0.341	1.16	0.328	0
1456461_at	Ewsr1	Ewing sarcoma breakpoint region 1	-1.23	0.593	1.27	0.704	-1.27	0.705	1.5	0.432	0.07
1447533_at	---	Transcribed locus	-1.03	0.906	-1.22	0.614	1.08	0.838	1.53	0.051	0.09
1442360_at	Auts2	Autism susceptibility candidate 2	-1.32	0.285	1.29	0.447	-1.22	0.204	1.31	0.332	0.01
1417165_at	Mbd2	methyl-CpG binding domain protein 2	-1.18	0.002	-1.04	0.361	1.06	0.65	1.1	0.451	-0.02
1427109_at	ORF61	open reading frame 61	1.13	0.014	-1.21	0.076	-1.1	0.501	1.01	0.915	-0.04
1450059_at	---	---	-1.37	0.312	1.14	0.652	-1	0.984	1.17	0.416	-0.02
1422519_at	Cask	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	-1.27	0.156	1	0.964	1.07	0.683	-1	0.967	-0.05
1444980_at	C730009D12	Hypothetical protein C730009D12	1.53	0.537	-1.27	0.042	-1.83	0.273	1.3	0.729	-0.07
1416579_a_at	Tacstd1	tumor-associated calcium signal transducer 1	1.03	0.795	-1.09	0.877	-1.09	0.706	1.21	0.47	0.01
1421334_x_at	Mynn	myoneurin	-1.14	0.591	-1.14	0.61	1.11	0.661	1.19	0.55	0.01
1440471_x_at	---	---	1.39	0.345	-1.13	0.68	-1.68	0.176	1.11	0.703	-0.08
1454946_at	Mybl2	myeloblastosis oncogene-like 2	-1.23	0.147	1.14	0.765	-1.1	0.346	3.27	0.148	0.52
1435330_at	---	---	1.06	0.849	1.15	0.503	-1.51	0.006	-3.08	0.03	-0.6
1456597_at	Heatr3	HEAT repeat containing 3	-1.18	0.419	-1.07	0.616	1.08	0.664	1.14	0.673	-0.01
1429776_a_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	-1.38	0.385	-1.06	0.671	1.2	0.456	1.05	0.869	-0.05
1422203_at	Slc18a3	solute carrier family 18 (vesicular monoamine), member 3	-1.31	0.644	1.24	0.699	-1.16	0.476	1.69	0.344	0.11
1430601_at	Tbccd1	TBCC domain containing 1	1.01	0.945	-1.16	0.713	-1.01	0.955	1.33	0.546	0.04
1417418_s_at	Cox6a1 /// LOC665	cytochrome c oxidase, subunit VI a, polypeptide 1 /// similar to Cytochrome c oxid	-1.11	0.324	-1.16	0.122	1.1	0.25	1.33	0.097	0.04
1423240_at	Src	Rous sarcoma oncogene	-1.07	0.88	-1.2	0.746	1.1	0.66	1.58	0.152	0.1
1417797_a_at	1810019J16Rik	RIKEN cDNA 1810019J16 gene	-1.1	0.174	-1.15	0.515	1.08	0.714	1.02	0.942	-0.03
1454004_at	5033414K04Rik	RIKEN cDNA 5033414K04 gene	-1.89	0.155	1.33	0.29	1.01	0.984	-1.36	0.552	-0.23
1418114_at	Rbpsuh	recombining binding protein suppressor of hairless (Drosophila)	-1.01	0.9	-1.18	0.311	1.03	0.803	1.15	0.508	0
1459264_at	Trim33 /// 8030451I	tripartite motif protein 33 /// RIKEN cDNA 8030451N04 gene	1.04	0.953	-1.02	0.98	-1.18	0.446	1.19	0.674	0.01
1415838_at	Serinc1	serine incorporator 1	-1.05	0.61	-1.13	0.194	1.03	0.856	1.56	0.136	0.1
1423786_at	8430410A17Rik	RIKEN cDNA 8430410A17 gene	-1.03	0.929	-1.16	0.355	1.03	0.751	1.05	0.573	-0.03
1428285_at	8430427H17Rik	RIKEN cDNA 8430427H17 gene	-1.03	0.945	-1.61	0.428	1.27	0.255	2.74	0.077	0.34
1457430_at	Spock2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	-1.07	0.83	1.08	0.859	-1.17	0.54	1.06	0.64	-0.02
1427914_a_at	Tceb1	transcription elongation factor B (SIII), polypeptide 1	1.2	0.379	-1.06	0.095	-1.39	0	1.09	0.446	-0.04
1432460_at	1700125F08Rik	RIKEN cDNA 1700125F08 gene	-3.1	0.11	1.5	0.392	1.04	0.894	-1.37	0.703	-0.48
1421717_at	V1rd4	vomeronasal 1 receptor, D4	1.31	0.659	-2.95	0.002	1.21	0.627	-1.32	0.561	-0.44
1446509_at	Smox	spermine oxidase	1.35	0.097	-1.92	0.196	-1	0.997	4.29	0.212	0.68
1450113_at	---	---	1.03	0.903	-1	0.988	-1.19	0.527	1.66	0.348	0.12
1450135_at	Fzd3	frizzled homolog 3 (Drosophila)	1.26	0.258	-1.47	0.459	-1.08	0.275	1.84	0.21	0.14

1459579_at	---	---	-2.14	0.294	1.49	0.321	-1.1	0.855	2.44	0.132	0.17
1428439_at	Nub1	negative regulator of ubiquitin-like proteins 1	-1.11	0.872	1.08	0.889	-1.13	0.813	1.47	0.167	0.08
1424661_at	Pmpca	peptidase (mitochondrial processing) alpha	-1.3	0.063	-1.23	0.101	1.29	0.143	1.14	0.637	-0.03
1456696_x_at	Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	1.04	0.492	1	1	-1.2	0.556	-1.14	0.571	-0.08
1449614_s_at	AI314976 /// LOC67	expressed sequence AI314976 /// similar to Protein C6orf130 homolog	-1.05	0.561	-1.21	0.185	1.09	0.644	1.14	0.296	-0.01
1422284_at	Nkx2-9	NK2 transcription factor related, locus 9 (Drosophila)	1.06	0.847	-1.09	0.372	-1.12	0.664	1.07	0.744	-0.02
1456657_at	AA415437	expressed sequence AA415437	1.07	0.821	-1.09	0.625	-1.14	0.388	1.09	0.807	-0.02
1451389_at	Zcsl3	zinc finger, CSL-type containing 3	-1.21	0.614	1.24	0	-1.26	0.445	1.12	0.539	-0.03
1452959_a_at	Capn10	calpain 10	-1.19	0.527	-1.48	0.032	1.35	0.037	1.34	0.244	0.01
1430090_at	Ccdc28b	coiled coil domain containing 28B	1.48	0.33	-1.88	0.137	-1.16	0.501	1.35	0.195	-0.06
1455896_a_at	Kcnk1	potassium channel, subfamily K, member 1	1.16	0.176	-1.37	0.445	-1.02	0.945	1.38	0.586	0.03
1452176_at	Nup153	nucleoporin 153	-1.16	0.297	1.05	0.373	-1.05	0.441	1.04	0.655	-0.03
1447841_x_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.14	0.628	-1.06	0.793	1.04	0.849	2.41	0.103	0.31
1447932_at	Ccdc16	coiled-coil domain containing 16	1.27	0.564	-1.21	0.559	-1.29	0.403	1.21	0.616	-0.01
1448230_at	Usp10	ubiquitin specific peptidase 10	-1.12	0.291	-1.12	0.214	1.08	0.33	1.39	0.233	0.06
1442253_at	---	---	-1.38	0.555	-1.38	0.666	1.42	0.281	1.82	0.108	0.12
1448857_a_at	Zdhhc12	zinc finger, DHHC domain containing 12	-1.16	0.545	-1.02	0.936	1.03	0.924	1.38	0.316	0.06
1444906_at	Lphn2	latrophilin 2	-1.28	0.752	1.36	0.373	-1.38	0.649	1.02	0.961	-0.07
1423772_x_at	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.13	0.011	-1.13	0.098	1.1	0.384	1.01	0.809	-0.04
1436360_at	Hkr2	GLI-Kruppel family member HKR2	-1.2	0.06	-1.42	0.003	1.33	0.179	1.08	0.54	-0.05
1442455_at	C79845	expressed sequence C79845	-1.14	0.774	-1.1	0.854	1.08	0.472	1.1	0.505	-0.01
1436380_at	Cdc42bpa	Cdc42 binding protein kinase alpha	1.07	0.101	-1.12	0.289	-1.1	0.379	1.42	0.127	0.07
1436952_at	Klf9	Kruppel-like factor 9	-1.21	0.344	-1.49	0.3	1.37	0.467	1.06	0.893	-0.07
1426405_at	Rnf11	ring finger protein 11	-1.29	0.378	1.27	0.329	-1.21	0.248	1.6	0.354	0.09
1420551_at	2310039E09Rik	RIKEN cDNA 2310039E09 gene	-1.53	0.477	-1.05	0.851	1.26	0.605	1.3	0.663	0
1457985_at	Clmn	calmin	1.2	0.865	-1.57	0.142	1.03	0.951	-1.09	0.758	-0.11
1424013_at	Etf1	eukaryotic translation termination factor 1	-1.13	0.195	1.04	0.399	-1.06	0.554	1.28	0.282	0.03
1455214_at	Mitf	microphthalmia-associated transcription factor	-1.07	0.429	1.06	0.518	-1.14	0.336	1.13	0.737	-0.01
1437200_at	Fcho2	FCH domain only 2	-1.06	0.685	1.05	0.405	-1.14	0.022	1.35	0.094	0.05
1439629_at	Nrxn3	neurexin III	-1.18	0.737	1.07	0.547	-1.06	0.882	2.01	0.098	0.21
1422205_at	Sox1	SRY-box containing gene 1	-1.21	0.583	-1.12	0.867	1.15	0.355	2	0.097	0.2
1460275_at	Gpr3	G-protein coupled receptor 3	-1.6	0.392	1.4	0.437	-1.19	0.395	1.58	0.548	0.05
1455401_at	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-1.25	0.363	1.07	0.785	-1	0.976	1.12	0.397	-0.01
1416597_at	Hdgfrp2	hepatoma-derived growth factor, related protein 2	-1.12	0.607	-1.08	0.48	1.05	0.705	1.01	0.944	-0.04
1440501_at	AU041480	expressed sequence AU041480	1.33	0.589	-1.41	0.106	-1.2	0.668	1.09	0.829	-0.05
1456411_at	Rccd1	RCC1 domain containing 1	1.01	0.97	1.1	0.759	-1.32	0.085	-1.19	0.421	-0.1
1439058_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associat	-1.12	0.576	1.22	0.536	-1.33	0.375	1.23	0.318	0
1448900_at	D16H22S680E	DNA segment, Chr 16, human D22S680E, expressed	-1.19	0.106	-1.04	0.806	1.07	0.587	1.76	0.151	0.15
1438215_at	---	---	-1.14	0.61	-1.16	0.451	1.13	0.478	1.03	0.788	-0.03
1440992_at	3110052M02Rik	RIKEN cDNA 3110052M02 gene	1.08	0.611	1.02	0.882	-1.3	0.085	-1.61	0.255	-0.2
1429931_at	4930553P18Rik	RIKEN cDNA 4930553P18 gene	-4.3	0.199	1.92	0.181	-1.4	0.367	1.2	0.519	-0.65
1431251_at	1300011L04Rik	RIKEN cDNA 1300011L04 gene	-1.11	0.718	-1.36	0.038	1.23	0.5	1.35	0.708	0.03
1433018_at	4930560O18Rik	RIKEN cDNA 4930560O18 gene	-1.91	0.208	1.48	0.33	-1.15	0.382	1	0.996	-0.15
1429584_at	Mynn	myoneurin	-1.36	0.076	-1.06	0.712	1.19	0.3	1.48	0.14	0.06
1421672_at	Il17a	interleukin 17A	-1.75	0.139	-1.04	0.895	1.33	0.369	1.3	0.427	-0.04
1420980_at	Pak1	p21 (CDKN1A)-activated kinase 1	-1.11	0.045	1.09	0.653	-1.13	0.495	1.25	0.325	0.02
1445062_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	1.59	0.263	-1.32	0.333	-1.92	0.077	1	0.995	-0.16
1444108_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730040G	-1.07	0.845	1	0.999	-1.07	0.398	1.36	0.377	0.06
1416699_at	1110008F13Rik	RIKEN cDNA 1110008F13 gene	-1.04	0.852	1.07	0.665	-1.2	0.343	1.13	0.428	-0.01
1431437_at	Foxp4	forkhead box P4	1.03	0.781	1.11	0.691	-1.38	0.187	-1.13	0.747	-0.09
1431485_at	4833447I15Rik	RIKEN cDNA 4833447I15 gene	-1.02	0.937	-1.71	0.267	1.31	0.327	1.12	0.249	-0.08
1420441_at	Cenpc1	centromere protein C1	-1.22	0.31	-1	0.999	1.05	0.844	1.59	0.294	0.1
1441993_at	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	-1.07	0.683	1.02	0.889	-1.08	0.677	1.19	0.607	0.01

1417336_a_at	Sytl4	synaptotagmin-like 4	1.04	0.803	-1.18	0.53	-1.02	0.942	1.86	0.126	0.17
1422563_at	Crry	complement receptor related protein	-1.1	0.48	1.03	0.254	-1.08	0.181	1.07	0.349	-0.02
1459478_at	AA408396	expressed sequence AA408396	-1.01	0.973	1.03	0.866	-1.18	0.74	1.26	0.521	0.03
1454861_at	Txlna	taxilin alpha	1.05	0.708	-1.16	0.054	-1.05	0.728	1	0.935	-0.04
1456163_at	2700049P18Rik	RIKEN cDNA 2700049P18 gene	-1.35	0.212	1.02	0.93	1.11	0.129	-1.09	0.591	-0.08
1428082_at	Acsl5	acyl-CoA synthetase long-chain family member 5	1.11	0.57	-1.12	0.345	-1.16	0.25	1.11	0.269	-0.01
1420352_at	Prss22	protease, serine, 22	-1.21	0.534	-1.56	0.017	1.4	0.286	1.09	0.752	-0.07
1416865_at	Fgd1	FYVE, RhoGEF and PH domain containing 1	-1.22	0.622	1.04	0.92	1.01	0.949	-1.59	0.181	-0.19
1455337_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	-1.1	0.264	-1.07	0.732	1.03	0.835	1.17	0.427	0.01
1431397_at	---	---	1.32	0.354	-1.51	0.341	-1.13	0.813	1.21	0.828	-0.03
1452493_s_at	Hoxb8	homeo box B8	1.1	0.841	-1.11	0.531	-1.16	0.777	2.07	0.137	0.23
1420466_at	Spt2	salivary protein 2	1.75	0.391	-1.7	0.278	-1.86	0.258	1.1	0.823	-0.18
1459629_at	---	---	1.52	0.118	-1.1	0.882	-2.26	0.039	1.42	0.528	-0.11
1427959_at	Abhd10	abhydrolase domain containing 10	-1.17	0.158	1.1	0.633	-1.09	0.555	1.17	0.399	0
1418593_at	Taf6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1	0.996	-1.19	0.389	1.03	0.706	1.04	0.806	-0.03
1453784_at	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C	-1.23	0.106	-1.13	0.278	1.18	0.574	1.12	0.69	-0.02
1457916_at	---	---	1.01	0.921	1.08	0.891	-1.27	0.619	-1.45	0.478	-0.16
1450435_at	L1cam	L1 cell adhesion molecule	1.16	0.492	-1.56	0.164	1.07	0.506	-1.18	0.402	-0.13
1453939_x_at	LOC677168	hypothetical protein LOC677168	-1.75	0.57	-1.03	0.878	1.33	0.397	1.82	0.379	0.09
1458445_at	6530409C15Rik	RIKEN cDNA 6530409C15 gene	-1.24	0.063	1.49	0.526	-1.73	0.327	1.07	0.861	-0.1
1430291_at	1110060D06Rik ///	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	-1.21	0.298	1	0.965	1.04	0.829	-1.04	0.838	-0.05
1419814_s_at	S100a1	S100 calcium binding protein A1	-1.14	0.244	1.1	0.007	-1.12	0.486	1.14	0.04	0
1418984_at	Inadl	InaD-like (Drosophila)	1.07	0.099	-1.24	0.303	1	0.999	-2.03	0.002	-0.3
1422568_at	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	1.01	0.897	-1.11	0.165	-1.04	0.611	1.01	0.944	-0.03
1425226_x_at	Tcrb-V13 /// LOC66	T-cell receptor beta, variable 13 /// similar to T-cell receptor beta-2 chain C region	1.03	0.875	-1.25	0.577	1.04	0.753	-2.61	0.076	-0.45
1417605_s_at	Camk1 /// LOC669	calcium/calmodulin-dependent protein kinase I /// similar to calcium/calmodulin-de	1.11	0.117	-1.11	0.262	-1.15	0.41	1.17	0.404	0
1447926_at	Arl5a	ADP-ribosylation factor-like 5A	1.01	0.947	-1.85	0.227	1.32	0.598	-1.6	0.331	-0.28
1440323_at	Syt2	synaptotagmin II	-1.44	0.719	-1.42	0.481	1.47	0.505	3.49	0.091	0.53
1415685_at	Mtif2	mitochondrial translational initiation factor 2	-1.01	0.926	-1.15	0.023	1.02	0.9	1.13	0.378	0
1444486_at	Klhl5	kelch-like 5 (Drosophila)	1.25	0.581	-1.77	0.29	1.06	0.863	-1.47	0.321	-0.23
1437403_at	E130306M17Rik	RIKEN cDNA E130306M17 gene	1.53	0.131	-1.18	0.726	-2.01	0.076	1.06	0.801	-0.15
1429171_a_at	5730507H05Rik	RIKEN cDNA 5730507H05 gene	-2.26	0.089	-1.01	0.988	1.44	0.498	3.37	0.257	0.39
1438225_x_at	Tram1	translocating chain-associating membrane protein 1	-1.22	0.567	1.26	0.54	-1.25	0.491	1.07	0.85	-0.04
1415775_at	Rbbp7	retinoblastoma binding protein 7	-1.08	0.693	-1.11	0.136	1.05	0.359	1.23	0.123	0.02
1457872_at	---	---	-1.37	0.704	1.21	0.798	-1.08	0.83	1.42	0.524	0.05
1453177_at	4631426E05Rik	RIKEN cDNA 4631426E05 gene	-1.63	0.073	1.3	0.361	-1.05	0.88	1.46	0.359	0.02
1453200_at	Rai1	retinoic acid induced 1	-1.48	0.009	1.19	0.038	1	0.978	-1.14	0.504	-0.11
1435314_at	Tph2	tryptophan hydroxylase 2	1.95	0.294	-1.97	0.408	-2.4	0.178	1.6	0.308	-0.21
1447880_x_at	Edg5	Endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	-1.64	0.261	1.48	0.253	-1.27	0.244	1.12	0.642	-0.08
1439605_at	---	---	1.04	0.92	-1.11	0.793	-1.08	0.802	2.27	0.127	0.28
1450086_at	Gmeb1	glucocorticoid modulatory element binding protein 1	1.1	0.472	-1.02	0.787	-1.26	0.236	1.29	0.252	0.03
1430257_at	Card11	caspase recruitment domain family, member 11	1.27	0.587	-1.74	0.231	1.03	0.65	-2.25	0.04	-0.42
1456918_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1.18	0.47	1.09	0.528	-1.65	0.067	-1.33	0.549	-0.18
1425473_at	Crsp6	cofactor required for Sp1 transcriptional activation, subunit 6	-1.15	0.052	1.01	0.963	1	0.976	-1.28	0.114	-0.11
1428234_at	Cpsf6	cleavage and polyadenylation specific factor 6	-1.23	0.522	-1.21	0.305	1.24	0.208	1.14	0.508	-0.02
1449434_at	Car3	carbonic anhydrase 3	-2.18	0.174	-1.82	0.232	1.87	0.468	35.48	0.196	8.34
1416404_s_at	Rps16	ribosomal protein S16	1.04	0.588	1.03	0.509	-1.24	0.016	-1.34	0.015	-0.13
1445638_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	-3.02	0.023	1.29	0.554	1.26	0.28	-1.82	0.402	-0.58
1444278_at	---	---	1.32	0.639	-1.09	0.719	-1.58	0.459	1.02	0.862	-0.08
1421927_at	Tbl2	transducin (beta)-like 2	-1.18	0.676	-1	0.965	1.03	0.773	1.56	0.262	0.1
1446461_at	Sox5	SRY-box containing gene 5	1.15	0.011	-1.28	0.177	-1.06	0.799	2.06	0.04	0.22
1450980_at	Gtpbp3	GTP binding protein 3	1.08	0.701	-1.3	0.387	1.03	0.849	-1.08	0.7	-0.07
1427939_s_at	Mycbp	c-myc binding protein	-1.06	0.692	-1.16	0.137	1.07	0.659	1.45	0.284	0.07

1457573_at	Top1	Topoisomerase (DNA) I	1.07	0.84	-1.13	0.806	-1.09	0.737	1.43	0.386	0.07
1442250_at	Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	-1.44	0.377	1.05	0.92	1.13	0.688	-1.07	0.784	-0.08
1426211_at	Tmem161a	transmembrane protein 161A	-1.07	0.694	-1.59	0.088	1.31	0.142	1.28	0.273	-0.02
1425238_at	LOC625603	40S ribosomal protein S20 pseudogene	-1.43	0.436	1.17	0.549	1.01	0.982	-1.85	0.142	-0.28
1427786_at	Sp6	trans-acting transcription factor 6	-1.01	0.963	1.04	0.899	-1.19	0.325	1.91	0.391	0.19
1418709_at	Cox7a1	cytochrome c oxidase, subunit VIIa 1	-1.23	0.003	-1.03	0.929	1.09	0.776	1.26	0.557	0.02
1428418_s_at	3110050N22Rik	RIKEN cDNA 3110050N22 gene	1.05	0.554	1.07	0.565	-1.31	0.051	-1.14	0.539	-0.08
1434666_at	Pcgf5	polycomb group ring finger 5	1.04	0.778	-1.16	0.151	-1.03	0.76	1.26	0.397	0.03
1430898_s_at	4931428L18Rik	RIKEN cDNA 4931428L18 gene	-1	0.998	1.07	0.718	-1.24	0.72	1.02	0.975	-0.04
1441987_at	Mbd5	methyl-CpG binding domain protein 5	1.11	0.61	1.3	0.511	-2.16	0.006	-1.54	0.123	-0.32
1429713_at	Sumf2	sulfatase modifying factor 2	1.25	0.569	-1.17	0.728	-1.29	0.172	1.15	0.424	-0.02
1445748_at	Cd3e	CD3 antigen, epsilon polypeptide	-1.1	0.89	-1.07	0.8	1.03	0.912	1.31	0.719	0.04
1422795_at	Cul3	cullin 3	-1.29	0.038	-1.06	0.732	1.16	0.342	1.42	0.259	0.06
1440975_at	1810057P16Rik	RIKEN cDNA 1810057P16 gene	1.43	0.209	-1	0.957	-2.21	0.02	1.01	0.93	-0.19
1419543_a_at	Sfrs10	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila)	-1.19	0.122	-1.02	0.942	1.05	0.624	1.03	0.911	-0.03
1460229_at	Stag3	stromal antigen 3	-1.67	0.591	1.92	0.44	-2.81	0.082	1.96	0.002	-0.15
1426661_at	Rpl27a /// LOC665	ribosomal protein L27a /// similar to ribosomal protein L27a	1.04	0.461	1.05	0.242	-1.28	0.016	-1.26	0.03	-0.11
1425879_at	Zfp352	zinc finger protein 352	-1.14	0.786	-1.32	0.38	1.24	0.036	1.65	0.367	0.11
1422429_at	Rnf14	ring finger protein 14	-1.13	0.114	1.01	0.457	-1.02	0.796	1.16	0.356	0
1433440_x_at	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B	-1.12	0.08	1.01	0.882	-1.02	0.817	1.11	0.158	-0.01
1433396_at	4921504P13Rik	RIKEN cDNA 4921504P13 gene	-2.27	0.466	-2.34	0.216	2.01	0.156	1.65	0.336	-0.24
1430844_at	1700018M17Rik	RIKEN cDNA 1700018M17 gene	1.02	0.956	1.24	0.458	-1.61	0.032	-1.18	0.551	-0.13
1423667_at	Mat2a	methionine adenosyltransferase II, alpha	1.25	0.271	-1.14	0.44	-1.32	0.174	1.11	0.549	-0.03
1437425_at	Gdap1	ganglioside-induced differentiation-associated-protein 1	-1.56	0.391	1.1	0.778	1.14	0.768	-1	0.986	-0.08
1444660_at	4932438A13Rik	RIKEN cDNA 4932438A13 gene	1.01	0.979	1.16	0.52	-1.41	0.077	-1.31	0.293	-0.14
1434859_at	Umps	uridine monophosphate synthetase	-1.15	0.18	-1.01	0.935	1.02	0.707	1.55	0.164	0.1
1420345_at	Cldn14	claudin 14	-1.01	0.985	1.25	0.231	-1.58	0.176	1.13	0.734	-0.05
1457290_at	Mab21l1	mab-21-like 1 (C. elegans)	1.03	0.95	1.2	0.774	-1.55	0.147	-1.64	0.443	-0.24
1443547_at	---	---	1.2	0.656	-1.02	0.954	-1.44	0.165	1.2	0.299	-0.01
1447646_at	Heatr2	HEAT repeat containing 2	-1.15	0.893	-2.41	0.075	1.59	0.333	1.17	0.634	-0.2
1429070_at	4933440H19Rik	RIKEN cDNA 4933440H19 gene	1.16	0.601	-1.2	0.079	-1.13	0.094	1.17	0.128	0
1424925_at	Sec63	SEC63-like (S. cerevisiae)	1.03	0.688	1.02	0.805	-1.22	0.103	-1.03	0.849	-0.05
1424171_a_at	Hagh	hydroxyacyl glutathione hydrolase	-1.04	0.807	-1.31	0.004	1.15	0.604	3.21	0.212	0.5
1427399_a_at	Nxf7	nuclear RNA export factor 7	1.31	0.482	-1.15	0.855	-1.42	0.413	2.37	0.192	0.28
1448204_at	Sav1	salvador homolog 1 (Drosophila)	-1.13	0.477	-1.1	0.071	1.08	0.551	1.25	0.244	0.03
1451993_at	9130404D08Rik	RIKEN cDNA 9130404D08 gene	1.21	0.319	-1.08	0.734	-1.35	0.254	1.23	0.086	0
1441363_at	---	---	-1.12	0.843	1.1	0.821	-1.14	0.397	1.01	0.988	-0.04
1420329_at	4930455C21Rik	RIKEN cDNA 4930455C21 gene	1.03	0.705	1.01	0.906	-1.21	0.167	-1.28	0.154	-0.11
1430544_at	5830404H04Rik	RIKEN cDNA 5830404H04 gene	-1.21	0.265	-1.15	0.533	1.18	0.518	1.25	0.404	0.02
1436407_at	9430069J07Rik	RIKEN cDNA 9430069J07 gene	-1.05	0.959	1.28	0.599	-1.55	0.28	1.12	0.885	-0.05
1424009_at	Reg3d	regenerating islet-derived 3 delta	-1.57	0.418	-1.15	0.076	1.37	0.518	1.24	0.507	-0.03
1429132_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	1.2	0.465	-1.28	0.179	-1.12	0.661	1.7	0.329	0.13
1447394_at	Clca6 /// AI747448	chloride channel calcium activated 6 /// expressed sequence AI747448 /// similar	1.9	0.466	-1.65	0.479	-2.68	0.046	1.34	0.382	-0.27
1416161_at	Rad21	RAD21 homolog (S. pombe)	1	0.998	-1.03	0.831	-1.1	0.356	1.48	0.23	0.09
1435827_at	4933404O12Rik	RIKEN cDNA 4933404O12 gene	-1.06	0.904	-1.48	0.143	1.26	0.477	2.09	0.041	0.2
1450699_at	Selenbp1	selenium binding protein 1	-1.06	0.754	1.06	0.727	-1.14	0.244	2	0.166	0.21
1435151_a_at	Rps3	ribosomal protein S3	1.02	0.783	1.05	0.426	-1.24	0.062	-1.41	0.031	-0.14
1418751_at	Sit1	suppression inducing transmembrane adaptor 1	1.15	0.837	-1.63	0.38	1.12	0.489	-2.04	0.172	-0.35
1449186_at	Bag4	BCL2-associated athanogene 4	1.02	0.848	-1.14	0.062	-1.03	0.829	1.26	0.336	0.03
1450929_at	Zfp57	zinc finger protein 57	1.15	0.696	1.18	0.734	-1.82	0.059	-1.8	0.3	-0.32
1422898_s_at	Slc22a12	solute carrier family 22 (organic anion/cation transporter), member 12	-1.24	0.199	-1.41	0.394	1.36	0.056	1.4	0.365	0.03
1454914_at	2610101N10Rik	RIKEN cDNA 2610101N10 gene	-1.11	0.645	1.09	0.065	-1.12	0.257	1.17	0.358	0.01
1424190_at	Pigc	phosphatidylinositol glycan anchor biosynthesis, class C	1.18	0.082	-2.56	0.068	1.31	0.441	-1.47	0.156	-0.39

1454343_at	6430710M23Rik	RIKEN cDNA 6430710M23 gene	-1.42	0.257	-1.04	0.838	1.21	0.619	1.24	0.316	0
1443881_at	Pofut1	protein O-fucosyltransferase 1	-1.07	0.664	-1.09	0.446	1.03	0.864	1.21	0.14	0.02
1450902_at	Brd3	bromodomain containing 3	-1.2	0.275	-1.16	0.057	1.18	0.523	1.01	0.952	-0.04
1451481_s_at	Osta	organic solute transporter alpha	-1.3	0.545	1.01	0.969	1.09	0.716	-1.07	0.822	-0.07
1417941_at	Nanp	N-acetylneuraminic acid phosphatase	-1.07	0.817	1.01	0.944	-1.07	0.724	2.08	0.161	0.24
1452284_at	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	1.06	0.941	-1.73	0.101	1.23	0.333	-1.05	0.913	-0.12
1422591_at	Tceb3	transcription elongation factor B (SIII), polypeptide 3	-1.19	0.063	-1.04	0.756	1.08	0.394	1.19	0.468	0.01
1454220_at	9330185C12Rik	RIKEN cDNA 9330185C12 gene	1.43	0.271	-1.21	0.399	-1.63	0.125	2.38	0.375	0.24
1424213_at	Ubiad1	UbiA prenyltransferase domain containing 1	-1.06	0.785	-1.08	0.416	1.01	0.946	1.05	0.497	-0.02
1439023_at	Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	-1.26	0.47	-1.11	0.739	1.19	0.321	1.03	0.844	-0.04
1425263_a_at	Mbp	myelin basic protein	-1.03	0.865	-1.78	0.005	1.35	0.49	1.16	0.736	-0.08
1438050_x_at	---	---	1.13	0.451	-1.12	0.603	-1.18	0.523	1.61	0.027	0.11
1450515_at	Kcnj11	potassium inwardly rectifying channel, subfamily J, member 11	1.19	0.513	-1.4	0.44	-1.02	0.952	1.25	0.646	0
1440381_at	2410085M17Rik	RIKEN cDNA 2410085M17 gene	-1.24	0.456	1.18	0.52	-1.11	0.433	1.1	0.639	-0.02
1441160_at	D330050G23Rik	RIKEN cDNA D330050G23 gene	1.01	0.927	1.06	0.89	-1.24	0.239	-1.21	0.2	-0.09
1439730_at	Ncald	Neurocalcin delta	-2	0.061	1.78	0.284	-1.68	0.334	1.33	0.455	-0.14
1431472_at	2310043D23Rik	RIKEN cDNA 2310043D23 gene	-1.16	0.831	1.47	0.291	-1.82	0.354	1.45	0.377	-0.02
1428000_at	Tmem60	transmembrane protein 60	-1.05	0.328	1.06	0.416	-1.16	0.239	1.22	0.428	0.02
1424810_at	Tasp1	taspase, threonine aspartase 1	-1.13	0.668	-1.07	0.639	1.06	0.684	1.14	0.252	0
1432795_at	2310058F05Rik	RIKEN cDNA 2310058F05 gene	-2.12	0.249	1.41	0.298	-1	0.967	1.29	0.637	-0.1
1436120_at	Setdb2	SET domain, bifurcated 2	-1.56	0.272	1.02	0.9	1.22	0.217	-1.16	0.251	-0.12
1421958_at	L1cam	L1 cell adhesion molecule	1.24	0.294	-4.66	0.12	1.43	0.23	-2.07	0.153	-1.02
1450251_a_at	Lnx1	ligand of numb-protein X 1	-1.17	0.416	1.19	0.581	-1.2	0.398	1.17	0.675	0
1429238_a_at	Ogfod2	2-oxoglutarate and iron-dependent oxygenase domain containing 2	-1.07	0.496	-1.13	0.284	1.07	0.703	1.14	0.43	0
1422907_at	Gnat2	guanine nucleotide binding protein, alpha transducing 2	-1.21	0.651	-1.57	0.147	1.42	0.058	1.2	0.646	-0.04
1427396_a_at	Csde1	cold shock domain containing E1, RNA binding	1.12	0.2	-1.02	0.84	-1.3	0.006	1.02	0.819	-0.04
1426735_at	Iars2	isoleucine-tRNA synthetase 2, mitochondrial	-1.13	0.258	-1.1	0.399	1.09	0.334	1.01	0.953	-0.03
1447503_at	BC016495	CDNA sequence BC016495	-1.22	0.271	1.38	0.486	-1.47	0.13	1.03	0.889	-0.07
1434298_at	Zfhx1b	zinc finger homeobox 1b	-1.19	0.415	1.23	0.456	-1.24	0.079	1.13	0.157	-0.02
1434158_at	Gmds	GDP-mannose 4, 6-dehydratase	1.01	0.967	-1.17	0.199	1.02	0.758	-1.1	0.523	-0.06
1444072_at	---	Transcribed locus	-1.04	0.843	-1.44	0.33	1.23	0.499	1.23	0.501	-0.01
1428936_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	1.15	0.767	1.1	0.64	-1.59	0.17	-1.12	0.55	-0.11
1436868_at	Rtn4rl1	reticulon 4 receptor-like 1	1	0.994	-1.06	0.571	-1.07	0.456	1.02	0.941	-0.03
1435067_at	B230208H17Rik	RIKEN cDNA B230208H17 gene	1.11	0.721	-1.05	0.792	-1.22	0.081	1.02	0.393	-0.04
1445281_a_at	B230311B06Rik	RIKEN cDNA B230311B06 gene	1.16	0.877	-1.01	0.975	-1.38	0.682	3.02	0.008	0.45
1420937_at	Cpsf2	cleavage and polyadenylation specific factor 2	-1.07	0.732	-1.06	0.022	1	0.985	1	0.991	-0.03
1443048_at	---	---	1.15	0.608	-1.67	0.252	1.13	0.873	-1.82	0.089	-0.3
1439304_at	B230216N24Rik	RIKEN cDNA B230216N24 gene	-1.27	0.432	1.62	0.406	-2.09	0.002	1.09	0.817	-0.17
1447155_at	D730039F16Rik	RIKEN cDNA D730039F16 gene	-1.15	0.541	1.08	0.754	-1.08	0.847	1.64	0.119	0.12
1432401_a_at	4930511M11Rik	RIKEN cDNA 4930511M11 gene	1.07	0.937	1.3	0.561	-1.95	0.052	-1.64	0.422	-0.3
1438187_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), mem	-1.04	0.592	-1.11	0.753	1.02	0.872	1.06	0.411	-0.02
1430035_at	1700034M03Rik	RIKEN cDNA 1700034M03 gene	1.12	0.779	-1.36	0.254	1.03	0.908	-1.25	0.262	-0.12
1433820_a_at	1110012D08Rik	RIKEN cDNA 1110012D08 gene	1.1	0.618	-1.3	0.084	1.01	0.888	-1.58	0.054	-0.19
1434761_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	-1.42	0.19	1.64	0.436	-1.87	0.292	1.17	0.814	-0.12
1443748_x_at	Ankrd44	ankyrin repeat domain 44	-2.11	0.267	-1.48	0.27	1.73	0.496	2.1	0.256	0.06
1443330_at	D1Ertd646e	DNA segment, Chr 1, ERATO Doi 646, expressed	1.03	0.941	1.09	0.652	-1.31	0.187	-1.08	0.782	-0.07
1448283_a_at	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B	-1.03	0.712	1.06	0.555	-1.18	0.185	1.12	0.479	-0.01
1433020_at	5830413G11Rik	RIKEN cDNA 5830413G11 gene	-1.33	0.701	1.31	0.672	-1.22	0.408	1.49	0.498	0.06
1416284_at	Mrpl28	mitochondrial ribosomal protein L28	1.09	0.497	-1.2	0.192	-1.05	0.641	1.1	0.515	-0.01
1454763_at	Ankrd17	ankyrin repeat domain 17	-1.03	0.523	1.02	0.824	-1.12	0.264	1.26	0.22	0.03
1458178_at	1700012H17Rik	RIKEN cDNA 1700012H17 gene	-1.12	0.865	-2.69	0.196	1.62	0.408	1.3	0.537	-0.22
1454045_a_at	Pgs1	phosphatidylglycerophosphate synthase 1	1.05	0.68	-1.23	0.444	1.02	0.868	-1.33	0.188	-0.12
1460183_at	Adprh	ADP-ribosylarginine hydrolase	-1	0.999	-1.31	0.49	1.12	0.718	1.24	0.467	0.01

1424859_at	Homer3	homer homolog 3 (Drosophila)	1.04	0.923	1.06	0.903	-1.28	0.006	-1.48	0.086	-0.16
1441660_at	Actr2	ARP2 actin-related protein 2 homolog (yeast)	1.06	0.805	1.16	0.329	-1.5	0.058	-1.71	0.209	-0.25
1430048_at	7630402I04Rik	RIKEN cDNA 7630402I04 gene	1.22	0.647	-1.59	0.346	1.03	0.934	-1.14	0.814	-0.12
1449312_at	Npy5r	neuropeptide Y receptor Y5	1.47	0.64	-1.49	0.162	-1.36	0.49	2.2	0.151	0.21
1434548_at	Serinc3	serine incorporator 3	1.13	0.637	-1.07	0.7	-1.23	0.246	1.41	0.177	0.06
1435204_at	Prmt8	protein arginine N-methyltransferase 8	1.37	0.659	-1.57	0.548	-1.14	0.639	2.12	0.283	0.19
1418753_at	Gfpt2	glutamine fructose-6-phosphate transaminase 2	-1.19	0.699	-1.14	0.628	1.17	0.496	1.19	0.621	0.01
1415946_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.01	0.908	-1.22	0.164	1.08	0.328	3.95	0.134	0.7
1431893_a_at	Pdss1	prenyl (solanesyl) diphosphate synthase, subunit 1	-1.16	0.085	1.08	0.581	-1.06	0.635	1.44	0.269	0.08
1435993_at	RP23-298F22.2	zinc finger protein 306-like	-1.09	0.757	-1.15	0.782	1.09	0.602	1.05	0.846	-0.02
1446524_at	---	PREDICTED: Mus musculus similar to HYPOTHETICAL PROTEIN ORF-1137 (L	-1.44	0.191	1.28	0.586	-1.1	0.557	1.21	0.564	-0.01
1433670_at	Emp2	epithelial membrane protein 2	1.1	0.529	1.08	0.581	-1.42	0.076	-1.63	0.226	-0.22
1449037_at	Crem	cAMP responsive element modulator	-1.2	0.346	1.03	0.895	1.01	0.949	-1.44	0.25	-0.15
1418347_at	Ccdc22	coiled-coil domain containing 22	-1.07	0.297	1	0.964	-1.06	0.65	1.09	0.333	-0.01
1432267_at	6720483E21Rik	RIKEN cDNA 6720483E21 gene	-1.24	0.503	1.41	0.377	-1.51	0.256	1.96	0.259	0.16
1450326_at	Shc3	src homology 2 domain-containing transforming protein C3	-1.02	0.895	1.48	0.209	-2.36	0.366	1.82	0.086	-0.02
1420680_at	Cts8	cathepsin 8	1.1	0.776	-1.6	0.321	1.16	0.694	-1.31	0.683	-0.16
1418470_at	Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	-1.25	0.455	-1.48	0.22	1.41	0.36	1.73	0.536	0.1
1436351_at	Coq3	coenzyme Q3 homolog, methyltransferase (yeast)	-1.03	0.684	-1.23	0.047	1.1	0.546	1.09	0.678	-0.02
1435522_a_at	2310016E02Rik	RIKEN cDNA 2310016E02 gene	-1.01	0.855	1.09	0.092	-1.24	0.109	1.02	0.848	-0.04
1431058_at	Htatsf1	HIV TAT specific factor 1	1.22	0.294	-1.51	0	1	0.977	-1.35	0.181	-0.16
1454882_at	L3mbtl3	l(3)mbt-like 3 (Drosophila)	-1.22	0.206	1.01	0.955	1.06	0.68	-1.9	0.091	-0.26
1415735_at	Ddb1	damage specific DNA binding protein 1	-1.12	0.267	-1.02	0.625	1	0.965	1.36	0.207	0.06
1437892_at	Zfp306	zinc finger protein 306	1.14	0.529	-1.15	0.345	-1.14	0.567	1.14	0.423	0
1450887_at	Rqcd1	rcd1 (required for cell differentiation) homolog 1 (S. pombe)	1.02	0.546	-1.04	0.46	-1.11	0.091	1.2	0.483	0.02
1436947_a_at	Txnl1	thioredoxin-like 1	-1.02	0.838	1.04	0.535	-1.17	0.162	1.35	0.176	0.05
1438088_at	---	Adult male cecum cDNA, RIKEN full-length enriched library, clone:9130222J03 p	1.28	0.765	-1.54	0.344	-1.05	0.832	1.57	0.16	0.07
1450985_a_at	Tjp2	tight junction protein 2	1.03	0.895	-1.08	0.506	-1.08	0.499	1.19	0.298	0.01
1427466_at	Cdc91l1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	-2.34	0.26	-1.09	0.833	1.54	0.205	1.02	0.969	-0.22
1417712_at	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	1.1	0.389	-1.05	0.64	-1.2	0.306	1.29	0.247	0.04
1441110_at	Lrrc21	leucine rich repeat containing 21	1.4	0.279	-1.47	0.349	-1.24	0.578	1.36	0.488	0.01
1451530_at	Egfr	epidermal growth factor receptor	-1.07	0.714	1.25	0.735	-1.42	0.296	1.33	0.481	0.02
1455503_at	Zfp85-rs1 /// Zfp273	zinc finger protein 85, related sequence 1 /// zinc finger protein 273	1.02	0.927	1.17	0.632	-1.43	0.301	-2.36	0.114	-0.4
1457045_at	Galnt13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.08	0.826	-1.42	0.633	1.1	0.706	-2.24	0.28	-0.37
1460010_a_at	Ptdss2	phosphatidylserine synthase 2	-1.16	0.508	1.03	0.838	-1	0.985	3.72	0.132	0.65
1452486_a_at	Cryaa	crystallin, alpha A	1.01	0.945	-1.04	0.841	-1.1	0.683	1	0.999	-0.03
1429851_at	1700003M02Rik	RIKEN cDNA 1700003M02 gene	-1.2	0.777	1.07	0.898	-1.02	0.94	1.1	0.862	-0.01
1440834_at	Slc5a10	solute carrier family 5 (sodium/glucose cotransporter), member 10	1.13	0.606	1.11	0.535	-1.54	0.26	-1.17	0.246	-0.12
1448376_at	Wrnip1	Werner helicase interacting protein 1	1.04	0.771	-1.26	0.032	1.05	0.75	-1.33	0.067	-0.12
1436368_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	-1.46	0.01	-1.05	0.698	1.25	0.252	3.25	0.165	0.5
1438096_a_at	Dtymk	deoxythymidylate kinase	-1.2	0.237	-1.04	0.714	1.09	0.121	1.21	0.448	0.01
1439332_at	Ddit4l	DNA-damage-inducible transcript 4-like	-1	0.979	-1.19	0.63	1.05	0.832	1.08	0.744	-0.02
1452506_a_at	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C	1.01	0.781	-1.14	0.158	-1.01	0.977	1.06	0.675	-0.02
1434701_at	AW215868	expressed sequence AW215868	-1.09	0.575	-1.09	0.071	1.05	0.69	1.27	0.015	0.03
1431388_at	Mphosph10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	-1.15	0.486	-1.02	0.907	1.04	0.878	1.04	0.744	-0.02
1437087_at	---	---	-1.2	0.029	1.3	0.275	-1.32	0.001	1.65	0.278	0.11
1456073_s_at	Panx3	pannexin 3	1.56	0.164	-1.35	0.283	-1.71	0.1	1.13	0.743	-0.09
1450812_at	Bcl2a1a /// Bcl2a1b	B-cell leukemia/lymphoma 2 related protein A1a /// B-cell leukemia/lymphoma 2 r	-1.64	0.626	1.23	0.795	1.04	0.813	-1.02	0.973	-0.09
1435776_at	2310009B15Rik	RIKEN cDNA 2310009B15 gene	1.04	0.852	-1.27	0.268	1.06	0.668	-1.31	0.31	-0.12
1459054_at	BC035954	cDNA sequence BC035954	-1.02	0.957	-1.12	0.698	1	0.981	1.38	0.115	0.06
1420923_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	1.11	0.64	-1.49	0.092	1.1	0.832	-1.19	0.501	-0.12
1441224_at	Drp2	Dystrophin related protein 2	1.37	0.765	-1.29	0.728	-1.36	0.669	3.14	0.031	0.47
1435467_at	Fgd6	FYVE, RhoGEF and PH domain containing 6	1.21	0.126	-1.37	0.243	-1.06	0.84	1.21	0.531	0

1436532_at	Dcamkl3	doublecortin and CaM kinase-like 3	-1.1	0.274	-1.15	0.689	1.11	0.752	1.65	0.371	0.13
1434893_at	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	-1.09	0.687	-1.21	0.711	1.14	0.685	1.54	0.077	0.1
1427654_a_at	Htr4	5 hydroxytryptamine (serotonin) receptor 4	1.45	0.519	-1.7	0.365	-1.17	0.509	1.98	0.03	0.14
1430553_at	Vsig1	V-set and immunoglobulin domain containing 1	-1.91	0.032	1.21	0.315	1.16	0.154	-2.61	0.036	-0.54
1430509_at	---	---	1.04	0.592	-1.09	0.842	-1.08	0.85	1.37	0.362	0.06
1432481_a_at	Lyzl6	lysozyme-like 6	-1.68	0.308	-1.43	0.492	1.59	0.323	1.88	0.192	0.09
1450406_a_at	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	1.02	0.939	-1.15	0.177	-1	0.986	1.08	0.763	-0.01
1421439_at	Wnt8b	wingless related MMTV integration site 8b	1.59	0.496	-1.44	0.348	-1.67	0.386	1.43	0.586	-0.02
1415889_a_at	Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1	-1.12	0.532	1.12	0.473	-1.15	0.023	1.01	0.962	-0.03
1444416_at	Cenpa	Centromere autoantigen A	-1.01	0.99	-1.6	0.323	1.27	0.486	2.32	0.255	0.24
1428949_at	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	-1.02	0.892	-1.23	0.035	1.09	0.077	1.23	0.166	0.02
1433295_at	4930449I04Rik	RIKEN cDNA 4930449I04 gene	-1.49	0.542	1.26	0.618	-1.05	0.912	1.22	0.799	-0.01
1453065_at	Aldh5a1	aldhehyde dehydrogenase family 5, subfamily A1	-1.15	0.021	-1.26	0.305	1.22	0.381	1.25	0.705	0.02
1423302_a_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	-1.36	0.091	-1.04	0.894	1.19	0.31	1.28	0.549	0.02
1419443_at	Sap18	Sin3-associated polypeptide 18	-1.01	0.921	-1.11	0.17	1	0.993	1.09	0.616	-0.01
1441722_at	Aatf	Apoptosis antagonizing transcription factor	1.18	0.396	1.09	0.714	-1.62	0.029	-1.13	0.497	-0.12
1452079_s_at	Dcun1d1	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	1.05	0.5	-1.17	0.629	-1.02	0.95	1.83	0.4	0.17
1441151_at	AU044157	expressed sequence AU044157	-1.65	0.42	-1.16	0.764	1.42	0.372	1.45	0.026	0.01
1456828_at	C030023E24Rik	RIKEN cDNA C030023E24 gene	-2.16	0.153	1.47	0.361	-1.05	0.922	1.32	0.576	-0.1
1447297_at	Slc25a36	Solute carrier family 25, member 36	-2.43	0.099	1.69	0.093	-1.27	0.448	1.17	0.644	-0.21
1444468_at	Paqr8	progestin and adipoQ receptor family member VIII	-1.17	0.445	1.04	0.913	-1.01	0.974	1.42	0.023	0.07
1444590_at	Ddhd2	DDHD domain containing 2	1.52	0.678	-1.14	0.86	-2.06	0.145	1.59	0.311	-0.02
1457762_at	Ttc15	Tetratricopeptide repeat domain 15	-1.14	0.035	-1.12	0.774	1.12	0.686	1.01	0.913	-0.03
1421945_a_at	Bxdc1	brix domain containing 1	-1.22	0.131	-1.07	0.559	1.14	0.558	1.02	0.922	-0.04
1429750_at	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	1.06	0.283	-1.05	0.816	-1.14	0.578	2.69	0.211	0.39
1452698_at	Tsfm	Ts translation elongation factor, mitochondrial	-1.32	0.124	-1.06	0.616	1.18	0.189	1.17	0.414	-0.01
1428151_x_at	Ccbl1	cysteine conjugate-beta lyase 1	1.08	0.409	-1.02	0.903	-1.21	0.058	1.07	0.769	-0.02
1458586_at	---	---	-1.18	0.296	1.49	0.043	-1.82	0.041	1.06	0.901	-0.11
1448981_x_at	Tcl1b1	T-cell leukemia/lymphoma 1B, 1	-1.2	0.71	1.24	0.134	-1.23	0.406	1.25	0.334	0.02
1456877_at	Duox1 /// LOC6405	dual oxidase 1 /// similar to dual oxidase 1	1.04	0.865	1.03	0.802	-1.23	0.677	-1.24	0.491	-0.1
1437933_at	Hhip	Hedgehog-interacting protein	1.86	0.154	-1.53	0.347	-2.65	0.018	1.57	0.186	-0.19
1450197_at	Rpe65	retinal pigment epithelium 65	-1.41	0.499	-1.32	0.381	1.42	0.063	1.53	0.259	0.05
1439013_x_at	Acyp1	acylphosphatase 1, erythrocyte (common) type	-1.26	0.226	1.27	0.265	-1.21	0.332	1.27	0.512	0.02
1415676_a_at	Psmb5	proteasome (prosome, macropain) subunit, beta type 5	-1.06	0.679	-1.11	0	1.04	0.727	1.03	0.7	-0.03
1435429_x_at	Rps27l	ribosomal protein S27-like	1	0.962	-1.03	0.524	-1.1	0.394	1.34	0.158	0.06
1450609_at	Lcn8	lipocalin 8	-1.57	0.495	1.38	0.398	-1.14	0.643	1.36	0.42	0.01
1458892_at	9430047G12Rik	RIKEN cDNA 9430047G12 gene	1.13	0.434	-1.05	0.843	-1.24	0.259	1.31	0.146	0.04
1427712_at	Ceacam1	CEA-related cell adhesion molecule 1	1.21	0.696	-1.04	0.95	-1.39	0.596	2.2	0.14	0.25
1451641_at	Dbr1	debranching enzyme homolog 1 (S. cerevisiae)	-1.04	0.897	-1.19	0.091	1.08	0.584	1.08	0.791	-0.02
1420197_at	Gadd45b	Growth arrest and DNA-damage-inducible 45 beta	-1.06	0.902	1.05	0.83	-1.12	0.783	1.5	0.145	0.09
1439658_at	Lmod3	leiomodin 3 (fetal)	-1.6	0.546	-1.16	0.779	1.4	0.603	1.21	0.785	-0.04
1425140_at	Lactb2	lactamase, beta 2	-1.07	0.786	-1.13	0.464	1.07	0.695	1.49	0.261	0.09
1445891_at	AF529169	cDNA sequence AF529169	-2.09	0.04	1.31	0.491	1.09	0.863	-1.04	0.965	-0.18
1420616_at	Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	-1.09	0.344	-1.1	0.537	1.06	0.262	1.22	0.155	0.02
1451170_s_at	Nomo1	nodal modulator 1	-1.12	0.621	1	0.983	-1.01	0.94	1.38	0.354	0.06
1458923_at	Msra	Methionine sulfoxide reductase A	1.16	0.814	-1.08	0.7	-1.26	0.675	1.29	0.448	0.03
1435450_at	Cpne3	copine III	-1.05	0.635	1.09	0.468	-1.18	0.214	1.16	0.098	0.01
1423642_at	Tubb2c	tubulin, beta 2c	-1.16	0.123	-1.16	0.273	1.17	0.425	2.14	0.166	0.24
1453257_at	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransf	-1.1	0.068	1	0.972	-1.03	0.875	1.36	0.301	0.06
1431900_a_at	Foxa3	forkhead box A3	1.04	0.883	-1.09	0.739	-1.08	0.693	1.35	0.585	0.06
1442004_at	Trim65	tripartite motif-containing 65	-1.92	0.088	1.14	0.367	1.22	0.137	-1.28	0.257	-0.21
1452384_at	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	-1.11	0.506	1.21	0.415	-1.29	0.221	1.67	0.22	0.12
1426548_a_at	Atpbd4	ATP binding domain 4	1	0.991	1.04	0.858	-1.18	0.23	-1.02	0.677	-0.04

1445385_at	---	Adult inner ear cDNA, RIKEN full-length enriched library, clone:F930025M14 proc	1.42	0.222	-1.59	0.186	-1.2	0.311	1.22	0.136	-0.03
1439624_at	Ugt2b35	UDP glucuronosyltransferase 2 family, polypeptide B35	1.21	0.787	-1.27	0.17	-1.13	0.619	1.12	0.834	-0.02
1429181_at	1700009P17Rik	RIKEN cDNA 1700009P17 gene	-1.09	0.596	1.1	0.424	-1.14	0.524	1.11	0.196	-0.01
1419346_a_at	Svs5	seminal vesicle secretion 5	-2.47	0.18	-3.99	0.084	2.23	0.139	1.99	0.339	-0.56
1419787_a_at	Zfp628	zinc finger protein 628	-1.23	0.052	-1.11	0.433	1.17	0.606	1.24	0.406	0.02
1438401_at	Ubn1	ubinuclein 1	1.03	0.792	1.02	0.722	-1.19	0.183	-1.13	0.636	-0.07
1427972_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	-1.38	0.315	-1.08	0.437	1.24	0.276	1.2	0.678	-0.01
1450100_a_at	Tcerg1	transcription elongation regulator 1 (CA150)	-1.15	0.792	-2.93	0.047	1.68	0.37	2.47	0.181	0.02
1458017_at	Phf20	PHD finger protein 20	1.05	0.822	1.02	0.945	-1.23	0.345	-1.27	0.075	-0.11
1427274_at	D130054N24Rik	RIKEN cDNA D130054N24 gene	-1.16	0.186	-1.3	0.093	1.26	0.284	1.29	0.236	0.02
1458843_at	Depdc5	DEP domain containing 5	1.32	0.115	-1.71	0.05	-1.02	0.965	1.07	0.803	-0.08
1442131_at	1700048M11Rik	RIKEN cDNA 1700048M11 gene	-3.06	0.101	1.2	0.725	1.37	0.598	-1.62	0.233	-0.53
1436502_at	Mtus1	mitochondrial tumor suppressor 1	-1.22	0.112	-1.01	0.965	1.07	0.752	1.29	0.28	0.04
1440842_at	C230085N15Rik	RIKEN cDNA C230085N15 gene	1.12	0.841	1.25	0.509	-1.93	0.056	-2.98	0.038	-0.63
1423906_at	Hsbp1	heat shock factor binding protein 1	1.04	0.592	1.01	0.904	-1.2	0.224	-1.37	0.201	-0.13
1431521_at	5033428B15Rik	RIKEN cDNA 5033428B15 gene	1.26	0.651	-1.31	0.436	-1.15	0.729	1.27	0.481	0.02
1438212_at	Usp37	ubiquitin specific peptidase 37	1.34	0.034	-1.37	0.29	-1.22	0.565	1.18	0.417	-0.02
1455750_at	BC053994	cDNA sequence BC053994	-1.05	0.651	-1.12	0.597	1.04	0.777	1.07	0.75	-0.01
1423237_at	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.04	0.697	-1.1	0.311	-1.07	0.448	1.41	0.248	0.07
1438510_a_at	Hars	histidyl-tRNA synthetase	-1	0.99	1.12	0.48	-1.3	0.22	1.58	0.403	0.1
1450956_at	Scd3	stearoyl-coenzyme A desaturase 3	-1.15	0.32	-1.01	0.981	1.03	0.948	1.47	0.487	0.09
1457750_at	D16Ertd780e	DNA segment, Chr 16, ERATO Doi 780, expressed	-1.06	0.912	1.02	0.97	-1.08	0.722	1.03	0.94	-0.02
1432930_at	4930453O09Rik	RIKEN cDNA 4930453O09 gene	1.1	0.802	-1.09	0.864	-1.15	0.71	1.89	0.292	0.19
1454858_x_at	Mettl7a	methyltransferase like 7A	-1.13	0.674	-1.32	0.141	1.25	0.329	1.48	0.225	0.07
1435212_at	P2rx2	purinergic receptor P2X, ligand-gated ion channel, 2	-1.43	0.485	1.2	0.604	-1	0.992	1.4	0.204	0.04
1448778_at	Sfrs4	splicing factor, arginine/serine-rich 4 (SRp75)	-1.18	0.39	-1.1	0.644	1.14	0.52	1.65	0.08	0.13
1436098_at	Bche	butyrylcholinesterase	1.15	0.51	-1.35	0.115	-1	0.992	1.26	0.62	0.02
1422535_at	Ccne2	cyclin E2	-1.18	0.604	1.13	0.652	-1.1	0.542	5.74	0.208	1.15
1438294_at	Atxn1	ataxin 1	1.05	0.702	-1.15	0.341	-1.04	0.804	1.2	0.523	0.02
1420601_at	Gcm1	glial cells missing homolog 1 (Drosophila)	1.28	0.367	-1.19	0.726	-1.29	0.649	1.24	0.484	0.01
1433459_x_at	Prss2	protease, serine, 2	1.14	0.873	-1.11	0.674	-1.18	0.777	1.14	0.784	0
1437714_x_at	Usp14	Ubiquitin specific peptidase 14	-1.27	0.171	-1.05	0.739	1.15	0.372	1.59	0.247	0.11
1441963_at	Prosapip1	ProSAPiP1 protein	1.08	0.542	-1.05	0.803	-1.16	0.375	1.68	0.324	0.14
1451207_at	Cbara1	calcium binding atopy-related autoantigen 1	1.12	0.696	-1.29	0.202	-1.01	0.944	1.16	0.544	0
1428837_at	Klhl14	kelch-like 14 (Drosophila)	1.08	0.702	-1.63	0.394	1.2	0.646	-3.35	0.061	-0.68
1416415_a_at	H2afz /// LOC66663	H2A histone family, member Z /// similar to H2A histone family, member Z /// simil	-1.12	0.124	1.07	0.4	-1.08	0.315	1.16	0.456	0.01
1459041_at	Snx12	Sorting nexin 12	1.41	0.664	-2.27	0.168	1.05	0.911	-1.39	0.586	-0.3
1449372_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	1.33	0.345	-1.08	0.619	-1.58	0.029	1.19	0.329	-0.03
1435859_x_at	Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	1.06	0.027	-1.01	0.79	-1.19	0.061	1.32	0.096	0.05
1460369_at	BC003267	cDNA sequence BC003267	1.12	0.594	1.11	0.778	-1.5	0.024	-1.01	0.966	-0.07
1457337_at	---	---	-1.4	0.611	1.36	0.66	-1.22	0.481	1.58	0.536	0.08
1433403_at	2810489J07Rik	RIKEN cDNA 2810489J07 gene	1.14	0.744	-1.02	0.898	-1.3	0.118	2.54	0.202	0.34
1455262_at	Thsd4	thrombospondin, type I, domain containing 4	-1.19	0.018	1.29	0.612	-1.32	0.031	1.42	0.179	0.05
1420106_at	D9Mgi7	DNA Segment, Chr 9, Mouse Genome Informatics 7	-1.13	0.655	1.29	0.014	-1.4	0.274	1.21	0.355	-0.01
1453115_at	Oaz3	ornithine decarboxylase antizyme 3	-2.28	0.3	1.43	0.382	1.02	0.973	-2.1	0.244	-0.48
1439909_at	Zfp521	zinc finger protein 521	-1.71	0.367	1.63	0.238	-1.48	0.168	1.06	0.776	-0.12
1425790_a_at	Grik2	glutamate receptor, ionotropic, kainate 2 (beta 2)	1.03	0.944	-1.06	0.725	-1.08	0.721	1.05	0.587	-0.02
1428217_at	1600012H06Rik	RIKEN cDNA 1600012H06 gene	1.03	0.55	1.01	0.844	-1.17	0.084	-1.22	0.205	-0.09
1441636_at	---	Transcribed locus	-1.4	0.429	1.12	0.707	1.06	0.668	-2.06	0.207	-0.32
1450128_at	Pla2g2a	phospholipase A2, group IIA (platelets, synovial fluid)	-1.36	0.724	-1.08	0.759	1.23	0.604	1.13	0.824	-0.02
1457618_at	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	-1.01	0.967	1.11	0.711	-1.25	0.477	1.12	0.716	-0.01
1448630_a_at	Sdhc	succinate dehydrogenase complex, subunit C, integral membrane protein	-1.09	0.461	-1.14	0.043	1.1	0.361	1.14	0.362	0
1427940_s_at	Mycbp	c-myc binding protein	-1.02	0.806	-1.14	0.323	1.04	0.92	1.16	0.613	0.01

1441064_at	E330039K12Rik	RIKEN cDNA E330039K12 gene	-1.64	0.084	-1.69	0.325	1.69	0.321	1.12	0.884	-0.13
1455354_at	Wdr22	WD repeat domain 22	1.03	0.918	-1.26	0.165	1.07	0.605	-1.52	0.297	-0.17
1418988_at	Pex7	peroxisome biogenesis factor 7	-1.06	0.388	-1.18	0.071	1.1	0.357	1.06	0.645	-0.02
1424702_a_at	2410024A21Rik	RIKEN cDNA 2410024A21 gene	-1.31	0.14	-1.05	0.771	1.18	0.356	1.05	0.773	-0.03
1416418_at	Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	-1.09	0.342	-1.3	0.019	1.2	0.249	1.49	0.105	0.08
1441809_at	A930009A15Rik	RIKEN cDNA A930009A15 gene	1.7	0.172	-2.52	0.079	-1.25	0.519	1.16	0.855	-0.23
1455875_x_at	Tm9sf2	transmembrane 9 superfamily member 2	1.01	0.914	1.06	0.502	-1.23	0.053	-1.21	0.329	-0.09
1423419_at	Lig3	ligase III, DNA, ATP-dependent	-1.11	0.2	-1.17	0.235	1.14	0.299	1.27	0.214	0.03
1449626_s_at	Acbd4	acyl-Coenzyme A binding domain containing 4	-1.16	0.366	-1.15	0.34	1.16	0.612	1.16	0.063	0
1417301_at	Fzd6	frizzled homolog 6 (Drosophila)	-1.15	0.524	-1.12	0.543	1.13	0.392	2.23	0.039	0.27
1417316_at	Them2	thioesterase superfamily member 2	-1	0.999	-1.12	0.544	1	1	1.17	0.356	0.01
1449483_at	Polk	polymerase (DNA directed), kappa	1.06	0.632	-1.07	0.708	-1.11	0.19	1.1	0.432	0
1436307_at	Myo9a	myosin IXa	-1.02	0.915	1.17	0.621	-1.35	0.061	1.22	0.333	0
1444971_at	Rbm5	RNA binding motif protein 5	1.06	0.849	1.23	0.524	-1.67	0.088	-1.37	0.457	-0.19
1454491_at	2900040J22Rik	RIKEN cDNA 2900040J22 gene	-1.14	0.873	1.16	0.692	-1.16	0.35	2.29	0.234	0.29
1442779_at	1700071K01Rik	RIKEN cDNA 1700071K01 gene	1.14	0.865	1.08	0.908	-1.47	0.412	-1.2	0.807	-0.12
1460445_at	Sfrs2ip	splicing factor, arginine/serine-rich 2, interacting protein	-1.07	0.681	-1.13	0.349	1.07	0.377	1.34	0.219	0.05
1439498_at	Punc	putative neuronal cell adhesion molecule	1.31	0.738	-2.1	0.112	1.11	0.884	-1.27	0.683	-0.24
1441960_x_at	5730494M16Rik	RIKEN cDNA 5730494M16 gene	-1.29	0.179	1.03	0.809	1.09	0.688	-1.23	0.331	-0.1
1434271_at	Gba2	glucosidase beta 2	1.06	0.724	-1.4	0.242	1.12	0.588	-1.08	0.599	-0.08
1427220_a_at	Svs5	seminal vesicle secretion 5	1.2	0.068	-1.91	0.078	1.17	0.738	-3.21	0.018	-0.69
1434071_a_at	Pelo	pelota homolog (Drosophila)	1.14	0.386	-1.11	0.506	-1.17	0.301	1.67	0.105	0.13
1450723_at	Isl1	ISL1 transcription factor, LIM/homeodomain	1.09	0.762	-1.16	0.6	-1.06	0.859	1.11	0.476	0
1428970_at	Nat13	N-acetyltransferase 13	-1.11	0.079	-1.2	0.059	1.17	0.16	1.46	0.301	0.08
1429478_at	6720463M24Rik	RIKEN cDNA 6720463M24 gene	-1.07	0.803	1.09	0.863	-1.16	0.472	2.04	0.193	0.23
1426473_at	Dnajc9	DnaJ (Hsp40) homolog, subfamily C, member 9	-1.12	0.191	-1.22	0.089	1.18	0.014	1.04	0.856	-0.03
1434948_at	Rab11fip2	RAB11 family interacting protein 2 (class I)	1.03	0.859	-1.19	0.042	1.02	0.878	-1.07	0.744	-0.05
1456232_at	Gmeb1	glucocorticoid modulatory element binding protein 1	-1.01	0.847	1.03	0.803	-1.15	0.567	1.43	0.061	0.08
1444409_at	Kbtbd8	Kelch repeat and BTB (POZ) domain containing 8	1.01	0.884	-1.07	0.614	-1.05	0.568	1.12	0.605	0
1457265_at	B230333C21Rik	RIKEN cDNA B230333C21 gene	1.11	0.094	-1.08	0.43	-1.18	0.129	1.4	0.181	0.07
1433012_at	Mga	MAX gene associated	-1.41	0.252	1.12	0.742	1.06	0.746	-1.16	0.474	-0.1
1425824_a_at	Pcsk4	proprotein convertase subtilisin/kexin type 4	-1.12	0.768	-1.11	0.762	1.1	0.443	1.14	0.578	0
1442578_at	---	---	-1.06	0.883	1.17	0.561	-1.29	0.1	2.78	0.202	0.4
1451787_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	-1.08	0.855	-1.08	0.829	1.05	0.815	4.93	0.053	0.95
1417206_at	Urod	uroporphyrinogen decarboxylase	-1.02	0.923	-1.18	0.064	1.07	0.63	4.85	0.181	0.93
1451305_at	Pgea1	PKD2 interactor, golgi and endoplasmic reticulum associated 1	1.15	0.731	-1.07	0.599	-1.23	0.347	1.14	0.691	0
1419863_at	Tmod1	Tropomodulin 1	-1.91	0.266	1.68	0.281	-1.45	0.341	4.84	0.212	0.79
1450628_at	Slc2a8	solute carrier family 2, (facilitated glucose transporter), member 8	-1.08	0.436	-1.2	0.138	1.14	0.418	1.41	0.094	0.07
1441194_at	Nrg3	Neuregulin 3	-1.68	0.28	1.62	0.404	-1.46	0.269	2.84	0.051	0.33
1444511_at	Slc41a1	solute carrier family 41, member 1	-1.73	0.43	-1.56	0.441	1.68	0.327	1.87	0.012	0.06
1420540_a_at	Rit1	Ras-like without CAAX 1	1.07	0.687	1.08	0.512	-1.34	0.108	-1.04	0.811	-0.06
1416135_at	Apex1	apurinic/apyrimidinic endonuclease 1	-1.27	0.032	1.09	0.333	1.01	0.942	-1.13	0.35	-0.07
1423907_a_at	Ndufs8	NADH dehydrogenase (ubiquinone) Fe-S protein 8	1.13	0.568	-1.17	0.291	-1.11	0.415	1.14	0.692	0
1460372_at	Duoxa1	dual oxidase maturation factor 1	-1.28	0.222	-1.39	0.072	1.39	0.196	2.42	0.31	0.29
1446142_at	---	---	1.38	0.064	-1.07	0.936	-1.7	0.411	1.11	0.79	-0.07
1455833_at	AU041783	expressed sequence AU041783	-1.15	0.491	1.04	0.897	-1.01	0.947	1.02	0.956	-0.03
1453641_at	Bcas1	breast carcinoma amplified sequence 1	1.31	0.704	-2.4	0.005	1.17	0.476	-1.83	0.143	-0.44
1460464_at	2700089E24Rik	RIKEN cDNA 2700089E24 gene	-1.03	0.857	-1.13	0.436	1.04	0.849	1.23	0.196	0.03
1453909_at	4930505N22Rik	RIKEN cDNA 4930505N22 gene	1.24	0.139	-1.19	0.558	-1.23	0.704	1.2	0.526	0.01
1460382_at	BC020535	cDNA sequence BC020535	-1.03	0.886	-1.28	0.193	1.14	0.571	1.01	0.956	-0.04
1449748_at	AA517023	expressed sequence AA517023	-2.43	0.411	1.26	0.647	1.22	0.292	-1	0.99	-0.24
1418887_a_at	D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	-1.06	0.233	-1.06	0.453	1.01	0.805	1.22	0.33	0.03
1436023_at	Bclaf1	BCL2-associated transcription factor 1	1.02	0.955	-1.23	0.329	1.06	0.815	-1.04	0.898	-0.05

1426217_at	2810441K11Rik	RIKEN cDNA 2810441K11 gene	1.09	0.696	-1.13	0.5	-1.08	0.555	1.15	0.617	0.01
1418856_a_at	Fanca	Fanconi anemia, complementation group A	-1.53	0.014	-1.23	0.478	1.43	0.091	1.15	0.646	-0.05
1434856_at	Ankrd44	ankyrin repeat domain 44	1.01	0.977	1.05	0.629	-1.19	0.177	-1.84	0.187	-0.24
1442984_at	C80060	expressed sequence C80060	1.22	0.759	-1.03	0.948	-1.41	0.343	1.66	0.417	0.11
1459713_s_at	Tmem16a	transmembrane protein 16A	-1.14	0.678	1.21	0.589	-1.23	0.416	1.3	0.368	0.04
1422780_at	Pxmp4	peroxisomal membrane protein 4	1.2	0.553	-1.32	0.142	-1.07	0.603	1.22	0.474	0.01
1422410_at	Ferd3l	Fer3-like (Drosophila)	-1.09	0.705	-2.28	0.214	1.54	0.371	1.64	0.216	-0.05
1436357_at	---	6 days neonate spleen cDNA, RIKEN full-length enriched library, clone:F430010L	1.15	0.433	-1.07	0.691	-1.23	0.136	1.46	0.401	0.08
1417112_at	Arl2bp	ADP-ribosylation factor-like 2 binding protein	-1.47	0.028	1.04	0.866	1.18	0.5	-1.35	0.216	-0.15
1434453_at	Polr3a	polymerase (RNA) III (DNA directed) polypeptide A	-1.26	0.123	1.04	0.596	1.06	0.729	-1.05	0.404	-0.05
1454244_at	Mcm10	minichromosome maintenance deficient 10 (S. cerevisiae)	-1.16	0.32	-2.18	0.172	1.58	0.435	1.1	0.565	-0.17
1416150_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	-1.03	0.673	1.01	0.96	-1.09	0.401	1.03	0.718	-0.02
1455031_at	---	---	-1.33	0.011	1.01	0.933	1.14	0.144	-1.22	0.236	-0.1
1438489_at	---	---	1.25	0.022	1	0.984	-1.56	0.076	-1.15	0.193	-0.11
1423610_at	Metap2	methionine aminopeptidase 2	-1.08	0.606	-1.08	0.178	1.05	0.577	2.63	0.207	0.38
1424142_at	Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associate	-1.27	0.59	-1.11	0.514	1.21	0.31	1.11	0.751	-0.02
1454321_at	1500005C15Rik	RIKEN cDNA 1500005C15 gene	-1.46	0.288	1.03	0.961	1.18	0.596	-1.02	0.94	-0.07
1425693_at	Braf	Braf transforming gene	1.05	0.813	-1.32	0.265	1.09	0.671	-1.04	0.843	-0.05
1449437_at	D6Wsu163e	DNA segment, Chr 6, Wayne State University 163, expressed	-1.07	0.29	1.08	0.38	-1.14	0.146	1.17	0.186	0.01
1443756_at	Serpini1	Serine (or cysteine) peptidase inhibitor, clade I, member 1	-1.08	0.896	-1.9	0.283	1.45	0.453	1.12	0.796	-0.1
1454801_at	Ankrd28	ankyrin repeat domain 28	1.11	0.357	-1.17	0.166	-1.07	0.374	1.5	0.348	0.09
1421815_at	Epdr2	ependymin related protein 2 (zebrafish)	-1.39	0.259	-1.09	0.823	1.26	0.386	4.32	0.293	0.78
1418472_at	Aspa	aspartoacylase (aminoacylase) 2	-1.05	0.786	-1.13	0.57	1.06	0.573	1.52	0.078	0.1
1440646_at	BC052040	CDNA sequence BC052040	1.2	0.367	1.01	0.977	-1.46	0.133	-1.08	0.761	-0.08
1453347_at	4930589P08Rik	RIKEN cDNA 4930589P08 gene	-1	0.993	-1.18	0.288	1.05	0.689	1.14	0.713	0
1432829_at	Eno1 /// LOC43318	enolase 1, alpha non-neuron /// similar to enolase 1, alpha non-neuron /// similar t	-1.78	0.082	1.1	0.772	1.23	0.118	-1.21	0.247	-0.16
1429614_at	Prpf18	PRP18 pre-mRNA processing factor 18 homolog (yeast)	-1.12	0.074	1.07	0.566	-1.08	0.64	1.46	0.347	0.08
1449267_at	3110023E09Rik	RIKEN cDNA 3110023E09 gene	-1.19	0.425	1.2	0.396	-1.16	0.478	1.38	0.013	0.06
1438549_a_at	Srr	serine racemase	-1.02	0.925	-1.13	0.401	1.03	0.92	1.1	0.693	0
1451468_s_at	Xpo5	exportin 5	-1.01	0.922	-1.27	0.074	1.12	0.469	1.3	0.366	0.04
1448245_at	Rpsa	ribosomal protein SA	1.01	0.55	1.08	0.201	-1.24	0.136	-1.4	0.007	-0.14
1432568_at	1700121K02Rik	RIKEN cDNA 1700121K02 gene	-1.05	0.941	1.38	0.098	-1.77	0.234	1.34	0.667	-0.02
1435573_at	Otud5	OTU domain containing 5	1.09	0.619	-1.03	0.844	-1.19	0.328	1.73	0.142	0.15
1438319_x_at	Fastkd2	FAST kinase domains 2	-1.26	0.373	-1.06	0.845	1.17	0.507	1.35	0.179	0.05
1453040_at	2810402A17Rik	RIKEN cDNA 2810402A17 gene	-1.27	0.71	1.07	0.667	1.05	0.851	-1.23	0.43	-0.1
1421040_a_at	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	-1.23	0.133	1.15	0.829	-1.07	0.816	1.37	0.096	0.06
1418015_at	Pum2	pumilio 2 (Drosophila)	1.37	0.215	1.08	0.679	-2.22	0.019	-1.1	0.67	-0.22
1439073_at	LOC627912	similar to Afadin (Af-6 protein)	-1.04	0.909	-1.22	0.658	1.12	0.51	1.29	0.507	0.04
1442629_at	Nt5c2	5'-nucleotidase, cytosolic II	1.15	0.535	-1.12	0.664	-1.17	0.437	1.16	0.486	0.01
1452518_a_at	Itk	IL2-inducible T-cell kinase	1.02	0.971	-1.67	0.469	1.28	0.509	-2.51	0.339	-0.47
1418710_at	Cd59a	CD59a antigen	1.04	0.57	-1.05	0.459	-1.1	0.451	2.63	0.239	0.38
1450945_at	Prkca	protein kinase C, alpha	-1.11	0.656	-1.41	0.049	1.29	0.129	1.12	0.591	-0.03
1437381_x_at	Gpr172b	G protein-coupled receptor 172B	-1.16	0.301	-1	0.872	1.04	0.602	1.07	0.736	-0.01
1416290_a_at	Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	1	0.993	1.05	0.827	-1.19	0.069	-1.17	0.552	-0.07
1433083_at	4930448K20Rik	RIKEN cDNA 4930448K20 gene	-1.26	0.24	-1.02	0.86	1.12	0.576	1.24	0.273	0.02
1432754_at	---	---	1.16	0.54	-1.45	0.338	1.05	0.927	-1.22	0.792	-0.12
1436412_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.2	0.61	1.03	0.906	1.04	0.743	-1.11	0.458	-0.06
1445969_at	---	Transcribed locus	1.02	0.905	1.22	0.542	-1.52	0.138	-1.04	0.953	-0.08
1418253_a_at	Hspa4l	heat shock protein 4 like	-1.2	0.282	-1.18	0.339	1.22	0.36	2.52	0.251	0.34
1435972_at	Cast	calpastatin	-1.01	0.882	1.07	0.391	-1.19	0.151	1.09	0.537	-0.01
1416902_a_at	Cox5b	cytochrome c oxidase, subunit Vb	-1.09	0.268	-1.08	0.332	1.06	0.388	1.42	0.158	0.08
1424126_at	Alas1	aminolevulinic acid synthase 1	-1.15	0.736	-1.76	0.281	1.46	0.082	1.19	0.087	-0.07
1431072_a_at	Ccdc50	coiled-coil domain containing 50	-1.27	0.125	1	0.986	1.11	0.581	-1.39	0.381	-0.14

1454841_at	4921511H13Rik	RIKEN cDNA 4921511H13 gene	-1.45	0.361	1.16	0.514	1.05	0.866	-1.43	0.093	-0.17
1421732_at	Glrp1	glutamine repeat protein 1	-1.43	0.02	-1.25	0.512	1.4	0.259	1.07	0.804	-0.05
1449955_at	Cacna1f	calcium channel, voltage-dependent, alpha 1F subunit	-1.8	0.262	-1.51	0.117	1.68	0.172	1.12	0.429	-0.13
1450306_at	Zp1	zona pellucida glycoprotein 1	-1.3	0.393	-1.18	0.537	1.28	0.583	1.06	0.922	-0.03
1423546_at	Zfp207	zinc finger protein 207	1.81	0.07	-1.56	0.118	-2.23	0.088	1.14	0.68	-0.21
1439709_at	---	---	1.16	0.84	-1.01	0.983	-1.33	0.533	1.38	0.435	0.05
1438216_at	Rreb1	ras responsive element binding protein 1	1.48	0.061	-1.41	0.212	-1.41	0.263	1.07	0.711	-0.07
1450398_at	Kcnk5	potassium channel, subfamily K, member 5	1.01	0.992	-1.13	0.786	1.01	0.987	-1.69	0.414	-0.2
1455968_x_at	Tmed2	transmembrane emp24 domain trafficking protein 2	1.14	0.116	-1.02	0.804	-1.28	0.07	1.06	0.735	-0.02
1417896_at	Tjp3	tight junction protein 3	1.01	0.92	-1.21	0.124	1.07	0.741	-1.38	0.183	-0.13
1418828_at	Thex1	three prime histone mRNA exonuclease 1	1	0.979	-1.1	0.424	-1.01	0.927	1.84	0.123	0.18
1426076_at	Cdc27	cell division cycle 27 homolog (S. cerevisiae)	-1.08	0.536	1.18	0.658	-1.25	0.421	1.36	0.421	0.05
1420776_a_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	-1.14	0.115	-1.2	0.302	1.19	0.238	1.29	0.347	0.03
1457024_x_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	-1.08	0.669	1.18	0.319	-1.26	0.198	1.18	0.058	0.01
1460375_at	0610038D11Rik	RIKEN cDNA 0610038D11 gene	-1.82	0.327	1.12	0.771	1.23	0.585	-1.82	0.096	-0.32
1455386_at	---	Transcribed locus	1.16	0.68	1.02	0.98	-1.39	0.159	-2.03	0.295	-0.31
1446129_at	Rab5a	RAB5A, member RAS oncogene family	1.33	0.514	-1.33	0.32	-1.23	0.222	1.1	0.557	-0.03
1446540_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930047B	-1.18	0.295	-1.41	0.199	1.35	0.402	1.55	0.056	0.07
1449588_at	Abca4	ATP-binding cassette, sub-family A (ABC1), member 4	-1.2	0.563	1.05	0.886	1.02	0.917	-1.05	0.933	-0.05
1456488_at	Wdr33	WD repeat domain 33	-1.97	0.23	-1.28	0.151	1.61	0.158	1.77	0.224	0.03
1453050_at	Gins3	GINS complex subunit 3 (Psf3 homolog)	-1.12	0.709	1.11	0.642	-1.12	0.617	1.56	0.369	0.11
1459752_at	Mcc	mutated in colorectal cancers	-1.64	0.442	1.5	0.558	-1.26	0.732	1.09	0.211	-0.08
1433348_at	2810414N06Rik	RIKEN cDNA 2810414N06 gene	-1.63	0.683	1.72	0.472	-1.77	0.287	1.52	0.468	-0.04
1441248_at	---	---	-1.07	0.742	1.13	0.32	-1.19	0.14	2.44	0.233	0.33
1429130_at	Ttc25	tetratricopeptide repeat domain 25	1.01	0.968	-1.27	0.415	1.1	0.471	-1.39	0.506	-0.14
1448604_at	Uck2	uridine-cytidine kinase 2	-1.28	0.327	-1.07	0.632	1.19	0.271	1.39	0.407	0.06
1425858_at	Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	-1.22	0.198	-1.16	0.258	1.22	0.676	1.16	0.181	0
1434168_at	Peo1	progressive external ophthalmoplegia 1 (human)	-1.14	0.543	-1.13	0.32	1.14	0.33	1.16	0.559	0.01
1441924_x_at	Edn3	endothelin 3	-1.72	0.007	1.17	0.501	1.15	0.628	-1.7	0.148	-0.28
1453061_at	2610018O07Rik	RIKEN cDNA 2610018O07 gene	1.01	0.929	-1.13	0.336	1.01	0.913	-1.28	0.45	-0.1
1425031_at	Fcmd	Fukuyama type congenital muscular dystrophy homolog (human)	1.09	0.836	1	0.994	-1.23	0.232	-1.24	0.561	-0.1
1448108_at	Serinc1	serine incorporator 1	-1.03	0.542	1.01	0.889	-1.09	0.349	1.35	0.117	0.06
1459288_at	Kcnd2	Potassium voltage-gated channel, Shal-related family, member 2	-1.51	0.064	-1.04	0.941	1.27	0.442	1.46	0.271	0.05
1434238_at	Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.09	0.515	1.08	0.38	-1.1	0.297	1.12	0.168	0
1436227_at	Lefty2	Left-right determination factor 2	-1.27	0.647	-2.98	0.175	1.78	0.355	1.47	0.452	-0.25
1451396_at	Pomt2	protein-O-mannosyltransferase 2	-1.06	0.611	-1.07	0.711	1.02	0.884	1.07	0.73	-0.01
1423289_a_at	1810029B16Rik	RIKEN cDNA 1810029B16 gene	-1.17	0.252	-1.08	0.209	1.11	0.713	1.01	0.96	-0.03
1426492_at	Tdp1	tyrosyl-DNA phosphodiesterase 1	-1.11	0.254	1.1	0.407	-1.11	0.643	1.29	0.204	0.04
1429729_at	Syt11	synaptotagmin XI	-1.06	0.923	1.15	0.846	-1.24	0.611	1.3	0.325	0.04
1416389_a_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	-1.18	0.004	-1.01	0.919	1.07	0.524	1.28	0.495	0.04
1434374_at	B930006L02Rik	RIKEN cDNA B930006L02 gene	1.01	0.977	-1.29	0.07	1.13	0.641	-1.23	0.343	-0.1
1433038_at	---	Visual cortex cDNA, RIKEN full-length enriched library, clone:K230311O21 produ	1.52	0.527	1	0.998	-2.65	0.19	-1.4	0.166	-0.38
1427033_at	Dnmbp	dynamin binding protein	1.04	0.707	-1.29	0.218	1.08	0.594	-1.45	0.105	-0.15
1448296_x_at	Tuba3 /// Tuba7 ///	tubulin, alpha 3 /// tubulin, alpha 7 /// similar to tubulin, alpha 1	1.13	0.882	-1.24	0.429	-1.03	0.908	1.21	0.643	0.02
1430161_at	Dlst	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate comple	-1.03	0.742	-1.09	0.705	1.02	0.938	1.02	0.941	-0.02
1456106_x_at	Sdccag3	serologically defined colon cancer antigen 3	-1.15	0.307	1.01	0.939	1.02	0.872	-1.29	0.117	-0.1
1447925_at	D630033A02Rik	RIKEN cDNA D630033A02 gene	-1.18	0.608	1.18	0.446	-1.14	0.863	3.08	0.003	0.48
1446122_at	4732416N19Rik	RIKEN cDNA 4732416N19 gene	-3.01	0.146	-1.59	0.22	1.94	0.004	1.19	0.296	-0.37
1440951_x_at	Wapal	Wings apart-like homolog (Drosophila)	1.81	0.609	-1.24	0.408	-3.46	0.099	1.77	0.496	-0.28
1449092_at	Ppm1d	protein phosphatase 1D magnesium-dependent, delta isoform	-1.32	0.191	-1.05	0.753	1.19	0.148	1.71	0.335	0.13
1456436_x_at	Rps20	ribosomal protein S20	1.05	0.386	1.05	0.453	-1.23	0.036	-1.3	0.023	-0.11
1432418_a_at	Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	-1.05	0.914	-1.46	0.112	1.26	0.644	1.85	0.332	0.15
1439955_at	Rad9b	RAD9 homolog B (S. cerevisiae)	1.13	0.671	-1.27	0.399	-1.01	0.883	1.29	0.49	0.04

1451208_at	Etf1	eukaryotic translation termination factor 1	1.18	0.242	-1.07	0.434	-1.26	0.246	1.27	0.405	0.03
1433658_x_at	Pcbp4	poly(rC) binding protein 4	1.07	0.196	1.01	0.951	-1.22	0.19	-1.63	0.186	-0.19
1456641_at	1190007F08Rik	RIKEN cDNA 1190007F08 gene	1.18	0.486	-1.12	0.745	-1.2	0.591	1.54	0.338	0.1
1444544_at	Prim1	DNA primase, p49 subunit	1.18	0.804	-1.2	0.594	-1.12	0.473	1.94	0.147	0.2
1452590_a_at	Plac9	placenta specific 9	1.1	0.536	1.21	0.08	-1.69	0.01	-1.44	0.258	-0.2
1428565_at	Unkl	unkempt-like (Drosophila)	1.02	0.771	1	0.98	-1.13	0.428	-1.09	0.559	-0.05
1452813_a_at	5033428A16Rik	RIKEN cDNA 5033428A16 gene	-1.03	0.562	1.08	0.531	-1.18	0.184	1.25	0.123	0.03
1451723_at	Cnot6l	CCR4-NOT transcription complex, subunit 6-like	1.11	0.42	-1.31	0.04	1.03	0.826	-1.24	0.224	-0.1
1442007_at	9830124H08Rik	RIKEN cDNA 9830124H08 gene	1.07	0.737	1.1	0.44	-1.36	0.09	-1.35	0.112	-0.14
1441983_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.12	0.886	-1.06	0.901	-1.18	0.545	1.09	0.562	-0.01
1415754_at	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	1.06	0.542	-1.1	0.403	-1.07	0.604	1.2	0.296	0.02
1451056_at	Psmd7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.04	0.679	-1.06	0.788	-1.09	0.676	1.1	0.783	0
1437953_at	Prei4	preimplantation protein 4	-1.17	0.325	-1.11	0.661	1.15	0.29	1.54	0.153	0.1
1428493_at	2610511M17Rik ///	RIKEN cDNA 2610511M17 gene /// similar to signal-induced proliferation-associa	1.03	0.684	-1.1	0.608	-1.03	0.871	1.13	0.483	0.01
1437283_at	Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	1.07	0.807	-1.12	0.521	-1.06	0.69	1.31	0.275	0.05
1431356_at	6430710C18Rik	RIKEN cDNA 6430710C18 gene	-1.99	0.577	-1.02	0.882	1.42	0.602	1.25	0.668	-0.08
1421824_at	Bace1	beta-site APP cleaving enzyme 1	1.03	0.9	-1.15	0.025	1	0.976	-1.25	0.084	-0.09
1453471_at	4833421E05Rik	RIKEN cDNA 4833421E05 gene	-1.17	0.763	1.04	0.831	1	0.983	-1.58	0.451	-0.17
1454886_x_at	---	---	1.67	0.392	-1.37	0.569	-1.97	0.421	1.48	0.547	-0.05
1452217_at	Ahnak	AHNAK nucleoprotein (desmoyokin)	1.09	0.393	1.05	0.781	-1.31	0.055	-1.1	0.824	-0.07
1447235_at	Sh3rf1	SH3 domain containing ring finger 1	1.55	0.542	-1.05	0.945	-2.48	0.101	1.38	0.422	-0.15
1460403_at	Psip1	PC4 and SFRS1 interacting protein 1	-1.08	0.246	-1.11	0.608	1.08	0.601	1.15	0.598	0.01
1458461_at	E330021D16Rik	RIKEN cDNA E330021D16 gene	-1.18	0.647	1.06	0.68	1	0.988	-1.16	0.343	-0.07
1429164_at	Prss36	protease, serine, 36	-1.31	0.102	-1.03	0.822	1.17	0.032	1.08	0.616	-0.02
1444328_at	Clta	clathrin, light polypeptide (Lca)	1.06	0.636	-1.29	0.021	1.07	0.796	-1.35	0.154	-0.13
1433493_at	5730472N09Rik	RIKEN cDNA 5730472N09 gene	-1.21	0.496	-1.03	0.796	1.11	0.371	1.99	0.115	0.21
1433767_at	1110018G07Rik	RIKEN cDNA 1110018G07 gene	-1.12	0.058	-1.05	0.159	1.06	0.293	1.27	0.388	0.04
1452213_at	Tex2	testis expressed gene 2	-1.07	0.622	-1.08	0.176	1.04	0.559	1.29	0.249	0.05
1446278_at	Utx	Ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1.34	0.077	-1.36	0.292	-1.2	0.487	1.51	0.083	0.07
1427842_at	Krtap6-3	keratin associated protein 6-3	-1.21	0.748	1.06	0.922	1.02	0.872	-1.37	0.603	-0.12
1421487_a_at	Nck1	non-catalytic region of tyrosine kinase adaptor protein 1	1.04	0.621	1.1	0.561	-1.31	0.099	-1.67	0.076	-0.21
1438431_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	-1.52	0.4	-1.91	0.155	1.72	0.261	1.33	0.266	-0.09
1452391_at	Cxadr	coxsackievirus and adenovirus receptor	-1.22	0.311	-1.08	0.866	1.16	0.712	1.28	0.321	0.04
1427931_s_at	Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	1.02	0.946	-1.24	0.333	1.08	0.771	-1.18	0.605	-0.08
1446507_at	Prnp	Prion protein	-1.57	0.092	1.41	0.314	-1.16	0.527	3.27	0.295	0.49
1418598_at	Ubox5	U box domain containing 5	1.07	0.624	-1.09	0.629	-1.09	0.513	1.24	0.34	0.03
1440836_at	Setd1b	SET domain containing 1B	-1.13	0.307	-1.14	0.422	1.14	0.678	1.01	0.928	-0.03
1438632_x_at	Tnp1	transition protein 1	-1.38	0.5	-1.09	0.902	1.27	0.618	1.16	0.846	-0.01
1420744_at	Chrnb2	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	-1.03	0.911	-1.08	0.737	1.01	0.948	1.38	0.29	0.07
1416228_at	Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	-1.03	0.846	1.03	0.822	-1.1	0.482	1	0.991	-0.03
1450150_a_at	Rpl13	ribosomal protein L13	1.03	0.507	1.08	0.366	-1.26	0.038	-1.44	0.021	-0.15
1422869_at	Mertk	c-mer proto-oncogene tyrosine kinase	1.11	0.697	1.11	0.323	-1.46	0.164	-1.07	0.858	-0.08
1421225_a_at	Slc4a4	solute carrier family 4 (anion exchanger), member 4	-1.1	0.734	1.04	0.599	-1.04	0.808	1.34	0.214	0.06
1417983_a_at	Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	1.01	0.933	1.17	0.458	-1.37	0.017	-1.04	0.897	-0.06
1423825_at	Gpr177	G protein-coupled receptor 177	-1.26	0.166	1.32	0.083	-1.25	0.179	1.07	0.733	-0.03
1427569_a_at	Utrn	utrophin	-1.21	0.68	-1.19	0.512	1.24	0.537	1.21	0.63	0.01
1437354_at	C230091D08Rik	RIKEN cDNA C230091D08 gene	1.19	0.321	-1.19	0.228	-1.14	0.529	1.41	0.386	0.07
1447649_x_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	1.25	0.398	1.11	0.666	-1.8	0.012	-1.64	0.263	-0.27
1424500_at	Utp6	UTP6, small subunit (SSU) processome component, homolog (yeast)	-1.15	0.101	-1.08	0.732	1.12	0.671	1.02	0.952	-0.03
1445920_at	---	---	-1.75	0.465	-1	0.996	1.34	0.033	2.09	0.014	0.17
1422796_at	Prep	prolyl endopeptidase	-1.21	0.24	-1.14	0.236	1.21	0.415	1.15	0.417	0
1454434_at	9030607J07Rik	RIKEN cDNA 9030607J07 gene	-1.37	0.3	1.43	0.519	-1.33	0.486	1.46	0.563	0.04
1418963_at	2310047O13Rik	RIKEN cDNA 2310047O13 gene	-1.21	0.202	-1.05	0.553	1.13	0.281	1.1	0.446	-0.01

1448307_at	Dscr2	Down syndrome critical region homolog 2 (human)	-1.07	0.054	-1.16	0.068	1.11	0.409	1.14	0.421	0.01
1436292_a_at	Oaz1	ornithine decarboxylase antizyme	-1.1	0.296	-1.13	0.167	1.11	0.323	1.01	0.897	-0.03
1419800_at	---	Transcribed locus	-1.05	0.939	-1.07	0.885	1.02	0.979	1.52	0.566	0.1
1427202_at	4833442J19Rik	RIKEN cDNA 4833442J19 gene	1.11	0.706	1.07	0.813	-1.38	0.22	-1.18	0.557	-0.09
1451519_at	Rnf2	ring finger protein 2	-1.22	0.034	1.06	0.707	1.02	0.66	-1.47	0.035	-0.15
1434515_at	Ncoa1	nuclear receptor coactivator 1	1.01	0.949	1	0.983	-1.12	0.357	-1.15	0.623	-0.06
1454896_at	---	---	1.02	0.869	1.01	0.944	-1.13	0.218	-1.03	0.825	-0.04
1426991_at	1810048J11Rik	RIKEN cDNA 1810048J11 gene	-1.12	0.622	-1.22	0.352	1.19	0.385	1.06	0.647	-0.02
1459597_at	Mtpn	myotrophin	1.12	0.827	1.14	0.751	-1.54	0.055	-1.69	0.045	-0.24
1433615_at	Tmem117	transmembrane protein 117	-1.61	0.006	1.1	0.813	1.18	0.519	-1.81	0.476	-0.28
1459972_x_at	Sez6	seizure related gene 6	-1.32	0.382	-1.02	0.961	1.17	0.598	1.68	0.055	0.13
1431891_at	Zswim5	zinc finger, SWIM domain containing 5	-1.17	0.636	-1	0.998	1.05	0.792	1.19	0.351	0.02
1455964_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	-1.06	0.702	1.05	0.877	-1.09	0.59	1.11	0.627	0
1426145_at	---	---	-1.21	0.574	1.12	0.674	-1.04	0.932	1.55	0.426	0.11
1429649_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), m	-1.01	0.887	-1.24	0	1.11	0.557	1.12	0.427	-0.01
1449168_a_at	Akap2	A kinase (PRKA) anchor protein 2	-1.25	0.483	1.1	0.051	1.01	0.983	-1.44	0.2	-0.14
1439712_at	Ints10	integrator complex subunit 10	1.41	0.637	-1.35	0.558	-1.31	0.487	1.08	0.911	-0.05
1420712_a_at	Hpn	hepsin	-1.04	0.28	1.02	0.846	-1.07	0.625	2.97	0.128	0.47
1438620_x_at	Sfrp1	secreted frizzled-related sequence protein 1	1.31	0.325	-1.4	0.609	-1.13	0.673	1.15	0.552	-0.02
1418072_at	Hist1h2bc	histone 1, H2bc	-1.15	0.059	-1.08	0.399	1.11	0.31	1.21	0.583	0.02
1448614_at	Nt5c2	5'-nucleotidase, cytosolic II	1.07	0.793	-1.34	0.452	1.09	0.8	-1.35	0.273	-0.13
1453692_at	4930581F22Rik	RIKEN cDNA 4930581F22 gene	1.09	0.657	-1.08	0.455	-1.11	0.703	1.15	0.521	0.01
1415710_at	Cox18	COX18 cytochrome c oxidase assembly homolog (S. cerevisiae)	-1.1	0.28	-1.09	0.326	1.08	0.233	1.01	0.955	-0.03
1420657_at	Ucp3	uncoupling protein 3 (mitochondrial, proton carrier)	-1.12	0.555	-1.15	0.471	1.15	0.533	2.34	0.107	0.3
1417123_at	Vav3	vav 3 oncogene	1.38	0.41	-1.86	0.4	-1.01	0.963	1.2	0.185	-0.07
1432580_at	Rshl2a	radial spokehead-like 2A	-1.18	0.81	1.13	0.788	-1.08	0.738	1.37	0.207	0.06
1448927_at	Kcnn2	potassium intermediate/small conductance calcium-activated channel, subfamily	1.03	0.806	-1.21	0.218	1.05	0.89	-1.05	0.904	-0.04
1423196_at	Nedd1	neural precursor cell expressed, developmentally down-regulated gene 1	-1.08	0.516	-1.19	0.405	1.15	0.548	1.59	0.349	0.12
1453510_s_at	4930589M24Rik	RIKEN cDNA 4930589M24 gene	-1.19	0.384	1.46	0.29	-1.64	0.076	2.08	0.038	0.18
1437437_x_at	Dnpep	aspartyl aminopeptidase	-1.22	0.006	1.03	0.64	1.06	0.577	-1.24	0.058	-0.09
1450216_at	Pcdhb16	protocadherin beta 16	-1.35	0.131	1.41	0.467	-1.31	0.354	1.5	0.319	0.06
1449981_a_at	Nat2	N-acetyltransferase 2 (arylamine N-acetyltransferase)	-1.14	0.747	1.07	0.351	-1.04	0.777	1.05	0.792	-0.02
1426605_at	Brcc3	BRCA1/BRCA2-containing complex, subunit 3	-1.11	0.715	-1.07	0.837	1.07	0.672	1.08	0.825	-0.01
1431433_at	Sbf2	SET binding factor 2	1.29	0.472	1.08	0.739	-1.88	0.048	-1.39	0.499	-0.22
1415672_at	Golga7	golgi autoantigen, golgin subfamily a, 7	-1.08	0.199	1.07	0.174	-1.1	0.025	1.12	0.255	0
1431488_at	4833428L15Rik	RIKEN cDNA 4833428L15 gene	-1.25	0.048	1.44	0.488	-1.51	0.233	1.5	0.623	0.05
1417784_at	Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	1.07	0.754	-1.48	0.216	1.16	0.68	-1.22	0.737	-0.12
1416345_at	Timm8a1	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	-1.09	0.576	-1.14	0.13	1.12	0.61	1.67	0.181	0.14
1426233_at	Map2k4	mitogen activated protein kinase kinase 4	-1.14	0.023	-1.07	0.571	1.1	0.473	1.16	0.54	0.01
1454290_at	4930573O21Rik	RIKEN cDNA 4930573O21 gene	-1.24	0.675	1.08	0.748	1.02	0.957	-1.49	0.351	-0.16
1444943_at	Sh3rf1	SH3 domain containing ring finger 1	-1.14	0.618	1.59	0.051	-2.26	0.021	1.27	0.388	-0.13
1448567_at	Tmem115	transmembrane protein 115	1.12	0.209	-1.32	0.034	1.03	0.852	-1.3	0.137	-0.12
1417004_at	Tsg101	tumor susceptibility gene 101	-1.11	0.341	1.1	0.521	-1.09	0.577	1.12	0.631	0
1416571_at	Traf4	Tnf receptor associated factor 4	-1.04	0.909	1.1	0.839	-1.18	0.604	2.69	0.201	0.39
1417648_s_at	Snx5	sorting nexin 5	-1.15	0.583	1.04	0.377	1	0.967	-1.42	0.251	-0.13
1430994_at	5-Mar	membrane-associated ring finger (C3HC4) 5	-1.89	0.078	-1.01	0.979	1.39	0.428	2.63	0.177	0.28
1456206_at	Alkbh3	AlkB, alkylation repair homolog 3 (E. coli)	1.82	0.455	-1.53	0.444	-2.28	0.371	1.32	0.428	-0.17
1455131_at	Opa3	optic atrophy 3 (human)	-1.01	0.919	-1.26	0.023	1.13	0.353	1.13	0.637	0
1455998_at	LOC667118 /// LOC	similar to Zinc finger BED domain containing protein 4 /// similar to Zinc finger BE	1.3	0.052	1.18	0.218	-2.35	0.024	-1.13	0.686	-0.25
1437346_x_at	Igh-VJ558	Immunoglobulin heavy chain (J558 family)	-1.04	0.849	1.43	0.412	-1.93	0.113	1.1	0.873	-0.11
1451424_at	Gabrp	gamma-aminobutyric acid (GABA-A) receptor, pi	1.28	0.19	-1.74	0.387	1.05	0.878	-1.03	0.706	-0.11
1445336_at	1110032A03Rik	RIKEN cDNA 1110032A03 gene	-1.38	0.168	1.25	0.478	-1.07	0.84	2.98	0.313	0.44
1447566_at	Hdac4	Histone deacetylase 4	-1.21	0.828	-1.28	0.661	1.3	0.658	1.82	0.093	0.16

1438573_at	Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	1.09	0.705	-1.18	0.353	-1.03	0.91	1.14	0.264	0.01
1454292_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	-1.61	0.08	1.22	0.76	1.07	0.901	-1.32	0.723	-0.16
1458127_at	Cdon	Cell adhesion molecule-related/down-regulated by oncogenes	1.09	0.846	1.07	0.819	-1.32	0.21	-1.03	0.939	-0.05
1437168_at	Srrp	serine-arginine repressor protein	-3.17	0.268	1.53	0.461	1.07	0.929	-2.06	0.152	-0.66
1432147_at	4930447F24Rik	RIKEN cDNA 4930447F24 gene	1.25	0.452	-1.17	0.78	-1.24	0.441	1.06	0.919	-0.03
1417753_at	Pkd2	polycystic kidney disease 2	-1	0.967	1.1	0.043	-1.23	0.092	1	0.998	-0.03
1426317_at	Stard6	StAR-related lipid transfer (START) domain containing 6	1.03	0.82	-1.22	0.583	1.05	0.548	-1.26	0.262	-0.1
1447100_s_at	5730508B09Rik	RIKEN cDNA 5730508B09 gene	-1.16	0.515	1.34	0.005	-1.42	0.042	3.24	0.209	0.5
1452662_a_at	Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	1.01	0.75	-1.09	0.321	-1.02	0.885	1.08	0.75	0
1418975_at	Nckipsd	NCK interacting protein with SH3 domain	-1.15	0.25	-1.09	0.739	1.12	0.584	1.07	0.455	-0.01
1457061_at	Glcci1	glucocorticoid induced transcript 1	-1.5	0.477	-1.12	0.802	1.35	0.195	1.1	0.819	-0.04
1441254_at	1810008K04Rik	RIKEN cDNA 1810008K04 gene	-1.32	0.103	1.26	0.519	-1.12	0.487	1.4	0.281	0.06
1455101_at	---	Mus musculus, clone IMAGE:2647821, mRNA	-1.1	0.451	1.36	0.086	-1.55	0.044	1.32	0.419	0.01
1449692_at	Prkcz	protein kinase C, zeta	-1.08	0.431	1.16	0.655	-1.21	0.501	1.75	0.204	0.15
1442200_at	1810063B07Rik	RIKEN cDNA 1810063B07 gene	1.07	0.885	1.07	0.783	-1.3	0.275	-1.32	0.178	-0.12
1417994_a_at	Accn1	amiloride-sensitive cation channel 1, neuronal (degenerin)	-1.28	0.697	1.18	0.426	-1.06	0.853	1.2	0.177	0.01
1426459_s_at	AW549877	expressed sequence AW549877	-1.18	0.259	1.05	0.634	1.01	0.902	-1.41	0.414	-0.13
1422304_at	Lcn4	lipocalin 4	-1.15	0.79	-1.4	0.516	1.33	0.451	1.17	0.761	-0.01
1416543_at	Nfe2l2	nuclear factor, erythroid derived 2, like 2	-1.03	0.806	1.01	0.957	-1.07	0.501	1.14	0.332	0.01
1427090_at	Zbed4	zinc finger, BED domain containing 4	-1.16	0.292	1.08	0.625	-1.03	0.707	1.74	0.164	0.16
1447871_at	---	Transcribed locus	1.11	0.597	-1.25	0.219	1	0.999	-1.8	0.582	-0.23
1428130_at	Lman1	lectin, mannose-binding, 1	1.13	0.769	-1.18	0.275	-1.07	0.809	1.55	0.092	0.11
1453629_at	4930478L05Rik	RIKEN cDNA 4930478L05 gene	-1.29	0.436	1.19	0.691	-1.06	0.929	2.59	0.256	0.36
1435457_at	Pdzd4	PDZ domain containing 4	1.02	0.813	1.41	0.54	-2.08	0.021	-1.33	0.147	-0.25
1459208_at	AU021889	expressed sequence AU021889	-1.6	0.194	1.54	0.423	-1.33	0.274	1.02	0.977	-0.1
1460209_at	Usp39	ubiquitin specific peptidase 39	1.05	0.743	-1.12	0.43	-1.04	0.582	1.29	0.487	0.05
1443462_at	D8Ertd572e	DNA segment, Chr 8, ERATO Doi 572, expressed	-1.4	0.619	1.51	0.274	-1.46	0.191	1.45	0.201	0.03
1441612_at	Zfp148	Zinc finger protein 148	-1.14	0.419	1.02	0.955	1.01	0.911	-1.43	0.14	-0.13
1457496_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643051	-1.18	0.42	1.08	0.665	-1.02	0.966	1.41	0.413	0.07
1437738_at	Atp2c1	ATPase, Ca++-sequestering	1.05	0.684	-1.19	0.335	1.02	0.803	-1.09	0.567	-0.05
1428312_at	Lrrc57	leucine rich repeat containing 57	1.07	0.548	-1.09	0.351	-1.09	0.345	1.25	0.162	0.04
1442930_at	AW061147	expressed sequence AW061147	1.1	0.801	-1.06	0.9	-1.16	0.784	2.03	0.097	0.23
1417777_at	Ltb4dh	leukotriene B4 12-hydroxydehydrogenase	-1.09	0.702	1.18	0.588	-1.24	0.423	1.15	0.746	0
1427536_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643056	1.05	0.894	-1.63	0.122	1.25	0.062	-1.39	0.058	-0.18
1432276_at	4930519F16Rik	RIKEN cDNA 4930519F16 gene	-2.36	0.05	-1.25	0.64	1.69	0.09	1.22	0.733	-0.18
1438005_at	B230315F11Rik	RIKEN cDNA B230315F11 gene	1.14	0.47	-1.14	0.389	-1.11	0.652	1.29	0.468	0.04
1416007_at	Satb1	special AT-rich sequence binding protein 1	1.08	0.694	-1.39	0.348	1.11	0.624	-2.86	0.054	-0.51
1447231_at	Slc8a1	Solute carrier family 8 (sodium/calcium exchanger), member 1	1.16	0.584	1.21	0.729	-1.86	0.11	-1.04	0.931	-0.13
1458291_at	Inhba	Inhibin beta-A	1.32	0.345	-1.26	0.367	-1.26	0.024	1.22	0.372	0.01
1427697_a_at	Trp73	transformation related protein 73	1.05	0.919	-1.68	0.071	1.27	0.136	-1.16	0.86	-0.13
1449197_at	2310040A13Rik	RIKEN cDNA 2310040A13 gene	-1.17	0.06	1.19	0.115	-1.15	0.118	1.07	0.723	-0.01
1441090_at	Numa1	Nuclear mitotic apparatus protein 1	-1.31	0.453	1.01	0.967	1.14	0.247	-1.14	0.563	-0.07
1424164_at	Mrpl50	mitochondrial ribosomal protein L50	-1.15	0.587	-1.01	0.949	1.05	0.809	1.39	0.37	0.07
1424552_at	Casp8	caspase 8	1.01	0.872	-1.25	0.142	1.1	0.617	-1.35	0.384	-0.12
1422983_at	Itgb6	integrin beta 6	1.51	0.521	-1.33	0.697	-1.54	0.501	2.54	0.002	0.3
1428471_at	Sorbs1	sorbin and SH3 domain containing 1	-1.14	0.156	-1.15	0.52	1.16	0.647	1.82	0.182	0.17
1431027_at	2810455O05Rik	RIKEN cDNA 2810455O05 gene	-1.05	0.943	-1.3	0.521	1.19	0.742	1.23	0.61	0.02
1432893_at	9130011L11Rik	RIKEN cDNA 9130011L11 gene	-1.89	0.048	1.75	0.27	-1.59	0.425	1.04	0.923	-0.17
1418307_a_at	Sbp	spermine binding protein	1.39	0.358	-2.12	0.286	1.05	0.928	-1.22	0.054	-0.22
1433943_at	BC063749	cDNA sequence BC063749	1.05	0.635	-1.24	0.582	1.06	0.442	-2.06	0.155	-0.3
1455513_at	Taf1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.07	0.777	1.13	0.264	-1.18	0.413	1.31	0.232	0.05
1419388_at	Tm4sf20	transmembrane 4 L six family member 20	-1.26	0.724	1.06	0.891	1.06	0.922	-2.02	0.23	-0.29
1431374_at	6330407A03Rik	RIKEN cDNA 6330407A03 gene	1.06	0.831	1.11	0.476	-1.35	0.229	-1.4	0.481	-0.14

1455398_at	Lrrc8c	leucine rich repeat containing 8 family, member C	-1.01	0.869	1.04	0.861	-1.14	0.156	1.22	0.179	0.03
1455391_at	Rad23a	RAD23a homolog (S. cerevisiae)	1.01	0.976	-1.07	0.591	-1.03	0.845	2.39	0.184	0.33
1428313_at	Zswim3	zinc finger, SWIM domain containing 3	-1.22	0.399	-1.2	0.358	1.26	0.072	1.26	0.253	0.02
1444734_at	A330001L22Rik	RIKEN cDNA A330001L22 gene	-1.03	0.536	1.17	0.652	-1.3	0.379	1.28	0.558	0.03
1428365_a_at	Prss15	protease, serine, 15	-1.12	0.226	-1.41	0.019	1.31	0.203	1.59	0.289	0.09
1428042_at	MGC41410	Similar to RIKEN cDNA B430319H21 gene	1.08	0.903	-1.02	0.97	-1.17	0.672	1.46	0.476	0.09
1453053_at	2610036L11Rik	RIKEN cDNA 2610036L11 gene	-1.19	0.475	-1.1	0.752	1.17	0.352	2.19	0.311	0.27
1435231_at	Coq4	coenzyme Q4 homolog (yeast)	-1.06	0.53	1.04	0.454	-1.08	0.539	1.11	0.604	0
1447440_at	Nutf2	Nuclear transport factor 2	-1.39	0.077	-1.16	0.472	1.33	0.324	1.1	0.876	-0.03
1446794_at	Gpr176	G protein-coupled receptor 176	-1.33	0.217	1.21	0.602	-1.05	0.901	1.07	0.899	-0.03
1456118_at	Mettl2	methyltransferase like 2	-1.07	0.646	-1.05	0.383	1.02	0.619	1.43	0.345	0.08
1450576_a_at	Sf3a2	splicing factor 3a, subunit 2	-1.2	0.515	-1.24	0.09	1.27	0.272	1.28	0.391	0.03
1433257_at	A330102K18Rik	RIKEN cDNA A330102K18 gene	1.84	0.149	-2.47	0.339	-1.5	0.155	1.84	0.198	-0.07
1426254_at	Tm2d1	TM2 domain containing 1	1.14	0.643	1.01	0.838	-1.31	0.094	-1.05	0.762	-0.05
1456736_x_at	5230400G24Rik	RIKEN cDNA 5230400G24 gene	-1.09	0.043	1.1	0.336	-1.11	0.388	1	0.987	-0.03
1441865_at	---	---	1.54	0.54	-1.29	0.613	-1.66	0.223	1.24	0.408	-0.04
1460697_s_at	2610209M04Rik	RIKEN cDNA 2610209M04 gene	1.07	0	-1.11	0.38	-1.06	0.595	1.04	0.713	-0.02
1418332_a_at	Agtpbp1 /// LOC671	ATP/GTP binding protein 1 /// similar to ATP/GTP binding protein 1	1.15	0.196	1.01	0.965	-1.31	0.145	-1.16	0.449	-0.08
1458267_at	Zfp248	zinc finger protein 248	-1.9	0.601	1.12	0.758	1.27	0.549	-1.33	0.598	-0.21
1434209_at	Prmt6	protein arginine N-methyltransferase 6	1.09	0.644	-2.06	0.118	1.34	0.466	-1.23	0.606	-0.21
1426885_a_at	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	-1.03	0.788	-1.11	0.115	1.05	0.558	1.24	0.225	0.04
1422732_at	Poldip2	polymerase (DNA-directed), delta interacting protein 2	-1.06	0.642	-1.07	0.463	1.04	0.343	1.17	0.183	0.02
1449749_s_at	Tfb1m	transcription factor B1, mitochondrial	-1.05	0.844	1.05	0.46	-1.1	0.431	1.02	0.95	-0.02
1430554_at	Lrig3	leucine-rich repeats and immunoglobulin-like domains 3	-1.2	0.471	1.15	0.757	-1.07	0.719	1.08	0.772	-0.01
1416274_at	Ctns	cystinosis, nephropathic	1.06	0.814	-1.12	0.579	-1.04	0.852	1.01	0.828	-0.02
1452156_a_at	Nisch	nischarin	1.01	0.85	1.01	0.827	-1.13	0.423	-1.17	0.157	-0.07
1451462_a_at	Ifnar2	interferon (alpha and beta) receptor 2	-1.04	0.828	1.02	0.562	-1.07	0.298	1.09	0.481	0
1419053_at	Pex14	peroxisomal biogenesis factor 14	1.01	0.984	-1.13	0.566	1.02	0.913	-1.02	0.815	-0.03
1445603_at	Sri	Sorcin	1.14	0.636	1.19	0.711	-1.68	0.25	-2.87	0.081	-0.56
1452472_at	Rtp3	receptor transporter protein 3	1.09	0.805	-1.4	0.081	1.11	0.768	-1.38	0.404	-0.14
1438472_at	---	---	-1.34	0.582	-1.57	0.473	1.53	0.353	2.74	0.062	0.34
1434886_at	---	---	-1.1	0.351	1.09	0.463	-1.09	0.474	1.09	0.616	0
1425177_at	Shmt1	serine hydroxymethyl transferase 1 (soluble)	-1.16	0.147	-1.05	0.822	1.1	0.453	1.32	0.3	0.05
1447239_at	Tomm70a	Translocase of outer mitochondrial membrane 70 homolog A (yeast)	-1.38	0.543	1.61	0.406	-1.72	0.267	1.45	0.178	-0.01
1445972_at	Ush2a	Usher syndrome 2A (autosomal recessive, mild) homolog (human)	-1	0.987	1.26	0.732	-1.52	0.535	1.12	0.823	-0.04
1418006_at	5830416A07Rik	RIKEN cDNA 5830416A07 gene	1.13	0.059	-1.17	0.116	-1.07	0.453	1.21	0.366	0.02
1452420_at	Stk32b	serine/threonine kinase 32B	1.02	0.935	-1.22	0.732	1.07	0.798	-1.2	0.162	-0.08
1442873_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	1.12	0.441	-1.02	0.937	-1.22	0.36	1.22	0.076	0.02
1459070_at	---	Transcribed locus	1.16	0.568	1.17	0.681	-1.7	0.133	-2.08	0.041	-0.36
1457887_at	Sspo	SCO-spondin	-1.38	0.3	-1.02	0.946	1.21	0.044	1.16	0.527	-0.01
1440903_at	Herc1	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	-1.01	0.973	1.03	0.868	-1.12	0.131	2.16	0.145	0.27
1425328_at	BC008163	cDNA sequence BC008163	-1	0.988	1.03	0.917	-1.12	0.094	1.47	0.113	0.09
1451323_at	Zfp7	zinc finger protein 7	1	0.989	1.18	0.724	-1.36	0.01	-2.01	0.145	-0.3
1437641_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	-1.58	0.407	1.25	0.538	1.03	0.642	-1.19	0.385	-0.12
1454046_x_at	Pgs1	phosphatidylglycerophosphate synthase 1	1.12	0.388	-1.27	0.093	1.01	0.804	-1.31	0.199	-0.11
1419471_a_at	Nudc	nuclear distribution gene C homolog (Aspergillus)	-1.19	0.112	-1.17	0.155	1.22	0.126	1.23	0.451	0.02
1457425_at	C130038G02Rik	RIKEN cDNA C130038G02 gene	1.08	0.739	-1.1	0.846	-1.08	0.769	1.63	0.127	0.13
1448704_s_at	H47	histocompatibility 47	1.05	0.109	1.12	0.485	-1.34	0.029	-1.18	0.604	-0.09
1429521_at	Alkbh8	alkB, alkylation repair homolog 8 (E. coli)	1.17	0.682	-1.18	0.421	-1.11	0.706	2.34	0.286	0.3
1415913_at	Rps13 /// LOC6252	ribosomal protein S13 /// similar to ribosomal protein S13 /// similar to ribosomal p	1.01	0.985	-1.26	0.434	1.11	0.66	-1.64	0.08	-0.19
1428757_at	Aasdhppt	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	-1.01	0.919	-1.37	0.151	1.2	0.164	1.29	0.434	0.02
1459462_at	Gig1	Glucocorticoid induced gene 1	-1.12	0.842	1.03	0.956	-1.01	0.975	1.1	0.868	0
1426779_x_at	Dag1	dystroglycan 1	-1.16	0.435	1.03	0.806	1.02	0.928	-1.39	0.151	-0.12

1419107_at	Ophn1	oligophrenin 1	1.04	0.723	-1.07	0.851	-1.06	0.764	1.25	0.211	0.04
1423815_at	Ddx56	DEAD (Asp-Glu-Ala-Asp) box polypeptide 56	-1.4	0.274	-1.17	0.202	1.35	0.083	1.19	0.335	-0.01
1441457_at	---	---	1.12	0.635	-1.14	0.525	-1.09	0.726	1.19	0.359	0.02
1458188_at	Dpysl2	Dihydropyrimidinase-like 2	1.43	0.382	1.18	0.816	-3.34	0.005	-1.11	0.85	-0.46
1419330_a_at	Gpa33	glycoprotein A33 (transmembrane)	-1.53	0.026	-1.18	0.492	1.41	0.324	1.02	0.922	-0.07
1459569_at	---	Transcribed locus	-1.06	0.807	1.03	0.967	-1.05	0.91	1.18	0.48	0.02
1439057_x_at	Zdhhc6	zinc finger, DHHC domain containing 6	-1.03	0.493	-1.11	0.086	1.04	0.473	1.32	0.104	0.06
1436218_at	LOC676300	similar to leucine-rich repeat-containing G protein-coupled receptor 6 isoform 1	1.32	0.327	-1.57	0.388	-1.05	0.891	1.21	0.509	-0.02
1427934_at	2610208E05Rik	RIKEN cDNA 2610208E05 gene	1.02	0.642	1.09	0.125	-1.24	0.151	-1.95	0	-0.27
1430697_at	Ammecr1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chrom	1.3	0.463	-1.09	0.906	-1.44	0.237	4.15	0.195	0.73
1416942_at	Arts1	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	1.02	0.948	-1.11	0.189	1	0.977	-1.13	0.596	-0.06
1433940_at	Spag7	sperm associated antigen 7	1.07	0.608	1.02	0.865	-1.21	0.183	-1.02	0.9	-0.04
1443808_at	D2Bwg1423e	DNA segment, Chr 2, Brigham & Women's Genetics 1423 expressed	-1.39	0.578	-1.13	0.698	1.32	0.269	2.32	0.211	0.28
1443907_at	Lnpep	leucyl/cystinyl aminopeptidase	-1.1	0.83	-1.12	0.622	1.11	0.723	1.07	0.488	-0.01
1458978_at	---	---	-1.62	0.49	1.06	0.676	1.24	0.39	-4.97	0.127	-1.07
1456331_at	9130023H24Rik	RIKEN cDNA 9130023H24 gene	-1.21	0.049	-1.03	0.915	1.12	0.277	1.11	0.735	0
1425780_a_at	Tmem167	transmembrane protein 167	-1.12	0.265	1.05	0.719	-1.03	0.81	1.05	0.81	-0.01
1415975_at	Carhsp1	calcium regulated heat stable protein 1	-1.01	0.965	-1.1	0.366	1.02	0.92	3.41	0.203	0.58
1429805_at	Myo1a /// LOC6747	myosin IA /// similar to Myosin Ia (Brush border myosin I) (BBM-I) (BBMI) (Myosin	-1.11	0.826	-1.05	0.827	1.06	0.78	1.29	0.166	0.05
1423274_at	Ints6	integrator complex subunit 6	1.15	0.392	-1.59	0.367	1.14	0.525	-1.47	0.176	-0.19
1425203_at	Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	-3.06	0.262	1.65	0.507	-1.06	0.915	1.06	0.917	-0.36
1439662_at	Homer1	homer homolog 1 (Drosophila)	1.14	0.306	-1.06	0.748	-1.19	0.326	1.52	0.09	0.1
1443223_at	---	---	1.1	0.835	1.17	0.479	-1.55	0.011	-1.25	0.432	-0.13
1434779_at	Cbln2	cerebellin 2 precursor protein	1.78	0.554	-1.29	0.652	-2.76	0.279	1.13	0.794	-0.28
1436303_at	Mllt4	myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog (Drosoph	-1.06	0.527	1.07	0.649	-1.1	0.555	1.08	0.832	0
1459815_at	Zmynd12	zinc finger, MYND domain containing 12	1.17	0.741	-1.86	0.112	1.21	0.558	-1.18	0.295	-0.16
1433903_at	AU021838	expressed sequence AU021838	1.08	0.369	-1.17	0.04	-1.02	0.637	1.05	0.691	-0.01
1434972_x_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	-1.18	0.146	-1	0.993	1.07	0.421	1.09	0.526	-0.01
1442060_at	Prepl	prolyl endopeptidase-like	1.36	0.387	-2.65	0.228	1.18	0.718	-1.68	0.107	-0.45
1437771_at	1110067I12Rik	RIKEN cDNA 1110067I12 gene	1.04	0.859	-1.31	0.506	1.12	0.711	-1.36	0.389	-0.13
1438791_at	1700016P04Rik	RIKEN cDNA 1700016P04 gene	1.83	0.446	-1.82	0.354	-1.86	0.253	2.99	0.18	0.28
1460576_at	Exoc6	exocyst complex component 6	-1.06	0.752	1.05	0.667	-1.08	0.233	1.26	0.438	0.04
1418431_at	Kif5b	kinesin family member 5B	1.23	0.358	-1.07	0.487	-1.32	0.119	1.15	0.664	0
1450856_at	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome	-1.91	0.194	1.09	0.859	1.3	0.601	-1.13	0.812	-0.16
1451387_s_at	Cuta	cutA divalent cation tolerance homolog (E. coli)	-1.12	0.619	-1.11	0.41	1.12	0.537	1.05	0.694	-0.01
1450461_at	Tcf7	transcription factor 7, T-cell specific	1.42	0.696	-2.22	0.313	1.05	0.353	-3.45	0.11	-0.8
1451760_s_at	2010001E11Rik ///	RIKEN cDNA 2010001E11 gene /// expressed sequence AI317395	-1.02	0.922	-1.19	0.193	1.1	0.627	1.67	0.16	0.14
1434676_at	Mtmr9	myotubularin related protein 9	-1.03	0.743	-1.13	0.31	1.06	0.602	1	0.987	-0.02
1460370_at	Top1mt	DNA topoisomerase 1, mitochondrial	-1.06	0.253	-1.06	0.659	1.03	0.882	1.09	0.442	0
1450091_at	Ighmbp2	immunoglobulin mu binding protein 2	-1.33	0.409	1.16	0.734	-1	0.998	1.2	0.441	0.01
1438857_x_at	---	---	-1.15	0.27	1.04	0.586	1	0.984	-1.83	0.305	-0.23
1452143_at	Spnb2	spectrin beta 2	1.02	0.894	1.14	0.219	-1.32	0.012	-1.59	0.204	-0.19
1432842_s_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	-1.14	0.347	1.03	0.559	1.01	0.905	-1.07	0.609	-0.04
1452520_a_at	Chrng	cholinergic receptor, nicotinic, gamma polypeptide	-1.07	0.766	1.08	0.203	-1.11	0.316	1	0.985	-0.02
1418427_at	Kif5b	kinesin family member 5B	1.13	0.559	-1.17	0.235	-1.07	0.721	1.3	0.201	0.05
1423879_at	D030056L22Rik	RIKEN cDNA D030056L22 gene	-1.07	0.496	-1.04	0.763	1.02	0.894	1.87	0.267	0.2
1424908_at	Mtfmt	mitochondrial methionyl-tRNA formyltransferase	-1.11	0.072	1	0.981	1.01	0.847	-1.34	0.165	-0.11
1430810_at	5730409E15Rik	RIKEN cDNA 5730409E15 gene	-1.4	0.562	-1.25	0.436	1.4	0.304	1.31	0.613	0.02
1443849_x_at	Urod	uroporphyrinogen decarboxylase	-1.02	0.822	-1.07	0.117	1	0.972	3.26	0.187	0.54
1430561_at	Dnajb14	DnaJ (Hsp40) homolog, subfamily B, member 14	1.09	0.802	-1.02	0.81	-1.18	0.583	1.1	0.396	0
1446556_at	Kcnd1	potassium voltage-gated channel, Shal-related family, member 1	-1.47	0.221	-1.44	0.119	1.55	0.17	1.33	0.535	-0.01
1417775_at	Rpo1-4	RNA polymerase 1-4	-1.36	0.117	-1.3	0.019	1.42	0.031	1.04	0.591	-0.05
1438894_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130060L(	1.14	0.416	1.11	0.718	-1.5	0.27	-2.15	0.115	-0.35

1427493_at	Sclt1	sodium channel and clathrin linker 1	-2.22	0.027	1.23	0.524	1.23	0.572	-1.07	0.842	-0.21
1425123_at	BC025816	cDNA sequence BC025816	1.01	0.943	-1.4	0.201	1.19	0.506	-1.54	0.386	-0.18
1429787_x_at	Zwint	ZW10 interactor	1.16	0.313	-1.15	0.033	-1.12	0.473	1.35	0.449	0.06
1456455_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// similar to	-1.2	0.774	1.31	0.611	-1.29	0.653	2.09	0.181	0.23
1448874_a_at	Sh2b1	SH2B adaptor protein 1	-1.16	0.496	1.02	0.86	1.03	0.856	-1.49	0.021	-0.15
1443459_at	C86415	expressed sequence C86415	1.24	0.801	-1.44	0.399	-1.01	0.978	1.55	0.417	0.08
1425973_at	Lyst	lysosomal trafficking regulator	1.04	0.959	1.08	0.775	-1.25	0.461	-1.04	0.962	-0.04
1446784_at	Adamts6	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.88	0.337	1.12	0.834	1.27	0.427	-2.17	0.176	-0.42
1455509_at	AB182283	cDNA sequence AB182283	1.25	0.337	-1.31	0.572	-1.11	0.692	3.5	0.308	0.58
1459902_at	2700007P21Rik	RIKEN cDNA 2700007P21 gene	1.13	0.729	-1.21	0.67	-1.03	0.798	1.12	0.425	0
1424243_at	Rwdd4a	RWD domain containing 4A	-1	0.98	1.11	0.226	-1.24	0.148	1.04	0.744	-0.02
1459309_at	Rufy3	RUN and FYVE domain containing 3	1.16	0.656	-1.45	0.463	1.07	0.889	-1.14	0.673	-0.09
1436452_x_at	Tmed2	transmembrane emp24 domain trafficking protein 2	1.06	0.653	-1.01	0.854	-1.16	0.286	1.2	0.456	0.02
1457907_at	Nek7	NIMA (never in mitosis gene a)-related expressed kinase 7	-1.04	0.95	-1.14	0.669	1.08	0.562	1.2	0.662	0.03
1422746_s_at	Bicd2	bicaudal D homolog 2 (Drosophila)	-1.13	0.348	-1.39	0.137	1.31	0.33	1.37	0.449	0.04
1418357_at	Foxg1	forkhead box G1	-3.02	0.435	1.37	0.518	1.22	0.717	-2.32	0.03	-0.69
1456764_at	Slc35f3	solute carrier family 35, member F3	-1.12	0.359	1.17	0.803	-1.17	0.394	3.58	0.15	0.62
1436298_x_at	Paics	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoribosylaminoim	-1.16	0.56	1.14	0.162	-1.09	0.381	1.09	0.649	0
1447248_at	Slc39a12	solute carrier family 39 (zinc transporter), member 12	1.13	0.481	1.1	0.373	-1.44	0.086	-1.23	0.483	-0.11
1418274_at	Nutf2 /// LOC62183	nuclear transport factor 2 /// similar to Nuclear transport factor 2 (NTF-2) /// simila	-1.05	0.736	1.09	0.493	-1.13	0.203	1.49	0.195	0.1
1422614_s_at	Bloc1s1	biogenesis of lysosome-related organelles complex-1, subunit 1	1.04	0.543	1.18	0.066	-1.45	0.005	-1.3	0.337	-0.13
1436983_at	Crebbp	CREB binding protein	-1.12	0.457	-1.19	0.553	1.19	0.641	1.06	0.8	-0.01
1432237_at	5730522E02Rik	RIKEN cDNA 5730522E02 gene	1.52	0.598	-1.97	0.095	-1.12	0.731	2.26	0.07	0.17
1416594_at	Sfrp1	secreted frizzled-related sequence protein 1	1.64	0.121	-1.8	0.184	-1.38	0.389	1.53	0.153	0
1432390_at	4933400F21Rik	RIKEN cDNA 4933400F21 gene	-1.06	0.884	-1.21	0.622	1.15	0.749	2.34	0.156	0.3
1418484_at	Tekt2	tektin 2	1.12	0.841	-1.45	0.27	1.12	0.601	-2.2	0.069	-0.35
1430412_at	2310068C19Rik	RIKEN cDNA 2310068C19 gene	1.27	0.264	-1.16	0.723	-1.27	0.367	2.08	0.185	0.23
1445696_x_at	---	Transcribed locus	-1.31	0.376	1.31	0.321	-1.18	0.113	1.03	0.808	-0.04
1419925_s_at	---	---	1	0.984	1.14	0.11	-1.29	0.033	-1.12	0.564	-0.07
1429831_at	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	1	0.995	-1.29	0.309	1.14	0.372	-1.31	0.434	-0.11
1440131_at	Pvrl1	Poliovirus receptor-related 1	1.23	0.786	1.16	0.644	-1.88	0.161	-2.44	0.038	-0.48
1454800_at	Morn2	MORN repeat containing 2	-1.08	0.225	-1.03	0.822	1.02	0.907	1.26	0.265	0.04
1454206_a_at	Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)	-1.4	0.088	-1.67	0.279	1.61	0.527	1.25	0.246	-0.05
1458693_at	Scn8a	Sodium channel, voltage-gated, type VIII, alpha	-1.64	0.174	1.25	0.773	1.06	0.929	-1.7	0.302	-0.26
1417275_at	Mal	myelin and lymphocyte protein, T-cell differentiation protein	1.04	0.656	-1.06	0.831	-1.06	0.678	1.22	0.134	0.03
1415859_at	Eif3s8	eukaryotic translation initiation factor 3, subunit 8	1.12	0.373	-1.42	0.236	1.09	0.816	-1.23	0.738	-0.11
1429216_at	Paqr3	progestin and adipoQ receptor family member III	1.33	0.001	-1.07	0.75	-1.51	0.117	1.66	0.06	0.1
1445461_at	---	Transcribed locus	1.07	0.258	-1.23	0.689	1.04	0.809	-1.12	0.143	-0.06
1437535_at	Ppp3r2	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type II)	1.62	0.598	-1.87	0.191	-1.31	0.637	1.23	0.296	-0.08
1424774_s_at	3230401I01Rik	RIKEN cDNA 3230401I01 gene	1.06	0.878	1.02	0.905	-1.2	0.158	-1.15	0.322	-0.07
1448676_at	Camk2b	calcium/calmodulin-dependent protein kinase II, beta	1.02	0.965	-1.31	0.484	1.14	0.472	-1.63	0.027	-0.2
1451896_a_at	Cherp	calcium homeostasis endoplasmic reticulum protein	-1.25	0.153	1.01	0.9	1.11	0.505	-1.07	0.688	-0.05
1416089_at	Rps15	ribosomal protein S15	1.08	0.231	1.03	0.683	-1.23	0.059	-1.41	0.044	-0.13
1441166_at	A330050F15Rik	RIKEN cDNA A330050F15 gene	-1.42	0.713	-2.17	0.146	1.76	0.296	1.13	0.809	-0.18
1435181_at	AI461788	expressed sequence AI461788	-1.02	0.91	-1.19	0.142	1.11	0.017	1.9	0.185	0.2
1458101_at	Lrrc56	leucine rich repeat containing 56	-1.37	0.218	-2.24	0.081	1.75	0.048	1.55	0.452	-0.08
1444991_at	---	---	-3.25	0.034	1.26	0.615	1.35	0.422	-1.12	0.78	-0.44
1424000_a_at	Rps11	ribosomal protein S11	1.03	0.577	1.03	0.441	-1.16	0.109	-1.51	0.011	-0.15
1421935_at	Rps20 /// LOC2456	ribosomal protein S20 /// similar to 40S ribosomal protein S20 /// similar to 40S rib	1.15	0.803	-1.17	0.569	-1.09	0.552	1	0.978	-0.03
1450156_a_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	-1.44	0.57	1.25	0.424	-1.03	0.93	4.66	0.202	0.86
1448902_at	Ttc23	tetratricopeptide repeat domain 23	-1.03	0.925	1.11	0.574	-1.2	0.16	1.11	0.6	0
1428840_s_at	Wdr53	WD repeat domain 53	1.08	0.813	1.04	0.837	-1.24	0.348	-1.14	0.373	-0.07
1425914_a_at	Armcx1	armadillo repeat containing, X-linked 1	-1.1	0.396	1.16	0.55	-1.17	0.069	1.11	0.661	0

1436136_at	Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)	-1.32	0.1	1.12	0.558	1.04	0.767	-1.05	0.782	-0.05
1419900_at	---	---	1.08	0.914	-1.09	0.836	-1.09	0.783	1.01	0.926	-0.02
1439138_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	1.16	0.544	1.16	0.359	-1.65	0.006	-1.63	0.047	-0.24
1443648_at	9530003O04Rik	RIKEN cDNA 9530003O04 gene	1.46	0.706	-1.07	0.897	-1.91	0.045	1.04	0.894	-0.12
1452130_at	Txndc14	thioredoxin domain containing 14	1.01	0.843	-1.07	0.231	-1.02	0.749	1.07	0.704	0
1456545_at	Il18rap	interleukin 18 receptor accessory protein	-1.3	0.253	-1.14	0.652	1.28	0.512	1.2	0.415	0.01
1442315_at	AI426778	expressed sequence AI426778	-1.01	0.973	-1.32	0.559	1.17	0.442	1.25	0.648	0.02
1460627_at	D130067I03Rik	RIKEN cDNA D130067I03 gene	1.41	0.666	-1.65	0.371	-1.1	0.857	3.88	0.26	0.63
1452164_at	BC038286	cDNA sequence BC038286	-1.04	0.845	-1.05	0.751	1.01	0.942	1.58	0.1	0.12
1446050_at	Magi1	Membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.77	0.322	1.77	0.004	-1.71	0.123	1.08	0.885	-0.16
1425562_s_at	Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	-1.14	0.442	1.02	0.866	1.02	0.893	-1.21	0.146	-0.08
1453773_at	4931406I20Rik	RIKEN cDNA 4931406I20 gene	1.33	0.093	1.13	0.682	-2.13	0.046	-1.62	0.237	-0.32
1423651_at	Hbld2	HESB like domain containing 2	-1.08	0.196	-1.07	0.121	1.07	0.675	2.03	0.194	0.24
1417519_at	Plagl2	pleiomorphic adenoma gene-like 2	-1.01	0.922	1.02	0.971	-1.1	0.647	1.2	0.557	0.03
1430046_at	Otud3	OTU domain containing 3	-1.44	0.277	-1.49	0.008	1.56	0.036	1.14	0.42	-0.06
1423972_at	Etfa	electron transferring flavoprotein, alpha polypeptide	-1.08	0.203	-1.22	0.09	1.18	0.127	1.25	0.217	0.03
1448846_a_at	Rpl29 /// LOC43335	ribosomal protein L29 /// similar to 60S ribosomal protein L29 /// similar to 60S rib	1.04	0.683	1.01	0.873	-1.15	0.07	-1.37	0.04	-0.12
1427613_at	AY074887	cDNA sequence AY074887	1.24	0.783	-1.91	0.317	1.16	0.786	-1.03	0.974	-0.13
1431988_at	1700112E06Rik	RIKEN cDNA 1700112E06 gene	1.17	0.448	-1.25	0.473	-1.05	0.762	1.03	0.953	-0.02
1456608_at	---	---	1.01	0.945	1.04	0.85	-1.14	0.737	-1.07	0.836	-0.04
1440871_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	-1.83	0.407	1.3	0.546	1.08	0.788	-1	0.993	-0.11
1426630_at	Exosc2	exosome component 2	-1.15	0.437	-1.04	0.792	1.09	0.626	1.38	0.289	0.07
1415705_at	9130011J15Rik	RIKEN cDNA 9130011J15 gene	1.12	0.297	-1.03	0.706	-1.21	0.353	1.25	0.255	0.03
1440186_s_at	2310020A21Rik	RIKEN cDNA 2310020A21 gene	-1.19	0.808	1.07	0.932	1.02	0.974	-1.2	0.752	-0.08
1424247_at	Erc1	ELKS/RAB6-interacting/CAST family member 1	1.03	0.845	-1.06	0.343	-1.05	0.598	1.32	0.231	0.06
1451977_at	Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	-1.1	0.545	-1.23	0.149	1.21	0.293	1.3	0.214	0.04
1418193_at	LOC672705	similar to max binding protein	-2.45	0.19	-1.03	0.95	1.55	0.39	1.67	0.391	-0.07
1426346_at	Prepl	prolyl endopeptidase-like	-1.02	0.92	-1.28	0.203	1.17	0.417	1.18	0.18	0.01
1451395_at	Ccdc92	coiled-coil domain containing 92	-1.22	0.137	-1.13	0.373	1.22	0.436	1.33	0.042	0.05
1417681_at	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	-1.13	0.478	-1.04	0.78	1.08	0.691	1.11	0.439	0.01
1451508_at	1700108L22Rik	RIKEN cDNA 1700108L22 gene	-1.01	0.939	-1.21	0.081	1.11	0.325	2.24	0.157	0.28
1449645_s_at	Cct3	chaperonin subunit 3 (gamma)	-1.1	0.711	-1.12	0.612	1.12	0.663	1.03	0.926	-0.02
1429601_x_at	C630010D07Rik ///	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofolate dehydro	-1.06	0.433	1.19	0.548	-1.26	0.061	1.27	0.286	0.03
1417763_at	Ssr1 /// LOC636537	signal sequence receptor, alpha /// similar to signal sequence receptor, alpha	-1.08	0.351	1.06	0.432	-1.07	0.394	1.31	0.208	0.06
1423462_at	Map3k7ip2	mitogen-activated protein kinase kinase kinase 7 interacting protein 2	-1.08	0.502	1.17	0.458	-1.21	0.105	1.01	0.765	-0.03
1460638_at	Yars	tyrosyl-tRNA synthetase	-1.36	0.037	-1.18	0.036	1.34	0.008	1.57	0.138	0.09
1427284_a_at	Ttpa	tocopherol (alpha) transfer protein	1.43	0.492	-1.16	0.296	-1.57	0.474	2.25	0.097	0.24
1428573_at	Chn2	chimerin (chimaerin) 2	-1.06	0.755	-1.19	0.231	1.14	0.592	1.01	0.962	-0.02
1421176_at	Rasgrp1	RAS guanyl releasing protein 1	-1.31	0.582	1.05	0.876	1.11	0.589	-2.73	0.292	-0.47
1432367_a_at	Ufd1l	ubiquitin fusion degradation 1 like	-1.08	0.593	-1.03	0.6	1.04	0.811	1.3	0.44	0.06
1436188_a_at	Ndrg4	N-myc downstream regulated gene 4	-1.23	0.134	1.06	0.936	1.06	0.799	-1.11	0.464	-0.06
1417106_at	Tpd52l2	tumor protein D52-like 2	1.03	0.316	1.01	0.929	-1.13	0.078	-1.15	0.448	-0.06
1444539_at	D530039A21Rik	RIKEN cDNA D530039A21 gene	-1.41	0.505	1.11	0.868	1.11	0.814	-1.42	0.489	-0.15
1437742_at	Rab21	RAB21, member RAS oncogene family	1.07	0.304	1.05	0.661	-1.23	0.072	-1.35	0.209	-0.12
1427315_at	Tmed7	transmembrane emp24 protein transport domain containing 7	-1.21	0.635	1.12	0.836	-1.02	0.942	1.75	0.108	0.16
1440864_at	AI836737	expressed sequence AI836737	-1.04	0.944	-1.41	0.137	1.26	0.577	1.23	0.752	0.01
1446436_at	Rbpsuh	Recombining binding protein suppressor of hairless (Drosophila)	1.29	0.508	1.04	0.888	-1.69	0.081	-1.3	0.404	-0.17
1439063_at	Asxl2	additional sex combs like 2 (Drosophila)	1.06	0.709	-1.26	0.087	1.08	0.644	-1.04	0.708	-0.04
1426384_a_at	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsil	-1.04	0.848	1.05	0.604	-1.09	0.329	1.04	0.844	-0.01
1422408_at	Ifna4	interferon alpha 4	-1.09	0.722	1.26	0.251	-1.33	0.622	1.22	0.523	0.01
1418067_at	Cfl2	cofilin 2, muscle	1.01	0.954	-1.1	0.461	1	0.961	-1.06	0.544	-0.04
1416726_s_at	Ube2s	ubiquitin-conjugating enzyme E2S	-1.22	0.407	-1.31	0.126	1.35	0.063	2.38	0.304	0.3
1417177_at	Galk1	galactokinase 1	-1.07	0.582	-1.13	0.408	1.11	0.579	1.11	0.41	0.01

1423779_at	Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	-1.11	0.239	-1.04	0.716	1.06	0.821	1.42	0.151	0.08
1453643_at	1700001L19Rik	RIKEN cDNA 1700001L19 gene	1.08	0.845	-1.48	0.388	1.18	0.702	-2.45	0.105	-0.42
1429952_at	Mospd4	motile sperm domain containing 4	-1.1	0.866	1.1	0.798	-1.1	0.476	1.1	0.906	0
1448103_s_at	Nono	non-POU-domain-containing, octamer binding protein	1.1	0.156	1.05	0.544	-1.28	0.015	-1.09	0.251	-0.06
1454836_at	Tmem18	transmembrane protein 18	1.04	0.434	-1.09	0.5	-1.03	0.795	1.11	0.322	0.01
1436997_x_at	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	1.08	0.752	-1.04	0.581	-1.12	0.315	1.01	0.948	-0.02
1437975_a_at	Rpl23a /// LOC385	ribosomal protein L23a /// hypothetical gene supported by BC029892 /// similar to	1.07	0.41	1.09	0.27	-1.3	0.007	-1.37	0.029	-0.13
1438575_a_at	2900056M20Rik	RIKEN cDNA 2900056M20 gene	1.02	0.851	1.11	0.724	-1.26	0.244	-1.38	0.149	-0.13
1430985_at	1810027O10Rik	RIKEN cDNA 1810027O10 gene	-1.06	0.67	1.06	0.168	-1.08	0.641	1.62	0.283	0.13
1449042_at	Ctcf	CCCTC-binding factor	1	0.976	-1.16	0.447	1.06	0.816	-1.13	0.695	-0.06
1446321_at	B230208B08Rik	RIKEN cDNA B230208B08 gene	1.09	0.879	-2.44	0.021	1.42	0.507	-1.42	0.619	-0.34
1424538_at	Ubl4	ubiquitin-like 4	-1.08	0.15	-1.05	0.524	1.04	0.724	1.14	0.423	0.01
1436391_s_at	Clcc1	chloride channel CLIC-like 1	-1.12	0.166	1.03	0.842	1.01	0.892	-1.06	0.473	-0.04
1426769_s_at	Maml1	mastermind like 1 (Drosophila)	1.05	0.776	-1.16	0.228	1.02	0.901	-1.23	0.291	-0.08
1431814_at	4932443L11Rik	RIKEN cDNA 4932443L11 gene	1.16	0.499	-1.49	0.413	1.09	0.48	-1.02	0.917	-0.06
1443258_at	Foxp1	forkhead box P1	1.12	0.227	1.01	0.985	-1.26	0.28	-1.71	0.194	-0.21
1451473_a_at	Cryzl1	crystallin, zeta (quinone reductase)-like 1	-1.03	0.703	1.1	0.436	-1.16	0.254	1.1	0.595	0
1435034_at	AW060207	expressed sequence AW060207	-1.15	0.632	1.03	0.858	1.02	0.892	-1.08	0.703	-0.04
1439411_a_at	Xpo7	exportin 7	1.05	0.028	-1.05	0.462	-1.09	0.612	2.41	0.201	0.33
1431820_at	4632404H12Rik	RIKEN cDNA 4632404H12 gene	-1.21	0.517	1	0.998	1.1	0.407	-1.47	0.303	-0.14
1428244_at	Larp1 /// LOC6312	La ribonucleoprotein domain family, member 1 /// similar to la related protein isofo	-1.12	0.187	-1.05	0.553	1.08	0.574	1.1	0.264	0
1425185_at	5830417C01Rik	RIKEN cDNA 5830417C01 gene	1.01	0.325	1.12	0.372	-1.25	0.205	-1.05	0.749	-0.04
1426740_s_at	Armc5	armadillo repeat containing 5	1.08	0.154	-1.18	0.012	-1.01	0.973	1.02	0.906	-0.02
1453360_a_at	Tex9	testis expressed gene 9	-1.35	0.406	1.22	0.708	-1.03	0.631	1.01	0.814	-0.04
1448037_at	Zcchc6	Zinc finger, CCHC domain containing 6	-1.04	0.768	1.02	0.875	-1.06	0.568	2.46	0.216	0.35
1425373_a_at	Tnfsf5ip1	tumor necrosis factor superfamily, member 5-induced protein 1	-1.32	0.341	-1.13	0.558	1.28	0.036	1.35	0.119	0.05
1428338_at	2610039E05Rik	RIKEN cDNA 2610039E05 gene	1.19	0.191	-1.44	0.169	1.04	0.559	-1.53	0.034	-0.18
1435533_s_at	4933426K21Rik	RIKEN cDNA 4933426K21 gene	-1.49	0.595	1.32	0.451	-1.07	0.837	4.51	0.027	0.82
1426646_at	9130011J15Rik	RIKEN cDNA 9130011J15 gene	-1.06	0.544	1.09	0.359	-1.11	0.513	1.18	0.334	0.02
1436541_at	2310008H09Rik	RIKEN cDNA 2310008H09 gene	1.27	0.266	-1.26	0.187	-1.15	0.488	1.1	0.689	-0.01
1438180_x_at	Silg111 /// Hax1	silica-induced gene 111 /// HCLS1 associated X-1	1.16	0.143	-1.07	0.422	-1.19	0.107	1.34	0.026	0.06
1433855_at	Abat	4-aminobutyrate aminotransferase	-1.05	0.514	-1.21	0.07	1.15	0.637	1.25	0.471	0.03
1450857_a_at	Col1a2	procollagen, type I, alpha 2	1.14	0.224	1.12	0.341	-1.5	0.256	-1.22	0.556	-0.11
1448942_at	Gng11	guanine nucleotide binding protein (G protein), gamma 11	1.06	0.796	1.27	0.102	-1.66	0.014	-1	0.981	-0.08
1423990_at	Rab28	RAB28, member RAS oncogene family	-1.01	0.9	1.09	0.351	-1.18	0.086	1.05	0.2	-0.01
1443650_at	Anks1	Ankyrin repeat and SAM domain containing 1	1.13	0.611	1.03	0.939	-1.31	0.467	-1.33	0.237	-0.12
1443957_at	Dixdc1	DIX domain containing 1	1.12	0.763	-1.7	0.388	1.22	0.635	-1.37	0.63	-0.18
1448565_at	Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	-1.23	0.652	1.07	0.72	1.05	0.834	-1.45	0.36	-0.14
1423107_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	-1.09	0.379	-1.07	0.497	1.08	0.239	1.24	0.437	0.04
1454941_at	Nmt1	N-myristoyltransferase 1	1.04	0.824	-1.01	0.92	-1.1	0.303	1.07	0.493	0
1450755_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	1.01	0.675	-1	0.961	-1.08	0.434	1.08	0.769	0
1453162_at	Utp11l	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	1.02	0.91	1.13	0.459	-1.27	0.039	-1.17	0.392	-0.07
1425186_at	Lmbrd1	LMBR1 domain containing 1	1.04	0.775	-1.18	0.216	1.04	0.775	-1.41	0.216	-0.13
1457723_at	Pspc1	Paraspeckle protein 1	-1.12	0.711	-1.3	0.515	1.27	0.411	1.08	0.795	-0.02
1427598_at	Pwcr1	Prader-Willi chromosome region 1 homolog (human)	-1.63	0.43	1.61	0.5	-1.42	0.322	3.16	0.011	0.43
1459958_at	Rsrc1	arginine/serine-rich coiled-coil 1	1.11	0.592	1.06	0.808	-1.32	0.19	-1.66	0.196	-0.2
1456056_a_at	D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-1.15	0.217	1.02	0.567	1.03	0.669	-1.31	0.5	-0.1
1424587_at	BC023488	cDNA sequence BC023488	-1.19	0.171	-1.05	0.876	1.13	0.598	1.39	0.317	0.07
1443367_at	---	---	1.18	0.888	1.28	0.733	-2.12	0.006	-2.46	0.018	-0.53
1435787_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	-1.11	0.506	1.15	0.425	-1.14	0.442	2.04	0.203	0.23
1421904_at	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	1.02	0.915	1.05	0.714	-1.16	0.139	-1.17	0.141	-0.07
1431934_at	4930505O20Rik	RIKEN cDNA 4930505O20 gene	1.19	0.813	-3.64	0.003	1.46	0.215	-1.29	0.551	-0.57
1415678_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	1.03	0.398	-1.02	0.706	-1.09	0.456	1.24	0.177	0.04

1459182_at	---	Transcribed locus	-2.01	0.097	-1.11	0.593	1.53	0.078	1.03	0.947	-0.14
1431727_at	Smgc	submandibular gland protein C	-1.44	0.457	1.41	0.497	-1.22	0.676	1.81	0.449	0.14
1448052_at	Cgnl1 /// LOC6774	cingulin-like 1 /// similar to cingulin-like 1 isoform 1	1.3	0.004	-1.29	0.723	-1.17	0.295	1.5	0.238	0.08
1443519_at	---	---	-1.2	0.522	1.09	0.762	1.01	0.989	-1.17	0.691	-0.07
1430864_at	Ttll9	tubulin tyrosine ligase like family 9	-1.17	0.193	-1.74	0	1.5	0.634	1.53	0.308	0.03
1433874_at	Ssh1	slingshot homolog 1 (Drosophila)	-1.06	0.796	-1.2	0.579	1.15	0.64	1.09	0.707	-0.01
1460239_at	Tspan13	tetraspanin 13	1.03	0.806	1.15	0.474	-1.33	0.08	-1.16	0.449	-0.08
1423083_at	Rab33b	RAB33B, member of RAS oncogene family	1.08	0.139	1.11	0.112	-1.35	0.008	-1.67	0.128	-0.21
1426496_at	Wdr55	WD repeat domain 55	-1.13	0.504	-1.12	0.095	1.15	0.196	1.21	0.341	0.03
1421634_at	Capn8	calpain 8	1.12	0.819	1.23	0.613	-1.73	0.061	-1.07	0.833	-0.11
1455200_at	Pak6	p21 (CDKN1A)-activated kinase 6	-1.25	0.368	-1.34	0.642	1.38	0.217	1.33	0.298	0.03
1418241_at	Usf2	upstream transcription factor 2	-1.07	0.624	-1.06	0.383	1.05	0.749	1	0.993	-0.02
1453113_at	Wdsub1	WD repeat, SAM and U-box domain containing 1	-1.05	0.807	1.01	0.877	-1.03	0.786	1.69	0.072	0.15
1460458_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	1.36	0.237	-1.12	0.779	-1.47	0.189	1.64	0.212	0.1
1427958_at	Abhd10	abhydrolase domain containing 10	-1.13	0.091	1.14	0.511	-1.11	0.439	1.16	0.322	0.02
1420880_a_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	1.07	0.108	1.02	0.839	-1.18	0.389	-1.12	0.357	-0.05
1450070_s_at	Pak1	p21 (CDKN1A)-activated kinase 1	-1.04	0.647	1.3	0.39	-1.5	0.035	1.07	0.814	-0.04
1419596_at	Eda /// LOC675952	ectodysplasin-A /// similar to Ectodysplasin-A (EDA protein homolog) (Tabby prot	-2.47	0.028	1.59	0.331	-1.07	0.791	1.95	0.032	0
1435686_at	AA536717	expressed sequence AA536717	1.08	0.602	-1.24	0.065	1.04	0.819	-1.16	0.356	-0.07
1415690_at	Mrpl27	mitochondrial ribosomal protein L27	1.03	0.726	-1.01	0.902	-1.1	0.269	1.31	0.101	0.06
1459612_at	Phlpp	PH domain and leucine rich repeat protein phosphatase	1.26	0.344	-1.29	0.694	-1.11	0.665	1.12	0.675	-0.01
1438529_at	D4Ertd429e	DNA segment, Chr 4, ERATO Doi 429, expressed	-1.51	0.132	1.76	0.358	-1.96	0.106	1.27	0.383	-0.11
1437632_at	---	Adult male cecum cDNA, RIKEN full-length enriched library, clone:9130409M07 p	1.14	0.153	-1.12	0.079	-1.1	0.314	1.11	0.568	0
1454146_at	9530036M11Rik	RIKEN cDNA 9530036M11 gene	1.37	0.327	-1.46	0.118	-1.14	0.551	2.49	0.307	0.32
1440176_x_at	1700003F12Rik	RIKEN cDNA 1700003F12 gene	1.38	0.534	-2.1	0.294	1.08	0.871	-2.07	0.03	-0.43
1434287_at	Agpat5	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransf	-1.4	0.174	1.38	0.366	-1.19	0.258	1.77	0.33	0.14
1420277_at	---	---	1.07	0.018	1.02	0.924	-1.2	0.297	-1.26	0.381	-0.09
1425472_a_at	Lmna	lamin A	-1.07	0.826	1.02	0.685	-1.03	0.862	2.82	0.123	0.44
1433700_at	4933433P14Rik	RIKEN cDNA 4933433P14 gene	1.02	0.897	1.08	0.657	-1.21	0.086	-1.11	0.367	-0.05
1459108_a_at	Yeats2	YEATS domain containing 2	-1.21	0.185	-1.05	0.712	1.15	0.209	1.16	0.271	0.01
1454912_at	Pbx4	pre-B-cell leukemia transcription factor 4	1.58	0.698	-2.25	0.253	-1.1	0.817	1.09	0.887	-0.17
1457473_at	Chd1	chromodomain helicase DNA binding protein 1	1.04	0.817	-1.1	0.545	-1.02	0.952	1.33	0.243	0.06
1423404_at	Gkn1	gastrokine 1	-1.04	0.97	1.15	0.697	-1.22	0.472	1.21	0.144	0.02
1456326_at	Gm784	gene model 784, (NCBI)	-1.65	0.385	1.43	0.59	-1.11	0.862	1.49	0.192	0.04
1456359_at	Ppwd1	peptidylprolyl isomerase domain and WD repeat containing 1	-1.13	0.522	-1	0.986	1.05	0.732	1.67	0.232	0.15
1456157_at	D14Ertd209e	DNA segment, Chr 14, ERATO Doi 209, expressed	1.07	0.65	1.04	0.897	-1.22	0.274	-1.26	0.442	-0.09
1427793_at	AJ242955	hypothetical protein, P4(21)n gene	1.17	0.79	1.19	0.764	-1.73	0.373	-1.01	0.982	-0.1
1419400_at	Mttp	microsomal triglyceride transfer protein	-1.08	0.688	-1.04	0.762	1.05	0.832	1.65	0.154	0.14
1451490_at	Lyplal1	lysophospholipase-like 1	-1.02	0.886	1.11	0.306	-1.2	0.101	1.29	0.524	0.05
1449469_at	Pkd2l2	polycystic kidney disease 2-like 2	-1.13	0.655	-1.04	0.934	1.08	0.893	7.55	0.15	1.62
1453118_s_at	Rpl22	ribosomal protein L22	1.01	0.868	1.04	0.373	-1.14	0.285	-1.28	0.001	-0.09
1416524_at	Spop	speckle-type POZ protein	1.01	0.968	1.06	0.439	-1.16	0.177	-1.14	0.264	-0.06
1417584_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member	-1.04	0.722	-1.31	0.125	1.21	0.196	2.04	0.191	0.23
1429373_x_at	Crtc2	CREB regulated transcription coactivator 2	1.02	0.934	-1.18	0.672	1.06	0.868	-1.88	0.12	-0.24
1416137_at	Anxa7	annexin A7	-1.09	0.557	-1.09	0.064	1.1	0.314	1.18	0.439	0.03
1416220_at	Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	-1.15	0.026	1.08	0.48	-1.02	0.831	1.14	0.216	0.01
1448721_at	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	-1.05	0.881	-1.25	0.237	1.18	0.328	1.49	0.286	0.09
1456178_at	Bambi-ps1	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus laevis)	1.17	0.808	-1.59	0.466	1.14	0.718	-2.36	0.306	-0.41
1417137_at	Uck2	uridine-cytidine kinase 2	-1.36	0.119	-1.96	0.261	1.69	0.082	1.69	0.49	0.02
1450925_a_at	Rps27l /// LOC667	ribosomal protein S27-like /// similar to 40S ribosomal protein S27-like protein	1.1	0.419	-1.04	0.565	-1.15	0.287	1.26	0.149	0.04
1450727_a_at	Poldip2	polymerase (DNA-directed), delta interacting protein 2	-1.08	0.706	-1.12	0.436	1.11	0.296	1.1	0.64	0
1433519_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1.02	0.885	-1.04	0.698	-1.05	0.73	1.34	0.272	0.07
1454643_at	Ubap2l	ubiquitin associated protein 2-like	-1.21	0.098	1	0.975	1.1	0.227	-1.09	0.443	-0.05

1432270_a_at	Chmp5	chromatin modifying protein 5	1.07	0.417	1.03	0.605	-1.2	0.159	-1.21	0.296	-0.08
1424440_at	Mrps6	mitochondrial ribosomal protein S6	1.02	0.835	-1.27	0.04	1.12	0.27	-1.25	0.308	-0.09
1450163_a_at	Wrn	Werner syndrome homolog (human)	1.22	0.767	-1.3	0.714	-1.06	0.647	1.83	0.308	0.17
1417244_a_at	Irf7	interferon regulatory factor 7	-1.47	0.317	1.01	0.888	1.24	0.063	-1.28	0.192	-0.12
1434302_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1.01	0.963	1.22	0.314	-1.42	0.014	-1.25	0.596	-0.11
1460740_at	Cltb	clathrin, light polypeptide (Lcb)	-1.08	0.611	-1.17	0.57	1.15	0.344	1.82	0.113	0.18
1450437_a_at	Ncam1	neural cell adhesion molecule 1	1.01	0.969	-1.48	0.308	1.24	0.086	-1.08	0.54	-0.08
1416910_at	Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15	-1.17	0.225	1.01	0.661	1.07	0.601	-1.25	0.491	-0.08
1434231_x_at	Rpl35	ribosomal protein L35	1	0.995	1.14	0.037	-1.25	0.039	-1.36	0.02	-0.12
1426483_at	Prkrir	protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, rep	1.19	0.203	1.01	0.903	-1.37	0.009	-1.15	0.419	-0.08
1438744_at	Asb7	ankyrin repeat and SOCS box-containing protein 7	-1.1	0.378	-1.02	0.873	1.05	0.71	1.08	0.644	0
1417731_at	Pqbp1	polyglutamine binding protein 1	1.1	0.279	-1.27	0.041	1.04	0.773	-1.42	0.151	-0.14
1426416_a_at	Yipf4	Yip1 domain family, member 4	-1.06	0.665	-1.03	0.646	1.02	0.851	1.84	0.158	0.19
1418236_s_at	Atg5	autophagy-related 5 (yeast)	1.1	0.516	1.02	0.866	-1.24	0.512	-1.2	0.43	-0.08
1446199_at	Rgs20	regulator of G-protein signaling 20	-1.56	0.179	1.02	0.925	1.27	0.493	-1.16	0.611	-0.11
1435969_at	Btbd12	BTB (POZ) domain containing 12	-1.07	0.561	1.07	0.795	-1.08	0.774	1.14	0.509	0.01
1435864_a_at	1810063B05Rik	RIKEN cDNA 1810063B05 gene	1.06	0.7	1.13	0.251	-1.35	0.152	-1.54	0.228	-0.17
1448736_a_at	Hprt1	hypoxanthine guanine phosphoribosyl transferase 1	-1	0.941	-1.07	0.069	1	0.954	1.18	0.076	0.03
1415782_at	Sumo2	SMT3 suppressor of mif two 3 homolog 2 (yeast)	-1	0.836	1.04	0.566	-1.12	0.086	1.08	0.391	0
1449322_at	Ptp4a1 /// LOC269	protein tyrosine phosphatase 4a1 /// similar to protein tyrosine phosphatase 4a1 /	-1.09	0.673	-1.01	0.914	1.02	0.751	1.23	0.21	0.04
1424858_at	L2hgdh	L-2-hydroxyglutarate dehydrogenase	-1.24	0.555	-1.55	0.17	1.49	0.212	1.4	0.134	0.02
1450535_at	Krtap12-1	keratin associated protein 12-1	-1.44	0.614	-1.48	0.326	1.56	0.435	1.1	0.87	-0.06
1452329_at	Plekhn1	pleckstrin homology domain containing, family N member 1	-1.61	0.273	1.21	0.561	1.1	0.544	-1.19	0.385	-0.12
AFFX-CreX-5_at	---	---	1.15	0.415	1.01	0.952	-1.28	0.26	-1.08	0.617	-0.05
1448478_at	Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	1.03	0.829	-1.04	0.395	-1.06	0.241	1.14	0.558	0.02
1447430_at	---	Transcribed locus	-1.86	0.114	-1.15	0.746	1.52	0.312	1.72	0.182	0.06
1440866_at	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	1.05	0.822	1.03	0.859	-1.18	0.509	-1.35	0.192	-0.11
1435010_at	Asb7	ankyrin repeat and SOCS box-containing protein 7	-1.05	0.478	1.04	0.788	-1.06	0.697	1.04	0.778	-0.01
1422743_at	Phka1	phosphorylase kinase alpha 1	1.08	0.499	-1.18	0.473	1.01	0.962	-1.34	0.159	-0.11
1453155_at	Tmem50a	transmembrane protein 50A	1.08	0.668	-1.03	0.856	-1.14	0.252	1.05	0.632	-0.01
1448582_at	Ctnnbl1	catenin, beta like 1	1.02	0.611	-1.22	0.104	1.09	0.1	-1.27	0.051	-0.09
1455061_a_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiol	-1.1	0.409	-1.43	0.129	1.33	0.414	1.16	0.705	-0.01
1448888_at	Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	1.04	0.768	-1.07	0.476	-1.04	0.419	1.04	0.762	-0.01
1437715_x_at	Apex1	apurinic/apyrimidinic endonuclease 1	-1.39	0.218	1	0.96	1.22	0.375	-1.05	0.515	-0.06
1457852_at	Ltbp1	Latent transforming growth factor beta binding protein 1	-1.42	0.615	1.5	0.236	-1.37	0.519	1.62	0.106	0.08
1441268_at	1500011B03Rik	RIKEN cDNA 1500011B03 gene	-1.23	0.757	1.09	0.914	1.04	0.921	-1.03	0.918	-0.03
1417091_at	Chuk	conserved helix-loop-helix ubiquitous kinase	-1.34	0.033	1.04	0.558	1.14	0.273	-1.21	0.444	-0.09
1456691_s_at	Srd5a2l	steroid 5 alpha-reductase 2-like	-1.13	0.428	1.02	0.858	1.02	0.856	-1.18	0.686	-0.06
1438172_x_at	Exod1	exonuclease domain containing 1	1.07	0.698	-1.07	0.805	-1.07	0.831	1.53	0.204	0.12
1460590_s_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	1.04	0.649	1.03	0.652	-1.16	0.027	-1.12	0.473	-0.05
1435396_at	Stxbp6	syntaxin binding protein 6 (amisyn)	1.09	0.348	1.13	0.504	-1.39	0.065	-1.12	0.789	-0.07
1459022_at	---	---	-1.12	0.662	1.02	0.975	1.02	0.919	-1.25	0.051	-0.08
1428046_a_at	Zfx	zinc finger protein X-linked	1.16	0.138	-1.01	0.973	-1.27	0.19	1.28	0.355	0.04
1455400_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	-1.13	0.369	-1.17	0.593	1.19	0.15	1.97	0.306	0.22
1429425_at	Rnf139	ring finger protein 139	-1.15	0.409	-1.11	0.181	1.17	0.026	1.41	0.244	0.08
1434006_at	BC051227	cDNA sequence BC051227	-1	0.989	-1.11	0.687	1.04	0.346	1.04	0.802	-0.01
1442349_at	C630028N24Rik	RIKEN cDNA C630028N24 gene	1.15	0.289	-1.72	0.126	1.2	0.587	-2.99	0.054	-0.59
1423961_at	Wdr26	WD repeat domain 26	-1.13	0.488	-1.09	0.532	1.14	0.376	1.29	0.458	0.05
1421906_at	Pparbp	peroxisome proliferator activated receptor binding protein	1.05	0.877	1	0.99	-1.13	0.614	-1.18	0.598	-0.06
1433341_at	5730416F02Rik	RIKEN cDNA 5730416F02 gene	1.19	0.284	-1.28	0.342	-1.04	0.368	1.09	0.397	-0.01
1419001_at	Baat	bile acid-Coenzyme A: amino acid N-acyltransferase	-1.29	0.662	-1.14	0.301	1.28	0.574	2.03	0.508	0.22
1425518_at	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	1.19	0.457	-1.43	0.192	1.04	0.818	-2.86	0.016	-0.51
1431107_at	Stk35	serine/threonine kinase 35	-1.3	0.084	-1.09	0.867	1.25	0.615	1.02	0.946	-0.03

1448875_at	Zhx1	zinc fingers and homeoboxes protein 1	1.06	0.681	-1.05	0.509	-1.09	0.618	1.13	0.562	0.01
1436878_at	Baalc	brain and acute leukemia, cytoplasmic	1.22	0.759	-1.03	0.942	-1.34	0.497	1.18	0.831	0.01
1448939_at	Usp25	ubiquitin specific peptidase 25	-1.1	0.564	1.12	0.315	-1.11	0.396	1.5	0.192	0.1
1423194_at	Arhgap5	Rho GTPase activating protein 5	1.16	0.693	-1.43	0.119	1.08	0.83	-1.4	0.057	-0.15
1417152_at	Btbd14a	BTB (POZ) domain containing 14A	-1.05	0.601	-1.16	0.122	1.12	0.228	1.16	0.07	0.02
1452102_at	Copb2	coatomer protein complex, subunit beta 2 (beta prime)	-1.11	0.443	1	0.968	1.03	0.774	-1.1	0.529	-0.04
1451738_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:p	-1.02	0.849	-1.31	0.343	1.19	0.277	1.03	0.782	-0.03
1438750_at	Atrx	Alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-1.09	0.681	1.04	0.83	-1.02	0.935	1.24	0.049	0.04
1437287_at	1110020G09Rik	RIKEN cDNA 1110020G09 gene	-1.09	0.397	-1.15	0.194	1.15	0.362	3.21	0.166	0.53
1439460_a_at	Zfp289	zinc finger protein 289	-1.26	0.126	-1.01	0.816	1.16	0.323	1.01	0.964	-0.03
1460495_s_at	Htra2	HtrA serine peptidase 2	-1.03	0.698	-1.2	0.218	1.14	0.167	1.47	0.233	0.09
1457210_at	1700092E19Rik	RIKEN cDNA 1700092E19 gene	-1.16	0.576	-1.22	0.695	1.25	0.553	1.34	0.267	0.05
1433635_at	Wdr18	WD repeat domain 18	-1.32	0.395	-1.09	0.325	1.26	0.263	1.21	0.485	0.02
1424172_at	Hagh	hydroxyacyl glutathione hydrolase	-1.09	0.236	-1.25	0.007	1.22	0.225	3.75	0.22	0.66
1427956_at	Pcgf1	polycomb group ring finger 1	1.04	0.823	1.05	0.712	-1.19	0.466	-1.39	0.193	-0.12
1452603_at	5330431N19Rik	RIKEN cDNA 5330431N19 gene	-1.13	0.048	-1.03	0.362	1.08	0.713	1.01	0.918	-0.02
1455901_at	Chpt1	choline phosphotransferase 1	-1.04	0.733	1	0.986	-1.02	0.915	1.12	0.678	0.01
1425536_at	Stx3	syntaxin 3	-1.06	0.732	1.24	0.113	-1.33	0.171	1.08	0.751	-0.02
1433122_at	2900069G24Rik	RIKEN cDNA 2900069G24 gene	-1.05	0.803	-3.67	0.087	1.71	0.127	1.77	0.302	-0.31
1424258_at	Polr2d	polymerase (RNA) II (DNA directed) polypeptide D	1.03	0.794	-1.1	0.421	-1	0.977	1.11	0.736	0.01
1458201_at	---	---	1.18	0.377	1.24	0.508	-1.92	0.036	-1.48	0.126	-0.25
1450665_at	Gabpa	GA repeat binding protein, alpha	-1	0.975	-1.26	0.114	1.15	0.337	1.07	0.739	-0.01
1428529_at	2810026P18Rik	RIKEN cDNA 2810026P18 gene	-1.13	0.441	-1.08	0.53	1.13	0.184	1.34	0.523	0.06
1437899_at	Gm776	gene model 776, (NCBI)	-3.11	0.401	1.28	0.677	1.34	0.439	-2.02	0.547	-0.63
1448557_at	1200015N20Rik	RIKEN cDNA 1200015N20 gene	1.02	0.884	-1.11	0.57	1.01	0.945	-1.34	0.332	-0.1
1416615_at	Clpp	caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)	-1.05	0.792	-1.17	0.049	1.13	0.418	1.17	0.383	0.02
1459970_at	Ust	Uronyl-2-sulfotransferase	-1.06	0.915	1.21	0.659	-1.27	0.18	1.13	0.73	0
1426777_a_at	Wasl	Wiskott-Aldrich syndrome-like (human)	-1.03	0.439	-1.27	0.072	1.17	0.089	1.07	0.752	-0.01
1435078_at	Tanc2	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-1.47	0.322	1.5	0.27	-1.31	0.021	1.26	0.484	-0.01
1450578_at	Sry	sex determining region of Chr Y	1.06	0.937	-2.17	0.043	1.42	0.603	-3.4	0.037	-0.77
1424795_a_at	1700001O22Rik	RIKEN cDNA 1700001O22 gene	1.63	0.229	-1.31	0.3	-1.85	0.344	1.43	0.137	-0.02
1435050_at	D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	1.33	0.031	-1.04	0.936	-1.55	0.094	1.61	0.361	0.09
1427518_at	D10627	cDNA sequence D10627	-1.14	0.258	-1.03	0.9	1.09	0.554	1.06	0.844	-0.01
1416084_at	Zfand5	zinc finger, AN1-type domain 5	-1.15	0.429	-1.15	0.438	1.2	0.521	1.63	0.191	0.13
1430974_a_at	Senp7	SUMO1/sentrin specific peptidase 7	1.52	0.284	-3.21	0.085	1.11	0.866	-1.04	0.93	-0.4
1437397_at	Prlr	prolactin receptor	-1.47	0.176	-1.06	0.837	1.32	0.12	1.99	0.21	0.19
1425616_a_at	Ccdc23	coiled-coil domain containing 23	-1.04	0.712	1.08	0.301	-1.12	0.402	1.18	0.472	0.03
1440986_at	Rpap1	RNA polymerase II associated protein 1	1.11	0.419	1	0.998	-1.21	0.383	-1.42	0.178	-0.13
1426374_at	2410166I05Rik	RIKEN cDNA 2410166I05 gene	1.01	0.931	1.05	0.585	-1.15	0.205	-1.01	0.975	-0.02
1457885_at	Prkag2	Protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.38	0.546	-1.81	0.189	1.01	0.992	-1.83	0.359	-0.31
1458717_at	C030010L15Rik	RIKEN cDNA C030010L15 gene	1.05	0.858	1.09	0.846	-1.25	0.612	-2.93	0.224	-0.51
1418976_s_at	Cideb	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	-1.09	0.541	-1.31	0.044	1.26	0.121	1.23	0.316	0.02
1428659_at	Phf7	PHD finger protein 7	1.04	0.663	-1.12	0.564	1.01	0.962	-1.12	0.684	-0.05
1434296_at	BC049349	cDNA sequence BC049349	-1.13	0.281	1.01	0.928	1.04	0.516	-1.17	0.227	-0.06
1424617_at	Ifi35	interferon-induced protein 35	1.04	0.744	-1.19	0.264	1.06	0.801	-1.41	0.207	-0.13
1439927_at	Palm	Paralemmin	1.08	0.761	1.04	0.921	-1.22	0.368	-1.13	0.56	-0.06
1426433_at	Myct1	myc target 1	-1.29	0.642	-1.26	0.767	1.37	0.543	1.65	0.471	0.12
1447863_s_at	Nr4a2	nuclear receptor subfamily 4, group A, member 2	1.38	0.71	-1.52	0.324	-1.11	0.683	1.11	0.693	-0.04
1428569_at	B230217C12Rik	RIKEN cDNA B230217C12 gene	1.14	0.454	-1.37	0.634	1.07	0.873	-1.55	0.242	-0.18
1422719_s_at	Nup50	nucleoporin 50	-1.25	0.141	-1.05	0.811	1.19	0.251	1.59	0.319	0.12
1455827_at	Mbnl2	muscleblind-like 2	1.03	0.653	1.2	0.282	-1.41	0.022	-1.31	0.077	-0.12
1452960_at	Scyl3	SCY1-like 3 (S. cerevisiae)	1.04	0.763	-1.11	0.248	1	0.967	-1.35	0.069	-0.11
1419055_a_at	Ptpn21	protein tyrosine phosphatase, non-receptor type 21	-1.11	0.552	1.02	0.859	1.01	0.971	-1.04	0.927	-0.03

1457206_at	Zfp521	Zinc finger protein 521	-1.16	0.591	1.26	0.425	-1.23	0.14	1.38	0.171	0.06
1419650_at	Zfr	zinc finger RNA binding protein	-1.01	0.895	1	0.977	-1.06	0.703	1.01	0.939	-0.01
1439229_at	Plekha7	pleckstrin homology domain containing, family A member 7	-1.01	0.825	1.02	0.844	-1.07	0.694	1.3	0.433	0.06
1433261_at	9430052A13Rik	RIKEN cDNA 9430052A13 gene	1.12	0.462	-1.08	0.81	-1.11	0.83	1.89	0.444	0.2
1447851_x_at	---	---	1.27	0.341	-1.6	0.203	1.04	0.769	-1.33	0.345	-0.15
1452682_at	4632404H22Rik	RIKEN cDNA 4632404H22 gene	-1.11	0.409	-1.08	0.606	1.11	0.643	1.52	0.068	0.11
1417509_at	Rnf19	ring finger protein (C3HC4 type) 19	-1.19	0.035	-1.15	0.456	1.23	0.466	1.91	0.349	0.2
1457995_at	F730014I05Rik	RIKEN cDNA F730014I05 gene	1.25	0.015	-1.14	0.736	-1.24	0.193	1	0.985	-0.03
1432421_at	Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	1.06	0.883	-1.13	0.6	-1.01	0.974	1.21	0.39	0.03
1451631_at	BC021395	cDNA sequence BC021395	-1.21	0.572	-1.29	0.573	1.34	0.3	1.18	0.492	0
1448934_at	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	-1.07	0.649	-1.16	0.215	1.14	0.237	1.13	0.11	0.01
1431169_at	D230012E17Rik	RIKEN cDNA D230012E17 gene	1.1	0.238	-1.4	0.277	1.12	0.785	-1.21	0.073	-0.1
1424783_a_at	Ugt1a2 /// Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A2 /// UDP glucuronosyltransf	-1.08	0.375	-1.1	0.444	1.11	0.23	1.84	0.024	0.19
1449336_a_at	Slk	STE20-like kinase (yeast)	-1.01	0.924	1.08	0.616	-1.15	0.394	1.26	0.368	0.05
1457841_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420405G1	1.1	0.874	-1.25	0.721	1.04	0.868	-1.03	0.933	-0.04
1442517_a_at	9630013A20Rik	RIKEN cDNA 9630013A20 gene	1.21	0.274	1.04	0.917	-1.44	0.287	-1.23	0.577	-0.11
1440179_x_at	Ibrdc1	IBR domain containing 1	-1.04	0.904	-1.25	0.175	1.17	0.313	1.34	0.057	0.06
1442570_at	Zmym1	Zinc finger, MYM domain containing 1	-1.66	0.337	1.59	0.42	-1.33	0.487	1.16	0.401	-0.06
1435782_at	LOC668206	similar to ubiquitin A-52 residue ribosomal protein fusion product 1	1.08	0.669	-1.36	0.219	1.12	0.642	-1.16	0.608	-0.08
1447995_x_at	1700026B20Rik	RIKEN cDNA 1700026B20 gene	-1.07	0.691	1.15	0.66	-1.17	0.523	1.28	0.35	0.05
1417700_at	Rab38	Rab38, member of RAS oncogene family	-1.02	0.738	1.18	0.51	-1.27	0.251	1.35	0.438	0.06
1449868_at	Tbx6	T-box 6	-1.15	0.674	-1.28	0.527	1.29	0.122	1.55	0.224	0.1
1430359_a_at	Nadsyn1	NAD synthetase 1	-1.28	0.115	1.03	0.359	1.13	0.493	-1.42	0.013	-0.14
1458013_at	Rbm27	RNA binding motif protein 27	1.57	0.563	1.04	0.937	-2.97	0.114	-1.04	0.964	-0.35
1420725_at	Tmlhe	trimethyllysine hydroxylase, epsilon	-1.57	0.024	1.2	0.249	1.1	0.41	-1.21	0.313	-0.12
1452168_x_at	Gspt1	G1 to S phase transition 1	-1.14	0.256	-1.07	0.435	1.13	0.174	1.2	0.273	0.03
1425886_at	Fev	FEV (ETS oncogene family)	-1.09	0.907	1.2	0.747	-1.21	0.106	2.05	0.163	0.24
1445576_at	4930526H21Rik	RIKEN cDNA 4930526H21 gene	-1.1	0.675	-1.11	0.813	1.13	0.444	1.97	0.217	0.22
1436619_at	D630045M09Rik	RIKEN cDNA D630045M09 gene	1.14	0.154	-1.17	0.564	-1.05	0.57	1.38	0.287	0.07
1460685_at	Timm17b	translocase of inner mitochondrial membrane 17b	-1.03	0.892	-1.06	0.623	1.03	0.91	1.1	0.727	0.01
1424432_at	Ubtd1	ubiquitin domain containing 1	-1.13	0.699	-1.11	0.633	1.16	0.447	1.51	0.007	0.11
1422964_at	Rad23a	RAD23a homolog (S. cerevisiae)	1.18	0.667	-1.14	0.338	-1.12	0.64	2.41	0.215	0.33
1430423_s_at	2610528E23Rik ///	RIKEN cDNA 2610528E23 gene /// FGF receptor activating protein 1	-1.41	0.393	-1.14	0.146	1.36	0.268	1.36	0.412	0.04
1428618_at	Hcfc2	host cell factor C2	-1.05	0.839	1.21	0.106	-1.29	0.091	1.24	0.333	0.03
1438303_at	Tgfb2	transforming growth factor, beta 2	-1.35	0.268	1.07	0.825	1.13	0.83	-1.39	0.577	-0.13
1448956_at	Stard10	START domain containing 10	1.1	0.615	-1.14	0.503	-1.04	0.793	2.73	0.177	0.41
1454566_at	4933439C20Rik ///	RIKEN cDNA 4933439C20 gene /// RIKEN cDNA D030013I16 gene	1.08	0.827	1.53	0.263	-3.05	0.142	-1.95	0.129	-0.6
1415901_at	Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	-1.21	0.444	-1.01	0.838	1.13	0.236	1.21	0.289	0.03
1452786_at	Trmu	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	-1.07	0.754	-1.15	0.458	1.13	0.385	1.15	0.49	0.02
1434854_a_at	Rps10	ribosomal protein S10	1.03	0.835	1.07	0.187	-1.19	0.316	-1.5	0.028	-0.15
1429183_at	Pkp2	plakophilin 2	-1.02	0.857	-1.11	0.186	1.06	0.686	1.56	0.284	0.12
1438480_a_at	Thyn1	thymocyte nuclear protein 1	-1.19	0.03	-1.22	0.186	1.28	0.283	1.33	0.043	0.05
1456848_at	---	---	-1.41	0.198	1.08	0.822	1.16	0.616	-1.26	0.406	-0.11
1459176_at	---	---	1.53	0.278	-1.21	0.771	-1.7	0.125	1.09	0.778	-0.07
1433612_at	Ap2s1	adaptor-related protein complex 2, sigma 1 subunit	1.03	0.517	-1.02	0.805	-1.06	0.574	1.04	0.874	-0.01
1425228_a_at	Dguok	deoxyguanosine kinase	1.05	0.202	-1.23	0.15	1.09	0.293	-1.34	0.093	-0.11
1453030_at	Msl2l1	male-specific lethal 2-like 1 (Drosophila)	-1.3	0.211	1.11	0.178	1.06	0.667	-1.09	0.682	-0.05
1446476_at	A430107P09Rik	RIKEN cDNA A430107P09 gene	1.04	0.931	1.26	0.339	-1.56	0.007	-1.95	0.227	-0.3
1453691_at	4921528I07Rik	RIKEN cDNA 4921528I07 gene	-1.12	0.503	1.19	0.676	-1.17	0.677	1.12	0.819	0.01
1417453_at	Cul4b	cullin 4B	-1.21	0.361	-1.06	0.464	1.18	0.336	1.01	0.933	-0.02
1419577_at	A530089I17Rik	RIKEN cDNA A530089I17 gene	-1.07	0.28	-1.09	0.189	1.1	0.417	1.08	0.415	0
1448821_at	Tyr	tyrosinase	-2.15	0.392	1.41	0.364	1.07	0.726	-1.39	0.115	-0.26
1434042_s_at	Mtmr3	myotubularin related protein 3	-1.06	0.225	-1.03	0.564	1.03	0.69	1.69	0.268	0.16

1419223_a_at	Dtna	dystrobrevin alpha	1.16	0.735	-1.54	0.067	1.13	0.769	-1.48	0.185	-0.18
1417818_at	Wwtr1	WW domain containing transcription regulator 1	1.02	0.915	1.18	0.28	-1.35	0.104	-1.04	0.814	-0.05
1438508_at	Jmjd1b	Jumonji domain containing 1B	1.02	0.819	1.22	0.298	-1.43	0.145	-1.08	0.839	-0.07
1429261_at	LOC664968 /// LOC	hypothetical protein LOC664968 /// hypothetical protein LOC669621 /// hypothetic	1.17	0.519	-1.03	0.659	-1.25	0.262	1.53	0.312	0.11
1420802_at	Il13	interleukin 13	1.17	0.219	1.21	0.461	-1.77	0.28	-1.91	0.013	-0.33
1432977_at	9030607L02Rik	RIKEN cDNA 9030607L02 gene	1.59	0.06	-1.15	0.771	-2.07	0.025	1.32	0.715	-0.08
1423670_a_at	Srpr	signal recognition particle receptor ('docking protein')	-1.1	0.272	1.07	0.651	-1.03	0.478	1.04	0.515	-0.01
1434930_at	Tpcn1	two pore channel 1	-1.08	0.356	-1.13	0.503	1.14	0.738	2.28	0.189	0.3
1453330_at	0610010D24Rik	RIKEN cDNA 0610010D24 gene	-1.02	0.915	1.01	0.967	-1.05	0.79	1.02	0.852	-0.01
1455440_at	Clcn6	chloride channel 6	-1.34	0.192	1.12	0.776	1.08	0.753	-1.12	0.331	-0.07
1431869_at	5730419F03Rik	RIKEN cDNA 5730419F03 gene	-1.1	0.884	-1.49	0.076	1.36	0.561	1.82	0.325	0.15
1439234_a_at	Tm2d2	TM2 domain containing 2	1.04	0.853	1.06	0.61	-1.19	0.055	-1.35	0.017	-0.11
1432218_a_at	Nol9	nucleolar protein 9	-1.43	0.477	1.1	0.846	1.14	0.591	-1.22	0.611	-0.1
1425465_a_at	Senp2	SUMO/sentrin specific peptidase 2	-1.09	0.682	-1.48	0.203	1.35	0.311	1.63	0.325	0.1
1459792_at	---	---	1.47	0.478	-1.37	0.295	-1.34	0.462	2.34	0.087	0.28
1449646_s_at	Tigd5	tigger transposable element derived 5	-1.21	0.303	-1.02	0.883	1.14	0.602	1.03	0.659	-0.01
1449357_at	2310030G06Rik	RIKEN cDNA 2310030G06 gene	1	0.98	1.04	0.719	-1.11	0.728	-2.88	0.095	-0.49
1454036_a_at	Usp15	ubiquitin specific peptidase 15	-1.12	0.601	-1.17	0.2	1.19	0.231	2.28	0.231	0.3
1443601_at	LOC545677	Hypothetical protein LOC545677	1.78	0.445	-3.26	0.161	-1.16	0.729	1.18	0.704	-0.36
1424094_at	Nek9	NIMA (never in mitosis gene a)-related expressed kinase 9	1.03	0.699	-1.16	0.197	1.05	0.623	-1.45	0.382	-0.13
1454689_at	Srrm1	serine/arginine repetitive matrix 1	-1.07	0.353	-1.15	0.466	1.14	0.343	1.29	0.295	0.05
1452889_at	2310007H09Rik	RIKEN cDNA 2310007H09 gene	1.27	0.677	-1.29	0.408	-1.11	0.618	1.36	0.322	0.06
1444424_at	Uble1a	Ubiquitin-like 1 (sentrin) activating enzyme E1A	1.58	0.564	-1.18	0.627	-1.94	0.005	1.3	0.128	-0.06
1446040_at	2700049A03Rik	RIKEN cDNA 2700049A03 gene	1.36	0.198	-1.23	0.067	-1.29	0.031	1.2	0.459	0.01
1454505_at	6330562C20Rik	RIKEN cDNA 6330562C20 gene	-1.29	0.287	1.1	0.881	1.07	0.856	-1.58	0.317	-0.18
1458628_at	Limk2	LIM motif-containing protein kinase 2	1.01	0.959	-1.03	0.905	-1.04	0.776	1.1	0.702	0.01
1415750_at	Tbl3	transducin (beta)-like 3	-1.01	0.979	-1.13	0.619	1.07	0.67	1.2	0.249	0.03
1419572_a_at	Abcd4	ATP-binding cassette, sub-family D (ALD), member 4	1.03	0.914	1.1	0.548	-1.23	0.007	-1.16	0.746	-0.06
1449935_a_at	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	-1.06	0.438	-1.1	0.288	1.09	0.261	1.04	0.808	-0.01
1453777_a_at	Ndst3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	-2.91	0.083	-1.22	0.453	1.78	0.173	1.49	0.273	-0.21
1432144_a_at	Rchy1	ring finger and CHY zinc finger domain containing 1	-1.05	0.657	-1.09	0.349	1.07	0.573	1.03	0.817	-0.01
1434066_at	Gtf3c1	general transcription factor III C 1	-1.06	0.562	-1.1	0.204	1.1	0.411	1.08	0.523	0
1438711_at	Pklr	pyruvate kinase liver and red blood cell	-1.11	0.502	-1.37	0.194	1.31	0.585	4.04	0.204	0.72
1432862_at	Nkx2-4	NK2 transcription factor related, locus 4 (Drosophila)	1.02	0.804	-1.84	0.427	1.38	0.457	-1.43	0.283	-0.22
1416144_a_at	Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	-1.08	0.255	1.03	0.706	-1.01	0.928	1.02	0.701	-0.01
1452944_at	Afmid	arylformamidase	-1.36	0.146	-1.38	0.394	1.48	0.516	2.17	0.119	0.23
1455027_at	Rufy3	RUN and FYVE domain containing 3	-1.14	0.659	1.33	0.152	-1.37	0.266	1	0.989	-0.04
1425605_a_at	Lmbr1	limb region 1	-1.18	0.805	-1.25	0.656	1.3	0.592	1.34	0.329	0.05
1427434_at	---	---	-1.36	0.506	1.06	0.51	1.16	0.417	-1.19	0.223	-0.08
1453864_at	Rdh14	retinol dehydrogenase 14 (all-trans and 9-cis)	1.11	0.611	-1.27	0.327	1.05	0.844	-1.98	0.03	-0.27
1430427_a_at	Pcdh18	protocadherin 18	1.39	0.524	-1.25	0.666	-1.33	0.64	1.21	0.769	0.01
1444325_at	Pten	Phosphatase and tensin homolog	1.87	0.288	-3.13	0.01	-1.33	0.62	1.68	0.2	-0.23
1424123_at	BC011209	cDNA sequence BC011209	-1.14	0.71	1.15	0.758	-1.09	0.717	1.08	0.56	0
1456743_x_at	Morf4l2 /// LOC433	mortality factor 4 like 2 /// similar to Mortality factor 4-like protein 2 (MORF-relatec	-1.07	0.568	1.2	0.316	-1.24	0.076	1.11	0.211	0
1424803_at	BC020002	cDNA sequence BC020002	1.14	0.58	-1.01	0.93	-1.23	0.03	1.33	0.11	0.06
1416145_at	Dhx15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	1.04	0.648	-1.06	0.399	-1.04	0.543	1.04	0.739	0
1417562_at	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	-1.07	0.464	-1.08	0.299	1.09	0.588	1.39	0.221	0.08
1432419_a_at	2700078K21Rik	RIKEN cDNA 2700078K21 gene	1.13	0.471	-1.09	0.659	-1.11	0.547	1.28	0.518	0.05
1416315_at	Abhd4	abhydrolase domain containing 4	1.05	0.885	-1	0.984	-1.11	0.192	1.45	0.245	0.1
1440419_at	Gm1679	gene model 1679, (NCBI)	1.53	0.128	-1.92	0.189	-1.11	0.539	1.15	0.714	-0.09
1448225_at	Gpaa1	GPI anchor attachment protein 1	1.15	0.358	-1.21	0.054	-1.04	0.9	1.14	0.475	0.01
1428004_at	3300001G02Rik	RIKEN cDNA 3300001G02 gene	1.09	0.325	-1.12	0.358	-1.04	0.837	1.31	0.492	0.06
1430110_at	D230044M03Rik	RIKEN cDNA D230044M03 gene	1.1	0.903	-1.2	0.623	1.02	0.953	-1.35	0.549	-0.11

1451720_at	Vps39	vacuolar protein sorting 39 (yeast)	1.08	0.329	1.07	0.508	-1.26	0.038	-1.37	0.115	-0.12
1448491_at	Ech1	enoyl coenzyme A hydratase 1, peroxisomal	1.13	0.019	-1.32	0.098	1.06	0.726	-1.24	0.188	-0.09
1434906_at	0610005C13Rik	RIKEN cDNA 0610005C13 gene	1.1	0.559	1.16	0.04	-1.45	0.216	-2.84	0.203	-0.51
1455832_a_at	Umps	uridine monophosphate synthetase	-1.12	0.617	-1.09	0.741	1.13	0.397	1.34	0.319	0.07
1417820_at	Tor1b	torsin family 1, member B	1.34	0.305	-1.11	0.61	-1.41	0.124	1.09	0.799	-0.02
1427909_at	2410015M20Rik	RIKEN cDNA 2410015M20 gene	1.01	0.977	1.03	0.776	-1.1	0.542	-1.07	0.817	-0.03
1430389_at	4930509H03Rik	RIKEN cDNA 4930509H03 gene	1.38	0.247	-1.76	0.28	1	0.993	-1.33	0.417	-0.18
1416421_a_at	Ssb	Sjogren syndrome antigen B	1.02	0.932	1.03	0.915	-1.11	0.548	-1.05	0.884	-0.03
1458176_at	Per3	Period homolog 3 (Drosophila)	-1.06	0.902	1.07	0.937	-1.08	0.887	1.03	0.933	-0.01
1437731_at	5830404H04Rik	RIKEN cDNA 5830404H04 gene	-1.1	0.184	-1.14	0.51	1.16	0.316	1.16	0.433	0.02
1434039_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-1.05	0.821	1.02	0.907	-1.03	0.771	1	0.993	-0.01
1427853_a_at	Hspb1	heat shock protein 1	-1.11	0.412	1.11	0.595	-1.07	0.724	1.47	0.289	0.1
1438648_x_at	1190003M12Rik	RIKEN cDNA 1190003M12 gene	-1.06	0.385	1.28	0.056	-1.38	0.154	1.15	0.496	0
1434665_at	Aga	aspartylglucosaminidase	-1.12	0.356	-1.1	0.273	1.14	0.407	1.02	0.917	-0.01
1429265_a_at	Rnf130	ring finger protein 130	-1.08	0.084	1.02	0.66	1	0.964	-1.17	0.346	-0.06
1452303_at	Arhgef10	Rho guanine nucleotide exchange factor (GEF) 10	1.09	0.724	-1.55	0.184	1.22	0.368	-1.16	0.475	-0.1
1419162_s_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	1.04	0.629	1.09	0.642	-1.22	0.149	-1.1	0.466	-0.05
1443396_at	Smndc1 /// LOC545	survival motor neuron domain containing 1 /// similar to survival motor neuron dor	1.17	0.184	1.1	0.539	-1.47	0.074	-1.17	0.566	-0.09
1448897_at	Mkrn2	makorin, ring finger protein, 2	-1.09	0.638	-1.03	0.623	1.05	0.489	1.01	0.921	-0.01
1417998_at	Ptges3	prostaglandin E synthase 3 (cytosolic)	-1.01	0.945	1.02	0.902	-1.07	0.483	1.18	0.061	0.03
1434514_at	Rbm15	RNA binding motif protein 15	-1.08	0.664	-1	0.976	1.03	0.81	1.28	0.291	0.06
1453981_at	2900009I07Rik	RIKEN cDNA 2900009I07 gene	-1.42	0.674	1.57	0.599	-1.48	0.297	1.37	0.418	0.01
1441911_x_at	Gart	phosphoribosylglycinamide formyltransferase	-1.37	0.203	-1.1	0.802	1.31	0.344	1.15	0.736	0
1447867_x_at	4930444A02Rik	RIKEN cDNA 4930444A02 gene	-1.14	0.681	-1.02	0.935	1.09	0.903	1.86	0.103	0.2
1446172_at	---	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:95300	1.35	0.284	1.04	0.806	-1.78	0.006	-1.27	0.203	-0.17
1448795_a_at	Tbrg4	transforming growth factor beta regulated gene 4	-1.43	0.045	-1.27	0.177	1.46	0.163	1.5	0.289	0.07
1448708_at	Pparbp	peroxisome proliferator activated receptor binding protein	-1.02	0.948	1.06	0.568	-1.11	0.244	1.05	0.533	0
1423535_at	Strn3	striatin, calmodulin binding protein 3	-1.01	0.776	1.12	0.367	-1.18	0.008	1.03	0.819	-0.01
1456707_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.05	0.667	-1.07	0.539	-1.04	0.861	1.03	0.918	-0.01
1436827_at	Gm944	gene model 944, (NCBI)	-1.07	0.648	1.22	0.407	-1.26	0.265	6.52	0.182	1.35
1457492_at	Trio	Triple functional domain (PTPRF interacting)	1.1	0.162	1.26	0.274	-1.72	0.008	-1.15	0.239	-0.13
1437786_at	C80008	expressed sequence C80008	-1.37	0.756	1.15	0.718	1.06	0.851	-1.77	0.396	-0.23
1416316_at	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	-1.1	0.352	-1.35	0.221	1.3	0.436	1.51	0.079	0.09
1451845_a_at	Ptrh2	peptidyl-tRNA hydrolase 2	-1.04	0.804	1.08	0.472	-1.11	0.361	1.14	0.627	0.02
1423798_a_at	Eif1	eukaryotic translation initiation factor 1	1.03	0.773	-1.05	0.541	-1.04	0.648	1.12	0.164	0.02
1426780_at	D14Ertd436e	DNA segment, Chr 14, ERATO Doi 436, expressed	1.04	0.804	-1.04	0.809	-1.05	0.73	1.07	0.712	0
1450051_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	1.34	0.304	-1.09	0.703	-1.45	0.315	1.19	0.593	0
1456551_at	Aldh1l1	Aldehyde dehydrogenase 1 family, member L1	-1.11	0.854	-1.28	0.429	1.27	0.398	1.13	0.807	0
1460319_at	Fut8	fucosyltransferase 8	-1.05	0.513	1.02	0.897	-1.03	0.821	1.35	0.236	0.07
1424185_a_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// RIKEN cD	1.01	0.928	1	0.979	-1.07	0.343	-1.05	0.054	-0.03
1416079_a_at	Arpc1a	actin related protein 2/3 complex, subunit 1A	-1.04	0.387	-1.07	0.279	1.05	0.689	1.24	0.065	0.05
1443785_x_at	Pdlim7	PDZ and LIM domain 7	-1.26	0.505	-1.05	0.842	1.2	0.37	1.18	0.104	0.02
1447989_at	---	Transcribed locus, weakly similar to XP_576435.1 PREDICTED: similar to ORF4	-1.08	0.922	-3.16	0.375	1.71	0.468	1.55	0.643	-0.25
1450924_at	Hdgfrp3	hepatoma-derived growth factor, related protein 3	1.05	0.559	1.04	0.878	-1.17	0.286	-1.06	0.818	-0.03
1446285_at	A130034M23Rik	RIKEN cDNA A130034M23 gene	-1.05	0.955	-1.34	0.25	1.25	0.514	1.52	0.27	0.09
1443902_at	6430573F11Rik	RIKEN cDNA 6430573F11 gene	-1.75	0.504	-2.96	0.119	2.04	0.314	1.04	0.752	-0.41
1448659_at	Casp7	caspase 7	-1.03	0.852	1.01	0.964	-1.03	0.713	1.1	0.618	0.01
1457807_at	Gnpnat1	Glucosamine-phosphate N-acetyltransferase 1	-1.48	0.104	1.05	0.927	1.22	0.523	-1.2	0.522	-0.1
1431085_a_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.01	0.877	-1.05	0.524	-1.02	0.888	1.38	0.321	0.08
1419283_s_at	Tns1	tensin 1	1.21	0.296	-1.49	0.26	1.07	0.503	-1.08	0.87	-0.07
1428854_at	Tmed8	transmembrane emp24 domain containing 8	1.05	0.516	-1.31	0.112	1.13	0.308	-1.76	0.111	-0.22
1424284_at	Pomt1	protein-O-mannosyltransferase 1	-1.19	0.049	-1.07	0.391	1.17	0.23	1.38	0.367	0.07
1430901_at	1700003F17Rik	RIKEN cDNA 1700003F17 gene	1.29	0.494	1.01	0.969	-1.54	0.118	-1.27	0.282	-0.13

1459725_s_at	Dcpp /// LOC63053	demilune cell and parotid protein /// similar to common salivary protein 1	-2.79	0.197	-1.05	0.897	1.64	0.063	1.21	0.466	-0.25
1438395_at	---	---	1.09	0.877	-1.14	0.741	-1.02	0.931	2.83	0.009	0.44
1432275_at	Ikbkb	inhibitor of kappaB kinase beta	-1.27	0.72	-1.26	0.413	1.37	0.308	2.72	0.018	0.39
1420349_at	Ptgfr	prostaglandin F receptor	1.12	0.378	1.02	0.924	-1.24	0.317	-1.46	0.574	-0.14
1447597_at	Rpo1-4	RNA polymerase 1-4	-1.5	0.388	1.1	0.786	1.18	0.602	-1.34	0.734	-0.14
1438624_x_at	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	1.01	0.958	1.27	0.725	-1.49	0.183	-1.35	0.356	-0.14
1416794_at	Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	-1.14	0.287	-1.35	0.143	1.33	0.283	2	0.237	0.21
1415855_at	Kitl	kit ligand	1.05	0.831	1.3	0.058	-1.66	0.019	-1.05	0.803	-0.09
1441177_at	---	---	1.52	0.425	-1.56	0.052	-1.27	0.471	2.09	0.24	0.2
1439454_x_at	Tm2d2	TM2 domain containing 2	1	0.966	1.11	0.294	-1.19	0.185	-1.29	0.183	-0.09
1427879_at	1810031K17Rik	RIKEN cDNA 1810031K17 gene	-1.2	0.048	-1.05	0.537	1.17	0.354	1.12	0.32	0.01
1427000_at	Hnf4a	hepatic nuclear factor 4, alpha	-1.24	0.298	1.08	0.54	1.06	0.908	-1.87	0.561	-0.24
1447053_x_at	Ssr3	signal sequence receptor, gamma	-1.21	0.352	1.3	0.366	-1.22	0.037	1.07	0.626	-0.01
1452540_a_at	Hist1h2bc /// Hist1h	histone 1, H2bc /// histone 1, H2be /// histone 1, H2bl /// histone 1, H2bm /// histor	-1.08	0.595	-1.17	0.109	1.17	0.311	1.97	0.311	0.22
1431105_a_at	Tmem33	transmembrane protein 33	-1.03	0.837	-1.23	0.167	1.16	0.65	1.71	0.226	0.16
1433881_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	-1.18	0.133	1.12	0.528	-1.02	0.929	1.3	0.484	0.06
1423702_at	H1f0	H1 histone family, member 0	1.02	0.9	-1.04	0.72	-1.03	0.778	1.21	0.296	0.04
1415783_at	Vps35	vacuolar protein sorting 35	-1.07	0.151	1.09	0.11	-1.08	0.394	1.34	0.161	0.07
1422540_at	Fbln1	fibulin 1	-1.17	0.603	1.37	0.679	-1.38	0.463	2.17	0.064	0.25
1458362_at	D730005E14Rik	RIKEN cDNA D730005E14 gene	-1.85	0.362	-1.38	0.174	1.69	0.057	1.3	0.496	-0.06
1449709_s_at	Ate1	arginine-tRNA-protein transferase 1	-1.08	0.67	-1.11	0.448	1.12	0.409	1.01	0.967	-0.01
1442050_at	Zfp608 /// D430007	zinc finger protein 608 /// RIKEN cDNA D430007A19 gene	1.01	0.962	1.25	0.576	-1.44	0.015	-1.57	0.122	-0.19
1433803_at	Jak1	Janus kinase 1	1.15	0.513	1.14	0.124	-1.53	0.001	-1.48	0.212	-0.18
1419195_at	Wfdc15	WAP four-disulfide core domain 15	-1.12	0.165	1.16	0.731	-1.11	0.449	1.76	0.132	0.17
1423408_a_at	2500003M10Rik	RIKEN cDNA 2500003M10 gene	-1.11	0.513	1.04	0.668	1	0.9	-1.27	0.026	-0.08
1428025_s_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.04	0.833	1.25	0.246	-1.36	0.255	1.05	0.849	-0.02
1452584_at	1500032L24Rik	RIKEN cDNA 1500032L24 gene	-1.04	0.632	-1.02	0.647	1.01	0.919	1.2	0.211	0.04
1426839_at	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	-1.01	0.943	-1.08	0.758	1.03	0.911	1.58	0.252	0.13
1425275_at	Asph	aspartate-beta-hydroxylase	1.05	0.95	-1.01	0.959	-1.1	0.761	1.11	0.339	0.01
1416941_s_at	Wbscr1	Williams-Beuren syndrome chromosome region 1 homolog (human)	-1.08	0.216	-1.04	0.37	1.06	0.136	1.08	0.119	0.01
1456585_x_at	E130309D02Rik	RIKEN cDNA E130309D02 gene	1.02	0.927	-1.09	0.538	1.02	0.932	-1.13	0.773	-0.05
AFFX-r2-Ec-bioC-5_	---	---	1.19	0.085	1.08	0.463	-1.46	0.082	-1.17	0.441	-0.09
1421163_a_at	Nfia	nuclear factor I/A	1.26	0.248	-1.07	0.529	-1.32	0.047	2.04	0.04	0.23
1419266_at	Nfyb	nuclear transcription factor-Y beta	-1.05	0.452	1.06	0.347	-1.06	0.744	1.48	0.294	0.11
1456604_a_at	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.05	0.502	-1.05	0.692	-1.06	0.762	1.2	0.457	0.04
1460653_at	Atxn2	ataxin 2	-1.1	0.491	-1.29	0.23	1.27	0.237	1.64	0.298	0.13
1423841_at	Bxdc2	brix domain containing 2	1.02	0.727	-1.06	0.622	-1.01	0.937	1.25	0.348	0.05
1425493_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	-1.01	0.932	1	0.99	-1.04	0.537	1.31	0.158	0.06
1448460_at	Acvr1	activin A receptor, type 1	-1.05	0.638	1.11	0.425	-1.12	0.683	1.09	0.566	0.01
1424729_at	BC054059	cDNA sequence BC054059	-2.65	0.064	-1.76	0.369	2.01	0.397	1.75	0.029	-0.16
1442383_at	Triobp	TRIO and F-actin binding protein	-1.64	0.367	1.84	0.36	-2.01	0.085	1.82	0.282	0
1453064_at	5730466H23Rik	RIKEN cDNA 5730466H23 gene	-1.02	0.914	1.15	0.064	-1.22	0.285	1.21	0.475	0.03
1421636_at	9030605E16Rik	RIKEN cDNA 9030605E16 gene	1.11	0.868	-1.61	0.221	1.22	0.605	-2.05	0.302	-0.33
1440451_at	D730048J04Rik	RIKEN cDNA D730048J04 gene	-1.21	0.36	1.13	0.818	-1	0.985	1.13	0.811	0.01
1444701_at	A130001D14Rik	RIKEN cDNA A130001D14 gene	1.26	0.485	1.01	0.987	-1.46	0.201	-1.28	0.084	-0.12
1428969_at	D030074E01Rik	RIKEN cDNA D030074E01 gene	-1.11	0.705	1.02	0.8	1.04	0.641	-1.28	0.273	-0.08
1416181_at	Mesdc2	mesoderm development candiate 2	1.03	0.574	-1	0.967	-1.08	0.569	1.17	0.166	0.03
1453853_a_at	Arhgef12	Rho guanine nucleotide exchange factor (GEF) 12	1.17	0.622	-1.05	0.829	-1.2	0.261	2.44	0.291	0.34
1453782_at	3021401C12Rik	RIKEN cDNA 3021401C12 gene	1.1	0.452	-1.21	0.262	1.03	0.521	-1.11	0.454	-0.05
1439871_at	Lmtk2	Lemur tyrosine kinase 2	1.23	0.162	1.06	0.908	-1.51	0.178	-1.16	0.125	-0.09
1418140_at	Dcx	doublecortin	-1.36	0.241	1	0.993	1.21	0.564	-1.37	0.332	-0.13
1429374_at	Cypt12	cysteine-rich perinuclear theca 12	1.33	0.412	-1.63	0.094	1.01	0.953	-2.35	0.157	-0.41
1438904_at	Nhsl1	NHS-like 1	-1	0.991	1	0.996	-1.05	0.689	1.09	0.021	0.01

1423516_a_at	Nid2	nidogen 2	-1.22	0.205	-1.17	0.572	1.28	0.373	1.33	0.159	0.05
1437526_x_at	Hnrpr /// LOC66932	heterogeneous nuclear ribonucleoprotein R /// similar to heterogeneous nuclear ri	-1.17	0.11	1.06	0.708	1.03	0.825	-1.02	0.812	-0.02
1441145_at	D030065N23Rik	RIKEN cDNA D030065N23 gene	1.07	0.731	1.24	0.078	-1.56	0.019	-2.19	0.02	-0.36
1416152_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	-1.08	0.538	1.08	0.366	-1.06	0.319	1.17	0.341	0.03
1442024_at	Ppp1r3e	Protein phosphatase 1, regulatory (inhibitor) subunit 3E	1.08	0.581	-1.4	0.318	1.17	0.592	-1.01	0.94	-0.04
1421455_at	Sntb1	syntrophin, basic 1	-1.5	0.528	1.08	0.884	1.2	0.658	-1.45	0.61	-0.16
1422766_at	Stau1	staufen (RNA binding protein) homolog 1 (Drosophila)	-1.04	0.786	-1.11	0.431	1.09	0.592	1.09	0.483	0.01
1417360_at	Mlh1	mutL homolog 1 (E. coli)	-1.2	0.303	1.37	0.063	-1.34	0.188	1.09	0.662	-0.02
1453365_at	Rabgap1l	RAB GTPase activating protein 1-like	1.17	0.268	-1.36	0.029	1.05	0.772	-1.41	0.14	-0.14
1455734_at	Crbn	cereblon	-1.03	0.684	-1.13	0.219	1.1	0.572	1.02	0.879	-0.01
1449342_at	Ptplb	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	-1.11	0.304	-1.05	0.103	1.1	0.547	1.12	0.357	0.01
1429082_at	D5Ertd585e	DNA segment, Chr 5, ERATO Doi 585, expressed	-1.1	0.596	-1.1	0.625	1.14	0.16	1.26	0.077	0.05
1419724_at	Edar /// LOC66900	ectodysplasin-A receptor /// similar to Tumor necrosis factor receptor superfamily	1.25	0.714	-1.06	0.81	-1.32	0.063	1.81	0.452	0.17
1424856_at	Atp1a3	ATPase, Na+/K+ transporting, alpha 3 polypeptide	1.2	0.428	-1.33	0.442	1	0.98	-1.51	0.067	-0.16
1421197_a_at	Acin1	apoptotic chromatin condensation inducer 1	-1.04	0.704	1.02	0.856	-1.03	0.925	1.01	0.975	-0.01
1426707_at	Tubgcp3	tubulin, gamma complex associated protein 3	-1.04	0.755	1.04	0.757	-1.05	0.667	1.11	0.519	0.02
1416391_at	Ptcd1	pentatricopeptide repeat domain 1	1.24	0.371	-1.09	0.216	-1.26	0.297	1.03	0.879	-0.02
1451222_at	Btf3l4	basic transcription factor 3-like 4	-1.06	0.602	-1.04	0.474	1.05	0.619	1.17	0.265	0.03
1418002_at	Higd2a	HIG1 domain family, member 2A	1.02	0.71	-1.1	0.119	1.02	0.825	-1.31	0.149	-0.09
1449970_at	Capn12	calpain 12	-1.54	0.662	-2.84	0.245	1.95	0.04	1.65	0.268	-0.19
1451175_at	Spcs3	signal peptidase complex subunit 3 homolog (S. cerevisiae)	-1.05	0.44	1.04	0.654	-1.04	0.766	1.14	0.152	0.02
1429769_at	Pggt1b	protein geranylgeranyltransferase type I, beta subunit	-1.14	0.344	1.19	0.236	-1.12	0.367	1.09	0.6	0
1436678_at	---	---	1.07	0.897	1.21	0.662	-1.48	0.182	-1.58	0.246	-0.19
1419909_at	Mphosph9	M-phase phosphoprotein 9	1.01	0.949	-1.02	0.927	-1.04	0.704	1.32	0.342	0.07
1429115_at	2010003O02Rik	RIKEN cDNA 2010003O02 gene	1.36	0.027	1.09	0.431	-1.97	0.019	-1.58	0.103	-0.27
1459548_at	Spire1	spire homolog 1 (Drosophila)	-1.03	0.877	1.24	0.757	-1.34	0.135	2.81	0.31	0.42
1445832_at	---	---	1.33	0.501	-1.93	0.176	1.11	0.828	-1.94	0.254	-0.36
1421998_at	Tor3a	torsin family 3, member A	1.12	0.302	1.02	0.875	-1.23	0.108	-1.29	0.398	-0.1
1424230_at	Exoc6	exocyst complex component 6	-1.24	0.09	-1.05	0.785	1.19	0.359	1.17	0.471	0.02
1445331_at	---	Transcribed locus	1.11	0.477	-1.27	0.551	1.06	0.425	-1.15	0.191	-0.06
1429878_a_at	Nupl1	nucleoporin like 1	-1.76	0.033	-1.05	0.923	1.44	0.23	1.29	0.242	-0.02
1459587_at	2410015B03Rik	RIKEN cDNA 2410015B03 gene	-1.08	0.864	-1.16	0.862	1.16	0.823	1.15	0.82	0.02
1419747_at	Asgr2	asialoglycoprotein receptor 2	1.07	0.69	-1.07	0.394	-1.06	0.804	1.71	0.321	0.17
1424086_at	D9Ucla1	DNA segment, Chr 9, University of California at Los Angeles 1	-1.01	0.959	1.04	0.56	-1.09	0.71	2.83	0.246	0.45
1423843_at	Lrrc61	leucine rich repeat containing 61	1.02	0.917	-1.22	0.59	1.12	0.531	-1.2	0.467	-0.07
1457415_a_at	4930513N10Rik	RIKEN cDNA 4930513N10 gene	1.55	0.507	-1.26	0.606	-1.64	0.125	1.27	0.645	-0.02
1429910_at	5730499H23Rik	RIKEN cDNA 5730499H23 gene	1.18	0.033	-1.21	0.187	-1.05	0.765	2.24	0.286	0.29
1421843_at	Il1rap	interleukin 1 receptor accessory protein	-1.48	0.004	-1.16	0.748	1.42	0.366	1.05	0.664	-0.04
1423682_a_at	Cdca4	cell division cycle associated 4	-1.04	0.393	1.09	0.709	-1.1	0.61	1.39	0.355	0.08
1447306_at	4930545H06Rik	RIKEN cDNA 4930545H06 gene	1.22	0.49	-1.38	0.455	1.01	0.869	-1.07	0.794	-0.06
1431390_a_at	Grinl1a	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	-1.12	0.149	1.02	0.791	1.04	0.77	-1.08	0.484	-0.03
1439066_at	Angpt1	angiopoietin 1	-1.62	0.02	1.65	0.377	-1.45	0.033	1.84	0.296	0.1
1460020_at	LOC629623	hypothetical protein LOC629623	-1.34	0.555	1.11	0.658	1.1	0.671	-1.94	0.027	-0.27
1416197_at	Snrpc	U1 small nuclear ribonucleoprotein C	-1.09	0.588	-1.12	0.444	1.15	0.478	1.32	0.217	0.06
1416789_at	Idh3g	isocitrate dehydrogenase 3 (NAD+), gamma	-1.1	0.462	-1.17	0.219	1.19	0.015	1.06	0.226	0
1417042_at	Slc37a4	solute carrier family 37 (glycerol-6-phosphate transporter), member 4	-1.24	0.212	-1.13	0.456	1.27	0.503	1.25	0.272	0.04
1448601_s_at	Msx1	homeo box, msh-like 1	-1.15	0.478	1.01	0.97	1.08	0.702	-1.03	0.859	-0.02
1459636_at	Angpt2	Angiopoietin 2	1.43	0.706	1.03	0.902	-2.05	0.131	-1.59	0.442	-0.29
1428446_at	Dync2li1	dynein cytoplasmic 2 light intermediate chain 1	-1.16	0.049	1.06	0.767	1.03	0.856	-1.41	0.099	-0.12
1455963_at	6332401O19Rik	RIKEN cDNA 6332401O19 gene	-1.21	0.263	-1.17	0.649	1.27	0.488	1.63	0.237	0.13
1442796_at	Atf7ip2	activating transcription factor 7 interacting protein 2	1.06	0.799	-1.15	0.842	1.03	0.907	-2.26	0.247	-0.33
1441334_at	---	Transcribed locus	-1.27	0.404	1.52	0.124	-1.55	0.042	1.08	0.887	-0.05
1439783_at	C330018D20Rik	RIKEN cDNA C330018D20 gene	1.13	0.134	-1.09	0.312	-1.1	0.611	1.18	0.467	0.03

1459432_at	---	Transcribed locus	1.03	0.901	1.01	0.974	-1.09	0.62	-1.24	0.41	-0.07
1459651_s_at	Nup54	nucleoporin 54	-1.25	0.105	-1.02	0.885	1.17	0.347	1.15	0.632	0.01
1457597_at	---	Transcribed locus	1.3	0.748	-1.52	0.464	-1	0.996	1.04	0.956	-0.05
1440665_at	---	---	1.08	0.934	-1.42	0.079	1.17	0.616	-2.09	0.197	-0.31
1427556_at	Mylk2 /// LOC66927	myosin, light polypeptide kinase 2, skeletal muscle /// similar to Myosin light chain	-1.63	0.389	1.62	0.565	-1.4	0.575	1.79	0.43	0.1
1442573_at	A930028L21Rik	RIKEN cDNA A930028L21 gene	1.42	0.526	-1.41	0.219	-1.2	0.517	1.35	0.538	0.04
1426585_s_at	Mapk1	mitogen activated protein kinase 1	-1.07	0.486	-1.09	0.028	1.1	0.108	1.08	0.103	0.01
1438176_x_at	1110031B06Rik	RIKEN cDNA 1110031B06 gene	-1.13	0.339	1.06	0.679	1.01	0.875	-1.2	0.433	-0.07
1421172_at	Adam12	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	-1.25	0.171	1.1	0.818	1.06	0.839	-1.04	0.926	-0.03
1449045_at	Afg3l1	AFG3(ATPase family gene 3)-like 1 (yeast)	-1.02	0.774	-1.06	0.402	1.03	0.81	1.29	0.013	0.06
1444165_at	Layn	layilin	-1.65	0.567	-1.26	0.775	1.56	0.573	1.87	0.469	0.13
1455640_a_at	Txn2	thioredoxin 2	-1.1	0.587	1.1	0.429	-1.06	0.557	1.19	0.372	0.03
1444076_at	Zfp81	zinc finger protein 81	-1.13	0.437	1.08	0.651	-1.01	0.863	1.11	0.418	0.01
1440341_at	LOC629345	similar to SMF protein	1.03	0.906	-1.28	0.248	1.14	0.581	-1.39	0.23	-0.12
1452741_s_at	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	1.17	0.628	-1.35	0.181	1.05	0.852	-1.54	0.149	-0.17
1424503_at	Rab22a	RAB22A, member RAS oncogene family	-1.05	0.856	-1.01	0.972	1.01	0.953	1.17	0.21	0.03
AFFX-r2-Bs-dap-M_	---	---	1.09	0.853	-1.15	0.34	1	0.991	-1.43	0.265	-0.12
1424888_at	2-Mar	membrane-associated ring finger (C3HC4) 2	-1.1	0.243	-1.14	0.2	1.17	0.626	2.16	0.31	0.27
1440166_x_at	Htr1d	5-hydroxytryptamine (serotonin) receptor 1D	-1.61	0.611	-1	0.995	1.34	0.178	1.02	0.937	-0.06
1453231_at	Cdkl1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-1.03	0.962	-1.52	0.268	1.33	0.531	1.72	0.236	0.12
1426446_at	6430548M08Rik	RIKEN cDNA 6430548M08 gene	-1.24	0.391	-1.03	0.931	1.17	0.405	1.33	0.254	0.06
1460095_at	1110030E23Rik	RIKEN cDNA 1110030E23 gene	-2.65	0.442	1.2	0.738	1.38	0.456	-4.1	0.21	-1.04
1452027_a_at	Trp63	transformation related protein 63	-1.32	0.551	1.17	0.812	1.03	0.953	-2.17	0.353	-0.32
1428378_at	Zc3hav1	zinc finger CCCH type, antiviral 1	-1.17	0.313	-1.45	0.152	1.41	0.196	1.11	0.371	-0.03
1438531_at	A730054J21Rik	RIKEN cDNA A730054J21 gene	-1.16	0.549	-1.08	0.883	1.16	0.337	1.57	0.386	0.12
1418238_at	Ivd	isovaleryl coenzyme A dehydrogenase	1.04	0.599	-1.24	0.298	1.11	0.538	-1.59	0.144	-0.17
1449470_at	Dlx1	distal-less homeobox 1	-1.23	0.48	1.16	0.829	-1.02	0.91	1.01	0.903	-0.02
1428615_at	P2ry5	purinergic receptor P2Y, G-protein coupled, 5	-1.13	0.062	1	0.98	1.07	0.42	-1.99	0.021	-0.26
1448100_at	4833439L19Rik	RIKEN cDNA 4833439L19 gene	-1.07	0.159	-1.12	0.163	1.13	0.113	1.14	0.207	0.02
1439413_x_at	Morf4l2	mortality factor 4 like 2	-1.21	0.223	1.29	0.129	-1.2	0.138	1.23	0.094	0.03
1448796_s_at	Tbrg4	transforming growth factor beta regulated gene 4	-1.06	0.678	-1.13	0.43	1.13	0.463	1.09	0.695	0.01
1418775_at	AI837181	expressed sequence AI837181	-1.77	0.044	1.08	0.488	1.31	0.115	-1.22	0.19	-0.15
1416462_at	Gpiap1	GPI-anchored membrane protein 1	-1.06	0.532	-1.06	0.665	1.08	0.511	1.27	0.143	0.05
1451163_at	Tinf2	Terf1 (TRF1)-interacting nuclear factor 2	1.03	0.686	-1.05	0.782	-1.02	0.881	1.03	0.736	0
1451327_a_at	Tmed1	transmembrane emp24 domain containing 1	1.05	0.607	-1.1	0.533	-1	0.981	1.07	0.588	0
1453354_at	Ndufs1	NADH dehydrogenase (ubiquinone) Fe-S protein 1	1.2	0.794	1.31	0.535	-2.24	0.028	-1.15	0.566	-0.22
1416844_at	Prmt2	protein arginine N-methyltransferase 2	1	0.988	1.11	0.556	-1.19	0.299	-1.51	0.081	-0.14
1454567_at	4933404K13Rik	RIKEN cDNA 4933404K13 gene	-1.49	0.372	1.34	0.552	-1.06	0.921	1.01	0.954	-0.05
1424809_at	Crb3	crumbs homolog 3 (Drosophila)	-1.26	0.465	-1.07	0.688	1.23	0.491	1.32	0.345	0.05
1427559_a_at	Atf2	activating transcription factor 2	-1.02	0.88	-1.17	0.692	1.13	0.555	1.15	0.622	0.02
1450056_at	Apc	adenomatosis polyposis coli	1.08	0.275	-1.19	0.147	1.04	0.846	-1.24	0.527	-0.08
1418353_at	Cd5	CD5 antigen	-1.54	0.055	1.11	0.603	1.2	0.144	-2	0.125	-0.31
1437758_a_at	Slc4a1ap	solute carrier family 4 (anion exchanger), member 1, adaptor protein	1.06	0.334	1.03	0.817	-1.14	0.229	-1.21	0.252	-0.07
1433024_at	4930421C12Rik	RIKEN cDNA 4930421C12 gene	-1.64	0.317	-1.22	0.712	1.53	0.32	1.22	0.23	-0.03
1425114_at	Rbbp6	retinoblastoma binding protein 6	1.02	0.623	-1.18	0.309	1.09	0.445	-1.56	0.067	-0.16
1449348_at	Mpp6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	-1.06	0.586	-1.15	0.148	1.14	0.562	1.23	0.33	0.04
1446232_at	Ltbp1	Latent transforming growth factor beta binding protein 1	-1.1	0.81	-1.64	0.464	1.44	0.213	1.34	0.302	0.01
1448479_at	Psmd3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	-1.11	0.35	-1.08	0.429	1.13	0.115	1.02	0.822	-0.01
1424322_at	Apex2	apurinic/apyrimidinic endonuclease 2	-1.08	0.821	-1.3	0.459	1.27	0.222	1.2	0.625	0.02
1424614_at	Frag1	FGF receptor activating protein 1	1.03	0.809	-1.08	0.549	1	0.998	-1.03	0.801	-0.02
1441772_at	P2rx4	Purinergic receptor P2X, ligand-gated ion channel 4	-1.55	0.219	1.17	0.766	1.14	0.18	-1.06	0.903	-0.07
1459205_at	Cpeb1	Cytoplasmic polyadenylation element binding protein 1	1.01	0.988	1.01	0.979	-1.06	0.89	-2.56	0.004	-0.4
1443623_a_at	---	21 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:G63	1.02	0.928	-1.32	0.659	1.18	0.703	-2.02	0.301	-0.29

1425051_at	Isoc1	isochorismatase domain containing 1	-1.08	0.509	-1.05	0.707	1.09	0.654	1.07	0.755	0.01
1423644_at	Aco1	aconitase 1	-1.07	0.582	-1.22	0.119	1.2	0.269	1.3	0.267	0.05
1459060_at	Shcbp1	Shc SH2-domain binding protein 1	-1.46	0.051	-1.11	0.867	1.37	0.34	1.04	0.236	-0.04
1421081_a_at	Banf1	barrier to autointegration factor 1	-1.09	0.325	-1.05	0.431	1.09	0.519	1.11	0.638	0.01
1449255_a_at	Rpl15	ribosomal protein L15	1.05	0.672	1.04	0.48	-1.15	0.115	-1.29	0.001	-0.09
1454798_at	Armet	Arginine-rich, mutated in early stage tumors	1.14	0.353	-1.01	0.882	-1.21	0.141	1.32	0.04	0.06
1418108_at	Plekhk1	pleckstrin homology domain containing, family K member 1	1.39	0.7	-1.38	0.58	-1.18	0.45	1.09	0.845	-0.02
1420381_a_at	Rpl31	ribosomal protein L31	1.25	0.006	1.12	0.616	-1.69	0.047	-1.15	0.461	-0.12
AFFX-r2-Ec-bioC-3_	---	---	1.13	0.12	1.08	0.302	-1.34	0.172	-1.13	0.543	-0.06
1428326_s_at	Hrsp12	heat-responsive protein 12	-1.22	0.227	-1.13	0.465	1.26	0.258	1.23	0.365	0.03
1430144_at	5830411G16Rik	RIKEN cDNA 5830411G16 gene	1.15	0.856	-1.81	0.5	1.26	0.604	-1.59	0.165	-0.25
1433422_at	LOC626748	hypothetical protein LOC626748	-2.36	0.289	1.19	0.739	1.35	0.342	-1.19	0.705	-0.25
1444619_x_at	Psmb8	proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional pep	-1.79	0.342	1.37	0.404	1.03	0.954	-1.97	0.178	-0.34
1427213_at	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	-1	0.996	-1.16	0.366	1.1	0.804	1.33	0.491	0.07
1443092_at	Mtmr3	myotubularin related protein 3	-1.25	0.398	-1.11	0.685	1.27	0.561	1.23	0.704	0.03
1437563_at	Phf20l1	PHD finger protein 20-like 1	1.03	0.84	1.06	0.592	-1.15	0.432	-1.14	0.297	-0.05
1456065_at	Ubash3a	ubiquitin associated and SH3 domain containing, A	-1.16	0.736	1.25	0.59	-1.18	0.177	1.03	0.882	-0.01
1426868_x_at	Lmna	lamin A	1.41	0.432	-1.4	0.557	-1.19	0.479	1.13	0.788	-0.01
1441232_at	---	Transcribed locus	-1.06	0.812	-1.26	0.504	1.22	0.651	1.08	0.581	0
1433772_at	Stch	stress 70 protein chaperone, microsome-associated, human homolog	1.16	0.236	1.08	0.755	-1.39	0.1	-1.09	0.641	-0.06
1456779_a_at	4930414L22Rik	RIKEN cDNA 4930414L22 gene	-1.28	0.175	1.12	0.72	1.06	0.818	-1.19	0.542	-0.07
1421181_at	Nptxr	neuronal pentraxin receptor	1.37	0.267	-1.22	0.599	-1.3	0.341	1.02	0.876	-0.03
1442321_at	Commd2	COMM domain containing 2	1.18	0.543	-1.01	0.942	-1.27	0.149	1.08	0.522	0
1417044_at	Lcmt1	leucine carboxyl methyltransferase 1	1.1	0.039	-1	0.974	-1.15	0.305	1.7	0.135	0.16
1424367_a_at	Homer2	homer homolog 2 (Drosophila)	1.57	0.277	-1.4	0.032	-1.48	0.229	2.06	0.365	0.19
1426044_a_at	Prkcq	protein kinase C, theta	-1.68	0.018	1.36	0.479	1.01	0.962	-2.07	0.031	-0.34
1449489_at	Tssk2	testis-specific serine kinase 2	1.12	0.421	-1.65	0.201	1.23	0.706	-1.2	0.227	-0.12
1425053_at	Isoc1	isochorismatase domain containing 1	-1.08	0.623	-1.2	0.188	1.2	0.387	1.55	0.2	0.12
1436526_at	Gnptg	N-acetylglucosamine-1-phosphotransferase, gamma subunit	-1.07	0.457	1.01	0.782	1.02	0.842	-1.04	0.835	-0.02
1453600_at	Ccdc18	coiled-coil domain containing 18	2.01	0.076	-1.83	0.554	-2.47	0.105	2.37	0.297	0.02
1423040_at	Bzw1	basic leucine zipper and W2 domains 1	1.01	0.909	-1.11	0.592	1.05	0.733	-1.2	0.417	-0.06
1438523_x_at	1500001A10Rik	RIKEN cDNA 1500001A10 gene	-1.45	0.147	-1.55	0.481	1.63	0.175	1.33	0.277	-0.01
1438977_x_at	Ran /// LOC671251	RAN, member RAS oncogene family /// similar to RAN, member RAS oncogene f	-1.06	0.6	-1.01	0.945	1.03	0.771	1.13	0.437	0.02
1423031_at	Maea	macrophage erythroblast attacher	-1.07	0.113	-1.13	0.098	1.14	0.032	1.03	0.854	-0.01
1425485_at	Mtmr6	myotubularin related protein 6	-1.17	0.309	1.06	0.432	1.05	0.784	-1.29	0.367	-0.09
1451876_a_at	Trp63	transformation related protein 63	-1.01	0.993	1.39	0.656	-1.73	0.414	1.08	0.902	-0.07
1446990_at	Nfia	nuclear factor I/A	1.17	0.497	-1.14	0.329	-1.1	0.475	1.2	0.404	0.03
1417094_at	Acot7	acyl-CoA thioesterase 7	1.05	0.819	-1.14	0.449	1.03	0.771	-1.1	0.747	-0.04
1418408_at	Zfand1	zinc finger, AN1-type domain 1	-1.11	0.201	1.03	0.746	1.02	0.922	-1.56	0.068	-0.15
1428107_at	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	1.07	0.016	1.08	0.548	-1.23	0.007	-1.03	0.828	-0.03
1444158_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	-1.13	0.493	-1.11	0.439	1.18	0.125	1.18	0.404	0.03
1452438_s_at	Taf4a	TAF4A RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.18	0.328	-1.16	0.232	1.25	0.238	1.05	0.771	-0.01
1437806_x_at	Mtch2	mitochondrial carrier homolog 2 (C. elegans)	1.16	0.832	1.2	0.262	-1.68	0.1	-1.79	0.301	-0.28
1430007_a_at	Cabyr	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	-1.94	0.051	1.63	0.442	-1.22	0.737	1.97	0.097	0.11
1452998_at	2010200O16Rik	RIKEN cDNA 2010200O16 gene	1.22	0.757	1.01	0.974	-1.36	0.518	-1.01	0.92	-0.04
1416387_at	Pip5k2c	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	-1.09	0.401	-1.11	0.367	1.14	0.423	1.19	0.102	0.03
1424269_a_at	Myl6 /// LOC43329	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle /// similar to m	1.02	0.755	1.17	0.07	-1.29	0.013	-1.15	0.034	-0.06
1432491_at	Pcdh8	protocadherin 8	-1.32	0.31	1.42	0.568	-1.28	0.635	1.21	0.522	0.01
1436926_at	Esrrb	estrogen related receptor, beta	1.1	0.591	-1.33	0.407	1.12	0.647	-1.12	0.777	-0.06
1433321_at	9430087B13Rik	RIKEN cDNA 9430087B13 gene	-1.07	0.885	1.03	0.878	-1.01	0.989	1.04	0.734	0
1424012_at	4930506L13Rik	RIKEN cDNA 4930506L13 gene	-1.08	0.506	-1.11	0.727	1.14	0.409	1.09	0.693	0.01
1436232_a_at	Gabpb1	GA repeat binding protein, beta 1	-1.01	0.966	1.06	0.799	-1.09	0.564	1.14	0.569	0.02
1455362_at	---	---	1.16	0.428	1.04	0.825	-1.31	0.072	-1.29	0.146	-0.1

1419554_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.03	0.749	-1.07	0.59	-1	0.986	1.19	0.364	0.04
1454948_at	Usp7	ubiquitin specific peptidase 7	-1.03	0.853	1.02	0.807	-1.03	0.782	1.82	0.214	0.19
1422005_at	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	1.18	0.366	-1.16	0.592	-1.08	0.752	1.11	0.629	0.01
1436240_at	Sost	sclerostin	1.07	0.075	1.01	0.912	-1.14	0.655	-1.25	0.314	-0.08
1437235_x_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1.02	0.905	1.3	0.065	-1.55	0.001	-1.29	0.512	-0.13
1451313_a_at	1110067D22Rik	RIKEN cDNA 1110067D22 gene	-1.08	0.641	1.23	0.539	-1.23	0.077	1.03	0.934	-0.01
1423440_at	1110001A07Rik	RIKEN cDNA 1110001A07 gene	-1.38	0.086	1.43	0.28	-1.23	0.353	2.04	0.204	0.21
1456309_x_at	Lasp1	LIM and SH3 protein 1	-1.6	0.163	1.13	0.44	1.2	0.038	-1.26	0.168	-0.13
1416736_at	Casc3	cancer susceptibility candidate 3	-1.12	0.282	-1.11	0.609	1.17	0.505	1.12	0.679	0.02
1435485_at	C230096C10Rik	RIKEN cDNA C230096C10 gene	-1.01	0.943	1.01	0.891	-1.04	0.824	1.42	0.1	0.1
1436046_x_at	Rpl29 /// LOC4333	ribosomal protein L29 /// similar to 60S ribosomal protein L29 /// similar to 60S rib	1.03	0.411	1.05	0.471	-1.13	0.209	-1.34	0.078	-0.1
1429347_at	Bcl2l14	Bcl2-like 14 (apoptosis facilitator)	-2.18	0.123	1.36	0.545	1.15	0.622	-1.65	0.029	-0.33
1422892_s_at	H2-Ea	histocompatibility 2, class II antigen E alpha	1.15	0.644	1.31	0.677	-2.01	0.242	-1.07	0.928	-0.15
1427490_at	Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	-1.02	0.765	-1.37	0.354	1.26	0.574	1.4	0.46	0.07
1429457_at	2310020A21Rik	RIKEN cDNA 2310020A21 gene	-1.58	0.171	1.47	0.192	-1.15	0.416	1.35	0.375	0.02
1453818_a_at	9030025P20Rik	RIKEN cDNA 9030025P20 gene	-1.41	0.094	1.02	0.835	1.24	0.062	-1.38	0.085	-0.14
1424785_at	Angptl6	angiopoietin-like 6	-1.48	0.061	-1.15	0.297	1.42	0.324	1.67	0.225	0.11
1456807_at	Ppp1r3e	protein phosphatase 1, regulatory (inhibitor) subunit 3E	-1.11	0.696	-1.03	0.931	1.1	0.7	1.07	0.685	0.01
1430979_a_at	Prdx2	peroxiredoxin 2	-1.06	0.679	-1.06	0.767	1.07	0.347	6.45	0.16	1.35
1434867_at	Slc4a11	solute carrier family 4, sodium bicarbonate transporter-like, member 11	1.06	0.575	-1.42	0.106	1.19	0.337	-1.06	0.695	-0.05
1416807_at	Rpl36a	ribosomal protein L36a	1.07	0.194	1.04	0.656	-1.16	0.093	-1.41	0.031	-0.12
1429830_a_at	Cd59a	CD59a antigen	1.01	0.908	-1.02	0.879	-1.03	0.842	3.39	0.18	0.59
1440525_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420418N1	-1.32	0.324	1.39	0.5	-1.22	0.116	1.17	0.761	0
1444864_at	D12Ertd125e	DNA segment, Chr 12, ERATO Doi 125, expressed	-1.31	0.454	1.04	0.938	1.16	0.632	-1.34	0.504	-0.11
1432918_at	4921511E18Rik	RIKEN cDNA 4921511E18 gene	1.03	0.933	1.11	0.765	-1.21	0.064	-1.21	0.568	-0.07
1455451_at	AI449310	expressed sequence AI449310	1.45	0.129	-1.01	0.985	-1.9	0.074	1.62	0.319	0.04
1443329_at	7-Mar	membrane-associated ring finger (C3HC4) 7	-1.97	0.364	1.13	0.732	1.32	0.518	-1.98	0.089	-0.37
1449851_at	Per1	period homolog 1 (Drosophila)	1.05	0.912	-1	0.997	-1.09	0.819	1.31	0.355	0.07
1440344_at	---	Transcribed locus	-1.62	0.309	1.17	0.56	1.18	0.488	-1.06	0.819	-0.08
1425163_at	AI661453	expressed sequence AI661453	-1.03	0.836	-1.18	0.456	1.15	0.643	1.71	0.397	0.16
1430746_at	1110050P16Rik	RIKEN cDNA 1110050P16 gene	-2.26	0.007	1.4	0.203	1.12	0.579	-2.07	0.097	-0.45
1431555_at	4933409F18Rik	RIKEN cDNA 4933409F18 gene	-6.18	0.035	1.15	0.595	1.66	0.319	-1.01	0.966	-1.1
1445979_at	Cnnm1	Cyclin M1	-1.04	0.894	1.27	0.669	-1.37	0.448	1.01	0.983	-0.03
1454576_at	A230102O21Rik	RIKEN cDNA A230102O21 gene	-1.13	0.492	-1.18	0.788	1.23	0.627	1.63	0.223	0.14
1423256_a_at	Atp6v1g1 /// LOC66	ATPase, H+ transporting, lysosomal V1 subunit G1 /// similar to vacuolar H+ ATP	-1.14	0.404	1.3	0.072	-1.27	0.065	1.01	0.882	-0.02
1416247_at	Dctn3	dynactin 3	-1.04	0.703	-1.1	0.143	1.09	0.518	1.05	0.784	0
1439881_at	C030013E06Rik	RIKEN cDNA C030013E06 gene	-1.06	0.921	1.23	0.701	-1.25	0.18	1.05	0.818	-0.01
1453950_a_at	Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2	-1.58	0.279	-1.11	0.872	1.44	0.511	2.64	0.047	0.34
1443689_at	Usp32	Ubiquitin specific peptidase 32	1.49	0.31	-1.24	0.173	-1.49	0.004	3.71	0.146	0.62
1458634_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.18	0.544	-1.06	0.869	-1.19	0.276	1.93	0.187	0.22
1436986_at	Sntb2	syntrophin, basic 2	-1.16	0.616	1.18	0.78	-1.08	0.88	1.44	0.237	0.09
1460065_at	AA763515	expressed sequence AA763515	-1.16	0.882	1.56	0.561	-1.84	0.078	1.14	0.848	-0.07
1421631_at	Pcdhb1	protocadherin beta 1	-2.13	0.223	1.47	0.329	1.02	0.971	-1.68	0.275	-0.33
1457179_at	4930406H16Rik ///	RIKEN cDNA 4930406H16 gene /// NACHT, leucine rich repeat and PYD contain	1.01	0.986	1.04	0.947	-1.09	0.847	-2.09	0.227	-0.28
1455318_at	Timd4	T-cell immunoglobulin and mucin domain containing 4	-2.32	0.328	1.21	0.511	1.33	0.345	-1.5	0.496	-0.32
1429585_s_at	Mynn	myoneurin	-1.08	0.164	1.16	0.279	-1.13	0.292	1.02	0.772	-0.01
1457707_at	Gm489	gene model 489, (NCBI)	-1.73	0.203	1.19	0.574	1.2	0.422	-1.69	0.152	-0.26
1439095_at	Sfrs11	splicing factor, arginine/serine-rich 11	1.18	0.376	1.02	0.946	-1.3	0.391	-1.07	0.875	-0.04
1458233_at	9030227G01Rik	RIKEN cDNA 9030227G01 gene	-1.19	0.273	1.19	0.528	-1.07	0.765	1.76	0.025	0.17
1460701_a_at	Mrpl52	mitochondrial ribosomal protein L52	1.08	0.184	1.18	0.146	-1.42	0.025	-1.38	0.234	-0.13
1428748_at	5830428H23Rik	RIKEN cDNA 5830428H23 gene	1.05	0.779	1.08	0.727	-1.2	0.451	-1.38	0.25	-0.11
1424988_at	Mylip	myosin regulatory light chain interacting protein	-1.19	0.459	1.06	0.597	1.06	0.686	-1.19	0.444	-0.06
1458025_at	---	---	-1.53	0.276	-1.24	0.497	1.51	0.602	1.33	0.517	0.02

1440229_at	2310034G01Rik	RIKEN cDNA 2310034G01 gene	1.11	0.717	-2.55	0.142	1.47	0.221	-1.57	0.155	-0.39
1434290_at	Gtdc1	glycosyltransferase-like domain containing 1	1.05	0.029	1.02	0.878	-1.12	0.334	-1.09	0.698	-0.03
1451368_at	Alg1	asparagine-linked glycosylation 1 homolog (yeast, beta-1,4-mannosyltransferase)	1.03	0.769	-1.16	0.143	1.08	0.519	-1.32	0.048	-0.09
1451660_a_at	Hoxb6	homeo box B6	-1.14	0.438	-1.35	0.372	1.35	0.191	1.38	0.18	0.06
1442634_at	---	Transcribed locus	1.05	0.889	-1.05	0.827	-1.03	0.888	1.67	0.368	0.16
1447713_at	Tpm1	tropomyosin 1, alpha	-1.55	0.127	1.15	0.845	1.17	0.722	-1.24	0.383	-0.12
1455672_s_at	Cplx2	complexin 2	-1.1	0.483	1.04	0.887	1.02	0.936	-1.03	0.897	-0.02
1416638_at	Sall2	sal-like 2 (Drosophila)	-1.23	0.37	1.11	0.825	1.04	0.708	-1.06	0.861	-0.03
1439373_x_at	Wnt5b	wingless-related MMTV integration site 5B	1.15	0.706	1.32	0.124	-2.05	0	-1.07	0.841	-0.16
1428224_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	-1.23	0.143	1.06	0.764	1.09	0.474	-1.6	0.081	-0.17
1416787_at	Acvr1	activin A receptor, type 1	-1.07	0.745	1.08	0.708	-1.05	0.732	1.16	0.26	0.03
1454487_at	5830490A04Rik	RIKEN cDNA 5830490A04 gene	1.27	0.529	-1.34	0.591	-1.05	0.92	1.83	0.295	0.18
1435416_x_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.21	0.047	-1.01	0.905	1.15	0.062	2.72	0.158	0.41
1420290_at	---	Transcribed locus	1.13	0.305	-1.29	0.689	1.06	0.902	-1.45	0.53	-0.14
1432227_at	Suv39h1	suppressor of variegation 3-9 homolog 1 (Drosophila)	-1.31	0.553	-1.02	0.978	1.23	0.598	1.31	0.555	0.05
1421820_a_at	Nf2	neurofibromatosis 2	-1.04	0.647	-1.15	0.381	1.13	0.396	1.18	0.232	0.03
1434373_at	B930006L02Rik	RIKEN cDNA B930006L02 gene	1.06	0.195	1.12	0.167	-1.26	0.138	-1.05	0.867	-0.03
1430209_at	4930404H21Rik	RIKEN cDNA 4930404H21 gene	-1.79	0.561	-1.09	0.902	1.49	0.255	1	0.983	-0.1
1434539_at	Lrrn3	leucine rich repeat protein 3, neuronal	1.61	0.521	-1.49	0.086	-1.45	0.312	1.22	0.574	-0.03
1427298_at	Dnm3os	dynamin 3, opposite strand	1.01	0.992	1.01	0.979	-1.05	0.823	-1.1	0.843	-0.03
1460493_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	1.13	0.818	-1.5	0.561	1.17	0.617	-2.41	0.348	-0.4
1430636_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	1.01	0.976	1.06	0.868	-1.1	0.682	-1.12	0.772	-0.04
1432821_at	Nfatc4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	-1.38	0.268	1.2	0.638	1.04	0.826	-1.56	0.19	-0.17
1450613_x_at	Ifnab	interferon alpha B	-3.44	0.09	-1.14	0.641	1.8	0.276	1.16	0.336	-0.41
1436006_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	-1.04	0.706	-1.25	0.142	1.2	0.269	2.3	0.268	0.31
1422859_a_at	Rpl23	ribosomal protein L23	1.03	0.933	1.21	0.079	-1.36	0.067	-2.07	0.427	-0.3
1440826_s_at	Tmem103	transmembrane protein 103	1.12	0.698	-1.08	0.742	-1.09	0.693	1.01	0.97	-0.01
1421823_a_at	Ppp2cb	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	1.02	0.872	-1.05	0.372	1	0.988	-1.02	0.81	-0.01
1443576_at	---	Transcribed locus	-1.27	0.71	-1.21	0.782	1.35	0.382	1.13	0.456	0
1438321_x_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	-1.18	0.122	1	0.979	1.12	0.075	-1.19	0.166	-0.06
1449019_at	Akap1	A kinase (PRKA) anchor protein 1	-1.13	0.19	-1.12	0.15	1.19	0.199	1.84	0.098	0.2
1441027_at	---	Transcribed locus	-1.28	0.235	1.21	0.583	-1.02	0.952	1.24	0.605	0.04
1452208_at	Prdm4	PR domain containing 4	-1	0.985	1.02	0.902	-1.05	0.72	1.23	0.278	0.05
1440983_at	Ttc15	Tetratricopeptide repeat domain 15	-1.28	0.136	-1.2	0.591	1.36	0.371	1.06	0.92	-0.02
1458155_at	Rabgap1l	RAB GTPase activating protein 1-like	-1.06	0.895	1.04	0.893	-1.02	0.969	1.35	0.498	0.08
1452861_at	2010300C02Rik ///	RIKEN cDNA 2010300C02 gene /// similar to Y59A8B.19	1.12	0.57	-2.15	0.078	1.38	0.106	-1.27	0.381	-0.23
1433583_at	Zfp365 /// LOC674	zinc finger protein 365 /// similar to zinc finger protein 365	1.11	0.872	-1.28	0.446	1.08	0.819	-1.23	0.697	-0.08
1435261_at	4732416N19Rik	RIKEN cDNA 4732416N19 gene	1.06	0.66	1.12	0.811	-1.27	0.355	-1.42	0.327	-0.13
1434745_at	Ccnd2	cyclin D2	1.05	0.722	1.11	0.599	-1.25	0.294	-1.1	0.765	-0.04
1445366_at	---	---	-2.76	0.303	1.11	0.875	1.5	0.288	-1.05	0.919	-0.3
1451065_a_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-1.15	0.233	1.01	0.926	1.08	0.67	-1.11	0.73	-0.04
1449180_at	Kcmf1	potassium channel modulatory factor 1	1.21	0.233	-1.21	0.145	-1.07	0.42	1.56	0.028	0.12
1433349_at	4930553P13Rik	RIKEN cDNA 4930553P13 gene	1.08	0.664	-1.18	0.385	1.04	0.787	-1.28	0.122	-0.09
1454287_at	4931428A05Rik	RIKEN cDNA 4931428A05 gene	-2.83	0.059	1.34	0.589	1.28	0.566	-1.22	0.663	-0.36
1428216_s_at	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	-1.44	0.286	1.57	0.238	-1.42	0.258	1.58	0.411	0.07
1442251_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	1.23	0.482	-1.33	0.227	-1.01	0.957	1.08	0.666	-0.01
1423983_at	Sez6l2	seizure related 6 homolog like 2	1	0.791	-1.08	0.834	1.04	0.892	-1.21	0.612	-0.06
1448185_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like do	1	0.997	-1.46	0.288	1.28	0.171	-1.1	0.778	-0.07
1418750_at	Plxnb3	plexin B3	-1.29	0.363	-2.1	0.473	1.72	0.087	1.16	0.778	-0.13
1457768_at	Prune	prune homolog (Drosophila)	1.1	0.172	1.19	0.581	-1.48	0.064	-1.19	0.596	-0.09
1417058_a_at	Krtcap2	keratinocyte associated protein 2	1.1	0.412	1.17	0.211	-1.43	0.002	-1.37	0.515	-0.13
1433149_at	4930513N20Rik	RIKEN cDNA 4930513N20 gene	-1.38	0.033	1.33	0.484	-1.1	0.762	1.41	0.396	0.07
1443340_at	Cbara1	calcium binding atopy-related autoantigen 1	-1.53	0.294	1.46	0.404	-1.17	0.651	1.43	0.231	0.05

1420359_at	Sva	seminal vesicle antigen	-1.06	0.859	1.32	0.469	-1.42	0.118	1.34	0.421	0.05
1455111_at	Yipf6	Yip1 domain family, member 6	-1	0.973	1.11	0.339	-1.16	0.035	1.41	0.008	0.09
1415879_a_at	Rplp2	ribosomal protein, large P2	1.05	0.319	1.07	0.234	-1.17	0.097	-1.29	0	-0.09
1439091_at	Fancd2	Fanconi anemia, complementation group D2	-1.07	0.813	-1.13	0.784	1.14	0.526	2.72	0.287	0.42
1424963_at	Rp1h	retinitis pigmentosa 1 homolog (human)	1.24	0.768	-1.68	0.015	1.13	0.753	-1.58	0.511	-0.22
1455255_at	4833420G11Rik	RIKEN cDNA 4833420G11 gene	-1.48	0.137	-1	0.995	1.3	0.116	2.06	0.378	0.22
1434183_at	LOC546078 /// LOC	similar to sterile alpha motif domain containing 1 /// similar to sterile alpha motif d	1.18	0.576	-1.19	0.44	-1.05	0.873	1.54	0.134	0.12
1434273_at	A830073O21Rik	RIKEN cDNA A830073O21 gene	1.17	0.085	1.02	0.898	-1.3	0.07	-1.15	0.481	-0.06
1449714_at	5730472N09Rik	RIKEN cDNA 5730472N09 gene	-1.18	0.281	-1.02	0.544	1.15	0.363	1.73	0.323	0.17
1457815_at	Nup214	Nucleoporin 214	1.39	0.678	-1.44	0.659	-1.12	0.596	1.05	0.787	-0.03
1416142_at	Rps6 /// LOC21473	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	1.03	0.708	1.15	0.221	-1.27	0.048	-1.36	0.178	-0.11
1451773_s_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	1.26	0.653	-1.62	0.404	1.09	0.742	-1.27	0.726	-0.13
1445300_at	---	---	1.79	0.377	-1.73	0.309	-1.67	0.295	1.11	0.778	-0.13
1445387_at	Senp6	SUMO/sentrin specific peptidase 6	1.03	0.941	1.21	0.376	-1.37	0.123	-1.21	0.618	-0.08
1436286_at	B830017H08Rik	RIKEN cDNA B830017H08 gene	-1.05	0.924	-1.3	0.462	1.25	0.414	1.22	0.776	0.03
1416068_at	Kars /// LOC631033	lysyl-tRNA synthetase /// similar to lysyl-tRNA synthetase	-1.08	0.387	-1.02	0.739	1.07	0.32	1.03	0.785	0
1416915_at	Msh6	mutS homolog 6 (E. coli)	-1.05	0.782	-1.14	0.149	1.14	0.538	1.47	0.168	0.11
1454182_at	5430417C01Rik	RIKEN cDNA 5430417C01 gene	-1.27	0.345	1.15	0.027	1.04	0.847	-1.29	0.112	-0.09
1450489_at	Sall1	sal-like 1 (Drosophila)	1.01	0.958	1.17	0.332	-1.26	0.501	-1.24	0.555	-0.08
1425255_s_at	Hnrpll	heterogeneous nuclear ribonucleoprotein L-like	1.03	0.736	-1	0.944	-1.06	0.565	2.05	0.146	0.25
1424666_at	5430405G24Rik	RIKEN cDNA 5430405G24 gene	1.05	0.674	-1.06	0.477	-1.03	0.894	1.16	0.046	0.03
1426815_s_at	AU024582	expressed sequence AU024582	1.01	0.93	-1.09	0.121	1.04	0.556	-1.35	0.159	-0.1
1436483_at	Myt1l	myelin transcription factor 1-like	-3	0.402	1.85	0.27	-1.28	0.498	1.34	0.303	-0.27
1431134_at	Ing5	inhibitor of growth family, member 5	1.08	0.834	-1.24	0.384	1.08	0.791	-1.15	0.572	-0.06
1459688_at	---	Transcribed locus	-1.23	0.211	1.45	0.203	-1.42	0.096	1.18	0.144	0
1445719_at	Sf3a1	Splicing factor 3a, subunit 1	1.64	0.315	-1.67	0.584	-1.36	0.571	1.12	0.737	-0.07
1451999_at	Ldb3	LIM domain binding 3	-1.16	0.739	-1.12	0.458	1.22	0.241	1.83	0.026	0.19
1439027_at	C330023M02Rik	RIKEN cDNA C330023M02 gene	-1.15	0.107	-1.1	0.23	1.19	0.053	1.12	0.561	0.02
1436603_at	Tbl2	transducin (beta)-like 2	1.19	0.038	-1.44	0.526	1.09	0.704	-1.13	0.547	-0.07
1455301_at	BQ952480	expressed sequence BQ952480	-1.45	0.286	-1.37	0.355	1.55	0.37	9.89	0.001	2.15
1446843_at	---	---	1.3	0.798	-3.01	0.088	1.34	0.498	-3.42	0.095	-0.95
1429613_at	0710001B24Rik	RIKEN cDNA 0710001B24 gene	1.25	0.511	-1.33	0.019	-1.03	0.812	1.12	0.713	0
1449258_at	D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	1.14	0.196	-1.11	0.441	-1.08	0.702	1.44	0.36	0.1
1419472_s_at	Nudc /// Nudc-ps1	nuclear distribution gene C homolog (Aspergillus) /// nuclear distribution gene C h	1.01	0.733	-1.04	0.654	-1	0.986	1.09	0.545	0.02
1436810_x_at	2900010M23Rik	RIKEN cDNA 2900010M23 gene	-1.15	0.481	1.09	0.345	1.01	0.933	-1.03	0.878	-0.02
1417726_at	Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	-1.03	0.846	1.01	0.948	-1.01	0.953	1.02	0.889	0
1432057_a_at	Prdm5	PR domain containing 5	-1.33	0.477	1.58	0.544	-1.57	0.154	1.25	0.172	-0.02
1436441_at	Ptger4	Prostaglandin E receptor 4 (subtype EP4)	-1.41	0.061	1.43	0.108	-1.2	0.573	1.96	0.023	0.19
1447502_at	Cmah	Cytidine monophospho-N-acetylneuraminic acid hydroxylase	1.25	0.072	-1.46	0.167	1.03	0.885	-1.27	0.483	-0.11
1425273_s_at	Emp2	epithelial membrane protein 2	-1.34	0.635	1.22	0.686	1.01	0.987	-1.66	0.412	-0.19
1433795_at	Tgfbr3	transforming growth factor, beta receptor III	1.08	0.149	1.05	0.79	-1.18	0.448	-1.19	0.586	-0.06
1425986_a_at	Dcun1d1	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	1.05	0.712	-1.02	0.914	-1.06	0.48	1.73	0.4	0.17
1431525_at	9130002K18Rik	RIKEN cDNA 9130002K18 gene	-1.68	0.145	1.53	0.39	-1.18	0.702	1.21	0.448	-0.03
1455149_at	Sh3rf1	SH3 domain containing ring finger 1	1.01	0.983	1.06	0.884	-1.1	0.379	-1.43	0.216	-0.12
1428445_at	Yif1b	Yip1 interacting factor homolog B (S. cerevisiae)	1.08	0.733	-1.12	0.458	-1	0.972	1.15	0.325	0.03
1455850_at	2310003H01Rik	RIKEN cDNA 2310003H01 gene	-1.22	0.26	-1.15	0.63	1.28	0.21	1.04	0.785	-0.01
1444379_at	Pwwp2	PWWP domain containing 2	1.11	0.782	-1.34	0.407	1.11	0.446	-1.02	0.779	-0.03
1460210_at	Pkd1	polycystic kidney disease 1 homolog	-1.1	0.753	1.03	0.895	1.03	0.889	-1.2	0.641	-0.06
1458066_at	---	---	-2.08	0.313	1.61	0.513	-1.13	0.751	1.56	0.503	-0.01
1429299_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	-1.2	0.337	-1.25	0.549	1.34	0.132	1.37	0.422	0.06
1448420_a_at	Fbxl12	F-box and leucine-rich repeat protein 12	-1.21	0.243	1.07	0.744	1.08	0.443	-1.48	0.239	-0.14
1458276_x_at	Cit	citron	-1.48	0.221	1.32	0.049	-1.02	0.933	1.62	0.235	0.11
1446853_at	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	1.36	0.532	-1.36	0.416	-1.14	0.764	1.47	0.297	0.08

1436454_x_at	Fen1	flap structure specific endonuclease 1	1.18	0.24	-1.2	0.571	-1.04	0.811	2.5	0.195	0.36
1455830_s_at	C87414 /// LOC664	expressed sequence C87414 /// similar to PRAME family member 9 /// similar to F	1.27	0.721	-3.51	0.156	1.42	0.258	-1.54	0.583	-0.59
1452972_at	Ttc32	tetratricopeptide repeat domain 32	-1.13	0.261	1.04	0.565	1.05	0.665	-1.64	0.05	-0.17
1426691_at	Tjap1	tight junction associated protein 1	1.02	0.906	1.01	0.965	-1.06	0.741	-1.11	0.591	-0.03
1421957_a_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	-1.01	0.897	1.02	0.893	-1.04	0.894	2.87	0.191	0.46
1422666_at	Cblc	Casitas B-lineage lymphoma c	-1.14	0.486	-1.13	0.409	1.21	0.64	1.22	0.702	0.04
1442948_at	---	---	1.06	0.939	-1.1	0.797	1.01	0.974	-1.79	0.25	-0.21
1439825_at	Dtx3l	deltex 3-like (Drosophila)	1.04	0.91	1.12	0.498	-1.23	0.567	-1.13	0.751	-0.05
1421847_at	Wsb2	WD repeat and SOCS box-containing 2	-1.04	0.648	-1.02	0.668	1.03	0.705	1.02	0.873	0
1439456_x_at	Atp6ap2	ATPase, H+ transporting, lysosomal accessory protein 2	-1.05	0.664	1.1	0.355	-1.09	0.431	1.1	0.639	0.02
1449465_at	Reln	reelin	-1.08	0.819	-1	0.998	1.05	0.79	2.17	0.022	0.29
1430850_x_at	Cgrrf1	cell growth regulator with ring finger domain 1	1.07	0.873	-1.07	0.738	-1.03	0.905	1.43	0.409	0.1
1428116_a_at	Dynlt1	dynein light chain Tctex-type 1	-1.12	0.198	1.06	0.49	1.02	0.864	-1.03	0.788	-0.02
1445726_at	C330011K17Rik	RIKEN cDNA C330011K17 gene	1.09	0.933	1.32	0.568	-1.76	0.259	-1.08	0.267	-0.11
1418736_at	B3galnt1	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 1	-1.24	0.004	1.45	0.141	-1.39	0.131	1.25	0.519	0.02
1440518_at	1700029I01Rik	RIKEN cDNA 1700029I01 gene	-1.22	0.514	1.26	0.283	-1.11	0.612	1.04	0.863	-0.01
1444300_at	Gpr125	G protein-coupled receptor 125	1.04	0.91	-1.28	0.374	1.16	0.534	-1.18	0.543	-0.07
1446759_at	5830457H20Rik	RIKEN cDNA 5830457H20 gene	1.48	0.401	-1.26	0.585	-1.43	0.094	1.21	0.502	0
1433363_at	A930036I15Rik	RIKEN cDNA A930036I15 gene	-1.08	0.827	1.17	0.652	-1.13	0.492	1.75	0.277	0.18
1439999_at	---	---	1.31	0.164	1.06	0.717	-1.68	0.006	-1.27	0.425	-0.14
1450911_at	Ppib	peptidylprolyl isomerase B	1.1	0.2	1.06	0.747	-1.23	0.013	-1.13	0.033	-0.05
1427720_a_at	Nnp1	novel nuclear protein 1	1.02	0.894	-1.08	0.56	1.03	0.409	-1.18	0.066	-0.05
1441972_at	6230424C14Rik	RIKEN cDNA 6230424C14 gene	1.24	0.241	1.14	0.083	-1.68	0.016	-1.25	0.474	-0.14
1443395_at	D6Ertd490e	DNA segment, Chr 6, ERATO Doi 490, expressed	-1.08	0.901	-1.07	0.836	1.12	0.747	3.05	0.004	0.5
1436822_x_at	Hk1 /// Rpl17 /// LO	hexokinase 1 /// ribosomal protein L17 /// similar to 60S ribosomal protein L17 (L2	1.13	0.305	1.05	0.721	-1.27	0.01	-1.26	0.036	-0.08
1435178_x_at	Anapc5	anaphase-promoting complex subunit 5	-1.01	0.631	-1.04	0.607	1.02	0.873	1.36	0.094	0.08
1454663_at	Eif5	eukaryotic translation initiation factor 5	-1.07	0.709	-1.07	0.42	1.1	0.602	1.44	0.327	0.1
1454693_at	Hdac4	Histone deacetylase 4	1.14	0.624	-1.75	0.197	1.26	0.173	-1.04	0.835	-0.1
1430234_at	Arl14	ADP-ribosylation factor-like 14	1.15	0.195	1.38	0.459	-2.28	0.106	-1.36	0.64	-0.28
1451630_at	Ttl	tubulin tyrosine ligase	1.04	0.864	1.01	0.938	-1.09	0.54	-1.06	0.634	-0.02
1456378_s_at	Fbxl20	F-box and leucine-rich repeat protein 20	-1.25	0.05	-1.16	0.048	1.31	0.061	1.21	0.091	0.03
1451928_a_at	Rad18	RAD18 homolog (S. cerevisiae)	1.13	0.63	-1.16	0.48	-1.02	0.943	1.82	0.287	0.19
1436048_at	Exoc8	exocyst complex component 8	-1.03	0.777	-1.08	0.447	1.08	0.502	1.15	0.37	0.03
1430302_at	1500041B16Rik	RIKEN cDNA 1500041B16 gene	1.03	0.938	1.14	0.652	-1.25	0.437	-1.12	0.687	-0.05
1446169_at	Dgcr8	DiGeorge syndrome critical region gene 8	-1.66	0.045	1.27	0.468	1.1	0.768	-1.71	0.423	-0.25
1443435_at	3732413I11Rik	RIKEN cDNA 3732413I11 gene	1.11	0.83	1.06	0.829	-1.24	0.339	-1.17	0.426	-0.06
1433660_at	D2Ertd435e	DNA segment, Chr 2, ERATO Doi 435, expressed	-1.02	0.841	-1.21	0.212	1.17	0.423	1.18	0.562	0.03
1441831_x_at	Clcn5	Chloride channel 5	-1.39	0.204	1.1	0.72	1.15	0.617	-1.01	0.963	-0.03
1443177_at	---	Transcribed locus	-1.55	0.137	1.26	0.678	1.07	0.649	-1.01	0.974	-0.06
1444428_at	---	---	1.02	0.74	-1	0.993	-1.04	0.75	1.03	0.887	0
1435487_at	Grid2	glutamate receptor, ionotropic, delta 2	1.07	0.634	-1.14	0.482	1.03	0.941	-1.08	0.785	-0.03
1454666_at	Klf3	Kruppel-like factor 3 (basic)	-1	0.953	-1.09	0.097	1.06	0.539	1.48	0.114	0.11
1434512_x_at	Sfrs3 /// LOC63224	splicing factor, arginine/serine-rich 3 (SRp20) /// similar to Splicing factor, arginine	-1.17	0.016	1.16	0.483	-1.04	0.846	1.11	0.495	0.02
1419073_at	Tmeff2	transmembrane protein with EGF-like and two follistatin-like domains 2	1.53	0.235	-1.13	0.606	-1.77	0.193	1.55	0.168	0.04
1429884_at	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	-1.14	0.269	-1.02	0.885	1.12	0.554	1.13	0.121	0.02
1460676_at	Josd1	Josephin domain containing 1	1.2	0.121	-1.06	0.628	-1.21	0.006	1.81	0.179	0.19
1452593_a_at	Tceb1	transcription elongation factor B (SIII), polypeptide 1	-1.18	0.728	1.22	0.225	-1.1	0.486	1.06	0.777	0
1452806_at	1500016O10Rik	RIKEN cDNA 1500016O10 gene	1.24	0.666	-1.4	0.396	1.02	0.917	-1.17	0.803	-0.08
1434258_s_at	Phactr4	phosphatase and actin regulator 4	-1.14	0.208	-1.08	0.441	1.17	0.332	1.5	0.26	0.11
1418456_a_at	Cxcl14	chemokine (C-X-C motif) ligand 14	-1.15	0.403	1.54	0.256	-1.77	0.013	1.25	0.21	-0.03
1416215_at	Gosr1	golgi SNAP receptor complex member 1	-1.05	0.842	1	0.99	1.02	0.93	-1.14	0.65	-0.04
1450789_at	Rhpn1	rhophilin, Rho GTPase binding protein 1	1.36	0.295	-1.48	0.435	-1.06	0.862	3.78	0.251	0.65
1436774_at	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	1.1	0.389	-1.08	0.497	-1.05	0.298	1.15	0.511	0.03

1443995_at	Gm9	gene model 9, (NCBI)	1.01	0.947	-1.05	0.894	1.01	0.96	-1.35	0.348	-0.09
1428350_at	2310061F22Rik	RIKEN cDNA 2310061F22 gene	-1.5	0.017	1.12	0.423	1.19	0.049	-1.23	0.086	-0.1
1451640_a_at	1500011J06Rik	RIKEN cDNA 1500011J06 gene	1.02	0.916	-1.12	0.318	1.06	0.698	-1.27	0.343	-0.08
1424682_at	Atpbd1c	ATP binding domain 1 family, member C	-1.21	0.475	-1.22	0.016	1.33	0.026	1.1	0.674	0
1436280_at	Zfp31	zinc finger protein 31	1.12	0.838	-1.46	0.416	1.17	0.682	-1.82	0.234	-0.25
1424111_at	Igf2r	insulin-like growth factor 2 receptor	1.08	0.543	-1.03	0.834	-1.07	0.614	1.21	0.266	0.04
1424136_a_at	Ppih /// LOC433064	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomerase H /// hypothetica	1.07	0.545	-1.07	0.572	-1.03	0.857	1.39	0.385	0.09
1423329_at	Gdap1	ganglioside-induced differentiation-associated-protein 1	-1.12	0.027	-1.37	0.465	1.35	0.444	1.16	0.663	0.01
1459107_at	Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	-1.29	0.467	1.14	0.508	1.06	0.621	-1.13	0.437	-0.05
1431765_a_at	Rps2 /// LOC24364	ribosomal protein S2 /// similar to 40S ribosomal protein S2 /// similar to 40S ribos	-1.16	0.049	1.07	0.671	1.05	0.51	-1.2	0.003	-0.06
1423997_at	Csde1	cold shock domain containing E1, RNA binding	1.04	0.807	1.01	0.892	-1.07	0.425	-1.02	0.816	-0.01
1428742_at	Fbxo45	F-box protein 45	-1.14	0.508	-1.04	0.892	1.14	0.623	1.44	0.28	0.1
1424467_at	Phldb1	pleckstrin homology-like domain, family B, member 1	1.1	0.644	-1.1	0.711	-1.03	0.923	1.5	0.006	0.12
1435133_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1.09	0.216	1.04	0.622	-1.18	0.514	-1.02	0.86	-0.02
1454626_at	Cltc	clathrin, heavy polypeptide (Hc)	-1.02	0.842	1.15	0.07	-1.17	0.07	1.29	0.088	0.06
1417707_at	B230342M21Rik	RIKEN cDNA B230342M21 gene	1.06	0.576	-1.36	0.366	1.19	0.263	-1.67	0.171	-0.2
1423393_at	Clic4	chloride intracellular channel 4 (mitochondrial)	1.13	0.169	-1.08	0.077	-1.08	0.398	1.4	0.058	0.09
1460315_s_at	Tbk1	TANK-binding kinase 1	-1.03	0.892	1.04	0.659	-1.04	0.712	1.02	0.771	0
1435716_x_at	Snrpn	small nuclear ribonucleoprotein N	-1.24	0.517	1.11	0.602	1.06	0.911	-1.12	0.686	-0.05
1427516_a_at	Boc	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) b	-1.09	0.698	-1.1	0.789	1.16	0.454	1.18	0.41	0.04
1448227_at	Grb7	growth factor receptor bound protein 7	-1.06	0.78	1.12	0.246	-1.09	0.734	1.01	0.956	-0.01
1419137_at	Shank3	SH3/ankyrin domain gene 3	1.34	0.078	-1.16	0.296	-1.29	0.095	1.16	0.725	0.01
1456054_a_at	Pum1	pumilio 1 (Drosophila)	1.09	0.563	1.07	0.439	-1.23	0.23	-1.18	0.494	-0.06
1438727_at	Wdr32	WD repeat domain 32	1.12	0.644	-1.04	0.798	-1.11	0.433	1.26	0.474	0.06
1458526_at	---	---	-1.04	0.586	-1.06	0.763	1.08	0.603	1.3	0.365	0.07
1423939_a_at	Yif1a	Yip1 interacting factor homolog A (S. cerevisiae)	-1.05	0.546	-1.02	0.773	1.05	0.523	1.11	0.382	0.02
1449728_at	---	Transcribed locus	-1.08	0.85	-1.29	0.687	1.28	0.638	1.21	0.798	0.03
1433747_at	Lnpep	leucyl/cystinyl aminopeptidase	1.01	0.951	1.08	0.605	-1.12	0.452	-1.14	0.709	-0.04
1434191_at	A530016O06Rik	RIKEN cDNA A530016O06 gene	1.13	0.436	-1.1	0.258	-1.06	0.737	1.37	0.562	0.08
1459318_at	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.27	0.767	1.29	0.637	-1.12	0.827	1.2	0.737	0.03
1441419_at	1700030G06Rik	RIKEN cDNA 1700030G06 gene	1.03	0.906	-1.31	0.403	1.18	0.454	-1.74	0.24	-0.21
1459291_at	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	-1.02	0.96	-1.32	0.496	1.24	0.608	1.08	0.84	-0.01
1446781_at	D8Ertd54e	DNA segment, Chr 8, ERATO Doi 54, expressed	-3.56	0.089	1.72	0.196	-1.03	0.951	1.08	0.92	-0.45
1429861_at	Pcdh9 /// LOC6382	protocadherin 9 /// similar to protocadherin 9 isoform 1 precursor	1.47	0.585	-1.95	0.262	-1.01	0.988	1.03	0.919	-0.11
1422912_at	Bmp4	bone morphogenetic protein 4	1.33	0.066	-1.2	0.691	-1.23	0.373	1.03	0.92	-0.02
1454562_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930590N04 pr	1.37	0.207	-1.62	0.181	-1.01	0.989	1.27	0.635	0
1424711_at	Tmem2	transmembrane protein 2	-1.05	0.791	-1.03	0.803	1.06	0.804	1.02	0.934	0
1418579_at	Cetn2	centrin 2	1.01	0.753	1.05	0.603	-1.09	0.715	-1.22	0.264	-0.06
1438959_x_at	---	Transcribed locus	-1.63	0.023	1.33	0.618	1.03	0.908	-1.25	0.09	-0.13
1428270_at	Glt8d1	glycosyltransferase 8 domain containing 1	-1.13	0.074	1.22	0.24	-1.14	0.161	1.05	0.806	0
1426033_at	Rgs9	regulator of G-protein signaling 9	-1.24	0.329	1.47	0.431	-1.43	0.265	1.3	0.41	0.03
1450606_at	Pnmt	phenylethanolamine-N-methyltransferase	1.07	0.94	1.08	0.818	-1.2	0.813	-1.58	0.038	-0.16
1429298_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	-1.1	0.509	-1.14	0.441	1.19	0.317	1.85	0.139	0.2
1430379_at	5830411K21Rik	RIKEN cDNA 5830411K21 gene	1.24	0.094	1.05	0.87	-1.44	0.174	-1.07	0.812	-0.06
1434704_at	Mll5	myeloid/lymphoid or mixed-lineage leukemia 5	1.04	0.802	1.02	0.709	-1.09	0.611	-1.16	0.6	-0.05
1433524_at	AU042671	expressed sequence AU042671	-1.11	0.49	-1.15	0.304	1.2	0.273	2.92	0.192	0.47
1447717_x_at	Nrsn2	neurensin 2	-1.08	0.922	1.06	0.918	-1.01	0.983	1.02	0.93	0
1435444_at	Atf6	activating transcription factor 6	1.09	0.602	-1.08	0.32	-1.04	0.827	1.08	0.716	0.01
1451182_s_at	Ankrd54	ankyrin repeat domain 54	-1.15	0.117	1.14	0.319	-1.04	0.856	1.31	0.274	0.07
1423519_at	2210412D01Rik	RIKEN cDNA 2210412D01 gene	-1.15	0.037	-1.04	0.422	1.15	0.31	1.14	0.282	0.02
1425678_a_at	Snrk	SNF related kinase	1.06	0.793	-1.14	0.421	1.05	0.786	-1.48	0.085	-0.13
1416108_a_at	Tmed3	transmembrane emp24 domain containing 3	1.09	0.425	1.01	0.955	-1.14	0.223	-1.11	0.529	-0.04
1452860_at	Fbxl17	F-box and leucine-rich repeat protein 17	-1.09	0.121	1.02	0.71	1.04	0.643	-1.23	0.312	-0.06

1436794_at	Nalp4f	NACHT, leucine rich repeat and PYD containing 4F	1.23	0.8	-1.53	0.469	1.1	0.843	-1.14	0.781	-0.09
1424461_at	Dctn2	dynactin 2	-1.04	0.635	-1.04	0.686	1.06	0.471	1.16	0.176	0.04
1433436_s_at	Thtpa /// Zfhx2as	thiamine triphosphatase /// zinc finger homeobox 2, antisense	-1.14	0.047	1.02	0.77	1.08	0.491	-1.08	0.821	-0.03
1449671_at	---	---	1.04	0.892	-1.45	0.465	1.25	0.415	-1.7	0.041	-0.21
1419239_at	Zfp54	zinc finger protein 54	-1.21	0.378	1.11	0.254	1.04	0.702	-1.25	0.247	-0.08
1435316_at	Psma6	Proteasome (prosome, macropain) subunit, alpha type 6	-1.07	0.82	1.11	0.502	-1.07	0.753	1.02	0.925	0
1441391_at	Gnb1l	Guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-1.2	0.209	-1.08	0.505	1.22	0.661	1.51	0.27	0.11
1428087_at	Dnm1l	dynamin 1-like	-1	0.974	-1.2	0.382	1.15	0.605	1	0.984	-0.01
1431191_a_at	Syt1	synaptotagmin I	1.14	0.6	-1.65	0.303	1.23	0.491	-1	0.993	-0.07
1428542_at	2010003J03Rik	RIKEN cDNA 2010003J03 gene	-1.01	0.441	-1.14	0.122	1.12	0.281	1.35	0.366	0.08
1431220_at	2810416G20Rik	RIKEN cDNA 2810416G20 gene	-1.13	0.237	1.01	0.942	1.08	0.825	-1.36	0.235	-0.1
1460462_at	Med18	mediator of RNA polymerase II transcription, subunit 18 homolog (yeast)	-1.03	0.947	1.06	0.783	-1.05	0.861	1.11	0.735	0.02
1458839_at	Exoc8	exocyst complex component 8	-1.21	0.801	-1.15	0.774	1.28	0.518	1.13	0.765	0.01
1434036_at	Mtss1	metastasis suppressor 1	-1.05	0.834	1	0.985	1.02	0.915	-1.34	0.203	-0.09
1458766_at	Pak7	P21 (CDKN1A)-activated kinase 7	-1.82	0.38	1.23	0.717	1.2	0.611	-1.43	0.421	-0.21
1427059_at	4732495E13Rik	RIKEN cDNA 4732495E13 gene	-1.04	0.649	-1.09	0.76	1.1	0.535	1	0.993	-0.01
1448310_at	Ick	intestinal cell kinase	1.02	0.934	-1.04	0.726	-1	0.997	1.14	0.536	0.03
1426235_a_at	Glul	glutamate-ammonia ligase (glutamine synthetase)	-1.02	0.911	-1.29	0.012	1.23	0.42	2.04	0.14	0.24
1429095_at	Cenpp	centromere protein P	-1.18	0.776	1.14	0.85	-1.01	0.987	4.22	0.237	0.79
1455128_x_at	Tnrc6a	trinucleotide repeat containing 6a	1.19	0.222	1.08	0.383	-1.4	0.139	-1.16	0.624	-0.07
1457382_at	---	PREDICTED: Mus musculus similar to Heterogeneous nuclear ribonucleoprotein	-1.27	0.44	-1.06	0.833	1.24	0.57	2.36	0.103	0.32
1449122_at	3110003A22Rik	RIKEN cDNA 3110003A22 gene	-1.05	0.717	1.14	0.503	-1.11	0.43	1.37	0.455	0.08
1420444_at	Slc22a3	solute carrier family 22 (organic cation transporter), member 3	1.5	0.434	-2.08	0.056	1	0.998	-1.5	0.196	-0.27
1415768_a_at	Ube2r2	ubiquitin-conjugating enzyme E2R 2	-1.02	0.874	-1.08	0.153	1.08	0.496	1.5	0.239	0.12
1454073_at	4930455D15Rik	RIKEN cDNA 4930455D15 gene	1.03	0.848	-1.26	0.77	1.16	0.388	-2.55	0.168	-0.4
1459296_at	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	-2.58	0.083	1.7	0.41	-1.12	0.617	1.07	0.695	-0.23
1458436_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	1.13	0.55	-1.08	0.699	-1.09	0.6	1.22	0.22	0.05
1418381_at	Zfp148	zinc finger protein 148	1.07	0.292	1.02	0.927	-1.11	0.244	-1.53	0.029	-0.14
1460141_at	---	Transcribed locus	1.01	0.98	-1.1	0.77	1.06	0.914	-1.53	0.346	-0.14
1417469_at	Nit1	nitrilase 1	-1.42	0.377	1.02	0.866	1.25	0.099	-1.22	0.423	-0.09
1434303_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1.08	0.826	1.02	0.898	-1.13	0.506	-1.19	0.631	-0.06
1420822_s_at	Sgpp1	sphingosine-1-phosphate phosphatase 1	-1.24	0.224	1.07	0.547	1.11	0.221	-1.13	0.18	-0.05
1433592_at	Calm1	calmodulin 1	1.01	0.849	1.04	0.605	-1.08	0.57	-1.21	0.286	-0.06
1415842_at	Gbl	G protein beta subunit-like	-1.16	0.482	1.16	0.453	-1.04	0.787	1.04	0.86	0
1447811_s_at	Amigo1	adhesion molecule with Ig like domain 1	1.13	0.67	-1.48	0.158	1.17	0.38	-1.52	0.303	-0.17
1451073_at	Sppl3	signal peptide peptidase 3	-1.12	0.694	1.15	0.284	-1.06	0.4	1.35	0.16	0.08
1445855_at	A030007L17Rik	RIKEN cDNA A030007L17 gene	-1.61	0.072	1.14	0.733	1.22	0.727	-1.42	0.557	-0.17
1433510_x_at	LOC622534	similar to ribosomal protein L36	1.05	0.569	1.07	0.275	-1.16	0.57	-1.73	0.072	-0.19
1448195_at	Taf5l	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated fa	-1.01	0.795	-1.04	0.681	1.04	0.607	1.1	0.711	0.02
1423822_a_at	Tmem168	transmembrane protein 168	-1.17	0.191	1.08	0.423	1.05	0.499	-1.3	0.04	-0.09
1428635_at	Comtd1	catechol-O-methyltransferase domain containing 1	-1.22	0.578	1.28	0.425	-1.13	0.257	1.07	0.828	0
1424639_a_at	Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	-1.14	0.337	-1.22	0.058	1.29	0.17	1.09	0.388	0
1429376_s_at	Anapc10	anaphase promoting complex subunit 10	1.08	0.435	1.18	0.187	-1.38	0.024	-1.04	0.681	-0.04
1451752_at	Foxk1	forkhead box K1	-1.2	0.635	1.12	0.375	1.02	0.892	-1.23	0.096	-0.07
1447007_at	1700008I05Rik	RIKEN cDNA 1700008I05 gene	1.08	0.784	1.16	0.675	-1.34	0.52	-1.28	0.382	-0.1
1418442_at	Xpo1	exportin 1, CRM1 homolog (yeast)	-1.07	0.518	1.31	0.044	-1.35	0.038	1.04	0.843	-0.02
1456870_at	A430107D22Rik	RIKEN cDNA A430107D22 gene	-1.71	0.15	1.11	0.76	1.28	0.411	-1.97	0.291	-0.32
1450777_at	Xrn2	5'-3' exoribonuclease 2	1.05	0.534	-1.14	0.246	1.06	0.594	-1.4	0.15	-0.11
1417579_x_at	Gmppa	GDP-mannose pyrophosphorylase A	-1.06	0.816	-1.02	0.895	1.06	0.645	1	0.994	-0.01
1417012_at	Sdc2	syndecan 2	1.18	0.505	-1.03	0.836	-1.2	0.345	1.23	0.341	0.04
1428126_a_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	1.19	0.417	-1.05	0.452	-1.19	0.116	1.02	0.933	-0.01
1424585_at	Ranbp10	RAN binding protein 10	-1.11	0.164	-1.16	0.274	1.22	0.108	4.02	0.188	0.74
1442371_at	1110048D14Rik	RIKEN cDNA 1110048D14 gene	1.03	0.918	1.19	0.261	-1.31	0.07	-1.05	0.494	-0.04

1450069_a_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.01	0.968	1.01	0.949	-1.04	0.761	-1.51	0.291	-0.13
1451864_at	Cacng8	calcium channel, voltage-dependent, gamma subunit 8	1.76	0.41	-1.41	0.232	-1.94	0.169	1.08	0.693	-0.13
1419946_s_at	Rab2	RAB2, member RAS oncogene family	1.43	0.577	1.09	0.823	-2.18	0.078	-1.05	0.876	-0.18
1423826_at	Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	-1.04	0.865	-1.14	0.366	1.14	0.586	1.3	0.488	0.07
1426383_at	Cry2	cryptochrome 2 (photolyase-like)	-1.06	0.76	-1.03	0.938	1.07	0.801	1.04	0.778	0
1431460_at	4930519D14Rik	RIKEN cDNA 4930519D14 gene	-3.04	0.007	2.13	0.175	-1.9	0.434	1.03	0.754	-0.45
1426905_a_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	-1.05	0.729	1.22	0.285	-1.22	0.031	1.25	0.354	0.05
1419607_at	Tnf	tumor necrosis factor	-1.74	0.161	1.26	0.512	1.15	0.839	-1.51	0.46	-0.21
1416674_at	Ptpru	protein tyrosine phosphatase, receptor type, U	-1.34	0.051	-1.35	0.239	1.5	0.021	1.54	0.211	0.09
1424263_at	2810003C17Rik	RIKEN cDNA 2810003C17 gene	1.02	0.924	1.11	0.595	-1.17	0.434	-1.29	0.385	-0.08
1444443_at	A830039H10Rik	RIKEN cDNA A830039H10 gene	-1.11	0.824	-2.45	0.042	1.67	0.318	3.45	0.232	0.39
1451261_s_at	AW049765	expressed sequence AW049765	1.1	0.435	1.15	0.446	-1.36	0.043	-1.85	0.103	-0.24
1456128_at	Atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), i	1.11	0.534	-1.04	0.891	-1.09	0.855	1.19	0.52	0.04
1449607_at	A230070E04Rik	RIKEN cDNA A230070E04 gene	-2.61	0.19	1.73	0.398	-1.14	0.448	1.09	0.846	-0.24
1435988_x_at	Ik	IK cytokine	1.13	0.102	1.16	0.017	-1.44	0.08	-1.47	0.103	-0.16
1419045_at	Slc25a23	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	-1.09	0.734	1.01	0.865	1.06	0.717	-1.67	0.121	-0.17
1435028_at	Wdr7	WD repeat domain 7	-1.02	0.693	1.07	0.577	-1.07	0.311	1.36	0.109	0.09
1444164_at	Fkbp3	FK506 binding protein 3	-1.18	0.483	1.03	0.794	1.1	0.466	-1.4	0.136	-0.11
1455580_at	Usp6nl	USP6 N-terminal like	-1.02	0.898	-1.13	0.515	1.12	0.492	1.16	0.517	0.03
1416609_at	BC004004	cDNA sequence BC004004	1.02	0.858	-1.05	0.616	1.01	0.955	-1.1	0.623	-0.03
1425069_at	BC018285	cDNA sequence BC018285	-1.85	0.104	1.47	0.246	-1.03	0.962	1.5	0.257	0.02
1453095_at	Rab10	RAB10, member RAS oncogene family	-1.02	0.767	-1.08	0.108	1.08	0.321	1.38	0.109	0.09
1448196_at	Mat2b	methionine adenosyltransferase II, beta	-1.25	0.172	1.08	0.383	1.11	0.287	-1.07	0.442	-0.03
1426230_at	Sphk2	sphingosine kinase 2	-1.2	0.381	-1.12	0.727	1.26	0.342	1.16	0.469	0.02
1439688_at	Fbln1	fibulin 1	1.33	0.727	-1.35	0.599	-1.1	0.751	1.12	0.849	0
1430451_at	4930481B07Rik	RIKEN cDNA 4930481B07 gene	-1.38	0.02	1.26	0.396	-1	0.994	1.35	0.495	0.06
1451297_at	Gulo	gulonolactone (L-) oxidase	1.29	0.556	-1.09	0.392	-1.28	0.728	1.11	0.712	0.01
1415675_at	Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	1.02	0.82	1	0.999	-1.04	0.741	-1.1	0.403	-0.03
1434144_s_at	2410187C16Rik	RIKEN cDNA 2410187C16 gene	-1.08	0.584	-1.08	0.292	1.13	0.48	1.15	0.184	0.03
1432654_at	5830426C09Rik	RIKEN cDNA 5830426C09 gene	1.08	0.39	1.05	0.786	-1.16	0.268	-1.26	0.088	-0.07
1438320_s_at	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	1.14	0.276	-1	0.958	-1.18	0.429	1.9	0.161	0.21
1437600_at	Atp11c	Atpase, class VI, type 11C	-1.06	0.912	1.06	0.737	-1.02	0.903	1.46	0.183	0.11
1423187_at	Gabarapl2	gamma-aminobutyric acid (GABA-A) receptor-associated protein-like 2	-1.08	0.154	-1.25	0.062	1.25	0.076	1.5	0.295	0.11
1423151_at	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	-1.04	0.718	1.13	0.564	-1.12	0.343	1.05	0.786	0.01
1418488_s_at	Ripk4	receptor-interacting serine-threonine kinase 4	-1.13	0.7	1.06	0.822	1.03	0.81	-1.33	0.355	-0.09
1444935_at	---	---	1.09	0.596	1.05	0.743	-1.19	0.617	-1.8	0.066	-0.21
1426693_x_at	Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-1.03	0.157	-1.12	0.2	1.12	0.39	1.07	0.499	0.01
1418854_at	Birc2	baculoviral IAP repeat-containing 2	1.01	0.954	1.06	0.605	-1.1	0.655	-1.44	0.203	-0.12
1434993_at	B830045N13Rik	RIKEN cDNA B830045N13 gene	1.12	0.777	1.14	0.302	-1.39	0.212	-1.34	0.276	-0.12
1430693_at	Pnpla5	patatin-like phospholipase domain containing 5	1.02	0.97	1.01	0.977	-1.04	0.858	-1.52	0.269	-0.13
1416423_x_at	Ssb	Sjogren syndrome antigen B	1.02	0.73	1.21	0.02	-1.32	0.035	-1.05	0.545	-0.04
1447581_at	3110050K21Rik	RIKEN cDNA 3110050K21 gene	1.14	0.029	-1.4	0.478	1.12	0.795	-1.3	0.358	-0.11
1444103_at	Epsti1	Epithelial stromal interaction 1 (breast)	1.25	0.493	1.06	0.927	-1.48	0.05	-1.43	0.5	-0.15
1431948_a_at	Pank2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	1.01	0.851	-1.08	0.634	1.05	0.537	-1.03	0.79	-0.01
1443446_at	---	---	1.17	0.845	1.45	0.4	-2.72	0.055	-1.39	0.509	-0.37
1430638_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	-1.31	0.101	1	0.993	1.22	0.394	-1.29	0.433	-0.09
1426265_x_at	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase	-1.22	0.195	-1.34	0.149	1.42	0.086	1.56	0.102	0.1
1430900_at	4930430O22Rik	RIKEN cDNA 4930430O22 gene	-1.01	0.945	-1.31	0.448	1.23	0.472	1.21	0.356	0.03
1446880_at	Sash1	SAM and SH3 domain containing 1	1.17	0.503	1.14	0.745	-1.48	0.122	-1.11	0.598	-0.07
1436633_at	Bahcc1	BAH domain and coiled-coil containing 1	1.07	0.718	-1.48	0.01	1.24	0.126	-1.28	0.105	-0.11
1434286_at	Trps1	trichorhinophalangeal syndrome I (human)	1.15	0.314	1.04	0.864	-1.26	0.247	-1.57	0.134	-0.16
1454475_at	4921524M04Rik	RIKEN cDNA 4921524M04 gene	1.2	0.578	-1.02	0.928	-1.23	0.513	1.91	0.128	0.21
1424122_s_at	Commd1	COMM domain containing 1	1.04	0.591	1.03	0.726	-1.09	0.524	-1.02	0.952	-0.01

1417800_at	Parp2	poly (ADP-ribose) polymerase family, member 2	-1.16	0.475	1.03	0.846	1.09	0.559	-1.3	0.193	-0.08
1435682_at	Lars2	leucyl-tRNA synthetase, mitochondrial	-1.08	0.573	-1.04	0.697	1.09	0.402	1.09	0.619	0.02
1456664_x_at	Hnrpf /// LOC63700	heterogeneous nuclear ribonucleoprotein F /// similar to heterogeneous nuclear ri	1.11	0.007	-1.03	0.65	-1.1	0.39	1.08	0.342	0.01
1415956_a_at	Pctk1	PCTAIRE-motif protein kinase 1	-1.12	0.762	-1.02	0.871	1.11	0.685	1.97	0.132	0.24
1454264_at	2310046K23Rik	RIKEN cDNA 2310046K23 gene	1.87	0.206	-2.08	0.117	-1.58	0.635	1.04	0.843	-0.19
1428751_at	Pacrg	Park2 co-regulated	-1.22	0.381	1	0.995	1.16	0.553	-2.29	0.131	-0.33
1424670_s_at	Zfyve21	zinc finger, FYVE domain containing 21	1.07	0.067	-1.05	0.637	-1.03	0.856	1.34	0.004	0.08
1456339_at	2810410D24Rik	RIKEN cDNA 2810410D24 gene	-1.02	0.925	-1.19	0.377	1.17	0.364	1.14	0.603	0.02
1429982_at	4933426K21Rik	RIKEN cDNA 4933426K21 gene	-1.5	0.602	1.42	0.534	-1.11	0.8	1.37	0.585	0.04
1435735_x_at	H47	histocompatibility 47	1.02	0.848	1.14	0.309	-1.2	0.056	-1.2	0.511	-0.06
1423690_s_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-1.62	0.245	1.47	0.351	-1.12	0.687	1.15	0.652	-0.03
1432628_at	Cbx3	chromobox homolog 3 (Drosophila HP1 gamma)	1.22	0.473	-1.1	0.804	-1.17	0.467	1.29	0.261	0.06
1422000_at	Akr1c12	aldo-keto reductase family 1, member C12	1.33	0.094	-1.42	0.093	-1.05	0.903	1.84	0.359	0.17
1422846_at	Rbp2	retinol binding protein 2, cellular	-2.29	0.52	-1.05	0.873	1.6	0.417	2.25	0.236	0.13
1443000_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	1.14	0.561	1.07	0.791	-1.3	0.317	-1.96	0.396	-0.26
1448583_at	AA960436	expressed sequence AA960436	-1.16	0.369	1.11	0.32	1.01	0.933	-1.08	0.771	-0.03
1436741_at	Obox1 /// MGC117	oocyte specific homeobox 1 /// similar to oocyte specific homeobox 3 /// similar to	-1.03	0.952	1.18	0.579	-1.2	0.388	1.44	0.377	0.1
1451250_at	Gprin1	G protein-regulated inducer of neurite outgrowth 1	-2.51	0.414	1.56	0.319	1.02	0.938	-1.56	0.078	-0.37
1426633_s_at	Kctd14	potassium channel tetramerisation domain containing 14	1.48	0.18	-1.11	0.796	-1.64	0.037	1.39	0.475	0.03
1437649_x_at	Ppib	peptidylprolyl isomerase B	1.11	0.01	1.23	0.211	-1.55	0.006	-1.12	0.406	-0.08
1451781_at	Nfatc2ip	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interactir	1.29	0.726	-1.32	0.731	-1.07	0.862	1.2	0.793	0.03
1448489_at	Pafah2	platelet-activating factor acetylhydrolase 2	-1.04	0.547	-1.09	0.159	1.1	0.55	1.37	0.289	0.09
1426616_at	Tlcd1	TLC domain containing 1	1.06	0.216	-1.02	0.895	-1.05	0.858	3.95	0.246	0.73
1436739_at	Agtr1a	angiotensin II receptor, type 1a	1.07	0.675	-1.01	0.928	-1.08	0.692	1.23	0.674	0.05
1457359_at	Inpp4b	inositol polyphosphate-4-phosphatase, type II	1.54	0.454	-2.39	0.185	1.03	0.915	-2.1	0.128	-0.48
1450987_a_at	2310004I24Rik	RIKEN cDNA 2310004I24 gene	1.01	0.948	1.03	0.61	-1.05	0.747	-1.42	0.123	-0.11
1448985_at	Dusp22	dual specificity phosphatase 22	1.04	0.863	1.08	0.556	-1.15	0.395	-1.32	0.25	-0.09
1418443_at	Xpo1	exportin 1, CRM1 homolog (yeast)	-1.11	0.313	1.15	0.091	-1.07	0.415	1.12	0.495	0.02
1428910_at	2310022B05Rik	RIKEN cDNA 2310022B05 gene	-1	0.986	-1.04	0.716	1.03	0.886	1.95	0.174	0.23
1430483_a_at	Tmem79	transmembrane protein 79	1.11	0.837	-1.12	0.637	-1.01	0.948	1.55	0.345	0.13
1416634_at	5730536A07Rik	RIKEN cDNA 5730536A07 gene	-1.06	0.644	-1.02	0.817	1.06	0.642	1.08	0.59	0.02
1449317_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.05	0.704	-1.07	0.572	1	0.996	-1.38	0.066	-0.1
1444341_at	8030451F13Rik	RIKEN cDNA 8030451F13 gene	1.09	0.212	-1.65	0.33	1.29	0.482	-1.34	0.568	-0.15
1453336_at	Ccdc98	coiled-coil domain containing 98	1.23	0.412	-1.27	0.453	-1.03	0.904	1.02	0.77	-0.01
1458372_at	Tmc8	transmembrane channel-like 8	-1.46	0.231	-1.78	0.173	1.74	0.265	1.25	0.423	-0.06
1459455_at	Armet	Arginine-rich, mutated in early stage tumors	1.5	0.504	-1.26	0.718	-1.45	0.489	1.36	0.388	0.04
1438437_a_at	4933439C10Rik	RIKEN cDNA 4933439C10 gene	1.08	0.062	1.12	0.692	-1.27	0.082	-1.34	0.56	-0.1
1444219_at	AY702103	cDNA sequence AY702103	-1.57	0.495	-1.14	0.864	1.47	0.522	2.04	0.286	0.2
AFFX-r2-Ec-bioD-5_	---	---	1.15	0.137	1.12	0.224	-1.39	0.054	-1.2	0.389	-0.08
1448332_at	Pex19	peroxisome biogenesis factor 19	1.17	0.726	-1.19	0.507	-1.02	0.938	1.14	0.728	0.03
1450390_x_at	Rps18	ribosomal protein S18	1.1	0.827	1.32	0.601	-1.76	0.097	-1	0.998	-0.09
1431950_at	4930528G23Rik	RIKEN cDNA 4930528G23 gene	-1.11	0.79	1.01	0.987	1.08	0.889	-1.24	0.737	-0.07
1437251_at	Cdca2	cell division cycle associated 2	-1.14	0.353	-1.23	0.694	1.3	0.368	1.99	0.293	0.23
1445692_x_at	---	---	-1.63	0.437	1.45	0.665	-1.08	0.83	1.01	0.985	-0.06
1421864_at	Dbil5	diazepam binding inhibitor-like 5	-1.21	0.488	-1.09	0.644	1.24	0.513	1.62	0.2	0.14
1460552_at	Ascc3l1	activating signal cointegrator 1 complex subunit 3-like 1	1.03	0.423	-1.1	0.339	1.05	0.65	-1.27	0.126	-0.07
1423346_at	Degs1	degenerative spermatocyte homolog 1 (Drosophila)	1.02	0.017	1.15	0.013	-1.22	0.01	-1.05	0.549	-0.03
1457680_a_at	Tmem69	transmembrane protein 69	-1.04	0.781	-1.12	0.14	1.13	0.125	1.19	0.487	0.04
1451984_at	Hnrpul1	heterogeneous nuclear ribonucleoprotein U-like 1	-1.03	0.915	1.14	0.063	-1.14	0.469	1.13	0.345	0.03
1449016_at	Zp2	zona pellucida glycoprotein 2	1.27	0.617	-1.2	0.592	-1.13	0.706	2.51	0.288	0.36
1419784_x_at	---	---	-1.63	0.286	1.12	0.759	1.26	0.71	-1.18	0.589	-0.11
1444431_at	Rcsd1	RCSD domain containing 1	1.04	0.844	-1.1	0.864	1.04	0.895	-1.26	0.347	-0.07
1424877_a_at	Alad	aminolevulinate, delta-, dehydratase	-1.14	0.393	-1.21	0.145	1.29	0.042	4.6	0.124	0.88

1435431_at	2310047M15Rik	RIKEN cDNA 2310047M15 gene	1.14	0.088	-1.28	0.112	1.07	0.807	-1.63	0.091	-0.18
1443051_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-1.05	0.817	-1.13	0.516	1.15	0.194	1.19	0.161	0.04
1416993_at	Cog4	component of oligomeric golgi complex 4	1.02	0.856	-1.03	0.745	-1.01	0.938	1.19	0.087	0.04
1423371_at	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.11	0.371	1.02	0.903	-1.16	0.115	-1.09	0.53	-0.03
1417845_at	Cldn6	claudin 6	1.03	0.829	-1.44	0.33	1.27	0.301	-1.22	0.468	-0.09
1439094_at	Cltc	clathrin, heavy polypeptide (Hc)	1.16	0.423	1.1	0.561	-1.38	0.111	-1.08	0.067	-0.05
1418029_at	Faim	Fas apoptotic inhibitory molecule	-1.22	0.203	1.03	0.767	1.14	0.312	-1.27	0.218	-0.08
1428029_a_at	H2afv	H2A histone family, member V	1.07	0.422	-1.1	0.359	1.01	0.922	-1.02	0.752	-0.01
1416604_at	Cyc1	cytochrome c-1	-1.06	0.435	-1.2	0.148	1.21	0.235	1.24	0.341	0.05
1441241_at	9630013D21Rik	RIKEN cDNA 9630013D21 gene	-1.05	0.73	-1.27	0.272	1.24	0.622	2.62	0.089	0.39
1424880_at	Trib1	tribbles homolog 1 (Drosophila)	1.03	0.62	-1.12	0.628	1.07	0.701	-1.05	0.672	-0.02
1455701_at	Snx26	sorting nexin 26	-1.32	0.375	1.24	0.311	-1.01	0.953	2.18	0.158	0.27
1417949_at	Ilf2	interleukin enhancer binding factor 2	1.15	0.62	-1.12	0.476	-1.05	0.775	1.76	0.169	0.18
1416498_at	Ppic	peptidylprolyl isomerase C	1.22	0.007	1.21	0.135	-1.79	0.014	-1.28	0.387	-0.16
1442521_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930568O12 pr	1.05	0.91	-1.02	0.952	-1.04	0.849	1.76	0.224	0.19
1420198_at	---	---	-1.99	0.12	1.43	0.407	1.06	0.854	-2.16	0.029	-0.42
1424006_at	Aarsd1	alanyl-tRNA synthetase domain containing 1	-1.01	0.928	-1.05	0.804	1.05	0.592	1.57	0.37	0.14
1442574_at	Cryzl1	Crystallin, zeta (quinone reductase)-like 1	-1.16	0.705	-1.05	0.935	1.18	0.698	2.64	0.134	0.4
1455855_x_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	-1.07	0.155	-1	0.957	1.06	0.433	1.16	0.091	0.04
1437556_at	Zfhx4	zinc finger homeodomain 4	-1.51	0.537	-1.05	0.717	1.37	0.463	2.29	0.391	0.28
1453747_at	2810021J22Rik	RIKEN cDNA 2810021J22 gene	1.01	0.926	1.11	0.596	-1.15	0.154	-1.4	0.231	-0.11
1453968_at	4833439F03Rik	RIKEN cDNA 4833439F03 gene	1.03	0.717	1.04	0.845	-1.08	0.645	-1.09	0.717	-0.03
1429363_at	Vps37a	vacuolar protein sorting 37A (yeast)	-1.12	0.702	-1.02	0.732	1.12	0.315	1.01	0.904	0
1452826_s_at	Fbxl20	F-box and leucine-rich repeat protein 20	-1.17	0.009	-1.12	0.403	1.24	0.054	1.12	0.157	0.02
1447585_s_at	Mrps6	mitochondrial ribosomal protein S6	1.06	0.497	-1.17	0.25	1.07	0.568	-1.28	0.273	-0.08
1459147_at	---	---	1.04	0.964	-3.62	0.098	1.68	0.161	-1.27	0.599	-0.55
1430018_at	Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5	1.21	0.768	1.05	0.942	-1.37	0.431	-2.67	0.142	-0.44
1455341_at	2010003J03Rik	RIKEN cDNA 2010003J03 gene	-1.2	0.054	-1.2	0.459	1.32	0.163	1.07	0.634	0
1434387_at	Itfg3	integrin alpha FG-GAP repeat containing 3	-1.16	0.125	-1.16	0.138	1.27	0.044	1.23	0.469	0.04
1429583_at	2900053A13Rik	RIKEN cDNA 2900053A13 gene	1.01	0.967	1.27	0.491	-1.41	0.028	-1.4	0.426	-0.13
1431873_a_at	Tube1	epsilon-tubulin 1	-1.16	0.396	-1.8	0.084	1.57	0.241	1.12	0.595	-0.07
1418545_at	Wasf1	WASP family 1	1.06	0.628	1.12	0.518	-1.23	0.44	-1.65	0.21	-0.18
1454993_a_at	Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	-1.11	0.355	1.11	0.31	-1.02	0.733	1.15	0.452	0.03
1417080_a_at	Ecsit	ECSIT homolog (Drosophila)	-1.08	0.713	-1.18	0.102	1.21	0.089	1.08	0.697	0.01
1420123_at	Tcta	T-cell leukemia translocation altered gene	1.05	0.666	1.03	0.809	-1.09	0.26	-1.08	0.666	-0.02
1449147_at	Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	-1.54	0.067	1.47	0.395	-1.14	0.359	1.44	0.354	0.06
1449163_at	Sigirr	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	-1.05	0.599	1.01	0.874	1.03	0.818	-1.41	0.219	-0.11
1428882_at	Wipi2	WD repeat domain, phosphoinositide interacting 2	-1.03	0.849	-1.12	0.564	1.13	0.671	2.83	0.258	0.45
1418827_at	Thex1	three prime histone mRNA exonuclease 1	1.06	0.681	-1.01	0.926	-1.06	0.669	1.36	0.446	0.09
1440388_at	---	Transcribed locus	1.06	0.434	-1.1	0.603	1.03	0.839	-1.13	0.308	-0.04
1429639_at	Prei4	preimplantation protein 4	-1.18	0.423	-1.05	0.775	1.19	0.537	1.05	0.714	0
1451164_a_at	Mrps18b	mitochondrial ribosomal protein S18B	-1.04	0.749	-1.23	0.223	1.22	0.375	1.21	0.356	0.04
1454374_at	5730458M16Rik	RIKEN cDNA 5730458M16 gene	-1.04	0.852	1.26	0.464	-1.29	0.064	1.52	0.079	0.11
1429543_at	6230424C14Rik	RIKEN cDNA 6230424C14 gene	1.15	0.43	1.22	0.047	-1.62	0.009	-1.68	0.167	-0.23
1418602_at	Cdh15 /// LOC6729	cadherin 15 /// similar to Muscle-cadherin precursor (M-cadherin) (Cadherin-15) (	-1.51	0.189	-1.06	0.796	1.38	0.535	1.01	0.988	-0.04
1426881_at	Ube3c	ubiquitin protein ligase E3C	1.07	0.762	-1.02	0.894	-1.06	0.626	1.13	0.345	0.03
1456117_at	2600005C20Rik	RIKEN cDNA 2600005C20 gene	-1.06	0.658	-1.02	0.841	1.07	0.55	1.11	0.385	0.02
1429121_at	4921517N04Rik	RIKEN cDNA 4921517N04 gene	-1.05	0.782	1.15	0.167	-1.13	0.286	1.59	0.431	0.14
1436907_at	Nav1	neuron navigator 1	1.05	0.662	1.1	0.23	-1.19	0.223	-1.06	0.804	-0.02
1452381_at	Creb3l2	cAMP responsive element binding protein 3-like 2	-1.15	0.329	1.1	0.6	1.02	0.926	-1.04	0.861	-0.02
1439060_s_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	-1.1	0.565	-1.03	0.893	1.11	0.369	2.72	0.129	0.42
1442046_at	Shroom2 /// LOC67	shroom family member 2 /// similar to Apical-like protein (APXL protein)	1.04	0.617	-1.93	0.087	1.43	0.214	-1.37	0.148	-0.21
1459751_s_at	Ppp1r16a	protein phosphatase 1, regulatory (inhibitor) subunit 16A	-1.01	0.917	1.02	0.558	-1.02	0.847	1.02	0.682	0

1420131_s_at	Pttg1ip	pituitary tumor-transforming 1 interacting protein	-1.01	0.246	1.03	0.488	-1.03	0.754	1.02	0.632	0
1433473_x_at	Tm2d2	TM2 domain containing 2	1.03	0.848	1.25	0.029	-1.41	0.001	-1.08	0.551	-0.05
1454651_x_at	Mbp	myelin basic protein	-1.17	0.729	-2.56	0.078	1.74	0.187	1.06	0.925	-0.23
1435867_at	---	Visual cortex cDNA, RIKEN full-length enriched library, clone:K230008J08 produ	-1.18	0.175	-1.1	0.443	1.24	0.052	1.61	0.312	0.14
1452667_at	Rab2b	RAB2B, member RAS oncogene family	1.06	0.65	1.09	0.646	-1.19	0.155	-1.53	0.139	-0.14
1455008_at	Gna12	guanine nucleotide binding protein, alpha 12	1.08	0.764	-1.02	0.882	-1.07	0.728	1.66	0.001	0.16
1431514_at	5730453C05Rik	RIKEN cDNA 5730453C05 gene	1.36	0.256	-1.09	0.881	-1.39	0.051	1.37	0.097	0.06
1431153_at	Nrxn3	Neurexin III	-1.07	0.871	1.34	0.588	-1.4	0.411	1.41	0.227	0.07
1458339_at	Cdadc1	cytidine and dCMP deaminase domain containing 1	-1.06	0.818	-1.06	0.845	1.11	0.802	1.22	0.652	0.05
1431282_at	Thrap4	thyroid hormone receptor associated protein 4	1.36	0.594	-1.32	0.371	-1.15	0.653	1.02	0.937	-0.02
1419966_at	Tubb2b	tubulin, beta 2b	1.56	0.451	-1.16	0.761	-1.75	0.283	1.31	0.566	-0.01
1437687_x_at	Fkbp9	FK506 binding protein 9	1.03	0.864	1.07	0.445	-1.12	0.544	-1.23	0.145	-0.06
1425100_a_at	Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma	-1.4	0.528	1.04	0.823	1.24	0.502	-1.85	0.132	-0.24
1421450_a_at	Map3k4	mitogen activated protein kinase kinase kinase 4	1.03	0.84	-1.19	0.119	1.12	0.552	-1.09	0.663	-0.03
1458301_x_at	Zfp292	Zinc finger protein 292	-1.39	0.344	-1.07	0.884	1.34	0.488	1.2	0.747	0.02
1420961_a_at	Ivns1abp	influenza virus NS1A binding protein	-1.05	0.67	1.12	0.74	-1.09	0.719	1.1	0.795	0.02
1421819_a_at	Set /// LOC671392	SET translocation /// similar to SET protein (Phosphatase 2A inhibitor I2PP2A) (I-	1.18	0.138	-1.19	0.093	-1.03	0.892	1.03	0.812	0
1441727_s_at	Zfp467	zinc finger protein 467	1.13	0.471	-1.22	0.425	1.04	0.787	-1.19	0.656	-0.06
1439924_x_at	Tubgcp5	tubulin, gamma complex associated protein 5	-1.07	0.728	1.62	0.4	-2.26	0.052	1.09	0.82	-0.16
1421413_a_at	Pdlim5 /// LOC6696	PDZ and LIM domain 5 /// similar to PDZ and LIM domain protein 5 (Enigma hom	1.14	0.593	-1.5	0.199	1.19	0.578	-1.8	0.166	-0.24
1436699_x_at	Rpl18 /// LOC67285	ribosomal protein L18 /// similar to 60S ribosomal protein L18	1.1	0.135	1.11	0.259	-1.27	0.069	-1.6	0.055	-0.17
1417617_at	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminid	-1.5	0.678	-2.41	0.179	1.91	0.054	1.26	0.008	-0.18
1420726_x_at	Tmlhe	trimethyllysine hydroxylase, epsilon	-1.43	0.162	1.05	0.73	1.24	0.063	-1.12	0.564	-0.06
1424697_at	Dtwd1	DTW domain containing 1	-1.05	0.351	1.08	0.497	-1.04	0.837	1.48	0.35	0.12
1438218_at	Zbtb24	zinc finger and BTB domain containing 24	1	0.992	-1.02	0.813	1.01	0.892	-1.51	0.074	-0.13
1415858_at	Eif3s8	eukaryotic translation initiation factor 3, subunit 8	1.02	0.275	-1.05	0.49	1.02	0.848	-1.17	0.18	-0.04
1419068_at	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	1.12	0.592	-1.14	0.396	-1.01	0.886	1.56	0.19	0.13
1448154_at	Ndrg2	N-myc downstream regulated gene 2	1.06	0.715	-1.2	0.055	1.1	0.559	-1.06	0.848	-0.02
1453464_at	D530014G21Rik	RIKEN cDNA D530014G21 gene	1.01	0.94	-1.03	0.751	1.01	0.961	-1.73	0.037	-0.18
1460300_a_at	Ltk	leukocyte tyrosine kinase	1.23	0.774	-1.49	0.432	1.09	0.63	-2.55	0.031	-0.43
1422119_at	Rab5b	RAB5B, member RAS oncogene family	-1.01	0.975	-1.15	0.387	1.14	0.649	1.07	0.903	0.01
1432689_at	4631422I05Rik	RIKEN cDNA 4631422I05 gene	1.18	0.858	1.14	0.732	-1.48	0.344	-3.41	0.263	-0.64
1430284_at	1700008P02Rik	RIKEN cDNA 1700008P02 gene	-1.96	0.495	1.19	0.69	1.3	0.387	-1.24	0.617	-0.18
1446995_at	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	-1.49	0.56	1.54	0.232	-1.27	0.611	1.04	0.919	-0.05
1433797_at	E130309D02Rik	RIKEN cDNA E130309D02 gene	-1.07	0.726	-1.04	0.833	1.1	0.347	1.13	0.699	0.03
1426086_a_at	Fmr1	fragile X mental retardation syndrome 1 homolog	-1.25	0.798	-2.15	0.294	1.73	0.207	1.18	0.716	-0.12
1436131_at	Siglech	sialic acid binding Ig-like lectin H	1.19	0.644	-1.3	0.05	1.04	0.921	-5.49	0.022	-1.14
1426746_at	1810026J23Rik	RIKEN cDNA 1810026J23 gene	-1.3	0.149	-1.05	0.775	1.28	0.197	1.18	0.4	0.02
1419357_at	5830446M03Rik	RIKEN cDNA 5830446M03 gene	-1.52	0.224	1.15	0.37	1.19	0.456	-1.16	0.164	-0.09
1421771_a_at	Ipp	IAP promoted placental gene	-1.26	0.353	-1.08	0.509	1.27	0.066	1.74	0.117	0.17
1432309_at	9130410C08Rik	RIKEN cDNA 9130410C08 gene	-1.38	0.481	-1.01	0.948	1.28	0.387	2.92	0.251	0.45
1454015_a_at	Cdh13	cadherin 13	-1.38	0.498	-1.43	0.352	1.57	0.549	1.38	0.38	0.03
1439559_at	1700040D17Rik	RIKEN cDNA 1700040D17 gene	-1.11	0.844	1.07	0.796	1.03	0.958	-1.16	0.405	-0.04
1433108_at	Tcrb-J /// Tcrb-V8.2	T-cell receptor beta, joining region /// T-cell receptor beta, variable 8.2 /// T-cell re	-2.17	0.271	1.26	0.524	1.28	0.144	-1.02	0.858	-0.17
1451218_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	-1.22	0.093	1.14	0.355	1.03	0.819	-1.12	0.262	-0.04
1425602_a_at	Rabep2	rabaptin, RAB GTPase binding effector protein 2	1	0.99	-1.19	0.555	1.15	0.38	-1.76	0.139	-0.2
1450186_s_at	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	1.03	0.83	-1.16	0.135	1.11	0.39	-1.02	0.864	-0.01
1442725_at	---	---	1.04	0.903	1.01	0.98	-1.06	0.829	-1.83	0.044	-0.21
1448785_at	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1.14	0.425	1.31	0.317	-1.81	0.033	-1.04	0.659	-0.1
1447855_x_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	-2.23	0.509	1.29	0.513	1.25	0.491	-1.73	0.602	-0.35
1434268_at	Adar	adenosine deaminase, RNA-specific	-1.14	0.233	1	0.992	1.12	0.22	-1.28	0.136	-0.08
1436349_at	2700094K13Rik	RIKEN cDNA 2700094K13 gene	1.03	0.347	1.03	0.87	-1.07	0.527	-1.53	0.066	-0.14
1449721_at	---	PREDICTED: Mus musculus hypothetical protein LOC628408 (LOC628408), mR	-1.32	0.762	1.37	0.562	-1.16	0.566	1.46	0.026	0.09

1416520_x_at	LOC622534	similar to ribosomal protein L36	1.03	0.214	1.06	0.022	-1.11	0.523	-1.6	0.048	-0.15
1425743_at	Trim7	tripartite motif protein 7	1.11	0.771	1.13	0.843	-1.33	0.336	-2.03	0.199	-0.28
1448610_a_at	Sod2	superoxide dismutase 2, mitochondrial	-1.05	0.747	-1.14	0.235	1.16	0.02	1.36	0.173	0.09
1423437_at	---	---	-1.07	0.292	-1.21	0.513	1.24	0.495	1.3	0.143	0.06
1436934_s_at	Aco2	aconitase 2, mitochondrial	-1.21	0.164	-1.11	0.543	1.27	0.18	1.15	0.026	0.03
1433222_at	2610311E24Rik	RIKEN cDNA 2610311E24 gene	1.15	0.377	1.05	0.934	-1.25	0.597	-1.48	0.548	-0.13
1430724_at	Abhd9	abhydrolase domain containing 9	-1.37	0.341	1.12	0.784	1.15	0.455	-1.56	0.373	-0.17
1449001_at	Ivd	isovaleryl coenzyme A dehydrogenase	1	0.988	-1.17	0.212	1.14	0.466	-1.77	0.136	-0.2
1444840_at	---	---	1.07	0.878	1.14	0.655	-1.28	0.473	-1.01	0.989	-0.02
1441192_at	Scly	selenocysteine lyase	-1.08	0.179	1.13	0.197	-1.06	0.741	1.44	0.037	0.11
1438171_x_at	Mettl9	methyltransferase like 9	-1.29	0.206	1.12	0.287	1.1	0.661	-1.03	0.888	-0.02
1456744_x_at	Flcn	folliculin	1.1	0.489	1.09	0.823	-1.24	0.457	-2.38	0.048	-0.36
1439744_at	Csk	C-src tyrosine kinase	1.08	0.779	1.1	0.816	-1.21	0.596	-1.53	0.414	-0.14
1424441_at	Slc27a4	solute carrier family 27 (fatty acid transporter), member 4	-1.13	0.21	1.03	0.834	1.08	0.588	-1.23	0.306	-0.06
1451605_at	Dyx1c1	dyslexia susceptibility 1 candidate 1 homolog (human)	-1.43	0.159	1.11	0.809	1.19	0.562	-2.37	0.015	-0.37
1434556_at	---	Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I8300	1.01	0.872	1.15	0.107	-1.2	0.193	-1	0.982	-0.01
1416192_at	Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	-1.04	0.866	-1.11	0.535	1.13	0.385	1.22	0.253	0.05
1459666_at	Trak1	trafficking protein, kinesin binding 1	-1.12	0.717	1.05	0.865	1.05	0.774	-1.4	0.072	-0.1
1418217_at	Nme7	non-metastatic cells 7, protein expressed in	-1.17	0.308	-1.18	0.028	1.3	0.17	1.27	0.448	0.05
1437080_s_at	Psmd11 /// LOC627	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 /// similar to 26S	-1.12	0.406	-1.14	0.084	1.23	0.012	1.2	0.202	0.04
1433624_at	5830434P21Rik	RIKEN cDNA 5830434P21 gene	1.04	0.751	-1.21	0.065	1.13	0.648	-1.26	0.321	-0.07
1454079_at	4933400F03Rik	RIKEN cDNA 4933400F03 gene	-1.43	0.605	-1.15	0.772	1.42	0.334	1.56	0.64	0.1
1443575_at	2310040G24Rik	RIKEN cDNA 2310040G24 gene	1.14	0.616	-1.54	0.029	1.21	0.273	-1.13	0.427	-0.08
1440858_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	-1.46	0.107	-1.12	0.549	1.42	0.078	1.16	0.688	0
1419812_s_at	Ccdc56	coiled-coil domain containing 56	1	0.994	-1.03	0.665	1.03	0.884	-1.09	0.482	-0.02
1442461_at	Gfod1	glucose-fructose oxidoreductase domain containing 1	-1.7	0.163	1.28	0.699	1.13	0.662	-2.21	0.064	-0.37
1441741_at	1700049E17Rik ///	RIKEN cDNA 1700049E17 gene /// RIKEN cDNA 4930503E14 gene /// RIKEN cD	1.16	0.78	-1.47	0.414	1.16	0.604	-1.26	0.503	-0.1
1442811_at	Rgmb	RGM domain family, member B	1.18	0.596	1.05	0.905	-1.3	0.353	-1.14	0.636	-0.05
1442239_at	Tnfaip8	Tumor necrosis factor, alpha-induced protein 8	-1.72	0.066	1.13	0.764	1.29	0.435	-1.21	0.444	-0.13
1453324_at	6330509M23Rik	RIKEN cDNA 6330509M23 gene	-1.09	0.468	1.06	0.774	1.02	0.874	-1.14	0.138	-0.04
1445734_at	Tdh	L-threonine dehydrogenase	-1.32	0.373	1.28	0.721	-1.03	0.952	1.37	0.519	0.07
1419590_at	Cyp2b9	cytochrome P450, family 2, subfamily b, polypeptide 9	1.35	0.759	-1.56	0.215	1.01	0.982	-1.03	0.88	-0.06
1428907_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	1.12	0.491	1.05	0.822	-1.2	0.378	-1	0.977	-0.01
1434048_at	4930471M23Rik	RIKEN cDNA 4930471M23 gene	1.14	0.63	-1.02	0.891	-1.14	0.569	1.39	0.098	0.09
1427719_s_at	Krt2-ps1 /// Krt82	keratin complex 2, basic, pseudogene 1 /// keratin 82	1.3	0.396	-1.13	0.801	-1.22	0.451	1.32	0.31	0.07
1434348_at	Fez2	fasciculation and elongation protein zeta 2 (zygin II)	-1.03	0.399	1.1	0.457	-1.07	0.416	1.15	0.523	0.03
1419310_s_at	Rfxank	regulatory factor X-associated ankyrin-containing protein	1.03	0.935	-1.06	0.704	1.03	0.731	-1.37	0.003	-0.09
1438129_at	Wsb2	WD repeat and SOCS box-containing 2	-1.07	0.736	1.05	0.713	1.01	0.976	-1.16	0.321	-0.04
1416289_at	Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-1.18	0.395	1.16	0.028	-1.01	0.918	1.19	0.05	0.04
1428888_at	Tmem33	transmembrane protein 33	1.52	0.514	-1.74	0.106	-1.11	0.868	1.1	0.67	-0.06
1448568_a_at	Slc20a1	solute carrier family 20, member 1	-1.06	0.873	-1.03	0.892	1.08	0.439	1.54	0.255	0.13
1422473_at	Pde4b	phosphodiesterase 4B, cAMP specific	1.12	0.529	-1.2	0.535	1.04	0.932	-2.76	0.098	-0.45
1451080_at	Usp1	ubiquitin specific peptdiase 1	-1.05	0.759	1.1	0.373	-1.06	0.484	1.36	0.278	0.09
1418728_at	Star	steroidogenic acute regulatory protein	1.03	0.936	-1.06	0.606	1.03	0.918	-1.68	0.155	-0.17
1460104_at	Vps4b	vacuolar protein sorting 4b (yeast)	1.01	0.959	-1.21	0.7	1.16	0.532	-1.29	0.543	-0.08
1419994_s_at	D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	1.09	0.237	1.07	0	-1.19	0.418	-1.32	0.158	-0.09
1453096_x_at	Rpl27 /// LOC6211(	ribosomal protein L27 /// similar to ribosomal protein L27 /// similar to ribosomal p	1.03	0.839	1.05	0.637	-1.09	0.592	-1.45	0.107	-0.12
1428105_at	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	-1.32	0.589	1.46	0.44	-1.28	0.114	2.7	0.256	0.39
1424894_at	Rab13	RAB13, member RAS oncogene family	-1.02	0.827	-1	0.984	1.02	0.728	1.05	0.802	0.01
1445043_at	---	---	1.19	0.569	1.24	0.627	-1.78	0.015	-1.85	0.084	-0.3
1456337_at	Centd1	centaurin, delta 1	-1.05	0.915	1.25	0.058	-1.26	0.335	1.02	0.922	-0.01
1445863_at	E030013G06Rik	RIKEN cDNA E030013G06 gene	1.55	0.1	-1.58	0.393	-1.22	0.276	1.11	0.864	-0.04
1434849_at	Tspyl2	TSPY-like 2	-1.42	0.182	1.23	0.299	1.06	0.744	-1.06	0.838	-0.05

1434808_at	BC066140	cDNA sequence BC066140	-1.03	0.821	1.34	0.414	-1.46	0.024	1.5	0.373	0.09
1437509_x_at	Prkd2	protein kinase D2	-1.18	0.082	1.14	0.592	1.01	0.966	-1.09	0.75	-0.03
1442176_at	Arid5b	AT rich interactive domain 5B (Mrf1 like)	1.33	0.504	-2.05	0.243	1.18	0.535	-1.3	0.41	-0.21
1452248_at	Plekhg5	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	-1.12	0.112	-1.1	0.7	1.2	0.175	1.09	0.684	0.02
1454481_at	Mif	macrophage migration inhibitory factor	-2.72	0.315	1.19	0.412	1.44	0.469	-2.25	0.093	-0.58
1442744_at	C79248	expressed sequence C79248	1.3	0.348	1.14	0.193	-1.78	0.017	-2.18	0.049	-0.38
1440021_at	Gpr20	G protein-coupled receptor 20	1.16	0.811	-1.97	0.285	1.33	0.4	-1.03	0.965	-0.13
1454492_at	8430418B16Rik	RIKEN cDNA 8430418B16 gene	1.58	0.02	-1.06	0.816	-2.09	0.007	1.28	0.448	-0.07
1420705_at	Foxb1	forkhead box B1	1.08	0.889	-1.46	0.407	1.24	0.489	-1.16	0.814	-0.08
1453362_x_at	Rps24	ribosomal protein S24	1.01	0.937	1.12	0.141	-1.15	0.183	-1.36	0.009	-0.1
1417195_at	Wwc2	WW, C2 and coiled-coil domain containing 2	1.03	0.866	1.09	0.607	-1.14	0.545	-1.4	0.021	-0.1
1436981_a_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	-1.21	0.279	1.12	0.542	1.06	0.822	-1.29	0.17	-0.08
1448341_a_at	Stxbp2	syntaxin binding protein 2	-1.23	0.018	1.13	0.25	1.06	0.6	-1.21	0.236	-0.06
1460741_x_at	D17Wsu92e	DNA segment, Chr 17, Wayne State University 92, expressed	1.13	0.621	-1.05	0.721	-1.09	0.583	1.46	0.374	0.11
1417881_at	Slc39a3	solute carrier family 39 (zinc transporter), member 3	-1.11	0.745	1.05	0.855	1.05	0.657	-1.03	0.914	-0.01
1425857_at	Fbxw9	F-box and WD-40 domain protein 9	1.25	0.351	-1.31	0.53	-1.01	0.921	1.84	0.284	0.19
1425747_at	1110060D06Rik ///	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	-1.14	0.146	-1.27	0.134	1.33	0.329	1.09	0.562	0
1431657_at	9230112D13Rik	RIKEN cDNA 9230112D13 gene	-2.12	0.097	-1.26	0.705	1.73	0.288	1.62	0.238	-0.01
1425176_at	C1ql3	C1q-like 3	-1.03	0.931	-1.31	0.333	1.27	0.667	1.26	0.602	0.05
1417385_at	Npepps	aminopeptidase puromycin sensitive	-1.06	0.691	-1.06	0.576	1.11	0.364	1.12	0.469	0.03
1434735_at	Hlf	hepatic leukemia factor	-1.04	0.889	-1.15	0.521	1.17	0.754	1.51	0.312	0.12
1451031_at	Sfrp4	secreted frizzled-related sequence protein 4	-1.05	0.543	1.38	0.2	-1.49	0.076	2.18	0.217	0.25
1427144_at	Hnrpll	heterogeneous nuclear ribonucleoprotein L-like	1.07	0.073	-1.01	0.917	-1.07	0.477	1.93	0.079	0.23
1438691_at	Zzef1	zinc finger, ZZ-type with EF hand domain 1	1.09	0.463	1.03	0.365	-1.14	0.454	-1.44	0.078	-0.11
1435886_at	Dnajb12	DnaJ (Hsp40) homolog, subfamily B, member 12	-1.01	0.984	-1.15	0.049	1.14	0.561	1.28	0.075	0.07
1445094_at	---	---	-1.45	0.235	1.53	0.306	-1.28	0.46	1.25	0	0.01
1433724_at	D15Ertd621e	DNA segment, Chr 15, ERATO Doi 621, expressed	1.09	0.423	1.01	0.936	-1.11	0.601	-1.13	0.234	-0.03
1442413_at	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	-1.01	0.981	-1.13	0.458	1.13	0.552	1.25	0.549	0.06
1443578_at	---	Transcribed locus	-1.52	0.09	1.24	0.398	1.1	0.741	-1.17	0.772	-0.09
1434986_a_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	-1.09	0.188	-1.1	0.478	1.17	0.255	1.03	0.863	0.01
1446750_at	Impact	imprinted and ancient	-1.08	0.756	1.44	0.217	-1.58	0.054	1.01	0.972	-0.05
1433973_at	Sephs1	selenophosphate synthetase 1	1.2	0.188	-1.11	0.461	-1.11	0.51	1.44	0.196	0.1
1438439_at	Gpr171	G protein-coupled receptor 171	1.23	0.695	1.16	0.816	-1.63	0.057	-2.96	0.186	-0.55
1423113_a_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	-1.04	0.527	1.04	0.674	1	0.944	-1.13	0.039	-0.03
1420342_at	Gdap10	ganglioside-induced differentiation-associated-protein 10	1.05	0.831	1.2	0.308	-1.34	0.178	-1.15	0.357	-0.06
1434964_at	AA408420	expressed sequence AA408420	-1.22	0.131	1.02	0.941	1.16	0.126	-1.08	0.499	-0.03
1452199_at	2700094F01Rik	RIKEN cDNA 2700094F01 gene	1.15	0.47	1.1	0.251	-1.33	0.072	-1.13	0.605	-0.05
1453289_at	Eif2c4	eukaryotic translation initiation factor 2C, 4	1.07	0.611	1.16	0.462	-1.31	0.061	-1.31	0.427	-0.1
1445269_at	Ccdc98	Coiled-coil domain containing 98	-1.06	0.573	-1.32	0.617	1.3	0.446	1.22	0.275	0.04
1440334_at	Zfp90	Zinc finger protein 90	1.07	0.762	1.2	0.762	-1.36	0.328	-1.51	0.365	-0.15
1449065_at	Acot1	acyl-CoA thioesterase 1	1.18	0.151	-4.23	0.039	1.58	0.222	-1.51	0.269	-0.74
1424039_at	Tmem66	transmembrane protein 66	1.04	0.145	-1.05	0.431	1	0.958	-1.61	0.164	-0.15
1429764_at	1500005K14Rik	RIKEN cDNA 1500005K14 gene	1.07	0.801	-1.16	0.621	1.07	0.679	-1.72	0.087	-0.18
1451162_at	Hsbp1	heat shock factor binding protein 1	1.02	0.929	1.02	0.748	-1.03	0.824	-1.35	0.182	-0.09
1421228_at	Ccl7	chemokine (C-C motif) ligand 7	1.03	0.939	1.03	0.926	-1.07	0.893	-2.76	0.056	-0.44
1415915_at	Ddx1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	-1.07	0.698	-1	0.944	1.07	0.442	1.35	0.278	0.09
1446501_at	A830053O21Rik	RIKEN cDNA A830053O21 gene	1.17	0.409	-1.14	0.765	-1.05	0.767	1.08	0.614	0.01
1448447_at	Vps28	vacuolar protein sorting 28 (yeast)	-1.09	0.292	1.01	0.85	1.07	0.418	-1.28	0.346	-0.07
1452935_at	LOC546143	hypothetical protein LOC546143	1.07	0.605	-1.16	0.368	1.07	0.812	-1.12	0.519	-0.03
1426450_at	Plcl2	phospholipase C-like 2	-1.52	0.134	-1.27	0.046	1.56	0.19	2.04	0.313	0.2
1417742_a_at	Dmap1	DNA methyltransferase 1-associated protein 1	1.01	0.957	-1.14	0.117	1.12	0.524	-1.14	0.272	-0.04
1452990_at	Mtf1	metal response element binding transcription factor 1	-2.91	0.109	1.35	0.479	1.31	0.68	-1.19	0.683	-0.36
1436696_x_at	Ceacam11	CEA-related cell adhesion molecule 11	1.69	0.217	-1.26	0.62	-1.91	0.28	1.32	0.314	-0.04

1415900_a_at	Kit	kit oncogene	-1.09	0.827	-1.7	0.248	1.49	0.394	1.25	0.318	-0.01
1427245_at	Arfgap1	ADP-ribosylation factor GTPase activating protein 1	-1.01	0.917	1.08	0.57	-1.08	0.433	1.03	0.83	0.01
1453037_at	---	---	-1.08	0.771	1.16	0.593	-1.09	0.246	2.09	0.154	0.27
1434059_at	B230312A22Rik	RIKEN cDNA B230312A22 gene	-1.28	0.171	-1.04	0.898	1.26	0.219	3.1	0.195	0.51
1456614_at	Acn9	ACN9 homolog (S. cerevisiae)	-1.13	0.097	-1.02	0.864	1.13	0.314	1.08	0.601	0.02
1423066_at	Dnmt3a	DNA methyltransferase 3A	-1.22	0.559	-1.04	0.315	1.22	0.216	1.2	0.069	0.04
1439845_at	---	Transcribed locus	1.17	0.55	1	0.991	-1.21	0.096	-1.51	0.011	-0.14
1452171_at	Grwd1	glutamate-rich WD repeat containing 1	1.08	0.699	-1.19	0.048	1.08	0.687	-1.08	0.745	-0.03
1426650_at	Myh8	myosin, heavy polypeptide 8, skeletal muscle, perinatal	-1.07	0.918	-1.39	0.597	1.35	0.497	1.43	0.373	0.08
1416518_at	H1foo	H1 histone family, member O, oocyte-specific	-1.1	0.129	-2.14	0.182	1.63	0.295	1.38	0.089	-0.06
1425094_a_at	Lhx6	LIM homeobox protein 6	-1.74	0.436	1.56	0.289	-1.15	0.504	1.24	0.662	-0.02
1446931_at	---	Transcribed locus	1.19	0.682	-1.43	0.45	1.11	0.819	-1.1	0.836	-0.06
1433094_at	Slc1a2	solute carrier family 1 (glial high affinity glutamate transporter), member 2	-1.34	0.655	1.28	0.727	-1.02	0.954	1.22	0.749	0.03
1419470_at	Gnb4	guanine nucleotide binding protein, beta 4	1.2	0.409	1.15	0.486	-1.52	0.075	-1.09	0.611	-0.07
1429748_at	---	---	1.07	0.84	1.19	0.748	-1.35	0.457	-1.19	0.615	-0.07
1450833_at	Chrm1	cholinergic receptor, muscarinic 1, CNS	-1.03	0.766	-1.29	0.48	1.25	0.139	1.04	0.84	0
1435177_a_at	Anapc5	anaphase-promoting complex subunit 5	-1	0.982	-1.01	0.915	1.01	0.959	1.29	0.068	0.07
1416100_at	Eif3s7	eukaryotic translation initiation factor 3, subunit 7 (zeta)	-1.02	0.416	-1.17	0.045	1.17	0.163	1.03	0.689	0
1421119_at	Kif21b	kinesin family member 21B	1.29	0.387	-1.67	0.55	1.11	0.806	-1.08	0.748	-0.09
1458878_at	Yes1	Yamaguchi sarcoma viral (v-yes) oncogene homolog 1	1.05	0.654	-1.16	0.659	1.1	0.767	-1.57	0.524	-0.15
1438503_x_at	Edf1 /// LOC665181	endothelial differentiation-related factor 1 /// similar to Endothelial differentiation-r	1.05	0.672	-1.23	0.001	1.14	0.596	-1.24	0.224	-0.07
1424822_at	9630044O09Rik	RIKEN cDNA 9630044O09 gene	1.52	0.552	-2.13	0.17	1.02	0.957	-1.1	0.717	-0.17
1450655_at	Pten	phosphatase and tensin homolog	1.05	0.689	1.08	0.309	-1.15	0.42	-1.25	0.211	-0.07
1447105_at	Dcakd	Dephospho-CoA kinase domain containing	1.2	0.127	-1.45	0.091	1.11	0.53	-1.17	0.597	-0.08
1449051_at	Ppara	peroxisome proliferator activated receptor alpha	1.11	0.599	-1.49	0.183	1.23	0.511	-1.4	0.023	-0.14
1455311_at	Dgcr8	DiGeorge syndrome critical region gene 8	-1.01	0.941	1.17	0.229	-1.18	0.118	1.34	0.273	0.08
1431506_s_at	Ppih /// LOC433064	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomerase H /// similar to P	1.08	0.065	-1.07	0.68	-1.02	0.937	1.14	0.685	0.03
1460620_at	Zfp592	zinc finger protein 592	-1.27	0.494	1.04	0.633	1.18	0.421	-1.46	0.047	-0.13
1435111_at	2310011E23Rik	RIKEN cDNA 2310011E23 gene	1.2	0.817	1.2	0.298	-1.66	0.298	-1.25	0.763	-0.13
1416032_at	Tmem109	transmembrane protein 109	-1.3	0.09	-1.06	0.785	1.3	0.34	1.03	0.886	-0.01
1457652_x_at	Ptgs1	Prostaglandin-endoperoxide synthase 1	-1.02	0.922	1.16	0.372	-1.15	0.786	1.58	0.351	0.14
1450400_at	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	-1.06	0.69	1.03	0.831	1.04	0.846	-1.07	0.766	-0.02
1419508_at	Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	-1.12	0.335	1.14	0.461	-1.03	0.9	1	0.999	0
1443162_at	Ptpn3	Protein tyrosine phosphatase, non-receptor type 3	1.11	0.813	1.25	0.584	-1.55	0.333	-1.36	0.447	-0.14
1452720_a_at	Fip1l1	FIP1 like 1 (S. cerevisiae)	1.01	0.894	-1.14	0.278	1.12	0.121	-1.12	0.415	-0.03
1416241_at	Sec13l1	SEC13-like 1 (S. cerevisiae)	-1	0.978	1.04	0.763	-1.03	0.793	1.02	0.825	0.01
1437525_a_at	Polr3a	polymerase (RNA) III (DNA directed) polypeptide A	-1.24	0.442	1.03	0.829	1.17	0.076	-1.48	0.081	-0.13
1450941_at	---	---	-1.02	0.87	1.11	0.233	-1.1	0.406	1.44	0.076	0.11
1418703_at	Rbms1	RNA binding motif, single stranded interacting protein 1	1.16	0.518	1.08	0.503	-1.32	0.204	-1.49	0.143	-0.14
1432718_at	---	---	-1.11	0.878	-1.15	0.59	1.23	0.441	1.09	0.704	0.02
1449413_at	Mpv17l	Mpv17 transgene, kidney disease mutant-like	1.16	0.476	1.08	0.741	-1.31	0.067	-1.03	0.94	-0.02
1431149_at	B430105A11Rik	RIKEN cDNA B430105A11 gene	-1.04	0.928	-2.73	0.11	1.67	0.093	2.21	0.017	0.03
1458131_at	---	---	1.11	0.904	1.24	0.758	-1.52	0.121	-1.49	0.34	-0.17
1421219_at	Ttll3	tubulin tyrosine ligase-like family, member 3	-1.16	0.743	1.2	0.695	-1.06	0.886	1.16	0.63	0.04
1454086_a_at	Lmo2	LIM domain only 2	-1.08	0.625	1.12	0.523	-1.03	0.883	1.96	0.227	0.24
1420636_a_at	Dusp12	dual specificity phosphatase 12	-1.13	0.386	1.01	0.927	1.11	0.513	-1.08	0.322	-0.02
1422672_at	Sprr1b	small proline-rich protein 1B	-1.21	0.45	1.13	0.865	1.05	0.867	-1.4	0.501	-0.11
1440816_x_at	Ddx1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	-1.09	0.638	1.28	0.103	-1.22	0.064	1.19	0.295	0.04
1434974_at	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	1.2	0.475	1.21	0.579	-1.67	0.055	-1.81	0.12	-0.27
1453185_at	5730406M06Rik	RIKEN cDNA 5730406M06 gene	1.29	0.228	1.1	0.669	-1.61	0.044	-1.07	0.458	-0.07
1431607_at	Lypla1	lysophospholipase 1	1.3	0.292	-1.44	0.482	1.01	0.974	-2.02	0.085	-0.29
1441198_at	Zfp39	zinc finger protein 39	1.24	0.556	-1.07	0.812	-1.2	0.527	1.94	0.229	0.23
1447952_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	-1.2	0.307	-1.22	0.372	1.36	0.217	1.27	0.167	0.05

1429510_at	2810410L24Rik	RIKEN cDNA 2810410L24 gene	-1.01	0.978	1.16	0.698	-1.17	0.534	1.16	0.415	0.04
1454606_at	4933426M11Rik	RIKEN cDNA 4933426M11 gene	-1.04	0.751	1.01	0.97	1.03	0.85	-1.15	0.381	-0.04
1440017_at	Plekhg3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	1.84	0.361	-2.19	0.213	-1.41	0.549	2.24	0.323	0.12
1456660_a_at	0610010F05Rik	RIKEN cDNA 0610010F05 gene	-1.03	0.869	-1.03	0.875	1.07	0.674	1.34	0.007	0.09
1438243_at	---	---	-3.61	0.019	1.19	0.755	1.54	0.301	-1.46	0.056	-0.59
1450752_at	Cyct	cytochrome c, testis	-1.11	0.422	1.25	0.554	-1.17	0.325	1.32	0.544	0.07
1423810_at	Ppme1	protein phosphatase methylesterase 1	-1.12	0.119	-1.06	0.342	1.17	0.494	1.07	0.819	0.01
1420335_at	Dmc1h	disrupted meiotic cDNA 1 homolog	-1.21	0.426	1.31	0.525	-1.15	0.506	2.63	0.138	0.39
1423367_at	Wnt7a	wingless-related MMTV integration site 7A	-1.6	0.423	-2.06	0.028	1.89	0.075	1.53	0.132	-0.06
1428686_at	2810029C07Rik	RIKEN cDNA 2810029C07 gene	-1.08	0.868	1.04	0.93	1.04	0.954	-1.49	0.299	-0.12
1423232_at	Etv4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	1.33	0.254	-1.22	0.167	-1.16	0.429	1.15	0.667	0.02
1429089_s_at	2900026A02Rik	RIKEN cDNA 2900026A02 gene	-1.09	0.498	-1.13	0.525	1.21	0.306	1.03	0.775	0
1426582_at	Atf2	activating transcription factor 2	-1.05	0.049	-1.07	0.767	1.13	0.335	1.27	0.415	0.07
1424283_at	Jtb	jumping translocation breakpoint	1.03	0.719	1.06	0.421	-1.09	0.209	-1.26	0.253	-0.07
1432343_at	4930419G24Rik	RIKEN cDNA 4930419G24 gene	1.15	0.857	1.01	0.951	-1.19	0.701	-1.54	0.456	-0.14
1427560_at	Six5	sine oculis-related homeobox 5 homolog (Drosophila)	1.47	0.59	-1.63	0.211	-1.08	0.608	1.15	0.782	-0.02
1426160_a_at	Stk16	serine/threonine kinase 16	-1.26	0.249	-1.09	0.464	1.3	0.311	1.43	0.382	0.09
1436243_at	A930004K21Rik	RIKEN cDNA A930004K21 gene	1.06	0.764	-1.1	0.871	1.04	0.903	-1.23	0.63	-0.06
1438474_at	Ankrd35	ankyrin repeat domain 35	1.28	0.768	-1.32	0.289	-1.03	0.672	1.01	0.98	-0.02
1416045_a_at	Smarcb1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.08	0.392	-1.05	0.602	1.13	0.194	1.02	0.836	0.01
1437114_at	A930001N09Rik	RIKEN cDNA A930001N09 gene	1	0.985	-1.09	0.73	1.08	0.822	-1.38	0.017	-0.09
1451014_at	Ror1	receptor tyrosine kinase-like orphan receptor 1	1.44	0.57	-2.32	0.108	1.14	0.718	-1.64	0.153	-0.35
1428511_at	Phkg2	phosphorylase kinase, gamma 2 (testis)	1.13	0.013	1.01	0.876	-1.15	0.106	-1.35	0.053	-0.09
1445153_at	Abl1	V-abl Abelson murine leukemia oncogene 1	1.11	0.406	1.26	0.398	-1.55	0.074	-1.57	0.25	-0.19
1460735_at	Svil	supervillin	-1.07	0.361	-1.07	0.725	1.14	0.287	1.18	0.073	0.04
1442466_a_at	Hisppd2a	histidine acid phosphatase domain containing 2A	-1.03	0.878	1.22	0.561	-1.22	0.235	1.03	0.83	0
1459046_at	4930473A06Rik	RIKEN cDNA 4930473A06 gene	1.24	0.755	-1.21	0.684	-1.06	0.754	1.23	0.565	0.05
1429459_at	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	-1.11	0.513	1.05	0.495	1.05	0.885	-1.48	0.18	-0.12
1451430_at	Slit2	slit homolog 2 (Drosophila)	-1.04	0.871	-1.02	0.966	1.07	0.868	1.11	0.841	0.03
1427874_at	Zfp313	zinc finger protein 313	1.04	0.839	1	0.991	-1.03	0.581	-1.31	0.035	-0.08
1460720_at	Trpc4ap	transient receptor potential cation channel, subfamily C, member 4 associated pr	1.04	0.804	-1.16	0.512	1.11	0.326	-1.36	0.041	-0.09
1418447_at	Golga5	golgi autoantigen, golgin subfamily a, 5	1.02	0.891	1.08	0.325	-1.11	0.398	-1.23	0.349	-0.06
1437074_at	Snx5	sorting nexin 5	1.18	0.661	1.08	0.686	-1.34	0.088	-1.73	0.007	-0.2
1452831_s_at	Ppat	phosphoribosyl pyrophosphate amidotransferase	1.1	0.346	-1.01	0.927	-1.09	0.261	1.29	0.478	0.07
1458047_at	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	-2.55	0.323	-1.33	0.089	1.86	0.329	1.25	0.538	-0.19
1443222_at	Akt3	Thymoma viral proto-oncogene 3	1.52	0.275	1.01	0.975	-2.1	0.004	-1.76	0.172	-0.33
1418621_at	Rab2	RAB2, member RAS oncogene family	1.04	0.837	-1.08	0.623	1.04	0.668	-1.14	0.302	-0.04
1428655_at	1110018J12Rik	RIKEN cDNA 1110018J12 gene	1.03	0.77	1.01	0.9	-1.04	0.878	-1.52	0.365	-0.13
1427582_at	Fgf6	fibroblast growth factor 6	-1.17	0.46	1.05	0.94	1.11	0.759	-1.84	0.21	-0.22
1417148_at	Pdgfrb	platelet derived growth factor receptor, beta polypeptide	1.27	0.277	1.17	0.689	-1.77	0.238	-1.1	0.701	-0.11
1459813_at	1700012D01Rik	RIKEN cDNA 1700012D01 gene	1.22	0.474	1.01	0.974	-1.28	0.176	-1.76	0.144	-0.2
1433391_at	---	---	1	0.998	1.33	0.654	-1.47	0.214	-1.04	0.813	-0.05
1417991_at	Dio1	deiodinase, iodothyronine, type I	-1.16	0.377	-1.46	0.134	1.46	0.335	1.52	0.568	0.09
1424267_at	1810043G02Rik	RIKEN cDNA 1810043G02 gene	-1.07	0.347	-1.06	0.751	1.13	0.481	1.07	0.849	0.02
1452330_a_at	Mxra8	matrix-remodelling associated 8	1.11	0.442	1.01	0.942	-1.13	0.669	-1.23	0.041	-0.06
1433709_at	Cant1	calcium activated nucleotidase 1	-1.07	0.43	1.02	0.88	1.06	0.718	-1.14	0.309	-0.03
1428169_at	Atg16l1	autophagy-related 16-like 1 (yeast)	-1.14	0.069	1.06	0.549	1.08	0.309	-1.17	0.113	-0.04
1416994_at	Ttc1	tetratricopeptide repeat domain 1	1.17	0.662	-1.14	0.429	-1.05	0.867	1.25	0.628	0.06
1446510_at	Phip	Pleckstrin homology domain interacting protein	1.04	0.531	1.1	0.788	-1.15	0.119	-1.45	0.126	-0.11
1418180_at	Sp1	trans-acting transcription factor 1	1.21	0.346	1.12	0.259	-1.48	0.048	-1.03	0.876	-0.04
1419529_at	Il23a	interleukin 23, alpha subunit p19	-1.58	0.329	-1.32	0.318	1.62	0.165	1.16	0.772	-0.03
1419444_at	Sap18	Sin3-associated polypeptide 18	-1.09	0.02	1.08	0.497	1.01	0.971	-1.12	0.537	-0.03
1437545_at	Rcor1	REST corepressor 1	1.17	0.602	-1.14	0.345	-1.04	0.849	1.35	0.424	0.09

1458818_at	D3Ertd162e	DNA segment, Chr 3, ERATO Doi 162, expressed	-1.76	0.327	-1.4	0.246	1.73	0.201	1.01	0.965	-0.11
1429829_at	9530003J23Rik	RIKEN cDNA 9530003J23 gene	1.45	0.679	-2.9	0.114	1.22	0.452	-1.2	0.664	-0.36
1416459_at	Arf2	ADP-ribosylation factor 2	-1.06	0.864	-1.03	0.9	1.1	0.808	1.33	0.487	0.08
1422219_a_at	Tbx20	T-box 20	-2.23	0.3	1.27	0.63	1.29	0.708	-2.2	0.234	-0.47
1443325_at	---	Transcribed locus	1.29	0.021	-1.77	0.028	1.16	0.501	-1.18	0.624	-0.13
1428731_at	Usp54	ubiquitin specific peptidase 54	-1.03	0.734	1.08	0.633	-1.05	0.815	1.39	0.383	0.1
1416104_at	Mpdu1	mannose-P-dolichol utilization defect 1	-1.14	0.025	-1.35	0.091	1.39	0.197	1.13	0.498	0.01
1425413_at	Rfx3	regulatory factor X, 3 (influences HLA class II expression)	1.12	0.577	-1.05	0.833	-1.07	0.644	1.24	0.475	0.06
1430596_s_at	1700110N18Rik	RIKEN cDNA 1700110N18 gene	1.07	0.883	-1.38	0.434	1.21	0.413	-1.48	0.038	-0.14
1435018_at	5930434B04Rik	RIKEN cDNA 5930434B04 gene	-1.07	0.469	1.01	0.855	1.06	0.209	-1.39	0.168	-0.1
1452464_a_at	Metapl1	methionine aminopeptidase-like 1	1.13	0.699	1.22	0.012	-1.51	0.019	-1	0.994	-0.04
1419525_at	Car5a	carbonic anhydrase 5a, mitochondrial	1.25	0.15	-1.18	0.505	-1.1	0.77	1.69	0.207	0.17
1442225_at	Cdc2l6	Cell division cycle 2-like 6 (CDK8-like)	-1.52	0.514	-1.1	0.757	1.45	0.219	1.8	0.267	0.16
1454543_at	Stk40	serine/threonine kinase 40	-1.1	0.79	-2.2	0.309	1.65	0.347	2.2	0.143	0.14
1438075_at	Fem1c	fem-1 homolog c (C.elegans)	1.02	0.807	1.21	0.355	-1.3	0.052	-1.15	0.62	-0.05
1435852_at	Spred3	sprouty-related, EVH1 domain containing 3	1.48	0.247	-1.28	0.63	-1.34	0.398	1.09	0.735	-0.01
1424995_at	6230410P16Rik	RIKEN cDNA 6230410P16 gene	1.09	0.818	1.18	0.096	-1.34	0.185	-1.43	0.329	-0.13
1445419_at	Gtpbp8	GTP-binding protein 8 (putative)	-1.42	0.394	1.13	0.703	1.18	0.274	-1.18	0.348	-0.07
1417328_at	Ercc1	excision repair cross-complementing rodent repair deficiency, complementation g	1.06	0.831	1.03	0.812	-1.08	0.638	-1.19	0.298	-0.05
1421231_at	Msi2	Musashi homolog 2 (Drosophila)	1	0.937	1.13	0.791	-1.14	0.669	-1.86	0.195	-0.22
1425006_a_at	Vrk1	vaccinia related kinase 1	1.23	0.119	-1.03	0.717	-1.24	0.06	1.16	0.487	0.03
1418071_s_at	Cdyl	chromodomain protein, Y chromosome-like	-1.07	0.826	1.1	0.539	-1.03	0.795	1.63	0.195	0.16
1457662_x_at	Tpk1	thiamine pyrophosphokinase	-1.42	0.138	1.19	0.535	1.12	0.675	-1.1	0.645	-0.05
1453755_at	Lsm11	U7 snRNP-specific Sm-like protein LSM11	-1.22	0.641	1.11	0.866	1.09	0.601	-1.01	0.977	-0.01
1438093_x_at	Dbi	diazepam binding inhibitor	-1.11	0.536	1.23	0.046	-1.14	0.678	1.01	0.964	0
1444925_at	---	---	-1.28	0.652	1.54	0.146	-1.45	0.62	1.82	0.302	0.16
1454754_a_at	Aamp	angio-associated migratory protein	1	1	-1.05	0.553	1.06	0.565	-1.45	0.174	-0.11
1415745_a_at	Dscr3	Down syndrome critical region gene 3	-1.03	0.877	1.02	0.805	1.02	0.801	-1.4	0.039	-0.1
1448438_at	Derl2	Der1-like domain family, member 2	1.14	0.065	1.03	0.765	-1.19	0.093	-1.04	0.867	-0.01
1456721_at	Gm837	gene model 837, (NCBI)	-1.71	0.288	1.16	0.7	1.27	0.465	-1.46	0.397	-0.19
1434051_s_at	Hspa12a	heat shock protein 12A	-1.17	0.425	1.11	0.823	1.04	0.792	-1.22	0.462	-0.06
1438060_at	Npas3	neuronal PAS domain protein 3	1.59	0.129	-1.54	0.501	-1.3	0.591	1.01	0.969	-0.06
1422530_at	LOC673890	similar to peripherin 1	-2.78	0.404	1.24	0.735	1.41	0.282	-2.19	0.193	-0.58
1439319_at	Elf1	E74-like factor 1	1.35	0.156	1.04	0.832	-1.61	0.173	-1.23	0.608	-0.11
1449550_at	Myo1c	myosin IC	1.05	0.667	1.11	0.662	-1.16	0.604	-2.18	0.077	-0.3
1441137_at	Bicc1	bicaudal C homolog 1 (Drosophila)	1.09	0.795	1.37	0.417	-1.79	0.032	-1.28	0.018	-0.16
1426714_at	D11Ertd18e	DNA segment, Chr 11, ERATO Doi 18, expressed	1.25	0.159	-1.12	0.265	-1.15	0.767	1.86	0.347	0.21
1430377_at	1300015D01Rik	RIKEN cDNA 1300015D01 gene	-1.79	0.072	1.55	0.102	-1.1	0.866	1.66	0.331	0.08
1425278_at	Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	-1.04	0.941	1.37	0.551	-1.46	0.318	2.23	0.345	0.28
1437644_at	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	1.8	0.622	-2.89	0.12	-1.16	0.782	1.19	0.641	-0.26
1439754_at	Sox12	SRY-box containing gene 12	1.8	0.074	-2.09	0.323	-1.36	0.54	1.63	0.118	-0.01
1424918_at	Tbc1d19	TBC1 domain family, member 19	-1.01	0.888	1	0.998	1.02	0.828	-1.01	0.913	0
1418289_at	Nes	nestin	-1.25	0.423	1.14	0.565	1.07	0.256	-1.66	0.165	-0.17
1435978_at	Gmppa	GDP-mannose pyrophosphorylase A	1.35	0.124	-1.25	0.43	-1.16	0.66	1.13	0.191	0.02
1450879_at	Atp9b	ATPas, class II, type 9B	1.07	0.713	1.02	0.898	-1.08	0.505	-1.27	0.157	-0.07
1429619_a_at	8430406I07Rik	RIKEN cDNA 8430406I07 gene	-1.02	0.827	-1.18	0.046	1.19	0.472	1.25	0.192	0.06
1451919_a_at	Mpl	myeloproliferative leukemia virus oncogene	-1.22	0.599	-1.08	0.677	1.27	0.401	1.13	0.115	0.02
1432234_at	4933438B17Rik	RIKEN cDNA 4933438B17 gene	-1.06	0.528	1.22	0.418	-1.17	0.36	1.65	0.523	0.16
1434372_at	AW112010	expressed sequence AW112010	1.16	0.184	1.05	0.413	-1.24	0.232	-1.11	0.683	-0.04
1447752_x_at	Drg1	developmentally regulated GTP binding protein 1	-1.02	0.965	1.24	0.173	-1.26	0.477	1.07	0.789	0.01
1432741_at	9530071P10Rik	RIKEN cDNA 9530071P10 gene	-1.48	0.641	1.45	0.335	-1.13	0.28	1.01	0.961	-0.04
1444571_at	Zswim3	Zinc finger, SWIM domain containing 3	-1.08	0.909	-1	0.998	1.09	0.866	1.29	0.136	0.07
1437837_x_at	Poldip3	polymerase (DNA-directed), delta interacting protein 3	-1.13	0.392	-1.12	0.004	1.24	0.164	1.02	0.822	0

1418851_at	Trim39	tripartite motif protein 39	1.06	0.52	-1.08	0.499	1.03	0.814	-1.05	0.775	-0.01
1419461_at	Rpp14	ribonuclease P 14 subunit (human)	-1.03	0.516	1.03	0.819	1.01	0.966	-1	0.986	0
1454847_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	-1.16	0.045	1.23	0.016	-1.09	0.724	1.08	0.723	0.02
1417907_at	Ube2l3 /// Rps28	ubiquitin-conjugating enzyme E2L 3 /// ribosomal protein S28	-1.14	0.556	-1.08	0.401	1.21	0.153	1.27	0.151	0.06
1431586_at	4921529N20Rik	RIKEN cDNA 4921529N20 gene	-1.23	0.12	1.23	0.773	-1.03	0.908	1.16	0.691	0.03
1444037_at	Lman1	lectin, mannose-binding, 1	1.43	0.369	-1.21	0.124	-1.33	0.136	1.12	0.581	0.01
1418386_at	2510005D08Rik	RIKEN cDNA 2510005D08 gene	-1.1	0.347	1.07	0.672	1.04	0.799	-1.04	0.819	-0.01
1446392_at	Slit2	Slit homolog 2 (Drosophila)	1.12	0.413	1.09	0.843	-1.25	0.449	-1.36	0.526	-0.1
1456861_at	---	Activated spleen cDNA, RIKEN full-length enriched library, clone:F830206P12 pr	1.01	0.98	1.14	0.716	-1.15	0.634	-1.17	0.72	-0.04
1434971_x_at	---	---	-1.03	0.721	1.07	0.528	-1.02	0.9	1.36	0.07	0.09
1423111_at	Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform	-1.17	0.469	-1.25	0.053	1.35	0.012	1.03	0.509	-0.01
1420341_at	Tmco5	transmembrane and coiled-coil domains 5	-2.47	0.39	1.31	0.651	1.29	0.653	-1.33	0.576	-0.3
1460385_a_at	Zfp179	zinc finger protein 179	1.74	0.544	-2	0.084	-1.3	0.61	1.85	0.414	0.07
1436338_at	---	---	-1.17	0.208	-1.02	0.894	1.18	0.589	1.22	0.201	0.05
1435563_at	Mrps5	mitochondrial ribosomal protein S5	-1.37	0.455	-1.08	0.769	1.36	0.26	2.12	0.032	0.26
1434508_at	Ube2q	ubiquitin-conjugating enzyme E2Q (putative)	-1.04	0.546	1.04	0.795	1.01	0.945	-1.35	0.139	-0.08
1448382_at	Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	-1.07	0.622	-1.93	0.06	1.56	0.115	1.09	0.639	-0.09
1448811_at	Mrpl2	mitochondrial ribosomal protein L2	-1.09	0.613	-1.23	0.029	1.28	0.178	1.18	0.656	0.04
1425699_a_at	Abhd14a	abhydrolase domain containing 14A	-1.12	0.714	-1.33	0.029	1.37	0.099	1.43	0.161	0.09
1428904_at	E230022H04Rik	RIKEN cDNA E230022H04 gene	-1.02	0.877	-1.05	0.737	1.08	0.795	1.28	0.32	0.07
1449731_s_at	Nfkbia	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	1.03	0.866	1.19	0.215	-1.25	0.242	-1.71	0.134	-0.19
1416606_s_at	Nola2	nucleolar protein family A, member 2	-1.01	0.636	-1.07	0.614	1.09	0.71	1.13	0.63	0.03
1454883_at	AI987692	expressed sequence AI987692	1.13	0.726	1.29	0.71	-1.67	0.276	-2.92	0.11	-0.54
1415870_at	Calu	calumenin	1.01	0.829	1.26	0.117	-1.34	0.074	-1.03	0.866	-0.03
1423882_at	Rfwd3	ring finger and WD repeat domain 3	-1.02	0.862	1.04	0.688	-1.01	0.932	1.46	0.295	0.12
1449862_a_at	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	-1.1	0.617	-1.25	0.368	1.31	0.434	2.92	0.277	0.47
1419820_at	Pkhd1	polycystic kidney and hepatic disease 1	1.12	0.416	1.21	0.24	-1.45	0.213	-1.62	0.503	-0.19
1422631_at	Ahr	aryl-hydrocarbon receptor	1.01	0.95	1.22	0.21	-1.28	0.095	-1.2	0.412	-0.06
1458514_at	AA536887	expressed sequence AA536887	-1.71	0.276	-1.81	0.62	1.88	0.199	1.54	0.284	-0.03
1442540_at	C77609	expressed sequence C77609	-1.07	0.576	-1.07	0.863	1.14	0.712	1.38	0.31	0.1
1436712_at	Pla2g4c	phospholipase A2, group IVC (cytosolic, calcium-independent)	-1.12	0.845	-1.46	0.276	1.44	0.202	4.12	0.213	0.74
1418919_at	Sgol1	shugoshin-like 1 (S. pombe)	-1.22	0.442	-1.43	0.593	1.5	0.36	3.98	0.194	0.71
1440669_at	B230217O12Rik	RIKEN cDNA B230217O12 gene	1.03	0.749	-1.08	0.778	1.06	0.851	-1.37	0.68	-0.09
1449510_at	Zfp467	zinc finger protein 467	1.04	0.845	-1.19	0.251	1.13	0.51	-1.25	0.278	-0.07
1432320_at	9430065F17Rik	RIKEN cDNA 9430065F17 gene	1.01	0.979	1.25	0.221	-1.32	0.459	-1.56	0.114	-0.15
1426440_at	Dhrs7	dehydrogenase/reductase (SDR family) member 7	-1.17	0.423	1.04	0.841	1.13	0.278	-1.05	0.622	-0.02
1423030_at	Vcp /// LOC675857	valosin containing protein /// similar to Transitional endoplasmic reticulum ATPas	-1.05	0.03	-1.02	0.713	1.09	0.346	1.12	0.135	0.03
1432016_a_at	Idh3a	isocitrate dehydrogenase 3 (NAD+) alpha	-1.05	0.686	-1.28	0.073	1.28	0.143	1.54	0.323	0.12
1459250_at	Tshz2	teashirt zinc finger family member 2	-1.04	0.953	-1.21	0.778	1.23	0.774	2.17	0.376	0.29
1453345_at	Npal1	NIPA-like domain containing 1	1.15	0.472	1.4	0.312	-2.17	0.041	-2.42	0.11	-0.51
1432570_at	6030458E02Rik	RIKEN cDNA 6030458E02 gene	1.19	0.545	-1.52	0.247	1.17	0.778	-1.6	0.275	-0.19
1448153_at	Cox5a	cytochrome c oxidase, subunit Va	-1.16	0.074	-1.15	0.026	1.28	0.008	1	0.931	-0.01
1444612_at	3222402P14Rik	RIKEN cDNA 3222402P14 gene	1.08	0.739	-1.27	0.625	1.15	0.838	-1.09	0.66	-0.03
1455593_at	Apob	apolipoprotein B	-1.05	0.906	-1.35	0.187	1.32	0.42	1.51	0.46	0.11
1452691_at	Rbm17	RNA binding motif protein 17	-1.08	0.555	1.02	0.735	1.06	0.678	-1.1	0.089	-0.02
1451561_at	Prr12	proline rich 12	-1.02	0.838	-1.04	0.828	1.07	0.715	1.19	0.263	0.05
1424318_at	1110067D22Rik	RIKEN cDNA 1110067D22 gene	-1.03	0.917	1.22	0.564	-1.21	0.219	1.13	0.752	0.03
1418012_at	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	-1.02	0.741	1.04	0.729	-1	0.982	1.24	0.235	0.07
1418172_at	Hebp1	heme binding protein 1	-1.7	0.297	-1.23	0.353	1.61	0.396	1.33	0.473	0
1442505_at	Fndc3b	Fibronectin type III domain containing 3B	-1.06	0.537	1.37	0.138	-1.42	0.103	1.08	0.724	-0.01
1421834_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	-1.21	0.541	1.28	0.726	-1.11	0.578	5.06	0.238	1.01
1427973_s_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	-1.13	0.826	-1.34	0.183	1.38	0.086	1.44	0.148	0.09
1438107_x_at	BB236558	expressed sequence BB236558	-1.41	0.625	1.15	0.776	1.16	0.56	-1.67	0.211	-0.19

1422321_a_at	Sf1	splicing factor 1	-1.18	0.162	-1.18	0.59	1.32	0.088	1.33	0.435	0.07
1460453_at	Tagap	T-cell activation Rho GTPase-activating protein	1.03	0.879	-1.07	0.661	1.05	0.408	-2	0.047	-0.25
1426923_at	Hrb	HIV-1 Rev binding protein	-1.04	0.855	1.06	0.746	-1.01	0.91	1.21	0.542	0.06
1415762_x_at	Mrpl52	mitochondrial ribosomal protein L52	1.13	0.122	1.08	0.305	-1.23	0.155	-1.37	0.217	-0.1
1420046_s_at	Maf1	MAF1 homolog (S. cerevisiae)	-1.1	0.61	1.08	0.425	1.02	0.781	-1.27	0.033	-0.07
1427349_x_at	2810021G02Rik	RIKEN cDNA 2810021G02 gene	-1.11	0.12	1.01	0.956	1.11	0.539	-1.59	0.202	-0.15
1453197_at	Med25	mediator of RNA polymerase II transcription, subunit 25 homolog (yeast)	-1.13	0.269	-1.15	0.154	1.26	0.256	1.12	0.453	0.03
1420461_at	Mst1r	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	-1.41	0.488	1.3	0.73	1.01	0.988	-1.1	0.881	-0.05
1448252_a_at	Eef1b2	eukaryotic translation elongation factor 1 beta 2	1.01	0.787	1.06	0.54	-1.06	0.701	-1.35	0.025	-0.08
1446606_at	LOC625175	region containing RIKEN cDNA 1700028E10 gene; hypothetical protein A630054	1.08	0.705	-1.11	0.55	1.03	0.835	-1.25	0.455	-0.06
1432526_a_at	Snf8	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	-1.02	0.919	-1.12	0.274	1.14	0.067	1.12	0.47	0.03
1420960_at	Fancg	Fanconi anemia, complementation group G	-1.5	0.209	1.18	0.685	1.17	0.238	-1.13	0.381	-0.07
1455865_at	Insm1	insulinoma-associated 1	-1.19	0.759	1.15	0.828	1.03	0.854	-3.97	0.138	-0.75
1422801_at	RP23-336J1.4	Ras-GTPase-activating protein SH3-domain binding protein	-1.17	0.047	-1	0.981	1.17	0.521	1.12	0.506	0.03
1449151_at	Pctk3	PCTAIRE-motif protein kinase 3	-1.02	0.945	-1.04	0.886	1.07	0.686	1.94	0.311	0.24
1447071_at	Tcf7l2	Transcription factor 7-like 2, T-cell specific, HMG-box	1.65	0.332	-1.15	0.571	-1.98	0.12	1.67	0.046	0.05
1444344_at	---	---	1.11	0.816	1.39	0.456	-1.9	0.001	-1.27	0.602	-0.17
1417055_at	0610009D07Rik	RIKEN cDNA 0610009D07 gene	1.03	0.02	-1.05	0.511	1.04	0.828	-1.07	0.604	-0.01
1449332_at	Fhl5	four and a half LIM domains 5	-1.41	0.691	-1.08	0.839	1.39	0.437	1.23	0.151	0.03
1440915_at	Mphosph9	M-phase phosphoprotein 9	1.44	0.079	-1.61	0.527	-1.05	0.832	1.22	0.53	0
1448163_at	Gnpda1 /// LOC231	glucosamine-6-phosphate deaminase 1 /// similar to Glucosamine-6-phosphate is	-1.29	0.274	-1.11	0.745	1.34	0.1	1.23	0.124	0.04
1447861_x_at	Mrg1	Myeloid ecotropic viral integration site-related gene 1	1.08	0.437	-1.09	0.857	1.02	0.875	-1.97	0.205	-0.24
1451227_a_at	Slc10a3	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	1.01	0.943	-1.04	0.677	1.05	0.548	-1.12	0.422	-0.03
1423938_at	Llgl2	lethal giant larvae homolog 2 (Drosophila)	1.07	0.292	-1.13	0.161	1.07	0.368	-1.08	0.128	-0.02
1421908_a_at	Tcf12	transcription factor 12	1.13	0.647	-1.25	0.458	1.09	0.799	-1.05	0.867	-0.02
1418837_at	Qprt	quinolinate phosphoribosyltransferase	-1.21	0.225	1.02	0.831	1.17	0.74	-1.4	0.095	-0.1
1418330_at	Ctcf	CCCTC-binding factor	-1	0.989	1.03	0.782	-1.01	0.956	1.13	0.3	0.04
1442039_at	Tox	thymocyte selection-associated HMG box gene	-1.09	0.785	-1.38	0.363	1.37	0.069	1.12	0.621	0.01
1457134_at	Cyfip1	cytoplasmic FMR1 interacting protein 1	1.24	0.81	-1.12	0.525	-1.12	0.558	1.27	0.755	0.07
1428031_at	Mchr1	melanin-concentrating hormone receptor 1	-1.36	0.659	1.25	0.181	1.03	0.852	-1.18	0.644	-0.07
1416734_at	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	1.07	0.792	1.12	0.661	-1.21	0.723	-1.01	0.989	-0.01
1417807_at	2700038N03Rik	RIKEN cDNA 2700038N03 gene	-1.02	0.846	-1.21	0.496	1.21	0.515	2.81	0.284	0.45
1451339_at	Suox	sulfite oxidase	-1.17	0.497	-1.13	0.439	1.28	0.289	2.61	0.231	0.4
1442308_at	Smyd4	SET and MYND domain containing 4	-1.34	0.515	1.37	0.202	-1.1	0.68	1.26	0.498	0.05
1428205_x_at	C030002O17Rik	RIKEN cDNA C030002O17 gene	-1.09	0.924	-2.12	0.308	1.63	0.088	1.57	0.097	0
1459420_at	---	---	1.37	0.365	-1.14	0.709	-1.3	0.25	1.45	0.375	0.1
1452148_at	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	1.05	0.621	-1.1	0.334	1.06	0.824	-1.11	0.225	-0.03
1434620_s_at	2610024E20Rik	RIKEN cDNA 2610024E20 gene	1.05	0.542	1.16	0.368	-1.23	0.162	-1.01	0.939	-0.01
1421627_at	Evx1	even skipped homeotic gene 1 homolog	-1.52	0.005	1.78	0.072	-1.72	0.391	3.43	0.108	0.49
1417698_at	Gtf2f1	general transcription factor IIF, polypeptide 1	1.07	0.412	-1.04	0.727	-1.01	0.954	1.29	0.268	0.08
1431349_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	1.35	0.546	-1.09	0.507	-1.33	0.232	1.06	0.909	0
1444672_at	---	Transcribed locus	-1.3	0.057	1.03	0.908	1.22	0.648	-1.74	0.258	-0.2
1450005_x_at	Egfl9	EGF-like-domain, multiple 9	1.06	0.85	1.04	0.891	-1.09	0.86	-3.09	0.063	-0.52
1437848_x_at	Adpgk	ADP-dependent glucokinase	-1.52	0.084	1.08	0.752	1.29	0.284	-1.18	0.557	-0.08
1450819_at	Pvrl1	poliovirus receptor-related 1	-1.14	0.755	1.04	0.921	1.1	0.498	-1.14	0.729	-0.03
1452620_at	Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-1.14	0.473	-1.07	0.905	1.21	0.217	1.75	0.205	0.19
1422970_at	Mxd3	Max dimerization protein 3	1.14	0.562	-1.12	0.471	-1.02	0.977	4.01	0.214	0.75
1445384_at	Riok2	RIO kinase 2 (yeast)	1.34	0.534	-1.8	0.43	1.12	0.742	-1.57	0.572	-0.23
1447376_at	Mov10	Moloney leukemia virus 10	-1.54	0.396	1.37	0.267	-1	0.996	1.1	0.819	-0.02
1424605_at	Pcsk5	proprotein convertase subtilisin/kexin type 5	1.16	0.803	1.02	0.965	-1.19	0.38	-1.26	0.694	-0.07
1436765_at	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	-1.01	0.947	1.05	0.756	-1.03	0.802	1.06	0.879	0.02
1438092_x_at	H2afz /// LOC6318	H2A histone family, member Z /// similar to H2A histone family, member Z /// simil	-1.01	0.841	1.09	0.278	-1.06	0.699	1.2	0.203	0.05
1459036_at	4930402E16Rik	RIKEN cDNA 4930402E16 gene	-1.77	0.409	1.43	0.597	1.02	0.967	-1.81	0.175	-0.28

1450711_at	Brd4	bromodomain containing 4	-1.11	0.093	-1.04	0.719	1.16	0.365	1.06	0.578	0.02
1451281_at	Zfp96	zinc finger protein 96	1.24	0.396	-1.13	0.346	-1.12	0.564	1.13	0.612	0.03
1439451_x_at	Gpr172b	G protein-coupled receptor 172B	1.01	0.892	-1.13	0.573	1.13	0.684	-1.26	0.266	-0.06
1428028_at	Gt4-1	gene trap insertion site 4-1	-1.13	0.869	-1.29	0.189	1.35	0.415	1.03	0.96	-0.01
1452764_at	Socs6	suppressor of cytokine signaling 6	1.04	0.909	1.04	0.894	-1.06	0.584	-1.12	0.588	-0.03
1417743_at	Clk2	CDC-like kinase 2	1.06	0.833	1.12	0.396	-1.18	0.222	-1.34	0.151	-0.09
1420517_at	2310010I16Rik	RIKEN cDNA 2310010I16 gene	1.1	0.694	1.07	0.889	-1.18	0.683	-1.15	0.815	-0.04
1459592_a_at	LOC669005	similar to NFkB interacting protein 1	-1.05	0.862	-1.32	0.315	1.31	0.207	1.32	0.421	0.07
1437411_at	BC010584	cDNA sequence BC010584	-1.12	0.511	1.1	0.842	1.03	0.94	-1.52	0.367	-0.13
1432942_at	5730408A14Rik	RIKEN cDNA 5730408A14 gene	1.05	0.824	1.08	0.818	-1.12	0.827	-1.18	0.794	-0.04
1437835_a_at	0610011L14Rik	RIKEN cDNA 0610011L14 gene	1.32	0.4	-1.58	0.073	1.07	0.378	-1.9	0.222	-0.27
1440313_at	Fuca2	fucosidase, alpha-L- 2, plasma	-1.2	0.467	1.18	0.759	1.01	0.942	-1.05	0.773	-0.02
1451293_at	Rnu3ip2	RNA, U3 small nucleolar interacting protein 2	-1.06	0.719	-1.13	0.688	1.19	0.453	1.08	0.259	0.02
1426546_at	Tesk2	testis-specific kinase 2	-1.33	0.448	1.01	0.948	1.26	0.297	-1.2	0.392	-0.07
1417237_at	Pld2	phospholipase D2	-1.1	0.671	1.05	0.724	1.07	0.511	-1.12	0.569	-0.03
1428296_at	Polr2l	polymerase (RNA) II (DNA directed) polypeptide L	-1.03	0.579	1.15	0.271	-1.11	0.468	1.27	0.271	0.07
1418380_at	Terf1	telomeric repeat binding factor 1	-1.11	0.698	-1.04	0.692	1.16	0.104	1.6	0.221	0.15
1454887_at	Pak2	p21 (CDKN1A)-activated kinase 2	-1.05	0.609	1.03	0.623	1.04	0.726	-1.34	0.148	-0.08
1443571_at	---	Transcribed locus	1.58	0.247	-2.38	0.044	1.02	0.971	-1.13	0.782	-0.23
1452446_a_at	2010008E23Rik	RIKEN cDNA 2010008E23 gene	-1.01	0.939	-1.03	0.664	1.06	0.656	1.09	0.633	0.03
1455713_x_at	Phb2	prohibitin 2	-1.15	0.095	-1.04	0.557	1.19	0.404	1.07	0.63	0.02
1439580_at	B930053N05Rik	RIKEN cDNA B930053N05 gene	1.32	0.403	1.26	0.625	-2.25	0.01	-1.13	0.656	-0.2
1435436_at	Epas1	Endothelial PAS domain protein 1	1.06	0.664	1.14	0.296	-1.23	0.004	-1.39	0.469	-0.1
AFFX-r2-Ec-bioD-3_	---	---	1.12	0.284	1.14	0.218	-1.32	0.112	-1.06	0.727	-0.03
1445025_at	AU015536	expressed sequence AU015536	1.33	0.474	-1.15	0.775	-1.23	0.383	1.63	0.131	0.15
1435027_at	Golga1	golgi autoantigen, golgin subfamily a, 1	1.05	0.698	1.09	0.238	-1.14	0.397	-1.08	0.757	-0.02
1419305_a_at	Fbxo36	F-box only protein 36	-1.03	0.335	-1.22	0.045	1.23	0.6	1.01	0.983	0
1440248_at	Casc4	cancer susceptibility candidate 4	1.05	0.837	1.06	0.904	-1.1	0.801	-2.29	0.077	-0.32
1442894_at	Dnahc6	dynein, axonemal, heavy chain 6	-3.73	0.382	1.69	0.084	1.06	0.743	-2.07	0.231	-0.76
1435188_at	Gm129	gene model 129, (NCBI)	1.14	0.911	-1.29	0.823	1.1	0.844	-1.21	0.702	-0.06
1417309_at	Tob2	transducer of ERBB2, 2	1.18	0.652	1.14	0.63	-1.42	0.305	-1.03	0.886	-0.03
1454687_at	Lrfn5	leucine rich repeat and fibronectin type III domain containing 5	-1.54	0.667	1.71	0.15	-1.5	0.16	1.69	0.129	0.09
1446560_at	Prss23	protease, serine, 23	-1.19	0.65	1.17	0.505	1.01	0.878	-1.07	0.783	-0.02
AFFX-DapX-M_at	---	---	1.19	0.752	-1.26	0.101	1.04	0.865	-1.51	0.302	-0.13
1428692_at	Hddc3	HD domain containing 3	1.1	0.753	1.15	0.475	-1.29	0.413	-1.26	0.322	-0.08
1449086_at	Rnf141	ring finger protein 141	-1.15	0.096	-1.05	0.838	1.2	0.622	1.48	0.189	0.12
1423492_at	Mrpl45	mitochondrial ribosomal protein L45	-1.2	0.158	-1.22	0.031	1.37	0.252	1.07	0.736	0
1436302_at	2410193C02Rik	RIKEN cDNA 2410193C02 gene	1.02	0.814	1.09	0.63	-1.09	0.572	-1.17	0.085	-0.04
1427821_at	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2	-1.51	0.556	-1.29	0.446	1.59	0.179	1.17	0.624	-0.01
1428346_at	Trafd1	TRAF type zinc finger domain containing 1	-1.12	0.463	1.04	0.687	1.09	0.37	-1.36	0.31	-0.09
1457237_at	Mbnl2	muscleblind-like 2	-1.02	0.877	1.09	0.839	-1.05	0.817	1.36	0.235	0.1
1441475_at	Ptk2	PTK2 protein tyrosine kinase 2	1.24	0.707	1.21	0.471	-1.76	0.001	-1.69	0.326	-0.25
1419948_at	D4Ertd117e	DNA segment, Chr 4, ERATO Doi 117, expressed	1.65	0.357	-1.44	0.245	-1.46	0.323	1.88	0.207	0.16
1418036_at	Prim2	DNA primase, p58 subunit	-1.06	0.776	1.2	0.502	-1.14	0.321	2.29	0.222	0.32
1448585_at	Gtf2h4	general transcription factor II H, polypeptide 4	-1.07	0.437	-1.16	0.018	1.23	0.107	1.09	0.555	0.02
1434600_at	Tjp2	tight junction protein 2	1.1	0.272	-1	0.974	-1.08	0.588	1.25	0.147	0.07
1421322_a_at	Isgf3g	interferon dependent positive acting transcription factor 3 gamma	-1.11	0.172	1.11	0.239	1.02	0.89	-1.17	0.426	-0.04
1418936_at	Maff	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	1.16	0.295	1.01	0.982	-1.17	0.322	-1.23	0.599	-0.06
1437201_at	Lrrc4c	leucine rich repeat containing 4C	1.46	0.494	1.12	0.67	-2.25	0.219	-3.87	0.027	-0.88
1443323_at	A930028L21Rik	RIKEN cDNA A930028L21 gene	1.33	0.267	1.04	0.853	-1.53	0.096	-1.69	0.377	-0.21
1433487_at	Clcn3	chloride channel 3	-1.03	0.802	-1.02	0.897	1.07	0.496	3.04	0.244	0.52
1452834_at	2600010E01Rik	RIKEN cDNA 2600010E01 gene	1.12	0.346	1.12	0.711	-1.27	0.13	-1.31	0.243	-0.09
1441028_at	D2Ertd210e	DNA segment, Chr 2, ERATO Doi 210, expressed	1.69	0.073	-1.32	0.273	-1.75	0.436	1.45	0.202	0.02

1448289_at	Crmp1	collapsin response mediator protein 1	-1	0.999	-1.26	0.51	1.23	0.599	1.23	0.795	0.05
1430688_s_at	D730039F16Rik	RIKEN cDNA D730039F16 gene	-1.35	0.18	-1.1	0.129	1.37	0.417	1.26	0.708	0.05
1417047_at	Prom2	prominin 2	1.01	0.889	-2.43	0.245	1.6	0.068	-3.19	0.2	-0.75
1459957_at	Tnrc6a	Trinucleotide repeat containing 6a	1.34	0.262	1.17	0.62	-1.94	0.004	-1.72	0.233	-0.29
1419243_at	Rab14	RAB14, member RAS oncogene family	-1.06	0.679	-1.07	0.41	1.15	0.227	1.12	0.411	0.03
1430826_s_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.3	0.33	-1.81	0.077	1.17	0.743	-1.45	0.125	-0.2
1454934_at	Ppm1f	protein phosphatase 1F (PP2C domain containing)	-1.11	0.464	1.1	0.163	1.03	0.875	-1.1	0.657	-0.02
1445221_at	---	Transcribed locus	1.18	0.683	1.47	0.504	-2.68	0.095	-1.04	0.869	-0.27
1421398_at	Trim7	tripartite motif protein 7	1.21	0.44	1.04	0.908	-1.3	0.552	-1.49	0.421	-0.13
1421215_a_at	Slmap	sarcolemma associated protein	-1.11	0.081	1.27	0.405	-1.18	0.612	1.14	0.825	0.03
1418482_at	Cyb561d2	cytochrome b-561 domain containing 2	-1.18	0.301	1.06	0.553	1.12	0.509	-1.14	0.527	-0.04
1458782_at	---	Transcribed locus	1.7	0.333	-2.32	0.227	-1.12	0.787	1.99	0.288	0.06
1451500_at	Ushbp1	Usher syndrome 1C binding protein 1	1.21	0.34	1.08	0.579	-1.37	0.099	-1.26	0.343	-0.08
1423300_at	Zdhhc6	zinc finger, DHHC domain containing 6	-1.11	0.63	-1.1	0.432	1.22	0.116	1.4	0.455	0.1
1434385_at	Tom1l2	target of myb1-like 2 (chicken)	-1.2	0.078	-1.05	0.614	1.24	0.197	1.2	0.288	0.05
1424112_at	Igf2r	insulin-like growth factor 2 receptor	1.04	0.794	-1.16	0.008	1.13	0.529	-1.04	0.838	-0.01
1423949_at	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	-1.15	0.145	-1.09	0.321	1.24	0.256	1.34	0.051	0.08
1451022_at	Lrp6	low density lipoprotein receptor-related protein 6	1.14	0.463	1.04	0.782	-1.19	0.544	-1.58	0.198	-0.15
1447645_x_at	Kcnk13	potassium channel, subfamily K, member 13	1.28	0.604	-1.28	0.564	-1.04	0.928	2.28	0.099	0.31
1418089_at	Stx8	syntaxin 8	1.17	0.296	1.12	0.34	-1.35	0.076	-1.32	0.377	-0.1
1418861_at	Pias4	protein inhibitor of activated STAT 4	-1.32	0.017	-1.05	0.718	1.32	0.28	1.02	0.885	-0.01
1436068_at	Zbtb10 /// LOC669	zinc finger and BTB domain containing 10 /// similar to zinc finger and BTB domai	1.21	0.265	-1.22	0.565	-1	0.983	1.05	0.549	0.01
1419902_at	---	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library,	-1.47	0.345	-1.12	0.586	1.45	0.077	1.12	0.575	0
1453485_s_at	1110005A03Rik	RIKEN cDNA 1110005A03 gene	1.02	0.921	1.09	0.424	-1.08	0.629	-1.86	0.152	-0.21
1431941_at	Slc35b4	solute carrier family 35, member B4	1.36	0.668	-1.13	0.701	-1.27	0.381	1.48	0.1	0.11
1423044_at	Prosc	proline synthetase co-transcribed	-1.09	0.019	-1.03	0.755	1.14	0.253	1	0.985	0.01
1437743_at	Aebp2	AE binding protein 2	1.05	0.62	1.12	0.444	-1.16	0.14	-1.03	0.893	-0.01
1425842_at	Edil3	EGF-like repeats and discoidin I-like domains 3	1.78	0.515	-1.1	0.87	-3.01	0.025	1.31	0.509	-0.25
1428294_at	Zfp259	zinc finger protein 259	1.31	0.127	-1.34	0.171	-1.03	0.856	1.05	0.818	0
1417100_at	Cd320	CD320 antigen	-1.15	0.376	1.09	0.093	1.07	0.552	-1.09	0.751	-0.02
1427533_at	Als2cl	ALS2 C-terminal like	1.07	0.354	-1.2	0.336	1.13	0.694	-2.12	0.098	-0.28
1430158_at	3110021A11Rik	RIKEN cDNA 3110021A11 gene	-1.01	0.978	1.16	0.482	-1.14	0.644	1.26	0.702	0.07
1436367_at	Ptprb	Protein tyrosine phosphatase, receptor type, B	1.13	0.258	1.04	0.797	-1.17	0.227	-1.23	0.456	-0.06
1427207_s_at	Afg3l2	AFG3(ATPase family gene 3)-like 2 (yeast)	-1.09	0.51	-1.02	0.857	1.12	0.327	1.7	0.171	0.18
1429408_at	Tbc1d21	TBC1 domain family, member 21	-2.35	0.479	1.96	0.305	-1.57	0.371	1.85	0.062	-0.03
1451882_a_at	Fgf8	fibroblast growth factor 8	1.23	0.55	-1.43	0.473	1.1	0.555	-1.29	0.348	-0.1
1415914_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	-1.05	0.367	-1.07	0.421	1.15	0.279	1.42	0.129	0.11
1439462_x_at	Tmed10 /// LOC634	transmembrane emp24-like trafficking protein 10 (yeast) /// similar to transmembr	-1.05	0.755	1.08	0.32	-1	0.925	1.12	0.338	0.04
1457633_x_at	Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	-1.3	0.361	1.36	0.482	-1.11	0.685	1.11	0.547	0.01
1427229_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	-1.65	0.184	1.44	0.06	-1.02	0.919	1.14	0.573	-0.02
1429984_at	5730455O13Rik	RIKEN cDNA 5730455O13 gene	1.02	0.936	-1.01	0.967	1.02	0.917	-1.38	0.099	-0.09
1439561_at	2010012O05Rik	RIKEN cDNA 2010012O05 gene	-1.47	0.05	1.26	0.384	1.09	0.676	-1.23	0.03	-0.09
1429295_s_at	Trip13	thyroid hormone receptor interactor 13	-1.43	0.063	-1.32	0.245	1.57	0.055	2.02	0.166	0.21
1447720_x_at	Prkaca	protein kinase, cAMP dependent, catalytic, alpha	-1.13	0.137	-1.11	0.232	1.24	0.148	1.07	0.73	0.02
1460138_at	5730446C15Rik	RIKEN cDNA 5730446C15 gene	1.24	0.218	1.01	0.973	-1.29	0.372	-1.12	0.786	-0.04
1444618_at	Rbm5	RNA binding motif protein 5	-1.06	0.927	1.13	0.802	-1.05	0.935	2.35	0.144	0.34
1459386_at	Zfp709	zinc finger protein 709	-1.49	0.033	1.2	0.581	1.16	0.596	-1.05	0.851	-0.04
1456738_s_at	Brp16	brain protein 16	1.11	0.344	-1.25	0.054	1.11	0.735	-1.1	0.516	-0.03
1453653_at	6330576A10Rik	RIKEN cDNA 6330576A10 gene	-1.1	0.736	1.21	0.299	-1.1	0.58	1.03	0.919	0.01
1441692_at	Pftk1	PFTAIRE protein kinase 1	1.62	0.419	-1.09	0.863	-2.05	0.012	1.59	0.083	0.02
1426765_at	Commd7 /// LOC63	COMM domain containing 7 /// similar to COMM domain containing protein 7 /// si	-1.12	0.464	1.05	0.773	1.09	0.457	-1.32	0.078	-0.08
1455870_at	Akap2	A kinase (PRKA) anchor protein 2	-1.13	0.557	1.07	0.535	1.08	0.723	-1.52	0.075	-0.13
1447781_s_at	Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	1.08	0.848	1.1	0.777	-1.18	0.292	-1.22	0.403	-0.06

1443067_at	---	Transcribed locus	-1.3	0.583	-1.21	0.513	1.44	0.003	1.19	0.479	0.03
1436695_x_at	Rbed1	RNA binding motif and ELMO domain 1	1.32	0.171	-1.46	0.162	1.02	0.887	-1.25	0.266	-0.09
1433353_at	D530015H24Rik	RIKEN cDNA D530015H24 gene	1.2	0.335	-1.01	0.945	-1.18	0.364	1.07	0.85	0.02
1424748_at	Galnt11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.01	0.817	1.09	0.583	-1.08	0.483	-1.61	0.15	-0.15
1419588_at	Spag1	sperm associated antigen 1	-1.58	0.206	1.15	0.638	1.25	0.415	-1.13	0.668	-0.08
AFFX-LysX-5_at	---	---	1.06	0.912	-1.14	0.271	1.09	0.777	-1.92	0.452	-0.23
1454092_a_at	Gtf2h3	general transcription factor IIH, polypeptide 3	-1	0.978	-1.22	0.017	1.21	0.342	1.07	0.642	0.01
1460405_at	Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	1.04	0.884	-1.01	0.976	-1	0.971	1.44	0.506	0.12
1428102_at	Cpb1	carboxypeptidase B1 (tissue)	1.13	0.528	1.52	0.313	-2.67	0.068	-1.73	0.519	-0.44
1443638_at	Ctnnd2	Catenin (cadherin associated protein), delta 2	1.08	0.885	1.22	0.698	-1.38	0.414	-2	0.39	-0.27
1455190_at	Gng7	guanine nucleotide binding protein (G protein), gamma 7 subunit	-1.46	0.7	-1.34	0.47	1.6	0.195	1.22	0.526	0.01
AFFX-r2-Ec-bioB-5_	---	---	1.21	0.214	1.21	0.191	-1.64	0.034	-1.03	0.908	-0.06
1420223_at	---	---	-1.12	0.523	1.11	0.815	1.03	0.899	-1.31	0.323	-0.07
1436469_at	LOC634327	similar to bromodomain containing 7	1.44	0.085	1.01	0.987	-1.72	0.145	-1.12	0.6	-0.1
1452030_a_at	Hnrpr	heterogeneous nuclear ribonucleoprotein R	-1.04	0.897	-1.1	0.685	1.16	0.532	1.2	0.612	0.06
AFFX-BioDn-5_at	---	---	1.27	0.218	1.11	0.274	-1.55	0.033	-1.27	0.443	-0.11
1422028_a_at	Ets1	E26 avian leukemia oncogene 1, 5' domain	1.05	0.844	-1.09	0.807	1.06	0.787	-1.57	0.15	-0.14
1454927_at	Zfp41	zinc finger protein 41	-1.04	0.607	-1.07	0.647	1.13	0.699	1.11	0.522	0.03
1451971_at	Cul4a	cullin 4A	-1.13	0.357	-1.02	0.83	1.16	0.31	2.6	0.186	0.4
1430891_at	Dusp12	dual specificity phosphatase 12	-1.45	0.178	1.91	0.3	-2.32	0.032	1.29	0.575	-0.14
1423575_a_at	Wbscr22	Williams Beuren syndrome chromosome region 22	1.09	0.594	1.02	0.834	-1.08	0.589	-1.17	0.349	-0.04
1437109_s_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.04	0.607	1.11	0.442	-1.14	0.285	-1.13	0.244	-0.03
1447680_at	Anp32e	Acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-1.09	0.924	1.01	0.982	1.1	0.873	-1.84	0.402	-0.2
1417326_a_at	Anapc11	anaphase promoting complex subunit 11 homolog (yeast)	1.09	0.726	1.05	0.59	-1.13	0.372	-1.03	0.858	0
1420645_at	Pcgf2	polycomb group ring finger 2	-1.17	0.5	1.42	0.493	-1.33	0.253	1.61	0.359	0.13
1425148_a_at	Snx6	sorting nexin 6	1.06	0.809	1.2	0.342	-1.28	0.269	-1.34	0.473	-0.09
1438444_at	A230091H23Rik	RIKEN cDNA A230091H23 gene	-1.24	0.819	1.2	0.755	1.03	0.96	-1.27	0.648	-0.07
1444494_at	Kbtbd10	kelch repeat and BTB (POZ) domain containing 10	-1.59	0.509	-1.36	0.316	1.67	0.116	1.74	0.249	0.11
1418637_at	Etv3	ets variant gene 3	-1	0.997	1.02	0.851	1.01	0.938	-2.04	0.071	-0.25
1460467_at	Iqcg	IQ motif containing G	1.12	0.9	-1.04	0.943	-1.06	0.883	2.62	0.27	0.41
1443767_at	Pcmtd1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	-1.04	0.803	1.11	0.898	-1.04	0.87	2.36	0.284	0.35
1442386_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	-1.25	0.283	1.14	0.621	1.09	0.732	-1.14	0.749	-0.04
1454646_at	Tcp11l2	t-complex 11 (mouse) like 2	-1.17	0.368	-1.04	0.737	1.22	0.053	1.35	0.266	0.09
1450978_at	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	-1.02	0.882	1.03	0.429	1.02	0.666	-1.09	0.216	-0.02
1453017_at	D5Ertd585e	DNA segment, Chr 5, ERATO Doi 585, expressed	-1.16	0.13	-1.12	0.378	1.28	0.023	1.05	0.84	0.01
1455688_at	Ddr2	discoidin domain receptor family, member 2	1.33	0.432	1.11	0.433	-1.69	0.05	-1.23	0.439	-0.12
1430367_at	Stambpl1	Stam binding protein like 1	1.07	0.541	1.17	0.394	-1.27	0.288	-2.28	0.07	-0.33
1448987_at	Acadl	acyl-Coenzyme A dehydrogenase, long-chain	-1.03	0.767	-1.38	0.136	1.34	0.179	1.28	0.303	0.05
1456404_at	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.02	0.848	1.04	0.787	1.01	0.947	-1.07	0.774	-0.01
1415967_at	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	-1.08	0.497	-1.14	0.151	1.23	0.06	1.15	0.169	0.04
1430505_at	1110032O16Rik	RIKEN cDNA 1110032O16 gene	-1.18	0.622	1.07	0.708	1.11	0.38	-1.46	0.062	-0.11
1424694_at	2010011I20Rik	RIKEN cDNA 2010011I20 gene	-1	0.976	1.08	0.462	-1.05	0.842	4.62	0.197	0.91
1449704_at	C80171	expressed sequence C80171	1.96	0.332	-2.21	0.208	-1.61	0.52	2.09	0.071	0.06
1427622_at	Mem1	maternal embryonic message 1	-1.09	0.875	1.13	0.72	-1.02	0.9	1.37	0.274	0.1
1451751_at	Ddit4l	DNA-damage-inducible transcript 4-like	1.03	0.874	-1.15	0.702	1.13	0.486	-1.37	0.651	-0.09
1449115_at	Mtf2	metal response element binding transcription factor 2	1.11	0.181	1.1	0.448	-1.22	0.116	-1.06	0.622	-0.02
1447157_at	4930480K23Rik	RIKEN cDNA 4930480K23 gene	1.1	0.776	-1.53	0.258	1.28	0.372	-1.39	0.534	-0.13
1457087_at	2900083I11Rik	RIKEN cDNA 2900083I11 gene	-2.09	0.438	2	0.446	-1.81	0.133	2.29	0.141	0.1
1451797_at	Smg5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	-1.02	0.9	-1.08	0.782	1.13	0.666	1.12	0.724	0.04
1420365_a_at	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	-1.06	0.647	1.1	0.439	-1.01	0.907	1.09	0.547	0.03
1460376_a_at	Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-1.03	0.929	-1.76	0.116	1.5	0.175	1.61	0.205	0.08
1416354_at	Rbmx	RNA binding motif protein, X chromosome	-1.03	0.833	-1.04	0.726	1.1	0.497	1.04	0.891	0.02
1453034_at	Zfp251	zinc finger protein 251	1.1	0.317	1.1	0.86	-1.2	0.243	-1.11	0.419	-0.03

1429587_at	Rbm34	RNA binding motif protein 34	-1.09	0.526	1.03	0.856	1.08	0.655	-1.41	0.197	-0.1
1444983_at	4933437K13Rik	RIKEN cDNA 4933437K13 gene	-1.25	0.075	1.17	0.794	1.06	0.587	-2.06	0.056	-0.27
1449435_at	B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	1.03	0.801	1.01	0.964	-1.01	0.957	-1.12	0.285	-0.02
1417151_a_at	Ntsr2	neurotensin receptor 2	-1.02	0.974	-1.03	0.962	1.08	0.716	1.19	0.481	0.05
1435228_at	BC023829	cDNA sequence BC023829	1.01	0.95	1.09	0.293	-1.06	0.542	-1.06	0.783	-0.01
1447460_at	Rpl5	Ribosomal protein L5	-1.53	0.559	1.34	0.552	1.04	0.859	-1.64	0.039	-0.2
1458394_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	1.18	0.775	-1.4	0.178	1.14	0.467	-1.12	0.449	-0.05
1423888_at	1200003M09Rik	RIKEN cDNA 1200003M09 gene	-1.14	0.487	-1.34	0.41	1.41	0.051	1.09	0.398	0.01
1419062_at	Epb4.1l3	erythrocyte protein band 4.1-like 3	-1.03	0.805	1.3	0.235	-1.32	0.397	1.21	0.492	0.04
1454983_at	AI465301	expressed sequence AI465301	-1.35	0.043	1.5	0.026	-1.26	0.164	1.17	0.464	0.01
1450742_at	Bysl	bystin-like	-1	0.99	-1.09	0.728	1.12	0.725	1.18	0.607	0.05
1445823_at	Ccdc91	Coiled-coil domain containing 91	-2.02	0.159	1.85	0.286	-1.46	0.497	1.32	0.239	-0.08
1419505_a_at	Ggps1	geranylgeranyl diphosphate synthase 1	-1.35	0.376	1.1	0.604	1.2	0.564	-1.57	0.022	-0.16
1433116_at	5730552O08Rik	RIKEN cDNA 5730552O08 gene	1	0.99	-1.84	0.261	1.49	0.384	-1.17	0.616	-0.13
1423133_at	0610040D20Rik	RIKEN cDNA 0610040D20 gene	1.13	0.166	-1.12	0.017	1.01	0.887	-1.11	0.636	-0.02
1420552_s_at	Tsga8	testis specific gene A8	-1.39	0.728	-1.19	0.736	1.48	0.208	1.07	0.767	-0.01
1444361_at	---	---	1.17	0.704	1.07	0.508	-1.27	0.202	-1.12	0.701	-0.04
1453300_at	Slc35d2 /// LOC674	solute carrier family 35, member D2 /// similar to UDP-glucuronic acid/UDP-N-ace	1.16	0.459	1.02	0.93	-1.17	0.522	-1.14	0.508	-0.03
1421161_at	Btc	betacellulin, epidermal growth factor family member	1.02	0.974	-1.12	0.727	1.12	0.751	-1.07	0.822	-0.01
1436255_at	D830044I16Rik	RIKEN cDNA D830044I16 gene	-1.2	0.532	-1.07	0.12	1.27	0.319	1.03	0.878	0.01
1423079_a_at	Tomm20 /// LOC54	translocase of outer mitochondrial membrane 20 homolog (yeast) /// similar to tra	-1.09	0.125	1.06	0.54	1.06	0.389	-1.17	0.064	-0.04
1443016_at	Dnmt3b	DNA methyltransferase 3B	1.17	0.634	-1.02	0.966	-1.13	0.527	1.51	0.535	0.13
1458132_at	Cnnm2	cyclin M2	-1.52	0.379	-1.09	0.866	1.46	0.384	2.05	0.011	0.22
1421391_at	Vipr2	vasoactive intestinal peptide receptor 2	-1.18	0.862	1.12	0.819	1.06	0.836	-1.87	0.571	-0.21
1444798_at	---	---	-1.45	0.581	1.22	0.639	1.13	0.845	-2.33	0.262	-0.36
1424407_s_at	Cbx6	chromobox homolog 6	-1.04	0.775	-1.16	0.49	1.21	0.205	1.01	0.92	0
1421863_at	Vamp1	vesicle-associated membrane protein 1	1.06	0.852	-1.23	0.605	1.16	0.605	-1.83	0.222	-0.21
1455319_x_at	Rps8	ribosomal protein S8	1.24	0.164	1.03	0.575	-1.29	0.084	-1.48	0.019	-0.13
1442035_at	Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5	-1.25	0.817	-1.11	0.782	1.33	0.332	1.49	0.432	0.12
1441067_at	AL033314	Expressed sequence AL033314	1.3	0.647	1.22	0.436	-1.95	0.256	-1.87	0.479	-0.32
1426220_at	4930471M23Rik	RIKEN cDNA 4930471M23 gene	-1.16	0.311	-1.08	0.703	1.24	0.315	1.09	0.472	0.02
1434857_at	A230106D06Rik	RIKEN cDNA A230106D06 gene	1.28	0.615	-1.92	0.291	1.23	0.599	-1.5	0.277	-0.23
1427062_at	Rbbp8	retinoblastoma binding protein 8	-1.11	0.485	1.25	0.508	-1.13	0.495	2.39	0.186	0.35
1418164_at	Stx2	syntaxin 2	-1.04	0.787	1.15	0.083	-1.08	0.306	3.45	0.184	0.62
1456150_at	A630082K20Rik	RIKEN cDNA A630082K20 gene	-1.09	0.562	-1.08	0.555	1.19	0.422	1.37	0.305	0.1
1416608_a_at	BC004004	cDNA sequence BC004004	1.06	0.584	1	0.952	-1.03	0.839	-1.21	0.492	-0.04
1455422_x_at	4-Sep	septin 4	1.21	0.121	1.22	0.367	-1.63	0.041	-1.45	0.096	-0.16
1445115_at	D130067I03Rik	RIKEN cDNA D130067I03 gene	-1.35	0.573	1.65	0.333	-1.55	0.256	1.28	0.695	0.01
1435586_at	Pcid2	PCI domain containing 2	-1.12	0.543	-1.12	0.333	1.25	0.032	1.16	0.551	0.04
1454849_x_at	Clu	clusterin	1.09	0.368	-1.19	0.278	1.11	0.216	-1.88	0.158	-0.22
1419949_at	Tmem38b	Transmembrane protein 38B	-1.1	0.587	1.28	0.481	-1.18	0.279	1.05	0.82	0.01
1440688_at	Arhgap26	Rho GTPase activating protein 26	-1.15	0.392	1.16	0.492	1	0.99	-1.36	0.241	-0.09
1453750_x_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	-1.32	0.287	1.36	0.249	-1.09	0.732	1.17	0.518	0.03
1448533_at	Ckap1	cytoskeleton-associated protein 1	1.04	0.528	-1.1	0.259	1.09	0.391	-1.18	0.304	-0.04
1452681_at	Dtymk	deoxythymidylate kinase	-1.11	0.675	-1.07	0.337	1.21	0.024	1.47	0.306	0.12
1446308_at	1700106J16Rik	RIKEN cDNA 1700106J16 gene	-1	0.992	-1.02	0.966	1.06	0.867	1.27	0.077	0.08
1432260_at	Gpr39	G protein-coupled receptor 39	-1.09	0.537	1.15	0.386	-1.04	0.903	1.17	0.581	0.05
1429686_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	-1.01	0.965	1.06	0.341	-1.01	0.957	1.37	0.215	0.1
1434119_at	D2Wsu81e	DNA segment, Chr 2, Wayne State University 81, expressed	-1.51	0.08	1.09	0.767	1.28	0.152	-1.1	0.181	-0.06
1438207_at	Gbf1	golgi-specific brefeldin A-resistance factor 1	-1.07	0.776	-1.51	0.03	1.44	0.346	1.39	0.073	0.06
1449026_at	Ifnar1	interferon (alpha and beta) receptor 1	1.09	0.438	1.02	0.862	-1.08	0.533	-1.4	0.157	-0.09
1459231_at	Pkn1	protein kinase N1	1.79	0.48	-1.51	0.573	-1.71	0.094	1.08	0.786	-0.09
1442764_at	Suv420h1	suppressor of variegation 4-20 homolog 1 (Drosophila)	1.05	0.799	1.06	0.91	-1.08	0.594	-1.02	0.933	0

1422492_at	Cpox	coproporphyrinogen oxidase	-1.04	0.871	-1.09	0.488	1.15	0.309	3.69	0.14	0.68
1449918_at	Cd209g	CD209g antigen	-1.18	0.406	1.15	0.678	1.04	0.904	-1.21	0.628	-0.05
1420582_at	Cd209e	CD209e antigen	1.04	0.603	1.29	0.609	-1.42	0.466	-1.79	0.302	-0.22
1436192_at	Arfgef2 /// LOC670	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibite	1.02	0.656	-1.14	0.282	1.15	0.283	-1.13	0.35	-0.03
1430766_at	5033403F01Rik	RIKEN cDNA 5033403F01 gene	1.12	0.815	1.31	0.203	-1.64	0.189	-1.08	0.72	-0.07
1416633_a_at	5730536A07Rik	RIKEN cDNA 5730536A07 gene	-1.05	0.6	1.14	0.08	-1.06	0.699	1	0.963	0.01
1426813_at	Ltv1	LTV1 homolog (S. cerevisiae)	-1.21	0.291	1.06	0.721	1.15	0.442	-1.1	0.39	-0.03
1457423_at	LOC675405	similar to voltage gated channel like 1	-1.06	0.904	1.27	0.116	-1.22	0.454	1.03	0.933	0.01
1426596_a_at	Smn1	survival motor neuron 1	-1.14	0.756	-1.15	0.838	1.29	0.476	1.1	0.811	0.03
1421108_at	Cml2	camello-like 2	1.17	0.469	1.11	0.747	-1.32	0.649	-1.05	0.866	-0.02
1424572_a_at	H2afy	H2A histone family, member Y	1.09	0.235	-1.18	0.209	1.1	0.553	-1.23	0.473	-0.05
1443746_x_at	Dmp1	dentin matrix protein 1	1.69	0.163	1	0.989	-2.92	0.119	-1.99	0.124	-0.55
1455147_at	---	PREDICTED: Mus musculus similar to KIAA1913 (LOC622645), mRNA	-1.49	0.618	-3.37	0.086	2.07	0.185	1.38	0.418	-0.35
1427623_at	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	-1.65	0.104	1.1	0.866	1.33	0.257	-1.06	0.806	-0.07
1442269_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230001K	1.26	0.21	-1.87	0.095	1.24	0.312	-1.4	0.172	-0.19
1452512_a_at	Ank1	ankyrin 1, erythroid	-2.58	0.35	1.79	0.37	-1.17	0.518	9.08	0.223	1.78
1416568_a_at	Acin1	apoptotic chromatin condensation inducer 1	-1	0.997	-1.07	0.65	1.1	0.747	1.22	0.179	0.06
1433392_at	---	---	1.25	0.756	-1.87	0.057	1.26	0.647	-2.77	0.225	-0.53
AFFX-r2-Bs-lys-M_a	---	---	1.12	0.798	-1.16	0.216	1.06	0.815	-1.64	0.408	-0.16
1439966_x_at	Sfxn2	sideroflexin 2	1.11	0.531	1.03	0.848	-1.11	0.601	-1.35	0.289	-0.08
1435554_at	Tmcc3	transmembrane and coiled coil domains 3	1.08	0.687	1.21	0.122	-1.34	0.077	-1.48	0.221	-0.13
1444410_at	Acp6	acid phosphatase 6, lysophosphatidic	-1.54	0.396	1.06	0.837	1.33	0.414	-1.05	0.91	-0.05
1436512_at	Arl4c /// LOC63243	ADP-ribosylation factor-like 4C /// similar to ADP-ribosylation factor-like protein 7	1.08	0.627	1.07	0.888	-1.13	0.711	-1.21	0.739	-0.05
1423189_at	6720456B07Rik	RIKEN cDNA 6720456B07 gene	1.05	0.716	1.03	0.825	-1.04	0.797	-1.23	0.424	-0.05
1427418_a_at	Hif1a	hypoxia inducible factor 1, alpha subunit	-1.09	0.672	1.06	0.431	1.05	0.557	-1.25	0.471	-0.05
1444750_at	Rsn	Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	1.31	0.212	1.11	0.645	-1.62	0.091	-2.76	0.076	-0.49
1418449_at	Lad1	ladinin	1.01	0.971	-1.45	0.015	1.34	0.037	-1.61	0.094	-0.18
1421481_at	Tnfrsf9	tumor necrosis factor receptor superfamily, member 9	-1.53	0.017	1.11	0.81	1.27	0.486	-1.36	0.108	-0.13
1418338_at	Wdr33	WD repeat domain 33	-1.03	0.59	-1.04	0.626	1.11	0.486	1.01	0.773	0.01
1419761_a_at	Gabpb1	GA repeat binding protein, beta 1	-1.1	0.463	-1.08	0.734	1.2	0.209	1.27	0.448	0.07
1455265_a_at	Rgs16	regulator of G-protein signaling 16	-1.37	0.074	-1.46	0.592	1.62	0.392	1.57	0.256	0.09
1416496_at	Mrfap1	Morf4 family associated protein 1	1.01	0.296	1.17	0.038	-1.17	0.101	-1.11	0.343	-0.02
1457439_at	Ccnt2	Cyclin T2	1.14	0.814	-1.37	0.629	1.17	0.5	-1.7	0.145	-0.19
1454461_at	5830433M15Rik	RIKEN cDNA 5830433M15 gene	-1.63	0.255	-2.59	0.068	2.04	0.018	1.09	0.583	-0.28
1452577_at	Igh	Immunoglobulin heavy chain complex	1.24	0.426	-1.32	0.512	1.05	0.916	-1.23	0.774	-0.07
1432482_at	Lyzl6	lysozyme-like 6	-2.13	0.299	2.25	0.326	-3.12	0.03	1.08	0.893	-0.48
1444449_at	Usp18	Ubiquitin specific peptidase 18	1.12	0.511	1.06	0.824	-1.18	0.477	-1.13	0.647	-0.03
1456144_at	LOC676640	region containing RIKEN cDNA 9630020C08 gene; neuron navigator 3	1	0.917	-1.19	0.645	1.19	0.617	-1.29	0.144	-0.07
1444030_at	Dcp1b	DCP1 decapping enzyme homolog b (S. cerevisiae)	-1.47	0.516	1.45	0.218	-1.11	0.535	1.14	0.807	0.01
1451000_at	Tmem126a	transmembrane protein 126A	-1.05	0.623	1.02	0.754	1.07	0.624	-1.2	0.33	-0.04
1436475_at	---	Transcribed locus	1.06	0.539	1.03	0.822	-1.06	0.626	-1.29	0.436	-0.06
1427692_a_at	Cask	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	1.12	0.33	-1.19	0.558	1.08	0.726	-1.41	0.46	-0.1
1423198_a_at	AW011752	expressed sequence AW011752	1.05	0.827	-1.08	0.699	1.06	0.844	-1.11	0.794	-0.02
1421090_at	Epb4.1l1	erythrocyte protein band 4.1-like 1	-1.05	0.863	-1.9	0.174	1.56	0.414	1.73	0.426	0.09
1441870_s_at	Pkd2	polycystic kidney disease 2	1.06	0.627	1.05	0.472	-1.07	0.772	-1.11	0.725	-0.02
1441921_x_at	Esrrb	estrogen related receptor, beta	-1.04	0.943	-1.51	0.363	1.41	0.351	1.34	0.452	0.05
1459673_at	Gtf3c1	general transcription factor III C 1	-1.39	0.636	-1.14	0.817	1.44	0.513	1.73	0.422	0.16
1427314_at	Tmed7	transmembrane emp24 protein transport domain containing 7	1.03	0.734	1.02	0.899	-1.01	0.891	-1.01	0.903	0.01
1439653_at	Adam6	a disintegrin and metallopeptidase domain 6	1.06	0.935	-1.33	0.471	1.23	0.292	-3.73	0.239	-0.69
1455947_at	AK162044	cDNA sequence AK162044	1.06	0.884	-1.14	0.847	1.11	0.786	-1.25	0.21	-0.06
1429724_at	Prpf4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	-1	0.989	-1.08	0.526	1.12	0.494	1.55	0.256	0.15
1435883_at	AW413431	expressed sequence AW413431	1.09	0.708	-1.17	0.298	1.09	0.604	-1.07	0.852	-0.01
1447905_x_at	Nup62	nucleoporin 62	-1	0.964	-1.09	0.207	1.13	0.132	1.2	0.323	0.06

1427500_at	Spcs1	signal peptidase complex subunit 1 homolog (S. cerevisiae)	-1.71	0.042	1.11	0.775	1.35	0.042	-1.17	0.525	-0.11
1440043_at	Ank2	ankyrin 2, brain	1.41	0.436	-1.18	0.42	-1.28	0.667	1.27	0.301	0.06
1421818_at	Bcl6	B-cell leukemia/lymphoma 6	1.1	0.657	-1.28	0.532	1.17	0.232	-1.86	0.043	-0.22
1418955_at	Zfp93	zinc finger protein 93	-1.01	0.902	-1.01	0.964	1.06	0.725	1.07	0.533	0.03
1456325_at	Cep68	centrosomal protein 68	1.23	0.237	-1.3	0.291	1.04	0.876	-1.44	0.254	-0.12
1436923_at	Rab2b	RAB2B, member RAS oncogene family	1.07	0.779	-1.1	0.734	1.06	0.75	-1.38	0.149	-0.09
1438603_x_at	Masp1	Mannan-binding lectin serine peptidase 1	1.56	0.144	-1.1	0.452	-1.74	0.228	2.84	0.101	0.39
1436293_x_at	D1Ertd471e	DNA segment, Chr 1, ERATO Doi 471, expressed	-1.46	0.083	-1.07	0.619	1.42	0.4	2.05	0.038	0.23
1435957_at	B830032F12	hypothetical protein B830032F12	-1.31	0.333	1.49	0.474	-1.28	0.311	1.16	0.377	0.02
1426832_at	6330505F04Rik	RIKEN cDNA 6330505F04 gene	-1.26	0.281	1.35	0.193	-1.11	0.301	1.3	0.293	0.07
1441648_at	C1qtnf4	C1q and tumor necrosis factor related protein 4	1.16	0.732	1.42	0.485	-2.18	0.277	-1.11	0.879	-0.18
1457622_at	BE983540	cDNA sequence BE983540	1.17	0.75	1.14	0.76	-1.37	0.514	-1.09	0.887	-0.04
1431200_a_at	Zcsl2	zinc finger, CSL domain containing 2	-1.25	0.516	1.25	0.411	-1.01	0.96	1.03	0.849	0.01
1427937_at	2610030H06Rik	RIKEN cDNA 2610030H06 gene	-1.19	0.508	-1.08	0.656	1.27	0.233	1.11	0.533	0.03
1424618_at	Hpd	4-hydroxyphenylpyruvic acid dioxygenase	-1.01	0.968	-1.28	0.377	1.27	0.525	1.82	0.375	0.2
1417149_at	P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha	-1.03	0.855	1.02	0.957	1.05	0.796	-1.48	0.276	-0.11
1419559_at	Cyp4f14	cytochrome P450, family 4, subfamily f, polypeptide 14	1.45	0.058	-1.6	0.03	-1.03	0.792	1.3	0.558	0.03
1430720_at	Ybx1	Y box protein 1	-1.82	0.342	1.16	0.762	1.33	0.388	-1.36	0.241	-0.17
1433076_at	5430402O13Rik	RIKEN cDNA 5430402O13 gene	-1.14	0.841	1.03	0.928	1.14	0.732	-1.71	0.518	-0.17
1424536_at	Oas1e	2'-5' oligoadenylate synthetase 1E	-1.07	0.751	1.75	0.487	-2.84	0.116	2.8	0.322	0.16
1447041_at	9530066K23Rik	RIKEN cDNA 9530066K23 gene	1.05	0.937	1.43	0.485	-1.76	0.325	-1.2	0.71	-0.12
1447057_at	---	---	-1.37	0.424	1.69	0.248	-1.62	0.195	1.07	0.753	-0.05
1431075_a_at	Eif4enif1	eukaryotic translation initiation factor 4E nuclear import factor 1	-1.08	0.415	-1	0.961	1.12	0.157	1.35	0.236	0.1
1430556_at	Spag9	sperm associated antigen 9	1.11	0.048	1.3	0.22	-1.59	0.015	-1.47	0.241	-0.16
1430577_at	Cep27	centrosomal protein 27	1.13	0.506	-1.03	0.719	-1.06	0.78	1.66	0.016	0.17
1449924_at	Prg3	proteoglycan 3	1.18	0.472	1.3	0.405	-1.8	0.166	-2.32	0.144	-0.41
1420100_s_at	D13Ertd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	-1.63	0.075	1.8	0.347	-1.58	0.297	1.07	0.896	-0.09
1424571_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1.03	0.178	-1.03	0.695	1.04	0.759	-1.16	0.069	-0.03
1415741_at	Tmem165	transmembrane protein 165	1	0.992	1.18	0.269	-1.16	0.051	-1.02	0.864	0
1443189_at	---	---	-1.39	0.27	1.6	0.207	-1.37	0.517	2.03	0.145	0.21
1427188_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	-1.09	0.269	-1.24	0.461	1.32	0.443	1.22	0.564	0.05
1458040_at	D7Wsu130e	DNA segment, Chr 7, Wayne State University 130, expressed	1.21	0.805	-1.19	0.728	-1.01	0.966	1.37	0.449	0.09
1418898_at	Lin7c	lin-7 homolog C (C. elegans)	1.07	0.563	-1.13	0.734	1.09	0.827	-1	0.985	0.01
1456034_at	Ttc18	tetratricopeptide repeat domain 18	-1.04	0.867	-1.37	0.472	1.36	0.157	1.1	0.813	0.01
1460357_at	Ythdf2	YTH domain family 2	1	0.974	1.07	0.463	-1.03	0.678	-1.04	0.615	0
1454813_at	Ccdc72	coiled-coil domain containing 72	-1	0.985	1.08	0.323	-1.04	0.705	1	0.927	0.01
1435684_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	-1.6	0.094	1.53	0.196	-1.12	0.53	1.23	0.204	0.01
1433159_at	Kif13b	kinesin family member 13B	1.18	0.818	-1.38	0.549	1.14	0.801	-1.42	0.516	-0.12
1454043_a_at	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	-1.03	0.964	1.22	0.713	-1.16	0.814	1.36	0.436	0.1
1437317_at	Ube1l	ubiquitin-activating enzyme E1-like	-1.05	0.813	-1.1	0.694	1.18	0.188	1.66	0.337	0.17
1431155_at	Camsap1l1	calmodulin regulated spectrin-associated protein 1-like 1	1.23	0.782	1.29	0.675	-1.9	0.097	-1.46	0.392	-0.21
1415947_at	Creg1	cellular repressor of E1A-stimulated genes 1	1.15	0.463	-1.07	0.512	-1.04	0.824	1.34	0.256	0.09
1460690_at	BC003940	cDNA sequence BC003940	-1.11	0.455	1.14	0.14	1	0.985	-1.4	0.165	-0.09
1415683_at	Nmt1	N-myristoyltransferase 1	1.09	0.268	-1.01	0.926	-1.04	0.575	1.19	0.117	0.06
1440486_at	2310037I24Rik	RIKEN cDNA 2310037I24 gene	-1.19	0.538	1.32	0.107	-1.12	0.499	1.03	0.796	0.01
1448687_at	C1qdc2	C1q domain containing 2	-1.07	0.58	1.15	0.445	-1.05	0.74	4.02	0.164	0.76
1450272_at	Tnfsf8	tumor necrosis factor (ligand) superfamily, member 8	-1.58	0.549	-1.15	0.745	1.54	0.189	1.04	0.947	-0.04
1441168_at	Il1rapl2	Interleukin 1 receptor accessory protein-like 2	1.01	0.971	1.23	0.695	-1.25	0.645	-1.37	0.51	-0.09
1426451_at	6030465E24Rik	RIKEN cDNA 6030465E24 gene	-1.14	0.025	1.04	0.808	1.13	0.541	-1.34	0.281	-0.08
1427129_a_at	Hnrpr	heterogeneous nuclear ribonucleoprotein R	-1.03	0.782	1.09	0.269	-1.02	0.884	1.01	0.919	0.01
1433260_at	4930500E03Rik	RIKEN cDNA 4930500E03 gene	1.23	0.178	-1.17	0.716	-1.04	0.881	2.14	0.113	0.29
1435127_a_at	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	-1.07	0.35	-1.04	0.446	1.15	0.385	1.41	0.235	0.11
1440376_at	Fbxo41	F-box protein 41	1.29	0.39	-1.19	0.487	-1.09	0.622	1.09	0.435	0.02

1437810_a_at	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	-1.06	0.863	-1.14	0.563	1.22	0.449	1.76	0.283	0.2
1426533_at	Nol5a	nucleolar protein 5A	-1.02	0.96	-1.14	0.237	1.18	0.479	1.02	0.92	0.01
1456389_at	Zfhx1b	zinc finger homeobox 1b	-1.12	0.373	1.43	0.138	-1.37	0.048	1.01	0.968	-0.02
1443310_at	Nup210	nucleoporin 210	-1.12	0.591	1.11	0.716	1.04	0.948	-2.4	0.316	-0.34
1452074_at	Tmem135	transmembrane protein 135	1.01	0.881	1.1	0.59	-1.07	0.667	-1.17	0.416	-0.03
1449546_a_at	Zfp617	zinc finger protein 617	1.18	0.375	-1.11	0.328	-1.04	0.802	1.14	0.62	0.04
1437008_x_at	Tmem109	transmembrane protein 109	-1.02	0.393	1.03	0.592	1.03	0.63	-1.34	0.272	-0.07
1416920_at	Rbm4	RNA binding motif protein 4	1.02	0.706	-1.06	0.524	1.08	0.264	-1.38	0.266	-0.08
1417816_s_at	Serinc3	serine incorporator 3	1.45	0.108	-1.31	0.155	-1.21	0.276	1.26	0.441	0.05
1446764_at	Wnt3a	Wingless-related MMTV integration site 3A	1.09	0.74	1.52	0.32	-2.31	0.006	-1.64	0.347	-0.34
1432313_at	4933433F19Rik	RIKEN cDNA 4933433F19 gene	1.2	0.818	1.03	0.958	-1.23	0.668	-1.31	0.173	-0.08
1435822_at	D830012I24Rik	RIKEN cDNA D830012I24 gene	1.28	0.292	1.1	0.686	-1.5	0.084	-1.25	0.421	-0.09
1454096_a_at	4930555I21Rik	RIKEN cDNA 4930555I21 gene	-2.07	0.268	-1.05	0.907	1.61	0.269	1.05	0.418	-0.12
1415703_at	Huwe1	HECT, UBA and WWE domain containing 1	-1.02	0.775	1.05	0.277	1.01	0.91	-1.01	0.949	0.01
1447796_at	Nop17	NOP17	-2.56	0.456	1.49	0.206	1.17	0.5	-1.2	0.449	-0.28
1418208_at	Pax8	paired box gene 8	-1.01	0.957	1.24	0.78	-1.22	0.363	1.43	0.486	0.11
1451188_at	Wdr26	WD repeat domain 26	-1.02	0.596	-1.01	0.925	1.07	0.721	1.52	0.279	0.14
1432416_a_at	Npm1	nucleophosmin 1	1.05	0.435	-1.14	0.166	1.12	0.586	-1.14	0.132	-0.03
1416023_at	Fabp3	fatty acid binding protein 3, muscle and heart	-1.19	0.369	-1.06	0.819	1.26	0.567	1.02	0.923	0.01
1440654_at	MGC99845	Hypothetical protein LOC574403	-1.11	0.843	1.13	0.562	1.01	0.937	-2.18	0.093	-0.29
1425028_a_at	Tpm2	tropomyosin 2, beta	1.32	0.138	-1.55	0.387	1.07	0.595	-1.44	0.177	-0.15
1455051_at	Rnf31	ring finger protein 31	-1.14	0.215	1.03	0.715	1.14	0.388	-1.49	0.022	-0.11
1427691_a_at	Ifnar2	interferon (alpha and beta) receptor 2	1.08	0.618	1.06	0.707	-1.1	0.611	-1.05	0.255	0
1428754_at	3300001M20Rik	RIKEN cDNA 3300001M20 gene	1.03	0.808	1.03	0.598	-1.02	0.752	-1.04	0.832	0
1434784_s_at	Tmem106c	transmembrane protein 106C	1.04	0.838	-1.07	0.563	1.07	0.52	-1.05	0.8	0
1452210_at	Dna2l	DNA2 DNA replication helicase 2-like (yeast)	-1.02	0.916	-1.11	0.701	1.17	0.339	1.76	0.348	0.2
1455253_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	1.02	0.834	-1.42	0.12	1.32	0.126	-1.14	0.558	-0.06
1442701_at	---	---	-1.08	0.894	-1.01	0.976	1.13	0.588	1.42	0.022	0.12
1459405_at	Iqgap3	IQ motif containing GTPase activating protein 3	1.57	0.039	-1.57	0.429	-1.19	0.642	1.19	0.614	0
1436768_x_at	E130112L23Rik ///	RIKEN cDNA E130112L23 gene /// similar to quattro	-1.16	0.344	1.24	0.497	-1.06	0.827	1.33	0.617	0.09
1417964_at	Ap3d1	adaptor-related protein complex 3, delta 1 subunit	-1.09	0.369	1.08	0.396	1.05	0.661	-1.1	0.539	-0.01
1440584_at	9130221L21Rik	RIKEN cDNA 9130221L21 gene	1.21	0.632	1.04	0.912	-1.26	0.288	-1.13	0.466	-0.03
1434576_at	Tsga14	testis specific gene A14	-1.18	0.513	-1.16	0.462	1.33	0.051	1.07	0.478	0.02
1417972_s_at	Pop5	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)	1.01	0.774	1.07	0.485	-1.04	0.822	-1.13	0.555	-0.02
1455331_at	9430067K14Rik	RIKEN cDNA 9430067K14 gene	1.04	0.75	-1.12	0.465	1.12	0.534	-1.37	0.321	-0.09
1420889_at	Hccs	holocytochrome c synthetase	-1.25	0.19	-1.15	0.65	1.37	0.206	1.21	0.572	0.05
1433607_at	Cbln4	cerebellin 4 precursor protein	-1.11	0.863	-1	0.994	1.15	0.608	1.02	0.967	0.01
1416254_a_at	Vps16	vacuolar protein sorting 16 (yeast)	1.01	0.804	-1.08	0.533	1.11	0.522	-1.36	0.298	-0.08
1433336_at	4930405G09Rik	RIKEN cDNA 4930405G09 gene	-2.48	0.449	1.8	0.064	-1.19	0.629	1.21	0.705	-0.16
1452566_at	---	---	1.04	0.951	-1.28	0.528	1.23	0.654	-1.1	0.582	-0.03
1450244_a_at	Map4k2	mitogen activated protein kinase kinase kinase kinase 2	1.01	0.891	-1.24	0.091	1.22	0.421	-1.93	0.026	-0.23
1453253_a_at	Rpusd1	RNA pseudouridylate synthase domain containing 1	-1.06	0.743	-1.13	0.645	1.22	0.18	1.67	0.168	0.18
1426443_at	Rhbdd2	rhomboid domain containing 2	1.07	0.82	-1.25	0.326	1.18	0.033	-1.79	0.184	-0.2
1456790_at	AA407452	EST AA407452	1.24	0.497	-1.23	0.214	-1.01	0.969	1.44	0.322	0.11
1439208_at	Chek1	checkpoint kinase 1 homolog (S. pombe)	-1.07	0.822	1.24	0.067	-1.15	0.802	3.74	0.164	0.69
1427957_at	9530008L14Rik	RIKEN cDNA 9530008L14 gene	1.07	0.399	-1.33	0.001	1.22	0.614	-3.46	0.02	-0.62
1459819_at	5330439K02Rik	RIKEN cDNA 5330439K02 gene	1.36	0.571	1.17	0.783	-1.93	0.42	-1.69	0.419	-0.27
1435182_at	C530028I08Rik	RIKEN cDNA C530028I08 gene	-1.18	0.035	1.11	0.62	1.09	0.406	-1.22	0.206	-0.05
1457042_at	AI256396	EST AI256396	1.27	0.543	-1.19	0.827	-1.07	0.804	1.21	0.535	0.05
1444640_at	Pigg	phosphatidylinositol glycan anchor biosynthesis, class G	-1.17	0.045	-1.05	0.745	1.25	0.289	1.08	0.731	0.02
1456086_x_at	LOC631302	similar to polyglutamine binding protein 1	1.01	0.913	-1.19	0.014	1.2	0.362	-1.11	0.71	-0.02
1457569_at	D8Ertd51e	DNA segment, Chr 8, ERATO Doi 51, expressed	-1.03	0.908	1.33	0.48	-1.34	0.559	1.89	0.164	0.21
1426551_at	Sidt1	SID1 transmembrane family, member 1	-2.54	0.116	1.15	0.238	1.51	0.327	-1.06	0.926	-0.24

1439786_at	Gab2	growth factor receptor bound protein 2-associated protein 2	-1.02	0.913	1.3	0.196	-1.3	0.023	1.29	0.277	0.07
1434086_at	AI790205	expressed sequence AI790205	-1.3	0.04	1.24	0.238	1.03	0.798	-1.1	0.442	-0.03
1448916_at	Mafg	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein G (avian)	-1.1	0.434	-1.05	0.682	1.19	0.299	2.34	0.128	0.35
1457660_x_at	5430416O09Rik	RIKEN cDNA 5430416O09 gene	1.32	0.564	-1.72	0.247	1.15	0.734	-1.17	0.836	-0.11
1435202_at	Zfp574	zinc finger protein 574	1.02	0.921	-1.14	0.565	1.16	0.424	-1.13	0.175	-0.03
1433563_s_at	Derl1	Der1-like domain family, member 1	1.06	0.828	1.06	0.46	-1.07	0.728	-1.04	0.546	0
1424410_at	Ttc8	tetratricopeptide repeat domain 8	-1.06	0.058	-1.04	0.725	1.14	0.212	1.14	0.552	0.05
1454535_at	A430110A21Rik	RIKEN cDNA A430110A21 gene	-1.22	0.266	1.03	0.866	1.2	0.459	-1.07	0.867	-0.01
1423290_at	Hyou1	hypoxia up-regulated 1	-1.38	0.307	1.11	0.66	1.21	0.485	-1.01	0.942	-0.01
1452782_a_at	Txn2	thioredoxin 2	-1	0.996	-1.05	0.661	1.1	0.411	1.24	0.288	0.07
1434567_at	4732496O08Rik	RIKEN cDNA 4732496O08 gene	-1.06	0.696	1.08	0.361	1.02	0.834	-1.39	0.09	-0.09
1426728_x_at	Ptdss2	phosphatidylserine synthase 2	-1.1	0.173	-1.1	0.673	1.23	0.341	5.51	0.178	1.14
1446063_at	C730034F03Rik	RIKEN cDNA C730034F03 gene	-1.28	0.076	1.44	0.178	-1.21	0.613	1.29	0.304	0.06
1446163_at	---	---	1.1	0.686	-1.14	0.588	1.07	0.855	-1.08	0.81	-0.01
1445329_at	Dtnb	dystrobrevin, beta	1.08	0.668	1.15	0.54	-1.23	0.024	-1.24	0.248	-0.06
1433501_at	Ctso	cathepsin O	1.01	0.887	1.09	0.027	-1.06	0.637	-1.38	0.389	-0.08
1454780_at	Galntl4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.01	0.934	1	0.989	1.06	0.55	-1.04	0.869	0
1447961_s_at	Mrpl38	mitochondrial ribosomal protein L38	1.18	0.458	-1.13	0.213	-1.01	0.922	1.07	0.711	0.03
1431812_a_at	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-1.28	0.679	-1.47	0.176	1.59	0.129	5.22	0.187	1.01
1459937_at	Ass1	Argininosuccinate synthetase 1	1	0.997	-1.25	0.369	1.25	0.237	-1.11	0.488	-0.03
1423955_a_at	Lass2	longevity assurance homolog 2 (S. cerevisiae)	-1.02	0.947	-1.03	0.782	1.1	0.237	1.03	0.508	0.02
1438177_x_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	1.04	0.624	1.11	0.31	-1.11	0.307	-1.26	0.381	-0.05
1444091_a_at	6430571L13Rik	RIKEN cDNA 6430571L13 gene	1.43	0.201	1.16	0.765	-2.19	0.145	-1.7	0.408	-0.33
1447698_x_at	---	---	-2.25	0.15	1.45	0.296	1.15	0.818	-1.3	0.578	-0.24
1450707_at	Doc2g	double C2, gamma	1.05	0.885	1.01	0.984	-1	0.992	-1.44	0.145	-0.1
1458247_s_at	Dctn5	dynactin 5	1.15	0.489	1.02	0.779	-1.14	0.364	-1.12	0.002	-0.02
1454977_at	AU020772	expressed sequence AU020772	-1.3	0.167	1.05	0.756	1.23	0.19	-1.23	0.068	-0.06
1420246_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	-1.13	0.686	1.72	0.106	-2.26	0.063	2.28	0.093	0.15
1453772_at	Syngr1	synaptogyrin 1	-1.15	0.668	1.58	0.314	-1.67	0.292	1.02	0.951	-0.05
1460193_at	St13	suppression of tumorigenicity 13	-1.02	0.835	-1.11	0.139	1.16	0.198	1	0.951	0.01
1426491_at	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 ((	-1.14	0.53	-1.03	0.823	1.2	0.42	1.12	0.542	0.04
1450741_at	Stau1	staufen (RNA binding protein) homolog 1 (Drosophila)	1.16	0.159	-1.1	0.513	-1.02	0.841	1.12	0.128	0.04
1416932_at	Cog2	component of oligomeric golgi complex 2	1.03	0.639	-1.23	0.22	1.21	0.241	-1.04	0.353	-0.01
1441004_at	Exosc4	Exosome component 4	-1.01	0.973	-1.26	0.132	1.27	0.232	1.06	0.459	0.01
1449137_at	Pdha1	pyruvate dehydrogenase E1 alpha 1	-1.06	0.756	-1.23	0.279	1.3	0.365	1.16	0.613	0.04
1453739_at	Tmem126b	transmembrane protein 126B	1.05	0.825	-1.04	0.738	1.04	0.883	-1.41	0.383	-0.09
1431434_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	1.08	0.137	1.19	0.792	-1.27	0.356	-2.4	0.06	-0.35
1420332_x_at	Sprrl7	small proline rich-like 7	1.59	0.133	-1.13	0.778	-1.73	0.224	1.18	0.274	-0.02
1451887_at	Lrba	LPS-responsive beige-like anchor	1	0.997	1.35	0.213	-1.43	0.033	-1.43	0.213	-0.13
1444303_at	Mark2	MAP/microtubule affinity-regulating kinase 2	-2.06	0.34	1.06	0.921	1.51	0.282	-2.12	0.138	-0.4
1423268_at	Itga5	integrin alpha 5 (fibronectin receptor alpha)	-1.37	0.527	1.59	0.498	-1.38	0.47	1.54	0.426	0.1
1438311_at	2010002M12Rik	RIKEN cDNA 2010002M12 gene	-2.46	0.454	1.45	0.658	1.2	0.74	-1.41	0.421	-0.31
1454588_at	9430006E15Rik	RIKEN cDNA 9430006E15 gene	-1.87	0.608	1.72	0.462	-1.25	0.395	1.47	0.219	0.02
1432411_a_at	Fbxw2	F-box and WD-40 domain protein 2	1.03	0.788	-1.02	0.946	1.05	0.904	-1.14	0.734	-0.02
1459125_at	D030059C06Rik	RIKEN cDNA D030059C06 gene	1.14	0.841	-1.21	0.556	1.08	0.833	-1.12	0.777	-0.03
1435118_at	Tsen2	tRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	-1.21	0.213	-1.05	0.575	1.28	0.179	1.08	0.697	0.02
1418272_at	Oxct2a	3-oxoacid CoA transferase 2A	-1.78	0.171	1.6	0.387	-1.12	0.678	1.31	0.119	0
1418235_at	Atg5	autophagy-related 5 (yeast)	1.09	0.726	1.04	0.816	-1.09	0.576	-1.04	0.857	0
1444415_at	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.7	0.21	-1.29	0.543	-1.73	0.296	1.23	0.701	-0.02
1454542_at	9330179C17Rik	RIKEN cDNA 9330179C17 gene	-1.16	0.69	1.41	0.382	-1.27	0.276	1.08	0.404	0.01
1420008_s_at	---	---	1.28	0.002	1.01	0.944	-1.3	0.121	-1.38	0.349	-0.1
1448388_a_at	1110002B05Rik	RIKEN cDNA 1110002B05 gene	1.14	0.277	1.09	0.051	-1.21	0.038	-1.33	0.247	-0.08
1455493_at	Syne1	synaptic nuclear envelope 1	-1.17	0.402	1.11	0.505	1.09	0.387	-1.12	0.717	-0.02

1440628_at	---	---	2.09	0.5	-2.25	0.119	-1.92	0.106	1.98	0.002	-0.03
1443539_at	Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11	-1.11	0.89	-1.18	0.576	1.3	0.111	1.26	0.682	0.07
1430337_at	6530401N04Rik	RIKEN cDNA 6530401N04 gene	1.23	0.288	-1.37	0.097	1.09	0.713	-1.37	0.537	-0.11
1420523_at	Ccdc50	coiled-coil domain containing 50	1.01	0.982	-1.12	0.836	1.15	0.772	-1.56	0.488	-0.13
1448915_at	Zfp524	zinc finger protein 524	-1.07	0.695	1.07	0.638	1.05	0.837	-1.2	0.554	-0.04
1458956_at	A330068P14Rik	RIKEN cDNA A330068P14 gene	1.13	0.234	1.2	0.124	-1.38	0.056	-1.02	0.943	-0.02
1452099_at	AA408296	expressed sequence AA408296	-1.04	0.775	1.01	0.911	1.08	0.631	-1.48	0.036	-0.11
1435558_at	Bai2	brain-specific angiogenesis inhibitor 2	1.01	0.983	-1.44	0.236	1.35	0.375	-2.84	0.021	-0.48
1428579_at	Fmnl2	formin-like 2	1.01	0.92	1.28	0.017	-1.32	0.314	-1.37	0.341	-0.1
1426973_at	Gpr153	G protein-coupled receptor 153	1.33	0.183	-1.74	0.34	1.15	0.709	-1.07	0.867	-0.08
1458139_at	---	---	1.05	0.9	1.19	0.766	-1.23	0.498	-1.2	0.675	-0.05
1421883_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	-1.89	0.301	1.9	0.449	-1.6	0.464	1.52	0.454	-0.02
1455800_x_at	Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	-1.05	0.551	1.02	0.751	1.08	0.433	-1.42	0.271	-0.09
1455345_at	Phf15	PHD finger protein 15	1.03	0.801	-1.01	0.93	1.03	0.879	-1.26	0.499	-0.05
1419118_at	2900093B09Rik	RIKEN cDNA 2900093B09 gene	-1.17	0.811	-1.13	0.548	1.31	0.402	2.86	0.074	0.47
1442931_at	2600003E23Rik	RIKEN cDNA 2600003E23 gene	-1.26	0.503	1.49	0.218	-1.29	0.571	1.06	0.768	0
1448835_at	E2f6	E2F transcription factor 6	-1.02	0.666	-1.01	0.503	1.09	0.381	1.57	0.189	0.16
1457279_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.26	0.314	-1.06	0.785	1.32	0.282	1.69	0.358	0.17
1425749_at	Stxbp6	syntaxin binding protein 6 (amisyn)	1.05	0.577	1.2	0.465	-1.25	0.273	-1.06	0.925	-0.02
1426692_at	Ccdc97	coiled-coil domain containing 97	-1.17	0.225	1.02	0.86	1.18	0.267	-1.16	0.208	-0.03
1426523_a_at	Gnpda2	glucosamine-6-phosphate deaminase 2	1.05	0.709	1.07	0.724	-1.07	0.411	-1.5	0.121	-0.11
1448564_at	Cib1	calcium and integrin binding 1 (calmyrin)	-1.01	0.936	1.01	0.923	1.05	0.698	-1.3	0.127	-0.06
1416803_at	Fkbp7	FK506 binding protein 7	1.06	0.698	1.37	0.084	-1.6	0.016	-1.29	0.223	-0.12
1426049_a_at	---	---	1.01	0.948	-1.08	0.741	1.12	0.364	-1.27	0.066	-0.06
1421331_at	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1.09	0.827	-1.14	0.612	1.09	0.458	-1.12	0.56	-0.02
1444773_at	D430040D24Rik	RIKEN cDNA D430040D24 gene	-1.04	0.936	-1.04	0.951	1.13	0.771	1.22	0.575	0.07
1446460_at	Tmem61	transmembrane protein 61	-1.18	0.631	-1.01	0.988	1.21	0.765	2.85	0.292	0.47
1436041_at	---	---	-1.34	0.446	-1.2	0.5	1.48	0.18	1.26	0.547	0.05
1454868_at	D4Ertd429e	DNA segment, Chr 4, ERATO Doi 429, expressed	-1.02	0.919	-1.25	0.205	1.28	0.45	1.02	0.839	0.01
1440729_at	Eps15	epidermal growth factor receptor pathway substrate 15	1.17	0.814	1.15	0.649	-1.36	0.522	-1.07	0.638	-0.03
1428834_at	Dusp4	dual specificity phosphatase 4	-1.02	0.95	1.01	0.989	1.07	0.852	-1.55	0.276	-0.12
1460398_at	Phf8	PHD finger protein 8	-1.15	0.226	-1.2	0.034	1.35	0.068	1.01	0.928	0
1435804_at	Eif4e2	eukaryotic translation initiation factor 4E member 2	1.1	0.537	-1.07	0.773	1.03	0.949	-1.24	0.057	-0.05
1443119_at	Grm7	glutamate receptor, metabotropic 7	1.31	0.094	1.02	0.918	-1.38	0.595	-1.12	0.881	-0.04
1437857_at	Dpy19l3	dpy-19-like 3 (C. elegans)	-1.13	0.69	1.1	0.825	1.07	0.744	-1.48	0.045	-0.11
1416580_a_at	Stub1	STIP1 homology and U-Box containing protein 1	1.05	0.632	-1.04	0.479	1.04	0.599	-1.08	0.458	-0.01
1455868_a_at	Tubgcp2	tubulin, gamma complex associated protein 2	-1.17	0.525	-1.03	0.834	1.23	0.074	1.72	0.136	0.19
1442841_at	Tspan3	Tetraspanin 3	-3.2	0.357	1.7	0.245	1.04	0.931	-2.2	0.024	-0.66
1441315_s_at	Slc19a2	solute carrier family 19 (thiamine transporter), member 2	-1.06	0.805	-1.07	0.49	1.18	0.308	1.84	0.246	0.22
1416703_at	Mapk14	mitogen activated protein kinase 14	-1.12	0.669	1.03	0.664	1.13	0.084	-1.13	0.577	-0.02
1424246_a_at	Tes	testis derived transcript	1	0.933	1.12	0.808	-1.07	0.647	-1.24	0.522	-0.05
1420051_at	---	Transcribed locus	-1.49	0.623	1.86	0.346	-1.91	0.109	1.65	0.217	0.03
1422586_at	Ecel1	endothelin converting enzyme-like 1	-1.19	0.613	1.31	0.385	-1.1	0.822	1.09	0.818	0.03
1455396_at	Atp8b1	ATPase, class I, type 8B, member 1	-1.01	0.86	1.21	0.441	-1.17	0.135	1.51	0.281	0.13
1455847_at	Pak7	p21 (CDKN1A)-activated kinase 7	-1.41	0.286	1.1	0.838	1.25	0.422	-1.33	0.597	-0.1
1448683_at	Cyp2d26	cytochrome P450, family 2, subfamily d, polypeptide 26	-1.19	0.131	-1.18	0.379	1.37	0.362	4.31	0.289	0.83
1427345_a_at	Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	1.2	0.685	1.03	0.831	-1.22	0.606	-1.16	0.815	-0.04
1449904_at	Dopey2	dopey family member 2	1.13	0.701	-1.22	0.23	1.1	0.651	-1.01	0.972	0
1455018_at	Lmtk2	lemur tyrosine kinase 2	-1.03	0.799	-1.1	0.18	1.18	0.235	1.03	0.654	0.02
1415817_s_at	Cct7	chaperonin subunit 7 (eta)	1.1	0.341	-1.1	0.007	1.05	0.713	-1.02	0.923	0.01
1450662_at	Tesk1	testis specific protein kinase 1	1.24	0.374	-1.32	0.023	1.05	0.814	-1.3	0.279	-0.08
1449898_at	1-Sep	septin 1	-1.37	0.275	1.03	0.931	1.3	0.329	-1.2	0.557	-0.06
1454558_at	5430416B10Rik	RIKEN cDNA 5430416B10 gene	-1.13	0.694	1.09	0.769	1.08	0.629	-1.33	0.485	-0.07

1455251_at	Itga1	integrin alpha 1	1.09	0.322	1.13	0.275	-1.2	0.113	-1.25	0.395	-0.06
1436706_at	Tmem32	transmembrane protein 32	1.23	0.491	-1.19	0.544	-1.01	0.984	1.43	0.294	0.11
1424789_at	Hkr2	GLI-Kruppel family member HKR2	-1.04	0.776	1.13	0.176	-1.03	0.781	1.06	0.692	0.03
1419838_s_at	Plk4	polo-like kinase 4 (Drosophila)	-1.38	0.22	1.54	0.353	-1.26	0.042	3.11	0.148	0.5
1441945_s_at	Abhd14a	abhydrolase domain containing 14A	-1.06	0.573	-1.09	0.146	1.19	0.191	1.06	0.444	0.03
1442615_at	Adk	Adenosine kinase	1.53	0.53	-1.05	0.846	-1.73	0.326	1.33	0.463	0.02
1438593_at	LOC622461	hypothetical LOC622461	1.24	0.752	-1.41	0.488	1.1	0.389	-1.58	0.359	-0.16
1421586_a_at	Cd46	CD46 antigen, complement regulatory protein	-1.16	0.55	-1.07	0.746	1.25	0.136	1.31	0.215	0.08
1454655_at	Dgkd	diacylglycerol kinase, delta	1.2	0.73	-1.58	0.368	1.23	0.5	-1.13	0.766	-0.07
1434077_at	Wdr37	WD repeat domain 37	-1.13	0.033	-1.33	0.36	1.42	0.296	1.04	0.931	0
1460694_s_at	Svil	supervillin	-1.07	0.673	-1.04	0.819	1.16	0.32	1.27	0.005	0.08
1447671_x_at	Fbxo6b	F-box only protein 6b	1.37	0.621	-1.06	0.712	-1.34	0.212	1.03	0.955	0
1446117_at	Spire1	spire homolog 1 (Drosophila)	-1.98	0.198	2	0	-1.82	0.221	2.68	0.134	0.22
1448672_a_at	Zfp289	zinc finger protein 289	1.02	0.763	-1.01	0.923	1.05	0.49	-1.02	0.86	0.01
1432691_at	9030407C09Rik	RIKEN cDNA 9030407C09 gene	1.12	0.889	-1.47	0.603	1.26	0.377	-1.21	0.743	-0.08
1419739_at	Tpm2	tropomyosin 2, beta	-1.06	0.853	-1.13	0.722	1.22	0.627	1.41	0.013	0.11
1457402_at	Sulf1	Sulfatase 1	1.44	0.069	1.24	0.262	-2.67	0.065	-3.06	0.08	-0.76
1423188_a_at	6720456B07Rik	RIKEN cDNA 6720456B07 gene	1.08	0.247	1.09	0.054	-1.13	0.198	-1.24	0.198	-0.05
1451973_at	Ube1dc1	ubiquitin-activating enzyme E1-domain containing 1	1.14	0.659	1.22	0.007	-1.44	0.052	-1.26	0.34	-0.09
1450071_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	1.06	0.631	1.06	0.696	-1.08	0.458	-1.03	0.757	0.01
1450036_at	Sgk3	serum/glucocorticoid regulated kinase 3	-1.11	0.425	-1.25	0.02	1.35	0.224	1.04	0.81	0.01
1434224_at	Tbl2	transducin (beta)-like 2	-1.08	0.664	-1.08	0.626	1.21	0.339	1.38	0.064	0.11
1456036_x_at	Gsto1	glutathione S-transferase omega 1	-1.2	0.203	1.1	0.154	1.13	0.531	-1.06	0.744	-0.01
1422593_at	Ap3s1	adaptor-related protein complex 3, sigma 1 subunit	-1.01	0.675	-1.02	0.69	1.09	0.516	1.7	0.217	0.19
1447226_at	---	---	1.3	0.696	1.32	0.393	-2.28	0.106	-1.62	0.424	-0.32
1421992_a_at	Igfbp4	insulin-like growth factor binding protein 4	1.04	0.767	-1.02	0.862	1.04	0.803	-1.16	0.055	-0.03
1458435_at	2010000I03Rik	RIKEN cDNA 2010000I03 gene	-1.24	0.181	1.06	0.892	1.2	0.311	-1.04	0.816	-0.01
1432815_at	4833419A21Rik	RIKEN cDNA 4833419A21 gene	-1.61	0.546	1.86	0.326	-1.73	0.072	2.1	0.181	0.16
1459998_at	Zfp407	zinc finger protein 407	1.03	0.87	1.11	0.063	-1.09	0.649	-1.13	0.514	-0.02
1424138_at	Rhbdf1	rhomboid family 1 (Drosophila)	-1.12	0.437	1.12	0.519	1.04	0.661	-1.13	0.733	-0.02
1452693_at	Dhx35	DEAH (Asp-Glu-Ala-His) box polypeptide 35	-1.18	0.35	1.01	0.942	1.2	0.034	-1.59	0.123	-0.14
1452714_at	Tanc1	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	1.01	0.93	1.2	0.062	-1.17	0.419	-1.44	0.056	-0.1
1423745_at	1110031B06Rik	RIKEN cDNA 1110031B06 gene	1.04	0.802	-1	0.979	1.02	0.787	-1.25	0.26	-0.05
1447403_a_at	Zmynd19	Zinc finger, MYND domain containing 19	-1.02	0.924	-1.33	0.327	1.33	0.356	1.75	0.424	0.18
1450308_a_at	Xrn1	5'-3' exoribonuclease 1	-1	0.947	1.33	0.418	-1.36	0.035	1.23	0.187	0.05
1446213_at	Mtmr2	Myotubularin related protein 2	1.17	0.824	1.16	0.814	-1.37	0.361	-2.4	0.032	-0.36
1452290_at	Tmem106b	transmembrane protein 106B	-1.19	0.354	1.04	0.782	1.17	0.37	-1.13	0.365	-0.02
1437711_x_at	Odc1 /// LOC66623	ornithine decarboxylase, structural 1 /// similar to Ornithine decarboxylase (ODC)	-1.12	0.352	-1.05	0.653	1.21	0.414	1.85	0.143	0.22
1445326_at	Sdk1	sidekick homolog 1 (chicken)	1.71	0.153	-2.93	0.209	1.01	0.987	-1.47	0.072	-0.42
1454471_at	3110062G12Rik	RIKEN cDNA 3110062G12 gene	1.08	0.436	1.65	0.488	-3.03	0.178	-1.02	0.975	-0.33
1419031_at	Fads2	fatty acid desaturase 2	-1.14	0.424	-1.52	0.135	1.52	0.233	2.37	0.257	0.31
1448265_x_at	Eva1	epithelial V-like antigen 1	-1.08	0.664	-1.11	0.548	1.23	0.096	1.07	0.713	0.03
1449587_a_at	Muc10	mucin 10, submandibular gland salivary mucin	-1.91	0.49	1.09	0.8	1.44	0.356	-1.57	0.308	-0.24
1449659_s_at	Mphosph9	M-phase phosphoprotein 9	1.1	0.591	-1	0.987	-1.04	0.739	1.01	0.887	0.02
1429067_at	Capns2	calpain, small subunit 2	1.12	0.679	-1.49	0.072	1.27	0.315	-1.68	0.004	-0.19
1419714_at	Cd274	CD274 antigen	-1.19	0.609	1.12	0.658	1.1	0.673	-1.2	0.658	-0.04
1447734_x_at	Aldoa /// LOC6674	aldolase 1, A isoform /// similar to Fructose-bisphosphate aldolase A (Muscle-type	-1.45	0.092	1.18	0.247	1.19	0.131	-1.13	0.268	-0.05
1446071_at	Steap2	six transmembrane epithelial antigen of prostate 2	1.04	0.887	1.19	0.689	-1.21	0.721	-3.37	0.136	-0.59
1433708_at	Srp68	signal recognition particle 68	1.07	0.489	-1.05	0.541	1.04	0.638	-1.09	0.357	-0.01
1458573_at	---	Transcribed locus	1.08	0.649	1.45	0.403	-1.88	0.108	-1.01	0.989	-0.09
1417930_at	Nab2	Ngfi-A binding protein 2	1	0.982	1.19	0.28	-1.15	0.689	-1.69	0.032	-0.16
1427677_a_at	Sox6	SRY-box containing gene 6	-1.01	0.915	-1.24	0.148	1.26	0.322	9.64	0.169	2.16
1422702_at	Azin1	antizyme inhibitor 1	-1.01	0.87	-1.04	0.745	1.11	0.613	2.58	0.192	0.41

1418226_at	Orc2l	origin recognition complex, subunit 2-like (S. cerevisiae)	-1.08	0.538	-1.02	0.905	1.16	0.351	2.45	0.222	0.38
1443806_x_at	Epb4.1l1	Erythrocyte protein band 4.1-like 1	1.36	0.678	1.22	0.719	-2.08	0.147	-2.22	0.258	-0.43
1438161_s_at	Rfc4	replication factor C (activator 1) 4	-1.05	0.533	-1.03	0.761	1.13	0.474	2.3	0.157	0.34
1453405_at	Pla2g4d	phospholipase A2, group IVD	1.05	0.761	-1.11	0.677	1.1	0.793	-1.66	0.046	-0.15
1423117_at	Pum1	pumilio 1 (Drosophila)	-1.04	0.79	-1.2	0.263	1.26	0.264	1.32	0.142	0.09
1420666_at	Doc2b	double C2, beta	-1.01	0.979	-1.64	0.433	1.46	0.218	1.03	0.951	-0.04
1423506_a_at	Nnat	neuronatin	-1.59	0.46	1.52	0.368	-1.1	0.815	1.79	0.375	0.16
1426996_at	AA409316	expressed sequence AA409316	1.26	0.179	-1.06	0.883	-1.16	0.452	1.16	0.804	0.05
1427405_s_at	Rab11fip5	RAB11 family interacting protein 5 (class I)	-1.29	0.325	1.23	0.494	1.06	0.8	-1.14	0.669	-0.04
1449632_s_at	Fkbp10	FK506 binding protein 10	1.14	0.748	1.08	0.896	-1.19	0.692	-1.56	0.346	-0.13
1419076_a_at	Brca2	breast cancer 2	-1.24	0.103	-1.01	0.958	1.26	0.401	3.08	0.229	0.52
1424621_at	AA792894	EST AA792894	-1.04	0.732	1.06	0.615	1.04	0.707	-1.06	0.759	0
1447301_at	Akap5	A kinase (PRKA) anchor protein 5	1.29	0.386	1.11	0.893	-1.53	0.003	-2.63	0.057	-0.44
1432038_at	4930509J09Rik	RIKEN cDNA 4930509J09 gene	-1.41	0.652	1.02	0.942	1.34	0.285	-1.66	0.025	-0.18
1437194_x_at	1200011O22Rik	RIKEN cDNA 1200011O22 gene	-1.04	0.62	-1.25	0.048	1.3	0.007	1.18	0.44	0.05
1424936_a_at	Dnahc8	dynein, axonemal, heavy chain 8	1.1	0.506	1.46	0.331	-1.97	0.065	-1	0.983	-0.11
1426819_at	Hipk3	homeodomain interacting protein kinase 3	1.03	0.731	1.22	0.039	-1.23	0.131	-1.26	0.23	-0.06
1436645_a_at	Cnot4	CCR4-NOT transcription complex, subunit 4	-1.04	0.76	1.17	0.462	-1.07	0.522	1.08	0.793	0.03
1458163_at	BC066028	cDNA sequence BC066028	-1.15	0.741	1.07	0.828	1.12	0.805	-1.08	0.564	-0.01
1422302_s_at	Ftl1 /// Ftl2 /// LOC5	ferritin light chain 1 /// ferritin light chain 2 /// similar to Ferritin light chain 1 (Ferriti	-1.03	0.871	1.05	0.699	1.04	0.671	-1.07	0.413	0
1453202_at	E330016A19Rik	RIKEN cDNA E330016A19 gene	1.4	0.59	-1.27	0.532	-1.14	0.665	1.35	0.352	0.08
1417283_at	Lynx1	Ly6/neurotoxin 1	-1.18	0.07	1.06	0.884	1.15	0.308	-2.21	0.04	-0.3
1434124_x_at	2400001E08Rik	RIKEN cDNA 2400001E08 gene	1.02	0.822	1.14	0.265	-1.11	0.386	-1.05	0.756	0
1446639_at	---	---	1.31	0.133	1.06	0.843	-1.44	0.463	-1.5	0.59	-0.14
1442760_x_at	Rtn4	Reticulon 4	1.27	0.407	1.19	0.684	-1.66	0.061	-1.29	0.321	-0.12
1454642_a_at	Commd3	COMM domain containing 3	-1.11	0.572	1.09	0.193	1.07	0.742	-1.01	0.965	0.01
1456159_at	Setd5	SET domain containing 5	1.29	0.15	1.15	0.531	-1.59	0.188	-1.54	0.29	-0.18
1448444_at	---	---	1.26	0.008	-1.01	0.97	-1.23	0.535	1.17	0.592	0.05
1439932_at	3110003A22Rik	RIKEN cDNA 3110003A22 gene	-1.11	0.795	1.29	0.288	-1.15	0.301	1.27	0.452	0.08
1453766_a_at	4931407K02Rik	RIKEN cDNA 4931407K02 gene	-1.2	0.78	-1.44	0.509	1.53	0.228	1.22	0.805	0.03
1417015_at	Rassf3	Ras association (RalGDS/AF-6) domain family 3	-2.04	0.327	1.27	0.598	1.31	0.601	-1.21	0.166	-0.17
1415909_at	Stip1	stress-induced phosphoprotein 1	1.01	0.959	-1.04	0.514	1.1	0.693	-1.05	0.856	0
1441948_x_at	Zfand3	zinc finger, AN1-type domain 3	-1.04	0.867	1.05	0.722	1.05	0.781	-1.45	0.308	-0.1
1436961_at	Hspa12a	heat shock protein 12A	-1.07	0.868	1.03	0.91	1.1	0.712	-1.01	0.975	0.01
1423685_at	Aars	alanyl-tRNA synthetase	-1.04	0.626	-1.07	0.484	1.17	0.409	1.8	0.066	0.21
1454741_s_at	Tmem164	transmembrane protein 164	-1.06	0.323	-1.02	0.733	1.14	0.377	1.19	0.131	0.06
1447557_at	Rabif	RAB interacting factor	-1.33	0.284	1.08	0.887	1.23	0.483	-1.41	0.107	-0.11
1433596_at	Dnajc6	DnaJ (Hsp40) homolog, subfamily C, member 6	-1.05	0.77	1.24	0.528	-1.15	0.59	1.44	0.291	0.12
1427161_at	Cenpf	centromere protein F	-1.66	0.435	1.51	0.313	-1.05	0.813	5.39	0.158	1.05
1428122_s_at	2610528K11Rik	RIKEN cDNA 2610528K11 gene	-1.29	0.148	1.34	0.358	-1.06	0.613	1.91	0.222	0.23
1438685_at	Zmym6	zinc finger, MYM-type 6	1.08	0.684	1.14	0.209	-1.19	0.462	-1.46	0.29	-0.11
1437484_at	Zbtb5	zinc finger and BTB domain containing 5	-1.12	0.648	1.19	0.499	-1.02	0.88	1.02	0.95	0.02
1428509_at	Myo1e	myosin IE	1.16	0.435	-1.81	0.131	1.35	0.299	-1.17	0.698	-0.12
1431684_at	4933402J24Rik	RIKEN cDNA 4933402J24 gene	-1.42	0.141	-1.29	0.609	1.58	0.323	1.16	0.302	0.01
1439764_s_at	Igf2bp2	insulin-like growth factor 2 mRNA binding protein 2	1.05	0.754	1.4	0.23	-1.61	0.056	-1.02	0.925	-0.05
1415807_s_at	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	-1.18	0.428	-1.15	0.291	1.34	0.118	1.65	0.209	0.17
1433553_at	Garnl3	GTPase activating RANGAP domain-like 3	-1.37	0.504	1.11	0.803	1.22	0.501	-3.26	0.228	-0.57
1434675_at	1700065O13Rik	RIKEN cDNA 1700065O13 gene	1.1	0.035	1.23	0.219	-1.36	0.304	-1.04	0.71	-0.02
1439085_at	C130039O16Rik	RIKEN cDNA C130039O16 gene	-2.31	0.498	1.78	0.167	-1.18	0.73	1.37	0.709	-0.08
1452098_at	Chtf18	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	-1.54	0.223	-1.4	0.364	1.7	0.187	2.82	0.19	0.39
1458676_at	Nktr	natural killer tumor recognition sequence	1.17	0.69	-1.27	0.424	1.11	0.857	-1.12	0.843	-0.03
1454933_at	2610027C15Rik	RIKEN cDNA 2610027C15 gene	1.11	0.644	1.28	0.096	-1.49	0.012	-1.46	0.169	-0.14
1421141_a_at	Foxp1	forkhead box P1	1.21	0.618	-1.36	0.368	1.12	0.691	-1.47	0.388	-0.12

1416513_at	Lamb2	laminin, beta 2	1.08	0.646	-1.27	0.261	1.19	0.585	-1.1	0.729	-0.02
1456450_at	Ctns	Cystinosis, nephropathic	1.09	0.683	1.1	0.693	-1.15	0.724	-1.12	0.569	-0.02
1425277_at	Slit1	slit homolog 1 (Drosophila)	1.05	0.696	1.04	0.813	-1.03	0.944	-1.48	0.388	-0.11
1436533_at	Trove2	TROVE domain family, member 2	-1.06	0.578	1.28	0.039	-1.18	0.376	1.11	0.572	0.04
1452123_s_at	Frmd4b	FERM domain containing 4B	-1.25	0.635	1.31	0.173	-1.05	0.759	1.14	0.754	0.04
1443813_x_at	Bckdk	branched chain ketoacid dehydrogenase kinase	1.12	0.573	1.22	0.727	-1.38	0.138	-1.08	0.898	-0.03
1421072_at	Irx5	Iroquois related homeobox 5 (Drosophila)	1.05	0.539	1.09	0.786	-1.08	0.456	-1.07	0.749	0
1455241_at	BC037703	cDNA sequence BC037703	1.08	0.819	1.01	0.983	-1.02	0.966	-1.21	0.581	-0.04
1422881_s_at	Sypl	synaptophysin-like protein	-1.06	0.785	1.12	0.155	1.01	0.966	-1.32	0.265	-0.06
1419369_at	Rnf138	ring finger protein 138	1.16	0.164	1.03	0.794	-1.14	0.135	-1.34	0.191	-0.07
1459021_at	---	Transcribed locus	-1.05	0.867	1.34	0.276	-1.29	0.363	1.15	0.513	0.04
1444802_at	Sec22a	SEC22 vesicle trafficking protein-like A (S. cerevisiae)	1.84	0.317	-1.29	0.629	-2.23	0.049	1.56	0.252	-0.03
1419690_at	2610002M06Rik	RIKEN cDNA 2610002M06 gene	-1.3	0.106	-1.19	0.144	1.45	0.065	1.85	0.139	0.2
1422186_s_at	Cyb5r3	cytochrome b5 reductase 3	1.28	0.161	-1.2	0.363	-1.06	0.585	1.39	0.01	0.1
1416353_at	Nr1h2	nuclear receptor subfamily 1, group H, member 2	-1.03	0.891	1.04	0.612	1.06	0.472	-1.08	0.351	-0.01
1432599_at	2610301H18Rik	RIKEN cDNA 2610301H18 gene	1.54	0.676	-1.41	0.458	-1.22	0.722	2.08	0.113	0.25
1443889_at	9030619P08Rik	RIKEN cDNA 9030619P08 gene	1.14	0.325	-1.81	0.007	1.37	0.309	-1.07	0.718	-0.09
1441117_at	Ash1l	Ash1 (absent, small, or homeotic)-like (Drosophila)	1.23	0.305	1.19	0.299	-1.56	0.072	-1.17	0.44	-0.08
1460463_at	4632413I24Rik	RIKEN cDNA 4632413I24 gene	-1.31	0.232	1.34	0.343	-1.05	0.841	1.01	0.99	0
1417365_a_at	Calm1	calmodulin 1	1.16	0.582	1.13	0.126	-1.29	0.066	-1.25	0.472	-0.06
1452773_at	5730494N06Rik	RIKEN cDNA 5730494N06 gene	-1.01	0.717	1.01	0.728	1.06	0.448	-1.18	0.238	-0.03
1433558_at	Dab2ip	disabled homolog 2 (Drosophila) interacting protein	-1.06	0.631	1.04	0.614	1.08	0.697	-1.17	0.638	-0.03
1417608_a_at	Rpl13a	ribosomal protein L13a	1.05	0.71	1.1	0.266	-1.09	0.29	-1.28	0.01	-0.06
1424656_s_at	Usp19	ubiquitin specific peptidase 19	-1.08	0.359	-1.17	0.046	1.29	0.008	1.06	0.769	0.02
1459534_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930028F22 product	1.25	0.759	-2.5	0.118	1.41	0.257	-1.21	0.5	-0.26
1460724_at	Ap2a1	adaptor protein complex AP-2, alpha 1 subunit	-1.06	0.791	-1.04	0.77	1.16	0.549	1.54	0.282	0.15
1454517_at	C030011I16Rik	RIKEN cDNA C030011I16 gene	-3.18	0.232	1.76	0.156	-1.01	0.977	1.38	0.547	-0.26
1445125_at	D8Ertd107e	DNA segment, Chr 8, ERATO Doi 107, expressed	-1.16	0.724	-1.07	0.903	1.26	0.614	1.35	0.272	0.1
1444788_x_at	Chd1	Chromodomain helicase DNA binding protein 1	1.1	0.793	1.29	0.131	-1.49	0.04	-1.11	0.367	-0.05
1454072_at	4731417B20Rik	RIKEN cDNA 4731417B20 gene	-1.14	0.179	1.15	0.491	1.04	0.783	-1.25	0.087	-0.05
1458063_at	4930518F22Rik	RIKEN cDNA 4930518F22 gene	-1.13	0.883	1.9	0.333	-3.55	0.141	2.26	0.087	-0.13
1423728_at	Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	-1.05	0.302	-1.03	0.559	1.14	0.094	1.03	0.76	0.02
1451632_a_at	Igh-1a	immunoglobulin heavy chain 1a (serum IgG2a)	-1.32	0.635	-1.69	0.339	1.71	0.322	1.45	0.262	0.04
1426393_a_at	Sdf4	stromal cell derived factor 4	1.08	0.102	-1.02	0.461	1.01	0.9	-1.2	0.269	-0.03
1438312_s_at	Ltbp3	latent transforming growth factor beta binding protein 3	1.08	0.676	1.29	0.209	-1.45	0.039	-1.07	0.41	-0.04
1424312_at	Adipor1	adiponectin receptor 1	-1.07	0.407	-1.01	0.896	1.14	0.564	3.12	0.249	0.54
1431436_a_at	Katnal2	katanin p60 subunit A-like 2	-1.67	0.498	1.38	0.415	1.09	0.672	-2.18	0.381	-0.34
1435861_at	Ppfia1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	-1.05	0.803	-1.91	0.199	1.59	0.316	1.23	0.74	-0.03
1422615_at	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	1.04	0.862	-1.09	0.784	1.1	0.604	-1.9	0.11	-0.21
1450712_at	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	1.43	0.091	-1.48	0.505	-1.04	0.755	2.71	0.259	0.41
1417374_at	Tuba4	tubulin, alpha 4	-1.18	0.204	-1.22	0.12	1.4	0.207	2.45	0.253	0.36
1439303_at	Negr1	Neuronal growth regulator 1	1.27	0.617	1.32	0.662	-2.08	0.114	-1.02	0.969	-0.13
1459770_at	Taok1	TAO kinase 1	1.55	0.644	-1.83	0.26	-1.03	0.867	1.9	0.174	0.15
1450958_at	Tm4sf1	transmembrane 4 superfamily member 1	1.04	0.24	1.11	0.619	-1.09	0.457	-1.1	0.663	-0.01
1460561_x_at	Sepw1	selenoprotein W, muscle 1	1.18	0.156	1.11	0.014	-1.3	0.03	-1.32	0.286	-0.08
1448500_a_at	Lime1	Lck interacting transmembrane adaptor 1	-1.16	0.068	1.05	0.863	1.15	0.329	-1.3	0.476	-0.06
1422769_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	-1.13	0.237	-1.05	0.863	1.23	0.392	1.03	0.955	0.02
1446927_at	Dock9	Dedicator of cytokinesis 9	1.07	0.811	1.55	0.389	-2.25	0.046	-1.42	0.279	-0.26
1424425_a_at	Mtap	methylthioadenosine phosphorylase	1.04	0.563	-1.17	0.092	1.17	0.234	-1.2	0.308	-0.04
1460718_s_at	Mtch1	mitochondrial carrier homolog 1 (C. elegans)	1.1	0.59	1.08	0.525	-1.13	0.144	-1.23	0.274	-0.04
1452093_at	2500001K11Rik	RIKEN cDNA 2500001K11 gene	-1.07	0.187	1.03	0.774	1.1	0.533	-1.56	0.088	-0.12
1426567_a_at	Pqlc1	PQ loop repeat containing 1	1.2	0.37	-1.12	0.511	-1.03	0.761	2.6	0.222	0.41
1452134_at	3010001K23Rik	RIKEN cDNA 3010001K23 gene	1.04	0.869	1.08	0.765	-1.06	0.71	-1.26	0.334	-0.05

1428796_at	5530401J07Rik	RIKEN cDNA 5530401J07 gene	1.01	0.659	1.23	0.35	-1.21	0.176	-1.11	0.676	-0.02
1423526_at	Arid3b	AT rich interactive domain 3B (Bright like)	1.04	0.926	-1.07	0.849	1.1	0.7	-1.65	0.186	-0.15
1460288_a_at	Ppp4c	protein phosphatase 4, catalytic subunit	-1.05	0.883	1.03	0.87	1.09	0.707	-1.17	0.561	-0.03
1441423_at	Ece1	endothelin converting enzyme 1	1.34	0.606	1.09	0.736	-1.56	0.124	-1.18	0.711	-0.08
1441693_at	Adamts3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	-1.08	0.578	1.56	0.187	-1.72	0.036	1.89	0.249	0.16
1460167_at	Aldh7a1	aldehyde dehydrogenase family 7, member A1	-1.1	0.478	-1.11	0.299	1.25	0.162	1.05	0.217	0.03
1452629_at	Safb2	scaffold attachment factor B2	-1.04	0.841	-1.14	0.055	1.23	0.311	1.02	0.921	0.02
1446387_at	---	---	1.71	0.555	-1.52	0.417	-1.43	0.015	1.09	0.638	-0.04
1449764_x_at	Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	1.52	0.63	-1.27	0.783	-1.32	0.607	1.05	0.92	0
1434087_at	Mthfr	5,10-methylenetetrahydrofolate reductase	-1.26	0.455	1.04	0.901	1.23	0.163	-1	0.996	0
1417181_a_at	Kifap3	kinesin-associated protein 3	1.03	0.79	1.31	0.117	-1.38	0.238	-1.12	0.311	-0.04
1426236_a_at	Glul	glutamate-ammonia ligase (glutamine synthetase)	1.07	0.732	-1.07	0.605	1.07	0.754	-1.01	0.969	0.01
1449183_at	Comt	catechol-O-methyltransferase	-1.05	0.891	-1.06	0.65	1.17	0.346	1.73	0.069	0.2
1416510_at	Mrpl4	mitochondrial ribosomal protein L4	-1.04	0.888	1.01	0.954	1.1	0.249	-1.06	0.568	0
1428202_at	1810037C20Rik	RIKEN cDNA 1810037C20 gene	-1.05	0.738	1.06	0.511	1.05	0.346	-1.07	0.619	0
1440411_at	---	Transcribed locus	-1.14	0.291	1.47	0.536	-1.4	0.095	1.05	0.947	0
1429395_at	Gstcd	glutathione S-transferase, C-terminal domain containing	-1.03	0.673	-1.22	0.294	1.28	0.234	1.18	0.394	0.05
1446839_at	Odz4	Odd Oz/ten-m homolog 4 (Drosophila)	-1	0.997	1.09	0.743	-1.02	0.964	1.4	0.508	0.12
1457940_at	Rps17	Ribosomal protein S17	-1.56	0.549	-1.26	0.679	1.63	0.192	1.42	0.648	0.06
1452215_at	9130401M01Rik	RIKEN cDNA 9130401M01 gene	-1.24	0.244	1.17	0.224	1.09	0.542	-1.19	0.358	-0.04
1429655_at	Nudcd1	NudC domain containing 1	-1.17	0.767	-1.17	0.629	1.36	0.07	1.42	0.229	0.11
1416719_a_at	Rps10 /// LOC6217	ribosomal protein S10 /// similar to ribosomal protein S10 /// similar to ribosomal p	1.06	0.576	1.08	0.264	-1.08	0.46	-1.28	0.072	-0.05
1423755_at	Zcchc8	zinc finger, CCHC domain containing 8	-1.06	0.602	1.16	0.423	-1.04	0.853	1.12	0.585	0.05
1420714_at	Lbx2	ladybird homeobox homolog 2 (Drosophila)	-1.57	0.07	1.27	0.413	1.16	0.401	-1.28	0.271	-0.11
1442428_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	1.33	0.401	-2.3	0.194	1.3	0.661	-1.14	0.795	-0.2
1424470_a_at	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	-1.05	0.283	-1.1	0.542	1.21	0.277	1.23	0.416	0.07
1441343_at	---	---	-1.02	0.968	1.01	0.965	1.08	0.9	-1.39	0.355	-0.08
1437101_at	Lats2	large tumor suppressor 2	1.02	0.828	-1.08	0.646	1.12	0.592	-1.26	0.062	-0.05
1451380_at	Zfyve19	zinc finger, FYVE domain containing 19	-1.05	0.644	1.16	0.119	-1.05	0.765	1.04	0.762	0.03
1454743_at	Nup205	nucleoporin 205	-1.01	0.921	1.1	0.236	-1.02	0.889	1.03	0.698	0.02
1421688_a_at	Ccl1	chemokine (C-C motif) ligand 1	-1.35	0.128	1.33	0.635	-1	0.996	3.55	0.02	0.63
1431598_a_at	Lhx9	LIM homeobox protein 9	-1.31	0.567	1.21	0.634	1.09	0.798	-1.7	0.302	-0.18
1431100_at	9930116N10Rik	RIKEN cDNA 9930116N10 gene	-1.11	0.129	1.13	0.501	1.04	0.791	-1.21	0.537	-0.04
1431644_a_at	Ica1	islet cell autoantigen 1	-1.03	0.869	1.14	0.677	-1.05	0.879	1.39	0.456	0.11
1434937_at	Phr1	pam, highwire, rpm 1	-1.08	0.606	1.09	0.18	1.06	0.542	-1.76	0.165	-0.18
1448838_at	Topors	topoisomerase I binding, arginine/serine-rich	1.05	0.876	1.12	0.502	-1.11	0.216	-1.09	0.543	-0.01
1423386_at	Psmd9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	-1.04	0.768	-1.12	0.464	1.21	0.257	1.83	0.094	0.22
1452697_at	Ctdp1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase,	1.15	0.07	-1.05	0.741	-1.04	0.84	1.34	0.003	0.1
1435800_a_at	Csda	cold shock domain protein A	-1.1	0.382	-1.06	0.701	1.22	0.235	1.99	0.154	0.26
1445226_at	BC023969	cDNA sequence BC023969	1.24	0.613	-1.2	0.753	-1	0.992	1.6	0.261	0.16
1441598_at	Tmeff2	transmembrane protein with EGF-like and two follistatin-like domains 2	1.22	0.523	1.16	0.429	-1.45	0.021	-2.3	0.388	-0.34
1435213_at	Nhlrc1	NHL repeat containing 1	-1.07	0.63	1.19	0.374	-1.06	0.818	1.03	0.869	0.02
1435049_s_at	AI854703	expressed sequence AI854703	-1	0.992	-2.72	0.016	1.7	0.373	1.66	0.548	-0.09
1425130_a_at	Ptpn5	protein tyrosine phosphatase, non-receptor type 5	1.74	0.308	-1.75	0.465	-1.31	0.675	1.04	0.831	-0.07
1460164_at	Spin	spindlin	1.06	0.443	-1.1	0.693	1.1	0.54	-1.28	0.297	-0.05
1423508_at	Myst4	MYST histone acetyltransferase monocytic leukemia 4	-1.05	0.665	1.11	0.324	1.01	0.89	-1.47	0.185	-0.1
1438998_at	Rasa1	RAS p21 protein activator 1	1.19	0.463	1.27	0.691	-1.64	0.121	-1.25	0.678	-0.11
1424327_at	3200002M19Rik	RIKEN cDNA 3200002M19 gene	-1.21	0.004	1.18	0.23	1.06	0.615	-1.14	0.2	-0.03
1452033_at	Gle1l	GLE1 RNA export mediator-like (yeast	1.11	0.111	-1.01	0.897	-1.03	0.869	1.07	0.675	0.03
1447228_at	1110051M20Rik	RIKEN cDNA 1110051M20 gene	-2	0.093	-1.11	0.213	1.67	0.125	1.37	0.354	-0.02
1415770_at	Wdr6	WD repeat domain 6	1.14	0.548	-1.36	0.145	1.2	0.53	-1.4	0.429	-0.11
1433832_at	Unc84b	unc-84 homolog B (C. elegans)	1.02	0.862	-1.28	0.173	1.27	0.174	-1.29	0.208	-0.07
1455411_at	Aqp11	aquaporin 11	1.19	0.588	-1.05	0.625	-1.08	0.825	1.39	0.441	0.11

1451763_at	Cnga1	cyclic nucleotide gated channel alpha 1	1.06	0.608	1.35	0.577	-1.53	0.397	-3.41	0.012	-0.63
1433599_at	Baz1a	bromodomain adjacent to zinc finger domain 1A	-1.24	0.461	1.08	0.571	1.18	0.332	-1.11	0.199	-0.02
1441979_at	BC060267	cDNA sequence BC060267	-1.03	0.913	-1.05	0.522	1.14	0.41	1.18	0.748	0.06
1424732_s_at	3110005G23Rik	RIKEN cDNA 3110005G23 gene	1.02	0.719	-1.1	0.381	1.14	0.195	-1.26	0.351	-0.05
1426751_s_at	Nup107	nucleoporin 107	-1.03	0.886	-1.01	0.973	1.1	0.132	1.25	0.405	0.08
1448378_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	-1.27	0.429	1.04	0.886	1.24	0.41	-1.54	0.044	-0.13
1416556_at	Tspan31	tetraspanin 31	1.1	0.538	-1.05	0.411	1.02	0.875	-1.05	0.696	0
1426848_at	Sec24b	SEC24 related gene family, member B (S. cerevisiae)	-1.04	0.864	-1.09	0.134	1.19	0.006	1.05	0.304	0.03
1427156_s_at	Ascc2	activating signal cointegrator 1 complex subunit 2	-1.1	0.535	1.13	0.216	1.03	0.718	-1.24	0.094	-0.05
1451988_s_at	Chmp4b	chromatin modifying protein 4B	-1.07	0.631	1.11	0.176	1.03	0.84	-1.09	0.61	-0.01
1438459_x_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associat	-1.04	0.874	1.06	0.793	1.05	0.822	-1.19	0.188	-0.03
1455971_at	2810032E02Rik	RIKEN cDNA 2810032E02 gene	1.47	0.505	1.04	0.95	-1.78	0.27	-1.01	0.984	-0.07
1447485_at	Gpr150	G protein-coupled receptor 150	1.61	0.252	-1.38	0.678	-1.35	0.348	6.17	0.301	1.26
1422784_at	Krt6a	keratin 6A	1.25	0.422	-1.31	0.294	1.06	0.887	-1.84	0.192	-0.21
1435110_at	Unc5b	unc-5 homolog B (C. elegans)	-1.11	0.296	1.08	0.627	1.09	0.501	-1.17	0.424	-0.03
1444719_at	D7Mgi29	DNA Segment, Chr 7, Mouse Genome Informatics 29	-2.21	0.339	1.13	0.854	1.49	0.505	-2.48	0.118	-0.52
1454611_a_at	Calm1	calmodulin 1	1.04	0.749	1.23	0.027	-1.24	0.153	-1.24	0.42	-0.05
1452865_at	Lrrc27	leucine rich repeat containing 27	-1.66	0.385	1.59	0.251	-1.13	0.591	1.15	0.867	-0.01
1422895_at	Vamp4	vesicle-associated membrane protein 4	1.03	0.185	1.1	0.209	-1.07	0.453	-1.57	0.119	-0.12
1459659_at	---	PREDICTED: Mus musculus hypothetical protein LOC623278 (LOC623278), mR	1.23	0.419	-1.33	0.687	1.09	0.826	-1.17	0.411	-0.04
1418791_at	Sh3gl2	SH3-domain GRB2-like 2	1.15	0.525	1.13	0.79	-1.26	0.477	-2.07	0.137	-0.26
1422578_at	Cs	citrate synthase	-1.01	0.926	-1.32	0.063	1.33	0.168	1.26	0.074	0.06
1418302_at	Ppt2	palmitoyl-protein thioesterase 2	-1.11	0.504	-1.08	0.516	1.24	0.469	1.15	0.268	0.05
1444374_at	---	PREDICTED: Mus musculus hypothetical LOC381451 (LOC381451), mRNA	1.25	0.756	1.3	0.419	-1.9	0.186	-1.07	0.621	-0.11
1439969_at	4930500O05Rik	RIKEN cDNA 4930500O05 gene	1.17	0.114	-1.18	0.591	1.05	0.662	-1.02	0.919	0.01
1452072_at	Myct1	myc target 1	-1.18	0.644	1.28	0.412	-1.07	0.834	1.33	0.567	0.09
1430635_at	Mlana	melan-A	-1.06	0.767	1.15	0.439	-1.02	0.961	1.05	0.774	0.03
1435412_at	1700007E06Rik	RIKEN cDNA 1700007E06 gene	1.3	0.703	1.14	0.831	-1.59	0.174	-1.06	0.351	-0.05
1430805_s_at	Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	1.05	0.886	1.06	0.373	-1.04	0.871	-1.18	0.355	-0.03
1456158_at	---	---	-3.62	0.054	1.33	0.473	1.46	0.195	-1.04	0.883	-0.46
1434436_at	Morc4	microrchidia 4	-1.1	0.673	1.05	0.903	1.11	0.707	-1.17	0.368	-0.03
1438542_at	---	---	-1.03	0.936	1.1	0.774	1.01	0.983	-1.19	0.699	-0.03
1433925_at	Dync1li2	dynein, cytoplasmic 1 light intermediate chain 2	1.01	0.94	1.17	0.328	-1.12	0.534	-1.02	0.928	0.01
1455609_at	C030025P15Rik	RIKEN cDNA C030025P15 gene	-1.47	0.11	-1.1	0.76	1.48	0.057	4.44	0.16	0.84
1437304_at	Cblb	Casitas B-lineage lymphoma b	-1.1	0.35	1.02	0.781	1.14	0.433	-1.23	0.471	-0.04
1434790_a_at	Lta4h	leukotriene A4 hydrolase	-1.15	0.02	1.01	0.755	1.19	0.127	-1.07	0.501	0
1415955_x_at	Prm1	protamine 1	-1.21	0.493	-1.05	0.894	1.3	0.114	1.01	0.94	0.01
1425859_a_at	Psmd4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	-1.04	0.707	-1.18	0.094	1.26	0.298	1.19	0.55	0.06
1438236_at	Nfia	nuclear factor I/A	1.42	0.402	-1.1	0.599	-1.35	0.177	1.4	0.486	0.09
1422004_at	D730048I06Rik	RIKEN cDNA D730048I06 gene	-1.12	0.827	1.77	0.03	-2.47	0.02	1.24	0.498	-0.14
1421113_at	Pga5	pepsinogen 5, group I	1.18	0.301	-1.03	0.873	-1.08	0.808	1.35	0.182	0.1
1433860_at	6030458C11Rik	RIKEN cDNA 6030458C11 gene	-1.07	0.531	-1.09	0.18	1.22	0.047	1.63	0.115	0.17
1429980_x_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	1.11	0.211	1.01	0.973	-1.05	0.827	-1.32	0.503	-0.06
1454659_at	Dctd	dCMP deaminase	1.09	0.311	-1.01	0.973	-1.01	0.966	1.64	0.146	0.18
1427008_at	Rnf43	ring finger protein 43	1.14	0.688	1.03	0.937	-1.11	0.734	-1.05	0.827	0
1446797_at	A330075M08Rik	RIKEN cDNA A330075M08 gene	1.03	0.971	1.71	0.199	-2.96	0.035	-1.21	0.614	-0.36
1437741_at	Rab21	RAB21, member RAS oncogene family	-1	0.995	1.01	0.881	1.06	0.661	-1.27	0.17	-0.05
1428621_a_at	Vps25	vacuolar protein sorting 25 (yeast)	1	0.977	-1.08	0.527	1.14	0.485	-1.02	0.754	0.01
1442697_at	---	---	1.34	0.462	-1.16	0.051	-1.15	0.645	1.03	0.857	0.01
AFFX-BioDn-3_at	---	---	1.18	0.202	1.06	0.562	-1.2	0.447	-1.05	0.793	0
1428265_at	Ppp2r1b	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	-1.08	0.311	-1.06	0.59	1.2	0.23	2.56	0.201	0.41
1441416_at	Inpp4b	inositol polyphosphate-4-phosphatase, type II	-1.09	0.761	1.01	0.984	1.14	0.736	-1.41	0.16	-0.09
1417581_at	Dhodh	dihydroorotate dehydrogenase	1.03	0.913	-1.23	0.409	1.23	0.228	-1.21	0.354	-0.05

1437127_at	A630033E08Rik	RIKEN cDNA A630033E08 gene	1.06	0.841	1.15	0.679	-1.17	0.308	-1.32	0.442	-0.07
1423057_at	Capza2	capping protein (actin filament) muscle Z-line, alpha 2	1.08	0.212	1.02	0.854	-1.02	0.859	-1.13	0.591	-0.02
1448784_at	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.07	0.533	-1.02	0.584	1.02	0.913	-1.13	0.441	-0.02
1449189_at	BC003266	cDNA sequence BC003266	1.01	0.897	1.11	0.034	-1.05	0.739	-1.21	0.179	-0.04
1423320_at	Dnase1l2	deoxyribonuclease 1-like 2	-1.29	0.375	1.01	0.966	1.29	0.181	-1.68	0.021	-0.17
1455346_at	Masp1	mannan-binding lectin serine peptidase 1	-1.22	0.597	-1.14	0.703	1.37	0.478	1.27	0.552	0.07
1451226_at	Pex6	peroxisomal biogenesis factor 6	1.02	0.95	-1.13	0.512	1.17	0.315	-1.29	0.151	-0.06
1446745_at	LOC433637	hypothetical LOC433637	-1.06	0.946	1.08	0.895	1.04	0.785	-1.29	0.489	-0.06
1433543_at	Anln	anillin, actin binding protein (scraps homolog, Drosophila)	1.18	0.495	-1.08	0.815	-1.03	0.903	5.99	0.209	1.27
1455117_at	Mcmdc1	minichromosome maintenance deficient domain containing 1	-1.15	0.148	-1.11	0.512	1.3	0.198	1.06	0.761	0.03
1448385_at	Slc15a4	solute carrier family 15, member 4	-1.12	0.36	1.04	0.829	1.14	0.478	-1.67	0.154	-0.15
1450572_at	Akp3	alkaline phosphatase 3, intestine, not Mn requiring	1.37	0.475	-1.21	0.594	-1.14	0.588	2.2	0.052	0.3
1457171_at	---	---	-1.26	0.059	1.39	0.58	-1.12	0.805	1.15	0.781	0.04
1437702_at	Tgm6	transglutaminase 6	-1.18	0.817	1.3	0.48	-1.08	0.904	1.93	0.435	0.24
1426654_at	Zc3hc1	zinc finger, C3HC type 1	-1.34	0.004	-1.04	0.826	1.37	0.017	1.16	0.592	0.04
1422671_s_at	Naalad2	N-acetylated alpha-linked acidic dipeptidase 2	1.23	0.305	1.35	0.19	-2.02	0.014	-1.08	0.85	-0.13
1440859_at	Akap6	A kinase (PRKA) anchor protein 6	-1.07	0.761	1.17	0.647	-1.03	0.84	1.28	0.264	0.09
1429260_at	1810014B01Rik	RIKEN cDNA 1810014B01 gene	1.13	0.56	-1.09	0.533	1.02	0.806	-1.13	0.369	-0.01
1418356_at	Mpst	mercaptopyruvate sulfurtransferase	-1.31	0.512	-1.59	0.214	1.68	0.141	2.41	0.313	0.3
1437915_at	Tom1l2	target of myb1-like 2 (chicken)	1.22	0.019	-1.02	0.92	-1.14	0.53	1.04	0.901	0.02
1425202_a_at	Ank3	ankyrin 3, epithelial	-1.15	0.226	-1.1	0.334	1.3	0.276	1.26	0.485	0.08
1424739_at	4932432K03Rik	RIKEN cDNA 4932432K03 gene	-1.14	0.46	-1.1	0.665	1.29	0.653	1.8	0.219	0.21
1424989_at	Tmem142a	transmembrane protein 142A	1.01	0.963	1.1	0.713	-1.04	0.698	-1.32	0.438	-0.06
1418073_at	Acot9	acyl-CoA thioesterase 9	1.06	0.431	1.16	0.183	-1.17	0.128	-1.29	0.064	-0.06
1448242_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	-1.11	0.592	1.22	0.122	-1.05	0.539	1.15	0.467	0.05
1455889_at	Mlstd1	male sterility domain containing 1	1.06	0.898	1.29	0.531	-1.38	0.223	-1	0.988	-0.01
1452253_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	1.05	0.909	1.06	0.85	-1.03	0.897	-1.25	0.433	-0.04
1453314_x_at	2610039C10Rik	RIKEN cDNA 2610039C10 gene	1.07	0.731	1.22	0.114	-1.27	0.098	-1.07	0.598	-0.01
1425898_x_at	Olfm3	olfactomedin 3	-1.36	0.196	1.72	0.132	-1.61	0.294	2.19	0.08	0.24
1419564_at	Zfp467	zinc finger protein 467	1.06	0.602	-1.16	0.513	1.15	0.763	-1.31	0.162	-0.06
1427375_at	Rg9mtd2	RNA (guanine-9-) methyltransferase domain containing 2	-1.11	0.538	-1.05	0.863	1.22	0.063	1.18	0.653	0.06
1418160_at	Mkrn3	makorin, ring finger protein, 3	1.57	0.407	-1.21	0.754	-1.46	0.283	2.95	0	0.46
1417927_at	Ddx19a	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19a	-1.09	0.662	-1.04	0.744	1.2	0.157	1.26	0.391	0.08
1426984_at	2310067B10Rik	RIKEN cDNA 2310067B10 gene	-1.26	0.525	1.17	0.419	1.11	0.48	-1.14	0.577	-0.03
1425866_a_at	Plekha4	pleckstrin homology domain containing, family A (phosphoinositide binding specif	1.11	0.653	1.12	0.46	-1.18	0.211	-1.29	0.41	-0.06
1454563_at	4930573C08Rik	RIKEN cDNA 4930573C08 gene	1.14	0.506	1.11	0.827	-1.21	0.643	-1.41	0.576	-0.09
1419474_a_at	Ehf	ets homologous factor	1.15	0.396	1.02	0.914	-1.11	0.614	-1.04	0.892	0.01
1436137_at	Slc6a17	solute carrier family 6 (neurotransmitter transporter), member 17	1.01	0.962	-1	0.996	1.07	0.491	-1.4	0.048	-0.08
1430458_at	Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	1.13	0.672	1.15	0.144	-1.24	0.323	-1.55	0.462	-0.13
1433052_at	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	-2.03	0.022	1.37	0.21	1.21	0.407	-1.03	0.959	-0.12
1451115_at	Pias3	protein inhibitor of activated STAT 3	1.14	0.153	-1.15	0.446	1.07	0.689	-1.18	0.325	-0.03
1452032_at	Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	-1.04	0.739	1	0.912	1.11	0.187	-1.3	0.102	-0.06
1425855_a_at	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	1	0.989	-1.21	0.399	1.25	0.644	-1.22	0.667	-0.04
1431655_a_at	Mulk	multiple substrate lipid kinase	1.15	0.848	-1.29	0.411	1.16	0.615	-1.16	0.798	-0.04
1430100_at	Mrps15	mitochondrial ribosomal protein S15	1.01	0.982	1.42	0.562	-1.55	0.517	-1.77	0.59	-0.22
1415911_at	Impact	imprinted and ancient	-1.01	0.881	1.16	0.248	-1.07	0.748	1.07	0.854	0.03
1428604_at	2610305D13Rik	RIKEN cDNA 2610305D13 gene	1.25	0.727	-1.43	0.483	1.13	0.703	-1.33	0.718	-0.1
1457320_at	Wapal	Wings apart-like homolog (Drosophila)	1.68	0.517	-1.59	0.589	-1.31	0.549	6.94	0.142	1.43
1453152_at	Mamdc2	MAM domain containing 2	1.06	0.874	1.22	0.387	-1.25	0.451	-1.18	0.824	-0.04
1457287_at	---	Transcribed locus	-1.05	0.856	1.09	0.133	1.03	0.817	-1.18	0.437	-0.03
1452095_a_at	H47	histocompatibility 47	-1.01	0.897	1.06	0.625	1.03	0.831	-1.17	0.494	-0.02
1418505_at	Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	-1.12	0.303	-1.02	0.815	1.2	0.079	2.93	0.172	0.5
1427197_at	Atr	ataxia telangiectasia and Rad3 related	-1.09	0.686	1	0.931	1.15	0.328	-1.17	0.364	-0.03

1422761_at	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	-1.23	0.274	-1.1	0.903	1.36	0.123	1.03	0.753	0.01
1429032_at	Micalcl	MICAL C-terminal like	-1.31	0.564	1.6	0.157	-1.4	0.186	1.21	0.626	0.03
1418200_at	Hkr3	GLI-Kruppel family member HKR3	1.16	0.271	-1.11	0.485	1.02	0.911	-1.32	0.008	-0.06
1452064_at	Crsp3	cofactor required for Sp1 transcriptional activation, subunit 3	-1.09	0.369	1.06	0.224	1.1	0.504	-1.11	0.126	-0.01
1460456_at	2010316F05Rik	RIKEN cDNA 2010316F05 gene	1	0.962	1.1	0.474	-1.03	0.88	-1.3	0.238	-0.06
1447780_x_at	Tufm /// LOC66983	Tu translation elongation factor, mitochondrial /// similar to Tu translation elongati	-1.16	0.592	-1.16	0.039	1.35	0.029	1.14	0.561	0.04
1457855_at	Rbp3	retinol binding protein 3, interstitial	1.03	0.967	1.23	0.656	-1.23	0.678	-1.63	0.547	-0.15
1445233_at	9130416B15	hypothetical protein 9130416B15	1.06	0.789	1.03	0.951	-1.01	0.98	-1.74	0.119	-0.17
1422474_at	Pde4b	phosphodiesterase 4B, cAMP specific	1.05	0.27	-1.17	0.558	1.17	0.705	-2.43	0.049	-0.34
1416349_at	Mrpl34	mitochondrial ribosomal protein L34	-1.12	0.559	-1.01	0.873	1.2	0.373	1.2	0.268	0.07
1422295_at	Mds1	myelodysplasia syndrome 1 homolog (human)	-1.11	0.794	1.49	0.607	-1.45	0.159	1.57	0.333	0.12
1439360_x_at	D15Ertd785e /// LO	DNA segment, Chr 15, ERATO Doi 785, expressed /// similar to kleisin beta isofo	-1.14	0.009	-1.05	0.465	1.25	0.315	1.22	0.292	0.07
1434645_at	C530008M17Rik	RIKEN cDNA C530008M17 gene	-1.16	0.49	-2.02	0.189	1.72	0.11	5.94	0.174	1.12
1421684_at	2310051M13Rik	RIKEN cDNA 2310051M13 gene	-1.21	0.666	1.17	0.832	1.08	0.855	-1.47	0.527	-0.11
1420307_a_at	Pitpnb	phosphatidylinositol transfer protein, beta	-1.04	0.869	-1.03	0.749	1.14	0.527	1.28	0.495	0.09
1455950_x_at	Rpl35	ribosomal protein L35	1.06	0.098	1.19	0.032	-1.2	0.084	-1.31	0.018	-0.07
1427125_s_at	Lrrc41	leucine rich repeat containing 41	1.11	0.693	1.1	0.54	-1.16	0.511	-1.16	0.573	-0.03
1417294_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	1	1	-1.08	0.666	1.15	0.286	-1.35	0.115	-0.07
1443272_at	Nope	neighbor of Punc E11	-1.49	0.661	1.23	0.389	1.18	0.637	-1.33	0.699	-0.1
1439030_at	Gmppb	GDP-mannose pyrophosphorylase B	1.22	0.321	-1.11	0.674	-1.04	0.498	1.06	0.736	0.03
1419493_a_at	Tpd52	tumor protein D52	-1.11	0.079	1.09	0.46	1.09	0.551	-1.45	0.111	-0.1
1446743_at	Las1l	LAS1-like (S. cerevisiae)	1.11	0.751	-1.43	0.26	1.27	0.25	-1.07	0.704	-0.03
1415757_at	Gbf1	golgi-specific brefeldin A-resistance factor 1	1.07	0.84	-1.1	0.302	1.1	0.442	-1.16	0.681	-0.02
1447967_at	Tmem69	transmembrane protein 69	-1.18	0.75	-1.3	0.568	1.46	0.461	1.27	0.617	0.06
1420656_at	Abcg8	ATP-binding cassette, sub-family G (WHITE), member 8	1.01	0.902	-1.45	0.154	1.39	0.499	-1.44	0.139	-0.12
1439419_at	2310057M21Rik	RIKEN cDNA 2310057M21 gene	1.01	0.984	-1.13	0.846	1.18	0.711	-1.39	0.254	-0.08
1429003_at	Snw1	SNW domain containing 1	1.15	0.233	-1.04	0.747	-1.03	0.907	1.09	0.784	0.04
1427785_x_at	Solh	Small optic lobes homolog (Drosophila)	-1.04	0.567	-1.08	0.311	1.19	0.242	1.04	0.899	0.03
1428528_at	1110007L15Rik	RIKEN cDNA 1110007L15 gene	-1.05	0.692	1.08	0.767	1.05	0.788	-1.05	0.867	0.01
1427566_at	Wfikkn1	WAP, FS, Ig, KU, and NTR-containing protein 1	-1.08	0.931	-1.39	0.311	1.43	0.33	1.72	0.246	0.17
1458644_at	AI661708 /// Gm15(	expressed sequence AI661708 /// gene model 150, (NCBI)	1.2	0.567	1.07	0.749	-1.23	0.559	-2.74	0.042	-0.43
1431567_at	1700018A04Rik	RIKEN cDNA 1700018A04 gene	-1.1	0.873	1.4	0.6	-1.29	0.347	2.36	0.065	0.34
1432116_at	1700031F05Rik	RIKEN cDNA 1700031F05 gene	-1.22	0.721	-1.12	0.768	1.36	0.542	1.08	0.84	0.03
1427831_s_at	Zfp260 /// LOC635(	zinc finger protein 260 /// similar to Zinc finger protein OZF (Zinc finger protein 26	1.11	0.645	-1.26	0.549	1.17	0.693	-1.65	0.342	-0.16
1424336_at	Ppcdc	phosphopantothenoylcysteine decarboxylase	1.09	0.678	-1.25	0.638	1.18	0.378	-1.46	0.425	-0.11
1418081_at	Wbscr18	Williams-Beuren syndrome chromosome region 18 homolog (human)	1.05	0.018	-1.13	0.022	1.15	0.103	-1.07	0.233	0
1460451_at	Tmem52	transmembrane protein 52	-1.8	0.068	-1.47	0.475	1.84	0.269	1.28	0.585	-0.04
1432108_at	Pcgf6	polycomb group ring finger 6	1.16	0.505	1.19	0.617	-1.37	0.217	-1.36	0.492	-0.09
1424024_at	Mcfd2	multiple coagulation factor deficiency 2	1.01	0.892	1.15	0.125	-1.1	0.495	-1.1	0.728	-0.01
1420318_at	LOC626877	Similar to zinc finger protein 709	1.35	0.012	1.05	0.871	-1.48	0.556	-1.43	0.486	-0.13
1424695_at	2010011I20Rik	RIKEN cDNA 2010011I20 gene	-1.07	0.786	-1.17	0.456	1.29	0.376	5.4	0.246	1.11
1441922_x_at	Vps11	vacuolar protein sorting 11 (yeast)	1.34	0.349	-1.64	0.355	1.13	0.488	-1.03	0.938	-0.05
1454811_a_at	Serinc1	serine incorporator 1	-1.05	0.588	-1.12	0.529	1.23	0.345	1.34	0.368	0.1
1431625_at	Pde1a	phosphodiesterase 1A, calmodulin-dependent	-3.57	0.023	-1.18	0.114	1.95	0.199	1.19	0.754	-0.4
1431842_at	4930422C21Rik	RIKEN cDNA 4930422C21 gene	1.14	0.54	-1.18	0.47	1.1	0.773	-1.06	0.909	0
1430934_at	2810043G22Rik	RIKEN cDNA 2810043G22 gene	1.43	0.187	-1.3	0.286	-1.14	0.493	2.53	0.196	0.38
1444755_at	Mad1l1	mitotic arrest deficient 1-like 1	1.06	0.619	1.07	0.885	-1.05	0.599	-1.32	0.691	-0.06
1415944_at	Sdc1	syndecan 1	-1.03	0.959	1.29	0.213	-1.22	0.072	2.06	0.114	0.28
1428207_at	Bcl7a	B-cell CLL/lymphoma 7A	1.05	0.655	-1.25	0.112	1.22	0.063	-1.2	0.331	-0.04
1423395_at	Tsnax	translin-associated factor X	1.08	0.725	1.04	0.227	-1.04	0.775	-1.3	0.131	-0.06
1428657_at	Rreb1	ras responsive element binding protein 1	1.01	0.945	-1.1	0.395	1.17	0.389	-1.28	0.286	-0.05
1450318_a_at	P2ry2	purinergic receptor P2Y, G-protein coupled 2	1.49	0.503	-1.56	0.454	-1.05	0.94	1.59	0.212	0.12
1425543_s_at	Plekha5	pleckstrin homology domain containing, family A member 5	-1.22	0.165	1.03	0.903	1.23	0.501	-1.96	0.218	-0.23

1420165_s_at	Dnajc17	DnaJ (Hsp40) homolog, subfamily C, member 17	1.39	0.261	-2.38	0.082	1.27	0.416	-1.21	0.361	-0.23
1422650_a_at	Riok3	RIO kinase 3 (yeast)	-1.02	0.734	-1.03	0.763	1.13	0.336	1.2	0.461	0.07
1459091_at	---	---	1.13	0.129	1.25	0.727	-1.44	0.321	-1.11	0.746	-0.04
1422135_at	LOC677248	similar to zinc finger protein 146	1.04	0.912	-1.07	0.825	1.11	0.763	-1.02	0.962	0.01
1441846_x_at	Tmed3	Transmembrane emp24 domain containing 3	1.44	0.495	1.05	0.831	-1.69	0.13	-1.65	0.06	-0.21
1423647_a_at	Zdhhc3	zinc finger, DHHC domain containing 3	1.27	0.416	-1.16	0.721	-1.05	0.876	1.38	0.465	0.11
1424117_at	BC056474	cDNA sequence BC056474	-1.06	0.792	-1.18	0.159	1.29	0.22	1.19	0.113	0.06
1436496_at	1700012O15Rik	RIKEN cDNA 1700012O15 gene	-1.22	0.326	1.94	0.067	-3.09	0.019	1.7	0.468	-0.17
1447346_s_at	5530400B01Rik	RIKEN cDNA 5530400B01 gene	-1.46	0.067	-1.42	0.589	1.69	0.301	2.84	0.041	0.41
1436971_x_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	1	0.998	1.15	0.169	-1.08	0.479	-1.34	0.106	-0.07
1450249_s_at	Kif5a /// Kif5c	kinesin family member 5A /// kinesin family member 5C	-1.43	0.428	-1.38	0.264	1.66	0.193	1.56	0.12	0.1
1420690_at	Fgf10	fibroblast growth factor 10	-1.1	0.772	1.48	0.301	-1.44	0.169	1.48	0.167	0.1
1426353_at	Stat6	signal transducer and activator of transcription 6	1.08	0.507	-1.05	0.177	1.05	0.363	-1.85	0.157	-0.19
1437398_a_at	Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	-1.05	0.663	-1.23	0.342	1.31	0.008	1.16	0.041	0.05
1428952_at	Pdia2	protein disulfide isomerase associated 2	1.27	0.566	-1.14	0.827	-1.08	0.634	6.19	0.213	1.31
1420560_at	Chrne	cholinergic receptor, nicotinic, epsilon polypeptide	-1.12	0.498	1.32	0.117	-1.15	0.565	1	0.987	0.01
1428869_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	-1.02	0.899	-1.18	0.357	1.25	0.366	1.41	0.159	0.12
1459126_at	Negr1	Neuronal growth regulator 1	1.24	0.402	-1.06	0.885	-1.11	0.818	1.2	0.146	0.07
1457531_a_at	A930017K11Rik	RIKEN cDNA A930017K11 gene	-1.46	0.008	-1.13	0.769	1.51	0.315	1.56	0.207	0.12
1424657_at	Taok1	TAO kinase 1	1.58	0.522	-1.26	0.485	-1.41	0.33	1.06	0.905	-0.01
1440233_at	A930013B10Rik	RIKEN cDNA A930013B10 gene	-1.23	0.023	1.07	0.872	1.2	0.658	-1.23	0.808	-0.05
1449407_at	Ift81	intraflagellar transport 81 homolog (Chlamydomonas)	1.03	0.825	1.15	0.43	-1.1	0.425	-1.42	0.359	-0.09
1444476_at	D030007L05Rik	RIKEN cDNA D030007L05 gene	1.33	0.717	1.09	0.895	-1.52	0.592	-1.02	0.962	-0.03
1435545_at	BC032203	cDNA sequence BC032203	1.01	0.961	-1.05	0.783	1.13	0.559	-1.2	0.118	-0.03
1415700_a_at	Ssr3	signal sequence receptor, gamma	-1.03	0.671	1.19	0.267	-1.08	0.474	1.18	0.299	0.06
1451002_at	Aco2	aconitase 2, mitochondrial	-1.13	0.315	-1.25	0.186	1.39	0.124	1.25	0.095	0.07
1429493_at	Mettl4	methyltransferase like 4	-1.08	0.547	-1.06	0.696	1.21	0.309	1.16	0.623	0.06
1429915_at	4930426L09Rik	RIKEN cDNA 4930426L09 gene	1.28	0.71	-1.07	0.841	-1.15	0.714	1.05	0.88	0.03
1426701_at	4632419K20Rik	RIKEN cDNA 4632419K20 gene	1.03	0.699	-1.18	0.325	1.2	0.258	-1.07	0.739	0
1451673_at	Cd8a /// LOC63614	CD8 antigen, alpha chain /// similar to T-cell surface glycoprotein CD8 alpha chai	1.04	0.784	-1.62	0.021	1.42	0.21	-1.95	0.213	-0.28
1432397_at	Tssk3	testis-specific serine kinase 3	-1.34	0.407	1.41	0.336	-1.09	0.87	1.09	0.824	0.02
1436094_at	Vgf	VGF nerve growth factor inducible	1.08	0.58	1.05	0.82	-1.05	0.657	-1.52	0.159	-0.11
1424594_at	Lgals7	lectin, galactose binding, soluble 7	1.14	0.039	-1.01	0.957	-1.05	0.738	1.22	0.178	0.08
1434682_at	6430601A21Rik	RIKEN cDNA 6430601A21 gene	1.18	0.27	1.05	0.776	-1.17	0.297	-1.27	0.045	-0.05
1425769_x_at	Cklf	chemokine-like factor	1.04	0.883	1.19	0.423	-1.17	0.354	-1.35	0.515	-0.07
1453073_at	5830403F22Rik	RIKEN cDNA 5830403F22 gene	1.06	0.928	1.18	0.826	-1.18	0.716	-1.8	0.495	-0.19
1456765_at	6430511F03	hypothetical protein 6430511F03	-1	0.983	1.04	0.829	1.04	0.705	-1.09	0.817	0
1423946_at	Pdlim2	PDZ and LIM domain 2	1.05	0.264	1.19	0.479	-1.19	0.045	-1.91	0.072	-0.21
1425070_at	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	1.39	0.288	-1.42	0.204	-1.01	0.94	1.22	0.073	0.04
1424869_at	Dhrs7b	dehydrogenase/reductase (SDR family) member 7B	-1.02	0.759	1.02	0.767	1.08	0.652	-1.29	0.2	-0.05
1423008_at	Art2a	ADP-ribosyltransferase 2a	-2.42	0.227	-1	0.99	1.67	0.405	1.06	0.811	-0.17
1457025_at	4833413O15Rik	RIKEN cDNA 4833413O15 gene	-1.02	0.92	-1.04	0.909	1.15	0.798	2.24	0.011	0.33
1448246_at	Hdac1	histone deacetylase 1	-1.1	0.39	1.14	0.289	1.03	0.844	-1.17	0.395	-0.02
1423038_at	Stx6	syntaxin 6	1.06	0.423	-1.01	0.932	1.03	0.694	-1.13	0.525	-0.01
1448334_a_at	Ccni	cyclin I	-1.01	0.893	1.09	0.172	1.01	0.976	-1.03	0.687	0.01
1448717_at	Gcdh	glutaryl-Coenzyme A dehydrogenase	-1.08	0.666	-1.01	0.865	1.17	0.489	1.53	0.141	0.15
1426006_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	-1.34	0.476	-1.13	0.773	1.45	0.246	1.58	0.361	0.14
1422030_at	Atp6v0a4	ATPase, H+ transporting, lysosomal V0 subunit A4	-1.74	0.444	-1.31	0.592	1.74	0.237	1.01	0.987	-0.07
1423479_at	Nol11	nucleolar protein 11	-1.02	0.859	-1.13	0.519	1.22	0.054	1.05	0.787	0.03
1451687_a_at	Tcf2	transcription factor 2	1.05	0.859	-1.06	0.742	1.08	0.585	-1.07	0.614	0
1426576_at	Tmem23	transmembrane protein 23	-1.08	0.63	-1.03	0.913	1.19	0.52	1.07	0.569	0.04
1422166_at	Clec2i	C-type lectin domain family 2, member i	-1.68	0.072	1.14	0.71	1.35	0.451	-2.1	0.155	-0.32
1452910_at	Bcor	Bcl6 interacting corepressor	-1.34	0.279	1.13	0.673	1.21	0.49	-1.16	0.148	-0.04

1424622_at	Hsf1	heat shock factor 1	1.07	0.566	-1.24	0.051	1.21	0.245	-1.28	0.247	-0.06
1448126_at	Tera	teratocarcinoma expressed, serine rich	1.13	0.084	1.03	0.874	-1.09	0.745	-1.03	0.901	0.01
1434560_at	Wdtc1	WD and tetratricopeptide repeats 1	-1.4	0.107	-1.39	0.368	1.65	0.189	1.52	0.255	0.09
1438427_at	4932442K08Rik	RIKEN cDNA 4932442K08 gene	1.14	0.263	-1.16	0.616	1.08	0.698	-1.76	0.177	-0.17
1427711_a_at	Ceacam1	CEA-related cell adhesion molecule 1	1.19	0.682	-1.54	0.265	1.25	0.723	-1.14	0.666	-0.06
1421911_at	Stat2	signal transducer and activator of transcription 2	-1.33	0.023	1.01	0.941	1.32	0.097	-1.25	0.099	-0.06
1431361_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	-1.16	0.688	1.31	0.351	-1.09	0.754	1.4	0.211	0.11
1449324_at	Ero1l	ERO1-like (S. cerevisiae)	-1	0.986	1.12	0.353	-1.04	0.68	1.38	0.295	0.12
1437051_at	Dffb	DNA fragmentation factor, beta subunit	1.08	0.819	1.2	0.45	-1.25	0.267	-1.24	0.062	-0.05
1451819_at	Zswim6	zinc finger, SWIM domain containing 6	-1.31	0.372	1.09	0.807	1.23	0.469	-2.45	0.13	-0.36
1416792_at	Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	-1.02	0.313	-1.1	0.444	1.2	0.204	1.75	0.132	0.21
1422136_at	Uhmk1 /// LOC677	U2AF homology motif (UHM) kinase 1 /// similar to U2AF homology motif (UHM) k	-1.27	0.103	1.01	0.986	1.29	0.393	-1.23	0.193	-0.05
1436752_at	Tbccd1	TBCC domain containing 1	-1.03	0.68	-1	0.99	1.12	0.215	2	0.23	0.27
1441154_at	Chd7	Chromodomain helicase DNA binding protein 7	1.56	0.3	-2.27	0.238	1.08	0.853	-1.79	0.386	-0.35
1416259_at	Pex12	peroxisomal biogenesis factor 12	1.04	0.372	1.13	0.251	-1.09	0.686	-1.21	0.23	-0.03
1436288_at	1700049M11Rik	RIKEN cDNA 1700049M11 gene	-1.69	0.134	1.82	0.06	-1.49	0.401	1.16	0.769	-0.05
1423835_at	Zfp503	zinc finger protein 503	-1.19	0.108	1.04	0.896	1.21	0.176	-1.33	0.345	-0.07
1458866_at	A930001M12Rik	RIKEN cDNA A930001M12 gene	-1.4	0.015	-1.07	0.904	1.44	0.054	1.27	0.607	0.06
1428068_at	Samm50	sorting and assembly machinery component 50 homolog (S. cerevisiae)	-1.09	0.293	-1.07	0.043	1.23	0.052	1.04	0.719	0.03
1453826_at	1810008K04Rik	RIKEN cDNA 1810008K04 gene	-1.27	0.515	-1.06	0.909	1.35	0.387	2.65	0.071	0.42
1452152_at	Clint1	clathrin interactor 1	-1.13	0.278	-1.04	0.584	1.23	0.043	1.11	0.441	0.04
1425718_a_at	Ivns1abp	influenza virus NS1A binding protein	-1.3	0.196	-1.07	0.644	1.38	0.045	1.05	0.853	0.02
1418436_at	Stx7	syntaxin 7	-1.02	0.903	1.07	0.504	1.03	0.618	-1.35	0.175	-0.06
1437541_at	---	---	-1.28	0.316	1.31	0.589	1	0.993	-1.24	0.158	-0.05
1428118_at	Lrrn6a	leucine rich repeat neuronal 6A	-1.02	0.936	1.05	0.934	1.06	0.634	-1.24	0.647	-0.04
1420737_at	Pmfbp1	polyamine modulated factor 1 binding protein 1	1.23	0.758	-1.17	0.711	-1	0.998	1.74	0.151	0.2
1449100_at	Pard6a	par-6 (partitioning defective 6,) homolog alpha (C. elegans)	1.03	0.91	-1.03	0.681	1.09	0.529	-1.06	0.511	0.01
1455642_a_at	Tspan17	tetraspanin 17	1.11	0.571	1.07	0.544	-1.1	0.443	-1.1	0.329	0
1453052_at	3110005G23Rik	RIKEN cDNA 3110005G23 gene	-1.05	0.448	1.04	0.528	1.1	0.452	-1.12	0.4	-0.01
1417783_at	Als2	amyotrophic lateral sclerosis 2 (juvenile) homolog (human)	-1.21	0.235	-1.03	0.899	1.29	0.173	1.08	0.472	0.03
1433620_at	Wdr41	WD repeat domain 41	-1.07	0.444	1.08	0.472	1.07	0.512	-1.1	0.612	0
1438608_at	Tnni2	Troponin I, skeletal, fast 2	-1.21	0.344	1.34	0.264	-1.08	0.662	2.53	0.287	0.39
1422192_at	Gja5	gap junction membrane channel protein alpha 5	1.09	0.682	1.16	0.15	-1.19	0.728	-1.07	0.806	0
1454726_s_at	AW456874	expressed sequence AW456874	1.15	0.439	1.11	0.741	-1.22	0.167	-1.15	0.667	-0.03
1423050_s_at	Hnrpu	heterogeneous nuclear ribonucleoprotein U	-1.01	0.878	1.13	0.205	-1.03	0.733	1.12	0.453	0.05
1427530_at	Bicd1	bicaudal D homolog 1 (Drosophila)	-1.09	0.012	-1.17	0.645	1.31	0.589	1.78	0.139	0.21
1419441_at	Arbp	acidic ribosomal phosphoprotein P0	1.05	0.391	1.09	0.46	-1.06	0.604	-1.21	0.033	-0.03
1419969_at	C77370	expressed sequence C77370	1.02	0.978	1.14	0.805	-1.07	0.871	-1.02	0.956	0.02
1454545_at	4933403L11Rik	RIKEN cDNA 4933403L11 gene	-1	0.996	-1.63	0.528	1.48	0.532	1.77	0.136	0.15
1421833_at	Pip5k1a	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha	-1.18	0.05	-1.06	0.781	1.3	0.091	4.48	0.214	0.88
1433309_at	4930472F24Rik	RIKEN cDNA 4930472F24 gene	-1.28	0.683	-1.36	0.46	1.57	0.429	1.64	0.344	0.14
1431033_x_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	-1.08	0.449	-1.13	0.442	1.27	0.262	1.06	0.764	0.03
1420900_a_at	Rab18	RAB18, member RAS oncogene family	-1.02	0.783	1.12	0.426	-1.01	0.959	1.51	0.037	0.15
1459500_at	C85351	expressed sequence C85351	1.11	0.876	-1.24	0.4	1.17	0.657	-1.86	0.313	-0.21
1456229_at	Hoxb3	homeo box B3	-1.14	0.21	1.19	0.73	1.02	0.89	-1.05	0.337	0.01
1439473_at	Pus7	Pseudouridylate synthase 7 homolog (S. cerevisiae)	1.28	0.766	-1.63	0.237	1.2	0.748	-2.21	0.412	-0.34
1426783_at	Gcn5l2	GCN5 general control of amino acid synthesis-like 2 (yeast)	1.11	0.449	-1.12	0.089	1.09	0.658	-1.2	0.256	-0.03
1450965_at	Tex261	testis expressed gene 261	1.16	0.551	1.01	0.944	-1.09	0.346	-1.13	0.578	-0.01
1444849_at	C76872	expressed sequence C76872	1.09	0.347	-1	0.996	1	0.981	-1.07	0.765	0
1458364_s_at	Ifrg15	interferon alpha responsive gene	1.01	0.903	1.09	0.47	-1.02	0.926	-1.25	0.385	-0.04
1418227_at	Orc2l	origin recognition complex, subunit 2-like (S. cerevisiae)	-1.03	0.959	1.13	0.555	-1.02	0.907	1.57	0.434	0.16
1439515_at	Setd5	SET domain containing 5	-1.3	0.328	-1.22	0.283	1.5	0.066	1.02	0.827	0
1434217_at	C330019G07Rik	RIKEN cDNA C330019G07 gene	-1.02	0.703	-1.01	0.852	1.12	0.252	1.09	0.317	0.04

1455369_at	Apba1	amyloid beta (A4) precursor protein binding, family A, member 1	-1.44	0.223	1.07	0.619	1.33	0.149	-1.26	0.227	-0.08
1426698_a_at	Hnrpm	heterogeneous nuclear ribonucleoprotein M	-1.1	0.548	-1.02	0.884	1.19	0.233	1.26	0.177	0.09
1438362_x_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	-1.14	0.54	-1.24	0.747	1.4	0.684	1.34	0.691	0.09
1415697_at	E430034L04Rik	RIKEN cDNA E430034L04 gene	-1.06	0.403	1.01	0.956	1.14	0.268	-1.05	0.593	0.01
1422747_at	Chek2	CHK2 checkpoint homolog (S. pombe)	-1.14	0.02	-1.25	0.638	1.41	0.101	2.23	0.232	0.31
1448105_at	Prm2	protamine 2	1.12	0.773	-1.28	0.53	1.19	0.717	-1.35	0.546	-0.08
1418314_a_at	A2bp1	ataxin 2 binding protein 1	-1.26	0.457	1.01	0.985	1.28	0.535	-1.44	0.24	-0.1
1417189_at	Psme2	proteasome (prosome, macropain) 28 subunit, beta	1.04	0.464	-1.01	0.931	1.06	0.675	-1.59	0.083	-0.13
1448285_at	Rgs4	regulator of G-protein signaling 4	-1.43	0.602	1.59	0.366	-1.25	0.437	1.19	0.845	0.02
1436481_at	---	Transcribed locus	1.17	0.548	-1.05	0.821	-1.04	0.878	3.19	0.156	0.57
1455105_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	-1.04	0.885	1.2	0.08	-1.08	0.081	1.23	0.125	0.08
1443863_at	Fndc3a	fibronectin type III domain containing 3a	-1.2	0.563	1	0.993	1.25	0.433	-1.06	0.639	0
1446727_at	---	---	1.04	0.944	-1.07	0.92	1.12	0.833	-1.48	0.235	-0.1
1453585_at	1600010M07Rik	RIKEN cDNA 1600010M07 gene	-1.56	0.135	1.05	0.84	1.4	0.364	-1.17	0.443	-0.07
1423656_x_at	1500010J02Rik	RIKEN cDNA 1500010J02 gene	1.07	0.582	-1.06	0.831	1.07	0.696	-1.12	0.497	-0.01
1448451_at	Ak2	adenylate kinase 2	-1.09	0.566	-1.4	0.188	1.46	0.14	1.02	0.948	0
1431510_s_at	2010110K16Rik	RIKEN cDNA 2010110K16 gene	1.05	0.57	1.08	0.34	-1.04	0.731	-1.02	0.906	0.02
1456399_at	---	---	1.1	0.555	1.1	0.513	-1.13	0.634	-1.22	0.479	-0.04
1449572_at	Trhr	thyrotropin releasing hormone receptor	1.18	0.818	1.19	0.805	-1.39	0.451	-1.22	0.097	-0.06
1443871_at	Man1a2	Mannosidase, alpha, class 1A, member 2	-1.32	0.605	1.02	0.969	1.32	0.026	-1.05	0.755	-0.01
1448013_at	Usp24	ubiquitin specific peptidase 24	-1.02	0.929	1	0.974	1.1	0.649	-1.22	0.292	-0.03
1432000_a_at	Dedd	death effector domain-containing	1.09	0.088	-1.28	0.218	1.21	0.043	-1.06	0.598	-0.01
1441996_at	9530082P21Rik	RIKEN cDNA 9530082P21 gene	-1.08	0.42	1.19	0.674	-1.03	0.864	1.75	0.21	0.21
1433806_x_at	Calr	calreticulin	-1	0.994	1.15	0.357	-1.07	0.497	1.22	0.294	0.08
1421118_a_at	Gpr56	G protein-coupled receptor 56	-1.09	0.762	-1.02	0.882	1.19	0.389	3.78	0.084	0.72
1420369_a_at	Csn2	casein beta	-1.02	0.95	-1.24	0.765	1.3	0.623	2.41	0.18	0.36
1424406_at	Bcl2l13	BCL2-like 13 (apoptosis facilitator)	-1.06	0.425	-1.07	0.387	1.21	0.048	2.3	0.24	0.35
1453157_at	1700022A21Rik	RIKEN cDNA 1700022A21 gene	1.16	0.808	1.07	0.911	-1.17	0.766	-2	0.066	-0.23
1439565_at	AW492303	Expressed sequence AW492303	1.17	0.493	1.07	0.713	-1.18	0.457	-1.28	0.437	-0.05
1448879_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	-1.08	0.772	-1.02	0.868	1.19	0.272	1	0.998	0.02
1439791_at	Gm527	gene model 527, (NCBI)	1.18	0.095	1.31	0.308	-1.67	0.007	-1.17	0.594	-0.09
1430029_a_at	Tspan31	tetraspanin 31	1.02	0.887	-1.03	0.803	1.1	0.789	-1.06	0.407	0.01
1431771_a_at	Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	-1.02	0.785	1.2	0.174	-1.1	0.675	1.26	0.151	0.09
1438533_at	Myo9b	myosin IXb	1.26	0.679	1.3	0.659	-1.88	0.027	-1.41	0.307	-0.18
1456805_a_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	1.15	0.618	-1.06	0.89	1	0.994	-1.05	0.86	0.01
1439155_at	Mettl1	methyltransferase-like 1	-1.04	0.252	1.13	0.23	1	0.982	-1.07	0.747	0.01
1457611_x_at	2010309E21Rik	RIKEN cDNA 2010309E21 gene	-1.16	0.766	1.11	0.528	1.12	0.529	-1.08	0.813	0
1446047_at	Rbms3	RNA binding motif, single stranded interacting protein	1.04	0.652	1.67	0.098	-2.61	0.019	-1.11	0.55	-0.25
1445617_at	---	Transcribed locus	1.32	0.637	-1.32	0.56	1.02	0.916	-1.25	0.471	-0.06
1432721_at	5830424K16Rik	RIKEN cDNA 5830424K16 gene	1.1	0.864	-1.03	0.869	1.02	0.865	-1.05	0.934	0.01
1444709_at	Invs	inversin	1.11	0.605	1.13	0.169	-1.18	0.581	-1.53	0.2	-0.12
1416475_at	Ube2d2	ubiquitin-conjugating enzyme E2D 2	1.04	0.485	-1.06	0.404	1.11	0.523	-1.15	0.625	-0.02
1430070_at	1500035N22Rik	RIKEN cDNA 1500035N22 gene	1.47	0.525	-1.57	0.321	-1.01	0.906	2.18	0.209	0.27
1446800_at	---	---	-1.21	0.605	1.17	0.598	1.09	0.871	-1.51	0.599	-0.11
1454885_at	BC063263	cDNA sequence BC063263	1.05	0.809	-1.01	0.971	1.05	0.546	-1.17	0.565	-0.02
1420366_at	Spesp1	sperm equatorial segment protein 1	1.23	0.738	-1.13	0.592	-1.03	0.892	1.15	0.742	0.06
1422714_at	Ube2i /// LOC5462(	ubiquitin-conjugating enzyme E2I /// similar to Chain A, Human Ubiquitin-Conjuga	-1.17	0.44	1.14	0.165	1.1	0.286	-1.43	0.153	-0.09
1455156_at	Strn	striatin, calmodulin binding protein	1	0.988	1.13	0.313	-1.04	0.611	-1.05	0.564	0.01
1451017_at	Ergic3	ERGIC and golgi 3	1.09	0.498	-1.1	0.065	1.1	0.355	-1.13	0.443	-0.01
1433859_at	D030070L09Rik	RIKEN cDNA D030070L09 gene	-1.06	0.64	1.06	0.612	1.09	0.432	-1.03	0.883	0.01
1425340_a_at	Ptpra	protein tyrosine phosphatase, receptor type, A	-1.05	0.591	1.08	0.095	1.05	0.696	-1.18	0.111	-0.02
1419368_a_at	Rnf138	ring finger protein 138	1.17	0.182	-1.42	0.044	1.21	0.336	-1.87	0.087	-0.22
1423199_at	Brd3	bromodomain containing 3	1.06	0.756	-1.09	0.717	1.12	0.534	-1.15	0.442	-0.02

1429500_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	-1.08	0.698	1.01	0.957	1.16	0.312	-1.36	0.455	-0.07
1423461_a_at	Ubl3	ubiquitin-like 3	-1.09	0.305	1.1	0.101	1.07	0.435	-1.44	0.272	-0.09
1423505_at	Tagln	transgelin	1.5	0.012	1.08	0.651	-1.94	0.015	-1.5	0.385	-0.22
1429391_at	Acpl2	acid phosphatase-like 2	-1.02	0.981	-1.26	0.365	1.32	0.603	1.29	0.125	0.08
1420509_at	Srfbp1	serum response factor binding protein 1	1.27	0.136	-1.21	0.162	1	0.999	-1.02	0.883	0.01
1415985_at	Sf3b3	splicing factor 3b, subunit 3	-1.16	0.491	1.07	0.55	1.16	0.394	-1.05	0.296	0.01
1415732_at	Bat5	HLA-B associated transcript 5	-1.07	0.585	-1.04	0.498	1.19	0.172	1.32	0.317	0.1
1440315_at	Mbnl1	muscleblind-like 1 (Drosophila)	-1.74	0.292	1.29	0.552	1.23	0.386	-1.22	0.611	-0.11
1447229_x_at	1110051M20Rik	RIKEN cDNA 1110051M20 gene	-1.71	0.263	-1.19	0.108	1.67	0.075	1.59	0.241	0.09
1457128_at	---	---	1.26	0.304	-1.26	0.756	1.04	0.926	-2.54	0.085	-0.37
1423308_at	Tgoln1	trans-golgi network protein	1.22	0.557	-1.46	0.059	1.19	0.776	-1.29	0.667	-0.08
1427554_at	Hel308	helicase, mus308-like (Drosophila)	-1.24	0.368	-1.06	0.825	1.35	0.284	1.16	0.794	0.05
1452216_at	BC025519	cDNA sequence BC025519	-1.01	0.981	-1.01	0.892	1.11	0.407	1.18	0.489	0.07
1435342_at	Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6	1.03	0.851	1.2	0.061	-1.16	0.085	-1.19	0.24	-0.03
1434350_at	Axud1	AXIN1 up-regulated 1	-1.21	0.626	1.05	0.914	1.22	0.475	-1.53	0.128	-0.12
1455874_at	1810059G22Rik	RIKEN cDNA 1810059G22 gene	-1.1	0.615	-1	0.982	1.19	0.206	1	0.998	0.02
1445299_at	Ppm1h	Protein phosphatase 1H (PP2C domain containing)	1.21	0.734	1.04	0.842	-1.19	0.606	-1.21	0.403	-0.04
1445130_at	AA407111	expressed sequence AA407111	1.47	0.475	1.1	0.861	-1.91	0.135	-1.32	0.706	-0.16
1415815_at	Trim27	tripartite motif protein 27	1.81	0.54	-2.93	0.361	-1.06	0.748	1.33	0.425	-0.21
1427186_a_at	Mef2a	myocyte enhancer factor 2A	1.14	0.118	1.17	0.28	-1.28	0.123	-1.18	0.599	-0.03
1424568_at	Tspan2	tetraspanin 2	1.34	0.286	1.06	0.926	-1.44	0.094	-1.34	0.003	-0.09
1448166_a_at	Psmb1	proteasome (prosome, macropain) subunit, beta type 1	1.05	0.098	-1.12	0.009	1.15	0.209	-1.24	0.251	-0.04
1440810_x_at	---	PREDICTED: Mus musculus similar to ribosomal protein L27a (LOC628200), mR	-1.69	0.187	1.47	0.251	1.04	0.892	-1.1	0.808	-0.07
1444720_at	AA408456	expressed sequence AA408456	-1.04	0.93	1.71	0.215	-2.33	0.043	1.32	0.365	-0.09
1434314_s_at	Rab11fip5	RAB11 family interacting protein 5 (class I)	-1.15	0.38	1	0.988	1.22	0.133	-1.27	0.45	-0.05
1441789_at	Rsbn1	Rosbin, round spermatid basic protein 1	1.44	0.398	1.21	0.602	-2.23	0.018	-1.04	0.935	-0.16
1460269_at	Pnmt	Phenylethanolamine-N-methyltransferase	1.43	0.209	-1.12	0.636	-1.29	0.691	1.34	0.54	0.09
1434541_x_at	---	---	-1.13	0.311	1.04	0.707	1.17	0.176	-1.33	0.036	-0.06
1454920_at	Uhrf2	ubiquitin-like, containing PHD and RING finger domains 2	-1.03	0.919	1.17	0.016	-1.05	0.762	1.09	0.669	0.05
1455297_at	Spin2	spindlin family, member 2	-1.1	0.646	1.3	0.396	-1.13	0.284	1.39	0.616	0.11
1429015_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	-1.13	0.352	1.25	0.643	-1.05	0.851	1.25	0.127	0.08
1458010_at	---	---	1.01	0.98	-1.28	0.691	1.31	0.365	-1.87	0.071	-0.21
1455024_at	Tlk1	tousled-like kinase 1	1.16	0.058	-1.06	0.372	-1.01	0.936	1.27	0.14	0.09
1433575_at	LOC672274	similar to Transcription factor SOX-4	1.01	0.986	1.27	0.209	-1.22	0.526	-1.93	0.006	-0.22
1453911_at	---	---	1.56	0.183	1.1	0.793	-2.27	0.103	-3.88	0.051	-0.87
1426130_at	Txnl6	thioredoxin-like 6	-1.3	0.279	1.04	0.894	1.29	0.598	-2.29	0.328	-0.32
1448569_at	Cd8b1	CD8 antigen, beta chain 1	1.02	0.767	1.08	0.5	-1.01	0.948	-1.23	0.102	-0.03
1448217_a_at	Rpl27 /// LOC6211(	ribosomal protein L27 /// similar to ribosomal protein L27 /// similar to ribosomal pı	1.11	0.073	1	0.982	-1.01	0.965	-1.37	0.073	-0.07
1416508_at	Med28	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	1.14	0.266	1.14	0.126	-1.23	0.101	-1.19	0.202	-0.03
1457701_at	Tmem136	transmembrane protein 136	1.02	0.924	1.44	0.074	-1.58	0.025	-1.06	0.797	-0.04
1452933_at	Ankrd39	ankyrin repeat domain 39	-1.04	0.576	-1.03	0.93	1.17	0.459	1.12	0.459	0.05
1453634_a_at	Erp29	endoplasmic reticulum protein 29	-1.22	0.113	1.03	0.683	1.25	0.324	-1.48	0.134	-0.11
1433479_at	5730410I19Rik	RIKEN cDNA 5730410I19 gene	-1.12	0.578	-1.23	0.568	1.39	0.511	1.24	0.607	0.07
1446546_at	Tmlhe	trimethyllysine hydroxylase, epsilon	-1.09	0.789	-1.14	0.67	1.3	0.407	2.43	0.282	0.38
1435764_a_at	Gemin7	gem (nuclear organelle) associated protein 7	1.06	0.741	1.06	0.73	-1.03	0.849	-1.06	0.67	0.01
1434838_at	LOC240444	similar to Potassium voltage-gated channel subfamily G member 2 (Voltage-gate(	-1.52	0.416	-1.18	0.599	1.59	0.155	1.09	0.82	0
1418107_at	Tcea2	transcription elongation factor A (SII), 2	1.09	0.693	-1.11	0.872	1.11	0.526	-1.59	0.212	-0.13
1453209_at	Brf1	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S	-1.12	0.672	1.15	0.684	1.06	0.717	-1.04	0.798	0.01
1451964_at	Mia2	melanoma inhibitory activity 2	-1.08	0.826	-1.72	0.276	1.59	0.12	1.28	0.621	0.02
1437337_x_at	Fuk	fucokinase	-1.13	0.296	-1.31	0.029	1.45	0.115	1.01	0.91	0.01
1421751_a_at	Psmd14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	-1.11	0.664	-1.05	0.329	1.25	0.241	1.14	0.497	0.06
1431846_at	4930546C10Rik	RIKEN cDNA 4930546C10 gene	-1.16	0.857	1.46	0.465	-1.28	0.717	1.57	0.3	0.15
1418764_a_at	Bpnt1	bisphosphate 3'-nucleotidase 1	1.16	0.663	-1.18	0.313	1.09	0.709	-1.3	0.47	-0.06

1433568_at	Papd4	PAP associated domain containing 4	1.03	0.858	1.17	0.341	-1.11	0.17	-1.12	0.678	-0.01
1424934_at	Ugt2b1	UDP glucuronosyltransferase 2 family, polypeptide B1	1.67	0.509	-2.25	0.054	-1.02	0.976	1.22	0.514	-0.09
1454518_at	4930429L21Rik	RIKEN cDNA 4930429L21 gene	-1.17	0.579	1.32	0.462	-1.08	0.62	1.47	0.308	0.13
1433972_at	Camta1	calmodulin binding transcription activator 1	1.17	0.325	-1.27	0.549	1.14	0.233	-1.92	0.564	-0.22
1434968_a_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	-1.05	0.307	1.1	0.32	1.05	0.61	-1.3	0.134	-0.05
1424447_at	1700030K09Rik	RIKEN cDNA 1700030K09 gene	-1.23	0.152	1.22	0.075	1.07	0.64	-1.7	0.085	-0.16
1418285_at	Efnb1	ephrin B1	1.15	0.504	-1.12	0.306	1.06	0.787	-1.09	0.712	0
1417407_at	Fbxl14	F-box and leucine-rich repeat protein 14	-1.05	0.57	1.1	0.531	1.05	0.692	-1.28	0.077	-0.05
1422538_at	Extl2	exotoses (multiple)-like 2	1.2	0.107	-1.02	0.729	-1.09	0.379	1	0.989	0.02
1440049_at	Rpl10	Ribosomal protein 10	-1.27	0.195	1.27	0.3	1.04	0.932	-1.66	0.186	-0.15
1440055_at	AI848100	Expressed sequence AI848100	-1.03	0.714	-1.04	0.858	1.17	0.669	1.1	0.131	0.05
1454846_at	Utp15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	-1.13	0.582	1.17	0.17	1.04	0.558	-1.09	0.515	0
1429767_at	2810013P06Rik	RIKEN cDNA 2810013P06 gene	1.2	0.322	1.11	0.35	-1.27	0.106	-1.38	0.147	-0.09
1425508_s_at	Arfrp1	ADP-ribosylation factor related protein 1	-1.13	0.245	1.1	0.323	1.11	0.139	-1.63	0.031	-0.14
1435705_at	LOC232875	similar to hypothetical protein FLJ12895	1.26	0.433	-1.39	0.417	1.12	0.5	-1.54	0.169	-0.14
1431089_at	Cpsf2	cleavage and polyadenylation specific factor 2	1.24	0.634	-1.08	0.638	-1.07	0.8	3.06	0.229	0.54
1443488_at	---	---	1.17	0.717	1.53	0.312	-2.46	0.02	-1.47	0.34	-0.31
1424055_at	Ncoa5	nuclear receptor coactivator 5	1.16	0.744	1.04	0.876	-1.12	0.636	-1.15	0.22	-0.02
1435508_x_at	0610009D07Rik	RIKEN cDNA 0610009D07 gene	1.31	0.217	1.07	0.819	-1.39	0.36	-1.02	0.883	-0.01
1449964_a_at	Mlycd	malonyl-CoA decarboxylase	1.04	0.885	-1.28	0.163	1.27	0.036	-1.44	0.106	-0.1
1419653_a_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	-1.04	0.746	1.12	0.202	1.02	0.878	-1.35	0.281	-0.06
1454787_at	Zdhhc9	zinc finger, DHHC domain containing 9	-1.13	0.425	-1.06	0.496	1.27	0.024	1.1	0.781	0.05
1448379_at	Pot1	protection of telomeres 1	-1.02	0.833	1.22	0.242	-1.11	0.202	1.24	0.346	0.08
1434828_at	B430201A12Rik	RIKEN cDNA B430201A12 gene	1.27	0.083	1.14	0.136	-1.44	0.114	-1.16	0.413	-0.05
1420882_a_at	Nsd1 /// Acd	nuclear receptor-binding SET-domain protein 1 /// adrenocortical dysplasia	1.01	0.984	-1.2	0.153	1.26	0.241	-1.19	0.282	-0.03
1437163_x_at	Gtf2h4	general transcription factor II H, polypeptide 4	-1.24	0.081	1.02	0.785	1.27	0.115	-1.04	0.686	0
1447924_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	-1.03	0.854	-1.16	0.354	1.27	0.411	2.02	0.145	0.27
1420282_s_at	Prss29	protease, serine, 29	-1.23	0.22	1.51	0.259	-1.28	0.264	2.36	0.416	0.34
1460729_at	Rock1	Rho-associated coiled-coil containing protein kinase 1	-1.1	0.483	-1.03	0.879	1.22	0.205	1.44	0.281	0.13
1452369_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain containing 1	1.22	0.508	-1.19	0.72	1.04	0.796	-1.06	0.807	0
1426733_at	Itpk1	inositol 1,3,4-triphosphate 5/6 kinase	-1.11	0.412	1.12	0.301	1.08	0.535	-1.37	0.068	-0.07
1456164_at	AW011738	expressed sequence AW011738	-1.02	0.968	1.15	0.742	-1.04	0.857	1.13	0.275	0.06
1440770_at	Bcl2	B-cell leukemia/lymphoma 2	1.04	0.827	1.16	0.519	-1.12	0.758	-1.5	0.438	-0.1
1417656_at	Mybl2	myeloblastosis oncogene-like 2	-1.09	0.055	-1.09	0.572	1.27	0.302	3.96	0.206	0.76
1423087_a_at	1110002E23Rik	RIKEN cDNA 1110002E23 gene	1.04	0.904	1.08	0.408	-1.02	0.945	-1.07	0.739	0.01
1452920_a_at	Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	1.19	0.386	-1.2	0.245	1.08	0.497	-1.28	0.201	-0.05
1437104_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibite	-1.07	0.761	-1.02	0.931	1.18	0.324	1.24	0.245	0.08
1431139_at	Cdyl2	chromodomain protein, Y chromosome-like 2	1.24	0.555	-2.07	0.168	1.38	0.55	-1.19	0.81	-0.16
1426632_at	Kctd14	potassium channel tetramerisation domain containing 14	-1.12	0.776	1.39	0.246	-1.22	0.297	1.71	0.298	0.19
1456742_x_at	Tm9sf2	transmembrane 9 superfamily member 2	-2.14	0.018	-1.65	0.388	2.03	0.212	1.09	0.883	-0.17
1460603_at	Samd9l	sterile alpha motif domain containing 9-like	1.03	0.766	-1	0.978	1.07	0.39	-1.9	0.101	-0.2
1434738_at	Tarsl2	threonyl-tRNA synthetase-like 2	-1.04	0.789	-1.22	0.049	1.32	0.406	2.89	0.213	0.49
1456788_at	Mrpl54	mitochondrial ribosomal protein L54	1.47	0.482	-1.56	0.447	-1.01	0.98	1.13	0.803	0.01
1453299_a_at	Pnp /// LOC545044	purine-nucleoside phosphorylase /// similar to purine-nucleoside phosphorylase //	-1.14	0.287	1.24	0.341	-1.02	0.856	3.19	0.198	0.57
1456401_at	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	1.18	0.766	-1.14	0.786	1.04	0.901	-1.98	0.399	-0.22
1428521_at	Thap3	THAP domain containing, apoptosis associated protein 3	1.18	0.209	-1.24	0.235	1.11	0.536	-1.75	0.097	-0.17
1428124_at	Gtf2e1	general transcription factor II E, polypeptide 1 (alpha subunit)	-1.06	0.735	1.14	0.141	1.02	0.849	-1.09	0.406	0
1452514_a_at	Kit	kit oncogene	-1.19	0.614	1.16	0.346	1.1	0.588	-1.03	0.901	0.01
1423267_s_at	Itga5	integrin alpha 5 (fibronectin receptor alpha)	-1.2	0.678	1.43	0.134	-1.2	0.191	1.64	0.264	0.17
1449863_a_at	Dlx5	distal-less homeobox 5	1.75	0.266	-1.19	0.567	-1.97	0.069	1.27	0.597	-0.04
1436858_at	Mbnl2	muscleblind-like 2	1.06	0.878	-1.05	0.905	1.08	0.817	-1.09	0.801	0
1435446_a_at	Chpt1	choline phosphotransferase 1	-1.04	0.534	-1	0.994	1.14	0.448	1.11	0.675	0.05
1416521_at	Sepw1	selenoprotein W, muscle 1	1.19	0.677	1.19	0.477	-1.39	0.131	-1.1	0.821	-0.03

1455571_x_at	Calm1	calmodulin 1	1.12	0.525	1.27	0.05	-1.41	0.025	-1.22	0.377	-0.06
1460224_at	Snx2	sorting nexin 2	-1.16	0.054	1.12	0.302	1.12	0.346	-2.52	0.037	-0.36
1454736_at	Ankrd57	ankyrin repeat domain 57	1.02	0.931	1.2	0.381	-1.12	0.508	-1.15	0.246	-0.02
1433936_at	0610010E21Rik	RIKEN cDNA 0610010E21 gene	1.04	0.711	-1.02	0.841	1.07	0.651	-1.55	0.07	-0.11
1443136_at	LOC432459	hypothetical gene supported by AK082906	-1.78	0.061	-1.12	0.767	1.65	0.149	1.05	0.803	-0.05
1448435_at	Pcqap	positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated protein	-1.04	0.728	1.04	0.673	1.09	0.677	-1.07	0.793	0.01
1444123_at	Prdm2	PR domain containing 2, with ZNF domain	-1.21	0.707	-1.43	0.534	1.57	0.038	1.14	0.789	0.02
1451392_at	Rbed1	RNA binding motif and ELMO domain 1	1.21	0.38	-1.33	0.037	1.14	0.271	-1.7	0.109	-0.17
1438120_x_at	---	---	-1.16	0.387	1.06	0.592	1.18	0.052	-1.35	0.298	-0.07
1447255_at	2310015A10Rik	RIKEN cDNA 2310015A10 gene	1.11	0.878	-1.12	0.828	1.1	0.891	-3.87	0.25	-0.7
1446761_at	D8Ertd56e	DNA segment, Chr 8, ERATO Doi 56, expressed	-1.16	0.813	1.8	0.315	-2.27	0.048	2.19	0.409	0.14
1448159_at	Rab7	RAB7, member RAS oncogene family	-1.19	0.557	1.04	0.845	1.22	0.376	-1.15	0.492	-0.02
1453258_at	---	---	1.53	0.421	-1.02	0.931	-1.68	0.182	1.14	0.79	-0.01
1455378_at	BC057371	cDNA sequence BC057371	1.51	0.009	-2.21	0.081	1.14	0.424	-1.16	0.46	-0.18
1444737_at	D2Wsu107e	DNA segment, Chr 2, Wayne State University 107, expressed	1.11	0.781	1.03	0.932	-1.03	0.939	-1.57	0.144	-0.12
1424255_at	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	-1.05	0.683	1.01	0.885	1.13	0.155	-1.22	0.184	-0.03
1450933_at	Pde7a	phosphodiesterase 7A	1.08	0.809	1.1	0.818	-1.08	0.677	-1.67	0.248	-0.14
1444508_s_at	Arrdc1	arrestin domain containing 1	1	0.954	1.18	0.129	-1.09	0.496	-1.14	0.449	-0.01
1457340_at	Rufy1	RUN and FYVE domain containing 1	1.04	0.826	1.16	0.76	-1.1	0.659	-1.13	0.805	-0.01
1422073_a_at	Celsr2	cadherin EGF LAG seven-pass G-type receptor 2	-1.24	0.229	1.18	0.819	1.11	0.531	-1.47	0.474	-0.1
1429444_at	Rasl11a	RAS-like, family 11, member A	-1.19	0.406	1.23	0.657	1.03	0.931	-1.75	0.252	-0.17
1459459_at	Ptpn12	Protein tyrosine phosphatase, non-receptor type 12	-1.18	0.833	-1.66	0.45	1.65	0.233	1.84	0.099	0.16
1438452_at	Nebl	nebulette	1.04	0.707	1.17	0.712	-1.12	0.372	-2.1	0.137	-0.25
1445064_at	Drr1	developmentally regulated repeat element-containing transcript 1	-1.37	0.3	1.55	0.08	-1.21	0.491	1.06	0.888	0.01
1417164_at	Dusp10	dual specificity phosphatase 10	-1.36	0.274	1.2	0.511	1.16	0.575	-1.2	0.055	-0.05
1459853_x_at	---	---	1.19	0.187	-1.05	0.747	-1.03	0.818	1.23	0.461	0.08
1424575_at	Rabl5	RAB, member of RAS oncogene family-like 5	-1.2	0.341	1.09	0.471	1.18	0.552	-1.39	0.18	-0.08
1436942_at	A930035D04Rik	RIKEN cDNA A930035D04 gene	-1.07	0.44	1.32	0.49	-1.18	0.11	1	0.994	0.02
1451790_a_at	Tfpi	tissue factor pathway inhibitor	-1.35	0.049	1.47	0.263	-1.12	0.255	1.09	0.742	0.02
1426195_a_at	Cst3	cystatin C	1.27	0.242	1.22	0.026	-1.64	0.001	-1.32	0.416	-0.12
1448351_at	Coro1b	coronin, actin binding protein 1B	-1.06	0.754	1.02	0.89	1.14	0.238	-1.55	0.133	-0.11
1432125_at	Ap3m2	adaptor-related protein complex 3, mu 2 subunit	1.07	0.916	-1.08	0.874	1.11	0.794	-1.68	0.353	-0.15
1443837_x_at	Bcl2	B-cell leukemia/lymphoma 2	-1.29	0.416	1.17	0.582	1.15	0.758	-1.01	0.978	0.01
1445640_at	Hlcs	Holocarboxylase synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-h	-1.31	0.733	1.32	0.326	1.02	0.974	-1.77	0.127	-0.18
1458483_at	A330102I10Rik	RIKEN cDNA A330102I10 gene	1.27	0.562	-1.69	0.328	1.25	0.361	-1.41	0.172	-0.15
1433829_a_at	Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	1.08	0.634	1.19	0.048	-1.21	0.164	-1.17	0.358	-0.02
1460468_s_at	2810451A06Rik	RIKEN cDNA 2810451A06 gene	1.16	0.677	1.17	0.42	-1.29	0.491	-2.94	0.209	-0.47
1451457_at	Sc5d	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae)	1.06	0.85	-1.02	0.921	1.06	0.695	-1.61	0.249	-0.13
1416509_at	Tm9sf3	transmembrane 9 superfamily member 3	1.13	0.009	1.1	0.113	-1.14	0.121	-1.13	0.519	-0.01
1426238_at	Bmp1	bone morphogenetic protein 1	1.33	0.218	-1.03	0.827	-1.25	0.352	1.11	0.368	0.04
1450623_at	Gnb2	guanine nucleotide binding protein, beta 2	-1.03	0.669	1.01	0.899	1.13	0.403	-1.01	0.927	0.02
1440497_at	---	CDNA clone IMAGE:5690974	-1.01	0.948	1.05	0.831	1.06	0.418	-1.04	0.586	0.02
1454556_at	2700057C20Rik	RIKEN cDNA 2700057C20 gene	1.14	0.821	-1.41	0.197	1.25	0.253	-1.5	0.211	-0.13
1437943_s_at	Mea1	male enhanced antigen 1	1.09	0.638	-1.03	0.819	1.05	0.84	-1.15	0.446	-0.01
1447930_at	Baz1a	bromodomain adjacent to zinc finger domain 1A	1.04	0.873	-1.03	0.856	1.1	0.754	-1.1	0.59	0
1452439_s_at	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	-1.06	0.687	-1.06	0.317	1.22	0.076	1.45	0.203	0.14
1435984_at	1110033F14Rik	RIKEN cDNA 1110033F14 gene	1.07	0.745	1.17	0.703	-1.15	0.327	-1.25	0.184	-0.04
1430527_a_at	Rnf167	ring finger protein 167	1.04	0.859	-1.06	0.718	1.12	0.431	-1.37	0.044	-0.07
1426593_a_at	Fbxo22	F-box only protein 22	-1.16	0.1	1.05	0.496	1.19	0.183	-1.42	0.104	-0.08
1450099_a_at	Gba	glucosidase, beta, acid	-1.1	0.5	1.08	0.302	1.11	0.433	-1.03	0.887	0.02
1456563_at	4933429F08Rik	RIKEN cDNA 4933429F08 gene	-1.05	0.832	-1.3	0.371	1.39	0.14	1.51	0.257	0.14
1420091_s_at	Morc3	microrchidia 3	-1.05	0.73	1.14	0.55	1.01	0.935	-1.45	0.02	-0.09
1460478_at	2200002J24Rik	RIKEN cDNA 2200002J24 gene	1.01	0.95	1.11	0.634	-1.02	0.956	-1.01	0.973	0.02

1424328_s_at	3200002M19Rik	RIKEN cDNA 3200002M19 gene	-1.07	0.641	1.11	0.242	1.06	0.813	-1.08	0.771	0.01
1447083_at	4933407I05Rik	RIKEN cDNA 4933407I05 gene	-1.27	0.758	1.15	0.702	1.17	0.62	-1.41	0.445	-0.09
1429536_at	2310040C09Rik	RIKEN cDNA 2310040C09 gene	-1.17	0.333	1.1	0.64	1.15	0.662	-1.2	0.611	-0.03
1434438_at	Samhd1	SAM domain and HD domain, 1	-1.13	0.187	1.07	0.646	1.15	0.596	-1.55	0.292	-0.12
1418915_at	Mmachc	methylmalonic aciduria cblC type, with homocystinuria	-1.05	0.689	-1.07	0.626	1.21	0.165	1.19	0.349	0.07
1433137_at	5031415H12Rik	RIKEN cDNA 5031415H12 gene	-1	0.901	1.24	0.287	-1.15	0.092	1.16	0.058	0.06
1457571_at	Zfp68	zinc finger protein 68	1.15	0.643	1.38	0.221	-1.74	0.049	-1.12	0.69	-0.08
1416923_a_at	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	1.26	0.165	-1.07	0.485	-1.1	0.653	1.71	0.236	0.2
1460656_a_at	5630401J11Rik	RIKEN cDNA 5630401J11 gene	1.04	0.363	-1.05	0.317	1.12	0.291	-1.26	0.166	-0.04
1437637_at	Phtf2	putative homeodomain transcription factor 2	1.02	0.895	-1.05	0.928	1.13	0.606	-1.69	0.119	-0.15
1457476_at	D8Ertd362e	DNA segment, Chr 8, ERATO Doi 362, expressed	1.13	0.541	1.49	0.564	-2.07	0.172	-2.11	0.19	-0.39
1456945_at	Nudt6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	1.16	0.181	1.1	0.699	-1.18	0.372	-1.25	0.184	-0.04
1429877_at	Lrrc44	leucine rich repeat containing 44	-1.29	0.324	1.1	0.819	1.24	0.113	-1.35	0.234	-0.08
1415853_at	Def8	differentially expressed in FDCP 8	-1.03	0.841	-1.09	0.73	1.22	0.037	1.65	0.382	0.19
1457260_at	7530403E16Rik	RIKEN cDNA 7530403E16 gene	1.08	0.857	-1.22	0.357	1.2	0.426	-1.15	0.403	-0.02
1421585_at	4933439F11Rik	RIKEN cDNA 4933439F11 gene	1.08	0.454	1.1	0.771	-1.08	0.505	-1.11	0.281	0
1426156_at	Lats2	large tumor suppressor 2	-1.21	0.721	-1.32	0.284	1.52	0.262	1.07	0.702	0.02
1428127_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	1.12	0.639	-1.04	0.423	1.02	0.89	-1.15	0.679	-0.01
1437615_s_at	Vps37c	Vacuolar protein sorting 37C (yeast)	1.05	0.727	-1.06	0.545	1.11	0.331	-1.07	0.456	0.01
1438540_at	---	---	-1.37	0.631	1.48	0.583	-1.11	0.773	1.08	0.928	0.02
1424068_at	Tcta	T-cell leukemia translocation altered gene	-1.01	0.843	1.09	0.698	1.03	0.812	-1.41	0.31	-0.08
1445669_at	Spry4	sprouty homolog 4 (Drosophila)	-1.23	0.441	-1.65	0.133	1.69	0.173	1.15	0.521	-0.01
1436050_x_at	Hes6	hairy and enhancer of split 6 (Drosophila)	1.05	0.883	-1.1	0.625	1.15	0.342	-1.4	0.091	-0.08
1457924_at	Mbnl1	muscleblind-like 1 (Drosophila)	1.2	0.741	1.04	0.936	-1.15	0.789	-1.74	0.123	-0.16
1457338_at	Ppp1r12b	Protein phosphatase 1, regulatory (inhibitor) subunit 12B	1.53	0.013	-1.18	0.598	-1.38	0.111	1.31	0.312	0.07
1454629_at	A930037G23Rik	RIKEN cDNA A930037G23 gene	-1.1	0.732	1.03	0.957	1.17	0.189	-1	0.997	0.02
1448502_at	Slc16a7	solute carrier family 16 (monocarboxylic acid transporters), member 7	1.19	0.092	-1.1	0.798	1.01	0.977	-1.32	0.351	-0.06
1420426_at	Myo7b	myosin VIIb	1.01	0.954	1.54	0.575	-1.79	0.34	-1.25	0.287	-0.12
1459726_at	Ptprn2	Protein tyrosine phosphatase, receptor type, N polypeptide 2	1.12	0.663	-1.07	0.857	1.05	0.921	-1.28	0.561	-0.05
1415998_at	Vdac1	voltage-dependent anion channel 1	-1.45	0.095	-1.22	0.033	1.6	0.112	1.22	0.563	0.04
1443814_x_at	Ctsh	cathepsin H	1.11	0.018	1.04	0.488	-1.04	0.849	-1.45	0.314	-0.09
1435361_at	---	---	1.09	0.214	-1.73	0.196	1.44	0.049	-1.06	0.737	-0.07
1460045_at	Cdh7	cadherin 7, type 2	-1.69	0.24	1.83	0.319	-1.45	0.4	1.11	0.77	-0.05
1459277_at	Ncoa1	Nuclear receptor coactivator 1	1.36	0.32	1.06	0.898	-1.46	0.483	-1.97	0.166	-0.25
1424058_at	1190002C06Rik	RIKEN cDNA 1190002C06 gene	-1.36	0.03	1.01	0.946	1.36	0.022	-1.09	0.551	-0.02
1435793_at	Aph1b	anterior pharynx defective 1b homolog (C. elegans)	1.01	0.953	1.23	0.101	-1.16	0.469	-1.03	0.9	0.01
1451410_a_at	Crip3	cysteine-rich protein 3	-1.65	0.025	1.4	0.447	1.1	0.653	-1.85	0.136	-0.25
1446796_at	---	---	-1.4	0.6	1.58	0.569	-1.23	0.557	1.4	0.065	0.09
1439664_at	Wdr68	WD repeat domain 68	1.32	0.205	1.01	0.958	-1.29	0.239	-1.28	0.458	-0.06
1440890_a_at	BB114266	expressed sequence BB114266	1.25	0.292	1.08	0.34	-1.3	0.287	-1.12	0.254	-0.02
1417069_a_at	Gmfb	glia maturation factor, beta	1.25	0.331	1	0.987	-1.17	0.617	-1.16	0.802	-0.02
1428656_at	Rnasen	ribonuclease III, nuclear	-1.25	0.046	-1.03	0.846	1.34	0.26	1.6	0.199	0.17
1457390_at	Prpf3	PRP3 pre-mRNA processing factor 3 homolog (yeast)	1.85	0.028	-1.44	0.099	-1.78	0.071	1.24	0.221	-0.03
1417893_at	Sfxn3	sideroflexin 3	1.15	0.604	1.09	0.662	-1.15	0.189	-1.43	0.16	-0.09
1441299_at	---	Transcribed locus	1.03	0.968	-1.29	0.65	1.3	0.656	-3	0.058	-0.49
1430295_at	Gna13	guanine nucleotide binding protein, alpha 13	1.1	0.352	-1.05	0.882	1.05	0.79	-1.24	0.511	-0.03
1425193_at	2010106G01Rik	RIKEN cDNA 2010106G01 gene	-1.05	0.683	1.12	0.534	1.04	0.808	-1.1	0.546	0
1429063_s_at	Kif16b	kinesin family member 16B	-1.1	0.548	1.09	0.57	1.1	0.438	-1.22	0.394	-0.03
1437365_at	Nsun3	NOL1/NOP2/Sun domain family 3	-1.25	0.4	-1.12	0.698	1.42	0.141	1.21	0.228	0.06
1445365_at	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	-1.08	0.805	1.38	0.616	-1.24	0.658	1.26	0.449	0.08
1435668_at	4932442K08Rik	RIKEN cDNA 4932442K08 gene	1.1	0.381	-1.18	0.628	1.16	0.299	-1.18	0.74	-0.02
1432849_at	---	---	1.16	0.072	1.04	0.888	-1.1	0.802	-1.32	0.085	-0.05
1447018_at	---	---	1.26	0.787	-1.04	0.942	-1.13	0.864	1.58	0.372	0.17

1425663_at	Il1rn	interleukin 1 receptor antagonist	-1.29	0.468	1.09	0.848	1.25	0.372	-1.1	0.612	-0.01
1434336_s_at	Rcor1	REST corepressor 1	-1.08	0.634	-1.17	0.348	1.33	0.347	1.19	0.516	0.07
1442514_a_at	Ell3	elongation factor RNA polymerase II-like 3	-1.09	0.605	1.14	0.815	1.05	0.86	-3.25	0.06	-0.54
1460170_at	Ext2	exostoses (multiple) 2	1.1	0.283	-1.11	0.494	1.1	0.423	-1.19	0.273	-0.02
1428478_at	Reep4	receptor accessory protein 4	-1.37	0.179	-1.02	0.85	1.4	0.006	1.52	0.21	0.13
1455791_at	Cdt1	chromatin licensing and DNA replication factor 1	1.13	0.575	1.13	0.734	-1.18	0.273	-1.01	0.977	0.02
1436714_at	Lpp	LIM domain containing preferred translocation partner in lipoma	1.33	0.51	1.2	0.384	-1.73	0.053	-1.28	0.544	-0.12
1428104_at	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	-1.32	0.44	-1.25	0.379	1.55	0.085	4.27	0.175	0.81
1437032_x_at	Rbm14	RNA binding motif protein 14	1.31	0.416	-1.13	0.532	-1.1	0.462	1.15	0.329	0.06
1460341_at	Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2	-1.16	0.139	1.09	0.259	1.16	0.214	-1.02	0.924	0.02
1424331_at	Rab40c	Rab40c, member RAS oncogene family	1	0.964	-1.08	0.626	1.18	0.082	-1.17	0.522	-0.02
1433777_at	L3mbtl2	l(3)mbt-like 2 (Drosophila)	-1.04	0.841	-1.11	0.442	1.25	0.293	1.22	0.115	0.08
1449377_at	Nicn1	nicolin 1	-1.02	0.954	1.11	0.51	1.02	0.864	-1.64	0.125	-0.13
1439418_x_at	Tmem43	transmembrane protein 43	-1.61	0.246	1.11	0.857	1.38	0.146	-1.43	0.437	-0.14
1438810_at	D10Ertd755e	DNA segment, Chr 10, ERATO Doi 755, expressed	1.14	0.816	1.28	0.623	-1.47	0.146	-1.38	0.037	-0.1
1449412_at	1810046J19Rik	RIKEN cDNA 1810046J19 gene	-1.08	0.404	1.07	0.224	1.12	0.434	-1.19	0.503	-0.02
1425994_a_at	Asah2	N-acylsphingosine amidohydrolase 2	-1.05	0.488	1.15	0.677	1	0.985	-2.23	0.099	-0.28
1447488_at	E130016E03Rik	RIKEN cDNA E130016E03 gene	-1.09	0.906	-1.61	0.327	1.57	0.131	1.85	0.329	0.18
1438587_at	4933417M04Rik	RIKEN cDNA 4933417M04 gene	1.29	0.569	1.44	0.53	-2.59	0.325	-1.02	0.969	-0.22
1417915_at	Rap2b	RAP2B, member of RAS oncogene family	1.04	0.901	-1.62	0.474	1.45	0.302	-1.2	0.585	-0.08
1434589_x_at	Surf4	surfeit gene 4	-1.11	0.597	1.17	0.201	1.03	0.746	-1.32	0.107	-0.06
1460091_at	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B	-1.42	0.481	1.16	0.633	1.25	0.416	-1.08	0.91	-0.02
1417435_at	Large	like-glycosyltransferase	-1.11	0.467	1.2	0.087	1.01	0.95	-1.15	0.376	-0.01
1429239_a_at	Stard4	StAR-related lipid transfer (START) domain containing 4	-1.08	0.757	-1.19	0.641	1.34	0.527	1.37	0.65	0.11
1417260_at	U2af2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 2	-1.03	0.899	-1.01	0.934	1.14	0.485	1.14	0.393	0.06
1435415_x_at	Marcksl1	MARCKS-like 1	1.32	0.226	1.11	0.779	-1.47	0.184	-1.17	0.364	-0.05
1426911_at	Dsc2	desmocollin 2	-1.68	0.281	1.25	0.099	1.26	0.539	-2.01	0.393	-0.29
1459504_at	AU022121	expressed sequence AU022121	-1.21	0.589	-1.08	0.672	1.36	0.154	1.19	0.636	0.06
1423158_at	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	1.02	0.842	1.15	0.378	-1.06	0.78	-2.1	0.161	-0.25
1428581_at	1700024G10Rik	RIKEN cDNA 1700024G10 gene	1.89	0.275	-1.43	0.619	-1.9	0.041	1.28	0.389	-0.04
1417592_at	Frap1	FK506 binding protein 12-rapamycin associated protein 1	1.21	0.562	-1.21	0.24	1.07	0.672	-1.3	0.088	-0.06
1439976_at	Alg11	asparagine-linked glycosylation 11 homolog (yeast, alpha-1,2-mannosyltransfera	1.03	0.812	-1.15	0.483	1.22	0.438	-1.2	0.473	-0.03
1418840_at	Pdcd4 /// LOC6708	programmed cell death 4 /// similar to programmed cell death 4	1.03	0.572	-1.05	0.711	1.13	0.408	-1.17	0.681	-0.02
1457289_at	Nr2e1	nuclear receptor subfamily 2, group E, member 1	1.35	0.581	-1.36	0.294	1.03	0.944	-1.03	0.956	0
1455884_at	Dpp9	dipeptidylpeptidase 9	-1.08	0.568	1.15	0.272	1.04	0.749	-1.04	0.813	0.02
1451587_a_at	Tiprl	TIP41, TOR signalling pathway regulator-like (S. cerevisiae)	1.12	0.648	-1.05	0.8	1.04	0.836	-1.08	0.807	0.01
1423870_at	2610208M17Rik	RIKEN cDNA 2610208M17 gene	1.12	0.539	1.07	0.644	-1.09	0.29	-1.15	0.168	-0.01
1427960_at	Ugt2b34	UDP glucuronosyltransferase 2 family, polypeptide B34	-1.06	0.289	-1.24	0.005	1.37	0.067	1.32	0.155	0.1
1433110_at	5830474E16Rik	RIKEN cDNA 5830474E16 gene	1.21	0.009	1.6	0.351	-3.25	0.002	-1.69	0.165	-0.53
1418956_at	Tssk6	testis-specific serine kinase 6	-1.17	0.834	-1.35	0.383	1.52	0.213	1.56	0.223	0.14
1422656_at	Rasl2-9	RAS-like, family 2, locus 9	1.1	0.578	1.03	0.948	-1.02	0.967	-1.54	0.011	-0.11
1432826_a_at	Cd80	CD80 antigen	-2.36	0.162	1.01	0.931	1.68	0.128	-1.28	0.508	-0.24
1436210_at	C330018K18Rik	RIKEN cDNA C330018K18 gene	1.03	0.898	1.25	0.6	-1.2	0.423	-1.75	0.225	-0.17
1417637_a_at	Hmg20b	high mobility group 20 B	1.08	0.737	1.05	0.412	-1.02	0.649	-1	0.997	0.03
1424742_at	---	---	1.08	0.925	1.28	0.329	-1.33	0.395	-1.5	0.44	-0.12
1418344_at	Tmem8	transmembrane protein 8 (five membrane-spanning domains)	-1.12	0.424	1.24	0.087	-1.02	0.858	1.36	0.192	0.12
1423891_at	Gstt3	glutathione S-transferase, theta 3	-1.14	0.628	-1.21	0.54	1.41	0.217	2.02	0.093	0.27
1441969_at	Trim36	tripartite motif-containing 36	1.2	0.602	1.26	0.711	-1.52	0.031	-1.59	0.212	-0.16
1445897_s_at	Ifi35	interferon-induced protein 35	1.12	0.506	-1.03	0.015	1.03	0.82	-1.38	0.014	-0.07
1454804_at	Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	-1.01	0.936	-1.03	0.775	1.16	0.335	1.89	0.161	0.25
1450931_at	Dock9 /// LOC6703	dedicator of cytokinesis 9 /// similar to Dedicator of cytokinesis protein 9 (Cdc42 g	1.09	0.428	-1.11	0.731	1.12	0.6	-1.19	0.574	-0.02
1421252_a_at	Mef2a	myocyte enhancer factor 2A	1.06	0.702	1.08	0.07	-1.03	0.894	-1.2	0.457	-0.02
1445008_at	Fndc3b	Fibronectin type III domain containing 3B	-1.09	0.849	1.49	0.543	-1.42	0.4	1.72	0.086	0.18

1419917_s_at	Tmed7	transmembrane emp24 protein transport domain containing 7	1.13	0.444	1.06	0.667	-1.08	0.345	-1.03	0.826	0.02
1435055_a_at	Tom1 /// LOC54587	target of myb1 homolog (chicken) /// similar to TOM1	-1.07	0.314	1.08	0.121	1.1	0.325	-1.11	0.125	0
1432786_at	4833420D23Rik	RIKEN cDNA 4833420D23 gene	1.18	0.528	-1.11	0.873	1.04	0.933	-1.32	0.254	-0.06
1431962_a_at	Stambp	Stam binding protein	-1.06	0.625	-1.02	0.786	1.2	0.176	1.2	0.035	0.08
1433811_at	LOC639490 /// LOC	similar to myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog	1.1	0.197	1.03	0.857	-1.02	0.929	-1.68	0.28	-0.14
1437331_a_at	Arf3	ADP-ribosylation factor 3	1.14	0.463	1.01	0.934	-1.04	0.641	-1.18	0.622	-0.02
1453119_at	Otud1	OTU domain containing 1	-1.04	0.882	1.07	0.666	1.09	0.47	-1.58	0.23	-0.12
1423058_at	Capza2	capping protein (actin filament) muscle Z-line, alpha 2	-1.17	0.185	1.13	0.387	1.13	0.414	-1.34	0.172	-0.06
1440744_at	Pi16	Peptidase inhibitor 16	-2.27	0.331	2.21	0.121	-2.15	0.012	1.27	0.597	-0.23
1434092_at	Nos3as	nitric oxide synthase 3 antisense	-2.02	0.33	1.72	0.006	-1.11	0.635	1.33	0.629	-0.02
1419954_s_at	Zfand3	zinc finger, AN1-type domain 3	1.08	0.151	-1.02	0.847	1.06	0.686	-1.05	0.803	0.01
1422217_a_at	Cyp1a1	cytochrome P450, family 1, subfamily a, polypeptide 1	1.2	0.519	1.04	0.858	-1.13	0.785	-1.06	0.886	0.01
1457074_at	Kif24	kinesin family member 24	-1.59	0.149	1.75	0.078	-1.35	0.243	2.54	0.244	0.34
1444426_at	F730031O20Rik	RIKEN cDNA F730031O20 gene	-1.23	0.65	-1.05	0.926	1.35	0.378	1.33	0.468	0.1
1416749_at	Htra1	HtrA serine peptidase 1	-1.18	0.097	1.23	0.514	1.04	0.843	-1.85	0.103	-0.19
1449131_s_at	Cd1d1	CD1d1 antigen	1.06	0.855	-1.15	0.177	1.19	0.657	-1.59	0.295	-0.12
1421608_at	Il20	interleukin 20	-2.95	0.163	1.29	0.57	1.48	0.327	-1.29	0.614	-0.36
1448313_at	Tpp1	tripeptidyl peptidase I	-1.15	0.207	1.07	0.539	1.18	0.064	-1.03	0.851	0.02
1433037_at	5830434F19Rik	RIKEN cDNA 5830434F19 gene	-1.3	0.236	1.29	0.115	1.05	0.78	-1.17	0.591	-0.03
1440568_at	Pot1	protection of telomeres 1	1.18	0.281	-1.56	0.201	1.3	0.632	-1.04	0.816	-0.03
1436715_s_at	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synth	-1.02	0.693	1.03	0.811	1.1	0.258	-1.34	0.163	-0.06
1432949_at	5330421F21Rik	RIKEN cDNA 5330421F21 gene	-1.46	0.154	1.18	0.296	1.25	0.236	-1.33	0.567	-0.09
1444042_at	Trip11	thyroid hormone receptor interactor 11	-1.18	0.374	1.14	0.754	1.13	0.468	-1.09	0.819	0
1444924_at	---	---	-1.32	0.688	1.44	0.267	-1.09	0.762	1.17	0.819	0.05
1423750_a_at	Sf1	Splicing factor 1	-1.01	0.945	-1.07	0.688	1.19	0.38	1.18	0.447	0.07
1449618_s_at	2900092E17Rik	RIKEN cDNA 2900092E17 gene	-1.03	0.786	1.06	0.719	1.08	0.487	-1.33	0.038	-0.05
1458420_at	9430057O19Rik	RIKEN cDNA 9430057O19 gene	-2.03	0.003	1.77	0.279	-1.17	0.72	1.12	0.764	-0.08
1448967_at	Nipsnap3a	nipsnap homolog 3A (C. elegans)	1	0.998	-1.03	0.595	1.15	0.322	-1.07	0.638	0.01
1423548_s_at	Ergic3	ERGIC and golgi 3	1.15	0.447	-1.13	0.337	1.08	0.46	-1.04	0.858	0.02
1437115_at	AA673488	expressed sequence AA673488	1.11	0.463	-1.14	0.071	1.13	0.684	-1.08	0.34	0
1425814_a_at	Calcrl	calcitonin receptor-like	1.1	0.007	1.24	0.004	-1.29	0.001	-1.31	0.25	-0.07
1435646_at	Ikbkg	inhibitor of kappaB kinase gamma	-1.12	0.175	1.06	0.812	1.17	0.509	-1.05	0.712	0.01
1423297_at	Add3	adducin 3 (gamma)	-1.27	0.079	1.08	0.728	1.25	0.508	-2.28	0.088	-0.31
1418233_a_at	Trappc5	trafficking protein particle complex 5	1.14	0.161	-1.07	0.208	1.04	0.771	-1.78	0.189	-0.17
1447665_at	Lrrn6c	leucine rich repeat neuronal 6C	-4.5	0.001	-1.53	0.412	2.24	0.136	1.29	0.685	-0.62
1453473_a_at	Dynlt1 /// LOC6712	dynein light chain Tctex-type 1 /// similar to Cytoplasmic dynein light chain (T-con	-1.19	0.298	1.09	0.398	1.19	0.481	-1.02	0.899	0.02
1424385_at	---	---	1.08	0.525	-1.11	0.037	1.14	0.398	-1.12	0.491	0
1453310_at	Ppil6	peptidylprolyl isomerase (cyclophilin)-like 6	1.05	0.62	-1.01	0.989	1.07	0.804	-1.6	0.501	-0.12
1442327_at	4930482J15Rik	RIKEN cDNA 4930482J15 gene	-1.4	0.023	1.33	0.202	1.07	0.773	-1.29	0.231	-0.07
1416075_at	Sav1	salvador homolog 1 (Drosophila)	-1.08	0.688	-1.17	0.088	1.34	0.197	1.5	0.162	0.15
1423053_at	Arf4	ADP-ribosylation factor 4	-1.05	0.803	-1.01	0.93	1.18	0.434	1.07	0.695	0.05
1418068_at	Ndufa10	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 10	-1.19	0.396	-1.27	0.416	1.49	0.027	1.12	0.424	0.04
1445545_at	Tmem77	Transmembrane protein 77	1.22	0.576	1.09	0.395	-1.23	0.319	-2.12	0.081	-0.26
1435550_at	C430014K11Rik	RIKEN cDNA C430014K11 gene	1.08	0.617	-1.04	0.869	1.07	0.826	-1.11	0.726	0
1427130_x_at	1700021K02Rik	RIKEN cDNA 1700021K02 gene	-1.16	0.553	-1.16	0.47	1.39	0.316	1.04	0.913	0.03
1428608_at	Mylc2b	myosin light chain, regulatory B	1	0.976	1.18	0.004	-1.07	0.057	-1.35	0.237	-0.06
1433460_at	Ttc7b	tetratricopeptide repeat domain 7B	-1.08	0.806	-1.03	0.844	1.22	0.308	1.09	0.73	0.05
1428361_x_at	Hba-a1	hemoglobin alpha, adult chain 1	1.04	0.402	1.36	0.129	-1.39	0.007	-1.26	0.099	-0.06
1446890_at	---	---	-1.28	0.476	1.09	0.862	1.25	0.599	-1.25	0.486	-0.05
1433974_at	Sephs1	selenophosphate synthetase 1	-1.01	0.897	-1.16	0.487	1.27	0.401	1.66	0.377	0.19
1419715_at	1700029F12Rik	RIKEN cDNA 1700029F12 gene	1.63	0.427	-1.17	0.717	-1.57	0.155	1.2	0.669	0.02
1451676_at	Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	1.32	0.356	1.08	0.653	-1.4	0.052	-1.17	0.622	-0.04
1424088_at	Myg1	melanocyte proliferating gene 1	1.1	0.556	-1.03	0.687	1.05	0.79	-1.09	0.463	0.01

1453114_at	Nol9	nucleolar protein 9	-1.36	0.7	-1.19	0.676	1.54	0.192	1.23	0.57	0.06
1425276_at	Fbs1	fibrosin 1	-1.05	0.842	1.12	0.725	1.05	0.845	-1.14	0.497	-0.01
1437231_at	Slitrk6	SLIT and NTRK-like family, member 6	1.15	0.769	1.12	0.815	-1.18	0.441	-1.09	0.89	0
1435649_at	Nexn	nexilin	1.17	0.6	1.15	0.528	-1.26	0.262	-1.28	0.402	-0.05
1431551_at	2610028D06Rik	RIKEN cDNA 2610028D06 gene	1.41	0.619	-1.15	0.716	-1.19	0.254	1.57	0.199	0.16
1429803_at	1700021F07Rik	RIKEN cDNA 1700021F07 gene	1.3	0.641	-1.14	0.29	-1.06	0.102	1.06	0.655	0.04
1427965_at	Ssbp1	single-stranded DNA binding protein 1	-1.1	0.428	1.07	0.321	1.14	0.112	-1.36	0.036	-0.06
1426532_at	Zmynd11	zinc finger, MYND domain containing 11	1.01	0.983	-1.07	0.679	1.18	0.647	-1.33	0.395	-0.05
1440743_at	4931428F04Rik	RIKEN cDNA 4931428F04 gene	1	0.994	-1.16	0.487	1.25	0.463	-1.18	0.165	-0.02
1438440_at	Rnasen	ribonuclease III, nuclear	1.23	0.632	-2.21	0.459	1.44	0.316	-1.62	0.294	-0.29
1433590_at	Herc3	hect domain and RLD 3	-1.22	0.202	1.01	0.967	1.29	0.329	-1.11	0.764	-0.01
1447894_x_at	Vps52 /// LOC6317	vacuolar protein sorting 52 (yeast) /// similar to vacuolar protein sorting 52	-1.04	0.559	-1.09	0.531	1.24	0.279	1.06	0.582	0.04
1415928_a_at	Map1lc3b	microtubule-associated protein 1 light chain 3 beta	-1.03	0.558	1.17	0.351	-1.03	0.66	1.15	0.104	0.07
1423615_at	Zfp364	zinc finger protein 364	-1.21	0.135	1.01	0.937	1.28	0.082	-1.02	0.864	0.01
1434575_at	Epb4.1l1	erythrocyte protein band 4.1-like 1	-1.1	0.61	-1.04	0.832	1.25	0.067	1.2	0.044	0.08
1425132_at	Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	-1.23	0.172	-1.52	0.521	1.64	0.009	1.91	0.115	0.2
1416530_a_at	Pnp	purine-nucleoside phosphorylase	-1.12	0.476	1.25	0.327	-1.02	0.695	2.07	0.125	0.29
1418631_at	Ube2h	ubiquitin-conjugating enzyme E2H	-1.08	0.758	-1.09	0.344	1.27	0.368	1.78	0.343	0.22
1433359_at	---	---	-2.22	0.378	1.79	0.215	-1.14	0.611	1.76	0.191	0.05
1435965_at	Cnot3	CCR4-NOT transcription complex, subunit 3	1.17	0.185	-1.01	0.974	-1.04	0.842	1.08	0.625	0.05
1429317_at	Qrsl1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	1.01	0.964	-1.21	0.481	1.28	0.131	-1.58	0.066	-0.12
1443851_at	8430415E04Rik	RIKEN cDNA 8430415E04 gene	-1.17	0.053	1.11	0.721	1.16	0.563	-1.43	0.371	-0.08
1440125_at	A530054K11Rik	RIKEN cDNA A530054K11 gene	-1.17	0.232	1.01	0.963	1.25	0.222	-1.56	0.053	-0.12
1452200_at	D11Ertd497e	DNA segment, Chr 11, ERATO Doi 497, expressed	1.12	0.354	1	0.976	-1.01	0.853	-1.24	0.119	-0.03
1418535_at	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	-1	0.988	1.25	0.538	-1.14	0.341	1.18	0.667	0.07
1424301_at	Zfp219	zinc finger protein 219	1.06	0.852	-1.11	0.124	1.16	0.416	-1.11	0.602	0
1425762_a_at	Rxra	retinoid X receptor alpha	-1.28	0.043	-1.07	0.763	1.4	0.26	1.27	0.313	0.08
1457828_at	Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	2.03	0.267	-2.91	0.152	-1.35	0.256	1.38	0.53	-0.21
1454438_at	Rab27a	RAB27A, member RAS oncogene family	-1.01	0.994	-1.05	0.868	1.17	0.533	1.23	0.804	0.09
1433631_at	Eif5	eukaryotic translation initiation factor 5	-1.05	0.666	-1.12	0.136	1.27	0.05	1.33	0.238	0.11
1446377_at	Fbln5	fibulin 5	-1.06	0.857	-1.04	0.961	1.21	0.554	1.27	0.529	0.1
1436569_at	C030045D06Rik	RIKEN cDNA C030045D06 gene	1.28	0.378	1.14	0.07	-1.45	0.021	-1	0.992	-0.01
1417864_at	Pgk1 /// LOC43359	phosphoglycerate kinase 1 /// phosphoglycerate kinase 1-like /// phosphoglycerat	-1.24	0.063	1.02	0.804	1.29	0.089	-1.11	0.279	-0.01
1439552_at	Trio	triple functional domain (PTPRF interacting)	1.07	0.921	-1.1	0.829	1.14	0.689	-1.12	0.598	0
1437757_at	---	---	1.63	0.184	-1.49	0.359	-1.22	0.324	1.18	0.439	0.02
1418633_at	Notch1	Notch gene homolog 1 (Drosophila)	1.06	0.744	-1.31	0.298	1.3	0.141	-1.26	0.052	-0.05
1424427_at	Tada1l	transcriptional adaptor 1 (HFI1 homolog, yeast) like	1.08	0.139	1.08	0.706	-1.05	0.772	-1.19	0.336	-0.02
1459733_at	Pea15	Phosphoprotein enriched in astrocytes 15	1.19	0.384	1.2	0.234	-1.37	0.253	-1.39	0.44	-0.09
1435712_a_at	Rps18	ribosomal protein S18	1.13	0.071	1.08	0.328	-1.09	0.463	-1.4	0.006	-0.07
1420425_at	Prdm1	PR domain containing 1, with ZNF domain	-1.17	0.441	1.35	0.079	-1.1	0.703	1.9	0.207	0.25
1424871_s_at	1500031H01Rik	RIKEN cDNA 1500031H01 gene	1.09	0.505	-1.12	0.355	1.13	0.288	-1.1	0.563	0
1459298_at	---	---	-1.37	0.464	1.52	0.467	-1.15	0.684	1.69	0.391	0.17
1421519_a_at	Zfp120	zinc finger protein 120	1.04	0.724	-1.17	0.062	1.22	0.018	-1.93	0.051	-0.21
1421990_at	Syt1	synaptotagmin I	-1.3	0.647	-1.29	0.551	1.57	0.297	1.09	0.778	0.02
1422749_at	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	1.2	0.442	-1.4	0.216	1.21	0.269	-2.19	0.173	-0.3
1445847_at	---	---	-1.83	0.064	-1.31	0.55	1.81	0.186	1.28	0.671	-0.01
1450008_a_at	Ctnnb1	catenin (cadherin associated protein), beta 1	-1.2	0.011	1.01	0.942	1.28	0.222	-1.06	0.661	0.01
1431325_at	Cml3	camello-like 3	1.16	0.842	-1.21	0.697	1.13	0.776	-1.44	0.481	-0.09
1449634_a_at	Anks1b /// LOC544	ankyrin repeat and sterile alpha motif domain containing 1B /// similar to AIDA-1b	1.11	0.907	-6.72	0.034	1.86	0.091	-1.19	0.796	-1.23
1457909_at	Dna2l	DNA2 DNA replication helicase 2-like (yeast)	-1.28	0.491	1.48	0.192	-1.16	0.697	1.69	0.398	0.18
1436812_at	Fkrp	fukutin related protein	1.07	0.677	-1.17	0.636	1.19	0.089	-1.13	0.47	-0.01
1429321_at	Rnf149	ring finger protein 149	1.02	0.683	-1.07	0.54	1.17	0.45	-1.37	0.266	-0.06
1453179_at	Phca	phytoceramidase, alkaline	1.31	0.7	-1.31	0.5	1.05	0.888	-1.01	0.98	0.01

1417092_at	Pthr1	parathyroid hormone receptor 1	1.02	0.894	1.14	0.551	-1.04	0.91	-1.16	0.256	-0.01
1454386_at	6430500D05Rik	RIKEN cDNA 6430500D05 gene	1.21	0.678	1.24	0.709	-1.5	0.27	-1.66	0.482	-0.18
1444459_at	---	---	-1.18	0.53	1.3	0.322	-1.04	0.834	1.66	0.141	0.19
1434358_x_at	Rps21	ribosomal protein S21	1.08	0.55	1.21	0.11	-1.21	0.015	-1.26	0.09	-0.04
1417967_at	Mms19l	MMS19 (MET18 S. cerevisiae)-like	1.06	0.637	1.08	0.373	-1.02	0.915	-1.52	0.153	-0.1
1445072_at	---	---	1.21	0.779	1.2	0.471	-1.4	0.222	-2.29	0.183	-0.32
1441228_at	Apold1	apolipoprotein L domain containing 1	-1.23	0.322	1.66	0.189	-1.56	0.447	2.07	0.295	0.24
1458162_at	---	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C63003	1.29	0.675	1.27	0.584	-1.8	0.051	-1.21	0.684	-0.11
1457095_at	Pscd1	Pleckstrin homology, Sec7 and coiled-coil domains 1	-1.14	0.772	1.29	0.448	-1.05	0.922	1.17	0.714	0.07
1450842_a_at	Cenpa	centromere protein A	-1.05	0.862	-1.09	0.555	1.25	0.459	2.44	0.142	0.39
1451401_a_at	0610009K11Rik	RIKEN cDNA 0610009K11 gene	-1.03	0.793	1.02	0.826	1.13	0.555	-1.09	0.614	0.01
1447876_x_at	2310073E15Rik	RIKEN cDNA 2310073E15 gene	-2.4	0.426	1.6	0.167	1.1	0.797	-1.31	0.359	-0.25
1442714_at	LOC667963	hypothetical protein LOC667963	1.31	0.281	1.09	0.563	-1.37	0.18	-1.14	0.572	-0.03
1416939_at	Ppa1	pyrophosphatase (inorganic) 1	-1.03	0.703	-1.04	0.593	1.18	0.142	1.2	0.29	0.08
1424480_s_at	Akt2	thymoma viral proto-oncogene 2	-1.09	0.158	1.02	0.746	1.18	0.156	-1.06	0.396	0.01
1426227_s_at	Vps37c	vacuolar protein sorting 37C (yeast)	-1.13	0.193	1.01	0.956	1.23	0.223	-1.01	0.889	0.02
1440754_at	Ankhd1	Ankyrin repeat and KH domain containing 1	-1.48	0.441	1.76	0.326	-1.46	0.273	1.3	0.255	0.03
1426101_at	---	ORFs (putative primordial protein)	1.2	0.663	1.15	0.694	-1.29	0.633	-2	0.43	-0.24
1424707_at	Tmed10	transmembrane emp24-like trafficking protein 10 (yeast)	-1.01	0.923	1.06	0.426	1.06	0.479	-1.08	0.664	0.01
1442606_at	Dnmbp	Dynamin binding protein	1.26	0.234	1.1	0.819	-1.33	0.106	-1.28	0.281	-0.06
1440667_at	Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	-1.65	0.25	1.43	0.453	1.08	0.869	-1.2	0.258	-0.08
1423350_at	Socs5	suppressor of cytokine signaling 5	1.03	0.859	1.35	0.056	-1.36	0.053	-1.8	0.152	-0.19
1455559_at	E330039K12Rik	RIKEN cDNA E330039K12 gene	1.21	0.617	-1.31	0.538	1.15	0.646	-1.18	0.632	-0.03
1423820_at	Elof1	elongation factor 1 homolog (ELF1, S. cerevisiae)	-1.08	0.391	-1.09	0.327	1.28	0.362	1.13	0.481	0.06
1428333_at	2900062L11Rik	RIKEN cDNA 2900062L11 gene	-1.45	0.086	1.54	0.443	-1.12	0.797	1.49	0.293	0.12
1447856_x_at	Slc25a25	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 25	-1.8	0.613	-1.25	0.54	1.77	0.177	1.35	0.486	0.02
1442423_at	Nrxn3	Neurexin III	1.25	0.657	1.45	0.323	-2.36	0.023	-1.31	0.602	-0.24
1448798_at	Eps8l3	ESP8-like 3	1.17	0.315	-1.05	0.867	1	0.994	-1.24	0.136	-0.03
1427463_at	Casd1	CAS1 domain containing 1	-1.16	0.642	1.09	0.837	1.17	0.766	-1.38	0.038	-0.07
1458190_at	Arhgap4	Rho GTPase activating protein 4	-1.16	0.664	1.06	0.901	1.2	0.583	-1.93	0.417	-0.21
1421493_a_at	Rgs20	regulator of G-protein signaling 20	-1.13	0.54	-1.99	0.048	1.74	0.27	1.21	0.719	-0.04
1455821_x_at	C1qbp	complement component 1, q subcomponent binding protein	-1.02	0.913	-1.37	0.05	1.41	0.055	1.16	0.215	0.05
1448579_at	Glg1	golgi apparatus protein 1	-1.09	0.058	1.06	0.567	1.15	0.503	-1.05	0.799	0.01
1436813_x_at	Khsrp	KH-type splicing regulatory protein	-1.36	0.172	-1.71	0.049	1.8	0.067	1.68	0.217	0.1
1447372_at	Aldh16a1	aldehyde dehydrogenase 16 family, member A1	1	0.963	-1.09	0.289	1.2	0.407	-1.25	0.003	-0.03
1445146_at	B230219N05Rik	RIKEN cDNA B230219N05 gene	-1.55	0.273	1.19	0.668	1.28	0.591	-2.05	0.099	-0.28
1430533_a_at	Ctnnb1	catenin (cadherin associated protein), beta 1	1.04	0.861	-1.15	0.668	1.21	0.595	-1.38	0.308	-0.07
1457981_x_at	Gins1	GINS complex subunit 1 (Psf1 homolog)	-1.11	0.382	1.39	0.524	-1.2	0.612	1.99	0.341	0.27
1455364_a_at	Rps7 /// LOC64005	ribosomal protein S7 /// similar to 40S ribosomal protein S7 (S8)	1.02	0.857	1.14	0.238	-1.03	0.705	-1.48	0.001	-0.09
1435482_at	Fibcd1	fibrinogen C domain containing 1	-1.92	0.559	-1	0.995	1.6	0.342	2.46	0.251	0.29
1428739_at	2310040A07Rik	RIKEN cDNA 2310040A07 gene	1.25	0.132	1.51	0.514	-2.78	0.049	-1.05	0.896	-0.26
1433520_at	Scap	SREBP cleavage activating protein	1.08	0.304	-1.25	0.03	1.24	0.024	-1.12	0.202	-0.01
1439359_x_at	Nrxn1	neurexin I	1.13	0.633	1.31	0.31	-1.47	0.368	-1.84	0.177	-0.22
1457720_at	---	---	1.27	0.786	1.18	0.805	-1.48	0.498	-1.55	0.24	-0.15
1440728_at	Kcnma1	Potassium large conductance calcium-activated channel, subfamily M, alpha mer	-1.21	0.77	1.56	0.346	-1.36	0.391	1.35	0.529	0.08
1429242_at	1110054O05Rik	RIKEN cDNA 1110054O05 gene	1.11	0.129	-1.01	0.974	1.02	0.833	-1.26	0.146	-0.03
1436489_x_at	C85492	expressed sequence C85492	-1.11	0.218	-1.09	0.66	1.3	0.032	1.4	0.097	0.13
1434694_at	Lrrc8a	leucine rich repeat containing 8A	1.04	0.804	1.16	0.292	-1.09	0.06	-1.05	0.594	0.02
1418606_at	Hoxd10	homeo box D10	-1.22	0.094	-1.05	0.913	1.35	0.313	1.14	0.817	0.06
1432610_at	2900024J01Rik	RIKEN cDNA 2900024J01 gene	-1.22	0.721	-1.37	0.393	1.57	0.173	1.19	0.241	0.04
1453778_at	2810407C02Rik	RIKEN cDNA 2810407C02 gene	-1.45	0.274	1.15	0.685	1.29	0.339	-1.59	0.31	-0.15
1442430_at	BC048562	cDNA sequence BC048562	1.03	0.944	1.14	0.574	-1.05	0.82	-1.05	0.747	0.02
1427761_at	Prnpip1	prion protein interacting protein 1	1.01	0.96	1.25	0.594	-1.16	0.765	-1.12	0.838	0

1436815_x_at	Tpcn2	Two pore segment channel 2	1.91	0.271	-2.53	0.134	-1.23	0.479	1.49	0.352	-0.09
1435165_at	Cntn2	contactin 2	1.35	0.346	-1.09	0.802	-1.17	0.812	1.03	0.872	0.03
1428534_at	2310073E15Rik	RIKEN cDNA 2310073E15 gene	-1	0.989	1	0.98	1.12	0.122	-1.21	0.363	-0.02
1433619_at	AI894139	expressed sequence AI894139	-1.44	0.086	1.1	0.568	1.33	0.045	-1.35	0.425	-0.09
1459800_s_at	Map3k4	mitogen activated protein kinase kinase kinase 4	1.08	0.745	1.08	0.232	-1.03	0.84	-1.5	0.036	-0.09
1449574_a_at	Cdc42	cell division cycle 42 homolog (S. cerevisiae)	1.03	0.922	-1.12	0.601	1.2	0.525	-1.24	0.467	-0.03
1457127_at	Defb42	defensin beta 42	1.03	0.826	1.13	0.726	-1.04	0.9	-1.54	0.28	-0.1
1451140_s_at	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.01	0.933	-1.14	0.409	1.24	0.085	-1.28	0.47	-0.04
1456214_at	Pcdh7	protocadherin 7	1.08	0.782	1.16	0.716	-1.14	0.336	-1.32	0.055	-0.05
1441348_at	Zfp422-rs1	Zinc finger protein 422, related sequence 1	1.1	0.427	1.1	0.808	-1.08	0.612	-1.15	0.753	-0.01
1444899_at	D630037F22Rik	RIKEN cDNA D630037F22 gene	1.55	0.417	-1.37	0.636	-1.18	0.666	1.11	0.831	0.03
1432653_at	1700008H02Rik	RIKEN cDNA 1700008H02 gene	1.66	0.315	-1.05	0.939	-1.93	0.219	1.67	0.422	0.09
1419883_s_at	Atp6v1b2	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.33	0.031	1.03	0.706	1.34	0.225	-1.12	0.634	-0.02
1418361_at	Gas8	growth arrest specific 8	-1.02	0.833	-1.34	0.394	1.39	0.091	1.06	0.814	0.03
1426040_a_at	Odf2	outer dense fiber of sperm tails 2	-1.11	0.396	-1.18	0.781	1.38	0.64	2.57	0.132	0.41
1429773_at	2810451A06Rik	RIKEN cDNA 2810451A06 gene	-1.01	0.991	1.15	0.571	-1.02	0.978	1.32	0.655	0.11
1429628_at	6330407J23Rik	RIKEN cDNA 6330407J23 gene	1.24	0.675	-2.48	0.041	1.48	0.412	-1.11	0.809	-0.22
1437464_at	Spata7	spermatogenesis associated 7	-1	0.991	-1.12	0.874	1.24	0.473	1.01	0.978	0.03
1450867_at	Mrpl17	mitochondrial ribosomal protein L17	1.14	0.486	1.05	0.877	-1.06	0.707	-1.16	0.713	-0.01
1418553_at	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	-1.09	0.38	1.08	0.532	1.13	0.394	-1.94	0.195	-0.2
1447401_at	Wbp11	WW domain binding protein 11	-1.06	0.499	1.65	0.173	-1.9	0.271	1.15	0.546	-0.04
1441204_at	A130019P10Rik	RIKEN cDNA A130019P10 gene	1.12	0.751	-1.05	0.885	1.06	0.81	-1.47	0.178	-0.09
1423661_s_at	Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	1.04	0.831	-1.19	0.243	1.24	0.578	-1.04	0.849	0.01
AFFX-b-ActinMur/M	Actb	actin, beta, cytoplasmic	1.17	0.668	1.04	0.857	-1.1	0.494	-1.2	0.083	-0.02
1453273_at	Kcnv1	potassium channel, subfamily V, member 1	-1.34	0.65	1.51	0.34	-1.15	0.775	1.54	0.528	0.14
1430814_at	1300013D18Rik ///	RIKEN cDNA 1300013D18 gene /// similar to cytochrome P450, family 2, subfami	1.03	0.502	-1.07	0.726	1.16	0.37	-1.52	0.145	-0.1
1423372_at	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.05	0.782	1.11	0.348	-1.04	0.433	-1.1	0.68	0.01
1446155_at	2700089E24Rik	RIKEN cDNA 2700089E24 gene	-1.12	0.326	-1.15	0.068	1.37	0.017	1.28	0.069	0.09
1430298_at	4930473A06Rik	RIKEN cDNA 4930473A06 gene	1.17	0.372	1.18	0.599	-1.29	0.244	-1.61	0.135	-0.14
1433490_s_at	Epb4.1l2	erythrocyte protein band 4.1-like 2	1.03	0.725	1.28	0.051	-1.22	0.239	-1.46	0.264	-0.09
1455844_at	Cables1	Cdk5 and Abl enzyme substrate 1	1.06	0.77	-1.04	0.938	1.1	0.78	-2.87	0.049	-0.44
1451415_at	1810011O10Rik	RIKEN cDNA 1810011O10 gene	1.08	0.511	1.09	0.785	-1.04	0.687	-1.5	0.104	-0.09
1452688_at	Prpf39	PRP39 pre-mRNA processing factor 39 homolog (yeast)	1.15	0.349	-1.38	0.097	1.25	0.402	-1.09	0.767	-0.02
1418033_s_at	Zfp535	zinc finger protein 535	1.17	0.624	-1.05	0.903	1	0.99	-1.2	0.376	-0.02
1446495_at	---	---	1.77	0.045	-1.23	0.596	-1.82	0.38	1.11	0.367	-0.04
1417781_at	Lass4	longevity assurance homolog 4 (S. cerevisiae)	1.23	0.192	-1.41	0.076	1.19	0.277	-1.35	0.255	-0.08
1447453_x_at	A230083H22Rik	RIKEN cDNA A230083H22 gene	1.16	0.859	-1.52	0.272	1.31	0.352	-1.34	0.396	-0.1
1426253_at	4933428G09Rik	RIKEN cDNA 4933428G09 gene	-1.28	0.312	1.06	0.747	1.28	0.282	-1.19	0.238	-0.03
1449644_at	LOC236118	similar to T-cell receptor alpha chain V region CTL-F3 precursor	-1.26	0.434	1.3	0.574	1.04	0.915	-6.76	0.001	-1.42
1422880_at	Sypl	synaptophysin-like protein	1.17	0.422	-1.04	0.454	1	0.957	-1.18	0.511	-0.01
1430009_at	Hsfy2	heat shock transcription factor, Y linked 2	1.38	0.569	1.12	0.838	-1.59	0.28	-1.33	0.598	-0.11
1453452_at	4930517J16Rik	RIKEN cDNA 4930517J16 gene	1.47	0.588	-1.63	0.418	1.04	0.74	-1.54	0.134	-0.16
1446958_at	D13Ertd150e	DNA segment, Chr 13, ERATO Doi 150, expressed	1.25	0.326	1.17	0.705	-1.4	0.103	-1.24	0.558	-0.06
1441112_at	LOC667118 /// LOC	similar to Zinc finger BED domain containing protein 4 /// similar to Zinc finger BE	1.47	0.161	-1.06	0.825	-1.38	0.178	1.01	0.988	0.01
1455823_at	Bbs4	Bardet-Biedl syndrome 4 homolog (human)	-1.11	0.375	1.09	0.737	1.14	0.551	-1.23	0.299	-0.03
1418196_at	Tep1	telomerase associated protein 1	-1.07	0.718	1.13	0.569	1.06	0.592	-1.24	0.55	-0.03
1420773_at	Dub1	deubiquitinating enzyme 1	-1.6	0.37	-1.1	0.865	1.6	0.292	1.17	0.867	0.02
1419891_s_at	C77545	expressed sequence C77545	1	0.994	1.83	0.267	-3.36	0.041	-1.36	0.494	-0.47
1418369_at	Prim1	DNA primase, p49 subunit	-1.26	0.035	-1.22	0.034	1.51	0.218	2.5	0.194	0.38
1450910_at	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	1.27	0.577	-1.14	0.615	-1.02	0.948	1.53	0.415	0.16
1420521_at	Papln	papilin, proteoglycan-like sulfated glycoprotein	1.03	0.849	1.35	0.686	-1.34	0.264	-1.48	0.519	-0.11
1446559_at	D830016K09Rik	RIKEN cDNA D830016K09 gene	1.43	0.128	1	0.996	-1.43	0.337	-1.9	0.18	-0.22
1426648_at	Mapkapk2	MAP kinase-activated protein kinase 2	-1.16	0.376	1.11	0.45	1.15	0.29	-1.13	0.488	-0.01

1440822_x_at	Reps1	RalBP1 associated Eps domain containing protein	-1.19	0.48	1.05	0.565	1.24	0.123	-1.35	0.168	-0.06
1433143_at	9230118N17Rik	RIKEN cDNA 9230118N17 gene	-2.89	0.1	1.69	0.336	1.09	0.871	-1.66	0.446	-0.44
1458864_at	---	---	-2.22	0.094	1.54	0.327	1.14	0.818	-1.23	0.674	-0.19
1429848_at	Pvr	poliovirus receptor	1.35	0.511	1.15	0.798	-1.57	0.219	-2.13	0.127	-0.3
1426846_at	Cenpt	centromere protein T	-1.16	0.394	-1.04	0.902	1.31	0.079	1.8	0.263	0.23
1439506_at	Gm98	gene model 98, (NCBI)	-1.97	0.152	1.3	0.16	1.33	0.354	-1.69	0.495	-0.26
1438340_at	A930006D11Rik	RIKEN cDNA A930006D11Rik gene	-1.9	0.521	1.51	0.403	1.1	0.453	-1.82	0.128	-0.28
1453248_at	2810039B14Rik	RIKEN cDNA 2810039B14 gene	1.04	0.945	-1.28	0.179	1.31	0.27	-1.2	0.5	-0.03
1453450_at	C030006K11Rik	RIKEN cDNA C030006K11 gene	-1.01	0.931	-1.06	0.774	1.2	0.338	1.06	0.853	0.05
1438730_at	BC028801	cDNA sequence BC028801	1.41	0.307	1.06	0.837	-1.52	0.115	-1.05	0.721	-0.02
1438886_at	Heyl	hairy/enhancer-of-split related with YRPW motif-like	1.5	0.053	-1.4	0.278	-1.09	0.627	1.01	0.963	0
1459919_a_at	Mobkl2c	MOB1, Mps One Binder kinase activator-like 2C (yeast)	1.09	0.775	-1.1	0.746	1.13	0.55	-1.12	0.626	0
1435756_at	Samd10	sterile alpha motif domain containing 10	1.27	0.437	1.01	0.982	-1.17	0.526	-1.3	0.69	-0.05
1433589_at	D6Wsu116e	DNA segment, Chr 6, Wayne State University 116, expressed	-1.18	0.365	1.25	0.264	1.03	0.915	-1.02	0.947	0.02
1429737_a_at	Crls1	cardiolipin synthase 1	-1.12	0.133	-1.03	0.601	1.27	0.172	1.33	0.217	0.11
1452136_at	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	1.53	0.001	1.08	0.825	-1.91	0.177	-1.16	0.804	-0.12
1426024_a_at	Dbn1	drebrin 1	1.05	0.794	1.24	0.365	-1.19	0.342	-1.44	0.107	-0.08
1456469_x_at	Lasp1	LIM and SH3 protein 1	-1.47	0.527	-1.32	0.369	1.69	0.258	1.19	0.772	0.02
1437471_at	Lrrc45	leucine rich repeat containing 45	-1.03	0.862	1.02	0.884	1.15	0.283	-1.33	0.26	-0.05
1444347_at	Mgat4a	mannoside acetylglucosaminyltransferase 4, isoenzyme A	-1.22	0.324	1.26	0.084	1.05	0.866	-1.04	0.772	0.01
1424576_s_at	Cyp2c44	cytochrome P450, family 2, subfamily c, polypeptide 44	1.7	0.313	-1.53	0.047	-1.29	0.532	1.01	0.972	-0.03
1454058_at	4931406E20Rik	RIKEN cDNA 4931406E20 gene	-1.23	0.63	1.14	0.694	1.18	0.684	-1.52	0.571	-0.11
1415792_at	Rbck1	RanBP-type and C3HC4-type zinc finger containing 1	1.17	0.392	1.06	0.753	-1.1	0.542	-1.06	0.503	0.02
1454870_x_at	Gpr172b	G protein-coupled receptor 172B	1.08	0.57	-1.06	0.624	1.11	0.712	-1.12	0.371	0
1459843_s_at	Smad1	MAD homolog 1 (Drosophila)	1.1	0.133	1.22	0.011	-1.23	0.016	-1.21	0.514	-0.03
1459797_at	Epb4.1l2	Erythrocyte protein band 4.1-like 2	-2.11	0.29	-1.02	0.968	1.68	0.261	1.65	0.103	0.05
1423389_at	Smad7	MAD homolog 7 (Drosophila)	-1.16	0.466	1.18	0.636	1.09	0.567	-2.14	0.019	-0.26
1425601_a_at	Rtkn	rhotekin	1.31	0.332	1.15	0.404	-1.5	0.095	-1.49	0.565	-0.13
1418432_at	Cab39	calcium binding protein 39	1.17	0.549	1.06	0.739	-1.1	0.669	-1.2	0.685	-0.02
1425843_at	Mrpl33	mitochondrial ribosomal protein L33	-1.41	0.37	1.2	0.589	1.23	0.399	-1.38	0.53	-0.09
1426966_at	Axin1	axin 1	-1.05	0.594	1.11	0.107	1.07	0.674	-1.24	0.062	-0.03
1423521_at	Lmnb1	lamin B1	-1.81	0.183	-1.34	0.164	1.83	0.012	1.05	0.904	-0.07
1420534_at	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	1.55	0.46	1.02	0.974	-1.75	0.111	-1.12	0.689	-0.08
1452622_a_at	Tradd	TNFRSF1A-associated via death domain	1.12	0.086	1.04	0.658	-1.03	0.848	-1.38	0.142	-0.06
1443537_at	C130009A20Rik	RIKEN cDNA C130009A20 gene	1.64	0.196	-1.27	0.739	-1.41	0.169	1.15	0.447	0.03
1422731_at	Limd1	LIM domains containing 1	1.08	0.397	1.09	0.447	-1.04	0.74	-1.12	0.467	0
1421497_at	Gpha2	glycoprotein hormone alpha 2	-1.15	0.722	1.33	0.366	-1.07	0.798	2.06	0.253	0.29
1448887_x_at	Fxc1	fractured callus expressed transcript 1	1.02	0.907	1.19	0.323	-1.08	0.631	-1.17	0.553	-0.01
1446977_at	Traf6	Tnf receptor-associated factor 6	-1.05	0.465	1	0.998	1.18	0.079	-1.36	0.35	-0.06
1423701_at	Coasy	Coenzyme A synthase	1	0.975	-1.08	0.616	1.2	0.064	-1.23	0.099	-0.02
1454245_at	Csmd3	CUB and Sushi multiple domains 3	-1.03	0.963	1.09	0.895	1.07	0.847	-4.41	0.001	-0.82
1456745_x_at	Ergic3	ERGIC and golgi 3	1.17	0.297	-1.03	0.666	-1.01	0.889	1.03	0.751	0.04
1428456_at	Bola1	bolA-like 1 (E. coli)	-1.18	0.812	1.45	0.504	-1.2	0.666	1.89	0.235	0.24
1443664_s_at	Cd164l2	D164 sialomucin-like 2	1.36	0.53	-1.96	0.168	1.27	0.711	-1.77	0.323	-0.28
1421088_at	Gpc4	glypican 4	-1	0.972	-1.01	0.911	1.15	0.547	1.77	0.098	0.23
1423156_at	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	1.05	0.628	1.2	0.071	-1.13	0.443	-1.37	0.121	-0.06
1421205_at	Atm	ataxia telangiectasia mutated homolog (human)	1.19	0.473	-1.06	0.624	1	0.96	-1.45	0.282	-0.08
1449658_at	AA536748	expressed sequence AA536748	-1.25	0.62	1.25	0.762	1.09	0.687	-1.88	0.431	-0.2
1427045_at	Synpo	synaptopodin	-1.37	0.6	-1.01	0.976	1.41	0.376	1.14	0.853	0.04
1443191_at	---	---	1.1	0.883	-1.2	0.682	1.2	0.756	-1.46	0.324	-0.09
1459514_at	---	---	1.36	0.752	-1.04	0.945	-1.23	0.597	1.37	0.558	0.12
1445504_at	LOC331392	similar to Nucleolar phosphoprotein p130 (Nucleolar 130 kDa protein) (140 kDa n	-1.18	0.601	1.45	0.323	-1.2	0.496	1.07	0.64	0.04
1438400_at	4632411B12Rik	RIKEN cDNA 4632411B12 gene	-1.14	0.489	-1.02	0.881	1.28	0.236	1.04	0.814	0.04

1422499_at	Lima1	LIM domain and actin binding 1	1.06	0.26	-1.07	0.622	1.14	0.541	-1.44	0.324	-0.08
1444588_at	---	---	-1.02	0.962	1.2	0.495	-1.05	0.912	1.33	0.296	0.12
1451009_at	Rnf151	ring finger protein 151	-1.52	0.395	-1.22	0.617	1.66	0.157	1.43	0.407	0.09
1435619_at	---	Transcribed locus	-1.01	0.928	1.12	0.595	1.03	0.821	-1.24	0.241	-0.03
1429398_at	5730446D14Rik	RIKEN cDNA 5730446D14 gene	1.12	0.558	1.19	0.381	-1.21	0.706	-1.48	0.498	-0.1
1446557_at	E130309F12Rik	RIKEN cDNA E130309F12 gene	-1.01	0.968	1.01	0.964	1.14	0.698	-1.02	0.941	0.03
1453754_at	S100pbp	S100P binding protein	-1.99	0.14	1.17	0.764	1.46	0.248	-1.32	0.741	-0.17
1457414_at	---	9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone	1.95	0.202	-4.17	0.007	-1.05	0.914	1.5	0.545	-0.44
1436617_at	Cetn4	centrin 4	-1.18	0.122	1.37	0.537	-1.09	0.763	2.57	0.197	0.42
1426907_s_at	Dhx57	DEAH (Asp-Glu-Ala-Asp/His) box polypeptide 57	-1.09	0.501	1.19	0.047	1.03	0.848	-1.58	0.171	-0.11
1452146_a_at	Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	-1.19	0.067	1	0.987	1.29	0.063	-1.03	0.661	0.02
1417190_at	Pbef1	pre-B-cell colony-enhancing factor 1	-1.03	0.884	1.07	0.619	1.1	0.663	-1.15	0.159	0
1448767_s_at	Gjb1	gap junction membrane channel protein beta 1	1.38	0.169	-1.16	0.433	-1.13	0.635	1.16	0.408	0.06
1430188_at	1700037C18Rik	RIKEN cDNA 1700037C18 gene	1.12	0.563	-1.19	0.575	1.17	0.4	-1.22	0.004	-0.03
1443801_at	AW822216	Expressed sequence AW822216	-1.39	0.39	-1.02	0.971	1.44	0.286	1.46	0.446	0.12
1424415_s_at	Spon1	spondin 1, (f-spondin) extracellular matrix protein	1.11	0.35	1.26	0.46	-1.31	0.146	-1.02	0.922	0.01
1430929_at	9430082L08Rik	RIKEN cDNA 9430082L08 gene	-1.19	0.385	1.43	0.617	-1.15	0.811	1.16	0.666	0.06
1453802_at	3732412D22Rik	RIKEN cDNA 3732412D22 gene	-1.66	0.349	1.16	0.838	1.37	0.3	-1.07	0.863	-0.05
1458379_at	9330159F19Rik	RIKEN cDNA 9330159F19 gene	1.07	0.899	1.8	0.312	-3.68	0.01	-1.25	0.778	-0.51
1445973_at	C79461	expressed sequence C79461	-1.23	0.712	1.08	0.751	1.24	0.534	-1.4	0.648	-0.08
1454498_at	9230118N17Rik	RIKEN cDNA 9230118N17 gene	1.5	0.276	-2.54	0.138	1.24	0.324	-1.07	0.545	-0.22
1421639_at	1700082M22Rik	RIKEN cDNA 1700082M22 gene	1.15	0.529	-1.41	0.153	1.28	0.456	-2.9	0.272	-0.47
1457825_x_at	Tcn2	transcobalamin 2	-1.2	0.176	1.19	0.018	1.11	0.562	-1.02	0.944	0.02
1429695_at	Izumo1	izumo sperm-egg fusion 1	-1.02	0.969	-1.22	0.687	1.34	0.358	1.33	0.654	0.11
1431986_at	4933421A08Rik	RIKEN cDNA 4933421A08 gene	-1.06	0.842	1.36	0.53	-1.19	0.388	1.13	0.662	0.06
1448247_at	Bcl7b	B-cell CLL/lymphoma 7B	1.04	0.862	1.12	0.226	-1.02	0.831	-1.21	0.103	-0.02
1437580_s_at	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	-1.49	0.006	-1.12	0.78	1.58	0.155	4.5	0.165	0.87
1450992_a_at	Meis1	myeloid ecotropic viral integration site 1	1.01	0.963	1.43	0.177	-1.43	0.158	-1.04	0.779	-0.01
1448113_at	Stmn1 /// LOC6394	stathmin 1 /// similar to Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (	-1	0.991	1.28	0.319	-1.16	0.008	1.78	0.208	0.22
1434781_at	---	---	-1.19	0.537	1.39	0.117	-1.1	0.633	1.26	0.296	0.09
1433722_at	Akap13	A kinase (PRKA) anchor protein 13	1.02	0.916	-1	0.972	1.12	0.44	-1.2	0.266	-0.02
1421031_a_at	2310016C08Rik	RIKEN cDNA 2310016C08 gene	-1.21	0.422	1.29	0.242	1.02	0.95	-1.14	0.086	-0.01
1418293_at	Ifit2	interferon-induced protein with tetratricopeptide repeats 2	1.1	0.668	1.26	0.378	-1.3	0.314	-1.34	0.081	-0.07
1433921_s_at	Zcsl2	zinc finger, CSL domain containing 2	-1.06	0.718	1.21	0.249	-1.01	0.958	1.16	0.596	0.07
1437633_at	Ankrd11	ankyrin repeat domain 11	-1.08	0.545	-1.18	0.681	1.37	0.455	1.04	0.88	0.04
1442328_at	---	---	-1.24	0.179	1.54	0.39	-1.26	0.53	1.18	0.416	0.05
1439910_a_at	---	---	1.58	0.472	-1.28	0.372	-1.29	0.39	1.51	0.557	0.13
1439188_at	Cpsf6	cleavage and polyadenylation specific factor 6	1.14	0.152	-1.03	0.924	1.03	0.846	-1.79	0.129	-0.16
1429222_at	---	---	1.03	0.601	-1.01	0.967	1.13	0.372	-1.55	0.229	-0.1
1427289_at	Ddhd1	DDHD domain containing 1	-1.09	0.535	1.35	0.059	-1.16	0.578	1.15	0.642	0.07
1425724_at	Ptprn2	protein tyrosine phosphatase, receptor type, N polypeptide 2	-1.07	0.929	1.12	0.758	1.08	0.84	-1.57	0.014	-0.11
1430307_a_at	Mod1 /// LOC62489	malic enzyme, supernatant /// similar to NADP-dependent malic enzyme (NADP-I	-1.18	0.283	-1.57	0.094	1.66	0.176	1.29	0.367	0.05
1428997_at	Phf23	PHD finger protein 23	-1.16	0.242	1.04	0.602	1.23	0.007	-1.11	0.525	0
1450870_at	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	1.13	0.472	-1.09	0.658	1.09	0.058	-1.17	0.577	-0.01
1444747_at	Pcmtd1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1.4	0.362	-1.49	0.502	1.07	0.816	-1.95	0.16	-0.24
1430756_at	5430427G11Rik	RIKEN cDNA 5430427G11 gene	1.24	0.369	1.05	0.874	-1.17	0.356	-1.06	0.865	0.01
1440434_at	---	---	1.23	0.412	1.27	0.45	-1.56	0.059	-1.14	0.553	-0.05
1427760_s_at	Plf /// Plf2 /// Mrpplf	proliferin /// proliferin 2 /// mitogen regulated protein, proliferin 3	-2.37	0.045	1.62	0.376	1.1	0.866	-1.41	0.56	-0.27
1439873_at	Dgkd	diacylglycerol kinase, delta	-1.45	0.566	1.02	0.921	1.43	0.572	-3.27	0.041	-0.57
1444580_at	---	Transcribed locus	1.11	0.877	-2.03	0.214	1.54	0.52	-1.86	0.111	-0.31
1451486_at	1200006F02Rik	RIKEN cDNA 1200006F02 gene	-1.16	0.011	1.2	0.396	1.08	0.551	-1.31	0.253	-0.05
1446241_at	---	Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830471B11	-2.04	0.073	1.09	0.824	1.56	0.238	-1.6	0.545	-0.25
1451309_at	Arhgap1	Rho GTPase activating protein 1	-1.16	0.61	1.21	0.046	1.07	0.745	-1.32	0.145	-0.05

1458886_at	Spop	Speckle-type POZ protein	1.98	0.265	-1.29	0.574	-2.64	0.029	1.03	0.926	-0.23
1459806_x_at	Mrps23	mitochondrial ribosomal protein S23	1.13	0.637	-1.06	0.744	1.07	0.818	-1.26	0.068	-0.03
1427070_at	5730407K14Rik	RIKEN cDNA 5730407K14 gene	1.4	0.177	1.12	0.501	-1.63	0.114	-1.33	0.262	-0.11
1422334_a_at	Sftpa1	surfactant associated protein A1	1.22	0.77	1.15	0.619	-1.29	0.004	-2.09	0.218	-0.26
1457525_at	---	Activated spleen cDNA, RIKEN full-length enriched library, clone:F830103I17 pro	1.33	0.386	-1.37	0.682	1.08	0.837	-2.89	0.177	-0.46
1448957_at	Rbpsuh	recombining binding protein suppressor of hairless (Drosophila)	-1	0.993	-1.08	0.498	1.21	0.247	1.02	0.867	0.04
1439346_at	---	---	-1.07	0.776	-1.58	0.046	1.57	0.198	1.25	0.031	0.04
1449128_at	Ccdc43	coiled-coil domain containing 43	1.07	0.812	1.22	0.07	-1.16	0.601	-1.29	0.259	-0.04
1448699_at	Mrpl54	mitochondrial ribosomal protein L54	-1.01	0.947	1.02	0.599	1.13	0.64	-1.13	0.635	0
1452267_at	Flywch1	FLYWCH-type zinc finger 1	-1.06	0.728	1.01	0.962	1.19	0.301	-1.29	0.241	-0.04
1427121_at	Fbxo4	F-box only protein 4	1.11	0.655	1.2	0.583	-1.2	0.262	-1.67	0.203	-0.14
1451499_at	Cadps2	Ca2+-dependent activator protein for secretion 2	1.03	0.837	1.34	0.119	-1.3	0.045	-1.69	0.122	-0.15
1435897_at	Rpl32	ribosomal protein L32	-1.03	0.79	1.15	0.088	1.02	0.854	-1.36	0.025	-0.05
1426628_at	Tmem34	transmembrane protein 34	-1.16	0.283	1.15	0.576	1.13	0.486	-1.46	0.208	-0.09
1448114_a_at	Htf9c	HpaII tiny fragments locus 9c	1.15	0.009	-1.03	0.822	1.02	0.927	-1.23	0.148	-0.02
1434269_at	AA536717	expressed sequence AA536717	1.02	0.853	-1	0.993	1.12	0.609	-1.23	0.355	-0.02
1431888_s_at	Psg21	pregnancy-specific glycoprotein 21	1.2	0.626	1.27	0.617	-1.5	0.566	-1.04	0.831	-0.02
1432360_a_at	Tmtc4	transmembrane and tetratricopeptide repeat containing 4	1.15	0.128	-1.34	0.379	1.25	0.297	-1.51	0.018	-0.11
1458389_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.46	0.497	1.19	0.652	-2.05	0.004	-1.98	0.292	-0.34
1439807_at	Tmem74	transmembrane protein 74	-1.61	0.612	-1.59	0.015	1.89	0.061	1.49	0.45	0.05
1460679_at	Exosc4	exosome component 4	-1.14	0.306	-1.09	0.148	1.35	0.062	1.01	0.955	0.03
1452995_at	Nudt17	nudix (nucleoside diphosphate linked moiety X)-type motif 17	1.06	0.897	1.15	0.617	-1.07	0.875	-1.3	0.151	-0.04
1449160_at	Npr1	natriuretic peptide receptor 1	1.26	0.634	1.17	0.806	-1.39	0.13	-1.35	0.432	-0.08
1435868_at	Ankrd13c	ankyrin repeat domain 13c	-1	0.964	-1.29	0.051	1.37	0.149	1.2	0.621	0.07
1448836_s_at	Atpbd1b	ATP binding domain 1 family, member B	1.18	0.029	-1.21	0.205	1.13	0.521	-1.3	0.028	-0.05
1452161_at	Tiparp	TCDD-inducible poly(ADP-ribose) polymerase	-1.29	0.534	1.2	0.395	1.17	0.569	-1.02	0.861	0.01
1439187_at	Vps13d	vacuolar protein sorting 13 D (yeast)	1.05	0.787	-1.22	0.183	1.27	0.085	-1.05	0.859	0.01
1454596_at	A730089K16Rik	RIKEN cDNA A730089K16 gene	-1	0.998	1.33	0.275	-1.23	0.546	1.55	0.371	0.16
1416688_at	Snap91	synaptosomal-associated protein 91	1.05	0.843	1.32	0.267	-1.29	0.58	-2.54	0.08	-0.36
1424779_at	D10Ucla1	DNA segment, Chr 10, University of California at Los Angeles 1	1.2	0.09	-1.19	0.191	1.1	0.716	-1.32	0.258	-0.05
1460325_at	Pum1	pumilio 1 (Drosophila)	1	0.991	-1.02	0.691	1.16	0.379	-1.12	0.554	0
1457609_at	Adarb2	Adenosine deaminase, RNA-specific, B2	-1.29	0.5	1.36	0.413	1.01	0.979	-1.41	0.261	-0.08
1456596_at	6430550H21Rik	RIKEN cDNA 6430550H21 gene	1.17	0.795	-1.26	0.778	1.18	0.701	-1.21	0.473	-0.03
1436358_at	Atpaf1	ATP synthase mitochondrial F1 complex assembly factor 1	1.11	0.344	1.08	0.586	-1.06	0.738	-1.28	0.322	-0.03
1435322_at	1110011C06Rik	RIKEN cDNA 1110011C06 gene	1.13	0.435	1.08	0.438	-1.06	0.725	-1.18	0.128	-0.01
1423809_at	Tcf19	transcription factor 19	-1.11	0.737	1.27	0.09	-1.03	0.839	2.17	0.228	0.32
1455302_at	Vps29	vacuolar protein sorting 29 (S. pombe)	-1.16	0.252	1.05	0.878	1.23	0.512	-1.49	0.047	-0.09
1415839_a_at	Npm1	nucleophosmin 1	1.11	0.012	-1.03	0.743	1.06	0.69	-1.19	0.003	-0.01
1452887_at	Traf3ip1	TNF receptor-associated factor 3 interacting protein 1	-1.42	0.119	1.08	0.614	1.36	0.086	-1.3	0.047	-0.07
1452274_at	Zfand3	zinc finger, AN1-type domain 3	-1.04	0.887	-1.12	0.444	1.28	0.221	1.01	0.94	0.03
1438124_at	LOC195691 /// LOC	similar to putative pheromone receptor (Go-VN5) /// similar to putative pheromone	1.04	0.933	1.12	0.661	-1.02	0.962	-1.35	0.472	-0.05
1418103_at	Slc12a9	solute carrier family 12 (potassium/chloride transporters), member 9	-1.14	0.157	1.03	0.837	1.24	0.273	-1.02	0.879	0.03
1420597_a_at	Cabp2	calcium binding protein 2	1.11	0.481	1.22	0.699	-1.22	0.029	-1.07	0.645	0.01
1450173_at	Ripk2	receptor (TNFRSF)-interacting serine-threonine kinase 2	-1.19	0.482	1.11	0.189	1.2	0.332	-1.04	0.683	0.02
1428679_s_at	0610010K14Rik	RIKEN cDNA 0610010K14 gene	-1.03	0.855	1.12	0.367	1.05	0.787	-1.02	0.892	0.03
1429151_at	Wdr68	WD repeat domain 68	-1.05	0.606	1.11	0.072	1.08	0.554	-1.06	0.182	0.02
1437602_at	RP23-273O7.4	similar to Hypothetical protein MGC26988	1.17	0.799	1.09	0.883	-1.13	0.373	-2.23	0.029	-0.27
1438359_at	2010003K15Rik	RIKEN cDNA 2010003K15 gene	-1.19	0.722	-1.38	0.001	1.58	0.288	1.05	0.949	0.01
1428868_a_at	Oaz1	ornithine decarboxylase antizyme	-1.06	0.755	-1.15	0.346	1.33	0.013	1.15	0.427	0.07
1425619_s_at	Dsg2	desmoglein 2	1.23	0.008	-1.26	0.105	1.12	0.537	-1.09	0.792	0
1455090_at	Angptl2	angiopoietin-like 2	1.08	0.581	1.26	0.207	-1.24	0.431	-1.01	0.963	0.02
1450556_at	Spnb1	spectrin beta 1	1.16	0.668	-1	0.984	-1.01	0.97	6.33	0.163	1.37
1430239_at	5430421F17Rik	RIKEN cDNA 5430421F17 gene	1.29	0.758	-1.11	0.835	-1.05	0.833	1.33	0.509	0.11

1422700_at	Alox12	arachidonate 12-lipoxygenase	-2.39	0.19	-1.33	0.371	1.97	0.083	1.95	0.285	0.05
1426737_at	Gspt1	G1 to S phase transition 1	-1.1	0.702	1	0.995	1.23	0.438	-1.01	0.961	0.03
1420796_at	Ahrr	aryl-hydrocarbon receptor repressor	-1	1	1.51	0.484	-1.58	0.364	1.31	0.66	0.06
1446271_at	---	---	1.53	0.261	-1.22	0.259	-1.26	0.308	1.28	0.61	0.08
1448101_s_at	Trim27	tripartite motif protein 27	-1.01	0.931	-1.14	0.25	1.28	0.307	1.08	0.295	0.05
1434883_at	Mtdh	Metadherin	-1.07	0.279	1.21	0.31	-1	1	1.17	0.245	0.08
1424591_at	5830433M19Rik	RIKEN cDNA 5830433M19 gene	-1.09	0.453	1.21	0.275	1.01	0.906	-1.04	0.581	0.02
1458055_at	Dsc3	Desmocollin 3	1.23	0.831	-1.04	0.824	-1.04	0.554	1.21	0.712	0.09
1455759_a_at	Ankhd1	ankyrin repeat and KH domain containing 1	1.21	0	-1.04	0.634	-1.03	0.886	1.02	0.838	0.04
1450571_a_at	Bfsp1	beaded filament structural protein in lens-CP94	-1.65	0.339	1	0.996	1.54	0.293	-1.84	0.383	-0.24
1437455_a_at	Btg1	B-cell translocation gene 1, anti-proliferative	-1.15	0.426	1.04	0.598	1.24	0.479	-1.39	0.147	-0.07
1431029_at	Ttll9	tubulin tyrosine ligase like family 9	1.22	0.307	-1.46	0.275	1.24	0.617	-1.25	0.752	-0.06
1446699_at	Jmjd2a	jumonji domain containing 2A	1.19	0.848	-2.43	0.335	1.54	0.205	-1.27	0.231	-0.24
1442325_at	Tbc1d24	TBC1 domain family, member 24	-1.19	0.481	1.42	0.014	-1.13	0.737	2.93	0.147	0.51
1440676_at	A830043J08Rik	RIKEN cDNA A830043J08 gene	1.51	0.62	-1.38	0.256	-1.09	0.473	1	0.989	0.01
1451279_at	Erc1	ELKS/RAB6-interacting/CAST family member 1	-1.23	0.599	1.23	0.552	1.11	0.776	-2.2	0.072	-0.28
1438206_a_at	2610042O14Rik	RIKEN cDNA 2610042O14 gene	-1.02	0.879	1.06	0.51	1.1	0.59	-1.54	0.23	-0.1
1440405_at	Adcy3	Adenylate cyclase 3	1.16	0.854	-1.24	0.635	1.18	0.582	-2.08	0.248	-0.25
1434011_a_at	Ints5	integrator complex subunit 5	-1.05	0.766	-1.11	0.219	1.3	0.006	1.09	0.49	0.05
1425037_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	-1.18	0.355	-1.27	0.368	1.51	0.119	1.21	0.054	0.07
1449979_a_at	Spock3	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 3	-2.19	0.109	1.02	0.975	1.67	0.384	-2.48	0.248	-0.49
1440230_at	Lrrc54	leucine rich repeat containing 54	-1.02	0.943	1.14	0.604	1.03	0.869	-1.42	0.392	-0.07
1435509_x_at	Cdk2ap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	-1.01	0.9	-1.02	0.856	1.17	0.095	1.03	0.653	0.04
1434544_at	Bola2	bolA-like 2 (E. coli)	-1.06	0.809	1.12	0.259	1.08	0.712	-1.04	0.61	0.03
1418508_a_at	Grb2	growth factor receptor bound protein 2	-1.13	0.551	1.21	0.182	1.05	0.837	-1.08	0.691	0.01
1454827_at	Pogz	pogo transposable element with ZNF domain	1.22	0.554	1.22	0.717	-1.42	0.338	-1.43	0.058	-0.1
1432039_a_at	Lrp2bp	Lrp2 binding protein	-1.28	0.503	-1.13	0.773	1.48	0.432	1.79	0.007	0.22
1437078_at	LOC631721	similar to vacuolar protein sorting 52	-1.07	0.784	-1.1	0.292	1.3	0.037	1.31	0.106	0.11
1449281_at	Nrtn	neurturin	-1.15	0.645	1.36	0.58	-1.1	0.764	1.17	0.496	0.07
1433522_at	Pskh1	protein serine kinase H1	1.28	0.086	-1.07	0.496	-1.07	0.652	1.2	0.224	0.09
1437546_at	Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	1.16	0.159	1.08	0.447	-1.11	0.422	-1.24	0.464	-0.03
1452827_at	1500009C09Rik	RIKEN cDNA 1500009C09 gene	-2.52	0.007	1.78	0.104	-1.03	0.949	2.1	0.428	0.08
1454936_at	Vars2l	valyl-tRNA synthetase 2-like	1.12	0.587	-1.17	0.282	1.17	0.37	-1.25	0.321	-0.03
1449966_s_at	Cab39l	calcium binding protein 39-like	1.11	0.645	-1.19	0.508	1.19	0.525	-1.05	0.842	0.02
1437396_at	Creb3l2	cAMP responsive element binding protein 3-like 2	-1.29	0.028	-1.02	0.86	1.4	0.026	1.37	0.163	0.11
1449008_at	Tulp3	tubby-like protein 3	-1.06	0.565	1.04	0.718	1.17	0.267	-1.35	0.062	-0.05
1430909_at	Nup210l	nucleoporin 210-like	-1.1	0.548	1.15	0.581	1.09	0.568	-1.35	0.592	-0.05
1442114_at	Xab1	XPA binding protein 1	1.45	0.315	-1.34	0.389	-1.05	0.363	1.21	0.019	0.07
1445333_at	---	---	-1.72	0.469	-1.35	0.33	1.83	0.274	1.01	0.969	-0.06
1442480_at	---	Transcribed locus	1.06	0.854	1.37	0.635	-1.4	0.243	-1.31	0.582	-0.07
1436884_x_at	Ewsr1	Ewing sarcoma breakpoint region 1	1.39	0.087	1.05	0.841	-1.41	0.024	-1.09	0.602	-0.02
1443599_at	Dcst1	DC-STAMP domain containing 1	1.24	0.369	-1.04	0.942	-1.06	0.869	1.8	0.019	0.23
1418767_at	Cyp4f13	cytochrome P450, family 4, subfamily f, polypeptide 13	1.07	0.57	-1.38	0.003	1.36	0.077	-1.62	0.418	-0.14
1446301_at	Farsla	Phenylalanine-tRNA synthetase-like, alpha subunit	-1.39	0.024	1.39	0.154	1.04	0.935	-3.43	0.081	-0.6
1416974_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.12	0.19	-1.24	0.181	1.22	0.227	-1.36	0.105	-0.06
1448593_at	Wisp1	WNT1 inducible signaling pathway protein 1	-1.21	0.598	1.58	0.325	-1.35	0.589	1.28	0.185	0.08
1427412_s_at	Rapgef6	Rap guanine nucleotide exchange factor (GEF) 6	-1.13	0.37	1.01	0.968	1.26	0.177	-1.29	0.074	-0.04
1451443_at	Nfix	nuclear factor I/X	-1.2	0.518	1.49	0.462	-1.21	0.279	1.25	0.346	0.08
1450408_at	Clcn7	chloride channel 7	-1.08	0.838	-1.09	0.782	1.3	0.255	1.28	0.274	0.1
1458837_at	2810006K23Rik	RIKEN cDNA 2810006K23 gene	-1.06	0.79	-1	0.999	1.2	0.649	1.48	0.404	0.16
1416377_at	Pdcd7	programmed cell death protein 7	1.03	0.882	-1.16	0.177	1.25	0.396	-1.33	0.152	-0.05
1454525_at	15-Sep	selenoprotein	1.39	0.737	1.22	0.71	-1.84	0.035	-1.04	0.819	-0.07
1421140_a_at	Foxp1	forkhead box P1	1.16	0.606	-1.11	0.522	1.08	0.485	-1.86	0.133	-0.18

1426910_at	---	---	1.04	0.817	1.34	0.224	-1.29	0.145	-1.12	0.742	-0.01
1427469_at	Helz	helicase with zinc finger domain	1.11	0.384	1.25	0.087	-1.26	0.339	-1.63	0.128	-0.13
1458851_at	---	Transcribed locus	1.2	0.117	1.03	0.889	-1.09	0.883	-2.86	0.326	-0.43
1436745_at	Scyl1bp1	SCY1-like 1 binding protein 1	-1.1	0.238	1.23	0.211	1.01	0.947	-1.19	0.347	-0.01
1418656_at	Lsm5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.06	0.527	1.17	0.273	-1.09	0.722	-1.13	0.599	0
1432297_at	Zim2	zinc finger, imprinted 2	-3.88	0.002	1.45	0.301	1.44	0.12	-1.27	0.66	-0.56
1451241_at	Lamb1-1	laminin B1 subunit 1	1.22	0.325	-1.51	0.415	1.26	0.56	-2.18	0.041	-0.3
1443831_s_at	Mtl5	metallothionein-like 5, testis-specific (tesmin)	-1.1	0.181	-1.03	0.514	1.27	0.524	1.01	0.904	0.04
1453605_s_at	Ccdc91	coiled-coil domain containing 91	-1.07	0.849	-1.13	0.758	1.33	0.513	1.03	0.874	0.04
1443823_s_at	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	-1.02	0.951	1.02	0.979	1.15	0.795	-1.08	0.83	0.02
1447180_at	---	Transcribed locus	-3.19	0.397	1.82	0.278	1.02	0.982	-1.38	0.338	-0.43
1417625_s_at	Cmkor1	chemokine orphan receptor 1	1.18	0.49	1.21	0.563	-1.3	0.25	-1.41	0.163	-0.08
1453043_at	0610012H03Rik	RIKEN cDNA 0610012H03 gene	-1.01	0.901	1.27	0.081	-1.12	0.803	2.49	0.059	0.41
1453219_a_at	2410004F06Rik	RIKEN cDNA 2410004F06 gene	-1.12	0.659	-1.12	0.669	1.36	0.246	1.02	0.852	0.04
1440075_at	---	Transcribed locus	1.06	0.883	1.19	0.77	-1.11	0.589	-1.34	0.32	-0.05
1451346_at	Mtap	methylthioadenosine phosphorylase	1.02	0.89	-1.19	0.028	1.29	0.131	-1.11	0.622	0
1441332_at	---	---	1.06	0.939	-1.66	0.39	1.49	0.398	-1.91	0.375	-0.26
1445003_at	Farsla	phenylalanine-tRNA synthetase-like, alpha subunit	-1.51	0.207	2.03	0.268	-2.19	0.053	1.51	0.359	-0.04
1423720_a_at	Sar1a	SAR1 gene homolog A (S. cerevisiae)	1.01	0.966	1.14	0.69	-1	0.992	-1.02	0.943	0.03
1426350_at	Mgat2	mannoside acetylglucosaminyltransferase 2	-1.2	0.459	1.23	0.193	1.09	0.606	-1.27	0.461	-0.04
1431637_at	---	---	-1	0.999	1.25	0.647	-1.11	0.751	1.98	0.136	0.28
1425271_at	Psmc3ip	proteasome (prosome, macropain) 26S subunit, ATPase 3, interacting protein	1.36	0.169	-1.11	0.881	-1.12	0.518	2.83	0.208	0.49
1449346_s_at	Riok1	RIO kinase 1 (yeast)	1.05	0.811	1.33	0.042	-1.29	0.013	-1.02	0.832	0.02
1459476_s_at	Csrp2bp	cysteine and glycine-rich protein 2 binding protein	-1.06	0.153	1.09	0.335	1.12	0.385	-1.08	0.323	0.02
1419996_s_at	Arnt	aryl hydrocarbon receptor nuclear translocator	1.2	0.545	-1.01	0.898	-1.04	0.815	1.24	0.262	0.1
AFFX-BioC-5_at	---	---	1.36	0.098	1.14	0.134	-1.53	0.104	-1.24	0.419	-0.07
1421746_a_at	Fbxo17	F-box protein 17	1.15	0.427	-1.08	0.784	1.08	0.521	-1.13	0.677	0
1438681_at	Alkbh1	alkB, alkylation repair homolog 1 (E. coli)	-1.54	0.265	1.03	0.881	1.47	0.27	-1.26	0.193	-0.07
1429320_at	4921511I16Rik	RIKEN cDNA 4921511I16 gene	1.03	0.941	-1.2	0.116	1.29	0.238	-1.03	0.879	0.02
1417722_at	Pgls	6-phosphogluconolactonase	1.02	0.818	-1	0.988	1.13	0.542	-1.51	0.132	-0.09
1436456_at	9130023D20Rik	RIKEN cDNA 9130023D20 gene	-1.06	0.158	1.04	0.674	1.17	0.38	-1.11	0.624	0.01
1450299_at	Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7	1.91	0.257	-3.23	0.101	-1.08	0.868	1.1	0.835	-0.32
1429678_at	5730508B09Rik	RIKEN cDNA 5730508B09 gene	-1.17	0.569	1.3	0.295	-1.01	0.94	3.29	0.21	0.6
1425897_at	Birc1c	baculoviral IAP repeat-containing 1c	1.15	0.805	-1.66	0.455	1.4	0.507	-1.03	0.964	-0.04
1460346_at	Arsa	arylsulfatase A	1.14	0.146	-1.14	0.048	1.13	0.151	-1.04	0.839	0.02
1437223_s_at	Xbp1	X-box binding protein 1	-1.02	0.728	1.21	0.325	-1.04	0.408	1.1	0.652	0.06
1452925_a_at	5-Mar	membrane-associated ring finger (C3HC4) 5	-1.01	0.92	-1.06	0.504	1.22	0.02	3.01	0.245	0.54
1456797_at	Cltb	clathrin, light polypeptide (Lcb)	-1.23	0.66	1.71	0.158	-1.6	0.195	3.06	0.016	0.49
1455380_at	Pcyox1l	prenylcysteine oxidase 1 like	1.18	0.716	-1.03	0.929	-1.01	0.99	2.59	0.053	0.43
1436562_at	Ddx58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	-1.14	0.368	1.04	0.791	1.24	0.087	-1.6	0.143	-0.12
1425279_at	Pdik1l	PDLIM1 interacting kinase 1 like	1.34	0.418	-1.02	0.915	-1.19	0.663	1.26	0.45	0.1
1460046_at	Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	-2.5	0.148	1.74	0.275	1.01	0.934	-3.8	0.169	-0.89
1460332_at	Pln	phospholamban	-1.16	0.53	-1.18	0.57	1.44	0.295	1.25	0.418	0.09
1447775_x_at	Zfp622	zinc finger protein 622	1.46	0.28	-1.61	0.023	1.07	0.78	-2.23	0.11	-0.33
1425669_at	Mobkl2b	MOB1, Mps One Binder kinase activator-like 2B (yeast)	1.1	0.721	1.27	0.419	-1.28	0.472	-1.85	0.042	-0.19
1456285_at	Pola1	Polymerase (DNA directed), alpha 1	-2.23	0.023	1.73	0.457	-1.03	0.963	1.04	0.95	-0.12
1426835_at	Metap1	methionyl aminopeptidase 1	1.07	0.639	1.11	0.475	-1.03	0.665	-1.09	0.748	0.01
1422065_at	Klrb1d	killer cell lectin-like receptor subfamily B member 1D	-1.24	0.588	1.6	0.628	-1.34	0.389	1.15	0.436	0.04
1416086_at	Tpst2	protein-tyrosine sulfotransferase 2	1.08	0.348	1.11	0.624	-1.03	0.57	-1.31	0.281	-0.04
1449482_at	Hist3h2ba	histone 3, H2ba	-1.38	0.588	-1.89	0.307	1.9	0.029	1.66	0.457	0.07
1446228_at	D19Wsu12e	DNA segment, Chr 19, Wayne State University 12, expressed	-1.27	0.559	1.17	0.701	1.2	0.539	-1.17	0.431	-0.02
1457305_at	---	Transcribed locus	1.24	0.471	-1.04	0.865	-1.05	0.794	1.57	0.19	0.18
1436353_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	1.02	0.801	1.34	0.094	-1.27	0.156	-1.75	0.134	-0.16

1432533_a_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	-1.07	0.644	-1.21	0.329	1.4	0.03	1.32	0.43	0.11
1433994_at	4931406P16Rik	RIKEN cDNA 4931406P16 gene	1.16	0.048	1	0.988	-1.01	0.942	-1.2	0.537	-0.01
1443572_at	---	---	1.93	0.169	-1.17	0.628	-2.74	0.142	1.1	0.767	-0.22
1440002_at	Rnmt	RNA (guanine-7-) methyltransferase	1.53	0.15	1.17	0.616	-2.19	0.077	-1.73	0.14	-0.31
1442237_at	Sqstm1	Sequestosome 1	1.2	0.555	1.24	0.598	-1.39	0.239	-1.05	0.885	0
1416347_at	Men1	multiple endocrine neoplasia 1	-1.01	0.647	1.02	0.829	1.15	0.13	-1.18	0.317	-0.01
1416601_a_at	Dscr1	Down syndrome critical region homolog 1 (human)	1.12	0.83	-1.25	0.629	1.24	0.725	-1.36	0.522	-0.06
1426908_at	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransfe	1.06	0.647	-1.07	0.643	1.16	0.189	-1.3	0.202	-0.04
1457209_at	Ddhd2	DDHD domain containing 2	1.4	0.073	-1.05	0.85	-1.25	0.462	1.41	0.118	0.13
1417520_at	Nfe2l3	nuclear factor, erythroid derived 2, like 3	-1.32	0.136	1.03	0.899	1.37	0.186	-1.3	0.124	-0.05
1456026_at	8030451K01Rik	RIKEN cDNA 8030451K01 gene	-1.08	0.225	1.03	0.708	1.19	0.385	-1.34	0.314	-0.05
1422155_at	Hist2h3c2	histone 2, H3c2	1.22	0.115	-1.08	0.845	1.01	0.974	-1.75	0.084	-0.15
1441731_at	---	Transcribed locus	1.28	0.53	1.43	0.081	-2.22	0.238	-2.88	0.004	-0.6
1438579_at	Utp14b	UTP14, U3 small nucleolar ribonucleoprotein, homolog B (yeast)	-1.46	0.189	-1.14	0.397	1.59	0.189	1.32	0.317	0.08
1434707_at	Sbf1	SET binding factor 1	-1.11	0.709	1.02	0.779	1.23	0.168	-1.2	0.373	-0.02
1454879_s_at	1700052N19Rik	RIKEN cDNA 1700052N19 gene	-1.23	0.222	1.07	0.513	1.27	0.065	-1.09	0.683	0.01
1456433_at	Rcbtb1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	1.14	0.492	-1.07	0.559	1.09	0.65	-1.18	0.662	-0.01
1439953_at	Pmm2	phosphomannomutase 2	1.29	0.238	-1.1	0.79	-1.04	0.924	1.6	0.165	0.19
1443255_s_at	Cdgap	Cdc42 GTPase-activating protein	1.24	0.625	-1.26	0.534	1.12	0.638	-2.4	0.166	-0.33
1423292_a_at	Prx	periaxin	1.02	0.919	1.23	0.78	-1.11	0.602	-1.69	0.27	-0.14
1434023_at	AU016693	expressed sequence AU016693	1.02	0.772	1.14	0.345	-1.01	0.924	-1.08	0.706	0.02
1421469_a_at	Stat5a	signal transducer and activator of transcription 5A	-1.12	0.387	-1.29	0.017	1.49	0.056	1.14	0.465	0.05
1441729_at	---	Transcribed locus	-1.29	0.141	1.31	0.333	1.06	0.915	-3.21	0.146	-0.53
1447912_x_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	1.03	0.966	1.64	0.443	-2.08	0.105	-2.55	0.151	-0.49
1434064_at	Tmem142c	transmembrane protein 142C	-1.16	0.275	1.11	0.426	1.18	0.129	-1.37	0.047	-0.06
1452341_at	Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	1.03	0.84	-1.03	0.821	1.16	0.324	-1.16	0.194	0
1454454_at	---	---	-1	0.997	1.53	0.235	-1.6	0.064	1.21	0.547	0.04
1449931_at	Cpeb4	cytoplasmic polyadenylation element binding protein 4	-1.02	0.903	-1.08	0.899	1.25	0.726	1.91	0.465	0.26
1431969_at	4930402D18Rik	RIKEN cDNA 4930402D18 gene	1.21	0.859	1.04	0.953	-1.1	0.769	-1.44	0.627	-0.07
1425059_at	Prmt6	protein arginine N-methyltransferase 6	-1.22	0.315	1.12	0.634	1.22	0.316	-1.09	0.709	0.01
1425826_a_at	Sorbs1	sorbin and SH3 domain containing 1	-1.04	0.675	-1.34	0.116	1.45	0.296	1.68	0.234	0.19
1440054_at	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	1.11	0.884	1.37	0.202	-1.49	0.034	-2.07	0.131	-0.27
1453014_a_at	Sec31l1	SEC31-like 1 (S. cerevisiae)	-1.1	0.399	1.01	0.858	1.23	0.192	-1.08	0.797	0.02
1424844_at	Angel1	angel homolog 1 (Drosophila)	1.16	0.477	-1.11	0.667	1.1	0.447	-1.11	0.728	0.01
1419427_at	Csf3	colony stimulating factor 3 (granulocyte)	1.22	0.771	1.5	0.607	-2.28	0.064	-1.03	0.963	-0.15
1451253_at	Pxk	PX domain containing serine/threonine kinase	-1.16	0.354	1.07	0.689	1.22	0.161	-2.62	0.044	-0.37
1437239_x_at	Phc2	polyhomeotic-like 2 (Drosophila)	1.11	0.059	-1.07	0.65	1.11	0.041	-1.46	0.09	-0.08
1448485_at	Ggt1	gamma-glutamyltransferase 1	1.06	0.548	-8.5	0.016	1.97	0.106	-1	0.993	-1.61
1457871_at	Colec10	collectin sub-family member 10	1.24	0.618	1.17	0.022	-1.33	0.489	-1.04	0.936	0.01
1450649_at	Gng10	guanine nucleotide binding protein (G protein), gamma 10	1.06	0.586	1.17	0.293	-1.07	0.695	-1.83	0.043	-0.17
1431953_at	Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	-1.18	0.322	1.12	0.769	1.19	0.669	-1.07	0.904	0.02
1451280_at	Arpp21	cyclic AMP-regulated phosphoprotein, 21	-1.9	0.438	1.26	0.455	1.37	0.571	-2.92	0.183	-0.55
1434326_x_at	Coro2b	coronin, actin binding protein, 2B	-1.36	0.32	-1.04	0.845	1.45	0.011	1.65	0.232	0.18
1441345_at	C80143	expressed sequence C80143	1.04	0.798	1.45	0.165	-1.49	0.161	-1.16	0.721	-0.04
1439135_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330034C	-1.18	0.463	1.34	0.554	-1.03	0.961	1.51	0.598	0.16
1417840_at	1500031L02Rik	RIKEN cDNA 1500031L02 gene	1.13	0.242	-1.12	0.249	1.13	0.441	-1.14	0.212	0
1454389_at	Lrch4	Leucine-rich repeats and calponin homology (CH) domain containing 4	1.07	0.832	-1.05	0.921	1.13	0.842	-1.1	0.896	0.01
1435674_at	Rhobtb2	Rho-related BTB domain containing 2	-1.13	0.575	1.17	0.387	1.11	0.471	-1.26	0.063	-0.03
1421929_at	Epha4	Eph receptor A4	1.51	0.234	-1.18	0.531	-1.24	0.459	1.31	0.58	0.1
1434953_at	---	Adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:533043	1.16	0.179	1	0.995	-1	0.993	-1.55	0.118	-0.1
1422018_at	Hivep2	human immunodeficiency virus type I enhancer binding protein 2	1.15	0.207	-1.07	0.839	1.07	0.786	-1.93	0.214	-0.19
1460409_at	Cpt1a	carnitine palmitoyltransferase 1a, liver	-1.16	0.246	-1.27	0.142	1.51	0.051	1.03	0.904	0.03
1450407_a_at	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	1.22	0.792	-1.15	0.556	1.07	0.87	-1.23	0.602	-0.02

1421207_at	Lif	leukemia inhibitory factor	1.3	0.496	-1.8	0.21	1.3	0.428	-2.01	0.047	-0.3
1432770_at	0610040A22Rik	RIKEN cDNA 0610040A22 gene	-1.13	0.559	1.09	0.755	1.18	0.695	-1.68	0.241	-0.13
1456531_x_at	Prpf19	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)	-1.03	0.809	1.1	0.226	1.09	0.374	-1.21	0.132	-0.01
1425310_a_at	Emid2	EMI domain containing 2	-1.15	0.574	-1.37	0.636	1.56	0.129	1.14	0.759	0.04
1459764_x_at	Snx10	Sorting nexin 10	-1.03	0.787	1.04	0.922	1.15	0.312	-1.28	0.011	-0.03
1457122_at	Ap2m1	Adaptor protein complex AP-2, mu1	1.25	0.579	-1.19	0.541	1.07	0.81	-1.12	0.556	0
1434263_at	F630110N24Rik	RIKEN cDNA F630110N24 gene	-1.11	0.756	-1.07	0.44	1.33	0.24	1.53	0.344	0.17
1456519_at	AW493845	Expressed sequence AW493845	1.21	0.692	-1.35	0.578	1.21	0.557	-1.04	0.854	0.01
1431109_at	5430406M13Rik	RIKEN cDNA 5430406M13 gene	1.26	0.812	1.03	0.724	-1.16	0.615	-1.67	0.123	-0.13
1427507_at	Trim17	tripartite motif protein 17	-1.26	0.222	-1.14	0.557	1.49	0.217	1.11	0.893	0.05
1424560_at	Pstpip1	proline-serine-threonine phosphatase-interacting protein 1	-1.5	0.525	1.12	0.715	1.37	0.22	-1.55	0.146	-0.14
1437345_a_at	Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	-1.05	0.558	-1.03	0.594	1.24	0.05	1.02	0.931	0.04
1437583_x_at	Acss1	acyl-CoA synthetase short-chain family member 1	1.36	0.51	-2.61	0.025	1.42	0.168	-2.48	0.013	-0.58
1422598_at	Casq1	calsequestrin 1	-2.01	0.082	1.18	0.103	1.48	0.519	-1.12	0.455	-0.12
1452301_at	Aldh3b1	aldehyde dehydrogenase 3 family, member B1	-1.72	0.107	-1.04	0.859	1.61	0.107	1.54	0.015	0.1
1438220_at	Foxj3	forkhead box J3	1.06	0.768	-1.02	0.935	1.12	0.635	-1.21	0.426	-0.01
1437328_x_at	Cpsf3	cleavage and polyadenylation specificity factor 3	-2.62	0.484	2.04	0.152	-1.35	0.558	1.02	0.973	-0.23
1432551_at	LOC73317	hypothetical LOC73317	-1.83	0.533	2.18	0.047	-2.28	0.157	1.32	0.49	-0.16
1420820_at	2900073G15Rik	RIKEN cDNA 2900073G15 gene	1.12	0.031	1.19	0.013	-1.17	0.072	-1.2	0.257	-0.02
1423657_at	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synth	-1.02	0.653	1.13	0.337	1.05	0.638	-1.26	0.35	-0.02
1453945_at	2310005E17Rik	RIKEN cDNA 2310005E17 gene	1.15	0.756	-1.61	0.354	1.39	0.454	-1.44	0.118	-0.13
1422103_a_at	Stat5b	signal transducer and activator of transcription 5B	1.05	0.5	-1.06	0.506	1.17	0.29	-1.2	0.202	-0.01
1456308_x_at	Trim28	tripartite motif protein 28	-1.08	0.528	-1.17	0.009	1.37	0.035	1.15	0.365	0.07
1452150_at	AU040320	expressed sequence AU040320	-1.08	0.347	-1.07	0.599	1.3	0.134	1.07	0.749	0.05
1421876_at	Mapk9	mitogen activated protein kinase 9	-1.15	0.028	-1.13	0.453	1.4	0.157	1.34	0.457	0.12
1424396_a_at	Asrgl1	asparaginase like 1	-1.54	0.044	-1.06	0.712	1.57	0.345	1.3	0.213	0.07
1459834_x_at	---	---	-1.52	0.111	1.66	0.237	-1.19	0.764	1.15	0.477	0.03
1460202_at	Myoz1	myozenin 1	-2.4	0.235	-1.19	0.53	1.91	0.113	1.12	0.763	-0.14
1439465_x_at	9430057O19Rik	RIKEN cDNA 9430057O19 gene	-1.06	0.667	1.07	0.758	1.14	0.563	-1.32	0.093	-0.04
1458160_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4933400K21 pr	-1.07	0.918	1.13	0.818	1.09	0.745	-1.54	0.045	-0.1
1428564_at	Zfp579	zinc finger protein 579	-1.1	0.095	1.18	0.15	1.08	0.698	-1.06	0.889	0.02
1434816_at	Vps33a	vacuolar protein sorting 33A (yeast)	1.21	0.459	1.06	0.586	-1.12	0.442	-1.16	0.211	0
1455250_at	Sh3bp4	SH3-domain binding protein 4	1.01	0.957	1.19	0.689	-1.04	0.852	-1.45	0.246	-0.07
1457162_at	Ldlrap1	low density lipoprotein receptor adaptor protein 1	1.2	0.515	-1.21	0.655	1.14	0.28	-1.31	0.355	-0.05
1427206_at	Afg3l2	AFG3(ATPase family gene 3)-like 2 (yeast)	-1.13	0.353	-1.14	0.193	1.4	0.04	1.6	0.316	0.18
1453261_at	2610035D17Rik	RIKEN cDNA 2610035D17 gene	-1.06	0.77	1.22	0.291	1	0.988	-1.45	0.237	-0.07
1442835_at	---	0 day neonate lung cDNA, RIKEN full-length enriched library, clone:E030050O06	2.04	0.148	-2.02	0.279	-1.6	0.038	1.1	0.906	-0.12
1431278_s_at	Pla2g6	phospholipase A2, group VI	-2.01	0.113	-1.38	0.469	1.94	0.226	1.06	0.753	-0.1
1455242_at	Foxp1	forkhead box P1	1.09	0.68	-1.02	0.885	1.1	0.633	-1.67	0.191	-0.13
1417020_at	Spata4	spermatogenesis associated 4	1.11	0.801	-1.04	0.911	1.09	0.899	-1.35	0.421	-0.05
1440592_at	Cd80	CD80 antigen	1.06	0.918	1.35	0.471	-1.33	0.384	-1.39	0.028	-0.08
1458406_at	AI429294	Expressed sequence AI429294	-1.36	0.492	1.29	0.158	1.14	0.687	-1.06	0.788	0
1420769_at	D11Lgp2e	DNA segment, Chr 11, Lothar Hennighausen 2, expressed	-1.4	0.196	1.17	0.569	1.28	0.373	-1.41	0.234	-0.09
1454791_a_at	Rbbp4	retinoblastoma binding protein 4	-2.09	0.527	-2	0.043	2.18	0.048	1.68	0.189	-0.06
1423357_at	2610209A20Rik	RIKEN cDNA 2610209A20 gene	-1.1	0.408	1.36	0.113	-1.12	0.413	1.09	0.086	0.06
1440421_at	2700085M18Rik	RIKEN cDNA 2700085M18 gene	-1.14	0.537	1.44	0.221	-1.18	0.403	1.29	0.431	0.1
1450438_at	Ncam1	neural cell adhesion molecule 1	-1.08	0.859	1.52	0.246	-1.38	0.395	1.95	0.195	0.25
1452413_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	1.53	0.4	-2.05	0.17	1.14	0.607	-1.39	0.339	-0.19
1429367_at	Wipi2	WD repeat domain, phosphoinositide interacting 2	-1.05	0.788	-1.05	0.735	1.26	0.392	1.58	0.048	0.18
1422006_at	Eif2ak2	eukaryotic translation initiation factor 2-alpha kinase 2	-1.05	0.91	1.14	0.431	1.07	0.864	-1.39	0.466	-0.06
1427300_at	Lhx8	LIM homeobox protein 8	-1.01	0.99	1.04	0.93	1.13	0.789	-1.64	0.122	-0.12
1448067_at	AW011956	expressed sequence AW011956	1.13	0.396	1.43	0.371	-1.66	0.032	-1.06	0.702	-0.04
1443616_at	Sypl	Synaptophysin-like protein	1.46	0.47	-1.12	0.778	-1.23	0.668	1.09	0.892	0.05

1418249_at	Crcp	calcitonin gene-related peptide-receptor component protein	-1.01	0.978	1.23	0.328	-1.07	0.372	1	0.995	0.04
1441568_at	BC010311	cDNA sequence BC010311	-1.28	0.036	1.33	0.196	1.05	0.712	-1.19	0.668	-0.02
1428612_at	Atg7	autophagy-related 7 (yeast)	-1.1	0.667	-1.16	0.268	1.39	0.108	1.34	0.294	0.12
1437914_at	E2f6	E2F transcription factor 6	1.5	0.02	-1.24	0.736	-1.17	0.475	1.5	0.587	0.15
1423480_at	Nol11	nucleolar protein 11	1.07	0.592	1.31	0.095	-1.27	0.044	-1.01	0.917	0.02
1437496_at	9330129D05Rik	RIKEN cDNA 9330129D05 gene	-1.24	0.404	-1.06	0.617	1.41	0.343	1.05	0.815	0.04
1419540_at	Fthl17 /// LOC4347	ferritin, heavy polypeptide-like 17 /// similar to ferritin, heavy polypeptide-like 17 ///	1.37	0.715	1.26	0.573	-1.85	0.17	-3.43	0.028	-0.66
1441659_at	Dpf3	D4, zinc and double PHD fingers, family 3	-1.26	0.772	1.61	0.559	-1.33	0.449	1.02	0.949	0.01
1419358_at	Sorcs2	sortilin-related VPS10 domain containing receptor 2	-1.26	0.236	1.25	0.427	1.12	0.535	-1.38	0.375	-0.07
1430999_a_at	Scoc	short coiled-coil protein	-1.17	0.505	-1.01	0.992	1.31	0.522	3.54	0.279	0.67
1429090_at	A030007L17Rik	RIKEN cDNA A030007L17 gene	-1.33	0.175	-1.29	0.693	1.63	0.264	1.24	0.682	0.07
1434351_at	Nup214	nucleoporin 214	1.06	0.467	-1.09	0.35	1.18	0.319	-1.07	0.059	0.02
1419861_at	---	---	-1.09	0.475	1.04	0.87	1.2	0.663	-1.26	0.116	-0.02
1458906_at	---	---	1.83	0.046	1.02	0.925	-3.19	0.086	-1.44	0.486	-0.44
1424922_a_at	Brd4	bromodomain containing 4	1.05	0.669	-1.37	0.091	1.39	0.106	-1.15	0.34	-0.02
1450822_at	Lzp-s	P lysozyme structural	1.02	0.972	1.58	0.203	-1.78	0.018	-1.33	0.032	-0.13
1450041_a_at	Tub	tubby candidate gene	1.3	0.525	-1.15	0.783	-1	0.996	1.13	0.687	0.07
1450713_at	Cspg5	chondroitin sulfate proteoglycan 5	-1.67	0.087	1.35	0.149	1.21	0.351	-1.03	0.931	-0.03
1439789_at	---	---	1	0.993	1.17	0.812	-1.01	0.96	-2.48	0.056	-0.33
1443657_at	6330505N24Rik	RIKEN cDNA 6330505N24 gene	-1.18	0.794	1.65	0.494	-1.5	0.003	6.39	0.19	1.34
1426067_x_at	Cct3	chaperonin subunit 3 (gamma)	1.22	0.757	1.17	0.504	-1.3	0.427	-1.02	0.932	0.02
1440575_at	Hspa4	heat shock protein 4	1.53	0.219	-1.35	0.441	-1.11	0.469	1.04	0.882	0.02
1452942_at	Tmem65	transmembrane protein 65	-1.09	0.158	1.37	0.101	-1.15	0.416	1.17	0.619	0.08
1441930_x_at	Vat1	Vesicle amine transport protein 1 homolog (T californica)	-1.1	0.658	1.24	0.225	1.02	0.929	-1.17	0.627	0
1452665_at	Ttc27	tetratricopeptide repeat domain 27	1	0.993	-1.1	0.402	1.25	0.197	-1.21	0.091	-0.01
1453382_at	Fbxo42	F-box protein 42	1.34	0.48	-1.15	0.731	-1.05	0.73	1.52	0.213	0.17
1445822_at	LOC639112 /// LOC	similar to CG18631-PA /// similar to CG18631-PA /// similar to CG18631-PA	1.36	0.534	-1.2	0.538	-1.03	0.805	1.05	0.9	0.04
1418043_at	Abcc5	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	1.16	0.459	-1.21	0.671	1.18	0.334	-1.61	0.293	-0.12
1419565_a_at	Zfx	zinc finger protein X-linked	-1.06	0.788	1.46	0.281	-1.32	0.005	1.26	0.117	0.09
1418259_a_at	Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	1	0.994	1.18	0.108	-1.01	0.914	-1.4	0.388	-0.06
1442961_at	---	---	-1.09	0.765	1.02	0.92	1.23	0.169	-1.26	0.476	-0.03
1422791_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	-1.06	0.807	-1.06	0.758	1.28	0.343	1.38	0.363	0.13
1427024_at	5033405K12Rik	RIKEN cDNA 5033405K12 gene	-1.07	0.748	1.01	0.967	1.22	0.57	-1.44	0.174	-0.07
1429651_at	Phactr3	phosphatase and actin regulator 3	1.47	0.33	-1.26	0.771	-1.12	0.862	2.96	0.018	0.52
1423905_at	Pvr	poliovirus receptor	1.15	0.845	-1.09	0.831	1.1	0.837	-1.08	0.764	0.02
1422445_at	Itga6	integrin alpha 6	-1.22	0.563	1.34	0.289	1.01	0.886	-1.2	0.157	-0.02
1431295_a_at	Stx18	syntaxin 18	-1.07	0.687	1.13	0.662	1.1	0.724	-1.47	0.046	-0.08
1429267_at	Acot11	acyl-CoA thioesterase 11	-1.19	0.696	1.05	0.685	1.28	0.309	-1	0.969	0.03
1452014_a_at	Igf1	insulin-like growth factor 1	1.44	0.658	-1.15	0.338	-1.17	0.541	1.19	0.618	0.08
1426637_a_at	Six3	sine oculis-related homeobox 3 homolog (Drosophila)	-1.02	0.956	1.24	0.601	-1.05	0.803	1.29	0.053	0.11
1443567_at	BC032203	cDNA sequence BC032203	1.52	0.169	-1.1	0.745	-1.37	0.391	1.61	0.294	0.17
1443079_at	---	Transcribed locus	-1.62	0.305	1.29	0.738	1.26	0.69	-1.08	0.783	-0.04
1435820_x_at	Ddr1	discoidin domain receptor family, member 1	-1.27	0.155	1.33	0.399	1.05	0.847	-2.25	0.036	-0.28
1427962_at	Ccdc102a /// LOC6	coiled-coil domain containing 102A /// similar to CG31638-PA	-1.16	0.605	1.22	0.622	1.09	0.354	-1.8	0.047	-0.16
1420814_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	-1.03	0.681	1.07	0.503	1.13	0.278	-1.3	0.131	-0.03
1442702_at	Dmt2	Dorso-medial telencephalon gene 2	-1.8	0.53	2	0.011	-1.65	0.227	3.36	0.316	0.48
1419781_at	D630004N19Rik	RIKEN cDNA D630004N19 gene	1.17	0.781	-1.68	0.437	1.41	0.466	-1.01	0.987	-0.03
1430964_at	2310034O05Rik	RIKEN cDNA 2310034O05 gene	1.23	0.342	1.11	0.81	-1.21	0.502	-1.15	0.728	-0.01
1443682_at	AI662476	expressed sequence AI662476	2.03	0.03	-3.11	0.022	-1.23	0.333	1.05	0.868	-0.31
1440645_at	LOC546006	similar to deleted in malignant brain tumors 1 isoform c precursor	1.65	0.336	-1.81	0.057	-1.04	0.918	1.11	0.726	-0.02
1455849_at	---	---	1.17	0.399	1.11	0.646	-1.13	0.497	-1.05	0.866	0.03
1457788_at	Rassf1	Ras association (RalGDS/AF-6) domain family 1	1.28	0.648	1.24	0.344	-1.53	0.271	-1.41	0.232	-0.11
1431345_a_at	Taf1b	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, B	-1.08	0.508	1.1	0.771	1.14	0.68	-1.25	0.235	-0.02

1423122_at	Avpi1	arginine vasopressin-induced 1	1.05	0.885	1.38	0.041	-1.34	0.011	-1.44	0.419	-0.09
1438002_at	---	---	1.31	0.201	1.1	0.743	-1.34	0.388	-1.32	0.565	-0.06
1429366_at	Lrrc34	leucine rich repeat containing 34	1.53	0.319	-1.82	0.202	1.09	0.76	-1.36	0.599	-0.14
1434063_at	Zfp664	zinc finger protein 664	-1.09	0.591	1.19	0.316	1.07	0.709	-1.21	0.202	-0.01
1416431_at	Tubb6	tubulin, beta 6	1.05	0.769	1.48	0.128	-1.56	0.034	-1.25	0.358	-0.07
1419170_at	Tmem157	transmembrane protein 157	1.05	0.764	1.16	0.13	-1.04	0.776	-1.09	0.496	0.02
1424997_at	Sfrs8	splicing factor, arginine/serine-rich 8	1.23	0.312	1.09	0.703	-1.17	0.562	-1.04	0.911	0.03
1451624_a_at	Phospho2	phosphatase, orphan 2	1.04	0.859	-1.03	0.844	1.16	0.513	-2.03	0.159	-0.22
1424223_at	1700020C11Rik	RIKEN cDNA 1700020C11 gene	-1.13	0.355	-1.15	0.292	1.41	0	2.5	0.191	0.41
1419226_at	Cd96	CD96 antigen	1.08	0.662	1.17	0.722	-1.09	0.521	-2.25	0.117	-0.27
1440455_at	AI848599	expressed sequence AI848599	1.13	0.127	1.17	0.619	-1.14	0.089	-1.1	0.551	0.01
1453666_at	Rnf32	ring finger protein 32	-1.15	0.844	-1.26	0.473	1.51	0.389	1.17	0.56	0.07
1418599_at	Col11a1	procollagen, type XI, alpha 1	-1.9	0.109	1.18	0.757	1.46	0.436	-1.38	0.217	-0.16
1432129_a_at	Prrx1	paired related homeobox 1	1.29	0.546	-1.09	0.709	-1.05	0.705	1.46	0.476	0.15
1418762_at	Cd55	CD55 antigen	-1.25	0.64	1.27	0.067	1.1	0.519	-1.62	0.065	-0.13
1434606_at	Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	1.03	0.828	1.15	0.212	-1.01	0.753	-1.11	0.699	0.01
1442084_at	Prkrip1	Prkr interacting protein 1 (IL11 inducible)	-3.01	0.02	1.87	0.363	-1.03	0.934	1.09	0.393	-0.27
1453609_s_at	Ccdc9	coiled-coil domain containing 9	-1.03	0.759	1.27	0.159	-1.07	0.833	1.04	0.839	0.05
1428557_a_at	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	-1.06	0.534	-1.02	0.736	1.24	0.202	1.75	0.267	0.23
1448940_at	Trim21	tripartite motif protein 21	1.11	0.458	1.23	0.014	-1.2	0.279	-1.49	0.059	-0.09
1419343_at	Slc15a1	solute carrier family 15 (oligopeptide transporter), member 1	1.03	0.934	1.19	0.732	-1.05	0.83	-1.27	0.668	-0.03
1431792_a_at	Stk11ip	serine/threonine kinase 11 interacting protein	-1.2	0.337	1.27	0.404	1.07	0.432	-1.49	0.074	-0.09
1427992_a_at	Rab12	RAB12, member RAS oncogene family	-1	0.998	1.12	0.573	1.05	0.772	-1.25	0.262	-0.02
1420459_at	Dscr6	Down syndrome critical region homolog 6 (human)	-1.09	0.552	1.3	0.337	-1.05	0.599	1.3	0.212	0.12
1444298_at	A130090K04Rik	RIKEN cDNA A130090K04 gene	1.26	0.791	-1.36	0.558	1.18	0.784	-1.86	0.243	-0.2
1417609_at	Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	-1.03	0.753	1.23	0.097	-1.03	0.756	1.03	0.856	0.05
1451981_at	Gtrgeo22	gene trap ROSA b-geo 22	-1.1	0.669	-1.02	0.915	1.28	0.237	1.14	0.513	0.08
1434558_at	Wdr47	WD repeat domain 47	1.01	0.893	1.24	0.323	-1.09	0.377	-1.4	0.122	-0.06
1425299_s_at	0610038D11Rik ///	RIKEN cDNA 0610038D11 gene /// similar to UPF0315 protein /// similar to UPF0	1.03	0.834	-1.15	0.18	1.27	0.088	-1.17	0.405	0
1454087_at	Zfp618	zinc fingerprotein 618	1.13	0.776	1.13	0.834	-1.1	0.832	-1.59	0.453	-0.11
1451326_at	Abhd14b	abhydrolase domain containing 14b	1.11	0.367	-1.1	0.398	1.15	0.231	-1.21	0.539	-0.01
1430782_at	B130055D15Rik	RIKEN cDNA B130055D15 gene	1.67	0.477	-1.57	0.216	-1.16	0.795	2.12	0.209	0.27
1455127_at	Xkr5	X Kell blood group precursor-related family, member 5	-1.84	0.026	-1.14	0.588	1.75	0.195	1.45	0.332	0.05
1424916_x_at	8030466O12Rik	RIKEN cDNA 8030466O12 gene	1.06	0.412	1.25	0.058	-1.17	0.091	-1.64	0.198	-0.12
1443735_at	BC052688	CDNA sequence BC052688	1.02	0.906	1.31	0.445	-1.19	0.639	-1.02	0.93	0.03
1455863_at	Spata5l1	spermatogenesis associated 5-like 1	1.09	0.52	-1.17	0.444	1.22	0.444	-1.58	0.08	-0.11
1431693_a_at	Il17b	interleukin 17B	-2.05	0.334	1.78	0.469	-1.11	0.564	1.23	0.341	-0.04
1438640_x_at	Pgk1 /// LOC43359	phosphoglycerate kinase 1 /// phosphoglycerate kinase 1-like /// phosphoglycerat	-1.13	0.315	1.01	0.904	1.27	0.192	-1.29	0.034	-0.03
1451758_at	Lamc3	laminin gamma 3	1.07	0.822	-1.49	0.406	1.43	0.064	-1.02	0.974	0
1416717_at	Crisp2	cysteine-rich secretory protein 2	1.32	0.395	1.07	0.893	-1.28	0.634	-2.9	0.111	-0.45
1433382_at	1110065P19Rik	RIKEN cDNA 1110065P19 gene	1.44	0.383	-1.4	0.505	1.02	0.949	-1.18	0.718	-0.03
1441374_at	C79798	expressed sequence C79798	1.26	0.681	-1.38	0.697	1.19	0.674	-1.14	0.788	-0.02
1442482_at	1700106N22Rik	RIKEN cDNA 1700106N22 gene	1.23	0.641	-1.21	0.429	1.11	0.793	-1.13	0.865	0
1444487_at	Lrat	lecithin-retinol acyltransferase (phosphatidylcholine-retinol-O-acyltransferase)	-1.22	0.46	1.26	0.062	1.09	0.581	-2.58	0.067	-0.36
1418365_at	Ctsh	cathepsin H	1.2	0.015	1.16	0.002	-1.23	0.222	-1.52	0.27	-0.1
1438147_at	Srcrb4d	scavenger receptor cysteine rich domain containing, group B (4 domains)	-1.02	0.852	1.29	0.032	-1.11	0.652	1.16	0.573	0.08
1426283_at	Hnt	neurotrimin	-1.46	0.239	1.41	0.08	1.08	0.792	-2.19	0.311	-0.29
1439600_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.4	0.641	1.16	0.649	-1.64	0.18	-1	0.993	-0.02
1424808_at	Lama4	laminin, alpha 4	1.11	0.918	1.13	0.8	-1.07	0.857	-2.69	0.423	-0.38
1448523_at	Nphp1	nephronophthisis 1 (juvenile) homolog (human)	1.07	0.602	-1.05	0.915	1.15	0.083	-1.08	0.912	0.02
1439587_at	Lemd3	LEM domain containing 3	1.3	0.301	1.03	0.9	-1.19	0.127	-1.56	0.326	-0.11
1425098_at	Zfp106	zinc finger protein 106	-1	0.997	1.14	0.805	1.04	0.643	-1.19	0.485	-0.01
1439032_at	Cep27	centrosomal protein 27	1.38	0.086	-1.05	0.645	-1.18	0.412	1.55	0.221	0.17

1450724_at	Drctnnb1a	down-regulated by Ctnnb1, a	-1.09	0.355	1.49	0.067	-1.31	0.084	1.95	0.179	0.26
1428417_at	3110050N22Rik	RIKEN cDNA 3110050N22 gene	1.04	0.791	1.33	0.338	-1.23	0.272	-1.68	0.187	-0.14
1452949_at	Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	1.06	0.874	1.2	0.43	-1.09	0.537	-1.29	0.181	-0.03
1446954_at	Pdha1	Pyruvate dehydrogenase E1 alpha 1	1.05	0.927	1.28	0.316	-1.18	0.607	-2.03	0.054	-0.22
1455861_at	Epb4.1l5	erythrocyte protein band 4.1-like 5	-1.32	0.084	1.61	0.21	-1.24	0.445	1.03	0.841	0.02
1438084_at	Adam23	A disintegrin and metallopeptidase domain 23	1.14	0.692	1.19	0.563	-1.19	0.437	-2.57	0.088	-0.36
1453748_a_at	Kif23	kinesin family member 23	-1.26	0.535	-1.03	0.848	1.41	0.527	3.22	0.228	0.58
1450149_a_at	Ppp1cc /// LOC434	protein phosphatase 1, catalytic subunit, gamma isoform /// similar to protein phos	1.11	0.388	1.06	0.186	-1	0.971	-1.08	0.191	0.02
1431398_at	5730446D14Rik	RIKEN cDNA 5730446D14 gene	-1.24	0.086	1.49	0.303	-1.15	0.156	1.69	0.118	0.2
1429117_at	Tradd	TNFRSF1A-associated via death domain	1.11	0.711	1.21	0.204	-1.17	0.498	-1.27	0.361	-0.03
1435423_x_at	4933433P14Rik	RIKEN cDNA 4933433P14 gene	-1.13	0.616	1.14	0.351	1.16	0.342	-1.2	0.127	-0.01
1448416_at	Mgp	matrix Gla protein	1.86	0.043	-1.4	0.363	-1.68	0.007	1.66	0.367	0.11
1459522_s_at	Gyg	glycogenin	1.02	0.821	1.2	0.43	-1.05	0.82	-1.17	0.035	0
1423095_s_at	Crbn	cereblon	-1.04	0.546	1.06	0.405	1.15	0.475	-1.09	0.521	0.02
AFFX-BioC-3_at	---	---	1.29	0.127	1.12	0.144	-1.32	0.242	-1.21	0.394	-0.03
1444439_at	Bri3bp	Bri3 binding protein	1.19	0.809	-1.07	0.904	1.04	0.882	-1.73	0.019	-0.14
1459616_at	Plk1	polo-like kinase 1 (Drosophila)	-1.24	0.738	-1.91	0.427	1.85	0.168	2.25	0.409	0.23
1426390_a_at	Arf1	ADP-ribosylation factor 1	1.05	0.781	1.17	0.314	-1.05	0.503	-1.11	0.084	0.01
1432009_at	4933415D12Rik	RIKEN cDNA 4933415D12 gene	1.04	0.89	-1.02	0.851	1.15	0.222	-1	0.997	0.04
1443562_at	2610017I09Rik	RIKEN cDNA 2610017I09 gene	1.68	0.31	-1.2	0.789	-1.51	0.529	1.27	0.565	0.06
1430217_at	4921528H16Rik	RIKEN cDNA 4921528H16 gene	-1.19	0.731	-1.19	0.547	1.49	0.18	1.05	0.886	0.04
1451243_at	Rnpep	arginyl aminopeptidase (aminopeptidase B)	-1.05	0.475	-1.1	0.415	1.31	0.024	1.15	0.005	0.08
1448512_at	Hils1	histone H1-like protein in spermatids 1	-1.04	0.769	1.18	0.149	1.03	0.88	-1.07	0.539	0.03
1428103_at	---	---	-1.06	0.312	1.26	0.077	-1.04	0.731	1.6	0.107	0.19
1423235_at	Ap3b1	adaptor-related protein complex 3, beta 1 subunit	-1.04	0.649	1.02	0.87	1.19	0.029	-1.07	0.622	0.03
1415992_at	Pigo	phosphatidylinositol glycan anchor biosynthesis, class O	-1.18	0.415	1.03	0.845	1.3	0.092	-1.16	0.334	0
1425045_at	Pla2g4b	phospholipase A2, group IVB (cytosolic)	-1.02	0.914	1.13	0.188	1.07	0.768	-1.12	0.701	0.01
1424847_at	Nefh	neurofilament, heavy polypeptide	-1.87	0.193	-1.03	0.947	1.67	0.268	1.78	0.181	0.14
1455820_x_at	Scarb1	scavenger receptor class B, member 1	1.12	0.703	-1.14	0.327	1.18	0.244	-1	0.996	0.04
1433776_at	Lhfp	lipoma HMGIC fusion partner	1.22	0.054	1.31	0.03	-1.53	0.117	-1.27	0.534	-0.07
1424593_at	Ecd	ecdysoneless homolog (Drosophila)	-1.11	0.126	-1.05	0.827	1.32	0.076	1.23	0.458	0.1
1452057_at	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	-1.04	0.901	1.06	0.787	1.15	0.641	-1.08	0.721	0.02
1455929_x_at	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	-1.05	0.631	1.01	0.896	1.22	0.06	-1.14	0.408	0.01
1456510_x_at	Ubie	UbiE-YGHL1 fusion protein	-1.37	0.496	-1.4	0.228	1.73	0.175	1.18	0.298	0.04
1418902_at	3110023E09Rik	RIKEN cDNA 3110023E09 gene	1.09	0.65	1.14	0.067	-1.07	0.599	-1	0.988	0.04
1449779_at	---	---	1.32	0.265	-2.38	0.197	1.43	0.546	-1.13	0.522	-0.19
1427649_at	Wdr22	WD repeat domain 22	-2.14	0.147	1.31	0.505	1.4	0.24	-1.16	0.837	-0.15
1455138_x_at	Cfl1	cofilin 1, non-muscle	1.02	0.845	1.18	0.186	-1.02	0.805	-1.34	0.004	-0.04
1416780_at	Pfkm	phosphofructokinase, muscle	-1.14	0.05	-1.13	0.397	1.41	0.311	2.39	0.244	0.38
1455333_at	Tns3	tensin 3	1.06	0.374	1.16	0.535	-1.05	0.823	-1.08	0.844	0.02
1455172_at	AU020094	expressed sequence AU020094	1.32	0.49	-1	0.993	-1.16	0.499	1.35	0.191	0.13
1417234_at	Mmp11	matrix metallopeptidase 11	1.19	0.403	1.17	0.818	-1.23	0.483	-2.06	0.172	-0.23
1429046_at	Smurf2	SMAD specific E3 ubiquitin protein ligase 2	-1.02	0.933	1.17	0.621	1.03	0.924	-1.08	0.713	0.02
1443354_at	Trim59	Tripartite motif-containing 59	-1.42	0.289	1.53	0.457	-1.06	0.881	3.21	0.029	0.56
1430256_at	2310033K02Rik	RIKEN cDNA 2310033K02 gene	1.17	0.751	-2.68	0.313	1.64	0.443	-1.12	0.805	-0.25
1421543_at	Fbxo4	F-box only protein 4	1.06	0.672	1.57	0.555	-1.82	0.398	-1.44	0.682	-0.16
1420675_at	Zfp113	zinc finger protein 113	1.14	0.156	-1.04	0.873	1.07	0.609	-1.42	0.304	-0.06
1437723_s_at	Derl1	Der1-like domain family, member 1	-1.04	0.769	1.17	0.197	1.04	0.714	-1.02	0.888	0.04
1428730_at	Krit1	KRIT1, ankyrin repeat containing	1.56	0.099	1.08	0.819	-1.87	0.061	-1.09	0.63	-0.08
1454953_at	Rnf157	ring finger protein 157	-1.12	0.878	-1.44	0.354	1.59	0.221	1.01	0.975	0.01
1457145_at	Plekhg4	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	-1.49	0.068	1.73	0.3	-1.28	0.204	1.26	0.179	0.05
1421359_at	Ret	ret proto-oncogene	1.3	0.52	-1.86	0.206	1.34	0.541	-1.07	0.668	-0.07
1429142_at	1700012A03Rik	RIKEN cDNA 1700012A03 gene	1.2	0.145	1.21	0.397	-1.31	0.624	-1	0.998	0.03

1438921_at	Atr	Ataxia telangiectasia and Rad3 related	-1.39	0.353	1.33	0.349	1.13	0.486	-1.6	0.247	-0.13
1416085_s_at	Zfand5	zinc finger, AN1-type domain 5	-1.03	0.781	-1.03	0.709	1.24	0.158	1.53	0.177	0.18
1430446_at	2310057B04Rik	RIKEN cDNA 2310057B04 gene	-1.44	0.525	1.59	0.509	-1.12	0.76	1.71	0.034	0.19
1428491_at	Commd10	COMM domain containing 10	-1.1	0.632	1.26	0.279	1.01	0.934	-1.36	0.325	-0.05
1436661_at	Dpp10	dipeptidylpeptidase 10	-1.32	0.463	1.34	0.499	1.08	0.647	-1.49	0.386	-0.1
1456005_a_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	1.28	0.355	1.06	0.727	-1.2	0.134	-1.16	0.322	0
1458506_at	Gm1582	gene model 1582, (NCBI)	-1.03	0.963	-1.37	0.266	1.47	0.082	3.03	0.013	0.53
1455990_at	Kif23	kinesin family member 23	-2.45	0.424	1.88	0.201	-1.12	0.49	2.39	0.219	0.17
1422931_at	Fosl2	fos-like antigen 2	-1.18	0.502	1.22	0.428	1.11	0.477	-1.36	0.136	-0.05
1428805_at	Slc35e3	solute carrier family 35, member E3	1.02	0.85	1.16	0.489	-1	0.997	-1.35	0.133	-0.04
1460093_at	---	---	1.02	0.951	-1.86	0.347	1.62	0.46	-1.26	0.123	-0.12
1449804_at	Pnmt	phenylethanolamine-N-methyltransferase	-1.27	0.029	-1.03	0.95	1.42	0.1	1.23	0.382	0.09
1434529_x_at	Chfr	checkpoint with forkhead and ring finger domains	1.19	0.304	-1.07	0.647	1.06	0.479	-1.03	0.273	0.04
1419941_at	C030018P15Rik	RIKEN cDNA C030018P15 gene	-1.2	0.829	1.47	0.408	-1.14	0.739	1.59	0.013	0.18
1450122_at	Ptprg	protein tyrosine phosphatase, receptor type, G	-1.06	0.783	1.01	0.965	1.23	0.559	-1.15	0.397	0.01
1443207_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933019	-1.53	0.521	1.85	0.296	-1.48	0.306	1.02	0.971	-0.04
1438951_x_at	Nup54	nucleoporin 54	-1.17	0.46	1.32	0.082	-1	0.998	1.1	0.409	0.06
1426945_at	Ranbp5	RAN binding protein 5	-1.06	0.472	-1.02	0.824	1.25	0.023	1.46	0.093	0.16
1450656_at	Gna13	guanine nucleotide binding protein, alpha 13	1.21	0.426	1.16	0.245	-1.23	0.189	-1	0.986	0.03
1422384_at	Olfr1509	olfactory receptor 1509	-1.22	0.799	1.28	0.734	1.08	0.778	-1.28	0.786	-0.03
1437102_at	Ythdf1	YTH domain family 1	-1.13	0.213	1.09	0.634	1.21	0.247	-1.1	0.583	0.02
1425828_at	Nkx6-1	NK6 transcription factor related, locus 1 (Drosophila)	1.1	0.861	-1.06	0.748	1.14	0.044	-1.08	0.455	0.02
1460349_at	Prr14	proline rich 14	1.04	0.454	-1.05	0.38	1.19	0.087	-1.25	0.108	-0.02
1425500_x_at	LOC625794	Hypothetical protein LOC625794	-1.92	0.158	-1.04	0.876	1.7	0.356	1.39	0.529	0.03
1434903_s_at	Il1rl2	interleukin 1 receptor-like 2	1.38	0.298	-1.07	0.852	-1.15	0.282	1.01	0.952	0.04
1434932_at	Adarb1	adenosine deaminase, RNA-specific, B1	1.6	0.478	-1.92	0.1	1.05	0.889	-1.26	0.584	-0.13
1430747_at	Pqlc1	PQ loop repeat containing 1	1.28	0.55	1.1	0.764	-1.24	0.636	-1.19	0.689	-0.01
1444357_at	Akap6	A kinase (PRKA) anchor protein 6	-1.26	0.732	1.94	0.084	-2.25	0.013	1.16	0.8	-0.1
1449527_at	Pcdhb7	protocadherin beta 7	1.09	0.761	-1.13	0.697	1.2	0.456	-1.47	0.357	-0.08
1460153_at	Abi2	Abl-interactor 2	1.89	0.4	-3.72	0.093	1.02	0.95	-1.03	0.97	-0.46
1455824_x_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisia	-1.03	0.866	1.33	0.022	-1.13	0.14	1.03	0.708	0.05
1423913_at	Hectd3	HECT domain containing 3	-1.16	0.584	-1.34	0.061	1.58	0.008	1.1	0.335	0.04
1443591_at	Dlx4	distal-less homeobox 4	-1.13	0.41	1.71	0.061	-1.7	0.372	1.17	0.415	0.01
1454991_at	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-1.11	0.372	-1.07	0.819	1.34	0.187	1.77	0.082	0.23
1418509_at	Cbr2	carbonyl reductase 2	-1.44	0.031	1.71	0.631	-1.28	0.001	3.31	0.258	0.57
1457620_at	Htf9c	HpaII tiny fragments locus 9c	-2.85	0.074	1.94	0.042	-1.12	0.839	1.92	0.112	-0.03
1458174_at	Ccdc52	coiled-coil domain containing 52	1.24	0.157	1.04	0.932	-1.11	0.709	-1.16	0.478	0
1429484_at	1110002L01Rik	RIKEN cDNA 1110002L01 gene	1.31	0.363	-1.37	0.293	1.14	0.262	-1.29	0.14	-0.05
1451866_a_at	Hgf	hepatocyte growth factor	1.17	0.631	1.15	0.731	-1.16	0.658	-1.1	0.651	0.01
1421821_at	Ldlr	low density lipoprotein receptor	1.06	0.812	1.14	0.317	-1.03	0.836	-1.62	0.297	-0.11
1444911_at	9030605H24Rik	RIKEN cDNA 9030605H24 gene	-1.01	0.989	1.23	0.704	-1.04	0.901	1.42	0.08	0.15
1459389_at	Centg2	Centaurin, gamma 2	-2.22	0.002	1.75	0.302	-1.02	0.965	1.13	0.794	-0.09
1436525_at	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	-1.16	0.546	-1.08	0.774	1.4	0.059	1.04	0.875	0.05
1452817_at	Smyd3	SET and MYND domain containing 3	-1.54	0	-1.1	0.797	1.62	0.05	1.09	0.775	0.02
1442856_at	Adm2	adrenomedullin 2	1.46	0.398	-1.66	0.429	1.12	0.728	-1.82	0.025	-0.22
1429499_at	Fbxo5	F-box only protein 5	-1.37	0.55	-1.01	0.966	1.46	0.117	3.73	0.176	0.7
1442774_x_at	---	Transcribed locus	1.17	0.334	1.02	0.928	-1.01	0.952	-1.32	0.131	-0.03
1429472_at	4921525O09Rik	RIKEN cDNA 4921525O09 gene	1.51	0.518	1.11	0.747	-1.77	0.172	-1.38	0.411	-0.13
1436140_at	1700027J05Rik	RIKEN cDNA 1700027J05 gene	-1.08	0.623	1.25	0.515	1.01	0.978	-1.05	0.837	0.03
1453026_at	BC061039	cDNA sequence BC061039	-1.31	0.653	1.65	0.502	-1.31	0.365	1.14	0.77	0.04
1425157_x_at	Tspan33	tetraspanin 33	-1.04	0.756	-1.32	0.027	1.46	0.225	6.49	0.203	1.4
1440098_at	D030018L15Rik	RIKEN cDNA D030018L15 gene	-1.46	0.182	1.37	0.598	1.12	0.778	-1.17	0.82	-0.03
1424841_s_at	Rbks	ribokinase	-1.01	0.959	-1.27	0.067	1.4	0.122	1.51	0.316	0.16

1433507_a_at	Hmgn2	high mobility group nucleosomal binding domain 2	-1.16	0.43	1.31	0.02	1.01	0.947	-1.03	0.844	0.03
1455409_at	Spire1	spire homolog 1 (Drosophila)	-1.19	0.392	1.46	0.061	-1.13	0.372	2.31	0.208	0.36
1426814_at	AU024582	expressed sequence AU024582	-1.02	0.786	1.06	0.608	1.14	0.153	-1.26	0.32	-0.02
1420635_a_at	Tcirg1	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	-1	0.853	1.15	0.181	1.03	0.701	-1.28	0.196	-0.02
1458533_at	9330169L03Rik	RIKEN cDNA 9330169L03 gene	2.16	0.203	-2.87	0.214	-1.48	0.437	1.31	0.654	-0.22
1430299_at	Tsc22d4	TSC22 domain family 4	-1.66	0.063	1.83	0.007	-1.33	0.266	1.22	0.505	0.01
1420292_x_at	---	---	-2.5	0.092	2.38	0.293	-2.5	0.263	1.57	0.352	-0.26
1448314_at	Cdc2a	cell division cycle 2 homolog A (S. pombe)	-1.05	0.843	1.31	0.268	-1.09	0.704	4.18	0.18	0.84
1439219_at	A730082K24Rik	RIKEN cDNA A730082K24 gene	-1.18	0.453	-1.01	0.984	1.35	0.263	1.31	0.71	0.12
1423674_at	Usp1	ubiquitin specific peptdiase 1	1.45	0.237	-1.19	0.472	-1.12	0.681	1.71	0.395	0.21
1416430_at	Cat	catalase	-1.02	0.889	-1.05	0.684	1.25	0.237	1.47	0.232	0.16
1416268_at	Ets2	E26 avian leukemia oncogene 2, 3' domain	1.12	0.107	1.07	0.629	-1.01	0.968	-1.26	0.205	-0.02
1419381_at	Terf2ip	telomeric repeat binding factor 2, interacting protein	1.33	0.168	1.08	0.806	-1.29	0.008	-1.1	0.666	0
1429941_at	2410193C02Rik	RIKEN cDNA 2410193C02 gene	-1.74	0.008	1.39	0.468	1.22	0.692	-1.02	0.936	-0.04
1443292_at	---	Transcribed locus	-2	0.252	1.15	0.758	1.53	0.236	-1.02	0.949	-0.08
1454396_at	4632409D06Rik	RIKEN cDNA 4632409D06 gene	1.21	0.689	-1.39	0.547	1.26	0.622	-2.14	0.104	-0.27
1423803_s_at	Gltscr2	glioma tumor suppressor candidate region gene 2	1.05	0.832	-1.01	0.646	1.15	0.289	-1.55	0.071	-0.09
1416596_at	Slc44a4	solute carrier family 44, member 4	1.02	0.761	-1.6	0.022	1.54	0.298	-1.7	0.429	-0.18
1457627_x_at	Ropn1l	ropporin 1-like	-1.3	0.46	-1.06	0.536	1.47	0.054	1.17	0.627	0.07
1427093_at	Zfp707	zinc finger protein 707	-1.12	0.231	1.19	0.484	1.1	0.577	-1.52	0.147	-0.09
1456909_at	LOC676974	similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (P	-1.01	0.925	1.34	0.337	-1.18	0.274	1.07	0.803	0.06
1457185_at	---	---	1.3	0.202	1.02	0.964	-1.15	0.09	-1.81	0.076	-0.16
1456057_x_at	Tmem109	transmembrane protein 109	-1.12	0.312	1.11	0.126	1.18	0.196	-1.23	0.232	-0.01
1449368_at	Dcn	decorin	1.14	0.144	1.32	0.019	-1.38	0.213	-1.06	0.883	0
1454006_a_at	Ubxd6	UBX domain containing 6	-1.15	0.213	-1.04	0.794	1.35	0.162	1.4	0.217	0.14
1431562_at	4921513I03Rik	RIKEN cDNA 4921513I03 gene	-1.54	0.464	1.74	0.314	-1.26	0.574	1.17	0.825	0.03
1430301_at	Stxbp5	syntaxin binding protein 5 (tomosyn)	-1.12	0.54	1.5	0.281	-1.27	0.255	1.15	0.566	0.07
1452469_a_at	Smtn	smoothelin	1.08	0.795	-1.28	0.622	1.32	0.183	-1.01	0.903	0.03
1417298_at	Ebpl	emopamil binding protein-like	-1.04	0.038	1.1	0.15	1.13	0.188	-1.34	0.37	-0.04
1441857_x_at	Seh1l	SEH1-like (S. cerevisiae	1.26	0.747	-1.02	0.9	-1.06	0.766	1.01	0.979	0.05
1433114_at	4921504P20Rik	RIKEN cDNA 4921504P20 gene	-1.54	0.442	-1.51	0.44	1.87	0.083	1.02	0.947	-0.04
1441793_at	Rnf39	ring finger protein 39	1.39	0.513	-1.16	0.667	-1.07	0.72	1.17	0.72	0.08
1443116_at	---	---	1.16	0.654	1.18	0.751	-1.19	0.557	-1.61	0.287	-0.11
1418265_s_at	Irf2	interferon regulatory factor 2	1.12	0.693	-1.12	0.589	1.18	0.323	-1.42	0.283	-0.06
1454660_at	1100001E04Rik	RIKEN cDNA 1100001E04 gene	-1.08	0.921	1.15	0.81	1.1	0.723	-1.12	0.516	0.02
1428134_at	Coq9	coenzyme Q9 homolog (yeast)	-1.1	0.458	-1.09	0.362	1.36	0.064	1.12	0.165	0.07
1428721_at	Btbd5	BTB (POZ) domain containing 5	1.51	0.087	1.04	0.764	-1.57	0.112	-1.44	0.58	-0.11
1445313_at	Coq9	coenzyme Q9 homolog (yeast)	1.29	0.538	-1.05	0.837	-1.05	0.865	1.06	0.885	0.06
1441234_at	---	---	-1.57	0.576	-1.57	0.33	1.91	0.398	1.02	0.973	-0.05
1438928_x_at	Ninj1	ninjurin 1	-1.13	0.501	1.18	0.132	1.12	0.52	-1.12	0.712	0.01
1427515_at	A530088I07Rik	RIKEN cDNA A530088I07 gene	1.43	0.079	1.09	0.643	-1.51	0.079	-1.12	0.581	-0.03
1436589_x_at	Prkd2	protein kinase D2	-1.07	0.678	1.18	0.405	1.07	0.713	-2.88	0.02	-0.42
1417705_at	Otub1	OTU domain, ubiquitin aldehyde binding 1	1.23	0.618	-1.02	0.963	-1.03	0.938	1.33	0.269	0.13
1448791_at	Snx5	sorting nexin 5	-1.02	0.794	1.16	0.225	1.04	0.801	-2.01	0.047	-0.21
1417723_at	Ube2j1	ubiquitin-conjugating enzyme E2, J1	1.29	0.254	-1.01	0.619	-1.1	0.383	1.18	0.398	0.09
1429552_at	Wdr16	WD repeat domain 16	-1.57	0.536	1.33	0.618	1.22	0.456	-1.49	0.312	-0.13
1447687_x_at	---	---	1.03	0.893	-1.16	0.776	1.3	0.516	-1.25	0.547	-0.02
1443882_at	Slc26a2	Solute carrier family 26 (sulfate transporter), member 2	-1.01	0.927	1.37	0.004	-1.2	0.255	1.17	0.294	0.08
1445316_at	Armc9	Armadillo repeat containing 9	-2.57	0.079	1.94	0.477	-1.17	0.599	1.98	0.136	0.04
1436164_at	Slc30a1	solute carrier family 30 (zinc transporter), member 1	-1.04	0.687	1.4	0.064	-1.22	0.394	1.25	0.196	0.1
1458714_at	1700093C20Rik	RIKEN cDNA 1700093C20 gene	1.07	0.892	-1.06	0.855	1.17	0.721	-1.02	0.957	0.04
1437058_at	Megf6	multiple EGF-like-domains 6	1.17	0.065	1.03	0.952	-1.01	0.965	-1.34	0.344	-0.04
1449737_at	Pacs1	Phosphofurin acidic cluster sorting protein 1	1.6	0.037	-1.07	0.843	-1.51	0.143	1.14	0.712	0.04

1428818_at	Mon2	MON2 homolog (yeast)	1.09	0.659	-1.19	0.589	1.26	0.467	-1.21	0.585	-0.01
1451402_at	Ecd	ecdysoneless homolog (Drosophila)	-1.03	0.816	-1.04	0.705	1.26	0.248	1.1	0.279	0.07
1420182_x_at	Dmrt3	doublesex and mab-3 related transcription factor 3	-1.35	0.538	-1.17	0.714	1.59	0.181	1.08	0.77	0.04
1429506_at	Nkd1 /// LOC63437	naked cuticle 1 homolog (Drosophila) /// similar to naked cuticle 1 homolog /// sim	1.41	0.056	-1.17	0.623	-1.09	0.463	1.23	0.023	0.1
1455871_s_at	Tax1bp3 /// Rpl13	Tax1 (human T-cell leukemia virus type I) binding protein 3 /// ribosomal protein L	1.12	0.377	1.24	0.003	-1.22	0.037	-1.49	0.152	-0.08
1441835_x_at	Mtmr11	myotubularin related protein 11	-1.3	0.284	1.47	0.394	-1.06	0.74	1.07	0.486	0.05
1447812_x_at	Flnc	filamin C, gamma (actin binding protein 280)	1.79	0.424	-1.31	0.652	-1.59	0.39	1.64	0.213	0.13
1430491_at	Bop1	block of proliferation 1	-1.4	0.321	-1.22	0.588	1.65	0.116	1.02	0.932	0.01
1421728_at	Olig3	oligodendrocyte transcription factor 3	-1.44	0.592	-1.75	0.203	1.92	0.038	1.87	0.15	0.15
1425882_at	Gdf2	growth differentiation factor 2	-1.03	0.883	1.1	0.072	1.12	0.546	-1.29	0.054	-0.02
1441524_at	Tec	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	-1.14	0.834	-1.57	0.026	1.67	0.194	1.53	0.478	0.12
1419281_a_at	Zfp259	zinc finger protein 259	1.09	0.526	-1.01	0.95	1.11	0.364	-1.26	0.014	-0.02
1459600_at	Camk2d	Calcium/calmodulin-dependent protein kinase II, delta	-2.01	0.316	1.48	0.505	1.22	0.571	-1.29	0.72	-0.15
1433990_at	Lhfpl3	lipoma HMGIC fusion partner-like 3	-1.26	0.44	1.26	0.545	1.14	0.74	-1.49	0.322	-0.09
1446957_s_at	BC004022	cDNA sequence BC004022	-1.04	0.486	-1.12	0.044	1.33	0.21	1.14	0.518	0.08
1427890_a_at	Lrrc56	leucine rich repeat containing 56	-1	0.992	1.1	0.717	1.09	0.553	-1.11	0.636	0.02
1426264_at	Dlat	dihydrolipoamide S-acetyltransferase (E2 component of pyruvate dehydrogenase	-1.15	0.138	-1.28	0.176	1.54	0.092	1.57	0.263	0.17
1435226_at	Ibrdc3	IBR domain containing 3	1.07	0.765	-1.03	0.803	1.15	0.579	-1.06	0.787	0.03
1433637_at	Adck2	aarF domain containing kinase 2	-1.08	0.642	-1.04	0.817	1.31	0.188	1.01	0.966	0.05
1433905_at	Akap7	A kinase (PRKA) anchor protein 7	-1.08	0.696	1.45	0.005	-1.23	0.023	1.42	0.114	0.14
1426323_x_at	Siva	Cd27 binding protein (Hindu God of destruction)	-1.04	0.786	1.48	0.086	-1.34	0.083	1.23	0.502	0.08
1452999_at	Smndc1	survival motor neuron domain containing 1	-1.05	0.27	-1	0.978	1.24	0.102	1.07	0.651	0.06
1424655_at	Acp2	acid phosphatase 2, lysosomal	-1.02	0.879	1.1	0.635	1.11	0.17	-1.18	0.489	0
1428533_at	D1Bwg0212e	DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed	1.05	0.429	-1.05	0.74	1.19	0.011	-1.03	0.73	0.04
1429228_at	4930534B04Rik	RIKEN cDNA 4930534B04 gene	-1.05	0.927	-1.16	0.752	1.38	0.254	2.25	0.238	0.35
1442644_at	---	PREDICTED: Mus musculus hypothetical protein LOC622030 (LOC622030), mR	-1.27	0.13	1.42	0.483	-1.02	0.945	1.03	0.883	0.04
1427734_a_at	Dscaml1	Down syndrome cell adhesion molecule-like 1	1.13	0.138	-1.08	0.321	1.14	0.566	-1.16	0.484	0.01
1446011_at	C1galt1	Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransfe	-1.11	0.352	1.03	0.948	1.26	0.257	-1.17	0.502	0
1425592_at	Tnpo2	transportin 2 (importin 3, karyopherin beta 2b)	-1.27	0.357	-1.23	0.596	1.59	0.28	1.02	0.928	0.03
1440614_at	Arhgap23	Rho GTPase activating protein 23	-1.05	0.932	1.6	0.068	-1.58	0.109	1.77	0.355	0.19
1427706_a_at	Siglec1	sialic acid binding Ig-like lectin 1, sialoadhesin	-2.67	0.002	1.22	0.702	1.6	0.266	-1.93	0.258	-0.45
1456846_at	LOC382639	similar to RP58 protein	1.24	0.098	-1	0.993	-1.05	0.073	1.11	0.503	0.07
1452648_at	Tbrg1	transforming growth factor beta regulated gene 1	-1.06	0.408	1.09	0.48	1.15	0.08	-1.33	0.125	-0.03
1416548_at	Slc35b4	solute carrier family 35, member B4	-1.1	0.481	-1.02	0.463	1.3	0.032	1.06	0.737	0.06
1458172_at	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	1.3	0.086	1.4	0.559	-2.05	0.012	-1.47	0.304	-0.2
1453328_at	2700008G24Rik	RIKEN cDNA 2700008G24 gene	1.19	0.222	-1.03	0.853	1.03	0.864	-1.16	0.744	0.01
1435813_at	Mypn	myopalladin	-1.92	0.115	-1.09	0.826	1.75	0.336	1.84	0.105	0.15
1446319_at	Asb7	ankyrin repeat and SOCS box-containing protein 7	1.26	0.54	-1.11	0.734	1.03	0.911	-1.13	0.575	0.01
1451322_at	2310016A09Rik	RIKEN cDNA 2310016A09 gene	-1.16	0.247	-1.21	0.181	1.5	0.28	1.64	0.232	0.19
1447063_at	1700017B05Rik	RIKEN cDNA 1700017B05 gene	-1.08	0.385	-1.06	0.824	1.32	0.164	1.69	0.148	0.22
1445406_at	C77494	expressed sequence C77494	1.05	0.799	-1.45	0.211	1.45	0.183	-1.39	0.434	-0.09
1453039_at	Zfp335	zinc finger protein 335	1.24	0.223	-1.13	0.525	1.07	0.55	-1.11	0.449	0.02
1458965_at	---	---	-1.27	0.696	1.29	0.088	1.11	0.742	-3.17	0.221	-0.51
1433393_at	3300002I10Rik	RIKEN cDNA 3300002I10 gene	-1.02	0.977	1.12	0.858	1.09	0.829	-1.39	0.478	-0.05
1419639_at	Efnb2	ephrin B2	1.15	0.476	1.33	0.52	-1.41	0.097	-2.05	0.144	-0.24
1439343_at	---	---	-1.19	0.462	1.1	0.707	1.25	0.145	-2.11	0.108	-0.24
1444107_at	9430029N19Rik	RIKEN cDNA 9430029N19 gene	1.06	0.407	-1.03	0.904	1.16	0.201	-1.39	0.21	-0.05
1419361_at	Ss18	synovial sarcoma translocation, Chromosome 18	1.2	0.531	-1.05	0.729	1.04	0.825	-1.07	0.784	0.03
1416651_at	Znhit2	zinc finger, HIT domain containing 2	-1.01	0.96	-1.01	0.89	1.21	0.232	1.19	0.232	0.1
1425455_a_at	Churc1	churchill domain containing 1	1.2	0.403	1.01	0.827	-1.03	0.881	-1.06	0.74	0.03
1442154_at	U2af1-rs2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1, related sequence 2	1.01	0.977	1.41	0.189	-1.29	0.164	-1.3	0.087	-0.04
1430232_at	4933407E14Rik	RIKEN cDNA 4933407E14 gene	1.26	0.063	-1.53	0.038	1.27	0.355	-1.14	0.873	-0.03
1445902_at	Tanc2	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	-1.03	0.866	1.45	0.408	-1.29	0.307	1.01	0.977	0.03

1422012_at	Crhr2	corticotropin releasing hormone receptor 2	-1.34	0.492	1.52	0.124	-1.08	0.862	1.16	0.58	0.06
1426662_at	Cmas	cytidine monophospho-N-acetylneuraminic acid synthetase	-1.11	0.275	-1.05	0.417	1.34	0.312	2.21	0.259	0.35
1421530_a_at	Grm8	glutamate receptor, metabotropic 8	-1.26	0.101	1.4	0.402	-1	0.992	1.28	0.473	0.11
1418146_a_at	Rbl2 /// LOC63507	retinoblastoma-like 2 /// similar to retinoblastoma-like 2	1.18	0.467	-1.28	0.023	1.24	0.278	-1.01	0.963	0.03
1460195_at	Mrps11	mitochondrial ribosomal protein S11	-1	0.985	-1.04	0.794	1.23	0.114	1.28	0.457	0.12
1448978_at	Ngef	neuronal guanine nucleotide exchange factor	1.1	0.688	-1.06	0.885	1.15	0.396	-2.05	0.115	-0.22
1434177_at	Ece1	endothelin converting enzyme 1	1.18	0.809	-1.09	0.776	1.09	0.836	-1.32	0.436	-0.03
1458150_at	D030051N19Rik	RIKEN cDNA D030051N19 gene	1.39	0.321	1.08	0.794	-1.39	0.034	-1.52	0.152	-0.11
1455995_at	D10Bwg1379e	DNA segment, Chr 10, Brigham & Women's Genetics 1379 expressed	1.15	0.467	1.42	0.443	-1.62	0.075	-2.11	0.364	-0.29
1448254_at	Ptn	pleiotrophin	1.33	0.115	1.36	0.685	-1.99	0.025	-1.78	0.274	-0.27
AFFX-r2-Bs-thr-M_s	---	---	1.31	0.661	-1.15	0.477	1.01	0.973	-1.72	0.441	-0.14
1436559_a_at	Psmd10	proteosome (prosome, macropain) 26S subunit, non-ATPase, 10	-1	0.98	-1	0.932	1.2	0.247	1.09	0.526	0.07
1456794_at	E230016M11Rik	RIKEN cDNA E230016M11 gene	-1.05	0.843	-1.13	0.749	1.36	0.385	1.61	0.113	0.2
1455633_at	Zfp647	zinc finger protein 647	-1.21	0.296	1.35	0.217	1.02	0.907	-1.15	0.514	0
1449785_at	AA414993	expressed sequence AA414993	1.16	0.578	1.19	0.775	-1.19	0.501	-1.07	0.824	0.02
1431065_at	Eaf1	ELL associated factor 1	-1.07	0.707	-1.16	0.715	1.4	0.302	1.35	0.439	0.13
1434487_at	Mef2d	myocyte enhancer factor 2D	-1.01	0.868	1.11	0.429	1.09	0.586	-1.18	0.476	0
1456381_x_at	Mcl1	myeloid cell leukemia sequence 1	-1.04	0.863	1.21	0.172	1.02	0.872	-1.52	0.073	-0.08
1451829_a_at	Nf2	neurofibromatosis 2	-1.13	0.382	-1.04	0.9	1.35	0.313	1.88	0.445	0.27
1419048_at	Pcnx	pecanex homolog (Drosophila)	-1.01	0.905	1.14	0.41	1.07	0.525	-1.19	0.103	0
1427250_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1	0.999	-1.07	0.679	1.26	0.086	1.53	0.032	0.18
1429359_s_at	Rbpms	RNA binding protein gene with multiple splicing	-1.14	0.608	1.1	0.55	1.22	0.281	-1.3	0.425	-0.03
1453569_s_at	Mark3	MAP/microtubule affinity-regulating kinase 3	-1.08	0.786	-1.2	0.414	1.43	0.074	1.06	0.787	0.05
1454317_at	Adam1b	a disintegrin and metallopeptidase domain 1b	-1.46	0.635	1.69	0.252	-1.22	0.693	2.39	0.043	0.35
1438199_at	AI316807	expressed sequence AI316807	-1.01	0.952	1.04	0.827	1.16	0.061	-1.36	0.252	-0.04
1428450_at	2610034B18Rik	RIKEN cDNA 2610034B18 gene	1.08	0.629	1.19	0.291	-1.09	0.612	-1.73	0.158	-0.14
1456645_at	Wdr25	WD repeat domain 25	-1.27	0.541	1.4	0.198	1.01	0.952	-1.2	0.312	-0.02
1451571_s_at	9130019O22Rik ///	RIKEN cDNA 9130019O22 gene /// RIKEN cDNA E430018J23 gene /// RIKEN cD	1.06	0.685	1.14	0.262	-1	0.98	-1.78	0.16	-0.15
1443049_at	Tmem19	Transmembrane protein 19	1.12	0.456	1.21	0.067	-1.15	0.597	-1.62	0.127	-0.11
1435114_at	Wdhd1	WD repeat and HMG-box DNA binding protein 1	-1.04	0.837	-1.2	0.169	1.4	0.157	2.67	0.173	0.46
1426038_at	---	---	1.52	0.579	-2.15	0.382	1.21	0.468	-1.39	0.637	-0.2
1419789_at	Centg1	Centaurin, gamma 1	-1.59	0.164	1.79	0.212	-1.29	0.502	1.02	0.952	-0.02
1439429_x_at	Dtx2	deltex 2 homolog (Drosophila)	-1.15	0.674	1.02	0.965	1.3	0.013	-2.01	0.142	-0.21
1460594_a_at	Gmppa	GDP-mannose pyrophosphorylase A	1.11	0.67	-1	0.98	1.09	0.332	-1.12	0.453	0.02
1429059_s_at	1110004B13Rik	RIKEN cDNA 1110004B13 gene	-1.03	0.862	-1.08	0.827	1.3	0.435	3.05	0.107	0.56
1445549_at	---	---	-2.83	0.003	2.19	0.045	-1.52	0.131	1.43	0.429	-0.18
1457917_at	Lck	Lymphocyte protein tyrosine kinase	1.29	0.567	-1.65	0.309	1.31	0.411	-1.97	0.19	-0.26
1439410_x_at	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed	-1.05	0.357	-1.12	0.558	1.36	0.229	1.66	0.262	0.21
1451498_at	BC004853	cDNA sequence BC004853	1.04	0.948	-1.17	0.615	1.31	0.516	-1.16	0.45	0
1444614_x_at	6430537H07Rik	RIKEN cDNA 6430537H07 gene	-1.15	0.196	-1.29	0.36	1.55	0.055	1	0.992	0.03
1430892_at	1700011F03Rik	RIKEN cDNA 1700011F03 gene	1.12	0.717	1.52	0.476	-1.81	0.018	-1.49	0.726	-0.16
1431359_a_at	1110007C09Rik	RIKEN cDNA 1110007C09 gene	-1.11	0.732	1.02	0.926	1.28	0.409	-1.18	0.117	0
1457113_at	Nasp /// D4Ertd767	nuclear autoantigenic sperm protein (histone-binding) /// DNA segment, Chr 4, EF	-1.01	0.99	-1.45	0.549	1.51	0.54	2.37	0.167	0.36
1423284_at	Mansc1	MANSC domain containing 1	1.19	0.013	-1.29	0.402	1.23	0.14	-1.07	0.349	0.02
1458518_at	Cpeb2	cytoplasmic polyadenylation element binding protein 2	-1.16	0.382	-1.03	0.893	1.36	0.086	1.16	0.633	0.08
1437664_at	Hoxd3	homeo box D3	-1.26	0.519	1.03	0.955	1.37	0.591	-1.38	0.428	-0.06
1428602_at	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	1.2	0.682	1.06	0.822	-1.07	0.265	-1.1	0.778	0.02
1444082_at	A730017C20Rik	RIKEN cDNA A730017C20 gene	-2.06	0.27	1.08	0.855	1.63	0.259	-1.6	0.084	-0.24
1438780_at	---	---	-1.45	0.137	1.2	0.299	1.31	0.546	-1.07	0.861	0
1447398_at	---	---	-3.96	0.397	2.42	0.142	-1.91	0.057	3.02	0.135	-0.11
1429035_at	Dpep3	dipeptidase 3	1.44	0.605	1.06	0.93	-1.44	0.578	-1.56	0.489	-0.12
1438934_x_at	Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	-1.05	0.336	1.07	0.471	1.17	0.246	-1.37	0.456	-0.04
1436856_x_at	Tarsl1	threonyl-tRNA synthetase-like 1	1.02	0.872	-1.13	0.332	1.3	0.201	-1.32	0.011	-0.03

1433842_at	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	-1	0.997	1.19	0.122	1	0.979	-1.57	0.176	-0.09
1435547_at	---	17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920018H1	1.13	0.519	1.13	0.287	-1.07	0.145	-1.35	0.114	-0.04
1429892_at	Plac8l1	PLAC8-like 1	1.28	0.69	-1.01	0.971	-1.07	0.771	1.06	0.762	0.06
1416673_at	Bace2	beta-site APP-cleaving enzyme 2	-1.01	0.95	1.03	0.902	1.19	0.598	-1.22	0.361	-0.01
1444279_at	Huwe1	HECT, UBA and WWE domain containing 1	1.37	0.646	-1.7	0.495	1.24	0.595	-2.07	0.43	-0.29
1444128_at	Pip5k2b	Phosphatidylinositol-4-phosphate 5-kinase, type II, beta	1.07	0.925	-1.22	0.43	1.3	0.514	-1.63	0.239	-0.12
1438000_x_at	Zfp622	zinc finger protein 622	1.08	0.733	-1.08	0.55	1.2	0.359	-1.23	0.392	-0.01
1425428_at	Hif3a	hypoxia inducible factor 3, alpha subunit	-1.09	0.865	1.34	0.616	-1.06	0.88	1.93	0.285	0.28
1458601_at	8030447M02Rik	RIKEN cDNA 8030447M02 gene	1.37	0.137	1.25	0.298	-1.73	0.011	-1.32	0.218	-0.11
1416819_at	Cdc37	cell division cycle 37 homolog (S. cerevisiae)	1.09	0.622	-1.01	0.919	1.11	0.018	-1.03	0.736	0.04
1433693_x_at	Vamp3	vesicle-associated membrane protein 3	-1.46	0.336	1.11	0.659	1.41	0.23	-1.08	0.876	-0.01
1441417_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisia	1.66	0.024	-1.05	0.917	-1.71	0.322	1.51	0.42	0.1
1417669_at	Abhd12	abhydrolase domain containing 12	1.17	0.128	-1.05	0.743	1.08	0.195	-1.04	0.905	0.04
1415834_at	Dusp6	dual specificity phosphatase 6	1.02	0.831	-1.08	0.737	1.25	0.402	-1.36	0.457	-0.04
1419097_a_at	Stom	stomatin	-1	0.995	-1.08	0.594	1.27	0.136	3.9	0.161	0.77
1416605_at	Nola2	nucleolar protein family A, member 2	-1.03	0.369	1.02	0.912	1.21	0.365	-1.28	0.542	-0.02
1460417_at	AB041803	cDNA sequence AB041803	1.54	0.017	1.16	0.59	-1.98	0.039	-1.46	0.31	-0.19
1443506_at	Kctd2	potassium channel tetramerisation domain containing 2	-1.01	0.735	1.5	0.349	-1.4	0.157	2.27	0.174	0.34
1428924_at	Mocs3	molybdenum cofactor synthesis 3	1.17	0.39	-1.32	0.08	1.27	0.212	-1.11	0.491	0
1442554_s_at	Kalrn	kalirin, RhoGEF kinase	1.61	0.324	-1.22	0.397	-1.3	0.369	1.12	0.848	0.05
1451249_at	Trmt1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	1.06	0.732	-1.12	0.16	1.25	0.154	-1.57	0.028	-0.09
1429340_at	Hrasls5	HRAS-like suppressor family, member 5	1.54	0.494	-1.57	0.135	1.02	0.956	-1.83	0.159	-0.21
1421991_a_at	Igfbp4	insulin-like growth factor binding protein 4	1.21	0.533	-1.04	0.917	1.03	0.943	-1.14	0.791	0.01
1416109_at	Fuca1	fucosidase, alpha-L- 1, tissue	1.1	0.195	1.12	0.076	-1.03	0.814	-1.26	0.38	-0.01
1422834_at	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	-1.08	0.93	1.25	0.716	1.03	0.78	-1.08	0.622	0.03
1458451_at	Sbno1	Sno, strawberry notch homolog 1 (Drosophila)	-1.32	0.437	1.42	0.59	1.03	0.937	-1.15	0.793	-0.01
1431672_at	9430069I07Rik	RIKEN cDNA 9430069I07 gene	-1.03	0.806	-1.14	0.506	1.35	0.13	1.7	0.028	0.22
1428437_at	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	-1.07	0.772	1.26	0.056	1	0.954	-1.02	0.533	0.04
1456169_at	LOC226654	similar to KAT protein	1.13	0.247	1.22	0.688	-1.18	0.52	-1.87	0.132	-0.17
1429925_at	4933425B16Rik	RIKEN cDNA 4933425B16 gene	1.12	0.866	-1.05	0.942	1.12	0.697	-1.56	0.266	-0.09
1423018_at	Kcna3	potassium voltage-gated channel, shaker-related subfamily, member 3	-1.07	0.833	1.08	0.782	1.19	0.211	-1.57	0.061	-0.09
1455358_at	A2bp1	Ataxin 2 binding protein 1	1.23	0.093	-1.23	0.738	1.16	0.851	-3.95	0.192	-0.7
1459189_at	2610037D02Rik	RIKEN cDNA 2610037D02 gene	1.12	0.773	1.23	0.624	-1.18	0.446	-2	0.06	-0.21
1450476_at	Cnr2	cannabinoid receptor 2 (macrophage)	-2.03	0.297	1.38	0.04	1.32	0.444	-2.59	0.14	-0.48
1445382_at	---	Transcribed locus	-1.46	0.366	1.56	0.074	-1.05	0.689	1.21	0.645	0.07
1424148_a_at	AW049765	expressed sequence AW049765	1.18	0.413	1.2	0.362	-1.22	0.074	-1.72	0.207	-0.14
1434424_at	9630055N22Rik ///	RIKEN cDNA 9630055N22 gene /// similar to Feline leukemia virus subgroup C re	1.13	0.616	1.16	0.616	-1.1	0.63	-1.33	0.016	-0.03
1420945_at	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	-1.04	0.724	-1.45	0.261	1.55	0.524	1.01	0.989	0.02
1440594_at	Ppp1cc	Protein phosphatase 1, catalytic subunit, gamma isoform	1.6	0.451	-1.01	0.989	-1.64	0.165	1.18	0.605	0.03
1431314_a_at	5830417I10Rik	RIKEN cDNA 5830417I10 gene	-1.04	0.53	1.04	0.75	1.2	0.266	-1.33	0.093	-0.03
1452559_at	---	---	1.04	0.904	-1.1	0.703	1.26	0.204	-1.01	0.966	0.05
1418222_at	2610024G14Rik	RIKEN cDNA 2610024G14 gene	-1.16	0.406	-1.17	0.045	1.48	0.042	1.12	0.669	0.07
1449495_at	Reg3a	regenerating islet-derived 3 alpha	1.06	0.779	-1.35	0.616	1.4	0.363	-1	0.981	0.03
1425057_at	0610038K03Rik	RIKEN cDNA 0610038K03 gene	-1.09	0.56	-1.08	0.583	1.35	0.353	1.07	0.875	0.07
1447514_at	D030041N04Rik	RIKEN cDNA D030041N04 gene	1.63	0.238	-1.17	0.733	-1.4	0.335	1.15	0.775	0.06
1443433_at	Plxnc1	plexin C1	-1.27	0.106	1.45	0.47	-1.03	0.816	1.13	0.724	0.07
1428198_at	Adal	adenosine deaminase-like	-1.19	0.205	1.04	0.783	1.32	0.101	-1.04	0.718	0.03
1432996_at	---	---	-1.58	0.421	-1.63	0.439	1.96	0.252	1.19	0.642	-0.02
1418971_x_at	Bcl10	B-cell leukemia/lymphoma 10	-1.15	0.399	1.08	0.525	1.25	0.191	-1.24	0.211	-0.02
1455555_at	AV071699	Expressed sequence AV071699	1.27	0.292	1.12	0.328	-1.22	0.676	-3.42	0.003	-0.56
1424598_at	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	1.3	0.496	-1.05	0.868	-1.06	0.919	1.76	0.041	0.24
1431327_at	Vps13a	vacuolar protein sorting 13A (yeast)	1.26	0.66	-1.95	0.423	1.43	0.439	-1.11	0.705	-0.09
1429449_at	Samd4	sterile alpha motif domain containing 4	-1.16	0.574	-1.11	0.711	1.44	0.076	1.11	0.739	0.07

1439603_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.75	0.353	1.19	0.651	1.44	0.374	-1.02	0.962	-0.04
1458545_at	Tmem57	Transmembrane protein 57	2.02	0.517	-1.26	0.51	-2.56	0.051	1.39	0.111	-0.1
1459317_at	Ank2	ankyrin 2, brain	1.26	0.717	-1.02	0.946	-1.04	0.935	1.14	0.614	0.09
1419295_at	Creb3l1	cAMP responsive element binding protein 3-like 1	1.19	0.392	-1.26	0.641	1.22	0.212	-1.04	0.87	0.03
1431857_at	Phf19	PHD finger protein 19	-1.72	0.457	-1.27	0.433	1.83	0.165	1.22	0.614	0.02
1439714_at	---	---	1.05	0.48	-1.1	0.821	1.25	0.464	-1.21	0.671	0
1420503_at	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14	-1.12	0.532	1.1	0.886	1.21	0.476	-1.1	0.816	0.02
1428851_at	1300014I06Rik	RIKEN cDNA 1300014I06 gene	1.09	0.183	1.13	0.174	-1.01	0.935	-3.6	0.032	-0.6
1437146_x_at	Coro7	coronin 7	1.03	0.842	-1.11	0.674	1.27	0.083	-1.77	0.048	-0.15
1444171_at	Pdcd4	Programmed cell death 4	1.3	0.267	1.12	0.346	-1.27	0.429	-1.88	0.048	-0.18
1426128_a_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	1.05	0.661	-1.19	0.429	1.31	0.505	-1.38	0.035	-0.05
1433734_at	Slc13a4	solute carrier family 13 (sodium/sulfate symporters), member 4	1.14	0.285	-2.37	0.417	1.64	0.023	-1.26	0.732	-0.21
1427982_s_at	Syne2	synaptic nuclear envelope 2	1.27	0.075	-1.24	0.143	1.12	0.575	-1.32	0.438	-0.04
1433412_at	5730446C15Rik	RIKEN cDNA 5730446C15 gene	1.05	0.849	1.23	0.343	-1.09	0.766	-1.38	0.246	-0.05
1453474_at	1300007F04Rik	RIKEN cDNA 1300007F04 gene	1.14	0.427	1.1	0.581	-1.04	0.909	-1.29	0.197	-0.02
1454179_at	4933406K04Rik	RIKEN cDNA 4933406K04 gene	-1.53	0.548	1.84	0.036	-1.42	0.401	1.32	0.495	0.05
1458285_at	Gria1	Glutamate receptor, ionotropic, AMPA1 (alpha 1)	1.49	0.256	1.04	0.931	-1.48	0.167	-1.4	0.285	-0.09
1417059_at	Krtcap2	keratinocyte associated protein 2	1.14	0.585	1.1	0.228	-1.04	0.799	-1.06	0.822	0.04
1451830_a_at	Spnb2	spectrin beta 2	1.19	0.118	1.2	0.667	-1.23	0.075	-1.72	0.196	-0.14
1421392_a_at	Birc3	baculoviral IAP repeat-containing 3	1.17	0.484	1.1	0.414	-1.07	0.714	-2.05	0.151	-0.21
1449418_s_at	Fbxo36	F-box only protein 36	1.04	0.744	-1.05	0.767	1.21	0.53	-1.11	0.258	0.02
1452068_at	Asahl	N-acylsphingosine amidohydrolase (acid ceramidase)-like	1.68	0.052	-1.37	0.196	-1.26	0.095	1.02	0.959	0.02
1459805_x_at	Dus3l	dihydrouridine synthase 3-like (S. cerevisiae)	-1.09	0.34	1.03	0.707	1.26	0.237	-1.32	0.135	-0.03
1431091_at	Pygo1	pygopus 1	-1.37	0.662	-1.07	0.816	1.54	0.133	1.19	0.667	0.07
1424363_at	Mycbpap	Mycbp associated protein	1.1	0.809	-1.58	0.224	1.47	0.269	-1.22	0.774	-0.06
1459931_a_at	LOC626877	Similar to zinc finger protein 709	1.18	0.171	1.25	0.33	-1.29	0.396	-1.04	0.881	0.02
1429973_at	4921509B22Rik	RIKEN cDNA 4921509B22 gene	-1.51	0.577	1.49	0.163	1.05	0.921	-1.25	0.781	-0.05
1455229_x_at	Pgs1	phosphatidylglycerophosphate synthase 1	1.27	0.062	-1.14	0.655	1.06	0.654	-1.29	0.187	-0.03
1436970_a_at	Pdgfrb	platelet derived growth factor receptor, beta polypeptide	1.15	0.604	1.49	0.058	-1.77	0.097	-1.24	0.327	-0.09
1455667_at	Preb	prolactin regulatory element binding	-1.3	0.185	1.11	0.672	1.32	0.212	-1.1	0.642	0.01
1421474_a_at	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	-1.32	0.249	1.13	0.426	1.32	0.419	-1.05	0.86	0.02
1450739_at	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	1.34	0.068	-1.47	0.118	1.18	0.464	-1.1	0.33	-0.01
1430565_at	1700030J22Rik	RIKEN cDNA 1700030J22 gene	1	0.972	1.33	0.363	-1.14	0.136	-1.18	0.445	0
1423078_a_at	Sc4mol	sterol-C4-methyl oxidase-like	1	0.995	1.41	0.164	-1.25	0.293	-1.47	0.398	-0.08
1426277_at	C730025P13Rik	RIKEN cDNA C730025P13 gene	-1.01	0.932	-1.11	0.405	1.32	0.008	1.04	0.695	0.06
1428243_at	1700021K19Rik	RIKEN cDNA 1700021K19 gene	1.03	0.877	-1.04	0.792	1.21	0.218	-1.89	0.112	-0.17
1441367_a_at	---	Transcribed locus	-1.23	0.442	1.2	0.463	1.19	0.464	-1.04	0.833	0.03
1453366_at	Tdrkh	tudor and KH domain containing protein	1.18	0.543	-1.18	0.56	1.18	0.256	-2.13	0.38	-0.24
1440222_at	---	---	1.73	0.03	-1.17	0.576	-1.61	0.071	1.11	0.625	0.01
1439011_at	---	Transcribed locus	1.14	0.541	-1.02	0.966	1.08	0.731	-1.24	0.44	-0.01
1433923_at	Krt77	keratin 77	-1.34	0.649	1.63	0.272	-1.2	0.674	1.02	0.962	0.03
1428864_at	5530400B01Rik	RIKEN cDNA 5530400B01 gene	1.41	0.326	-1.12	0.752	-1.11	0.805	6.2	0.215	1.35
1455944_at	Zfp516	zinc finger protein 516	1.1	0.759	1.12	0.788	-1.01	0.964	-1.09	0.352	0.03
1431801_at	Dscam	Down syndrome cell adhesion molecule	-1.27	0.289	1.49	0.37	-1.08	0.737	1.81	0.245	0.24
1436999_at	5033414K04Rik	RIKEN cDNA 5033414K04 gene	1.41	0.233	1.09	0.644	-1.4	0.259	-1.1	0.814	0
1444323_at	Ccnd3	cyclin D3	1.56	0.566	-1.35	0.423	-1.11	0.705	1.25	0.599	0.09
1460454_at	2010001H14Rik	RIKEN cDNA 2010001H14 gene	-1.33	0.295	1.44	0.507	1.01	0.981	-1.04	0.902	0.02
1426046_a_at	Rabggta	Rab geranylgeranyl transferase, a subunit	1.08	0.078	-1.16	0.376	1.26	0.191	-1.5	0.063	-0.08
1454749_at	Pcnt	pericentrin (kendrin)	-1.27	0.298	-1.05	0.935	1.47	0.388	1.32	0.65	0.12
1423157_at	Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	1.08	0.353	1.26	0.081	-1.16	0.257	-1.33	0.061	-0.04
1444312_at	Slc22a15	solute carrier family 22 (organic anion/cation transporter), member 15	-1.34	0.57	1.55	0.275	-1.1	0.681	1.15	0.313	0.06
1448937_at	Slc35b3	solute carrier family 35, member B3	1.05	0.838	1.26	0.233	-1.12	0.102	-1.7	0.06	-0.13
1454494_at	5830448L01Rik	RIKEN cDNA 5830448L01 gene	1.39	0.579	-1.34	0.36	1.07	0.876	-1.58	0.233	-0.11

1421462_a_at	Lepre1	leprecan 1	-1.04	0.781	1.09	0.8	1.15	0.368	-1	0.992	0.05
1428773_s_at	Bcor	Bcl6 interacting corepressor	-1.34	0.172	1.06	0.716	1.4	0.242	-1.48	0.086	-0.09
1421597_a_at	Msx3	homeo box, msh-like 3	1.25	0.148	-1.23	0.26	1.14	0.661	-1.64	0.495	-0.12
1435252_at	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	-1.09	0.777	1.05	0.88	1.23	0.544	-1.28	0.197	-0.02
1449243_a_at	Rps19	ribosomal protein S19	1.11	0.006	1.17	0	-1.09	0.631	-1.45	0.013	-0.06
AFFX-BioB-M_at	---	---	1.44	0.062	1.09	0.473	-1.48	0.125	-1.12	0.681	-0.02
1458308_at	Stno	strawberry notch homolog (Drosophila)	-1.1	0.502	1.18	0.498	1.12	0.455	-1.19	0.332	0
1435309_at	BC019943	cDNA sequence BC019943	-1.07	0.92	1.02	0.927	1.25	0.408	-1.27	0.452	-0.02
1433189_at	4933433N18Rik	RIKEN cDNA 4933433N18 gene	-1.59	0.483	1.5	0.278	1.07	0.75	-1.44	0.219	-0.11
1428928_at	Cacnb4	calcium channel, voltage-dependent, beta 4 subunit	1.05	0.842	-1.14	0.786	1.28	0.515	-1.09	0.845	0.02
1433826_at	Tspyl3	TSPY-like 3	1.22	0.134	1.01	0.965	-1.02	0.873	-1.4	0.309	-0.05
1428903_at	3110037I16Rik	RIKEN cDNA 3110037I16 gene	1.11	0.458	1.22	0.274	-1.14	0.415	-1.46	0.172	-0.07
1421247_at	Pax9	paired box gene 9	1.1	0.464	1.19	0.741	-1.1	0.765	-3.78	0.124	-0.64
1447933_at	Kif26a /// LOC6683	kinesin family member 26A /// similar to CG14535-PA /// similar to CG14535-PA	1.07	0.469	-1.31	0.406	1.37	0.514	-1.4	0.356	-0.07
1451191_at	Crabp2	cellular retinoic acid binding protein II	-2.08	0.391	1.53	0.354	1.2	0.36	-2.14	0.145	-0.37
1436244_a_at	Tle2	transducin-like enhancer of split 2, homolog of Drosophila E(spl)	1.56	0.001	-1.1	0.662	-1.34	0.208	1.09	0.805	0.05
1454019_at	---	---	1.12	0.882	-1.08	0.872	1.17	0.751	-1.38	0.62	-0.05
1449426_a_at	Anxa10	annexin A10	-1.93	0.534	1.62	0.236	1.07	0.86	-1.06	0.945	-0.08
1440214_at	A630001G21Rik	RIKEN cDNA A630001G21 gene	-1.15	0.81	1.27	0.522	1.07	0.85	-1.98	0.068	-0.2
1417073_a_at	Qk	quaking	1.02	0.902	1.48	0.007	-1.42	0.017	-1.01	0.953	0.02
1442685_at	---	---	1.15	0.746	-1.41	0.646	1.35	0.226	-1.22	0.557	-0.03
1420906_at	Cd2ap	CD2-associated protein	-1.05	0.935	1.08	0.872	1.17	0.612	-1.41	0.357	-0.05
1460732_a_at	Ppl	periplakin	-1.13	0.269	1.17	0.323	1.15	0.41	-1.18	0.709	0
1420706_at	P140	P140 gene	1.18	0.754	1.65	0.323	-2.6	0	-2.43	0.168	-0.55
1423128_at	Aip	aryl-hydrocarbon receptor-interacting protein	1.19	0.175	-1.08	0.363	1.09	0.059	-1.01	0.964	0.05
1437694_at	BB114266	Expressed sequence BB114266	1.03	0.925	1.35	0.053	-1.2	0.525	-1.52	0.393	-0.09
1425854_x_at	Tcrb-V13 /// LOC66	T-cell receptor beta, variable 13 /// similar to T-cell receptor beta-2 chain C region	1.23	0.789	1.01	0.985	-1.03	0.8	-3.05	0.034	-0.46
1428992_at	Unc13d	unc-13 homolog D (C. elegans)	-1.12	0.373	1.11	0.7	1.21	0.08	-1.08	0.411	0.03
1459014_at	2900019G14Rik	RIKEN cDNA 2900019G14 gene	1.09	0.909	1.14	0.776	-1.03	0.949	-1.16	0.845	0.01
1418580_at	Rtp4	receptor transporter protein 4	1.11	0.461	1.17	0.239	-1.07	0.608	-1.72	0.122	-0.13
1415847_at	Ldhc	lactate dehydrogenase C	1.34	0.547	-1.27	0.353	1.09	0.805	-1.09	0.891	0.02
1435837_at	Cryab	crystallin, alpha B	1	0.986	1.29	0.455	-1.09	0.66	-2.02	0.015	-0.21
1454033_at	1700007B13Rik	RIKEN cDNA 1700007B13 gene	-1.14	0.761	-2.37	0.031	1.91	0.218	1.2	0.775	-0.1
1436250_at	5430405G05Rik	RIKEN cDNA 5430405G05 gene	1.23	0.739	1.15	0.74	-1.21	0.461	-1.22	0.504	-0.01
1453984_at	Pik3r2 /// Ifi30	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta) /// inter	-1.2	0.628	1.02	0.968	1.35	0.447	-1.42	0.435	-0.06
1432281_a_at	Itgb6	integrin beta 6	1.08	0.901	-1.24	0.602	1.32	0.375	-1.2	0.649	-0.01
1452650_at	Trim62	tripartite motif-containing 62	1.25	0.46	-1.35	0.392	1.21	0.248	-2.02	0.162	-0.22
1434043_a_at	---	---	-1.04	0.568	1.09	0.569	1.16	0.414	-1.13	0.664	0.02
1447708_x_at	Pde2a	phosphodiesterase 2A, cGMP-stimulated	-1.31	0.048	1.23	0.516	1.22	0.523	-1.35	0.588	-0.05
1446363_at	---	---	1.16	0.756	1.31	0.6	-1.35	0.161	-2.12	0.351	-0.25
1451841_a_at	Ncor2	nuclear receptor co-repressor 2	1.19	0.17	-1.01	0.979	1.03	0.846	-1.38	0.03	-0.04
1457401_at	Dnahc9	dynein, axonemal, heavy chain 9	1.01	0.967	-1.32	0.58	1.44	0.202	-1.78	0.339	-0.16
1416046_a_at	Fuca2	fucosidase, alpha-L- 2, plasma	-1.05	0.412	1.4	0.042	-1.16	0.219	1.21	0.335	0.1
1437159_at	---	---	1.16	0.333	-1.29	0.227	1.27	0.356	-1.51	0.173	-0.09
1426218_at	Glcci1	glucocorticoid induced transcript 1	-1.37	0.025	1.14	0.641	1.34	0.24	-1.41	0.203	-0.08
1447378_at	---	PREDICTED: Mus musculus hypothetical protein LOC628013 (LOC628013), mR	-1.12	0.797	1.26	0.213	1.05	0.763	-1.8	0.038	-0.15
1419259_at	Rsu1	Ras suppressor protein 1	-1.01	0.926	1.18	0.016	1.03	0.701	-1.04	0.71	0.04
1423878_at	Gypc	glycophorin C	1.31	0.353	-1.07	0.726	-1.04	0.744	3.84	0.192	0.76
1449747_at	Bcdin3	Bin3, bicoid-interacting 3, homolog (Drosophila)	1.34	0.084	-1.07	0.69	-1.07	0.822	1.72	0.387	0.23
1455059_at	9430093I07Rik	RIKEN cDNA 9430093I07 gene	-1.02	0.876	1.16	0.531	1.06	0.739	-1.37	0.4	-0.04
1449169_at	Has2	hyaluronan synthase 2	1.18	0.706	1.56	0.275	-2.13	0.073	-1.2	0.68	-0.15
1424374_at	Gimap4	GTPase, IMAP family member 4	-1.09	0.573	1.13	0.52	1.17	0.596	-1.38	0.445	-0.04
1421448_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.02	0.908	-1.01	0.98	1.24	0.621	1.02	0.95	0.06

1418906_at	Nubp1	nucleotide binding protein 1	1.09	0.034	-1.03	0.788	1.15	0.318	-1.09	0.584	0.03
1432188_s_at	Nup43	nucleoporin 43	-1.32	0.034	-1.02	0.904	1.48	0.199	1.17	0.444	0.08
1435296_at	Adra2c	adrenergic receptor, alpha 2c	1.04	0.768	-1.31	0.454	1.41	0.185	-1.01	0.978	0.03
1436031_at	Cachd1	cache domain containing 1	-1.18	0.185	-1	0.993	1.37	0.16	3.63	0.206	0.7
1456007_at	Arf3	ADP-ribosylation factor 3	1.2	0.845	1.04	0.939	-1.03	0.951	-1.29	0.574	-0.02
1454752_at	LOC380843 /// LOC	similar to RNA binding motif protein 24 /// similar to RNA binding motif protein 24	-1.83	0.289	1.42	0.466	1.25	0.07	-1.09	0.565	-0.06
1420660_at	Lrrc6	leucine rich repeat containing 6 (testis)	1.5	0.505	-2.52	0.409	1.32	0.39	-1.35	0.37	-0.26
1430258_at	2810422J05Rik	RIKEN cDNA 2810422J05 gene	1.14	0.438	-1.79	0.117	1.51	0.257	-1.15	0.25	-0.07
1438765_at	Dhx33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	-1.39	0.336	1.11	0.66	1.38	0.305	-1.05	0.823	0.01
1447685_x_at	Ets2	E26 avian leukemia oncogene 2, 3' domain	1.31	0.417	-1.18	0.776	1.05	0.66	-4.4	0.003	-0.8
1454241_at	Rwdd1	RWD domain containing 1	1.31	0.263	-1.6	0.608	1.27	0.484	-1.25	0.675	-0.07
1455956_x_at	Ccnd2	cyclin D2	1.19	0.444	-1.02	0.895	1.05	0.846	-1.48	0.228	-0.07
1447404_at	Gm96	Gene model 96, (NCBI)	1.42	0.628	1.25	0.702	-1.87	0.12	-2.29	0.019	-0.37
1452663_at	Svop	SV2 related protein	-1.88	0.191	1.08	0.68	1.6	0.292	-2.38	0.371	-0.4
1447966_a_at	Tmem69	transmembrane protein 69	1.37	0.371	-1	0.993	-1.19	0.594	1.02	0.967	0.05
1415827_a_at	D3Ucla1	DNA segment, Chr 3, University of California at Los Angeles 1	-1.02	0.853	1	0.993	1.23	0.226	-1.27	0.203	-0.02
1446595_at	Itsn2	intersectin 2	1.13	0.545	1.38	0.106	-1.43	0.017	-1.52	0.319	-0.11
1418581_a_at	Limk2	LIM motif-containing protein kinase 2	-1.1	0.761	1.24	0.193	1.07	0.642	-1.06	0.339	0.03
1426708_at	Antxr2	anthrax toxin receptor 2	1.18	0.196	1.19	0.196	-1.19	0.304	-1.08	0.835	0.03
1443159_at	9130221J17Rik	RIKEN cDNA 9130221J17 gene	1.29	0.24	-1.01	0.949	-1.07	0.366	1.2	0.622	0.1
1443361_at	Tspan9	Tetraspanin 9	-1.42	0.461	1.79	0.432	-1.39	0.119	1.09	0.743	0.02
1452882_at	Pgrmc2	progesterone receptor membrane component 2	-1.01	0.177	-1.03	0.837	1.26	0.078	1.09	0.629	0.08
1453840_at	Pabpc1	poly A binding protein, cytoplasmic 1	1.69	0.305	-1.02	0.959	-1.84	0.096	2.38	0.163	0.3
1433977_at	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1.05	0.749	-1.03	0.834	1.19	0.434	-1.77	0.123	-0.14
1449053_s_at	Cog1	component of oligomeric golgi complex 1	-1.11	0.458	1.01	0.963	1.3	0.119	-1.02	0.855	0.05
1452532_x_at	Ceacam1	CEA-related cell adhesion molecule 1	1.09	0.766	-1.38	0.278	1.4	0.495	-1.34	0.448	-0.06
1420207_at	---	---	-1.03	0.96	1.84	0.327	-2.47	0.24	1.17	0.197	-0.12
1422436_at	2210010C04Rik	RIKEN cDNA 2210010C04 gene	-1.58	0.294	1.12	0.697	1.46	0.334	-1.2	0.632	-0.05
1431473_at	5330423I11Rik	RIKEN cDNA 5330423I11 gene	-1.44	0.406	1.53	0.448	-1.01	0.984	1.69	0.436	0.19
1452872_at	2900054D09Rik	RIKEN cDNA 2900054D09 gene	-1.08	0.077	1.54	0.074	-1.34	0.063	1.29	0.317	0.1
1436781_at	Man2b1	mannosidase 2, alpha B1	-1.22	0.302	1.02	0.931	1.37	0.234	-1.98	0.001	-0.2
1446480_at	D8Ertd82e	DNA segment, Chr 8, ERATO Doi 82, expressed	1.32	0.228	-1.23	0.73	1.08	0.891	-1.23	0.69	-0.02
1454154_at	4933416I08Rik	RIKEN cDNA 4933416I08 gene	-2.32	0.352	1.94	0.154	-1.18	0.652	1.11	0.855	-0.11
1457942_at	---	Transcribed locus	-1.22	0.236	1.23	0.103	1.17	0.569	-1.06	0.719	0.03
1431798_a_at	Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	1	0.975	1.27	0.303	-1.06	0.695	-1.07	0.597	0.03
1452802_at	4933411K16Rik	RIKEN cDNA 4933411K16 gene	-3.11	0.125	1.35	0.696	1.54	0.484	-2.09	0.373	-0.58
1428403_at	2410025L10Rik	RIKEN cDNA 2410025L10 gene	-1.4	0.01	1.26	0.407	1.23	0.295	-1.55	0.001	-0.11
1420897_at	Snap23	synaptosomal-associated protein 23	-1.18	0.114	-1.13	0.165	1.48	0.224	1.01	0.869	0.05
1438078_at	---	Transcribed locus	1.04	0.674	1.35	0.361	-1.21	0.324	-1.17	0.673	0
1457362_at	Agrp	Agouti related protein	1.2	0.802	1.33	0.573	-1.46	0.13	-1.2	0.706	-0.03
1452690_at	Khsrp	KH-type splicing regulatory protein	-1.16	0.632	-1.1	0.718	1.44	0.442	1.8	0.212	0.25
1445824_at	Zfp458	zinc finger protein 458	1.36	0.434	1.02	0.951	-1.2	0.158	-1.39	0.04	-0.05
1459608_at	Trim24	Tripartite motif protein 24	-1.14	0.43	1.29	0.358	1.04	0.828	-1.26	0.181	-0.01
1425943_at	Nmur2	neuromedin U receptor 2	-2.86	0.093	1.5	0.295	1.36	0.173	-1.37	0.074	-0.34
1459526_at	Tnrc6a	Trinucleotide repeat containing 6a	1.8	0.335	-1.03	0.853	-2.24	0.055	1.08	0.815	-0.1
1430149_at	Ndufa3	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3	-1.13	0.807	-1.4	0.374	1.61	0.039	1.09	0.782	0.04
1424376_at	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	1.17	0.478	1.08	0.757	-1.03	0.873	-1.05	0.877	0.04
1450454_at	Tor3a	torsin family 3, member A	1	0.998	-1.46	0.002	1.53	0.246	-1.16	0.573	-0.02
1432939_at	5730405N03Rik	RIKEN cDNA 5730405N03 gene	1.1	0.89	-1.14	0.816	1.23	0.466	-1.88	0.186	-0.17
1457860_at	---	---	1.44	0.073	1.22	0.717	-1.8	0.369	-1.53	0.481	-0.17
1434360_s_at	Ptprg /// LOC63266	protein tyrosine phosphatase, receptor type, G /// similar to protein tyrosine phosp	1.12	0.58	-1.18	0.244	1.24	0.203	-1.33	0.023	-0.04
1431032_at	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	-1.22	0.038	-1.1	0.364	1.48	0.114	1.19	0.127	0.09
1433500_at	Dennd2a	DENN/MADD domain containing 2A	1.1	0.717	1.25	0.507	-1.16	0.406	-1.07	0.762	0.03

1439433_a_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	-1.15	0.585	1.34	0.047	1.01	0.969	-1.06	0.603	0.03
1441492_at	Zfp64	Zinc finger protein 64	-1.21	0.221	1.16	0.704	1.23	0.361	-1.09	0.65	0.02
1417364_at	Eef1g	eukaryotic translation elongation factor 1 gamma	-1.03	0.745	1.06	0.409	1.18	0.125	-1.32	0.102	-0.03
1453752_at	Rpl17	ribosomal protein L17	1.11	0.406	1.14	0.232	-1.04	0.875	-1.43	0.212	-0.05
1454679_at	D8Ertd457e	DNA segment, Chr 8, ERATO Doi 457, expressed	1.09	0.565	-1.01	0.959	1.13	0.367	-1.19	0.428	0.01
1441807_s_at	---	---	-1.07	0.902	-1.21	0.54	1.45	0.226	1.4	0.093	0.14
1445667_at	---	---	1.14	0.587	-1.04	0.944	1.11	0.57	-1.51	0.06	-0.07
1443859_at	Rsbn1	rosbin, round spermatid basic protein 1	1.06	0.767	-1.34	0.48	1.41	0.179	-1.33	0.113	-0.05
1448729_a_at	4-Sep	septin 4	1.36	0.042	1.14	0.164	-1.39	0.122	-1.22	0.307	-0.03
1432017_at	Hip1	huntingtin interacting protein 1	-1.89	0.245	1.8	0.263	-1.12	0.813	1.01	0.982	-0.05
1432301_a_at	1700074P13Rik	RIKEN cDNA 1700074P13 gene	-1.68	0.215	1.14	0.786	1.48	0.388	-3.04	0.053	-0.53
1433867_at	1810030O07Rik	RIKEN cDNA 1810030O07 gene	1.11	0.3	1.16	0.198	-1.06	0.437	-1.13	0.572	0.02
1439444_x_at	Tmed10 /// LOC634	transmembrane emp24-like trafficking protein 10 (yeast) /// similar to transmembr	-1.01	0.929	1.26	0.167	-1.03	0.704	1.18	0.341	0.1
1447172_at	---	---	1.41	0.187	-1.41	0.364	1.1	0.729	-1.36	0.515	-0.07
1421292_a_at	A730008L03Rik	RIKEN cDNA A730008L03 gene	1.04	0.792	-1.08	0.274	1.26	0.027	-1.2	0.131	0
1429099_at	1110051B16Rik	RIKEN cDNA 1110051B16 gene	1.29	0.009	1.33	0.354	-1.67	0.145	-1.13	0.743	-0.05
1438990_x_at	Iqcf3	IQ motif containing F3	1.69	0.557	1.01	0.993	-1.91	0.235	-1	0.998	-0.05
1449417_at	Ambn	ameloblastin	1.55	0.122	-1.64	0.251	1.06	0.821	-1.25	0.499	-0.07
1427880_at	Uqcrq	ubiquinol-cytochrome c reductase, complex III subunit VII	-1.12	0.853	1.59	0.13	-1.36	0.271	1.1	0.505	0.05
1416455_a_at	Cryab	crystallin, alpha B	1.22	0.582	-1.18	0.592	1.15	0.501	-1.18	0.672	0
1416110_at	Slc35a4	solute carrier family 35, member A4	-1.03	0.894	-1.04	0.758	1.28	0.098	1.43	0.206	0.16
1459896_at	Pogk	pogo transposable element with KRAB domain	-1.34	0.097	1.39	0.52	1.08	0.623	-1.05	0.844	0.02
1432954_at	4921520E09Rik	RIKEN cDNA 4921520E09 gene	-2.1	0.49	1.87	0.38	-1.14	0.8	2.24	0.27	0.22
1458650_at	---	---	-1.59	0.422	1	0.988	1.59	0.004	-1.38	0.363	-0.09
1428625_a_at	Rmi1	RMI1, RecQ mediated genome instability 1, homolog (S. cerevisiae)	1.2	0.535	1.16	0.499	-1.16	0.025	-1.19	0.38	0
1439494_at	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), member 9	1.22	0.062	1.33	0.452	-1.5	0.175	-1.39	0.684	-0.09
1440874_at	Slco5a1	solute carrier organic anion transporter family, member 5A1	1.16	0.818	-1.34	0.695	1.32	0.589	-1.59	0.087	-0.12
1420762_a_at	Ybx2	Y box protein 2	-1.12	0.487	1.26	0.219	1.06	0.92	-1.18	0.543	0.01
1430192_at	Casp3	caspase 3	-2.91	0.151	1.32	0.659	1.55	0.522	-1.14	0.856	-0.29
1458808_at	Sned1	Sushi, nidogen and EGF-like domains 1	2.24	0.016	-3.31	0.126	-1.48	0.202	1.21	0.713	-0.33
1419833_s_at	Centd3	centaurin, delta 3	1.09	0.309	1.19	0.126	-1.06	0.713	-1.11	0.681	0.03
1444254_at	Tns4	tensin 4	1.41	0.28	-1.06	0.9	-1.16	0.121	1.38	0.579	0.14
1423229_at	Inpp5e	inositol polyphosphate-5-phosphatase E	1.04	0.636	-1.09	0.475	1.26	0.274	-1.26	0.085	-0.01
1427624_s_at	Il22 /// Iltifb	interleukin 22 /// interleukin 10-related T cell-derived inducible factor beta	-2.41	0.366	1.63	0.334	1.17	0.73	-1.24	0.618	-0.21
1445738_at	---	---	1.23	0.664	-1.16	0.754	1.13	0.717	-1.97	0.052	-0.19
1418079_at	Psme3	proteaseome (prosome, macropain) 28 subunit, 3	-1.01	0.932	-1.26	0.108	1.44	0.105	2.11	0.292	0.32
1430545_at	Dbf4	DBF4 homolog (S. cerevisiae)	1.2	0.753	-1.39	0.69	1.31	0.483	-1.71	0.215	-0.15
1419908_at	Fcrla	Fc receptor-like A	1.15	0.877	-1.43	0.511	1.37	0.416	-1.59	0.157	-0.13
1454671_at	Insig1	insulin induced gene 1	1.05	0.706	1.27	0.166	-1.11	0.646	-1.07	0.72	0.03
1447059_at	---	---	1.29	0.76	1.14	0.81	-1.27	0.697	-1.34	0.491	-0.04
1434210_s_at	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	1.11	0.227	1.27	0.25	-1.18	0.102	-1.18	0.456	0
1425454_a_at	Il12a	interleukin 12a	-1.33	0.504	1.05	0.82	1.42	0.357	-1.18	0.023	-0.01
1451445_at	Umps	uridine monophosphate synthetase	-1.12	0.739	-1.15	0.595	1.46	0.305	1.34	0.456	0.13
1426078_a_at	Gpr108	G protein-coupled receptor 108	1.12	0.735	-1.03	0.844	1.14	0.63	-1.24	0.031	-0.01
1458944_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930542D16 pr	-1.45	0.511	2.04	0.068	-2.03	0.338	1.39	0.683	-0.01
1433633_at	Irf2bp2 /// LOC6729	interferon regulatory factor 2 binding protein 2 /// similar to interferon regulatory fa	1.02	0.741	-1.11	0.678	1.3	0.435	-1.17	0.477	0.01
1417970_at	Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	-1.05	0.711	1.31	0.009	-1.04	0.733	1.27	0.385	0.12
1437311_at	A930034L06Rik	RIKEN cDNA A930034L06 gene	1.08	0.768	1.3	0.496	-1.18	0.225	-1.13	0.749	0.02
1447643_x_at	Snai2	snail homolog 2 (Drosophila)	1.04	0.904	1.42	0.124	-1.32	0.442	-1.7	0.285	-0.14
1417540_at	Elf1	E74-like factor 1	1	0.973	1.26	0.067	-1.05	0.712	-1.48	0.065	-0.07
1457250_x_at	Nr1d2	Nuclear receptor subfamily 1, group D, member 2	-1.18	0.81	1.06	0.622	1.32	0.326	-1.11	0.851	0.02
1416622_at	Wbscr16	Williams-Beuren syndrome chromosome region 16 homolog (human)	1.1	0.652	-1.09	0.664	1.2	0.161	-1.02	0.925	0.05
1444729_at	E130317F20Rik	RIKEN cDNA E130317F20 gene	-1.35	0.56	1.35	0.206	1.12	0.7	-1.08	0.824	0.01

1416442_at	Ier2	immediate early response 2	1.01	0.945	-1.02	0.889	1.23	0.434	-1.76	0.083	-0.13
1429582_at	Btbd14a	BTB (POZ) domain containing 14A	-1.06	0.668	-1.07	0.279	1.34	0.187	1.31	0.331	0.13
1426906_at	Ifi203	interferon activated gene 203	-1.03	0.874	1.12	0.383	1.13	0.708	-2.33	0.098	-0.28
1451516_at	Rhebl1	Ras homolog enriched in brain like 1	1.06	0.373	1.19	0.319	-1.03	0.935	-1.17	0.438	0.01
1445916_at	Atp6v1a	ATPase, H+ transporting, lysosomal V1 subunit A	1.08	0.443	1.42	0.554	-1.39	0.147	-1.21	0.013	-0.02
1426635_at	Acbd3	acyl-Coenzyme A binding domain containing 3	-1.07	0.794	1	0.978	1.28	0.368	-1.09	0.806	0.03
1445595_at	---	Transcribed locus	1.7	0.477	-2.94	0.013	1.18	0.712	-2.52	0.195	-0.65
1431711_a_at	9030409G11Rik	RIKEN cDNA 9030409G11 gene	1.19	0.485	-1.03	0.967	1.06	0.86	-1.43	0.284	-0.05
1434132_at	E430025E21Rik	RIKEN cDNA E430025E21 gene	1.06	0.783	-1.04	0.616	1.2	0.015	-1.16	0.329	0.01
1459698_at	LOC622320	Similar to retinoic acid, EGF, and NGF upregulated	-1.06	0.793	1.24	0.432	1.04	0.841	-1.73	0.099	-0.13
1446534_at	---	---	-1.26	0.459	1.06	0.921	1.37	0.566	-1.59	0.3	-0.11
1418635_at	Etv3	ets variant gene 3	1.09	0.243	-1.04	0.836	1.17	0.596	-1.29	0.36	-0.02
1423932_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	-3.59	0.02	-1.06	0.87	2	0.107	1.26	0.567	-0.35
1416964_at	Eefsec	eukaryotic elongation factor, selenocysteine-tRNA-specific	-1.09	0.678	1.04	0.797	1.27	0.254	-1.22	0.098	0
1451601_a_at	BC011467	cDNA sequence BC011467	1.17	0.462	1.17	0.196	-1.14	0.601	-1.49	0.131	-0.07
1421424_a_at	Anpep	alanyl (membrane) aminopeptidase	1.22	0.395	1.04	0.7	-1.05	0.844	-1.03	0.921	0.05
1420766_at	Socs7	suppressor of cytokine signaling 7	-1.18	0.318	-1.41	0.512	1.67	0.063	1.2	0.67	0.07
1426774_at	Parp12	poly (ADP-ribose) polymerase family, member 12	-1.01	0.68	1.17	0.094	1.06	0.453	-1.03	0.801	0.05
1453369_a_at	Fundc1	FUN14 domain containing 1	-1.03	0.6	1.15	0.371	1.09	0.515	-1.3	0.296	-0.02
1433505_a_at	Lrrc8d	leucine rich repeat containing 8D	1.03	0.776	-1.09	0.145	1.28	0.296	-1.2	0.464	0
1433232_at	4933426I03Rik	RIKEN cDNA 4933426I03 gene	-1.36	0.415	1.17	0.833	1.32	0.356	-1.36	0.115	-0.06
1422556_at	Gna13	guanine nucleotide binding protein, alpha 13	1.43	0.264	-1.07	0.525	-1.16	0.66	1.53	0.114	0.18
1441222_x_at	---	---	-1.49	0.368	1.61	0.268	-1.07	0.901	1.37	0.201	0.11
1439567_at	Tbx3	T-box 3	-2.5	0.084	1.63	0.427	1.19	0.627	-1.81	0.461	-0.37
1449043_at	Naga	N-acetyl galactosaminidase, alpha	-1.01	0.921	-1.09	0.588	1.31	0.151	1.3	0.002	0.13
1459347_at	---	---	1.01	0.979	1.71	0.512	-2.01	0.031	-1.96	0.576	-0.31
1422690_at	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	1	0.991	-1.06	0.532	1.28	0.154	-1.13	0.443	0.02
1426787_at	Sfi1 /// LOC673404	Sfi1 homolog, spindle assembly associated (yeast) /// similar to spindle assembly	1.21	0.243	1.16	0.248	-1.17	0.448	-1.2	0.71	0
1434939_at	Foxf1a	forkhead box F1a	1.12	0.827	1.19	0.289	-1.1	0.702	-1.06	0.735	0.04
1421440_at	LOC677060	similar to wingless related MMTV integration site 8b	-2.79	0.369	2.08	0.352	-1.27	0.01	1.03	0.925	-0.24
1429040_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	1.42	0.617	-1.9	0.234	1.28	0.524	-1.08	0.839	-0.07
1434044_at	Repin1	replication initiator 1	-1.02	0.926	1.03	0.694	1.21	0.541	-1.12	0.582	0.03
1450106_a_at	Evl	Ena-vasodilator stimulated phosphoprotein	-1.33	0.295	1.17	0.429	1.29	0.114	-1.88	0.13	-0.18
1433518_at	Lcmt2	leucine carboxyl methyltransferase 2	1.04	0.578	-1.14	0.278	1.3	0.042	-1.08	0.651	0.03
1432259_s_at	4931415C17Rik ///	RIKEN cDNA 4931415C17 gene /// RIKEN cDNA 2810487C13 gene	1.84	0.455	-2.71	0.27	1.02	0.956	-2.62	0.2	-0.62
1437948_x_at	Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	-1.13	0.728	1.29	0.646	1.04	0.861	-1.75	0.017	-0.14
1444242_at	---	---	1.14	0.385	-1.13	0.431	1.2	0.062	-1.41	0.094	-0.05
1453632_at	4930538K18Rik	RIKEN cDNA 4930538K18 gene	-1.03	0.913	-1.03	0.941	1.28	0.596	1.1	0.755	0.08
1450529_at	H2-M9	histocompatibility 2, M region locus 9	-1.99	0.293	1.61	0.21	1.11	0.796	-1.24	0.707	-0.13
1430181_at	H1fnt	H1 histone family, member N, testis-specific	1.32	0.71	-1.02	0.876	-1.08	0.819	1.35	0.493	0.14
1438130_at	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.45	0.118	1.13	0.469	-1.56	0.091	-1.01	0.963	0
1436870_s_at	AU041783	expressed sequence AU041783	1.15	0.665	1.17	0.607	-1.11	0.62	-1.19	0.636	0.01
1420580_at	4930429B21Rik	RIKEN cDNA 4930429B21 gene	1.24	0.311	-1.08	0.742	1.06	0.877	-1.15	0.435	0.02
1437689_x_at	Clu	clusterin	1.05	0.498	-1	0.98	1.17	0.089	-1.89	0.141	-0.17
1427840_at	---	---	-1.13	0.786	1.02	0.874	1.31	0.436	-2.05	0.287	-0.21
1424216_a_at	Papola	poly (A) polymerase alpha	-1.1	0.383	1.08	0.706	1.23	0.396	-1.34	0.114	-0.03
1449149_at	Traf3	Tnf receptor-associated factor 3	2.05	0.104	-1.65	0.377	-1.78	0.055	1.18	0.566	-0.05
1441474_at	C130070B15Rik	RIKEN cDNA C130070B15 gene	-1.73	0.448	1.34	0.308	1.31	0.42	-1.48	0.343	-0.14
1433896_at	Tmem127	transmembrane protein 127	-1.02	0.879	1.11	0.805	1.13	0.318	-1.04	0.854	0.05
1447794_x_at	Plac8l1	PLAC8-like 1	1.65	0.413	-1.6	0.385	-1.05	0.809	1.62	0.489	0.15
1436230_at	Gpr114	G protein-coupled receptor 114	1.11	0.889	-1.04	0.946	1.15	0.806	-1.29	0.647	-0.02
1416502_a_at	Preb	prolactin regulatory element binding	-1.2	0.088	1.04	0.662	1.35	0.002	-1.16	0.439	0.01
1416283_at	Gart	phosphoribosylglycinamide formyltransferase	-1.19	0.292	-1.05	0.097	1.44	0.017	1.05	0.778	0.06

1424812_at	BC017158	cDNA sequence BC017158	-1.07	0.785	-1.03	0.878	1.32	0.234	1.8	0.158	0.25
1449155_at	Polr3g	polymerase (RNA) III (DNA directed) polypeptide G	-1.07	0.541	1.23	0.113	1.06	0.624	-1.24	0.545	-0.01
1459446_at	Lrrc41	leucine rich repeat containing 41	-1.6	0.307	1.96	0.391	-1.56	0.468	1.05	0.879	-0.04
1417993_at	Svs3	seminal vesicle secretion 3	1.3	0.111	1.15	0.65	-1.29	0.613	-1.14	0.789	0.01
1425364_a_at	Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), me	-1.29	0.254	-1.08	0.282	1.52	0.003	2.31	0.01	0.37
1418109_at	Gspt2	G1 to S phase transition 2	-1.16	0.365	1.23	0.653	1.13	0.712	-1.59	0.12	-0.1
1431980_a_at	As3mt	arsenic (+3 oxidation state) methyltransferase	-1.14	0.141	1.22	0.096	1.13	0.226	-1.08	0.797	0.03
1427002_s_at	Arsg	arylsulfatase G	-1.41	0.181	-1.08	0.79	1.59	0.073	1.45	0.053	0.14
1451209_at	Lass5	longevity assurance homolog 5 (S. cerevisiae)	1.16	0.427	1.18	0.078	-1.13	0.023	-1.65	0.113	-0.11
1433763_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	1.02	0.866	-1.03	0.894	1.24	0.237	-1.52	0.091	-0.07
1430450_at	2310004L02Rik	RIKEN cDNA 2310004L02 gene	1.31	0.722	-1.28	0.329	1.14	0.79	-2.47	0.129	-0.33
1449254_at	Spp1	secreted phosphoprotein 1	-1.22	0.062	1.54	0.251	-1.16	0.538	1.71	0.167	0.22
1459269_at	2310014G06Rik	RIKEN cDNA 2310014G06 gene	-1.69	0.403	1.55	0.08	1.08	0.624	-1.5	0.097	-0.14
1442429_at	Ap2m1	Adaptor protein complex AP-2, mu1	1.38	0.331	-1.29	0.613	1.07	0.848	-1.24	0.416	-0.02
1423150_at	Scg5	secretogranin V	1.53	0.117	1.1	0.784	-1.68	0.038	-2.77	0.181	-0.45
1429314_at	Syt11	synaptotagmin XI	1.16	0.52	-1.08	0.884	1.14	0.414	-1.19	0.514	0.01
1443118_at	---	---	-1.19	0.802	1.31	0.533	1.08	0.718	-1.27	0.632	-0.02
1456609_at	Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1	1.22	0.055	-1.01	0.85	1.02	0.806	-1.26	0.355	-0.01
1417288_at	Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specif	1.15	0.549	1.1	0.632	-1.02	0.908	-2.01	0.098	-0.2
1437457_a_at	Mtpn	myotrophin	1.06	0.554	1.29	0.002	-1.14	0.232	-1.41	0.217	-0.05
1416701_at	Rnd3	Rho family GTPase 3	1.15	0.672	-1.05	0.847	1.12	0.708	-1.26	0.058	-0.01
1451839_a_at	Pde7a	phosphodiesterase 7A	1.26	0.515	-1.46	0.527	1.28	0.422	-2.15	0.184	-0.27
1445334_at	LOC665155	similar to signal recognition particle 54	1.11	0.401	1.32	0.424	-1.25	0.319	-1.1	0.535	0.02
1424508_at	Ttc5	tetratricopeptide repeat domain 5	1.21	0.071	-1.09	0.502	1.1	0.492	-1.2	0.624	0.01
1452390_at	AA881470	EST AA881470	1.34	0.051	-1.24	0.08	1.08	0.798	-1.14	0.632	0.01
1430391_a_at	St8sia4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	-1.68	0.201	1.34	0.508	1.29	0.443	-1.29	0.423	-0.08
1444927_at	D11Ertd729e	DNA segment, Chr 11, ERATO Doi 729, expressed	1.92	0.322	-1.39	0.072	-1.7	0.185	1.17	0.83	0
1424725_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	1.19	0.567	-1.17	0.683	1.18	0.579	-1.02	0.975	0.05
1416922_a_at	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	1.3	0.131	-1.01	0.878	-1.06	0.794	1.85	0.278	0.27
1453726_s_at	2810407C02Rik	RIKEN cDNA 2810407C02 gene	-1	0.986	1.06	0.746	1.17	0.076	-1.02	0.933	0.05
1424262_at	2810003C17Rik	RIKEN cDNA 2810003C17 gene	-1.39	0.105	-1.31	0.778	1.74	0.185	1.38	0.465	0.11
1438411_at	Gpr81	G protein-coupled receptor 81	1.7	0.174	-1.87	0.309	-1.01	0.993	1.39	0.445	0.06
1418266_at	Alox12b	arachidonate 12-lipoxygenase, 12R type	-1.12	0.681	-1.24	0.012	1.52	0.181	1.24	0.285	0.1
1455654_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	1.46	0.421	-1.26	0.358	-1.03	0.891	1.86	0.113	0.26
1451111_at	Nup133	nucleoporin 133	-1.07	0.619	-1.05	0.828	1.34	0.086	1.66	0.269	0.22
1455908_a_at	Scpep1	serine carboxypeptidase 1	-1.28	0.031	1.29	0.016	1.16	0.435	-1.37	0.133	-0.05
1458088_at	Ubap2	Ubiquitin-associated protein 2	1.5	0.394	-1	0.998	-1.37	0.257	1.63	0.035	0.19
1457278_at	6720489N17Rik	RIKEN cDNA 6720489N17 gene	-1.5	0.533	1.45	0.378	1.11	0.821	-1.04	0.898	0.01
1422798_at	Cntnap2	contactin associated protein-like 2	1.03	0.934	-1.22	0.726	1.38	0.319	-1.1	0.857	0.02
1448792_a_at	Cyp2f2	cytochrome P450, family 2, subfamily f, polypeptide 2	1.64	0.613	-1.31	0.18	-1.21	0.001	2.76	0.088	0.47
1459089_at	LOC545637 /// LOC	hypothetical LOC545637 /// hypothetical LOC623272 /// hypothetical LOC623281	1.42	0.349	-1.24	0.623	-1	0.999	2.39	0.091	0.39
1436675_at	Wdr63	WD repeat domain 63	-2.07	0.075	1.76	0.15	-1.01	0.951	1.46	0.573	0.03
1423655_a_at	1500010J02Rik	RIKEN cDNA 1500010J02 gene	-1.1	0.48	-1.25	0.2	1.51	0.03	1.08	0.774	0.06
1449928_at	Dynlt3	dynein light chain Tctex-type 3	-1.05	0.907	-1.1	0.794	1.37	0.544	1.03	0.956	0.06
1432527_at	1700108M19Rik	RIKEN cDNA 1700108M19 gene	1.55	0.27	1.07	0.943	-1.64	0.092	-1.08	0.84	-0.03
1440855_at	Mjd	Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3	1.35	0.589	-1.12	0.559	-1.02	0.899	1.11	0.775	0.08
1456167_at	LOC241051	similar to PHD finger protein 19	-2.09	0.146	1.82	0.539	-1.08	0.849	1.26	0.258	-0.02
1433125_at	5330422M15Rik	RIKEN cDNA 5330422M15 gene	-1.38	0.627	1.35	0.054	1.15	0.637	-1.2	0.066	-0.02
1452752_at	Lepre1	leprecan 1	-1.26	0.041	1.37	0.298	1.07	0.711	-1.02	0.753	0.04
1434148_at	Tcf4	transcription factor 4	1.04	0.512	1.52	0.021	-1.5	0.025	-1.12	0.678	-0.01
1439035_at	---	12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C53(	1.44	0.171	1.04	0.763	-1.35	0.094	-1.02	0.955	0.03
1455839_at	Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	1	0.971	1.24	0.283	-1.01	0.835	-1.09	0.579	0.04
1446445_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	1.33	0.306	1.18	0.395	-1.38	0.075	-1.07	0.862	0.01

1416837_at	Bax	Bcl2-associated X protein	1.16	0.106	1.11	0.147	-1.05	0.713	-1.17	0.254	0.01
1437608_x_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	1.06	0.748	1.18	0.347	-1.01	0.963	-1.41	0.314	-0.05
1432471_at	5730419I09Rik	RIKEN cDNA 5730419I09 gene	-1.47	0.218	1.16	0.604	1.39	0.323	-1.25	0.435	-0.04
1449693_at	Map3k7	Mitogen activated protein kinase kinase kinase 7	-1.2	0.828	1.83	0.201	-1.77	0.284	1.44	0.317	0.08
1418287_a_at	Dmbt1	deleted in malignant brain tumors 1	-2.61	0.304	-24.4	0.384	2.8	0.031	1.02	0.969	-5.8
1428848_a_at	Macf1	microtubule-actin crosslinking factor 1	1.31	0.407	1.01	0.907	-1.11	0.564	-1.54	0.266	-0.08
1421191_s_at	Gopc	golgi associated PDZ and coiled-coil motif containing	-1.08	0.658	1.05	0.768	1.26	0.03	-1.25	0.415	-0.01
1422467_at	Ppt1	palmitoyl-protein thioesterase 1	-1.04	0.794	1.24	0.03	1.02	0.743	-1.39	0.181	-0.04
1444800_at	Nfib	Nuclear factor I/B	1.58	0.505	-1.84	0.195	1.11	0.835	-1.11	0.59	-0.07
1426761_at	Aof2	amine oxidase (flavin containing) domain 2	-1.02	0.83	1.1	0.334	1.15	0.483	-1.15	0.383	0.02
1446358_at	Bai3	Brain-specific angiogenesis inhibitor 3	1.4	0.154	1.3	0.508	-1.91	0.128	-2.16	0.081	-0.34
1455981_at	Rps6 /// LOC21473	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	1.18	0.652	1.14	0.596	-1.1	0.701	-1.35	0.11	-0.03
1438541_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	1.22	0.315	1.09	0.855	-1.09	0.757	-1.25	0.264	-0.01
1422584_at	Skiv2l	superkiller viralicidic activity 2-like (S. cerevisiae)	1.04	0.815	-1.05	0.503	1.24	0.032	-1.25	0.282	-0.01
1437959_at	Zfp324	zinc finger protein 324	1.2	0.521	-1.15	0.504	1.15	0.552	-1.27	0.005	-0.01
1426472_at	Zfp52	zinc finger protein 52	1.1	0.87	-1.02	0.942	1.15	0.774	-1.42	0.211	-0.05
1450286_at	Npr3	natriuretic peptide receptor 3	1.65	0.209	-1.82	0.099	1.03	0.912	-1.77	0.176	-0.23
1418245_a_at	Rbm9	RNA binding motif protein 9	1.47	0.353	1.15	0.617	-1.64	0.406	-1.08	0.812	-0.03
1429371_at	2810426N06Rik	RIKEN cDNA 2810426N06 gene	-1.21	0.546	1.33	0.478	1.08	0.687	-1.27	0.156	-0.02
1452347_at	Mef2a	myocyte enhancer factor 2A	1.2	0.233	1.16	0.389	-1.15	0.292	-1.09	0.748	0.03
1456620_at	Gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	-1.05	0.799	-1.06	0.683	1.33	0.139	1	0.997	0.06
1423055_at	Nsg1	neuron specific gene family member 1	-1.37	0.113	-1.05	0.836	1.55	0.146	1.13	0.497	0.07
1434003_a_at	Dhps	deoxyhypusine synthase	1.08	0.654	-1.01	0.839	1.15	0.257	-1.42	0.124	-0.05
1452452_at	---	PREDICTED: Mus musculus hypothetical protein LOC626156 (LOC626156), mR	-1.12	0.149	1.2	0.311	1.14	0.147	-1.16	0.562	0.02
1455712_at	Hist3h2a	histone 3, H2a	1.2	0.413	1.18	0.348	-1.18	0.345	-1.11	0.62	0.02
1426304_x_at	B4galt7	xylosylprotein beta1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase	1.08	0.702	1.41	0.175	-1.35	0.319	-1.35	0.364	-0.05
1447330_at	Zbtb32	zinc finger and BTB domain containing 32	1.13	0.802	1.19	0.787	-1.1	0.801	-1.42	0.214	-0.05
1417490_at	Ctsb	cathepsin B	-1.1	0.223	1.21	0.05	1.11	0.077	-1.05	0.668	0.04
1447425_at	2900093B09Rik	RIKEN cDNA 2900093B09 gene	1.14	0.774	1.36	0.62	-1.36	0.435	-1.12	0.81	0
1435507_x_at	Prss2	protease, serine, 2	1.3	0.149	1.01	0.969	-1.07	0.807	-2.96	0.189	-0.43
1457509_at	Sbno1	sno, strawberry notch homolog 1 (Drosophila)	1.32	0.058	1.4	0.204	-1.96	0.035	-1.27	0.092	-0.13
1450164_at	Ascl1	achaete-scute complex homolog-like 1 (Drosophila)	1.18	0.666	1.23	0.704	-1.22	0.712	-3.59	0.251	-0.6
1450290_at	Pdcd1lg2	programmed cell death 1 ligand 2	-1.11	0.904	1.26	0.494	1.07	0.855	-1.28	0.367	-0.01
1424195_a_at	Inpp5d	inositol polyphosphate-5-phosphatase D	-1.18	0.475	1.02	0.923	1.36	0.163	-1.33	0.305	-0.03
1433980_at	Htatip	HIV-1 tat interactive protein, homolog (human)	1.06	0.752	-1.04	0.817	1.22	0.385	-1.28	0.072	-0.01
1436091_at	2810022L02Rik	RIKEN cDNA 2810022L02 gene	1.26	0.421	1.18	0.361	-1.28	0.564	-1.18	0.726	0
1419039_at	Cyp2d22	cytochrome P450, family 2, subfamily d, polypeptide 22	1.2	0.079	-1.11	0.6	1.13	0.321	-1.43	0.124	-0.05
1415812_at	Gsn	gelsolin	1.03	0.605	1.36	0.092	-1.19	0.123	-1.27	0.34	-0.02
1448167_at	Ifngr1	interferon gamma receptor 1	1.03	0.891	1.31	0.039	-1.12	0.352	-1.58	0.174	-0.09
1430893_at	Mup1	major urinary protein 1	2.26	0.279	-1.59	0.155	-2.91	0.038	1.26	0.576	-0.24
1421723_at	Pcdhb18	protocadherin beta 18	1.59	0.522	-1.89	0.368	1.12	0.839	-1.58	0.344	-0.19
1450527_at	Sstr1	somatostatin receptor 1	1.18	0.315	-1.25	0.445	1.25	0.183	-1.78	0.004	-0.15
1440208_at	Rac2	RAS-related C3 botulinum substrate 2	1.04	0.899	-1.18	0.691	1.35	0.129	-1.4	0.057	-0.05
1436198_at	Prep	prolyl endopeptidase	1.26	0.342	1.31	0.394	-1.51	0.235	-1.28	0.309	-0.06
1451489_at	Slc25a35	solute carrier family 25, member 35	1.02	0.922	-1.04	0.911	1.25	0.333	-1.8	0.169	-0.14
1450491_at	Ptger1	prostaglandin E receptor 1 (subtype EP1)	-1.08	0.935	-1.03	0.463	1.34	0.12	1.16	0.213	0.1
1415923_at	Ndn	necdin	1.33	0.061	1.03	0.874	-1.15	0.732	-1.33	0.333	-0.03
1431120_a_at	Golga1	golgi autoantigen, golgin subfamily a, 1	1.06	0.783	1.21	0.583	-1.04	0.758	-1.7	0.45	-0.12
1416213_x_at	Surf4	surfeit gene 4	-1.02	0.742	1.13	0.391	1.12	0.512	-1.02	0.92	0.05
1441127_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.53	0.631	1.5	0.243	1.08	0.863	-2.35	0.425	-0.33
1436009_at	Usp30	ubiquitin specific peptidase 30	1.13	0.204	-1.22	0.325	1.28	0.152	-1.18	0.485	0
1437651_a_at	Dtnb	dystrobrevin, beta	1.04	0.618	-1.08	0.433	1.27	0.277	-1.07	0.714	0.04
1455955_s_at	Snx17	sorting nexin 17	-1.06	0.672	1.15	0.152	1.14	0.096	-1.11	0.457	0.03

1450279_at	Prokr1	prokineticin receptor 1	-1.46	0.239	1.03	0.955	1.52	0.558	-1.58	0.405	-0.12
1444256_at	Rae1	RAE1 RNA export 1 homolog (S. pombe)	1.03	0.755	1.59	0.178	-1.64	0.025	-1.13	0.721	-0.04
1448338_at	Pgcp	plasma glutamate carboxypeptidase	1.32	0.52	-1.03	0.933	-1.06	0.855	1.16	0.731	0.1
1416772_at	Cpt2	carnitine palmitoyltransferase 2	-1.05	0.724	-1.36	0.145	1.55	0.268	1.16	0.45	0.08
1455071_at	Zbtb7b	Vzinc finger and BTB domain containing 7B	-1.38	0.1	1.26	0.213	1.25	0.342	-1.08	0.753	0.01
1431383_at	1110028F11Rik	RIKEN cDNA 1110028F11 gene	1	0.996	-1.17	0.256	1.38	0.296	-1.02	0.938	0.05
1430101_at	6330406O05Rik	RIKEN cDNA 6330406O05 gene	1.48	0.675	-2.01	0.217	1.26	0.326	-2.03	0.415	-0.33
1427578_a_at	Itgb4bp	integrin beta 4 binding protein	-1.02	0.791	1.21	0.239	1.04	0.652	-1.07	0.578	0.04
1447977_x_at	3100002L24Rik /// 9	RIKEN cDNA 3100002L24 gene /// RIKEN cDNA 9230108I15 gene /// similar to g	-1.01	0.332	1.14	0.414	1.11	0.6	-1.29	0.132	-0.01
1456883_at	Stox1	storkhead box 1	1.76	0.438	-3.15	0.398	1.16	0.57	-1.28	0.449	-0.38
1439495_at	4933407H18Rik	RIKEN cDNA 4933407H18 gene	1.15	0.412	1.09	0.493	-1.01	0.964	-1.07	0.733	0.04
1425567_a_at	Anxa5	annexin A5	1.1	0.206	1.25	0.025	-1.13	0.278	-1.47	0.064	-0.06
1448642_at	Pcbp1	poly(rC) binding protein 1	-1.17	0.11	-1.01	0.885	1.39	0.03	1.12	0.405	0.08
1448070_at	Xpo1	exportin 1, CRM1 homolog (yeast)	-1.36	0.187	-1.48	0.037	1.83	0.416	4.37	0.002	0.84
1426260_a_at	Ugt1a2 /// Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A2 /// UDP glucuronosyltransf	-1.1	0.243	-1.15	0.424	1.46	0.043	1.73	0.064	0.23
1428496_at	Secisbp2	SECIS binding protein 2	-1.08	0.708	1.12	0.439	1.2	0.135	-1.44	0.132	-0.05
1451562_at	BC006662	cDNA sequence BC006662	1.43	0.233	-1.16	0.54	-1.06	0.679	1.28	0.505	0.12
1436964_at	D7Ertd715e	DNA segment, Chr 7, ERATO Doi 715, expressed	1.1	0.67	1.34	0.413	-1.26	0.287	-1.31	0.147	-0.03
1448666_s_at	Tob2	transducer of ERBB2, 2	-1.22	0.47	1.2	0.181	1.21	0.369	-1.4	0.254	-0.05
1441036_at	---	---	1.33	0.168	1.33	0.468	-1.73	0.293	-1.43	0.351	-0.13
1454252_at	8030453O22Rik	RIKEN cDNA 8030453O22 gene	1.19	0.653	1.12	0.871	-1.08	0.918	-1.39	0.538	-0.04
1419509_a_at	Nagk	N-acetylglucosamine kinase	1.07	0.647	-1	0.987	1.17	0.242	-1.17	0.637	0.02
1433506_at	Lrrc8d	leucine rich repeat containing 8D	-1.11	0.326	-1.09	0.435	1.42	0.062	1.32	0.11	0.13
1437628_s_at	Rhoa	ras homolog gene family, member A	-1.1	0.306	1.08	0.018	1.25	0.006	-1.03	0.778	0.05
1454194_at	9330118I20Rik	RIKEN cDNA 9330118I20 gene	1.6	0.473	1.11	0.839	-1.92	0.272	-1.25	0.639	-0.11
1452862_at	Rreb1	ras responsive element binding protein 1	-1.17	0.3	-1.04	0.733	1.42	0.1	1.22	0.11	0.11
1420775_at	Hdhd1a	haloacid dehalogenase-like hydrolase domain	1.66	0.365	-2.59	0.229	1.19	0.686	-1.42	0.291	-0.29
1454181_at	4930519B02Rik	RIKEN cDNA 4930519B02 gene	-1.27	0.145	1.2	0.638	1.25	0.355	-2.22	0.022	-0.26
1442153_at	Uty	Ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	1.04	0.877	1.39	0.418	-1.24	0.347	-3.22	0.061	-0.51
1455151_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	1.64	0.26	1.09	0.824	-1.96	0.185	-1.18	0.638	-0.1
1437390_x_at	Stx1a	syntaxin 1A (brain)	1.56	0.188	1.08	0.874	-1.67	0.009	-1.5	0.277	-0.13
1443665_at	AI852444	Expressed sequence AI852444	1.17	0.342	-1.04	0.914	1.1	0.693	-1.16	0.587	0.02
1419630_a_at	Trim11	tripartite motif protein 11	-1.15	0.196	1.01	0.784	1.36	0.054	-1.33	0.152	-0.03
1458399_at	Lrrc3	leucine rich repeat containing 3	1.25	0.406	1.07	0.737	-1.1	0.815	-1.43	0.492	-0.05
1446541_at	4930434E21Rik	RIKEN cDNA 4930434E21 gene	-1.82	0.006	-1.22	0.561	1.87	0.01	1.87	0.395	0.17
1460609_at	Ints8	Integrator complex subunit 8	-1.16	0.707	1.26	0.675	1.11	0.816	-1.47	0.033	-0.06
1444068_at	Thrap1	thyroid hormone receptor associated protein 1	1.33	0.031	1.25	0.743	-1.52	0.443	-1.33	0.683	-0.07
1424497_at	1110032O16Rik	RIKEN cDNA 1110032O16 gene	1.36	0.063	1.17	0.331	-1.41	0.036	-1.47	0.272	-0.09
1426555_at	Scpep1	serine carboxypeptidase 1	-1.16	0.366	1.06	0.69	1.32	0.078	-1.28	0.303	-0.02
1430053_a_at	2810409H07Rik	RIKEN cDNA 2810409H07 gene	-1.15	0.504	-1.07	0.671	1.43	0.141	1.05	0.862	0.06
1429870_at	C630040K21Rik	RIKEN cDNA C630040K21 gene	1.15	0.809	1.57	0.085	-1.92	0.132	-2.22	0.033	-0.36
1433828_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-1.04	0.962	1.34	0.572	-1.07	0.553	1.62	0.215	0.21
1424548_at	Zgpat	zinc finger, CCCH-type with G patch domain	-1.1	0.48	1.18	0.412	1.15	0.436	-1.59	0.072	-0.09
1451606_at	A530016L24Rik	RIKEN cDNA A530016L24 gene	1.4	0.07	-1.13	0.845	-1.06	0.827	1.52	0.497	0.18
1430867_at	4933431M02Rik	RIKEN cDNA 4933431M02 gene	1.41	0.627	-1.23	0.145	1.02	0.97	-1.22	0.5	-0.01
1432452_at	1700054O19Rik	RIKEN cDNA 1700054O19 gene	-1.67	0.132	1.94	0.264	-1.42	0.179	2.21	0.099	0.26
1431833_a_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	1.28	0.663	-1.74	0.135	1.38	0.241	-1.62	0.415	-0.17
1424113_at	Lamb1-1	laminin B1 subunit 1	1.04	0.818	1.39	0.393	-1.24	0.464	-1.55	0.257	-0.09
1416041_at	Sgk	serum/glucocorticoid regulated kinase	-1.01	0.965	1.21	0.09	1.04	0.84	-1.64	0.182	-0.1
1426500_at	Icmt	isoprenylcysteine carboxyl methyltransferase	1.03	0.4	-1.06	0.479	1.27	0.229	-1.16	0.261	0.02
1422359_at	Olfr690	olfactory receptor 690	-1.45	0.568	1.51	0.404	1.04	0.846	-1.39	0.356	-0.07
1427753_at	Igkv1-135	Immunoglobulin light chain variable region	-2.55	0.377	-1.13	0.758	1.96	0.415	1.16	0.561	-0.14
1438083_at	Hhip	Hedgehog-interacting protein	1.52	0.5	1.17	0.549	-1.83	0.218	-1.51	0.644	-0.16

1426062_a_at	Casp7	caspase 7	-1.24	0.191	-1.1	0.565	1.52	0.146	1.41	0.26	0.15
1439866_at	Parc	p53-associated parkin-like cytoplasmic protein	1.04	0.938	-1.43	0.229	1.5	0.334	-2.19	0.469	-0.27
1425785_a_at	Txk	TXK tyrosine kinase	-2.04	0.462	1.68	0.411	1.07	0.733	-1.78	0.254	-0.27
1431639_at	4930468A15Rik	RIKEN cDNA 4930468A15 gene	1.38	0.075	-1.18	0.7	1.02	0.915	-1.08	0.77	0.03
1443781_at	---	---	1.25	0.265	-2.15	0.406	1.53	0.438	-2.35	0.329	-0.43
1418663_at	Mpdz	multiple PDZ domain protein	1.02	0.887	-1.37	0.034	1.49	0.292	-1.22	0.744	-0.02
1440378_at	---	---	1.27	0.225	-1.41	0.158	1.26	0.469	-1.09	0.573	0.01
1426794_at	Ptprs	protein tyrosine phosphatase, receptor type, S	1.24	0.194	1.08	0.648	-1.09	0.552	-1.48	0.118	-0.06
1453262_at	2810032G03Rik	RIKEN cDNA 2810032G03 gene	1.69	0.329	-1.13	0.808	-1.51	0.373	1.31	0.754	0.09
1435279_at	BC059842	cDNA sequence BC059842	-1.11	0.361	1.07	0.123	1.26	0.415	-1.22	0.383	0
1443858_at	Trim34	Tripartite motif protein 34	1.22	0.314	1.08	0.43	-1.07	0.604	-1.82	0.044	-0.15
1416294_at	Scamp3	secretory carrier membrane protein 3	-1.04	0.808	1.09	0.332	1.2	0.078	-1.15	0.099	0.02
1440033_at	Pag1	Phosphoprotein associated with glycosphingolipid microdomains 1	1.09	0.686	1.57	0.215	-1.74	0.01	-1.8	0.172	-0.22
1435785_at	LOC673251	similar to EH-domain containing 2	1.18	0.277	1.09	0.812	-1.03	0.87	-1.36	0.178	-0.03
1424167_a_at	Pmm1	phosphomannomutase 1	-1.08	0.574	1.44	0.176	-1.14	0.506	1.33	0.309	0.14
1450012_x_at	Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polyp	1.01	0.93	-1	0.972	1.23	0.235	-1.08	0.666	0.04
1442230_at	---	---	-1.32	0.108	1.69	0.355	-1.27	0.279	1.65	0.52	0.19
AFFX-ThrX-M_at	---	---	1.36	0.631	-1.16	0.413	1.02	0.96	-1.81	0.459	-0.15
1446277_at	---	---	-1.2	0.538	1.94	0.373	-2.16	0.441	1.05	0.935	-0.09
1436761_s_at	1200015N20Rik	RIKEN cDNA 1200015N20 gene	1.33	0.045	1.14	0.807	-1.3	0.355	-1.1	0.538	0.02
1452767_at	Rrbp1	ribosome binding protein 1	1.15	0.081	1.19	0.194	-1.11	0.393	-1.02	0.923	0.05
1440704_at	Rxfp2	relaxin/insulin-like family peptide receptor 2	-1.13	0.687	1.01	0.94	1.34	0.644	-1.03	0.843	0.05
1432615_at	Wdr37	WD repeat domain 37	1.05	0.495	1.38	0.301	-1.23	0.19	-1.08	0.89	0.03
1421955_a_at	Nedd4	neural precursor cell expressed, developmentally down-regulted gene 4	-1.03	0.94	-1.07	0.84	1.33	0.617	1.04	0.907	0.07
1454221_a_at	Kif2c	kinesin family member 2C	-1.21	0.145	-1.01	0.985	1.42	0.535	2.2	0.33	0.35
1432432_a_at	Rab3c	RAB3C, member RAS oncogene family	-1.16	0.462	1.42	0.444	-1.04	0.938	1.27	0.213	0.12
1420344_x_at	Gzmd	granzyme D	1.47	0.431	-1.89	0.133	1.24	0.692	-4.03	0.002	-0.8
1433650_at	Haghl	hydroxyacylglutathione hydrolase-like	-1.22	0.719	1.23	0.536	1.19	0.551	-1.1	0.589	0.03
1422553_at	Pten	phosphatase and tensin homolog	1.24	0.66	-1.01	0.959	1.01	0.977	-1.79	0.209	-0.14
1444462_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430098J	-4.02	0.021	1.18	0.747	1.82	0.053	-1.2	0.628	-0.56
1440538_at	---	---	1.66	0.41	-1.19	0.727	-1.34	0.55	1.31	0.721	0.11
1451011_at	Zfp358	zinc finger protein 358	1.59	0.553	-1.56	0.326	1.01	0.959	-1.03	0.939	0
1419602_at	Hoxa2	homeo box A2	-1.61	0.442	1.41	0.333	1.21	0.488	-1.01	0.958	0
1424675_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	-1.24	0.657	1.19	0.776	1.25	0.363	-1.08	0.739	0.03
1425896_a_at	Fbn1	fibrillin 1	1.39	0.437	1.07	0.826	-1.27	0.487	-1.07	0.699	0.03
1452747_at	Atp13a2 /// LOC67(	ATPase type 13A2 /// similar to ATPase type 13A2	-1.31	0.484	-1.2	0.704	1.65	0.319	1.39	0.457	0.13
1446087_at	Golga1	Golgi autoantigen, golgin subfamily a, 1	1.62	0.522	-1.51	0.524	-1.04	0.934	1.08	0.869	0.04
1425026_at	Sft2d2	SFT2 domain containing 2	-1.17	0.061	1.03	0.833	1.36	0.203	-1.27	0.257	-0.01
1433770_at	Dpysl2	dihydropyrimidinase-like 2	1.13	0.299	1.39	0.006	-1.39	0.118	-1.33	0.473	-0.05
1424644_at	Tbcc	tubulin-specific chaperone c	-1.04	0.792	1.09	0.31	1.19	0.181	-1.07	0.649	0.04
1427678_at	Zim3	zinc finger, imprinted 3	-1.09	0.888	1.3	0.625	1.03	0.956	-1.55	0.267	-0.08
1424053_a_at	Tcf25	transcription factor 25 (basic helix-loop-helix)	1.01	0.915	-1.17	0.174	1.37	0.088	-1.04	0.704	0.04
1449119_at	Arih2	ariadne homolog 2 (Drosophila)	1.02	0.686	-1.05	0.877	1.26	0.425	-1	0.992	0.06
1429144_at	Prei4	preimplantation protein 4	-1.1	0.45	-1.14	0.6	1.46	0.075	1.63	0.29	0.21
1435636_at	2310051F07Rik	RIKEN cDNA 2310051F07 gene	-1.15	0.197	-1.12	0.378	1.48	0.125	2.25	0.208	0.36
1454668_at	Zubr1	zinc finger, UBR1 type 1	-1.03	0.693	-1.12	0.188	1.38	0.148	1.14	0.367	0.09
1455854_a_at	Ssh1	slingshot homolog 1 (Drosophila)	1.07	0.733	-1.12	0.35	1.28	0.231	-1.1	0.638	0.03
1449784_at	---	---	1.92	0.398	-1.88	0.383	-1.26	0.276	1.15	0.722	-0.02
1451594_s_at	Serpinb6c	serine (or cysteine) peptidase inhibitor, clade B, member 6c	1.23	0.775	-1.11	0.729	1.12	0.733	-1.02	0.973	0.05
1428747_at	Trspap1	tRNA selenocysteine associated protein 1	1.12	0.36	1.22	0.065	-1.11	0.456	-1.31	0.074	-0.02
1425452_s_at	Ptprj /// AW125753	protein tyrosine phosphatase, receptor type, J /// expressed sequence AW12575	-1.63	0.019	1.17	0.643	1.46	0.162	-1.59	0.26	-0.15
1421341_at	Axin2	axin2	1.05	0.928	1.26	0.551	-1.07	0.851	-1.22	0.745	0.01
1428972_at	0610012D17Rik	RIKEN cDNA 0610012D17 gene	-1.19	0.563	1.38	0.222	1.02	0.944	-2.32	0.109	-0.28

1445879_at	zfp507	zinc finger protein 507	1.17	0.151	-1.25	0.296	1.28	0.614	-1.58	0.299	-0.1
1453586_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	-1.03	0.896	1.54	0.195	-1.37	0.148	1.19	0.632	0.08
1450159_at	Rem1	rad and gem related GTP binding protein 1	1.2	0.231	1.2	0.465	-1.18	0.404	-1.32	0.441	-0.03
1454997_at	Msrb3	methionine sulfoxide reductase B3	1.1	0.59	1.46	0.152	-1.48	0.17	-1.06	0.86	0.01
1457965_at	---	Transcribed locus	1.69	0.09	-1.19	0.771	-1.4	0.526	1.62	0.251	0.18
1432896_at	9030409K20Rik	RIKEN cDNA 9030409K20 gene	-1.44	0.236	1.38	0.355	1.17	0.406	-1.2	0.615	-0.02
1422170_at	Slc5a3	solute carrier family 5 (inositol transporters), member 3	-1.29	0.473	1.48	0.527	-1.01	0.968	1.73	0.364	0.23
1424393_s_at	Adhfe1	alcohol dehydrogenase, iron containing, 1	-1.14	0.388	-1.01	0.923	1.37	0.268	1.13	0.726	0.09
1430539_at	1810057P16Rik	RIKEN cDNA 1810057P16 gene	1.32	0.674	1.22	0.439	-1.42	0.232	-1.01	0.959	0.03
1448470_at	Fbp1	fructose bisphosphatase 1	-1.18	0.064	-1.18	0.523	1.55	0.112	1.96	0.221	0.29
1428318_at	Smgc	submandibular gland protein C	1.13	0.877	1.16	0.788	-1.05	0.929	-1.75	0.47	-0.13
1460361_at	5033414D02Rik	RIKEN cDNA 5033414D02 gene	-1.12	0.445	1.32	0.111	1.04	0.695	-1.73	0.058	-0.12
1430321_at	A930040G15Rik	RIKEN cDNA A930040G15 gene	-1.34	0.54	1.47	0.636	1.03	0.939	-3.27	0.011	-0.53
1443721_x_at	Stno	strawberry notch homolog (Drosophila)	1.11	0.057	1.15	0.578	-1.02	0.941	-1.15	0.304	0.02
1423359_at	Pln	phospholamban	-1.61	0.035	1.16	0.703	1.47	0.382	-1.02	0.969	0
1418183_a_at	Pscd1	pleckstrin homology, Sec7 and coiled-coil domains 1	-1.05	0.814	1.15	0.442	1.14	0.574	-1.99	0.102	-0.19
1438637_x_at	Sf3b2	splicing factor 3b, subunit 2	-1.13	0.393	1	0.989	1.36	0.062	-1.24	0.161	0
1457529_x_at	2810021G02Rik	RIKEN cDNA 2810021G02 gene	1.19	0.615	1.1	0.725	-1.05	0.796	-1.37	0.363	-0.03
1457992_at	Rcl1	RNA terminal phosphate cyclase-like 1	1.03	0.957	-1.37	0.531	1.49	0.336	-1.95	0.483	-0.2
1434492_at	A130022J15Rik	RIKEN cDNA A130022J15 gene	-1.18	0.608	1.47	0.096	-1.08	0.774	1.08	0.725	0.07
1416184_s_at	Hmga1	high mobility group AT-hook 1	-1.21	0.437	-1.01	0.955	1.43	0.177	1.14	0.431	0.09
1435404_at	Disp2	dispatched homolog 2 (Drosophila)	-1.24	0.501	-1.07	0.782	1.51	0.145	1.15	0.753	0.09
1422454_at	Krt13	keratin 13	1.57	0.581	1.15	0.653	-1.88	0.416	-2.59	0.115	-0.44
1416168_at	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	1.63	0.583	-1.3	0.22	-1.18	0.294	1.31	0.19	0.11
1424226_at	9030617O03Rik	RIKEN cDNA 9030617O03 gene	1.04	0.688	-1.16	0.461	1.34	0.005	-1.11	0.664	0.03
1436946_s_at	Gng5	guanine nucleotide binding protein (G protein), gamma 5 subunit	1.1	0.574	1.19	0.011	-1.05	0.719	-1.04	0.847	0.05
1448333_at	Adprh	ADP-ribosylarginine hydrolase	1.05	0.127	-1.11	0.441	1.3	0.254	-1.08	0.497	0.04
1435430_at	Tmem1	transmembrane protein 1	-1.01	0.91	-1.03	0.467	1.29	0.016	1.49	0.178	0.18
1425553_s_at	Hip1r	huntingtin interacting protein 1 related	1.01	0.947	-1.3	0.214	1.47	0.099	-1.96	0.163	-0.2
1444125_at	Pafah1b1	Platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	1.21	0.802	1.29	0.604	-1.34	0.625	-1.28	0.644	-0.03
1441442_at	---	---	1.17	0.78	1.41	0.373	-1.49	0.012	-1.41	0.451	-0.08
1441774_at	Rab38	Rab38, member of RAS oncogene family	1.29	0.101	-1.16	0.765	1.1	0.502	-1.06	0.731	0.04
1444681_at	D14Ertd171e	DNA segment, Chr 14, ERATO Doi 171, expressed	-1.45	0.344	1.63	0.067	-1.08	0.763	1.96	0.281	0.27
1426920_x_at	Itgb1	integrin beta 1 (fibronectin receptor beta)	1.72	0.384	-1.04	0.94	-1.77	0.033	1.48	0.115	0.1
1442591_at	AW060207	Expressed sequence AW060207	-1.59	0.069	1.18	0.687	1.44	0.552	-1.67	0.386	-0.16
1418834_at	Cno	cappuccino	-1.03	0.86	1.09	0.631	1.18	0.485	-1.09	0.239	0.04
1437451_at	1110006O17Rik	RIKEN cDNA 1110006O17 gene	1.02	0.872	1.62	0.082	-1.64	0.01	-1.39	0.24	-0.1
1420969_at	Btbd14b	BTB (POZ) domain containing 14B	-1.07	0.702	1.03	0.788	1.29	0.461	-1.02	0.854	0.05
1430511_at	1500037O19Rik	RIKEN cDNA 1500037O19 gene	-1.39	0.495	1.06	0.862	1.47	0.096	-1.47	0.61	-0.08
1454775_at	Hdac10	histone deacetylase 10	-1.12	0.598	1.08	0.545	1.27	0.151	-1.36	0.222	-0.03
1432315_at	4930483C13Rik	RIKEN cDNA 4930483C13 gene	1.72	0.463	-1.25	0.597	-1.38	0.521	1.55	0.184	0.16
1433843_at	Hs1bp3	HS1 binding protein 3	-1.14	0.713	1.01	0.943	1.37	0.135	-1.25	0.165	0
1426800_at	Rab8b /// LOC6702	RAB8B, member RAS oncogene family /// similar to RAB8B, member RAS oncog	1.46	0.4	-1.88	0.358	1.26	0.445	-1.6	0.147	-0.19
1454609_x_at	6430527G18Rik	RIKEN cDNA 6430527G18 gene	1.27	0.121	-1.29	0.36	1.2	0.298	-1.96	0.109	-0.19
1431386_s_at	Mbtps1	membrane-bound transcription factor peptidase, site 1	1.19	0.751	1.26	0.758	-1.25	0.664	-1.21	0.75	0
1452605_at	Thnsl1	threonine synthase-like 1 (bacterial)	-1.08	0.647	1.1	0.351	1.22	0.474	-1.42	0.211	-0.04
1452574_x_at	Igh-VJ558	Immunoglobulin heavy chain (J558 family)	1.08	0.436	-1.02	0.968	1.19	0.391	-3.06	0.36	-0.45
1444111_at	---	---	1.47	0.183	-1.76	0.535	1.22	0.692	-1.01	0.958	-0.02
1425969_a_at	Hdh	Huntington disease gene homolog	-1.02	0.857	1.01	0.769	1.25	0.13	-1.06	0.491	0.05
1424926_at	Sec63	SEC63-like (S. cerevisiae)	1.09	0.683	-1.06	0.851	1.21	0.512	-1	0.988	0.06
1433235_at	C030011I16Rik	RIKEN cDNA C030011I16 gene	1.16	0.54	-1.1	0.769	1.18	0.746	-1.62	0.461	-0.1
1432791_at	9030218A15Rik	RIKEN cDNA 9030218A15 gene	1.23	0.009	1.34	0.206	-1.46	0.257	-1.28	0.242	-0.04
1451496_at	Mtss1	metastasis suppressor 1	-1.34	0.212	-1.23	0.304	1.69	0.188	1.14	0.514	0.07

1460557_at	Supv3l1	suppressor of var1, 3-like 1 (S. cerevisiae)	-1.09	0.339	-1.09	0.399	1.42	0.11	1.16	0.395	0.1
1420921_at	Cd151	CD151 antigen	-1.43	0.644	-1.16	0.784	1.69	0.054	1.34	0.673	0.11
1448627_s_at	Pbk	PDZ binding kinase	-1.12	0.702	1.46	0.065	-1.12	0.648	4.28	0.157	0.88
1417084_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	-1.09	0.526	-1.22	0.441	1.51	0.101	1.25	0.453	0.11
1430624_at	4921511M17Rik ///	RIKEN cDNA 4921511M17 gene /// hypothetical LOC434874 /// hypothetical LOC	1.13	0.624	-1.18	0.719	1.28	0.622	-2.08	0.009	-0.21
1418468_at	Anxa11	annexin A11	-1.05	0.694	1.06	0.499	1.24	0.248	-1.11	0.335	0.03
1460362_at	2410001C21Rik	RIKEN cDNA 2410001C21 gene	1.29	0.135	-1.4	0.067	1.25	0.418	-1.03	0.902	0.03
1457927_at	Trpm3	transient receptor potential cation channel, subfamily M, member 3	-1.28	0.309	1.63	0.431	-1.18	0.791	1.09	0.607	0.06
1448116_at	Ube1x	ubiquitin-activating enzyme E1, Chr X	-1.07	0.196	-1.08	0.14	1.39	0.025	1.1	0.319	0.09
1418845_at	Proc	protein C	1.4	0.043	-1.17	0.071	-1	0.99	1.53	0.343	0.19
1452120_at	Nat11	N-acetyltransferase 11	-1.04	0.835	-1.01	0.964	1.3	0.407	1.61	0.108	0.21
1446325_at	Pcyox1	Prenylcysteine oxidase 1	-1.29	0.363	1.23	0.419	1.25	0.506	-1.46	0.242	-0.07
1433825_at	Ntrk3	Neurotrophic tyrosine kinase, receptor, type 3	1.29	0.109	-1.31	0.278	1.19	0.551	-1.36	0.407	-0.05
1430233_a_at	4933425K02Rik	RIKEN cDNA 4933425K02 gene	-1.02	0.985	-1.25	0.769	1.47	0.455	1.19	0.741	0.1
1440558_at	---	---	-1.16	0.626	1.31	0.373	1.08	0.703	-1.72	0.085	-0.12
1447176_at	A930008G19Rik	RIKEN cDNA A930008G19 gene	-1.21	0.535	1.87	0.028	-1.79	0.053	2.43	0.215	0.32
1443739_at	Lrba	LPS-responsive beige-like anchor	1.07	0.779	1.31	0.581	-1.15	0.542	-1.32	0.339	-0.02
1419757_at	Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	1.17	0.393	-1.09	0.668	1.16	0.22	-1.59	0.192	-0.09
1421344_a_at	Jub	ajuba	1.46	0.528	-1	0.986	-1.26	0.436	1.32	0.598	0.13
1446788_at	A430091L06Rik	RIKEN cDNA A430091L06 gene	2.01	0.052	-1.41	0.334	-1.87	0.276	1.76	0.424	0.12
1458806_at	D230005D02Rik	RIKEN cDNA D230005D02 gene	-1.24	0.721	1.34	0.637	1.11	0.719	-1.05	0.767	0.04
1453837_at	6330500D04Rik	RIKEN cDNA 6330500D04 gene	-1.71	0.314	1.02	0.934	1.65	0.191	-1.34	0.327	-0.1
1449582_at	Cdx1	caudal type homeo box 1	-1.6	0.501	1.37	0.216	1.26	0.383	-1.88	0.457	-0.21
1423388_at	Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	-1.03	0.881	1.14	0.689	1.14	0.531	-1.5	0.141	-0.06
1448413_at	2410016O06Rik	RIKEN cDNA 2410016O06 gene	-1.11	0.599	-1.09	0.369	1.44	0.17	1.01	0.97	0.06
1445311_at	Akap13	A kinase (PRKA) anchor protein 13	1.63	0.17	-1.15	0.737	-1.31	0.44	1.87	0.209	0.26
1445805_x_at	Kcnh3	potassium voltage-gated channel, subfamily H (eag-related), member 3	-1.28	0.487	1.49	0.187	-1.02	0.866	1.03	0.784	0.06
1432860_at	Panx3	pannexin 3	-1.52	0.315	1.11	0.53	1.49	0.303	-1.43	0.37	-0.09
1416164_at	Fbln5	fibulin 5	1.04	0.53	1.27	0.127	-1.06	0.85	-1.19	0.467	0.02
1437246_x_at	Rps6 /// LOC21473	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 40S ribos	1.07	0.834	1.3	0.038	-1.13	0.594	-1.33	0.176	-0.02
1451952_at	Prok2	prokineticin 2	1.29	0.765	-1.42	0.323	1.26	0.713	-1.08	0.869	0.01
1447013_at	AK220484	CDNA sequence AK220484	1.49	0.697	1.26	0.47	-1.97	0.063	-1.61	0.178	-0.21
1457016_at	---	Transcribed locus	-1.39	0.192	-1.11	0.593	1.63	0.193	1.07	0.838	0.05
1425116_a_at	Spnb4	spectrin beta 4	-2.11	0.331	1.83	0.304	-1.05	0.93	1.02	0.92	-0.08
1436299_at	Gls	glutaminase	-1.18	0.034	1.27	0.28	1.14	0.512	-1.07	0.293	0.04
1434308_at	Slc43a2	solute carrier family 43, member 2	-1.22	0.286	1.47	0.098	-1.04	0.834	1.16	0.702	0.09
1455028_at	Mapt	microtubule-associated protein tau	-1.44	0.108	1.01	0.979	1.55	0.442	-1.17	0.67	-0.01
1425360_at	LOC639490 /// LOC	similar to myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homolog	-1.05	0.807	1.09	0.835	1.22	0.521	-1.18	0.541	0.02
1432407_at	4933426D04Rik	RIKEN cDNA 4933426D04 gene	-1.03	0.947	1.35	0.591	-1.07	0.916	1.23	0.783	0.12
1460058_at	---	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830028	1.03	0.914	-1.02	0.953	1.24	0.224	-1.03	0.843	0.06
1450182_at	Clcnka	chloride channel Ka	1.3	0.609	-2.1	0.295	1.48	0.437	-1.32	0.167	-0.16
1455692_x_at	1700097N02Rik	RIKEN cDNA 1700097N02 gene	-1.35	0.026	1.68	0.1	-1.21	0.508	1.73	0.411	0.22
1424674_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	1.06	0.834	1.34	0.024	-1.17	0.029	-1.53	0.068	-0.08
1428182_at	Prpsap1	phosphoribosyl pyrophosphate synthetase-associated protein 1	1.07	0.511	-1.05	0.375	1.24	0.006	-1.17	0.36	0.02
1444637_at	---	---	-1.48	0.501	-1.23	0.79	1.76	0.264	1.74	0.135	0.2
1451454_at	Pcdh20	protocadherin 20	1.19	0.21	1.43	0.601	-1.58	0.33	-3.67	0.252	-0.66
1439387_x_at	2310061F22Rik	RIKEN cDNA 2310061F22 gene	1.11	0.678	-1.07	0.549	1.21	0.479	-1.53	0.03	-0.07
1455953_x_at	Pstk	phosphoseryl-tRNA kinase	-1.13	0.591	1.04	0.857	1.33	0.288	-1.38	0.396	-0.04
1445947_at	Kns2	Kinesin 2	1.16	0.375	1.32	0.382	-1.29	0.296	-2.14	0.004	-0.24
1460734_at	Col9a3	procollagen, type IX, alpha 3	1.71	0.116	-1.85	0.031	1.01	0.975	-1.04	0.692	-0.04
1416122_at	Ccnd2	cyclin D2	-1.01	0.971	1.08	0.658	1.18	0.508	-1.06	0.818	0.05
1446309_at	5830483C08Rik	RIKEN cDNA 5830483C08 gene	-1.16	0.807	1.86	0.117	-1.88	0.331	2.44	0.279	0.32
1419464_at	2810046M22Rik	RIKEN cDNA 2810046M22 gene	-1.35	0.684	1.26	0.658	1.26	0.455	-1.86	0.251	-0.17

1455550_x_at	Serinc3	serine incorporator 3	1.09	0.473	1.3	0.11	-1.15	0.242	-1.03	0.615	0.05
1417817_a_at	Wwtr1	WW domain containing transcription regulator 1	1.46	0.22	1.12	0.549	-1.49	0.189	-1.09	0.772	0
1453762_at	Vps26b	vacuolar protein sorting 26 homolog B (yeast)	-1.1	0.618	-1.07	0.769	1.41	0.185	1.16	0.756	0.1
1431778_at	2310051N18Rik	RIKEN cDNA 2310051N18 gene	-2.24	0.062	1.66	0.059	1.14	0.737	-1.2	0.778	-0.16
1418201_at	Plekhg2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	1.11	0.653	1.33	0.07	-1.22	0.507	-2.17	0.052	-0.24
1439668_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	-1.68	0.281	1.54	0.126	1.12	0.685	-1.28	0.496	-0.07
1451712_at	8030411F24Rik	RIKEN cDNA 8030411F24 gene	-1.65	0.072	1.37	0.573	1.28	0.487	-1.2	0.463	-0.05
1440962_at	Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	-1.04	0.939	1.8	0.018	-2.02	0.182	1.95	0.346	0.17
1452038_at	Capza1 /// LOC672	capping protein (actin filament) muscle Z-line, alpha 1 /// similar to capping protei	-1.04	0.709	1.05	0.44	1.25	0.304	-1.15	0.24	0.03
1458012_at	Dach2	dachshund 2 (Drosophila)	-1.26	0.758	1.2	0.467	1.26	0.539	-1.16	0.728	0.01
1450551_x_at	Klra15	killer cell lectin-like receptor, subfamily A, member 15	1.33	0.047	-1.73	0.556	1.35	0.648	-3.65	0	-0.67
1440249_at	4921525H12Rik	RIKEN cDNA 4921525H12 gene	-1.53	0.355	-1.08	0.737	1.67	0.328	1.33	0.557	0.1
1448297_a_at	Tnk2 /// LOC67228	tyrosine kinase, non-receptor, 2 /// similar to Activated CDC42 kinase 1 (ACK-1) (	-1.12	0.643	-1.07	0.451	1.43	0.009	1.35	0.047	0.15
1422272_at	Phxr4	per-hexamer repeat gene 4	1.11	0.571	1.63	0.005	-1.91	0.013	-2.05	0.11	-0.31
1449910_at	2210418O10Rik	RIKEN cDNA 2210418O10 gene	-1.14	0.484	1.29	0.141	1.08	0.605	-1.01	0.988	0.06
1457474_at	Crtac1	Cartilage acidic protein 1	1.87	0.156	-2.09	0.284	-1.1	0.872	2.35	0.127	0.26
1428553_at	Glrx5	glutaredoxin 5 homolog (S. cerevisiae)	-1.07	0.044	-1.02	0.845	1.34	0.236	2.96	0.205	0.55
1423681_at	1300018I05Rik	RIKEN cDNA 1300018I05 gene	1.09	0.484	-1.14	0.254	1.29	0.049	-1.01	0.926	0.06
1418596_at	---	---	1.13	0.275	1.19	0.329	-1.07	0.754	-1.05	0.752	0.05
1434149_at	Tcf4	transcription factor 4	1.02	0.758	1.35	0.12	-1.13	0.476	-1.19	0.529	0.01
1449514_at	Gprk5	G protein-coupled receptor kinase 5	1.18	0.45	1.18	0.557	-1.11	0.279	-1.02	0.919	0.06
1454151_at	Tmem167	transmembrane protein 167	-1.1	0.753	1.66	0.104	-1.46	0.121	1.11	0.837	0.05
1428143_a_at	Pnpla2	patatin-like phospholipase domain containing 2	-1.15	0.158	-1.21	0.238	1.56	0.157	1.07	0.713	0.07
1426221_at	Loh11cr2a	loss of heterozygosity, 11, chromosomal region 2, gene A homolog (human)	1.08	0.621	1.22	0.262	-1.04	0.557	-1.2	0.157	0.01
1440283_at	1810059H22Rik	RIKEN cDNA 1810059H22 gene	-1.1	0.599	1.13	0.886	1.21	0.561	-1.31	0.713	-0.01
1424445_at	Tm4sf5	transmembrane 4 superfamily member 5	-1.28	0.587	1.2	0.372	1.28	0.648	-1.94	0.004	-0.19
1429140_at	9830002I17Rik	RIKEN cDNA 9830002I17 gene	-1.12	0.579	1.35	0.44	1.02	0.96	-1.13	0.598	0.03
1451349_at	BC020077	cDNA sequence BC020077	-1.04	0.851	-1.05	0.934	1.35	0.376	1.01	0.957	0.07
1443182_at	AW060207	Expressed sequence AW060207	1.13	0.621	-1.03	0.918	1.16	0.675	-1.07	0.767	0.05
1455582_at	---	Transcribed locus	1.18	0.448	1.44	0.185	-1.57	0.382	-1.33	0.525	-0.07
1458103_at	Ncor1	nuclear receptor co-repressor 1	-1.46	0.489	1.71	0.344	-1.15	0.571	1.08	0.516	0.04
1427637_a_at	Dsc3	desmocollin 3	-2.65	0.16	1.23	0.336	1.65	0.136	-1.46	0.094	-0.31
1454255_at	5430434F05Rik	RIKEN cDNA 5430434F05 gene	1.44	0.343	1.09	0.657	-1.38	0.167	-1.58	0.066	-0.11
1458422_at	D730002M21Rik	RIKEN cDNA D730002M21 gene	-1.45	0.326	1.21	0.657	1.36	0.386	-1.02	0.975	0.03
1450645_at	Mt4	metallothionein 4	1.53	0.49	-1.08	0.848	-1.25	0.651	1.83	0.112	0.26
1437308_s_at	F2r	coagulation factor II (thrombin) receptor	1.22	0.498	1.2	0.068	-1.18	0.06	-1.03	0.948	0.05
1442687_at	1700064N11Rik	RIKEN cDNA 1700064N11 gene	1.29	0.325	-1.33	0.397	1.21	0.384	-1.32	0.292	-0.03
1456377_x_at	Limd2 /// LOC6323	LIM domain containing 2 /// similar to epithelial protein lost in neoplasm	-1.03	0.846	1.11	0.384	1.18	0.203	-1.79	0.109	-0.13
1438935_at	BB234005	expressed sequence BB234005	-1.39	0.298	-1.31	0.538	1.77	0.262	1.03	0.939	0.03
1440428_at	Sfxn5	sideroflexin 5	1.37	0.496	1.03	0.965	-1.16	0.669	-1.39	0.517	-0.04
1443895_at	LOC621440 /// LOC	hypothetical protein LOC621440 /// hypothetical protein LOC633947 /// region cor	1.37	0.548	-1.46	0.532	1.21	0.652	-1.05	0.915	0.02
1421552_at	Cdx4	caudal type homeo box 4	1.16	0.721	1.18	0.763	-1.09	0.815	-1.49	0.382	-0.06
1453519_at	2610037D02Rik	RIKEN cDNA 2610037D02 gene	1.13	0.858	-2.7	0.021	1.76	0.281	-1.13	0.801	-0.23
1448571_a_at	Gmfb	glia maturation factor, beta	-1.19	0.056	1.1	0.585	1.32	0.237	-1.02	0.94	0.05
1422440_at	Cdk4 /// LOC64061	cyclin-dependent kinase 4 /// similar to Cell division protein kinase 4 (Cyclin-depe	-1.01	0.915	-1.04	0.712	1.31	0.23	1.28	0.451	0.14
1422577_at	Cs	citrate synthase	-1.09	0.818	-1.2	0.173	1.51	0.07	1.02	0.938	0.06
1457613_at	Rfxdc1	Regulatory factor X domain containing 1	1.19	0.474	-1.07	0.859	1.14	0.537	-1.2	0.731	0.02
1437754_at	AW146299	expressed sequence AW146299	-1.9	0.054	1.76	0.206	-1.03	0.967	1.98	0.175	0.2
1425331_at	Zfp106	zinc finger protein 106	1.34	0.131	-1.2	0.132	1.09	0.644	-1.29	0.027	-0.02
1426960_a_at	Fa2h	fatty acid 2-hydroxylase	1.1	0.516	-1.16	0.464	1.3	0.295	-1.07	0.799	0.04
1457955_at	Gga2	Golgi associated, gamma adaptin ear containing, ARF binding protein 2	1.04	0.829	1.24	0.621	-1.02	0.956	-2.5	0.043	-0.31
1451288_s_at	1810043G02Rik	RIKEN cDNA 1810043G02 gene	-1.14	0.553	1.05	0.81	1.33	0.214	-1.07	0.836	0.04
1441079_at	---	Transcribed locus	-1.22	0.634	1.4	0.618	1.04	0.921	-1.37	0.142	-0.04

1437293_x_at	Ust	uronyl-2-sulfotransferase	-2.26	0.17	1.92	0.25	-1.11	0.747	1.02	0.963	-0.11
1427446_s_at	Ttn	titin	-1.52	0.299	-1.27	0.602	1.82	0.469	1.11	0.873	0.03
1430408_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	1.21	0.819	-1.14	0.681	1.18	0.663	-2.5	0.209	-0.31
1428081_at	Klhl21	kelch-like 21 (Drosophila)	1.16	0.456	-1.1	0.819	1.2	0.387	-1.36	0.058	-0.03
1422466_at	Nxn	nucleoredoxin	-1.24	0.378	1.02	0.91	1.44	0.173	-1.2	0.349	0
1446915_at	D7Ertd316e	DNA segment, Chr 7, ERATO Doi 316, expressed	1.87	0.266	-1.39	0.318	-1.5	0.221	1.07	0.897	0.01
1436975_at	Gm24	Gene model 24, (NCBI)	1.4	0.522	-2.22	0.373	1.41	0.283	-1.72	0.357	-0.28
1420460_a_at	Pex11b	peroxisomal biogenesis factor 11b	-1.01	0.969	-1.04	0.765	1.32	0.285	1.15	0.533	0.1
1423435_at	---	---	1.87	0.215	-1.91	0.12	-1.16	0.699	1.91	0.359	0.18
1447261_at	---	PREDICTED: Mus musculus similar to CG12341-PA (LOC621976), mRNA	-1.26	0.48	1.4	0.585	1.07	0.723	-1.01	0.982	0.05
1432552_at	Tmem89	transmembrane protein 89	1.21	0.415	1.1	0.73	-1.05	0.491	-1.09	0.367	0.04
1427891_at	Gimap6	GTPase, IMAP family member 6	1.05	0.834	1.33	0.117	-1.14	0.503	-2.26	0.096	-0.25
1440329_s_at	Gpatc2	G patch domain containing 2	1	0.999	1.28	0.428	-1.02	0.898	-1.24	0.43	0.01
1424611_x_at	Trub2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	-1.01	0.968	1.19	0.228	1.08	0.646	-1.38	0.025	-0.03
1434128_a_at	Zfp574	zinc finger protein 574	-1.21	0.276	-1.01	0.968	1.45	0.039	1.1	0.685	0.08
1415819_a_at	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	1.01	0.958	-1.06	0.617	1.31	0.112	-1.15	0.391	0.03
1444561_at	Tmem39a	Transmembrane protein 39a	-1.07	0.783	-1.88	0.172	1.8	0.104	1.03	0.956	-0.03
1438968_x_at	Spint2	serine protease inhibitor, Kunitz type 2	1.04	0.866	1.25	0.023	-1.03	0.9	-1.22	0.511	0.01
1460393_a_at	Dusp7 /// LOC6749	dual specificity phosphatase 7 /// similar to dual specificity phosphatase 7	-1.08	0.437	1.11	0.791	1.22	0.393	-1.26	0.451	0
1457196_at	---	Transcribed locus	-1.67	0.081	1.6	0.206	1.06	0.816	-2.53	0.061	-0.38
1446092_at	---	Transcribed locus	-1.68	0.106	1.1	0.858	1.57	0.409	-1.76	0.438	-0.19
1441040_at	Klf12	Kruppel-like factor 12	-1.19	0.657	1.25	0.272	1.17	0.528	-1.07	0.813	0.04
1439072_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	1.52	0.449	-1.04	0.829	-1.29	0.625	2.36	0.001	0.39
1427209_at	Baz2a	bromodomain adjacent to zinc finger domain, 2A	-1.02	0.958	-1.01	0.953	1.29	0.193	1.2	0.597	0.11
1449586_at	Pkp1	plakophilin 1	-2.58	0.428	1.21	0.323	1.67	0.475	-1.18	0.842	-0.22
1421615_at	Myo15	myosin XV	-2.53	0.044	2.13	0.055	-1.36	0.462	1.12	0.503	-0.16
1441122_at	AU024342	expressed sequence AU024342	1.42	0.335	-1.37	0.556	1.11	0.821	-1.74	0.09	-0.14
1416806_at	Fdxr	ferredoxin reductase	-1.29	0.353	1.05	0.81	1.44	0.061	-1.19	0.049	0
1431062_a_at	Exoc4	exocyst complex component 4	1.14	0.693	-1.43	0.601	1.42	0.403	-1.09	0.826	0.01
1438160_x_at	Slco4a1	solute carrier organic anion transporter family, member 4a1	-1.58	0.272	1.28	0.6	1.35	0.407	-1.39	0.233	-0.09
1450129_a_at	Socs6	suppressor of cytokine signaling 6	1.19	0.063	-1.08	0.66	1.14	0.351	-1.09	0.574	0.04
1452050_at	Camk1d	calcium/calmodulin-dependent protein kinase ID	1.34	0.503	1.13	0.278	-1.25	0.199	-1.26	0.533	-0.01
1443768_at	---	---	1.96	0.309	-1.2	0.764	-2.12	0.019	1.08	0.84	-0.07
1422008_a_at	Aqp3	aquaporin 3	-1.16	0.368	1.18	0.396	1.22	0.679	-2.64	0.337	-0.35
1452139_at	Slc35c1	solute carrier family 35, member C1	1.07	0.86	-1.04	0.847	1.24	0.038	-1.02	0.944	0.06
1441820_at	Cdkl2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	1.04	0.896	-1.24	0.721	1.42	0.604	-1.97	0.269	-0.19
1454325_at	4930487N04Rik	RIKEN cDNA 4930487N04 gene	-1.06	0.874	1.56	0.287	-1.31	0.394	2.44	0.196	0.41
1441344_at	C80197	expressed sequence C80197	-1.51	0.257	1.23	0.688	1.38	0.262	-1.76	0.068	-0.17
1460623_at	Scap2	src family associated phosphoprotein 2	1	0.978	1.32	0.026	-1.06	0.546	-1.31	0.339	-0.01
1451122_at	Idi1	isopentenyl-diphosphate delta isomerase	-1.07	0.821	1.62	0.124	-1.42	0.045	1.26	0.584	0.1
1453402_at	6430500C12Rik	RIKEN cDNA 6430500C12 gene	1.12	0.749	1.41	0.368	-1.36	0.072	-1.07	0.871	0.03
1458405_at	B430201F14	hypothetical protein B430201F14	1.27	0.45	-1.7	0.37	1.41	0.468	-1.31	0.134	-0.08
1449278_at	Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	-1.06	0.694	1.05	0.789	1.27	0.186	-1.53	0.181	-0.07
1424736_at	Eef2	eukaryotic translation elongation factor 2	-1.12	0.103	1.05	0.606	1.32	0.036	-1.4	0.061	-0.04
1433694_at	Pde3b	phosphodiesterase 3B, cGMP-inhibited	1.07	0.758	-1.16	0.291	1.33	0.147	-2.11	0.143	-0.22
1428524_at	2310051N18Rik	RIKEN cDNA 2310051N18 gene	1.32	0.304	1.16	0.026	-1.28	0.233	-1.04	0.778	0.04
1433290_at	C030045M22Rik	RIKEN cDNA C030045M22 gene	-2.12	0.03	1.76	0.375	1.03	0.936	-1.79	0.285	-0.28
1435552_at	Otud7b	OTU domain containing 7B	1.22	0.674	1.08	0.251	-1.03	0.773	-1.32	0.167	-0.01
1451078_at	2510039O18Rik	RIKEN cDNA 2510039O18 gene	-1	0.996	1.01	0.879	1.25	0.078	-1.05	0.697	0.05
1423390_at	Siah1a	seven in absentia 1A	1.23	0.217	1.19	0.576	-1.18	0.596	-1.17	0.703	0.02
1453662_at	LOC77413	hypothetical LOC77413	1.53	0.309	-1.09	0.824	-1.23	0.438	1.28	0.64	0.12
1419595_a_at	Ggh /// LOC667301	gamma-glutamyl hydrolase /// similar to Gamma-glutamyl hydrolase precursor (G	1.02	0.887	1.31	0.064	-1.06	0.638	-1.13	0.696	0.03
1454667_at	Snx8	sorting nexin 8	-1.03	0.578	1.1	0.508	1.2	0.454	-1.94	0.107	-0.17

1446227_at	Gpr180	G protein-coupled receptor 180	1.12	0.894	-2.42	0.186	1.73	0.296	-2.63	0.088	-0.55
1433120_at	9530002O20Rik	RIKEN cDNA 9530002O20 gene	1.77	0.254	1.04	0.871	-2.19	0.138	-3.3	0.171	-0.67
1431334_a_at	4933433P14Rik	RIKEN cDNA 4933433P14 gene	1.12	0.489	1.24	0.51	-1.11	0.703	-1.24	0.61	0.01
1458425_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13008	-1.32	0.623	1.26	0.489	1.25	0.114	-1.19	0.233	0
1453959_at	1700065O13Rik	RIKEN cDNA 1700065O13 gene	1.77	0.333	-1.67	0.454	-1.11	0.699	1.51	0.596	0.12
1459927_at	4833445I07Rik	RIKEN cDNA 4833445I07 gene	1.13	0.353	-1.05	0.901	1.18	0.763	-1.1	0.793	0.04
1430154_at	4930543C13Rik	RIKEN cDNA 4930543C13 gene	-1.27	0.281	1.25	0.356	1.23	0.194	-1.06	0.766	0.04
1460090_at	Arih1	Ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	1.41	0.556	-1.06	0.921	-1.09	0.829	1.15	0.751	0.1
1416221_at	Fstl1	follistatin-like 1	1.1	0.244	1.62	0.014	-1.83	0.027	-1.3	0.279	-0.1
1434687_at	C730026J16	hypothetical protein C730026J16	1.2	0.594	1.21	0.585	-1.16	0.488	-1.15	0.744	0.02
1448908_at	Ppap2b	phosphatidic acid phosphatase type 2B	1.07	0.714	-1.13	0.281	1.32	0.086	-1.58	0.075	-0.08
1451066_at	Leng4	leukocyte receptor cluster (LRC) member 4	1.01	0.883	-1.14	0.241	1.38	0.058	-1.06	0.724	0.05
1419903_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.33	0.699	1.5	0.522	1.02	0.97	-1.94	0.295	-0.19
1421781_at	Upk2	uroplakin 2	1.24	0.674	1.07	0.896	-1.04	0.857	-1.63	0.173	-0.09
1452260_at	Cidec	cell death-inducing DFFA-like effector c	-1.84	0.336	-1.64	0.007	2.11	0.484	6.55	0.003	1.3
1426094_at	Rhbdl1	rhomboid, veinlet-like 1 (Drosophila)	1.09	0.728	1.23	0.628	-1.06	0.778	-1.08	0.682	0.05
1439501_at	Cbara1	calcium binding atopy-related autoantigen 1	1.03	0.962	1.59	0.199	-1.55	0.023	-1.26	0.272	-0.05
1423358_at	1810009K13Rik	RIKEN cDNA 1810009K13 gene	-1.13	0.683	1.27	0.02	1.12	0.686	-1.12	0.748	0.03
1422836_at	Mbnl3	muscleblind-like 3 (Drosophila)	1.44	0.532	-1.37	0.293	1.1	0.329	-1.05	0.786	0.03
1450351_a_at	Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	1.29	0.197	1.04	0.755	-1.07	0.727	-1.03	0.855	0.06
1431301_at	E130201N16Rik	RIKEN cDNA E130201N16 gene	-1.74	0.425	1.24	0.751	1.46	0.412	-1.14	0.745	-0.05
1431621_at	4930420G21Rik	RIKEN cDNA 4930420G21 gene	1.86	0.587	-2.78	0.042	1.05	0.822	-2.16	0.07	-0.51
1433308_at	9330159N22Rik	RIKEN cDNA 9330159N22 gene	-1.2	0.682	-1.2	0.729	1.6	0.293	1.91	0.11	0.28
1426891_at	Rpap1	RNA polymerase II associated protein 1	1.1	0.738	-1.3	0.047	1.4	0.107	-1.04	0.514	0.04
1426206_at	Robo4	roundabout homolog 4 (Drosophila)	-1.19	0.041	1.28	0.004	1.15	0.3	-1.06	0.687	0.04
1454876_at	Rab23	RAB23, member RAS oncogene family	1.07	0.768	1.27	0.14	-1.08	0.668	-1.17	0.549	0.02
1460366_at	Eml3	echinoderm microtubule associated protein like 3	1.04	0.696	-1.05	0.624	1.28	0.088	-1.06	0.786	0.05
1459435_at	---	Transcribed locus	-1.67	0.071	1.94	0.127	-1.36	0.541	1.2	0.611	0.03
1440026_at	Trps1	Trichorhinophalangeal syndrome I (human)	1.06	0.847	1.46	0.395	-1.34	0.057	-1.28	0.14	-0.02
1454186_a_at	2310051N18Rik	RIKEN cDNA 2310051N18 gene	1.06	0.582	-1.15	0.295	1.34	0.347	-1.07	0.795	0.05
1455443_at	Gdap1l1	ganglioside-induced differentiation-associated protein 1-like 1	1.88	0.428	-1.21	0.218	-1.77	0.384	1.23	0.532	0.03
1416238_at	Tie1	tyrosine kinase receptor 1	1.01	0.856	-1.06	0.735	1.31	0.357	-1.33	0.366	-0.02
1427030_at	Ccdc52	coiled-coil domain containing 52	-1.08	0.601	1.26	0.228	1.09	0.18	-1.15	0.448	0.03
1431797_at	4921518K17Rik	RIKEN cDNA 4921518K17 gene	-1.03	0.969	1.67	0.265	-1.59	0.362	1.25	0.651	0.08
1434858_x_at	Zfp511	zinc finger protein 511	1.31	0.218	-1.48	0.11	1.28	0.261	-1.23	0.32	-0.03
1438528_at	Pcm1	Pericentriolar material 1	1.09	0.384	1.51	0.145	-1.5	0.026	-1.4	0.315	-0.08
1439760_x_at	Upk1b	uroplakin 1B	-1.54	0.242	1.89	0.518	-1.37	0.131	2.02	0.172	0.25
1452228_at	Tbc1d23	TBC1 domain family, member 23	1.38	0.222	-1.14	0.48	1.01	0.977	-1.39	0.004	-0.03
1460664_at	Zfpn1a4	zinc finger protein, subfamily 1A, 4 (Eos)	1.2	0.47	1.08	0.693	-1.01	0.926	-1.04	0.816	0.06
1432467_at	Lrch3	leucine-rich repeats and calponin homology (CH) domain containing 3	-1.16	0.739	-2.33	0.33	1.98	0.243	1.45	0.591	-0.02
1448076_at	Sh2bp1	SH2 domain binding protein 1 (tetratricopeptide repeat containing)	1.04	0.803	1.45	0.073	-1.28	0.429	-1.11	0.726	0.02
1457192_at	---	---	1.04	0.795	1.64	0.571	-1.7	0.396	-1.89	0.36	-0.23
1447987_at	D030041N04Rik	RIKEN cDNA D030041N04 gene	1.39	0.181	-1.06	0.699	-1.07	0.455	1.15	0.305	0.1
1444293_at	BC028471	cDNA sequence BC028471	1.17	0.802	1.13	0.847	-1.04	0.951	-1.82	0.084	-0.14
1426194_x_at	Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerevisiae)	2.2	0.447	-2.1	0.145	-1.69	0.354	1.04	0.969	-0.14
1427138_at	0610010D24Rik	RIKEN cDNA 0610010D24 gene	1.14	0.428	-1.18	0.55	1.29	0.103	-1.01	0.941	0.06
1450026_a_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	1.13	0.328	-1.09	0.443	1.23	0.42	-1.15	0.518	0.03
1424620_at	D13Wsu177e	DNA segment, Chr 13, Wayne State University 177, expressed	-1.03	0.819	-1.04	0.755	1.33	0.238	1.2	0.354	0.12
1447544_at	---	Transcribed locus	-1.01	0.956	1.4	0.408	-1.14	0.562	1.02	0.938	0.07
1421164_a_at	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	-1.07	0.773	1.16	0.097	1.17	0.423	-1.97	0.144	-0.18
1454328_at	2900060K15Rik	RIKEN cDNA 2900060K15 gene	1.1	0.884	1.71	0.369	-2.18	0.026	-1.49	0.28	-0.21
1428035_at	Fsip1	fibrous sheath-interacting protein 1	-1.01	0.965	1.3	0.324	-1.02	0.926	1.02	0.885	0.07
1446732_at	---	---	1.46	0.219	-1.28	0.332	1.03	0.937	-1.1	0.404	0.03

1421014_a_at	Clybl	citrate lyase beta like	-1.07	0.247	-1.18	0.18	1.49	0.109	1.46	0.409	0.18
1442500_at	C77406	expressed sequence C77406	-1.55	0.095	2.07	0.23	-1.79	0.221	1.04	0.952	-0.06
AFFX-r2-Bs-lys-5_at	---	---	1.17	0.77	-1.14	0.259	1.23	0.54	-1.58	0.558	-0.08
1431179_at	Entpd7	ectonucleoside triphosphate diphosphohydrolase 7	-1.03	0.929	-1.09	0.432	1.38	0.068	1.07	0.734	0.08
1438527_at	Rpl3 /// LOC242809	ribosomal protein L3 /// similar to 60S ribosomal protein L3 (J1 protein) /// similar t	1.57	0.1	-1.16	0.751	-1.19	0.568	1.89	0.264	0.28
1426539_at	Usp11	ubiquitin specific peptidase 11	-1.23	0.338	1.28	0.097	1.19	0.535	-1.22	0.584	0
1432511_s_at	Cep27	centrosomal protein 27	-1.39	0.006	-1.29	0.46	1.78	0.052	1.16	0.671	0.06
1457300_at	Aftph	aftiphilin	1.19	0.858	1.09	0.894	-1.01	0.984	-1.77	0.291	-0.12
1452414_s_at	Ccdc86	coiled-coil domain containing 86	1.05	0.785	-1.16	0.609	1.36	0.308	-1.15	0.566	0.03
1441044_at	C130002M15Rik	RIKEN cDNA C130002M15 gene	1.12	0.76	1.24	0.413	-1.1	0.648	-1.02	0.94	0.06
1426514_at	4631426J05Rik	RIKEN cDNA 4631426J05 gene	1.06	0.613	1.28	0.33	-1.07	0.588	-1.36	0.275	-0.02
1450373_at	Prp15	proline-rich protein 15	1.3	0.525	-1.37	0.572	1.25	0.464	-1.44	0.551	-0.07
1438530_at	Tfpi	tissue factor pathway inhibitor	1.17	0.301	1.32	0.245	-1.27	0.042	-1.15	0.436	0.01
1423405_at	Timp4	tissue inhibitor of metalloproteinase 4	-1.06	0.77	-1.07	0.729	1.39	0.34	1.49	0.105	0.19
1439226_at	Dock8	Dedicator of cytokinesis 8	-1.02	0.905	1.15	0.459	1.14	0.606	-1.92	0.051	-0.16
1427358_a_at	Dapk1	death associated protein kinase 1	1.03	0.884	-1.02	0.949	1.26	0.386	-1.26	0.458	0
1423552_at	Leprotl1	leptin receptor overlapping transcript-like 1	1.08	0.584	-1.04	0.821	1.24	0.38	-1.43	0.236	-0.04
1420262_at	---	---	1.24	0.49	1.38	0.49	-1.52	0.318	-1.16	0.745	-0.02
1430560_at	Ppp1r10	protein phosphatase 1, regulatory subunit 10	1.17	0.509	-1.24	0.599	1.29	0.121	-1.09	0.733	0.04
1432492_a_at	Haao	3-hydroxyanthranilate 3,4-dioxygenase	-1.07	0.603	1.02	0.934	1.32	0.595	-2.54	0.176	-0.32
1423611_at	Akp2	alkaline phosphatase 2, liver	-1.09	0.561	-1.13	0.341	1.47	0.079	1.05	0.744	0.08
1451635_at	D630002G06Rik ///	RIKEN cDNA D630002G06 gene /// RIKEN cDNA C730048C13 gene /// similar to	1.05	0.509	1.27	0.468	-1.05	0.899	-1.2	0.761	0.02
1434825_at	LOC381742	similar to CAGL79	-1.16	0.473	1.17	0.394	1.24	0.513	-1.31	0.435	-0.01
1437841_x_at	Csdc2	cold shock domain containing C2, RNA binding	-1.01	0.98	-1.59	0.425	1.65	0.07	2.15	0.195	0.3
1457378_at	Mrpl54	Mitochondrial ribosomal protein L54	-1.67	0.003	1.6	0.092	1.07	0.696	-1.16	0.578	-0.04
1417304_at	Chrd	chordin	-1.14	0.864	1.2	0.455	1.2	0.076	-1.13	0.6	0.03
1417715_a_at	Got2	glutamate oxaloacetate transaminase 2, mitochondrial	-1.1	0.425	-1.18	0.167	1.52	0.03	1.23	0.173	0.12
1451770_s_at	Dhx9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	-1.05	0.143	1.03	0.734	1.29	0.15	-1.23	0.272	0.01
1455563_at	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	1.15	0.301	-1	0.993	1.12	0.42	-1.19	0.526	0.02
1420501_at	Dnajc1	DnaJ (Hsp40) homolog, subfamily C, member 1	1.31	0.098	1.14	0.57	-1.22	0.319	-1.31	0.359	-0.02
1418662_at	2210012G02Rik	RIKEN cDNA 2210012G02 gene	1.31	0.297	1.08	0.638	-1.13	0.213	-1.01	0.939	0.06
1418203_at	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1	-1.06	0.663	1.3	0.423	1.03	0.848	-1.64	0.315	-0.09
1460549_a_at	Cdc23	CDC23 (cell division cycle 23, yeast, homolog)	-1.07	0.848	-1.46	0.208	1.65	0.278	1.27	0.51	0.1
1440559_at	Hmga2-ps1	high mobility group AT-hook 2, pseudogene 1	-1.08	0.762	-1.18	0.525	1.5	0.071	1.19	0.602	0.11
1435528_at	D2Bwg1335e	DNA segment, Chr 2, Brigham & Women's Genetics 1335 expressed	1.01	0.965	-1.03	0.841	1.3	0.02	-1.03	0.736	0.06
1438404_at	Rnf144	ring finger protein 144	1.04	0.819	1.3	0.457	-1.07	0.709	-1.68	0.029	-0.1
1419113_at	Ap1g2	adaptor protein complex AP-1, gamma 2 subunit	-1.19	0.337	1.28	0.053	1.15	0.362	-1.63	0.096	-0.09
1455838_at	Slfnl1	schlafen like 1	-1.46	0.546	1.03	0.961	1.56	0.025	-5.69	0.021	-1.14
1435479_at	---	---	-1.31	0.214	-1.08	0.895	1.58	0.398	1.18	0.823	0.09
1416172_at	Pes1	pescadillo homolog 1, containing BRCT domain (zebrafish)	1.27	0.058	-1.14	0.277	1.12	0.267	-1.27	0.397	0
1457578_at	Ppargc1b	Peroxisome proliferative activated receptor, gamma, coactivator 1 beta	-1.08	0.853	1.26	0.649	1.09	0.808	-1.06	0.863	0.05
1460608_at	Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	1.47	0.711	-1.4	0.47	1.09	0.804	-3.28	0.056	-0.53
1440058_at	Slc22a14	solute carrier family 22 (organic cation transporter), member 14	1.16	0.8	-1.1	0.904	1.21	0.614	-1.16	0.698	0.03
1454621_s_at	5730472N09Rik	RIKEN cDNA 5730472N09 gene	-1.21	0.298	-1.02	0.905	1.46	0.056	1.81	0.249	0.26
1418031_at	Myo9b	myosin IXb	-1.19	0.064	1.32	0.057	1.11	0.286	-1.4	0.047	-0.04
1456795_at	D330027G24Rik	RIKEN cDNA D330027G24 gene	1.04	0.955	-1.14	0.555	1.36	0.132	-2.17	0.07	-0.23
1456365_at	LOC629750 /// LOC	similar to ubiquitin A-52 residue ribosomal protein fusion product 1 /// similar to ub	-1.09	0.661	1.32	0.116	1.03	0.885	-1.75	0.322	-0.12
1434969_at	Brunol5	bruno-like 5, RNA binding protein (Drosophila)	1.29	0.513	-1.22	0.565	1.17	0.344	-1.67	0.303	-0.11
1438559_x_at	Slc44a2	solute carrier family 44, member 2	-1.2	0.396	1.32	0.073	1.12	0.707	-1.75	0.199	-0.13
1452175_at	1810026J23Rik	RIKEN cDNA 1810026J23 gene	-1.12	0.399	-1.07	0.727	1.45	0.084	1.48	0.29	0.19
1424271_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	1.09	0.808	-1.02	0.968	1.21	0.471	-1.64	0.41	-0.09
1447245_at	---	Transcribed locus	-2.07	0.329	1.07	0.921	1.72	0.281	-1.2	0.53	-0.12
1420238_at	---	---	-1.52	0.134	1.81	0.348	-1.23	0.788	1.03	0.895	0.02

1456557_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	1.25	0.081	1.12	0.719	-1.1	0.558	-1.43	0.521	-0.04
1457130_at	2900035I09Rik	RIKEN cDNA 2900035I09 gene	1.05	0.889	-1.9	0.157	1.7	0.301	-1.44	0.579	-0.15
1438521_at	Ostm1	Osteopetrosis associated transmembrane protein 1	1.79	0.494	1.06	0.932	-2.34	0.227	-1.29	0.338	-0.2
1446726_at	LOC665490 /// LOC	hypothetical protein LOC665490 /// hypothetical protein LOC669883 /// hypothetic	-1.33	0.473	1.07	0.891	1.46	0.533	-1.21	0.524	0
1441054_at	Apol2	apolipoprotein L, 2	-3.24	0.18	-1.1	0.726	2.06	0.076	11.49	0.178	2.3
1424954_a_at	---	---	1.1	0.61	-1	0.997	1.18	0.457	-1.19	0.498	0.02
1453256_at	Polr3c	polymerase (RNA) III (DNA directed) polypeptide C	1.02	0.844	-1.05	0.292	1.3	0.084	-1.02	0.824	0.06
1457225_at	Olfr288	olfactory receptor 288	-1.03	0.975	1.05	0.782	1.26	0.529	-3.53	0.195	-0.56
1432855_at	Kctd3	potassium channel tetramerisation domain containing 3	-1.37	0.596	1.94	0.176	-1.65	0.324	1.15	0.774	0.02
1424290_at	BC010311	cDNA sequence BC010311	-1.09	0.676	-1.05	0.721	1.4	0.154	1.11	0.596	0.09
1425305_at	Zfp295	zinc finger protein 295	1.06	0.451	-1.01	0.957	1.23	0.155	-1.21	0.388	0.02
1432433_at	4930524N10Rik	RIKEN cDNA 4930524N10 gene	-1.8	0.314	1.55	0.096	1.18	0.377	-1.57	0.614	-0.16
1417003_at	0610012G03Rik ///	RIKEN cDNA 0610012G03 gene /// hypothetical protein LOC638521	1.05	0.878	-1.14	0.808	1.35	0.343	-1.05	0.792	0.05
1447252_s_at	Mep1a	meprin 1 alpha	1.53	0.516	-1.64	0.38	1.14	0.696	-1.07	0.668	-0.01
1424544_at	Nrbp2	nuclear receptor binding protein 2	1.22	0.139	1.31	0.355	-1.33	0.172	-1.01	0.974	0.05
1418740_at	Spert	spermatid associated	1.01	0.843	-1.24	0.678	1.46	0.108	-1.72	0.461	-0.12
1433645_at	2210409B22Rik	RIKEN cDNA 2210409B22 gene	-1.05	0.313	1.5	0.014	-1.2	0.178	1.2	0.413	0.11
1425110_at	Sorcs3	sortilin-related VPS10 domain containing receptor 3	-2.03	0.295	1.7	0.098	1.09	0.683	-1.31	0.382	-0.14
1453895_at	C330026N13Rik	RIKEN cDNA C330026N13 gene	1.05	0.802	1.39	0.57	-1.18	0.252	-1.38	0.145	-0.03
1441175_at	Arx	Aristaless related homeobox gene (Drosophila)	-1.34	0.652	1.13	0.422	1.41	0.564	-1.32	0.641	-0.03
1450890_a_at	Abi1	abl-interactor 1	1.02	0.891	-1.03	0.812	1.29	0.187	-1.59	0.064	-0.08
1440926_at	Flt1	FMS-like tyrosine kinase 1	-1.05	0.827	1.31	0.526	1.02	0.951	-1.1	0.648	0.04
1422876_at	Capn9 /// LOC6397	calpain 9 (nCL-4) /// similar to calpain 9 (nCL-4)	1.06	0.902	-1.03	0.944	1.25	0.675	-1.78	0.328	-0.12
1418056_at	Iqcf3	IQ motif containing F3	-1.66	0.102	-1.31	0.519	1.91	0.231	1.27	0.532	0.05
1422301_at	Ftl2	ferritin light chain 2	-1.3	0.476	1.16	0.077	1.35	0.323	-1.02	0.873	0.05
1429865_at	4931417G12Rik	RIKEN cDNA 4931417G12 gene	1.31	0.303	-1.08	0.831	1.04	0.93	-1.32	0.711	-0.01
1422673_at	Prkcm	protein kinase C, mu	1.12	0.47	1.41	0.505	-1.32	0.31	-1.64	0.142	-0.11
1436319_at	Sulf1	sulfatase 1	1.18	0.406	-1.03	0.937	1.14	0.673	-1.39	0.571	-0.03
1419682_a_at	Trp53rk /// 2810408	Trp53 regulating kinase /// RIKEN cDNA 2810408M09 gene	1.01	0.964	-1.14	0.544	1.39	0.209	-1.18	0.446	0.02
1445073_at	---	---	-1.01	0.983	1.88	0.16	-2.44	0.168	1.08	0.69	-0.12
1420541_at	Rdh16	retinol dehydrogenase 16	-1.05	0.776	-1.24	0.623	1.53	0.502	1.04	0.893	0.07
1439921_at	---	---	-1.11	0.697	1.68	0.316	-1.43	0.595	1.16	0.551	0.07
1422547_at	Ranbp1	RAN binding protein 1	-1.02	0.325	-1.03	0.675	1.33	0.07	1.31	0.194	0.15
1436100_at	Sh2d5	SH2 domain containing 5	-1.5	0.651	-1.43	0.454	1.92	0.037	1.08	0.838	0.02
1432146_at	Catsper3	cation channel, sperm associated 3	-1.08	0.608	1.49	0.323	-1.16	0.794	1.23	0.637	0.12
1433861_at	Cc2d1b	coiled-coil and C2 domain containing 1B	1.23	0.009	1.13	0.679	-1.08	0.724	-1.63	0.206	-0.09
1451245_at	Lrrc3b	leucine rich repeat containing 3B	1.09	0.766	1.26	0.487	-1.07	0.434	-1.04	0.843	0.06
1428206_at	Ccdc69	coiled-coil domain containing 69	1.29	0.592	-1.34	0.6	1.24	0.674	-1.32	0.351	-0.03
1444382_at	4930579G22Rik	RIKEN cDNA 4930579G22 gene	1.24	0.36	-1.11	0.752	1.14	0.577	-1.44	0.419	-0.04
1450548_at	Htr1f	5-hydroxytryptamine (serotonin) receptor 1F	1.11	0.588	1.4	0.3	-1.29	0.596	-1.67	0.368	-0.11
1416434_at	Bcl2l10	Bcl2-like 10	-1.14	0.601	-2.09	0.085	1.93	0.052	4.14	0.029	0.71
1432415_at	Rab3c	RAB3C, member RAS oncogene family	1.51	0.68	-2.71	0.107	1.4	0.469	-1.17	0.524	-0.24
1439697_at	Il1rap	interleukin 1 receptor accessory protein	1.13	0.79	1.2	0.558	-1.05	0.948	-2.15	0.477	-0.22
1438383_x_at	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	-1.03	0.799	1.04	0.4	1.27	0.034	-1.21	0.27	0.02
1422323_a_at	Lbx1	ladybird homeobox homolog 1 (Drosophila)	1.07	0.805	1.5	0.37	-1.41	0.209	-1.09	0.847	0.02
1433029_at	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	-1.51	0.497	1.26	0.675	1.35	0.442	-1.08	0.894	0.01
1425404_a_at	Tmem110	transmembrane protein 110	-1.54	0.15	1.5	0.026	1.13	0.139	-1.08	0.621	0
1451528_at	BC025833	cDNA sequence BC025833	-1.16	0.664	-1.16	0.279	1.56	0.43	1.15	0.861	0.1
1454200_at	Zfhx1b	zinc finger homeobox 1b	-1	0.992	1.76	0.035	-1.91	0.207	1.16	0.662	0
1453172_at	Stch	stress 70 protein chaperone, microsome-associated, human homolog	1.41	0.122	-1.05	0.826	-1.08	0.691	1.41	0.077	0.17
1432464_a_at	2310057J16Rik	RIKEN cDNA 2310057J16 gene	1.13	0.444	-1.09	0.435	1.24	0.077	-1.05	0.894	0.06
1452864_at	Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	-1.18	0.461	1.48	0.427	-1.05	0.244	2.11	0.04	0.34
1459890_s_at	1110008P14Rik	RIKEN cDNA 1110008P14 gene	1.11	0.698	1.22	0.216	-1.04	0.842	-1.14	0.645	0.04

1429049_at	Nuak2	NUAK family, SNF1-like kinase, 2	1.05	0.909	-1.04	0.699	1.27	0.202	-1.67	0.132	-0.1
1435829_at	B930008K04Rik	RIKEN cDNA B930008K04 gene	1.12	0.588	1.18	0.353	-1.03	0.867	-1.51	0.259	-0.06
1447623_s_at	C130009A20Rik	RIKEN cDNA C130009A20 gene	1.08	0.773	1.3	0.655	-1.11	0.635	-1.64	0.306	-0.09
1441593_at	Pten	Phosphatase and tensin homolog	1.81	0.158	1.1	0.682	-2.66	0.031	-1.7	0.491	-0.36
1424180_a_at	Thrap4	thyroid hormone receptor associated protein 4	-1.14	0.141	-1.04	0.86	1.45	0.061	1.28	0.25	0.14
1430854_at	Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucos	1.25	0.027	1.64	0.518	-2.48	0.271	-1.07	0.723	-0.17
1429719_at	Foxp4	forkhead box P4	-1.07	0.518	1.11	0.352	1.24	0.509	-1.14	0.732	0.03
1418812_a_at	Barhl1	BarH-like 1 (Drosophila)	1.79	0.028	1.09	0.679	-2.44	0.397	-1.17	0.79	-0.18
1450468_at	Myoc	myocilin	-3.09	0.14	1.44	0.303	1.53	0.226	-1.05	0.897	-0.3
1420535_a_at	Nub1	negative regulator of ubiquitin-like proteins 1	1.28	0.069	1.04	0.636	-1.03	0.772	-1.09	0.584	0.05
1437737_at	AV340375	expressed sequence AV340375	1.22	0.159	1.09	0.673	-1.02	0.935	-1.09	0.659	0.05
1452375_at	Aldh4a1	aldehyde dehydrogenase 4 family, member A1	-1.08	0.793	-1.05	0.852	1.41	0.25	1.2	0.577	0.12
1460688_s_at	AA407659	expressed sequence AA407659	-1.01	0.96	1.06	0.588	1.24	0.094	-1.44	0.153	-0.04
1420235_at	Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antig	-1.7	0.549	-1.34	0.456	1.95	0.143	2.53	0.144	0.36
1452956_a_at	D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed	-1.09	0.176	1.21	0.159	1.16	0.328	-1.12	0.123	0.04
1426564_at	Zfp553	zinc finger protein 553	-1.14	0.677	1.22	0.491	1.19	0.379	-1.06	0.734	0.05
1423796_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associat	-1.04	0.907	-1.15	0.357	1.45	0.014	1.13	0.213	0.1
1419423_at	Stab2	stabilin 2	-1.23	0.191	1.35	0.119	1.12	0.608	-1.03	0.899	0.05
1431985_at	2210010B09Rik	RIKEN cDNA 2210010B09 gene	1.02	0.902	-1.2	0.248	1.43	0.352	-1.56	0.016	-0.08
1442132_at	BC057552	CDNA sequence BC057552	-1.02	0.968	1.23	0.419	1.07	0.651	-1.32	0.017	-0.01
1437414_at	Zfp217	zinc finger protein 217	-1.08	0.592	1.06	0.567	1.29	0.159	-1.1	0.309	0.05
1429853_at	1700018C11Rik	RIKEN cDNA 1700018C11 gene	-1.32	0.532	-1.17	0.453	1.67	0.156	1.24	0.624	0.11
1418970_a_at	Bcl10	B-cell leukemia/lymphoma 10	-1.11	0.131	1.13	0.359	1.25	0.146	-1.55	0.11	-0.07
1448374_at	Med28	mediator of RNA polymerase II transcription, subunit 28 homolog (yeast)	1.2	0.432	1.15	0.387	-1.07	0.669	-1.4	0.12	-0.03
1433907_at	Pknox2	Pbx/knotted 1 homeobox 2	1.47	0.208	-1.73	0.395	1.24	0.3	-1.09	0.699	-0.03
1423476_at	Tscot	thymic stromal cotransporter	1.14	0.874	-1.06	0.837	1.2	0.365	-1.18	0.65	0.03
1458689_at	Atg10	Autophagy-related 10 (yeast)	1.21	0.656	-1.05	0.906	1.12	0.583	-1.3	0.291	0
1457126_at	Myl4	myosin, light polypeptide 4	-1.58	0.429	1.09	0.886	1.57	0.05	-1.05	0.944	0.01
1452140_at	Tbc1d20	TBC1 domain family, member 20	-1.1	0.784	1.11	0.653	1.27	0.424	-1.28	0.643	0
1447550_at	LOC666892 /// LOC	hypothetical protein LOC666892 /// hypothetical protein LOC671332	-1.09	0.781	1.53	0.48	-1.18	0.455	1.05	0.899	0.08
1422151_at	Gats	opposite strand transcription unit to Stag3	-1.74	0.547	1.01	0.978	1.7	0.379	-3.41	0.275	-0.61
1424866_at	Usp43	ubiquitin specific peptidase 43	-1.14	0.759	1.25	0.25	1.16	0.17	-1.11	0.723	0.04
1430453_a_at	Bcl2l2	Bcl2-like 2	1.15	0.624	1.18	0.781	-1.05	0.619	-2.44	0.193	-0.29
1430361_at	2610005M20Rik	RIKEN cDNA 2610005M20 gene	-2.53	0.173	1.31	0.522	1.58	0.266	-1.28	0.235	-0.23
1448788_at	Cd200	Cd200 antigen	1.06	0.773	1.31	0.135	-1.09	0.21	-1.82	0.085	-0.14
1417541_at	Hells	helicase, lymphoid specific	-1.61	0.29	-1.39	0.154	1.94	0.211	1.37	0.318	0.08
1418028_at	Dct	dopachrome tautomerase	-1.21	0.741	1.42	0.192	1.04	0.897	-1.07	0.722	0.05
1449478_at	Mmp7	matrix metallopeptidase 7	2.04	0.469	-3.3	0.155	-1.06	0.922	1.42	0.329	-0.22
1428106_at	1300001I01Rik	RIKEN cDNA 1300001I01 gene	-1.31	0.173	-1.21	0.003	1.7	0.023	1.24	0.165	0.1
1447011_at	Ergic2	ERGIC and golgi 2	1.42	0.417	-1.4	0.37	1.16	0.379	-1.08	0.863	0.02
1459356_at	Dst	Dystonin	-1.2	0.645	1.46	0.222	-1	0.989	1.16	0.767	0.1
1429271_at	9130011E15Rik	RIKEN cDNA 9130011E15 gene	-1.45	0.326	1.28	0.29	1.32	0.245	-1.57	0.111	-0.11
1460610_at	9430057O19Rik	RIKEN cDNA 9430057O19 gene	-1.11	0.544	1.28	0.347	1.11	0.322	-1.17	0.265	0.03
1423672_at	2510042P03Rik	RIKEN cDNA 2510042P03 gene	-1.03	0.767	1.11	0.047	1.2	0.475	-1.43	0.475	-0.04
1442444_at	Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	-1.07	0.916	-1.03	0.975	1.38	0.356	1.01	0.919	0.07
1437663_at	Pigv	phosphatidylinositol glycan anchor biosynthesis, class V	-1.04	0.815	1.24	0.219	1.09	0.57	-1.35	0.287	-0.02
1460534_at	5530401A10Rik	RIKEN cDNA 5530401A10 gene	1.2	0.818	-1.16	0.81	1.22	0.681	-3.28	0.246	-0.5
1458261_at	Cbll1	Casitas B-lineage lymphoma-like 1	1.06	0.723	1.39	0.607	-1.19	0.22	-1.32	0.523	-0.01
1429471_at	1110017D15Rik	RIKEN cDNA 1110017D15 gene	-1.07	0.768	1.13	0.829	1.23	0.521	-1.57	0.619	-0.07
1444457_at	---	---	1.31	0.69	1.19	0.185	-1.27	0.465	-1.61	0.014	-0.09
1433984_a_at	Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	-1.13	0.448	1.09	0.3	1.31	0.148	-1.14	0.312	0.03
1446441_at	Slc20a1	solute carrier family 20, member 1	-1.07	0.933	1.51	0.204	-1.19	0.508	1.42	0.331	0.17
1432126_at	1700072H12Rik	RIKEN cDNA 1700072H12 gene	1.21	0.434	-1.41	0.503	1.37	0.372	-2.51	0.336	-0.33

1452886_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.13	0.673	-1.17	0.707	1.3	0.501	-1.28	0.26	0
1417196_s_at	Wwc2	WW, C2 and coiled-coil domain containing 2	1.04	0.797	1.32	0.21	-1.07	0.673	-1.47	0.122	-0.05
1417253_at	Frg1	FSHD region gene 1	1.34	0.113	1.04	0.756	-1.09	0.595	-1.05	0.694	0.06
1452051_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	-1.1	0.112	1.05	0.523	1.33	0.035	-1.38	0.168	-0.02
1420512_at	Dkk2	dickkopf homolog 2 (Xenopus laevis)	1.2	0.306	1.18	0.829	-1.09	0.833	-1.56	0.481	-0.07
1457400_at	Snx19	sorting nexin 19	-1.11	0.194	1.11	0.901	1.28	0.706	-1.43	0.549	-0.04
1451810_at	ORF63	open reading frame 63	-1.06	0.883	1.18	0.584	1.17	0.627	-4.32	0.055	-0.76
1449896_at	---	---	-1.08	0.395	1.28	0.224	1.08	0.481	-1.03	0.958	0.06
1454891_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	1.11	0.056	1.23	0.073	-1.05	0.511	-1.01	0.954	0.07
1457391_at	Vamp3	Vesicle-associated membrane protein 3	1.33	0.564	-1.38	0.045	1.24	0.351	-3.39	0.242	-0.55
1420439_at	Tsx	testis specific X-linked gene	-1.28	0.629	1.16	0.73	1.35	0.583	-2.05	0.155	-0.2
1437825_at	Lrrc4c	leucine rich repeat containing 4C	1.08	0.843	1.46	0.417	-1.33	0.261	-5.23	0.032	-1
1455996_x_at	Prap1	proline-rich acidic protein 1	1.33	0.63	-1.72	0.426	1.38	0.191	-1.55	0.348	-0.14
1458920_at	Stx6	Syntaxin 6	1.18	0.754	1.25	0.562	-1.16	0.578	-1.8	0.035	-0.13
1455798_at	Galk2	galactokinase 2	-1.17	0.243	1.18	0.128	1.26	0.328	-1.35	0.081	-0.02
1425525_a_at	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	-1.04	0.669	1.31	0.023	1.02	0.752	-1.17	0.622	0.03
1454944_at	Hic2	hypermethylated in cancer 2	1.26	0.244	1.11	0.883	-1.08	0.662	-1.01	0.972	0.07
1426901_s_at	Camta2	calmodulin binding transcription activator 2	-1.03	0.35	1.14	0.101	1.19	0.121	-1.16	0.583	0.03
1417647_at	Snx5	sorting nexin 5	-1.17	0.643	1.35	0.04	1.08	0.414	-1.74	0.156	-0.12
1422821_s_at	Stard5	StAR-related lipid transfer (START) domain containing 5	1.07	0.679	-1.08	0.592	1.3	0.225	-1.14	0.305	0.04
1421268_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1	0.992	-1.06	0.887	1.35	0.386	-1.13	0.706	0.04
1434536_at	Gpr75	G protein-coupled receptor 75	-1.45	0.433	1.73	0.44	-1.14	0.498	1.42	0.552	0.14
1445812_at	---	---	-2.01	0.104	1.02	0.969	1.78	0.361	-1.25	0.646	-0.12
1458259_x_at	Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	1.39	0.344	1.11	0.776	-1.26	0.514	-1.94	0.451	-0.18
1428442_at	BC029722	cDNA sequence BC029722	1.03	0.692	1.28	0.065	-1.02	0.862	-1.45	0.201	-0.04
1437353_at	Setd1b	SET domain containing 1B	-1.21	0.129	-1.06	0.642	1.52	0.144	1.21	0.16	0.11
1421920_a_at	Ccr9	chemokine (C-C motif) receptor 9	1.12	0.907	1.2	0.733	-1.03	0.896	-2.98	0.032	-0.42
1453378_at	Zfpn1a3	zinc finger protein, subfamily 1A, 3 (Aiolos)	1.06	0.897	1.26	0.713	-1.02	0.96	-1.61	0.364	-0.08
1452757_s_at	Hba-a1	hemoglobin alpha, adult chain 1	1.07	0.6	1.48	0.088	-1.34	0.007	-1.15	0.222	0.01
1420480_at	Cnnm3	cyclin M3	-1.02	0.953	-1.02	0.95	1.34	0.162	1.21	0.469	0.13
1430208_at	Krt42	keratin 42	-1.15	0.48	1.46	0.106	-1.04	0.723	1.12	0.478	0.1
1433725_at	Acvr1b	activin A receptor, type 1B	-1.18	0.403	1.13	0.19	1.32	0.04	-1.49	0.184	-0.06
AFFX-r2-Bs-phe-5_a	---	---	1.43	0.557	-1.18	0.374	1.02	0.959	-2.2	0.493	-0.23
1447847_x_at	---	---	1.35	0.649	-1.54	0.278	1.3	0.45	-1.3	0.561	-0.05
1420475_at	Mtpn	myotrophin	1.06	0.663	-1.07	0.459	1.3	0.33	-1.2	0.438	0.02
1420876_a_at	6-Sep	septin 6	-1.18	0.071	1.06	0.879	1.39	0.213	-2.12	0.091	-0.21
1449212_at	Pip	prolactin induced protein	1.36	0.718	-1.32	0.527	1.18	0.469	-1.98	0.13	-0.19
1421685_at	Clec4b1	C-type lectin domain family 4, member b1	-1.02	0.925	1.72	0.252	-1.66	0.022	2.59	0.047	0.4
1428735_at	Cd69	CD69 antigen	1.26	0.227	-1.26	0.595	1.24	0.589	-2.72	0.036	-0.37
1424179_at	Plekhj1	pleckstrin homology domain containing, family J member 1	1.33	0.446	-1.01	0.957	-1.03	0.914	1.03	0.896	0.08
1449059_a_at	Oxct1	3-oxoacid CoA transferase 1	-1.18	0.003	1.36	0.088	1.09	0.292	-1.12	0.545	0.04
1453936_at	---	---	-1.34	0.402	-1.51	0.397	1.89	0.047	1.42	0.128	0.11
1417329_at	Slc23a2	solute carrier family 23 (nucleobase transporters), member 2	-1.02	0.754	1.04	0.758	1.28	0.053	-1.34	0.28	-0.01
1442638_at	---	---	-2.61	0.031	-1.29	0.426	2.14	0.051	1.14	0.778	-0.16
1423495_at	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	1.16	0.524	-1.38	0.085	1.41	0.202	-1.07	0.576	0.03
1431226_a_at	Fndc4	fibronectin type III domain containing 4	1.07	0.75	1.25	0.129	-1.03	0.884	-1.02	0.946	0.07
1434747_at	Ctrc	chymotrypsin C (caldecrin)	1.24	0.065	1.54	0.191	-1.95	0.161	-2.09	0.053	-0.31
1419009_at	Actl7a	actin-like 7a	-1.3	0.356	-1.48	0.539	1.85	0.08	1.16	0.733	0.06
1426686_s_at	Map3k3	mitogen activated protein kinase kinase kinase 3	1.17	0.022	1.13	0.353	-1.01	0.956	-1.24	0.447	0.01
1434167_at	Slc35e4	solute carrier family 35, member E4	-1.29	0.315	1.42	0.551	1.1	0.78	-1.81	0.468	-0.14
1419649_s_at	Myo1c	myosin IC	1.09	0.266	1.23	0.016	-1.02	0.882	-1.56	0.068	-0.07
1448999_at	Trappc5	trafficking protein particle complex 5	-1.07	0.761	1.12	0.381	1.24	0.05	-1.34	0.114	-0.01
1433354_at	D530015H24Rik	RIKEN cDNA D530015H24 gene	1.4	0.303	1.08	0.852	-1.22	0.55	-1.43	0.465	-0.04

1418937_at	Dio2	deiodinase, iodothyronine, type II	-1.28	0.665	1.74	0.433	-1.29	0.29	2.29	0.081	0.36
1449188_at	Midn	midnolin	1.2	0.294	1.16	0.309	-1.07	0.777	-1.24	0.408	0.01
1418304_at	Pcdh21	protocadherin 21	1.16	0.367	-1.27	0.67	1.35	0.312	-1.36	0.455	-0.03
1443111_at	Plekha1	pleckstrin homology domain containing, family A (phosphoinositide binding specif	1.24	0.73	1.34	0.193	-1.39	0.244	-1.48	0.046	-0.07
1421235_s_at	Recql5	RecQ protein-like 5	1.03	0.842	-1.23	0.134	1.45	0.274	-1	0.943	0.06
1420573_at	Hoxd1	homeo box D1	1.19	0.695	-1.12	0.799	1.21	0.791	-2.07	0.263	-0.2
1426838_at	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	1.33	0.107	-1.01	0.93	-1.02	0.905	1.52	0.276	0.21
1421941_at	Camk4	calcium/calmodulin-dependent protein kinase IV	-1.36	0.603	1.01	0.987	1.55	0.172	-1.08	0.869	0.03
1452499_a_at	Kif2a	kinesin family member 2A	-1	0.985	-1.13	0.678	1.42	0.16	2.16	0.256	0.36
1423215_at	Spcs2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	-1.05	0.393	1.38	0.225	-1.04	0.558	1.09	0.452	0.1
1417167_at	Exosc5	exosome component 5	-1.13	0.711	-1.19	0.171	1.57	0.065	1.04	0.796	0.07
1427628_at	Tcrb-V8.2	T-cell receptor beta, variable 8.2	-4.25	0.053	1.46	0.259	1.6	0.262	-1.32	0.151	-0.63
1447431_at	Dera	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	1.05	0.96	-1.13	0.856	1.37	0.465	-1.27	0.531	0
1435736_x_at	Rabl4	RAB, member of RAS oncogene family-like 4	-1.18	0.453	1.39	0.268	1.06	0.652	-1.22	0.467	0.01
1437059_at	Sox21	SRY-box containing gene 21	-1.03	0.957	-1.36	0.59	1.59	0.114	1.62	0.021	0.21
1453743_x_at	Phf14	PHD finger protein 14	1.58	0.407	1.03	0.953	-1.45	0.069	-1.45	0.269	-0.07
1450759_at	Bmp6	bone morphogenetic protein 6	-1	0.967	-1.09	0.848	1.39	0.137	1.02	0.926	0.08
1426627_at	Map3k7	mitogen activated protein kinase kinase kinase 7	1.19	0.594	-1.17	0.693	1.25	0.507	-1.12	0.695	0.04
1455737_at	C030002B11Rik	RIKEN cDNA C030002B11 gene	-1.08	0.588	1.27	0.409	1.1	0.448	-1.31	0.331	0
1430052_at	C030048H21Rik	RIKEN cDNA C030048H21 gene	1.27	0.396	-1.27	0.625	1.24	0.434	-1.16	0.544	0.02
1427373_at	Amigo1	adhesion molecule with Ig like domain 1	-1.45	0.038	1.41	0.46	1.2	0.526	-2.74	0.048	-0.4
1453089_at	3110079O15Rik	RIKEN cDNA 3110079O15 gene	-1.15	0.854	1.22	0.636	1.21	0.58	-1.37	0.164	-0.02
1454672_at	---	---	1.38	0.27	1.29	0.57	-1.58	0.154	-1.17	0.665	-0.02
1450017_at	Ccng1	cyclin G1	1.12	0.324	-1.03	0.841	1.21	0.114	-1.12	0.234	0.05
1450184_s_at	Tef	thyrotroph embryonic factor	1.31	0.492	-1.72	0.313	1.41	0.638	-1.07	0.916	-0.02
1441073_at	---	---	2.03	0.388	-1.39	0.497	-1.81	0.063	1.06	0.896	-0.03
1445296_at	D7Ertd715e	DNA segment, Chr 7, ERATO Doi 715, expressed	-1.98	0.14	1.22	0.313	1.57	0.334	-1.48	0.713	-0.17
1431207_at	2900024O10Rik	RIKEN cDNA 2900024O10 gene	-1.37	0.291	1.73	0.07	-1.19	0.324	1.02	0.955	0.05
1423431_a_at	Mybbp1a	MYB binding protein (P160) 1a	1.09	0.424	-1.04	0.692	1.24	0.41	-1.18	0.125	0.03
1446891_at	Als2cr13	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (hum	-1.18	0.707	1.13	0.803	1.33	0.481	-1.34	0.748	-0.02
1424819_a_at	Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	-1.13	0.249	1.13	0.596	1.28	0.159	-1.32	0.168	-0.01
1440442_at	Map2k7	mitogen activated protein kinase kinase 7	1.04	0.953	-1.12	0.857	1.36	0.569	-2.27	0.399	-0.24
1423370_a_at	Csnk1g2	casein kinase 1, gamma 2	1.25	0.476	1.14	0.261	-1.11	0.256	-1.18	0.129	0.03
1448189_a_at	Fliih	flightless I homolog (Drosophila)	-1.01	0.881	1.03	0.819	1.28	0.11	-1.21	0.395	0.02
1425079_at	Tm6sf2	transmembrane 6 superfamily member 2	1.1	0.722	1.28	0.016	-1.09	0.642	-1.19	0.769	0.03
1456515_s_at	Tcfl5	transcription factor-like 5 (basic helix-loop-helix)	-1.21	0.763	-1.17	0.743	1.62	0.091	1.06	0.914	0.08
1441183_at	Jmjd2b	Jumonji domain containing 2B	1.22	0.355	1.23	0.472	-1.18	0.37	-1.16	0.521	0.03
1439038_at	9130227C08Rik	RIKEN cDNA 9130227C08Rik gene	1.14	0.774	-1.05	0.783	1.21	0.392	-1.47	0.188	-0.04
1425080_at	Zfp286	zinc finger protein 286	-1.15	0.261	1.04	0.923	1.4	0.521	-1.18	0.865	0.03
1437979_at	Zcchc2	Zinc finger, CCHC domain containing 2	-1.53	0.554	1.04	0.941	1.61	0.206	-1.21	0.441	-0.02
1423691_x_at	Krt8	keratin 8	-1.01	0.961	1.32	0.13	-1.01	0.931	4.42	0.094	0.93
1430740_at	---	---	-1.99	0.3	1.82	0.379	-1.02	0.945	1.31	0.568	0.03
1448503_at	Mcl1	myeloid cell leukemia sequence 1	-1.02	0.655	1.2	0.258	1.12	0.591	-1.22	0.346	0.02
1436335_at	Plcl4	phospholipase C-like 4	-1.47	0.503	1.12	0.851	1.5	0.306	-1.06	0.863	0.02
1450579_x_at	Sry	sex determining region of Chr Y	-1.79	0.283	1.94	0.342	-1.24	0.332	1.73	0.167	0.16
1426982_at	Flywch1	FLYWCH-type zinc finger 1	-1.1	0.662	1.19	0.102	1.21	0.129	-1.22	0.463	0.02
1424523_at	Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	-1.19	0.712	1.3	0.121	1.16	0.251	-1.32	0.336	-0.01
1447448_s_at	Klf6	Kruppel-like factor 6	1.07	0.419	1.43	0.144	-1.26	0.317	-1.48	0.119	-0.06
1442113_at	5330417C22Rik	RIKEN cDNA 5330417C22 gene	1.73	0.152	-1.86	0.404	1.03	0.862	-1.13	0.769	-0.06
1435857_s_at	Aplp1	amyloid beta (A4) precursor-like protein 1	-1.08	0.564	1.12	0.793	1.25	0.452	-1.07	0.829	0.06
1421251_at	Zfp40	zinc finger protein 40	1.18	0.569	1.32	0.526	-1.24	0.182	-1.49	0.142	-0.06
1426499_at	Sh3glb2	SH3-domain GRB2-like endophilin B2	1.19	0.673	-1.11	0.52	1.21	0.403	-1.02	0.91	0.07
1430360_at	4833412C15Rik	RIKEN cDNA 4833412C15 gene	1.79	0.31	-1.14	0.457	-1.56	0.255	1.38	0.317	0.12

1416735_at	Asah1	N-acylsphingosine amidohydrolase 1	1.11	0.461	1.27	0.018	-1.09	0.292	-1.04	0.819	0.06
1451727_at	D11Ertd730e	DNA segment, Chr 11, ERATO Doi 730, expressed	1.08	0.173	1.45	0.147	-1.29	0.103	-1.43	0.053	-0.05
1450849_at	Hnrpu	heterogeneous nuclear ribonucleoprotein U	-1.04	0.594	-1.1	0.47	1.43	0.034	1.12	0.53	0.1
1426158_at	Tcrb-V13	T-cell receptor beta, variable 13	1.35	0.544	1.05	0.891	-1.11	0.798	-8.4	0.128	-1.78
1427633_a_at	Pappa	pregnancy-associated plasma protein A	1.54	0.524	1.18	0.724	-1.71	0.341	-1.54	0.503	-0.13
1453091_s_at	Letmd1	LETM1 domain containing 1	1.03	0.878	-1.06	0.6	1.33	0.116	-1.17	0.386	0.03
1458645_at	---	Transcribed locus	1.13	0.854	1.57	0.559	-1.67	0.095	-1.33	0.641	-0.07
1439381_x_at	Marveld1	MARVEL (membrane-associating) domain containing 1	1.25	0.177	-1.18	0.055	1.2	0.336	-1.68	0.209	-0.1
1423321_at	Myadm	myeloid-associated differentiation marker	-1.04	0.817	-1.08	0.371	1.42	0.267	1.03	0.95	0.08
1419957_at	C77144	expressed sequence C77144	1.16	0.81	1.15	0.846	-1.01	0.976	-1.1	0.776	0.05
1446515_at	Jak3	Janus kinase 3	-1.29	0.764	1.01	0.973	1.52	0.182	-1.08	0.867	0.04
1457009_at	Rhobtb3	Rho-related BTB domain containing 3	1.5	0.635	-1.17	0.648	-1.06	0.729	1.07	0.826	0.09
1423705_at	2310057D15Rik	RIKEN cDNA 2310057D15 gene	1.02	0.882	1.31	0.2	-1.02	0.926	-1.17	0.512	0.03
1439457_x_at	Atg12	autophagy-related 12 (yeast)	-1.23	0.578	1.33	0.57	1.16	0.644	-1.86	0.051	-0.15
1459758_at	Usf1	upstream transcription factor 1	-1.3	0.513	-1.28	0.56	1.75	0.208	1.16	0.812	0.08
1427019_at	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	1.56	0.378	-1.72	0.383	1.16	0.596	-1.17	0.656	-0.04
1443414_at	C78513	EST C78513	-1.04	0.92	-1.62	0.039	1.73	0.077	1.21	0.786	0.07
1433600_at	Adra2a	adrenergic receptor, alpha 2a	-1.01	0.966	-5.52	0.088	2.14	0.051	1.38	0.021	-0.75
1421964_at	Notch3	Notch gene homolog 3 (Drosophila)	1.16	0.606	-1.26	0.232	1.35	0.273	-1.49	0.073	-0.06
1420720_at	Nptx2	neuronal pentraxin 2	1.03	0.939	-1.45	0.203	1.59	0.192	-1.13	0.844	0.01
1423596_at	Nek6 /// LOC67424	NIMA (never in mitosis gene a)-related expressed kinase 6 /// similar to NIMA (ne	-1	0.974	1.23	0.439	1.08	0.373	-1.1	0.571	0.05
1442950_at	Nrg3	Neuregulin 3	-1.26	0.628	1.31	0.361	1.2	0.617	-1.18	0.549	0.02
1431212_a_at	3300001M20Rik	RIKEN cDNA 3300001M20 gene	-1.17	0.632	-1.05	0.85	1.49	0.171	1.2	0.335	0.12
1427137_at	Ces5	carboxylesterase 5	1.95	0.047	-1.52	0.137	-1.43	0.499	1.04	0.856	0.01
1448611_at	Wwc2	WW, C2 and coiled-coil domain containing 2	1.17	0.345	1.23	0.041	-1.11	0.489	-1.06	0.758	0.06
1419504_at	Mogat1	monoacylglycerol O-acyltransferase 1	-1.08	0.293	-1.38	0.625	1.65	0.26	1.55	0.303	0.19
1439492_at	C130053K05Rik	RIKEN cDNA C130053K05 gene	-1.17	0.485	1.51	0.427	-1.07	0.76	1.51	0.517	0.2
1442627_at	---	---	1.43	0.31	-1.49	0.093	1.2	0.472	-1.27	0.75	-0.03
1426479_a_at	Tnrc5	trinucleotide repeat containing 5	-1.25	0.483	1.3	0.151	1.2	0.442	-1.28	0.147	-0.01
1434538_x_at	Eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta	1.09	0.329	-1.07	0.514	1.28	0.021	-1.14	0.002	0.04
1453631_at	Stx8	syntaxin 8	-1.27	0.417	1.78	0.088	-1.34	0.275	1.2	0.737	0.09
1445872_at	Nr6a1	nuclear receptor subfamily 6, group A, member 1	1.02	0.946	-1.65	0.447	1.68	0.443	-1.21	0.626	-0.04
1437809_x_at	Ets2	E26 avian leukemia oncogene 2, 3' domain	1.35	0.605	-1.23	0.778	1.14	0.617	-1.22	0.8	0.01
1434107_at	Spata2	spermatogenesis associated 2	1.09	0.516	-1.01	0.901	1.23	0.435	-1.11	0.274	0.05
1432557_at	1700045I11Rik /// L	RIKEN cDNA 1700045I11 gene /// similar to RIKEN cDNA 1700045I11 gene	-1.26	0.477	1.2	0.604	1.32	0.416	-1.61	0.275	-0.09
1428498_at	2610206B13Rik	RIKEN cDNA 2610206B13 gene	1.25	0.19	1.17	0.508	-1.12	0.408	-1.03	0.752	0.07
1439482_at	F830021D11Rik	RIKEN cDNA F830021D11 gene	-1.18	0.033	-1.09	0.426	1.54	0.001	2.3	0.147	0.39
1425801_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	-1.18	0.62	1.24	0.024	1.22	0.373	-1.59	0.099	-0.08
1454592_at	9430012M22Rik	RIKEN cDNA 9430012M22 gene	1.14	0.812	1.45	0.522	-1.39	0.213	-1.93	0.129	-0.18
1444429_at	Lrtm1	leucine-rich repeats and transmembrane domains 1	-1.5	0.054	1.53	0.045	1.12	0.813	-1.36	0.543	-0.06
1421592_at	Ncam2	neural cell adhesion molecule 2	1.31	0.768	1.32	0.579	-1.48	0.656	-1.38	0.703	-0.06
1426623_a_at	Arhgap17	Rho GTPase activating protein 17	-1.09	0.329	1.07	0.598	1.32	0.249	-1.49	0.157	-0.05
1458195_at	Vps13d	vacuolar protein sorting 13 D (yeast)	1.52	0.431	1.27	0.439	-1.92	0.087	-1.21	0.352	-0.09
1432156_a_at	Rnf32	ring finger protein 32	-1.23	0.227	1.47	0.306	1.03	0.905	-1.79	0.096	-0.13
1420793_at	Mup4	major urinary protein 4	1.48	0.597	-1.3	0.337	1.06	0.882	-1.11	0.678	0.03
1437161_x_at	Rbpms	RNA binding protein gene with multiple splicing	1.07	0.384	-1.14	0.176	1.37	0.076	-1.18	0.446	0.03
1418481_at	Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	-1.05	0.955	-1.36	0.632	1.62	0.183	1.59	0.258	0.2
1443621_at	1700010H23Rik	RIKEN cDNA 1700010H23 gene	1	0.99	1.53	0.297	-1.29	0.097	-1.04	0.783	0.05
1424297_at	Zfp282	zinc finger protein 282	-1.03	0.752	1.19	0.571	1.15	0.295	-1.19	0.033	0.03
1419061_at	Rhod	ras homolog gene family, member D	1.21	0.275	1.14	0.437	-1.04	0.824	-2.58	0.08	-0.32
1422670_at	Rnd2	Rho family GTPase 2	-1.03	0.857	1.67	0.005	-1.5	0.039	1.06	0.806	0.05
1429353_a_at	4930511M11Rik	RIKEN cDNA 4930511M11 gene	-1.01	0.957	1.78	0.203	-1.85	0.226	1.01	0.961	-0.02
1442249_at	---	Transcribed locus	1.27	0.804	-1.2	0.113	1.21	0.82	-2.76	0.24	-0.37

1430210_at	C330024D12Rik	RIKEN cDNA C330024D12 gene	-1.05	0.79	1.31	0.349	1.04	0.733	-1.14	0.54	0.04
1426249_at	Adrbk1	adrenergic receptor kinase, beta 1	-1.04	0.513	1.05	0.753	1.3	0.38	-1.27	0.45	0.01
1438352_at	Mapre2	Microtubule-associated protein, RP/EB family, member 2	1.52	0.29	1.27	0.692	-1.9	0	-1.16	0.626	-0.07
1422619_at	Ppap2a	phosphatidic acid phosphatase 2a	1.06	0.718	1.37	0.103	-1.13	0.37	-1.33	0.443	-0.01
1430660_at	5830417I10Rik	RIKEN cDNA 5830417I10 gene	1.48	0.605	-1.53	0.15	1.17	0.359	-1.16	0.722	-0.01
1420971_at	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	1.04	0.862	-1.27	0.582	1.48	0.327	-1.03	0.908	0.06
1444584_at	LOC238535 /// 492	piggyBac transposable element derived 1 (Pgbd1) pseudogene /// RIKEN cDNA 4	1.06	0.872	-1.18	0.19	1.41	0.163	-1.43	0.26	-0.04
1454218_at	4930405D01Rik	RIKEN cDNA 4930405D01 gene	1.45	0.132	-1.35	0.207	1.12	0.737	-1.24	0.654	0
1417889_at	Apobec2	apolipoprotein B editing complex 2	1.23	0.445	-1.27	0.489	1.3	0.383	-1.08	0.423	0.04
1416132_at	C920006C10Rik	RIKEN cDNA C920006C10 gene	-1.02	0.891	1.03	0.916	1.3	0.254	-1.25	0.342	0.01
1437887_at	E130306M17Rik	RIKEN cDNA E130306M17 gene	-1.06	0.738	1.1	0.855	1.27	0.354	-1.55	0.494	-0.06
1433556_at	Centa1	centaurin, alpha 1	-1.15	0.406	-1	0.97	1.44	0.045	1.12	0.279	0.1
1438991_x_at	Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	-1.02	0.834	1.05	0.366	1.29	0.05	-1.21	0.235	0.03
1453015_at	5830471E12Rik	RIKEN cDNA 5830471E12 gene	-1.23	0.036	1.13	0.499	1.37	0.018	-1.18	0.028	0.02
1424650_at	Pdia5	protein disulfide isomerase associated 5	1.25	0.284	1.31	0.194	-1.34	0.233	-1.35	0.417	-0.03
1432167_at	---	---	1.79	0.016	-1.16	0.762	-1.5	0.222	1.54	0.18	0.16
1429929_at	Mei1	meiosis defective 1	1	0.998	1.37	0.081	-1.06	0.87	-1.22	0.6	0.02
1419040_at	Cyp2d22	cytochrome P450, family 2, subfamily d, polypeptide 22	1.33	0.314	-1.14	0.432	1.11	0.675	-1.15	0.353	0.04
1430473_at	9530034A14Rik	RIKEN cDNA 9530034A14 gene	2.04	0.146	-1.34	0.636	-1.9	0.358	2.29	0.078	0.27
1436885_a_at	Cherp	calcium homeostasis endoplasmic reticulum protein	-1.05	0.677	1.15	0.195	1.21	0.316	-1.12	0.266	0.05
1424008_a_at	Rbpms2	RNA binding protein with multiple splicing 2	-1.2	0.018	-1.23	0.2	1.66	0.003	1.86	0.398	0.27
1447509_at	1810057P16Rik	RIKEN cDNA 1810057P16 gene	1.6	0.018	1.2	0.545	-1.96	0.051	-1.86	0.018	-0.25
1452672_at	Thoc5	THO complex 5	1.08	0.701	-1.04	0.405	1.26	0.298	-1.37	0.203	-0.02
1427372_at	Cyp27b1	cytochrome P450, family 27, subfamily b, polypeptide 1	1.22	0.556	-1.89	0.326	1.56	0.371	-1.14	0.668	-0.06
1422118_at	Sync	syncoilin	-1.64	0.253	1.33	0.77	1.37	0.388	-1.24	0.729	-0.04
1421874_a_at	Mrps23	mitochondrial ribosomal protein S23	1.08	0.666	-1.02	0.917	1.25	0.249	-1.27	0.488	0.01
1442507_at	Whrn	whirlin	-1.34	0.376	1.53	0.205	1.04	0.913	-1.47	0.468	-0.06
1418283_at	Cldn4	claudin 4	-1.63	0.243	1.08	0.917	1.62	0.061	-1.13	0.66	-0.01
1459145_at	A930033H14Rik	RIKEN cDNA A930033H14 gene	1.39	0.534	1.07	0.901	-1.18	0.535	-1.08	0.532	0.05
1454788_at	LOC632433	similar to ADP-ribosylation factor-like protein 7	1.12	0.29	1.41	0.187	-1.27	0.346	-1.65	0.329	-0.1
1425306_at	BC027072	cDNA sequence BC027072	-1.35	0.385	1.75	0.334	-1.22	0.67	1.01	0.984	0.05
1437762_at	Rab39	RAB39, member RAS oncogene family	-1.08	0.807	1.37	0.265	1.02	0.911	-1.72	0.071	-0.1
1453364_x_at	9130019O22Rik	RIKEN cDNA 9130019O22 gene	-1.18	0.387	1.43	0.112	1.03	0.746	-1.21	0.54	0.02
1448328_at	Sh3bp2	SH3-domain binding protein 2	-1.15	0.738	1.07	0.458	1.38	0.357	-1.55	0.065	-0.06
1438141_at	BC029684	cDNA sequence BC029684	1.14	0.637	-1.05	0.879	1.22	0.42	-1.35	0.058	-0.01
1459052_at	Hif3a	Hypoxia inducible factor 3, alpha subunit	-3.63	0.052	-1.57	0.544	2.4	0.216	1.5	0.457	-0.32
1416173_at	Pes1	pescadillo homolog 1, containing BRCT domain (zebrafish)	-1.08	0.517	1.27	0.377	1.12	0.441	-1.26	0.217	0.01
1442005_at	AW987390	expressed sequence AW987390	1.28	0.099	1.17	0.516	-1.16	0.673	-1.23	0.14	0.02
1425894_at	Mrgprf	MAS-related GPR, member F	-1.4	0.381	1.77	0.061	-1.2	0.617	1.43	0.114	0.15
1422084_at	Bmx	BMX non-receptor tyrosine kinase	1.36	0.649	-1.04	0.911	-1.01	0.976	1.29	0.65	0.15
1446388_at	Tex9	Testis expressed gene 9	-1.22	0.401	1.69	0.482	-1.24	0.559	1.08	0.863	0.08
1434050_at	AI315068	expressed sequence AI315068	1.07	0.757	-1.1	0.707	1.34	0.095	-1.11	0.493	0.05
1437756_at	Gimap9	GTPase, IMAP family member 9	1.01	0.865	1.34	0.285	-1.03	0.9	-1.99	0.095	-0.17
1453811_at	Hspa9a	heat shock protein 9A	1.96	0.534	-1.16	0.737	-2.02	0.097	1.86	0.043	0.16
1439096_at	Ddo	D-aspartate oxidase	-1.13	0.558	1.14	0.616	1.29	0.443	-1.81	0.192	-0.13
1444156_at	9230112E08Rik	RIKEN cDNA 9230112E08 gene	1.34	0.211	1.01	0.978	-1.03	0.857	-1.61	0.276	-0.07
1437710_x_at	1700021P22Rik	RIKEN cDNA 1700021P22 gene	-1.05	0.825	-1.1	0.712	1.45	0.035	1.22	0.663	0.13
1456119_at	Grm5	glutamate receptor, metabotropic 5	-2.2	0.178	1.61	0.493	1.25	0.659	-1.3	0.517	-0.16
1458664_at	---	Transcribed locus	1.13	0.776	1.37	0.352	-1.24	0.283	-1.16	0.61	0.03
1460727_at	Ercc2	excision repair cross-complementing rodent repair deficiency, complementation g	1.14	0.571	-1.22	0.509	1.36	0.035	-1.33	0.119	-0.01
1439812_at	4930402H24Rik	RIKEN cDNA 4930402H24 gene	-1.48	0.364	1.68	0.418	-1.04	0.893	1.11	0.754	0.07
1418157_at	Nr2f1	nuclear receptor subfamily 2, group F, member 1	1.45	0.335	1.2	0.391	-1.51	0.008	-1.15	0.654	0
1453308_at	8430429K09Rik	RIKEN cDNA 8430429K09 gene	-1.07	0.466	1.2	0.314	1.19	0.495	-1.06	0.544	0.06

1423980_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), mem	1.1	0.558	-1.22	0.735	1.39	0.023	-2.86	0.083	-0.39
1456484_at	Dhrsx	dehydrogenase/reductase (SDR family) X chromosome	1.94	0.286	-1.2	0.709	-1.83	0.17	1.64	0.224	0.14
1442968_at	D9Ertd241e	DNA segment, Chr 9, ERATO Doi 241, expressed	-1.04	0.924	1.56	0.166	-1.26	0.272	2.07	0.275	0.33
1432898_at	4930544L18Rik	RIKEN cDNA 4930544L18 gene	-1.38	0.076	1.26	0.115	1.33	0.501	-1.63	0.66	-0.1
1445308_at	Tssc1	tumor suppressing subtransferable candidate 1	-1.07	0.833	1.58	0.291	-1.25	0.516	1.11	0.874	0.09
1423945_a_at	Pkig	protein kinase inhibitor, gamma	-1.01	0.952	1.13	0.028	1.2	0.489	-1.17	0.031	0.04
1451421_a_at	Rogdi	rogdi homolog (Drosophila)	1.06	0.825	-1.02	0.913	1.28	0.189	-1.56	0.249	-0.06
1418300_a_at	Mknk2	MAP kinase-interacting serine/threonine kinase 2	1.15	0.287	-1.04	0.892	1.2	0.131	-1.16	0.052	0.04
1440300_at	---	Transcribed locus	-1.48	0.175	1.39	0.123	1.25	0.391	-1.45	0.051	-0.07
1432029_a_at	Smap1	stromal membrane-associated protein 1	-1.11	0.254	-1.02	0.862	1.44	0.034	2.77	0.127	0.52
1436917_s_at	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	1.27	0.61	1.26	0.399	-1.28	0.375	-2.03	0.081	-0.19
1443644_at	Bre	Brain and reproductive organ-expressed protein	1.42	0.013	1.08	0.868	-1.24	0.406	-1.5	0.063	-0.06
1428577_at	Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	-1.05	0.756	1.33	0.343	1.04	0.872	-1.64	0.217	-0.08
1452224_at	Morc3	microrchidia 3	1.28	0.2	1.06	0.726	-1.02	0.862	-1.31	0.145	0
1417134_at	Srpk2	serine/arginine-rich protein specific kinase 2	-1.03	0.573	1.11	0.367	1.24	0.18	-1.36	0.165	-0.01
1444617_at	Dcc	Deleted in colorectal carcinoma	1.46	0.496	-1.2	0.727	1.02	0.957	-1.28	0.595	0
1437903_at	Lox	lysyl oxidase	1.26	0.491	-1.19	0.623	1.22	0.322	-1.14	0.895	0.04
1419759_at	Abcb1a	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	-1.04	0.807	1.09	0.833	1.27	0.337	-1.38	0.563	-0.02
1455202_at	Gm50	gene model 50, (NCBI)	1.77	0.262	1.03	0.954	-1.93	0.057	-2.53	0.253	-0.41
1435016_at	Trak2	trafficking protein, kinesin binding 2	-1.03	0.432	1.43	0.156	-1.09	0.349	3.41	0.194	0.68
1426964_at	3110003A17Rik	RIKEN cDNA 3110003A17 gene	-1.03	0.723	1.34	0.026	1.01	0.905	-1.42	0.099	-0.03
1421987_at	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.1	0.769	-1.48	0.409	1.54	0.318	-1.28	0.449	-0.03
1427908_at	Bnip1	BCL2/adenovirus E1B interacting protein 1, NIP1	1.02	0.94	-1.08	0.294	1.37	0.228	-1.03	0.87	0.07
1454484_at	4933424L07Rik	RIKEN cDNA 4933424L07 gene	1.42	0.072	-1.1	0.754	-1.01	0.975	1.23	0.656	0.14
1419186_a_at	St8sia4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	1.4	0.257	1.37	0.141	-1.82	0.001	-1.71	0.238	-0.19
1431688_at	LOC73899	hypothetical LOC73899	-4.24	0.105	1.39	0.385	1.69	0.153	-1.57	0.094	-0.68
1451835_at	Sox21	SRY-box containing gene 21	-1.15	0.691	1.46	0.678	-1.01	0.983	1.21	0.439	0.13
1431879_at	9030417H13Rik	RIKEN cDNA 9030417H13 gene	1.64	0.341	-1.81	0.134	1.13	0.332	-1.03	0.946	-0.02
1457818_at	Gtf2h2	General transcription factor II H, polypeptide 2	1.19	0.363	1.19	0.702	-1.06	0.895	-1.25	0.56	0.02
1446479_at	Tnni3k	TNNI3 interacting kinase	1.75	0.208	-1.19	0.735	-1.37	0.56	2.91	0.201	0.52
1448605_at	Rhoc	ras homolog gene family, member C	1.29	0.357	1.25	0.354	-1.29	0.223	-1.33	0.276	-0.02
1448577_x_at	Syngr2	synaptogyrin 2	-1.06	0.83	1.05	0.573	1.32	0.096	-1.13	0.664	0.05
1436386_x_at	LOC195531	Similar to reduced expression 2	-1.06	0.886	1.11	0.504	1.27	0.199	-1.18	0.652	0.03
1452706_a_at	1700027J05Rik	RIKEN cDNA 1700027J05 gene	1.39	0.518	-1.23	0.435	1.12	0.552	-1.03	0.925	0.06
1445071_at	---	---	1.85	0.18	-1.56	0.602	-1.2	0.717	1.35	0.545	0.11
1458987_at	Cdk7	Cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	1.27	0.497	1.13	0.635	-1.09	0.778	-1.11	0.764	0.05
1422386_at	Olfr65	olfactory receptor 64	-1.03	0.861	1.57	0.298	-1.27	0.688	1.08	0.793	0.08
1425150_at	C730036D15Rik	RIKEN cDNA C730036D15 gene	1.28	0.639	1.36	0.354	-1.47	0.149	-2.39	0.497	-0.3
1460204_at	Tec	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	1.03	0.746	-1.31	0.052	1.53	0.413	-2.32	0.01	-0.27
1436862_at	Doc2a	double C2, alpha	-1.15	0.821	-1.67	0.452	1.85	0.439	1.97	0.162	0.25
1442918_at	Nav3 /// 9630020C(	neuron navigator 3 /// RIKEN cDNA 9630020C08 gene /// region containing RIKE	-1.12	0.855	1.3	0.429	1.13	0.617	-1	0.985	0.08
1445276_at	C80154	expressed sequence C80154	-1.83	0.491	1.14	0.44	1.63	0.439	-1.02	0.957	-0.02
1427163_at	Ubr2	ubiquitin protein ligase E3 component n-recognin 2	-1.03	0.853	-1.05	0.778	1.4	0.046	1.16	0.297	0.12
1440875_a_at	Rsad1	radical S-adenosyl methionine domain containing 1	1.34	0.386	1.01	0.983	-1.03	0.859	-1.32	0.543	0
1459799_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	-1.21	0.514	1.69	0.238	-1.23	0.727	1.56	0.19	0.2
1449945_at	Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta	-1.05	0.583	-1.57	0.339	1.74	0.272	1.04	0.902	0.04
1429206_at	Rhobtb1	Rho-related BTB domain containing 1	-1.03	0.853	-1.06	0.805	1.41	0.109	1.37	0.354	0.17
1439427_at	Cldn9	claudin 9	1.44	0.036	1.32	0.592	-1.76	0.324	-1.02	0.975	-0.01
1459383_at	Zfp52	Zinc finger protein 52	-1.35	0.707	1.03	0.971	1.56	0.162	-1.14	0.522	0.02
1428726_at	Thumpd2	THUMP domain containing 2	-1.26	0.469	1.52	0.015	1.01	0.978	-1.29	0.167	0
1431717_at	3526401B18Rik	RIKEN cDNA 3526401B18 gene	1.34	0.715	1.09	0.737	-1.13	0.725	-1.4	0.31	-0.02
1423460_at	Perq1	PERQ amino acid rich, with GYF domain 1	-1.14	0.13	1.09	0.743	1.36	0.266	-1.2	0.388	0.03
1460641_a_at	3100004P22Rik ///	RIKEN cDNA 3100004P22 gene /// RIKEN cDNA 2310022K01 gene	-1.04	0.85	1.08	0.762	1.28	0.133	-1.15	0.106	0.04

1454873_at	C130032F08Rik	RIKEN cDNA C130032F08 gene	1.4	0.319	-1.29	0.574	1.14	0.378	-2.32	0.117	-0.27
1431186_at	Dlg5	discs, large homolog 5 (Drosophila)	-1.79	0.143	1.93	0.117	-1.19	0.638	1.32	0.669	0.07
1452346_at	B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	-1.01	0.775	1.15	0.139	1.18	0.201	-1.1	0.414	0.06
1445519_at	Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3	-1.06	0.763	1.54	0.411	-1.19	0.424	1.13	0.642	0.11
1453442_at	2310043M15Rik	RIKEN cDNA 2310043M15 gene	-1.2	0.676	1.39	0.343	1.1	0.779	-2.16	0.061	-0.22
1428782_a_at	Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	-1.03	0.85	-1.24	0.222	1.55	0.003	1.15	0.211	0.11
1419671_a_at	Il17rc	interleukin 17 receptor C	1.31	0.49	-1.02	0.924	1.04	0.816	-1.22	0.222	0.03
1425253_a_at	Madcam1	mucosal vascular addressin cell adhesion molecule 1	-1.35	0.338	1.21	0.552	1.37	0.089	-3.34	0.073	-0.53
1438622_x_at	Tubb2c	tubulin, beta 2c	-2.3	0.012	-1.28	0.437	2.11	0.05	1.47	0.396	0
1456694_x_at	Ptpn6	protein tyrosine phosphatase, non-receptor type 6	1.2	0.593	-1.13	0.385	1.24	0.359	-1.21	0.328	0.03
1460165_at	Ppp1ca	protein phosphatase 1, catalytic subunit, alpha isoform	1.06	0.793	-1.01	0.952	1.27	0.15	-1.29	0.273	0.01
1450449_a_at	2900002H16Rik	RIKEN cDNA 2900002H16 gene	-1.15	0.202	1.43	0.142	1.03	0.751	-1.05	0.771	0.06
1447471_at	---	Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library,	1.21	0.209	1.25	0.032	-1.16	0.03	-1.29	0.222	0
1433176_at	4930563F15Rik	RIKEN cDNA 4930563F15 gene	1.18	0.491	1.47	0.304	-1.49	0.072	-1.44	0.168	-0.07
1456375_x_at	Trim27	tripartite motif protein 27	1.06	0.447	-1	0.99	1.27	0.296	-1.1	0.567	0.06
1454812_at	5730601F06Rik	RIKEN cDNA 5730601F06 gene	1.11	0.088	1.38	0.262	-1.19	0.385	-1.14	0.262	0.04
1436851_at	Ptger1 /// Pkn1	prostaglandin E receptor 1 (subtype EP1) /// protein kinase N1	1.13	0.302	-1.03	0.805	1.22	0.08	-1.31	0.306	0.01
1423205_at	Tm9sf4	transmembrane 9 superfamily protein member 4	-1.05	0.499	1.03	0.749	1.34	0.037	-1.19	0.253	0.03
1419179_at	Txnl4	thioredoxin-like 4	1.22	0.395	1.17	0.637	-1.07	0.494	-1.07	0.608	0.06
1421656_at	Spry2	sprouty homolog 2 (Drosophila)	-1.21	0.815	1.39	0.439	1.11	0.76	-1.25	0.408	0.01
1418718_at	Cxcl16	chemokine (C-X-C motif) ligand 16	1.02	0.902	1.5	0.095	-1.24	0.107	-1.37	0.09	-0.02
1429816_at	Armc3	armadillo repeat containing 3	1.79	0.414	-2.28	0.109	1.1	0.727	-3.43	0.107	-0.7
1424375_s_at	Gimap4	GTPase, IMAP family member 4	-1.01	0.833	1.22	0.057	1.12	0.645	-1.42	0.409	-0.02
1419109_at	Hrc	histidine rich calcium binding protein	-1.13	0.139	1.17	0.256	1.27	0.506	-1.04	0.884	0.07
1427617_at	Fut10	fucosyltransferase 10	1.51	0.391	-1.4	0.366	1.11	0.627	-1.42	0.368	-0.05
1447664_x_at	AA986860	expressed sequence AA986860	-1.06	0.81	1.15	0.621	1.23	0.319	-1.1	0.856	0.06
1429656_at	Rhobtb1	Rho-related BTB domain containing 1	-1.07	0.402	-1.16	0.593	1.53	0.125	1.23	0.637	0.13
1418871_a_at	1810007E14Rik	RIKEN cDNA 1810007E14 gene	1.01	0.989	1.51	0.566	-1.24	0.298	-1.03	0.957	0.06
1452457_a_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-1.05	0.897	1.4	0.316	-1.02	0.949	1.29	0.71	0.15
1455518_at	---	Transcribed locus, weakly similar to XP_232745.3 PREDICTED: hypothetical pro	-1.11	0.479	1.18	0.352	1.25	0.151	-1.54	0.314	-0.06
1449680_at	C80678	expressed sequence C80678	-1.61	0.275	1.28	0.052	1.42	0.337	-1.23	0.111	-0.03
1449971_a_at	Cd209f	CD209f antigen	-1.31	0.485	1.38	0.461	1.19	0.661	-1.08	0.708	0.04
1450597_at	Olfr870	olfactory receptor 870	1.63	0.268	-1	1	-1.44	0.493	2.31	0.009	0.38
1431599_at	2310069B03Rik	RIKEN cDNA 2310069B03 gene	-1.55	0.525	1.23	0.712	1.45	0.291	-1.06	0.924	0.02
1442051_at	Hist2h3c1	histone 2, H3c1	1.17	0.452	-1.06	0.798	1.21	0.114	-1.11	0.59	0.05
1457554_at	Apob	apolipoprotein B	1.75	0.363	-1.04	0.838	-1.62	0.18	1.07	0.895	0.04
1443694_at	Rgs20	regulator of G-protein signaling 20	-1.33	0.555	1.39	0.534	1.19	0.805	-1.34	0.522	-0.02
1459652_at	C79356	expressed sequence C79356	1.12	0.876	-1.09	0.775	1.29	0.332	-1.07	0.757	0.06
1447553_x_at	Ric3	Resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	1.5	0.216	-1.77	0.377	1.26	0.684	-1.05	0.937	-0.01
1460105_at	B3galnt2	UDP-GalNAc:betaGlcNAc beta 1,3-galactosaminyltransferase, polypeptide 2	1.18	0.828	-1.01	0.994	1.16	0.827	-1.13	0.689	0.05
1421954_at	Crkl	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	1.15	0.713	-1.46	0.115	1.5	0.306	-1.07	0.913	0.03
1447644_at	Wnt5b	Wingless-related MMTV integration site 5B	-1.83	0.279	-1.57	0.487	2.14	0.063	2.32	0.029	0.27
1439905_at	A330062J17Rik	RIKEN cDNA A330062J17 gene	1.84	0.443	-1.73	0.388	-1.1	0.875	1.99	0.04	0.25
1416092_a_at	Mtap4	microtubule-associated protein 4	-1.01	0.937	1.1	0.337	1.24	0.256	-1.29	0.452	0.01
1420125_at	Tcta	T-cell leukemia translocation altered gene	2.07	0.471	-1.48	0.49	-1.72	0.143	1.3	0.458	0.04
1455768_at	Npc2	Niemann Pick type C2	1.27	0.025	1.07	0.452	-1.01	0.953	-1.36	0.18	-0.01
1423027_at	Foxl1	forkhead box L1	1.15	0.388	1.39	0.325	-1.26	0.011	-1.1	0.326	0.04
1445978_at	---	---	-1.08	0.875	1.61	0.297	-1.26	0.588	1.42	0.548	0.17
1439556_at	Ncam1	neural cell adhesion molecule 1	1.62	0.304	1.02	0.975	-1.45	0.382	-1.71	0.089	-0.13
1444041_at	AU041133	expressed sequence AU041133	1.41	0.005	1.06	0.728	-1.16	0.225	-1.73	0.065	-0.11
1437980_at	9130230N09Rik	RIKEN cDNA 9130230N09 gene	-1.09	0.839	1.11	0.74	1.3	0.452	-1.5	0.262	-0.04
1445122_at	A830082N09Rik	RIKEN cDNA A830082N09 gene	1.19	0.379	1.31	0.731	-1.19	0.578	-2.06	0.309	-0.19
1440987_at	---	---	-1.29	0.108	1.32	0.683	1.24	0.3	-1.06	0.757	0.05

1457097_at	Scap2	src family associated phosphoprotein 2	-1.1	0.6	1.2	0.276	1.22	0.186	-1.16	0.345	0.04
1433681_x_at	Capn3	calpain 3	-1.44	0.005	-1.17	0.4	1.79	0.073	1.16	0.749	0.08
1443713_at	Chl1	cell adhesion molecule with homology to L1CAM	-1.61	0.26	1.39	0.549	1.32	0.569	-1.14	0.845	-0.01
1450151_at	Zfp316	zinc finger protein 316	-1.2	0.718	1.1	0.528	1.4	0.325	-2.05	0.334	-0.19
1448952_at	A030009H04Rik	RIKEN cDNA A030009H04 gene	-1.03	0.863	1.4	0.551	-1.04	0.853	1.16	0.49	0.12
1454418_at	5330421C15Rik	RIKEN cDNA 5330421C15 gene	1	0.99	1.51	0.149	-1.22	0.022	-1.04	0.83	0.06
1431915_at	4930442E04Rik	RIKEN cDNA 4930442E04 gene	1.43	0.723	-2.17	0.325	1.44	0.384	-1.08	0.87	-0.09
1422661_at	Lgals8	lectin, galactose binding, soluble 8	1.12	0.711	-1.01	0.97	1.23	0.669	-1.35	0.505	0
1444413_at	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	1.71	0.115	-3.05	0.038	1.3	0.563	-1.3	0.615	-0.34
1419416_a_at	Rarg	retinoic acid receptor, gamma	1.29	0.534	-1.38	0.422	1.32	0.598	-1.44	0.642	-0.05
1425264_s_at	Mbp	myelin basic protein	-1.01	0.845	1.15	0.792	1.19	0.159	-1.02	0.917	0.08
1420752_at	Dtx3	deltex 3 homolog (Drosophila)	-1.32	0.132	1.91	0.06	-1.5	0.161	1.42	0.212	0.13
1423094_at	Crbn	cereblon	-1.12	0.624	1.18	0.274	1.26	0.053	-1.22	0.481	0.02
1444054_at	---	---	-1.21	0.526	1.42	0.459	1.09	0.437	-1.68	0.313	-0.09
1446895_at	---	---	1.02	0.975	-1.07	0.791	1.37	0.386	-1.21	0.604	0.03
1426202_at	H2-Ea	Histocompatibility 2, class II antigen E alpha /// MHC class II E-sub-alpha (E-sub-	1.38	0.681	1.04	0.918	-1.09	0.846	-1.49	0.286	-0.04
1458347_s_at	Tmprss2	transmembrane protease, serine 2	-1.26	0.157	1.61	0.334	-1.08	0.43	2.06	0.056	0.33
1429452_x_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	1.39	0.346	1.11	0.423	-1.21	0.346	-1.39	0.48	-0.02
1452006_x_at	Zbtb8os	zinc finger and BTB domain containing 8 opposite strand	1.33	0.362	1.07	0.475	-1.08	0.469	-1.94	0.113	-0.15
1446704_at	Tpk1	Thiamin pyrophosphokinase	-1.28	0.219	1.46	0.341	1.09	0.737	-1.28	0.493	0
1450172_at	Pknox1	Pbx/knotted 1 homeobox	1.27	0.578	1.1	0.72	-1.04	0.869	-1.08	0.871	0.06
1430525_at	2310001K24Rik	RIKEN cDNA 2310001K24 gene	1.58	0.394	-1.25	0.21	-1.05	0.769	1.09	0.876	0.09
1458475_at	Brunol4	Bruno-like 4, RNA binding protein (Drosophila)	1.25	0.682	1.15	0.733	-1.07	0.806	-2.15	0.077	-0.2
1433179_at	Morn1	MORN repeat containing 1	-1.39	0.579	1.51	0.242	1.11	0.855	-1.55	0.5	-0.08
1427047_at	Nup188	nucleoporin 188	1.74	0.365	-1.55	0.472	-1.05	0.27	1.36	0.108	0.13
1423975_s_at	Numa1	nuclear mitotic apparatus protein 1	1.12	0.221	-1.08	0.387	1.29	0.046	-1.26	0.053	0.02
1434430_s_at	Adora2b	adenosine A2b receptor	-1.32	0.394	1.62	0.38	-1.04	0.81	1.51	0.339	0.19
1417946_at	Abhd3	abhydrolase domain containing 3	-1.25	0.022	-1.09	0.488	1.61	0.155	1.44	0.05	0.18
1440939_at	6-Sep	Septin 6	1.2	0.001	-2.75	0.235	1.77	0.086	-2.19	0.179	-0.49
1455282_x_at	Alas1	aminolevulinic acid synthase 1	-1.24	0.671	-1.65	0.337	1.93	0.038	1.1	0.148	0.03
1421699_at	Enam	enamelin	-1.03	0.888	1.07	0.872	1.29	0.568	-2.01	0.429	-0.17
1429722_at	Zbtb4	zinc finger and BTB domain containing 4	1.19	0.113	1.17	0.051	-1.02	0.874	-1.65	0.195	-0.08
1435973_at	---	Transcribed locus	-1.01	0.961	1.31	0.166	1.03	0.853	-1.22	0.388	0.03
1443186_at	4930425N13Rik	RIKEN cDNA 4930425N13 gene	-1.34	0.746	-2.35	0.228	2.17	0.167	1.68	0.187	0.04
1418746_at	Pnkd	paroxysmal nonkinesiogenic dyskinesia	1.29	0.015	-1.05	0.679	1.09	0.524	-1.17	0.641	0.04
1433684_at	Chmp6	chromatin modifying protein 6	-1.11	0.736	1.13	0.364	1.31	0.124	-1.07	0.369	0.06
1422971_at	Gcn5l2	GCN5 general control of amino acid synthesis-like 2 (yeast)	-1.14	0.312	1.29	0.511	1.17	0.676	-1.37	0.129	-0.01
1452779_at	3110006E14Rik	RIKEN cDNA 3110006E14 gene	2.07	0.158	-1.37	0.609	-1.87	0.246	1.22	0.733	0.01
1421136_at	Edn3	endothelin 3	1.53	0.533	-1.01	0.972	-1.23	0.627	1.06	0.905	0.09
1433294_at	4930449I04Rik	RIKEN cDNA 4930449I04 gene	-1.27	0.012	1.43	0.557	1.12	0.766	-1.38	0.258	-0.02
1435031_at	2010310D06Rik	RIKEN cDNA 2010310D06 gene	-1.06	0.795	1.14	0.285	1.26	0.266	-1.28	0.321	0.01
1455930_at	LOC673503	hypothetical protein LOC673503	1.64	0.105	-1.37	0.115	-1.03	0.946	2.06	0.396	0.32
1437389_x_at	---	---	-1.05	0.533	1.21	0.213	1.18	0.181	-1.27	0.198	0.02
1460074_x_at	Epdr2	ependymin related protein 2 (zebrafish)	-2.07	0.184	1.95	0.172	-1.11	0.559	2.74	0.155	0.38
1443105_at	Zfp398	Zinc finger protein 398	1.16	0.504	1.24	0.325	-1.07	0.777	-1.34	0.221	0
1415787_at	Ganab	alpha glucosidase 2 alpha neutral subunit	-1.09	0.493	-1.16	0.042	1.57	0.02	1.05	0.569	0.09
1427552_a_at	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	-1.05	0.7	-1.09	0.385	1.47	0.206	1.33	0.328	0.17
1440321_at	Mast2	Microtubule associated serine/threonine kinase 2	1.04	0.944	1.69	0.074	-1.64	0.456	-1.33	0.507	-0.06
1421209_s_at	Ikbkg	inhibitor of kappaB kinase gamma	-1.19	0.299	1.04	0.817	1.45	0.189	-1.11	0.467	0.05
1433100_at	Tmem153	transmembrane protein 153	1.34	0.562	-1.19	0.607	1.16	0.381	-1.16	0.748	0.04
1438564_at	Gas2	Growth arrest specific 2	1.13	0.837	1.44	0.502	-1.29	0.081	-1.13	0.757	0.04
1442719_at	Prmt3	protein arginine N-methyltransferase 3	1.72	0.125	1.06	0.938	-1.79	0.135	-1.07	0.646	-0.02
1420003_at	Nsun5	NOL1/NOP2/Sun domain family, member 5	1.44	0.287	-1.15	0.648	1.03	0.889	-1.44	0.357	-0.03

1428669_at	Bmyc	brain expressed myelocytomatosis oncogene	1.13	0.46	-1.03	0.873	1.24	0.15	-1.84	0.116	-0.13
1423999_at	Abl1	v-abl Abelson murine leukemia oncogene 1	1.12	0.411	1.31	0.11	-1.1	0.425	-1.07	0.57	0.07
1448121_at	Wbp2	WW domain binding protein 2	-1.13	0.569	-1.03	0.668	1.48	0.032	1.43	0.04	0.19
1418047_at	Neurod6	neurogenic differentiation 6	1.27	0.693	-1.03	0.96	1.1	0.836	-1.15	0.845	0.05
1457494_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:C030(	1.83	0.467	1.02	0.908	-2.06	0.345	-2.44	0.397	-0.41
1460004_x_at	Stx6	syntaxin 6	1.07	0.281	1.33	0.029	-1.07	0.676	-1.21	0.449	0.03
1430314_at	4933437F05Rik	RIKEN cDNA 4933437F05 gene	1.08	0.822	-1.35	0.669	1.52	0.218	-1.41	0.241	-0.04
1447237_at	Pde4b	Phosphodiesterase 4B, cAMP specific	1.72	0.364	-1.84	0.253	1.07	0.854	-2.39	0.315	-0.36
1443992_at	Nipbl	Nipped-B homolog (Drosophila)	-1.03	0.296	1.51	0.114	-1.17	0.364	1.23	0.225	0.14
1429943_at	Ctbs	chitobiase, di-N-acetyl-	-1.07	0.564	1.13	0.607	1.27	0.442	-1.26	0.219	0.02
1435075_at	Tmem106b	transmembrane protein 106B	1.16	0.237	-1.28	0.245	1.39	0.26	-1.19	0.318	0.02
1423883_at	Acsl1	acyl-CoA synthetase long-chain family member 1	-1.16	0.361	-1.58	0.027	1.85	0.162	2.83	0.199	0.48
1438053_at	Tfg	Trk-fused gene	1.09	0.838	1.47	0.393	-1.29	0.402	-1.27	0.363	0
1456261_at	Sh3kbp1	SH3-domain kinase binding protein 1	1.03	0.453	1.44	0.536	-1.16	0.612	-1.9	0.217	-0.15
1455308_at	Tmem16f	transmembrane protein 16F	1.13	0.074	1.47	0.005	-1.36	0.013	-1.17	0.56	0.02
1425586_a_at	Mlph	melanophilin	-1.09	0.854	-1.4	0.601	1.7	0.024	2.07	0.116	0.32
1445223_at	---	---	1.39	0.169	-1.18	0.596	1.11	0.604	-1.07	0.868	0.06
1432093_at	2310005A03Rik	RIKEN cDNA 2310005A03 gene	-1.1	0.03	1.44	0.175	-1.01	0.986	2.01	0.035	0.33
1457119_at	---	---	-1.09	0.343	1.16	0.734	1.26	0.079	-1.35	0.32	0
1454450_at	4930572C08Rik	RIKEN cDNA 4930572C08 gene	2.02	0.194	-1.83	0.104	-1.3	0.583	1.59	0.476	0.12
1426125_a_at	Casp9	caspase 9	1.47	0.171	-1.09	0.856	-1.05	0.902	1.12	0.59	0.11
1442247_at	---	---	-3.69	0.398	2.14	0.429	-1.07	0.71	1.08	0.913	-0.39
1425120_x_at	1810023F06Rik	RIKEN cDNA 1810023F06 gene	-1.84	0.086	1.69	0.304	1.11	0.779	-1.01	0.971	-0.01
1427077_a_at	Ap2b1	adaptor-related protein complex 2, beta 1 subunit	-1.02	0.815	-1.14	0.499	1.49	0.095	1.17	0.432	0.12
1436594_at	Zfp719	zinc finger protein 719	1.28	0.124	1.15	0.355	-1.1	0.453	-1.23	0.374	0.02
1441532_at	---	Transcribed locus	1.74	0.424	-1.72	0.433	1.02	0.95	-2.38	0.143	-0.33
1439459_x_at	Acly	ATP citrate lyase	-1.04	0.681	1.29	0.29	1.09	0.632	-1.36	0.211	0
1434922_at	Phf12	PHD finger protein 12	1.02	0.944	-1.01	0.946	1.34	0.24	-1.16	0.304	0.04
1446768_at	---	Transcribed locus	1.45	0.203	-1.17	0.657	1.04	0.836	-4.99	0.164	-0.92
1426971_at	Ube1l	ubiquitin-activating enzyme E1-like	1.45	0.354	-1.26	0.025	1.1	0.458	-1.04	0.728	0.06
1450525_at	Gli3	GLI-Kruppel family member GLI3	-1.59	0.232	1.77	0.394	-1.06	0.898	1.37	0.598	0.12
1435486_at	---	---	1.74	0.585	-1.48	0.064	-1.08	0.885	1.22	0.764	0.1
1441414_at	Eef2	Eukaryotic translation elongation factor 2	1.69	0.136	1.04	0.753	-1.63	0.012	-1.52	0.359	-0.11
1421853_at	Psen1	presenilin 1	1.03	0.095	-1.03	0.723	1.34	0.002	-1.11	0.36	0.06
1444761_at	Ccdc8	Coiled-coil domain containing 8	-1.51	0.207	1.34	0.556	1.34	0.156	-1.04	0.894	0.03
1428749_at	Dmxl2	Dmx-like 2	-1.09	0.785	-1.03	0.724	1.45	0.331	1.3	0.42	0.16
1444833_at	2410012H22Rik	RIKEN cDNA 2410012H22 gene	1.66	0.227	-1.11	0.797	-1.27	0.119	1.12	0.786	0.1
1417394_at	Klf4	Kruppel-like factor 4 (gut)	1.32	0.438	1.17	0.51	-1.17	0.653	-1.58	0.109	-0.06
1449603_at	AI594671	expressed sequence AI594671	1.39	0.626	-1.87	0.059	1.42	0.295	-1.16	0.371	-0.06
1420792_at	4930433N12Rik	RIKEN cDNA 4930433N12 gene	-1.02	0.948	1.16	0.812	1.21	0.604	-1.67	0.12	-0.08
1429123_at	Rab27a	RAB27A, member RAS oncogene family	1.02	0.786	1.48	0.25	-1.18	0.17	-1.06	0.673	0.06
1416339_a_at	Prkcsh	protein kinase C substrate 80K-H	-1.08	0.593	-1.11	0.072	1.52	0.027	1.15	0.51	0.12
1432706_at	5330428N10Rik	RIKEN cDNA 5330428N10 gene	1.17	0.841	1.3	0.318	-1.14	0.745	-2.75	0.101	-0.36
1446103_at	Rab8b	RAB8B, member RAS oncogene family	-1.66	0.266	1.78	0.226	-1.05	0.833	1.47	0.115	0.14
1451328_at	Pcnxl3	pecanex-like 3 (Drosophila)	-1.08	0.711	1.03	0.793	1.38	0.083	-1.12	0.446	0.06
1442502_at	Lrch1	leucine-rich repeats and calponin homology (CH) domain containing 1	1.48	0.272	1.01	0.956	-1.16	0.594	-1.5	0.15	-0.05
1425318_a_at	Tmem116	transmembrane protein 116	-1.17	0.264	1.61	0.312	-1.13	0.197	1.68	0.311	0.25
1421754_at	AY036118	cDNA sequence AY036118	1.32	0.653	1.07	0.863	-1.05	0.901	-1.45	0.635	-0.03
1426806_at	5830411E10Rik	RIKEN cDNA 5830411E10 gene	-1.23	0.455	1.17	0.329	1.36	0.061	-1.61	0.127	-0.08
1442827_at	Tlr4	Toll-like receptor 4	1.49	0.475	-1.08	0.589	-1.08	0.863	1.68	0.054	0.25
1437352_at	Acox3	acyl-Coenzyme A oxidase 3, pristanoyl	-2.09	0.071	1.13	0.584	1.74	0.198	-1.63	0.562	-0.21
1459077_at	Cyp2d26	Cytochrome P450, family 2, subfamily d, polypeptide 26	-1.3	0.002	1.75	0.106	-1.21	0.606	1.33	0.354	0.14
1445944_at	Slc25a5	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	1.19	0.726	1.51	0.474	-1.54	0.188	-1.27	0.511	-0.03

1433931_at	C030046I01Rik	RIKEN cDNA C030046I01 gene	-1.03	0.879	-1.12	0.385	1.48	0.136	1.53	0.027	0.22
1443975_at	Trip11	thyroid hormone receptor interactor 11	-1.53	0.017	1.77	0.222	-1.08	0.854	1.08	0.907	0.06
1443640_at	Zfp617	Zinc finger protein 617	-1.48	0.646	1.38	0.479	1.29	0.493	-1.12	0.763	0.02
1460380_at	Dsg2	desmoglein 2	-1.07	0.689	-1.24	0.581	1.61	0.304	1.09	0.744	0.1
1423748_at	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	-1.02	0.878	1.09	0.787	1.28	0.027	-1.49	0.184	-0.04
1432597_at	4930599N24Rik	RIKEN cDNA 4930599N24 gene	1.22	0.796	1.17	0.781	-1.05	0.934	-1.49	0.614	-0.04
1438536_at	5830411N06Rik	RIKEN cDNA 5830411N06 gene	1.3	0.165	1.16	0.819	-1.14	0.544	-1.02	0.952	0.08
1429125_at	Zbtb9	zinc finger and BTB domain containing 9	1.39	0.03	-1.08	0.687	1.02	0.845	-1.56	0.025	-0.05
1440723_at	---	---	-1.53	0.112	-1.13	0.698	1.8	0.277	1.18	0.755	0.08
1417363_at	Zfp61	zinc finger protein 61	1.07	0.761	1.37	0.644	-1.11	0.587	-1.49	0.131	-0.04
1416940_at	Ppif	peptidylprolyl isomerase F (cyclophilin F)	-1.27	0.341	-1.09	0.485	1.64	0.009	1.07	0.766	0.09
1421980_at	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	1.19	0.628	1.4	0.574	-1.32	0.604	-1.12	0.801	0.04
1417448_at	1810008A18Rik	RIKEN cDNA 1810008A18 gene	-1.02	0.911	1.05	0.709	1.32	0.065	-1.13	0.49	0.05
1425701_a_at	Rgs3	regulator of G-protein signaling 3	1.19	0.809	-1.78	0.428	1.6	0.301	-1.15	0.75	-0.04
1440715_s_at	D11Ertd497e	DNA segment, Chr 11, ERATO Doi 497, expressed	1.06	0.644	1.33	0.032	-1.05	0.715	-1.17	0.209	0.04
1429209_at	Col23a1	procollagen, type XXIII, alpha 1	-1.14	0.706	1.33	0.485	1.14	0.479	-1.81	0.055	-0.12
1422824_s_at	Eps8	epidermal growth factor receptor pathway substrate 8	-1.09	0.427	1.37	0.024	1.06	0.268	-1.1	0.448	0.06
1420891_at	Wnt7b	wingless-related MMTV integration site 7B	-1.02	0.933	1.18	0.751	1.19	0.46	-1.15	0.821	0.05
1444505_at	Rai17	retinoic acid induced 17	1.02	0.857	1.96	0.027	-2.67	0.02	-1.95	0.39	-0.41
1426146_a_at	Chpt1	choline phosphotransferase 1	1.08	0.492	-1.03	0.822	1.29	0.4	-1.11	0.637	0.06
1451088_a_at	Oxa1l	oxidase assembly 1-like	-1.02	0.94	-1.1	0.368	1.46	0.031	1.05	0.846	0.1
1452402_at	Uchl3	Ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	-1.1	0.759	1.09	0.75	1.35	0.502	-2.04	0.084	-0.17
1444610_at	---	Transcribed locus	-1.04	0.893	1.87	0.349	-1.94	0.331	1.48	0.498	0.09
1444151_at	2600009P04Rik	RIKEN cDNA 2600009P04 gene	-1.44	0.671	1.31	0.488	1.34	0.381	-1.07	0.668	0.04
1452778_x_at	Nap1l1	nucleosome assembly protein 1-like 1	1.14	0.332	-1.07	0.431	1.28	0.303	-1.12	0.136	0.06
1429644_at	1700011I03Rik /// L	RIKEN cDNA 1700011I03 gene /// hypothetical gene supported by AK005868; BC	1.22	0.475	1.18	0.654	-1.05	0.797	-1.62	0.256	-0.07
1450546_at	Ammecr1	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chrom	1.76	0.475	-1.71	0.014	-1	0.999	2.32	0.468	0.34
1417895_a_at	Tmem54	transmembrane protein 54	1.11	0.621	-1.85	0.418	1.69	0.187	-1.11	0.831	-0.04
1416836_at	Lrp10	low-density lipoprotein receptor-related protein 10	-1.07	0.69	1.02	0.767	1.39	0.078	-1.01	0.969	0.08
1427154_at	Krt2	keratin 2	1.23	0.804	1.44	0.611	-1.48	0.402	-3.05	0.123	-0.46
1458571_at	D430047D06Rik	RIKEN cDNA D430047D06 gene	1.87	0.036	-1.51	0.38	-1.23	0.586	1.12	0.718	0.06
1456889_at	---	PREDICTED: Mus musculus similar to aspartoacylase-3 (LOC629627), mRNA	2.02	0.008	-1.81	0.159	-1.28	0.221	1.05	0.845	-0.01
1450693_at	---	---	1.34	0.646	1.12	0.83	-1.13	0.714	-1.03	0.881	0.08
1420104_at	---	---	1.75	0.116	-1.33	0.308	-1.18	0.355	1.16	0.608	0.1
1425707_a_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	-1.28	0.685	-2.4	0.192	2.15	0.096	1.82	0.29	0.07
1451475_at	Plxnd1	Plexin D1	1.32	0.213	1.14	0.095	-1.13	0.66	-1.4	0.378	-0.02
1455315_at	Trp53i13	tumor protein p53 inducible protein 13	1.35	0.289	-1.03	0.853	1.03	0.766	-1.4	0.332	-0.01
1419748_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	1.46	0.537	-2.05	0.145	1.4	0.389	-1.61	0.072	-0.2
1424767_at	Cdh22	cadherin 22	1.35	0.536	1.14	0.784	-1.16	0.588	-1.33	0.355	0
1443904_at	Fads6	fatty acid desaturase domain family, member 6	-1.01	0.946	1.14	0.515	1.22	0.473	-1.7	0.226	-0.09
1434225_at	Swap70	SWA-70 protein	-1.05	0.559	1.12	0.665	1.28	0.268	-1.59	0.198	-0.06
1450153_at	Gopc	golgi associated PDZ and coiled-coil motif containing	1.05	0.28	-1.12	0.561	1.41	0.116	-1.28	0.55	0.02
1430943_at	6030498E09Rik	RIKEN cDNA 6030498E09 gene	-1.23	0.765	1.63	0.394	-1.11	0.285	1.51	0.591	0.2
1441113_at	A430071A18Rik	RIKEN cDNA A430071A18 gene	-2.36	0.061	2.05	0.258	-1.14	0.499	1.58	0.248	0.03
1422879_at	Sypl	synaptophysin-like protein	-1.01	0.966	-1.01	0.965	1.38	0.326	1.08	0.334	0.11
1419502_at	Ghdc	GH3 domain containing	1.14	0.456	-1.04	0.843	1.25	0.255	-1.19	0.481	0.04
1439737_x_at	Med6	Mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	-1.26	0.42	1.56	0.199	-1	0.997	1.22	0.672	0.13
1454024_at	Lrrc9	leucine rich repeat containing 9	-1.49	0.328	2	0.48	-1.47	0.338	1.32	0.319	0.09
1429859_a_at	Arl2bp	ADP-ribosylation factor-like 2 binding protein	-1.44	0.153	1.18	0.744	1.48	0.496	-1.26	0.698	-0.01
1432001_at	Zmynd17	zinc finger, MYND domain containing 17	-1.51	0.617	1.99	0.055	-1.43	0.433	1.38	0.376	0.11
1423281_at	Stmn2	stathmin-like 2	1.59	0.122	1.03	0.973	-1.36	0.163	-1.92	0.151	-0.17
1434958_at	Sacs	sacsin	-1.07	0.297	1.43	0.312	-1.01	0.881	1.07	0.735	0.1
1416593_at	Glrx	glutaredoxin	-1.03	0.923	-1.49	0.012	1.7	0.413	1.37	0.335	0.14

1454196_at	4930568A13Rik	RIKEN cDNA 4930568A13 gene	1.63	0.425	1.13	0.829	-1.67	0.078	-1.85	0.074	-0.19
1459509_at	Morf4l1	Mortality factor 4 like 1	1.33	0.391	1.07	0.849	-1.05	0.799	-1.05	0.84	0.08
1455044_at	Tmem44	transmembrane protein 44	1.35	0.58	-1.46	0.345	1.32	0.04	-1	0.956	0.05
1454625_at	Phf6	PHD finger protein 6	-1.17	0.347	1.4	0.2	1.1	0.583	-1.1	0.665	0.06
1452521_a_at	Plaur	plasminogen activator, urokinase receptor	-1.6	0.114	1.56	0.118	1.16	0.615	-1.65	0.327	-0.13
1418494_at	Ebf2	early B-cell factor 2	-1.02	0.976	1.15	0.717	1.22	0.712	-3.04	0.241	-0.42
1453561_x_at	8430431K14Rik	RIKEN cDNA 8430431K14 gene	2.23	0.402	-2.09	0.099	-1.56	0.108	1.4	0.152	0
1446770_at	2610208K16Rik	RIKEN cDNA 2610208K16 gene	-1.96	0.106	1.56	0.243	1.28	0.49	-1.2	0.679	-0.08
1439171_at	C530008M17Rik	RIKEN cDNA C530008M17 gene	-2.02	0.382	2.09	0.179	-1.31	0.404	1.71	0.075	0.12
1418371_at	Dynll2	dynein light chain LC8-type 2	-1.07	0.171	-1.07	0.735	1.48	0.037	1.55	0.243	0.22
1437252_at	Gats	opposite strand transcription unit to Stag3	-1.12	0.05	1.42	0.216	1.04	0.874	-1.28	0.558	0.01
1433745_at	Trio	triple functional domain (PTPRF interacting)	1.05	0.666	-1.08	0.342	1.37	0.201	-1.12	0.428	0.06
1434369_a_at	Cryab	crystallin, alpha B	1.35	0.196	-1.02	0.893	1.02	0.94	-1.53	0.341	-0.04
1458038_at	---	---	1.69	0.229	1.03	0.859	-1.56	0.026	-1.34	0.574	-0.05
1447114_x_at	4930414L22Rik	RIKEN cDNA 4930414L22 gene	-1.54	0.371	-1.86	0.269	2.16	0.044	1.12	0.775	-0.03
1434751_at	Ids	iduronate 2-sulfatase	1.24	0.255	-1.27	0.265	1.32	0.395	-1.22	0.371	0.02
1430580_at	2810030E01Rik	RIKEN cDNA 2810030E01 gene	-1.6	0.257	-1.4	0.481	2.01	0.192	1.12	0.827	0.03
1420478_at	Nap1l1	nucleosome assembly protein 1-like 1	1.14	0.107	-1.03	0.807	1.24	0.163	-1.1	0.543	0.06
1441026_at	Parp4	poly (ADP-ribose) polymerase family, member 4	1.25	0.713	1.14	0.649	-1.03	0.862	-1.84	0.252	-0.12
1415902_at	Aldh7a1	aldehyde dehydrogenase family 7, member A1	1.42	0.537	-1.19	0.835	1.1	0.485	-1.01	0.962	0.08
1425696_at	Txnl6	thioredoxin-like 6	-1.13	0.61	1.07	0.662	1.4	0.66	-2.19	0.18	-0.21
1435585_at	Tceal7	transcription elongation factor A (SII)-like 7	1.59	0.566	-1.61	0.386	1.14	0.747	-1.23	0.633	-0.03
1439162_at	1700011J10Rik	RIKEN cDNA 1700011J10 gene	1.09	0.923	1.29	0.541	-1.02	0.981	-3.19	0.028	-0.46
1441427_at	Vwc2	von Willebrand factor C domain containing 2	-1.1	0.796	1.25	0.265	1.2	0.612	-1.07	0.813	0.07
1452771_s_at	Acsl3	acyl-CoA synthetase long-chain family member 3	-1.15	0.201	1.37	0.102	1.11	0.465	-1.06	0.743	0.07
1448840_at	Tmub1	transmembrane and ubiquitin-like domain containing 1	-1.11	0.35	1.12	0.482	1.33	0.1	-1.41	0.065	-0.02
1423652_at	Hbld2	HESB like domain containing 2	-1.03	0.892	-1.01	0.964	1.4	0.216	3.94	0.263	0.82
1427239_at	Ift122	intraflagellar transport 122 homolog (Chlamydomonas)	-1.02	0.872	-1.22	0.483	1.55	0.15	1.07	0.503	0.1
1437815_at	1700111A04Rik	RIKEN cDNA 1700111A04 gene	2.12	0.004	-2.4	0.244	-1.21	0.64	1.21	0.174	-0.07
1447668_x_at	Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	-1.54	0.521	1.3	0.452	1.4	0.215	-1.28	0.198	-0.03
1447075_at	C2ta	Class II transactivator	1.23	0.516	-1.03	0.938	1.16	0.644	-1.92	0.124	-0.14
1451050_at	Nt5c3	5'-nucleotidase, cytosolic III	-1.07	0.584	-1.12	0.125	1.52	0.229	3.99	0.166	0.83
1456815_at	Foxn1	forkhead box N1	2.06	0.01	-1.27	0.613	-1.97	0.138	2.7	0.081	0.38
1431744_a_at	Smap1	stromal membrane-associated protein 1	-1.35	0.404	-1.01	0.967	1.63	0.002	1.97	0.331	0.31
1421645_at	9930013L23Rik	RIKEN cDNA 9930013L23 gene	1.48	0.579	1.03	0.973	-1.18	0.7	-1.18	0.585	0.04
1427112_at	2700049H19Rik	RIKEN cDNA 2700049H19 gene	-1.08	0.74	1.37	0.581	1.06	0.688	-1.44	0.357	-0.02
1424485_at	Angptl3	angiopoietin-like 3	1.75	0.205	-1.09	0.319	-1.46	0.491	1.49	0.605	0.17
1456886_at	Brp44l	Brain protein 44-like	-1.07	0.249	1.04	0.752	1.38	0.087	-1.24	0.421	0.03
1431491_at	9430087N24Rik	RIKEN cDNA 9430087N24 gene	1.04	0.866	-2.33	0.147	1.89	0.027	-1.38	0.589	-0.19
1438517_at	Wwox	WW domain-containing oxidoreductase	-1.3	0.334	1.46	0.328	1.13	0.666	-1.54	0.131	-0.06
1454089_at	Apobec4	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 4 (putative)	-1.98	0.212	1.75	0.264	1.1	0.609	-1.06	0.941	-0.05
1418159_at	Tcfcp2	transcription factor CP2	-1.05	0.788	-1.05	0.109	1.45	0.208	1.22	0.117	0.14
1416625_at	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	1.54	0.213	1.05	0.657	-1.31	0.137	-1.2	0.595	0.02
1436888_at	Nhlh2	nescient helix loop helix 2	1.47	0.648	1.07	0.857	-1.23	0.579	-2.66	0.148	-0.34
1444787_at	Chd1	Chromodomain helicase DNA binding protein 1	1.27	0.434	1.59	0.13	-2.02	0.073	-1.11	0.671	-0.06
1416237_at	Eva1	epithelial V-like antigen 1	-1.09	0.49	-1.26	0.246	1.65	0.2	2.81	0.033	0.53
1445462_at	---	---	1.87	0.129	-1.35	0.53	-1.35	0.31	1.64	0.142	0.2
1447283_at	Tsga10	testis specific 10	-1.03	0.931	1.23	0.667	1.15	0.311	-1.11	0.726	0.06
1416264_at	Abcb9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	1.67	0.22	-1.37	0.513	-1.05	0.835	1.03	0.941	0.07
1428941_at	Zmym2	zinc finger, MYM-type 2	1.3	0.448	-1.11	0.492	1.15	0.66	-1.19	0.449	0.04
1426880_at	BC026657	cDNA sequence BC026657	-1.15	0.045	1.29	0.018	1.2	0.179	-1.05	0.81	0.07
1456953_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	1.64	0.356	-1.51	0.225	1.05	0.904	-1.35	0.529	-0.04
1427823_at	---	---	-1.19	0.536	1.45	0.24	1.06	0.588	-1.16	0.707	0.04

1442599_at	Slc12a9	Solute carrier family 12 (potassium/chloride transporters), member 9	1.25	0.714	-1.2	0.823	1.28	0.311	-1.58	0.054	-0.06
1455892_x_at	LOC622147 /// LOC	similar to melanoma antigen /// similar to melanoma antigen /// similar to melanon	-1.01	0.987	1.02	0.951	1.35	0.132	-1.13	0.654	0.06
1444029_at	Parp11	poly (ADP-ribose) polymerase family, member 11	-1.01	0.985	1.29	0.712	1.08	0.403	-1.9	0.293	-0.14
1438304_at	Cxxc4	CXXC finger 4	1.26	0.553	1.35	0.517	-1.34	0.33	-1.17	0.414	0.03
1420654_a_at	Gbe1	glucan (1,4-alpha-), branching enzyme 1	-1.03	0.884	1.06	0.74	1.33	0.425	-1.19	0.571	0.04
1455360_at	4833412L08Rik	RIKEN cDNA 4833412L08 gene	1.27	0.045	1.24	0.213	-1.17	0.586	-1.07	0.659	0.07
1440978_at	C920011G20Rik	RIKEN cDNA C920011G20 gene	-1.19	0.5	-1.24	0.519	1.71	0.166	1.5	0.373	0.2
1430021_a_at	Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A	-1.03	0.779	-1.16	0.203	1.52	0.025	1.31	0.348	0.16
1419467_at	Clec14a	C-type lectin domain family 14, member a	1.36	0.03	1.17	0.453	-1.2	0.099	-1.16	0.541	0.04
1435694_at	Arhgap26	Rho GTPase activating protein 26	1.12	0.586	-1.03	0.833	1.26	0.01	-1.9	0.217	-0.14
1437090_at	Ccdc63	coiled-coil domain containing 63	1.86	0.422	-1.09	0.886	-1.72	0.517	1.82	0.267	0.22
1431742_at	1810053B23Rik	RIKEN cDNA 1810053B23 gene	1.55	0.564	-1.09	0.884	-1.12	0.743	2.69	0.015	0.51
1418752_at	Aldh3a1	aldehyde dehydrogenase family 3, subfamily A1	-1.51	0.336	1.34	0.565	1.36	0.435	-1.47	0.408	-0.07
1437174_at	Tfdp2	transcription factor Dp 2	-1.07	0.464	-1.12	0.118	1.54	0.156	3.55	0.242	0.72
1431630_a_at	Klf3	Kruppel-like factor 3 (basic)	-1.16	0.591	-1.09	0.724	1.59	0.368	2.04	0.151	0.34
1435652_a_at	Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	1.14	0.436	1.28	0.005	-1.06	0.718	-1.07	0.631	0.07
1434574_at	9430008C03Rik	RIKEN cDNA 9430008C03 gene	-1.24	0.48	1.44	0.094	1.11	0.574	-1.49	0.188	-0.04
1435906_x_at	Gbp2	guanylate nucleotide binding protein 2	-1.03	0.73	1.35	0.465	1.04	0.793	-1.02	0.891	0.08
1444320_at	Ddhd2	DDHD domain containing 2	-1.06	0.853	1.51	0.329	-1.11	0.698	1.51	0.174	0.21
1424990_at	Tmem142a	transmembrane protein 142A	1.34	0.301	1.04	0.792	-1.02	0.932	-1.18	0.618	0.04
1417877_at	2310005P05Rik	RIKEN cDNA 2310005P05 gene	-1.12	0.563	1.21	0.265	1.26	0.214	-1.18	0.215	0.04
1460396_at	Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	1.02	0.756	-1.1	0.052	1.44	0.092	-1.39	0.062	-0.01
1430312_at	Wrb	tryptophan rich basic protein	1.1	0.814	1.41	0.5	-1.18	0.37	-1.33	0.184	0
1459744_at	Cd53	CD53 antigen	-1.45	0.497	1.33	0.399	1.35	0.101	-1.82	0.044	-0.15
1457405_at	Dnm3	Dynamin 3	1.48	0.385	1.31	0.603	-1.73	0.123	-1.05	0.823	0
1425549_at	Psen1	presenilin 1	-1.56	0.539	1.19	0.734	1.53	0.336	-1.04	0.929	0.03
1426168_a_at	Tcra /// A130082M0	T-cell receptor alpha chain /// RIKEN cDNA A130082M07 gene /// RIKEN cDNA A	-1.25	0.679	1.06	0.898	1.5	0.119	-2.36	0.086	-0.26
1431108_at	2410131K14Rik	RIKEN cDNA 2410131K14 gene	-1.4	0.741	1.76	0.409	-1.13	0.795	1.36	0.547	0.15
1440671_at	A130012E19Rik	RIKEN cDNA A130012E19 gene	1.19	0.294	1.36	0.082	-1.23	0.359	-1.15	0.295	0.04
1422997_s_at	Acot1 /// Acot2	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase 2	1.18	0.103	-3.95	0.026	1.93	0.23	-1.01	0.946	-0.46
1424522_at	Heatr1	HEAT repeat containing 1	-1.06	0.605	1.21	0.31	1.21	0.171	-1.18	0.126	0.04
1445444_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.77	0.247	-1.05	0.953	-1.56	0.204	2.41	0.253	0.39
1438838_at	B230206F22Rik	RIKEN cDNA B230206F22 gene	-1.05	0.834	1.08	0.713	1.33	0.108	-1.14	0.391	0.05
1450015_x_at	Sgpp1	sphingosine-1-phosphate phosphatase 1	-1.06	0.336	-1	0.984	1.43	0.323	1.14	0.618	0.13
1429066_at	4930565B19Rik	RIKEN cDNA 4930565B19 gene	1.19	0.298	-1.03	0.941	1.2	0.46	-1.33	0.174	0.01
1428148_s_at	Coro7	coronin 7	-1.18	0.507	1.42	0.007	1.09	0.565	-1.26	0.142	0.02
1415961_at	Itm2c	integral membrane protein 2C	1.09	0.42	1.4	0.047	-1.15	0.093	-1.13	0.633	0.05
1449558_at	F8	coagulation factor VIII	1.36	0.157	1.21	0.349	-1.27	0.242	-1.09	0.667	0.05
1432023_a_at	1700019H03Rik	RIKEN cDNA 1700019H03 gene	1.27	0.627	-1.07	0.711	1.15	0.38	-1.36	0.064	0
1420859_at	Pkia	protein kinase inhibitor, alpha	1.15	0.525	1.29	0.639	-1.08	0.483	-1.18	0.497	0.04
1426725_s_at	Ets1	E26 avian leukemia oncogene 1, 5' domain	1.09	0.272	1.39	0.031	-1.13	0.5	-2.13	0.095	-0.2
1432235_at	Epsti1	epithelial stromal interaction 1 (breast)	-2.24	0.036	1.13	0.735	1.79	0.091	-1.78	0.215	-0.28
1451992_at	Adrbk1	adrenergic receptor kinase, beta 1	1.14	0.369	-1.05	0.055	1.27	0.214	-1.46	0.145	-0.02
1440576_at	Cpn1	carboxypeptidase N, polypeptide 1	-1.3	0.509	-1.04	0.753	1.63	0.317	1.08	0.784	0.09
1455219_at	1110030E23Rik	RIKEN cDNA 1110030E23 gene	1.27	0.184	1.38	0.468	-1.4	0.019	-1.3	0.177	-0.01
1422703_at	Gyk	glycerol kinase	-1.04	0.856	-1.18	0.048	1.56	0.193	1.66	0.281	0.25
1454240_at	Nfe2l3	nuclear factor, erythroid derived 2, like 3	1.73	0.316	-1.13	0.796	-1.34	0.175	1.26	0.498	0.13
1438263_at	9430020K01Rik	RIKEN cDNA 9430020K01 gene	1.7	0.361	-1.36	0.47	-1.07	0.913	2.62	0.023	0.47
1455069_x_at	Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	-1.25	0.123	1.51	0.017	1.06	0.657	-1.5	0.121	-0.05
1438316_a_at	Ccdc102a /// LOC6	coiled-coil domain containing 102A /// similar to CG31638-PA	1.19	0.349	-1.02	0.94	1.19	0.177	-2.4	0.021	-0.26
1457512_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13009	1.88	0.216	-1.1	0.533	-1.73	0.277	1.34	0.629	0.1
1453599_at	Trim71	tripartite motif-containing 71	-2.01	0.272	1.99	0.095	-1.13	0.814	2.16	0.075	0.25
1432620_at	---	---	1.56	0.415	-1.06	0.922	-1.16	0.635	1.08	0.902	0.11

1421280_at	Gabra1	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	1.64	0.494	-1.31	0.298	-1.04	0.928	1.18	0.635	0.12
1422132_at	Mthfr	5,10-methylenetetrahydrofolate reductase	1.44	0.5	-1.27	0.251	1.14	0.264	-2.01	0.462	-0.18
1429129_at	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1	1.12	0.384	1.42	0.136	-1.22	0.17	-1.36	0.37	-0.01
1417977_at	Eif4e3	eukaryotic translation initiation factor 4E member 3	1.29	0.159	1.22	0.124	-1.17	0.365	-1.5	0.055	-0.04
1454777_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	1.09	0.649	-1.04	0.774	1.32	0.342	-1.27	0.6	0.02
1444043_at	Gli3	GLI-Kruppel family member GLI3	1.28	0.708	1.48	0.345	-1.64	0.135	-1.29	0.659	-0.04
1446189_at	Myst4	MYST histone acetyltransferase monocytic leukemia 4	1.31	0.529	1.56	0.485	-2.02	0.062	-1.07	0.909	-0.06
1421896_at	Elk1	ELK1, member of ETS oncogene family	-1.19	0.828	1.53	0.22	-1.01	0.964	1.01	0.98	0.09
1447250_a_at	2610301F02Rik	RIKEN cDNA 2610301F02 gene	1.75	0.162	-1.02	0.97	-1.58	0.251	1.43	0.123	0.15
1459303_at	Gpm6a	Glycoprotein m6a	1.57	0.254	1.03	0.923	-1.31	0.581	-1.1	0.794	0.05
1438298_a_at	---	---	-1.6	0.613	1.09	0.809	1.65	0.278	-2.74	0.235	-0.4
1440879_at	Abca9	ATP-binding cassette transporter sub-family A member 9	1.25	0.282	1.27	0.323	-1.18	0.561	-1.27	0.669	0.02
1453541_at	Pfkl	phosphofructokinase, liver, B-type	-1.07	0.161	1.34	0.387	1.09	0.553	-1	0.958	0.09
1442246_at	LOC668224 /// LOC	hypothetical protein LOC668224 /// hypothetical protein LOC669738 /// hypothetic	-1.4	0.224	1.28	0.659	1.37	0.625	-2.27	0.268	-0.25
1437488_at	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	1.27	0.775	1.24	0.483	-1.16	0.444	-1.18	0.539	0.04
1441683_at	1110033M05Rik	RIKEN cDNA 1110033M05 gene	1.35	0.425	1.35	0.139	-1.49	0.054	-1.28	0.488	-0.02
1447833_x_at	Mfap2	microfibrillar-associated protein 2	-1.37	0.619	1.74	0.392	-1.11	0.775	1.02	0.885	0.07
1445976_at	C80279	expressed sequence C80279	-1.05	0.907	1.2	0.754	1.22	0.513	-1.51	0.137	-0.04
1456869_at	2210018M03Rik	RIKEN cDNA 2210018M03 gene	1.13	0.838	-1.45	0.495	1.55	0.185	-1.36	0.662	-0.03
1444213_at	1700012D14Rik	RIKEN cDNA 1700012D14 gene	1.19	0.522	-1.23	0.428	1.36	0.418	-1.45	0.206	-0.03
1438621_x_at	Axl	AXL receptor tyrosine kinase	1.22	0.687	-1.59	0.056	1.53	0.277	-1	0.993	0.04
1436423_at	E430004N04Rik	RIKEN cDNA E430004N04 gene	1.22	0.755	1.19	0.592	-1.04	0.771	-1.84	0.138	-0.12
1454143_at	4930442H23Rik	RIKEN cDNA 4930442H23 gene	1.94	0.082	-3.11	0.051	1.11	0.815	-2.02	0.408	-0.52
1460334_at	Dbnl	drebrin-like	-1.13	0.403	1.06	0.688	1.42	0.033	-1.53	0.132	-0.04
1437366_at	AI608492	expressed sequence AI608492	-1.37	0.241	1.17	0.793	1.47	0.119	-1.96	0.089	-0.17
1444129_at	---	---	-1.03	0.9	1.25	0.648	1.14	0.647	-1.54	0.253	-0.04
1437800_at	Edaradd	EDAR (ectodysplasin-A receptor)-associated death domain	-1.27	0.642	1.26	0.672	1.32	0.611	-3.24	0.051	-0.48
1456241_a_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	-1.07	0.614	1.03	0.804	1.4	0.036	-1.11	0.422	0.06
1435405_at	Setd4	SET domain containing 4	1.26	0.222	1.4	0.387	-1.42	0.101	-1.61	0.066	-0.09
1445220_at	Btbd9	BTB (POZ) domain containing 9	1.15	0.814	1.57	0.453	-1.54	0.166	-2.79	0.278	-0.4
1454965_at	D430039N05Rik	RIKEN cDNA D430039N05 gene	1.51	0.174	1.23	0.236	-1.59	0.188	-1.79	0.046	-0.16
1435234_at	Ncoa2	nuclear receptor coactivator 2	1.05	0.75	-1.02	0.868	1.34	0.319	-1.02	0.831	0.09
1453584_at	Stk36	serine/threonine kinase 36 (fused homolog, Drosophila)	-1.24	0.138	1.01	0.944	1.55	0.573	-1.15	0.328	0.04
1419500_at	Pabpc2	poly A binding protein, cytoplasmic 2	-1.08	0.833	-1.02	0.94	1.46	0.361	1.68	0.539	0.26
1416523_at	Rnase1	ribonuclease, RNase A family, 1 (pancreatic)	1.41	0.59	1.5	0.409	-2.16	0.167	-2.08	0.418	-0.33
1435419_at	Rgag4	retrotransposon gag domain containing 4	-1.48	0.308	1.53	0.076	1.17	0.512	-1.99	0.089	-0.19
1416785_at	Kcnip1	Kv channel-interacting protein 1	-1.24	0.587	1.58	0.115	-1.02	0.929	1.02	0.974	0.09
1450630_at	Qtrt1	queuine tRNA-ribosyltransferase 1	1.19	0.577	-1.13	0.794	1.29	0.089	-1.18	0.254	0.04
1428223_at	Mfsd2	major facilitator superfamily domain containing 2	1.09	0.718	-1.15	0.705	1.41	0.01	-1.13	0.585	0.06
1440700_a_at	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	-1.13	0.264	1.31	0.618	1.17	0.516	-1.46	0.654	-0.03
1438712_at	Dennd2d	DENN/MADD domain containing 2D	1.19	0.234	1.25	0.37	-1.08	0.59	-1.79	0.158	-0.11
1430150_at	Dcp2	DCP2 decapping enzyme homolog (S. cerevisiae)	-1.38	0.657	1.13	0.868	1.52	0.033	-1.21	0.316	0.01
1430184_at	Zfp597	zinc finger protein 597	-1.36	0.475	1.49	0.525	1.14	0.363	-1.26	0.409	0
1457063_at	9530033F24Rik	RIKEN cDNA 9530033F24 gene	1.07	0.824	1.58	0.009	-1.37	0.169	-1.54	0.125	-0.07
1420189_at	---	---	-1.62	0.354	1.61	0.154	1.14	0.743	-1.88	0.147	-0.18
1422913_at	Prm3	protamine 3	2.37	0.282	-1.34	0.613	-3.9	0.045	1.27	0.685	-0.4
1436792_at	Whdc1	WAS protein homology region 2 domain containing 1	1.35	0.233	1.04	0.762	-1.02	0.954	-1.19	0.305	0.05
1446886_at	Usp3	Ubiquitin specific peptidase 3	1.52	0.184	1.25	0.564	-1.67	0.148	-2.74	0.093	-0.41
1422985_at	Fzd1	frizzled homolog 1 (Drosophila)	-1.06	0.883	-1.09	0.753	1.51	0.202	1.31	0.481	0.17
1425121_a_at	BC006965	cDNA sequence BC006965	1.43	0.515	-1.2	0.603	1.11	0.79	-2.32	0.027	-0.25
1439872_at	---	Transcribed locus	1.13	0.851	1.59	0.23	-1.52	0.096	-1.4	0.149	-0.05
1448311_at	Usp5	ubiquitin specific peptidase 5 (isopeptidase T)	-1.1	0.686	-1.08	0.429	1.54	0.116	1.17	0.591	0.13
1448656_at	Cacnb3	calcium channel, voltage-dependent, beta 3 subunit	1.45	0.009	-1.22	0.476	1.1	0.784	-2.06	0.095	-0.18

1424900_at	Slc29a4	solute carrier family 29 (nucleoside transporters), member 4	-1.1	0.632	1.01	0.983	1.45	0.096	-1.03	0.915	0.08
1460130_at	LOC433632	hypothetical LOC433632	-1.67	0.621	1.84	0.005	-1.07	0.822	1.08	0.87	0.05
1451437_at	Zdhhc20	zinc finger, DHHC domain containing 20	1.45	0.023	1.03	0.855	-1.12	0.464	-1.62	0.365	-0.07
1427630_x_at	Ceacam1	CEA-related cell adhesion molecule 1	1.52	0.17	-1.17	0.381	1	0.992	-1.1	0.482	0.06
1426928_at	Ccdc93	coiled-coil domain containing 93	1.51	0.037	-1.47	0.265	1.18	0.481	-1.61	0.213	-0.1
1427184_at	Tcrb-V13	T-cell receptor beta, variable 13	1.04	0.903	1.68	0.557	-1.52	0.079	-3.13	0.098	-0.48
1439839_at	D130051D11Rik	RIKEN cDNA D130051D11 gene	1.26	0.421	1.54	0.319	-1.74	0.001	-1.33	0.168	-0.07
1439127_at	AI314180	expressed sequence AI314180	1.28	0.568	-1.04	0.936	1.13	0.729	-1.16	0.774	0.05
1446645_at	A730037C10Rik	RIKEN cDNA A730037C10 gene	-1.85	0.137	1.1	0.753	1.74	0.333	-1.15	0.537	-0.04
1428469_a_at	Dzip1	DAZ interacting protein 1	-1.12	0.87	1.17	0.763	1.31	0.276	-2.07	0.136	-0.18
1420716_at	Cd247	CD247 antigen	1.73	0.456	-1.69	0.368	1.05	0.945	-2.08	0.012	-0.25
1435938_at	Ckap2l	cytoskeleton associated protein 2-like	-1.2	0.176	1.57	0.263	-1.03	0.894	2.51	0.215	0.46
1434818_at	9330159K06	hypothetical protein 9330159K06	1.36	0.618	1.36	0.55	-1.51	0.287	-1.94	0.049	-0.18
1422592_at	Ctnnd2	catenin (cadherin associated protein), delta 2	1.5	0.358	1.05	0.939	-1.22	0.486	-1.52	0.007	-0.05
1460725_at	Xpa	xeroderma pigmentosum, complementation group A	1.23	0.319	-1.08	0.46	1.22	0.091	-1.33	0.371	0.01
1420651_at	Ate1	arginine-tRNA-protein transferase 1	-1.07	0.745	-1.5	0.433	1.78	0.474	1.05	0.922	0.06
1446928_at	Dnajc17 /// LOC638	DnaJ (Hsp40) homolog, subfamily C, member 17 /// similar to DnaJ (Hsp40) hom	1.32	0.657	1.26	0.717	-1.25	0.65	-2	0.106	-0.17
1419289_a_at	Syngr1	synaptogyrin 1	-1.06	0.88	-1.04	0.933	1.47	0.117	3.54	0.237	0.73
1424879_at	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	1.09	0.737	1.49	0.368	-1.26	0.495	-1.47	0.312	-0.04
1420363_at	Bik	Bcl2-interacting killer	1.29	0.43	1.27	0.678	-1.22	0.503	-1.91	0.365	-0.14
1455840_at	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	1.35	0.141	1.24	0.146	-1.28	0.029	-1.43	0.23	-0.03
1448275_at	Tmem19	transmembrane protein 19	1.16	0.519	-1.06	0.739	1.27	0.416	-1.22	0.129	0.04
1447798_at	1700123O21Rik	RIKEN cDNA 1700123O21 gene	1.09	0.93	1.34	0.778	-1.05	0.68	-1.35	0.565	0.01
1449486_at	Ces1	carboxylesterase 1	-1.91	0.265	1.32	0.01	1.53	0.028	-1.24	0.767	-0.07
1431193_at	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor	-2.21	0.509	1.46	0.088	1.47	0.383	-2.73	0.038	-0.5
1449087_at	Rnf141	ring finger protein 141	-1.15	0.653	-1.27	0.501	1.72	0.369	1.63	0.276	0.23
1428893_at	Osbpl7	oxysterol binding protein-like 7	-1.23	0.184	1.42	0.174	1.15	0.269	-1.05	0.764	0.07
1444665_at	4930402E16Rik	RIKEN cDNA 4930402E16 gene	1.31	0.612	1.1	0.669	-1.03	0.905	-1.39	0.659	0
1451794_at	Tmcc3	transmembrane and coiled coil domains 3	1.39	0.139	-1.08	0.758	1.07	0.807	-1.25	0.588	0.03
1428397_at	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	1.13	0.156	-2.09	0.106	1.77	0.06	-1.8	0.185	-0.25
1415795_at	Spin	spindlin	-1.09	0.15	1.16	0.565	1.3	0.258	-1.53	0.3	-0.04
1444489_at	Slc25a12	Solute carrier family 25 (mitochondrial carrier, Aralar), member 12	-1.07	0.744	1.38	0.044	1.06	0.56	-1.02	0.918	0.09
1453056_at	Slc16a13	solute carrier family 16 (monocarboxylic acid transporters), member 13	-1.03	0.87	1.36	0.547	1.04	0.791	-1.16	0.357	0.05
1433805_at	Jak1	Janus kinase 1	-1	0.944	1.2	0.053	1.18	0.291	-1.29	0.296	0.02
1436182_at	---	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:261(	1.18	0.808	1.3	0.521	-1.11	0.683	-2.73	0.074	-0.34
1449015_at	Retnla	resistin like alpha	-1.84	0.107	1.97	0.111	-1.16	0.357	3.58	0.301	0.64
1449120_a_at	Pcm1	pericentriolar material 1	1.08	0.771	1.32	0.294	-1.02	0.859	-1.58	0.035	-0.05
1459747_at	---	---	1.56	0.615	-1.14	0.766	-1.05	0.921	1.07	0.853	0.11
1458649_at	AI662245	expressed sequence AI662245	-1.11	0.761	1.27	0.685	1.21	0.665	-2.14	0.308	-0.19
1441926_x_at	Tmie	transmembrane inner ear	1.06	0.575	-1	0.994	1.32	0.053	-1.62	0.206	-0.06
1448928_at	Hdac6 /// LOC6691	histone deacetylase 6 /// similar to Histone deacetylase 6 (HD6) (Histone deacety	-1.06	0.51	-1.03	0.82	1.47	0.074	1.09	0.748	0.12
1436422_at	BC026590	cDNA sequence BC026590	-1.01	0.905	1.29	0.128	1.1	0.433	-1.22	0.005	0.04
1449275_at	2310038H17Rik	RIKEN cDNA 2310038H17 gene	-1.03	0.57	1.03	0.746	1.38	0.166	-1.03	0.76	0.09
1422830_s_at	Drd4	dopamine receptor 4	1.47	0.226	1.21	0.185	-1.44	0.281	-1.18	0.571	0.02
1420254_at	---	---	-1.09	0.714	1.7	0.493	-1.3	0.606	1.93	0.292	0.31
1416403_at	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	-1.07	0.702	-1.23	0.407	1.63	0.283	6.51	0.204	1.46
1427082_at	4632417N05Rik	RIKEN cDNA 4632417N05 gene	1.37	0.689	-1.09	0.267	1.1	0.868	-2.14	0.397	-0.19
1452363_a_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.23	0.095	-1.4	0.026	1.85	0.181	1.23	0.54	0.11
1417335_at	Sult2b1	sulfotransferase family, cytosolic, 2B, member 1	1.48	0.011	1.03	0.951	-1.16	0.436	-1.38	0.177	-0.01
1432881_at	4932437C15Rik	RIKEN cDNA 4932437C15 gene	-1.6	0.304	1.01	0.988	1.74	0.197	-2.45	0.199	-0.32
1454076_at	Lrrc17	leucine rich repeat containing 17	1.4	0.037	1.16	0.643	-1.21	0.029	-1.31	0.228	0.01
1427811_at	Tyms	thymidylate synthase	-1.7	0.179	-1.55	0.359	2.15	0.088	1.35	0.494	0.06
1440727_at	---	Transcribed locus	1.04	0.901	-1.32	0.561	1.59	0.048	-1.29	0.524	0.01

1425889_at	Wnt9a	wingless-type MMTV integration site 9A	-1.12	0.589	1.31	0.237	1.18	0.73	-1.76	0.402	-0.1
1455187_at	Zbtb40 /// LOC638(	zinc finger and BTB domain containing 40 /// similar to zinc finger and BTB domai	-1.2	0.684	1.15	0.568	1.4	0.052	-1.23	0.255	0.03
1451132_at	Pbxip1	pre-B-cell leukemia transcription factor interacting protein 1	-1.03	0.635	1.11	0.255	1.31	0.141	-1.43	0.269	-0.01
1447004_at	Plcb1	Phospholipase C, beta 1	-1.4	0.358	-1.17	0.68	1.81	0.085	1.2	0.726	0.11
1421395_at	Zik1	zinc finger protein interacting with K protein 1	1.27	0.689	-1.11	0.725	1.2	0.7	-1.35	0.536	0.01
1449662_at	Reep1	Receptor accessory protein 1	1.58	0.304	-1.49	0.366	1.13	0.739	-1.25	0.602	-0.01
1434495_at	Zfp278	zinc finger protein 278	1.1	0.003	-1.03	0.971	1.31	0.115	-1.09	0.729	0.07
1422622_at	Nos3	nitric oxide synthase 3, endothelial cell	-1.05	0.831	1.2	0.223	1.23	0.224	-1.16	0.247	0.06
1434382_at	Serinc2	serine incorporator 2	1.26	0.095	1.21	0.527	-1.09	0.695	-1.23	0.325	0.04
1432170_at	Tsfm	Ts translation elongation factor, mitochondrial	1.53	0.422	-1.04	0.93	-1.11	0.878	1.16	0.74	0.13
1455415_at	A730056A06Rik	RIKEN cDNA A730056A06 gene	-1.35	0.503	1.39	0.088	1.26	0.278	-1.32	0.753	-0.01
1450632_at	LOC433749 /// LOC	similar to aplysia ras-related homolog A2 /// similar to aplysia ras-related homolog	-1.11	0.273	1.1	0.585	1.39	0.1	-1.03	0.827	0.09
1456627_at	Ubqln2	Ubiquilin 2	-1.04	0.85	1.24	0.564	1.19	0.758	-1.45	0.455	-0.02
1426456_a_at	Pias2	protein inhibitor of activated STAT 2	-1.1	0.078	-1.02	0.819	1.5	0.029	1.33	0.101	0.18
1429288_x_at	Stx18	syntaxin 18	-1.07	0.69	1.21	0.117	1.24	0.219	-1.16	0.346	0.05
1442800_x_at	A830059I20Rik	RIKEN cDNA A830059I20 gene	-1.04	0.88	1.64	0.263	-1.27	0.223	1.12	0.619	0.11
1447836_x_at	4921525O09Rik	RIKEN cDNA 4921525O09 gene	1.51	0.005	-1.15	0.748	1.01	0.992	-1.16	0.819	0.05
1427981_a_at	Csad	cysteine sulfinic acid decarboxylase	1.39	0.286	-1.1	0.797	1.08	0.686	-1.2	0.441	0.04
1420612_s_at	Ptp4a2	protein tyrosine phosphatase 4a2	1.23	0.232	-1	0.981	1.16	0.476	-1.2	0.172	0.05
1427575_at	Fbxw14	F-box and WD-40 domain protein 14	-1.14	0.748	-1	0.996	1.51	0.535	1.8	0.316	0.29
1458429_at	Arhgap30	Rho GTPase activating protein 30	-1.67	0.428	1.41	0.457	1.38	0.444	-1.11	0.739	0
1422431_at	Magee1	melanoma antigen, family E, 1	-1.04	0.897	1.05	0.815	1.37	0.285	-1.08	0.722	0.08
1455030_at	Ptprj	protein tyrosine phosphatase, receptor type, J	-1.11	0.302	1.22	0.294	1.27	0.418	-1.43	0.414	-0.01
1458963_at	1810054D07Rik	RIKEN cDNA 1810054D07 gene	-1.39	0.625	1.04	0.906	1.63	0.011	-1.03	0.907	0.06
1448941_at	B4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	-1.34	0.172	-1.31	0.622	1.88	0.306	2.06	0.286	0.32
1460222_at	Sh3bp1	SH3-domain binding protein 1	-1.01	0.901	1.27	0.273	1.13	0.634	-1.42	0.471	-0.01
1425522_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	1.96	0.221	-1.68	0.099	-1.2	0.507	1.23	0.621	0.08
1457941_at	---	PREDICTED: Mus musculus similar to serine-threonine protein kinase pim-2 isof(	1.28	0.744	1.11	0.801	-1.01	0.982	-1.41	0.415	-0.01
1428960_at	4933434I06Rik	RIKEN cDNA 4933434I06 gene	1.67	0.638	-1.34	0.55	-1.03	0.898	2.97	0.009	0.57
1433139_at	Btbd14b	BTB (POZ) domain containing 14B	-1.71	0.321	1.37	0.513	1.43	0.352	-1.17	0.793	-0.02
1430960_at	4933440J02Rik	RIKEN cDNA 4933440J02 gene	1.65	0.194	-1.38	0.455	1.02	0.972	-1.13	0.898	0.04
1421722_at	---	---	1.25	0.353	1.66	0.425	-2.09	0.383	-1.1	0.691	-0.07
1422293_a_at	Kctd1	potassium channel tetramerisation domain containing 1	-1.08	0.529	1.43	0.455	1.03	0.774	-1.47	0.256	-0.02
1451807_at	Nr1i2	nuclear receptor subfamily 1, group I, member 2	-1.35	0.262	-1.55	0.29	2	0.316	2.29	0.217	0.35
1417978_at	Eif4e3	eukaryotic translation initiation factor 4E member 3	1.11	0.433	1.51	0.096	-1.31	0.076	-1.19	0.205	0.03
1456025_at	Dcamkl2	doublecortin and CaM kinase-like 2	1.32	0.436	1.24	0.576	-1.21	0.705	-1.06	0.419	0.07
1438314_at	Pctk1	PCTAIRE-motif protein kinase 1	-1.77	0.063	1.56	0.258	1.26	0.698	-1.58	0.536	-0.13
1436235_x_at	4732471D19Rik	RIKEN cDNA 4732471D19 gene	1.18	0.177	-1.36	0.18	1.47	0.063	-1.22	0.127	0.02
1455062_at	AU017455	expressed sequence AU017455	1.13	0.868	1.28	0.515	-1.02	0.943	-1.17	0.699	0.05
1416684_at	Fbl	fibrillarin	-1.14	0.185	1	0.978	1.51	0.217	-1.15	0.421	0.06
1432839_at	6430598H11Rik	RIKEN cDNA 6430598H11 gene	-2.84	0.014	2.25	0.162	-1.27	0.39	1.14	0.812	-0.18
1434537_at	Slco3a1	solute carrier organic anion transporter family, member 3a1	1.11	0.501	1.37	0.231	-1.11	0.207	-1.26	0.524	0.03
1448926_at	Hoxa5	homeo box A5	-1.2	0.089	1.56	0.264	-1	0.996	1.54	0.195	0.22
1418688_at	Calcr	calcitonin receptor	1.43	0.115	1.15	0.85	-1.24	0.384	-1.1	0.829	0.06
1449885_at	Tmem47	transmembrane protein 47	1.19	0.072	1.27	0.455	-1.08	0.785	-1.72	0.268	-0.08
1417339_a_at	Dynll1 /// LOC6277	dynein light chain LC8-type 1 /// similar to dynein, cytoplasmic, light peptide /// sin	1.04	0.393	1.58	0.239	-1.31	0.005	-1.12	0.534	0.05
1441251_a_at	2010001A14Rik	RIKEN cDNA 2010001A14 gene	1.24	0.698	1.16	0.616	-1.01	0.988	-4.05	0.164	-0.67
AFFX-DapX-5_at	---	---	1.38	0.602	-1.13	0.679	1.12	0.812	-1.89	0.459	-0.13
1436892_at	Spred2	sprouty-related, EVH1 domain containing 2	1.56	0.309	-1.26	0.321	1.03	0.902	-1.67	0.176	-0.08
1420143_at	Mnab	membrane associated DNA binding protein	-1.46	0.503	1.83	0.089	-1.15	0.602	1.95	0.053	0.29
1434247_at	Ldhal6b	lactate dehydrogenase A-like 6B	-1.11	0.742	1.2	0.568	1.29	0.051	-2.49	0.273	-0.28
1437048_x_at	Stxbp2	syntaxin binding protein 2	1.14	0.261	-1.06	0.48	1.31	0.035	-1.27	0.271	0.03
1440508_at	---	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C63003	1	0.998	1.42	0.13	-1.03	0.949	-1.54	0.387	-0.04

1460069_at	Smc6	structural maintenance of chromosomes 6	1.65	0.007	1.01	0.978	-1.37	0.544	-1.33	0.484	-0.01
1460110_at	Rttn	rotatin	1.08	0.746	-1.13	0.771	1.43	0.013	-1.1	0.742	0.07
1447681_x_at	Ptcd2	Pentatricopeptide repeat domain 2	-1.44	0.135	1.58	0.355	1.12	0.791	-1.02	0.792	0.06
1416887_at	C1d	nuclear DNA binding protein	1.76	0.18	-1.38	0.433	-1.1	0.799	1.86	0.389	0.28
1424048_a_at	Cyb5r1	cytochrome b5 reductase 1	-1.01	0.848	1.26	0.014	1.15	0.164	-1.03	0.378	0.09
1453553_at	---	---	1.38	0.288	1.22	0.803	-1.27	0.407	-1.17	0.414	0.04
1419859_at	---	Transcribed locus	-1.44	0.432	2.45	0.066	-4.16	0	1.81	0.295	-0.33
1431469_a_at	Cxxc5	CXXC finger 5	1.15	0.59	-1.09	0.089	1.32	0.137	-1.75	0.105	-0.09
1435191_at	Cdsn	corneodesmosin	-1.01	0.985	1.6	0.155	-1.25	0.004	1.41	0.248	0.19
1448411_at	Wfs1	Wolfram syndrome 1 homolog (human)	-1.01	0.939	-1.05	0.742	1.44	0.018	1.11	0.745	0.13
1425686_at	Cflar	CASP8 and FADD-like apoptosis regulator	1.33	0.16	-1.04	0.684	1.1	0.623	-1.08	0.651	0.08
1440032_at	E130008O17Rik	RIKEN cDNA E130008O17 gene	1.53	0.449	1.25	0.574	-1.65	0.058	-1.55	0.076	-0.1
1419617_at	Kcnn1	potassium intermediate/small conductance calcium-activated channel, subfamily	-1.17	0.715	1.29	0.367	1.25	0.723	-1.45	0.687	-0.02
1420794_at	Art2b	ADP-ribosyltransferase 2b	-1.69	0.352	1.37	0.145	1.43	0.325	-2.47	0.135	-0.34
1427179_at	Krt33b	keratin 33B	-1.15	0.648	1.32	0.491	1.2	0.184	-1.02	0.853	0.09
1436464_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330003D	1.76	0.23	-1.18	0.147	-1.28	0.285	1.32	0.751	0.16
1416728_at	Csnk2b	casein kinase 2, beta polypeptide	-1.04	0.511	-1.21	0.032	1.6	0.008	1.24	0.109	0.15
1433495_at	Glt25d1	glycosyltransferase 25 domain containing 1	1.23	0.375	1.16	0.099	-1	0.988	-1.38	0.2	0
1441577_at	C530014P21Rik	RIKEN cDNA C530014P21 gene	-1.37	0.11	2.11	0.141	-1.8	0.115	1.25	0.687	0.05
1424129_at	Mfsd1	major facilitator superfamily domain containing 1	-1.1	0.578	-1.01	0.947	1.49	0.224	1.1	0.416	0.12
1418394_a_at	Cd97	CD97 antigen	-1.25	0.16	1.15	0.139	1.44	0.005	-1.51	0.311	-0.04
1451092_a_at	Rangap1	RAN GTPase activating protein 1	-1.07	0.775	-1.05	0.773	1.51	0.025	2.18	0.238	0.39
1417279_at	Itpr1	inositol 1,4,5-triphosphate receptor 1	-1.06	0.632	1.16	0.324	1.29	0.199	-1.25	0.19	0.04
1432900_at	BC026657	cDNA sequence BC026657	-2.11	0.396	1.68	0.535	1.24	0.379	-1.56	0.033	-0.19
1446171_at	A230107N01Rik	RIKEN cDNA A230107N01 gene	1.49	0.121	-1.26	0.558	1.11	0.756	-1.19	0.766	0.04
1446204_at	8030451K01Rik	RIKEN cDNA 8030451K01 gene	1.59	0.236	1.06	0.923	-1.35	0.057	-1.51	0.367	-0.05
1451082_at	1300018I05Rik	RIKEN cDNA 1300018I05 gene	1.02	0.942	-1.16	0.495	1.52	0.18	-1.01	0.983	0.09
1441281_s_at	Ninj1	ninjurin 1	-1.01	0.981	1.17	0.166	1.23	0.408	-1.18	0.545	0.05
1445201_at	Zfp53	zinc finger protein 53	1.29	0.034	1.2	0.397	-1.11	0.672	-1.97	0.078	-0.15
1460585_x_at	Pisd	phosphatidylserine decarboxylase	1.11	0.523	-1.02	0.529	1.31	0.003	-1.22	0.315	0.04
1421947_at	Gng12	guanine nucleotide binding protein (G protein), gamma 12	-1.06	0.792	-1.01	0.907	1.46	0.112	1.85	0.018	0.31
1435713_at	Mettl2	methyltransferase like 2	1.42	0.046	1.09	0.7	-1.12	0.592	-1.18	0.016	0.05
1457897_at	---	Transcribed locus	-1.22	0.564	1.04	0.85	1.53	0.126	-1.38	0.097	0
1460216_at	Acads	acyl-Coenzyme A dehydrogenase, short chain	-1	0.982	-1.05	0.695	1.45	0.086	1.04	0.707	0.11
1449181_at	Fech	ferrochelatase	-1.09	0.316	-1.05	0.548	1.52	0.152	5.03	0.164	1.11
1434483_at	Usp12	ubiquitin specific peptidase 12	1.47	0.11	1.18	0.37	-1.35	0.082	-1.15	0.603	0.04
1431716_at	Herc4	hect domain and RLD 4	-1.3	0.463	1.58	0.125	1.04	0.868	-1.36	0.279	-0.01
1434024_at	Nphp4	nephronophthisis 4 (juvenile) homolog (human)	-1.36	0.032	-1.23	0.72	1.85	0.028	1.17	0.468	0.11
1431350_at	C130036L24Rik	RIKEN cDNA C130036L24 gene	-1.06	0.858	1.69	0.131	-1.31	0.414	1.3	0.485	0.16
1456511_x_at	Eras	ES cell-expressed Ras	1.54	0.244	1.06	0.942	-1.24	0.522	-1.8	0.318	-0.11
1436374_x_at	F11r	F11 receptor	-1.45	0.413	-1.02	0.961	1.72	0.062	1.39	0.216	0.16
1433817_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	1.13	0.465	-1.23	0.07	1.45	0.068	-1.11	0.709	0.06
1458403_at	Tnik /// LOC665113	TRAF2 and NCK interacting kinase /// similar to [Segment 1 of 2] Traf2 and NCK-	1.21	0.288	1.31	0.693	-1.15	0.638	-2.29	0.12	-0.23
1429609_at	1700001D09Rik	RIKEN cDNA 1700001D09 gene	-1.5	0.438	1.24	0.681	1.49	0.141	-1.22	0.608	0
1443311_at	Thap4	THAP domain containing 4	1.52	0.281	-2.18	0.095	1.42	0.466	-1.18	0.714	-0.11
1446976_at	D7Ertd758e	DNA segment, Chr 7, ERATO Doi 758, expressed	1.55	0.026	1.29	0.636	-1.81	0.131	-1.58	0.337	-0.13
1458653_at	Panx1	Pannexin 1	1.42	0.502	1.1	0.8	-1.14	0.463	-1.47	0.314	-0.02
1425745_a_at	Tacc2	transforming, acidic coiled-coil containing protein 2	-1.04	0.64	1.4	0.269	1.03	0.895	-1.4	0.282	0
1416583_at	Bad	Bcl-associated death promoter	1.25	0.211	1.27	0.365	-1.14	0.389	-1.03	0.934	0.09
1418215_at	Mep1b	meprin 1 beta	-1.03	0.743	1.47	0.406	-1.05	0.748	1.12	0.467	0.13
1442867_at	---	---	1.47	0.229	1.11	0.677	-1.23	0.622	-1.14	0.352	0.05
1433138_at	---	---	-1.17	0.739	-1.03	0.912	1.57	0.29	2.21	0.341	0.39
1451295_a_at	Chd4	chromodomain helicase DNA binding protein 4	1.18	0.382	-1.07	0.603	1.29	0.257	-1.1	0.712	0.07

1454838_s_at	AW548124	expressed sequence AW548124	1.02	0.943	-1.18	0.117	1.53	0.032	-1.82	0.132	-0.11
1438558_x_at	Foxq1	Forkhead box Q1	1.27	0.213	-1.17	0.607	1.27	0.131	-1.44	0.486	-0.02
1447551_x_at	Lphn3	latrophilin 3	1.44	0.62	1.4	0.114	-1.78	0.097	-1.6	0.452	-0.14
1425611_a_at	Cutl1	cut-like 1 (Drosophila)	-1.03	0.905	-1.03	0.931	1.46	0.089	1.24	0.101	0.16
1427367_at	Efcab4a	EF-hand calcium binding domain 4A	1.51	0.201	1.08	0.757	-1.24	0.12	-1.01	0.958	0.08
1458224_at	Lrrc2	Leucine rich repeat containing 2	1.16	0.761	1.37	0.442	-1.16	0.663	-1.44	0.533	-0.02
1458486_at	---	---	1.33	0.576	1.2	0.554	-1.15	0.49	-1.69	0.111	-0.08
1421630_at	Zfy1 /// Zfy2	zinc finger protein 1, Y linked /// zinc finger protein 2, Y linked	-1.86	0.162	1.77	0.276	1.09	0.73	-1.1	0.351	-0.02
1458990_at	Setd5	SET domain containing 5	-2.03	0.482	2.37	0.147	-1.87	0.203	1.08	0.892	-0.11
1427304_at	Vps18	vacuolar protein sorting 18 (yeast)	1.13	0.642	-1.06	0.856	1.32	0.176	-1.14	0.41	0.06
1428663_at	5133401H06Rik	RIKEN cDNA 5133401H06 gene	-1.01	0.979	-1.13	0.376	1.52	0.195	2.32	0.321	0.43
1420643_at	Lfng	lunatic fringe gene homolog (Drosophila)	1.49	0.109	1.06	0.759	-1.18	0.377	-1.29	0.232	0.02
1440310_at	Runx1t1	Runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1.8	0.272	-1.01	0.984	-1.64	0.265	1.22	0.702	0.09
1458754_at	---	---	1.3	0.78	1.11	0.872	-1.01	0.983	-2.42	0.188	-0.25
1449411_at	Dscam	Down syndrome cell adhesion molecule	1.21	0.248	1.41	0.516	-1.28	0.062	-1.51	0.546	-0.04
1422949_at	Nos1	nitric oxide synthase 1, neuronal	2.07	0.078	-1.74	0.206	-1.32	0.602	1.42	0.675	0.11
1455636_at	Lsamp	limbic system-associated membrane protein	-1.12	0.414	1.97	0.273	-1.85	0.311	1.06	0.946	0.01
1422899_at	Slc6a20	solute carrier family 6 (neurotransmitter transporter), member 20	-1.09	0.121	-1.03	0.942	1.51	0.367	1.14	0.858	0.13
1444950_at	Zfp509	zinc finger protein 509	1.76	0.44	-1.18	0.453	-1.27	0.376	1.2	0.756	0.13
1450403_at	Stat2	signal transducer and activator of transcription 2	-1.03	0.92	1.22	0.59	1.2	0.511	-1.38	0.318	0.01
1421527_at	Epha6	Eph receptor A6	1.28	0.077	1.16	0.786	-1.05	0.903	-1.07	0.829	0.08
1423639_at	Hrh2	histamine receptor H 2	-1.65	0.213	-1.17	0.529	1.94	0.004	1.14	0.55	0.07
1436242_a_at	Cklf	chemokine-like factor	1.17	0.38	1.36	0.039	-1.14	0.448	-1.34	0.159	0.01
1439424_x_at	Herpud2	HERPUD family member 2	-1.26	0.049	1.28	0.058	1.33	0.07	-1.18	0.446	0.04
1459558_at	Mast2	Microtubule associated serine/threonine kinase 2	-1.63	0.317	1.25	0.423	1.53	0.172	-1.07	0.91	0.02
1453293_a_at	2810408A11Rik	RIKEN cDNA 2810408A11 gene	-1.6	0.475	2.06	0.238	-1.4	0.39	1.04	0.87	0.02
1426267_at	Zbtb8os	zinc finger and BTB domain containing 8 opposite strand	1.31	0.458	1.11	0.765	-1.03	0.781	-1.13	0.631	0.07
1421111_at	Rybp	RING1 and YY1 binding protein	1.12	0.738	-1.06	0.919	1.34	0.627	-1.14	0.744	0.06
1422102_a_at	Stat5b	signal transducer and activator of transcription 5B	1.03	0.946	-1.1	0.602	1.47	0.057	-1.18	0.532	0.05
1451491_at	4930556P03Rik	RIKEN cDNA 4930556P03 gene	1.52	0.048	1.01	0.99	-1.14	0.449	-1.43	0.343	-0.01
1458621_at	Wdr78	WD repeat domain 78	1.53	0.515	-1.44	0.173	1.18	0.642	-1.24	0.181	0.01
1423503_at	Jam3	junction adhesion molecule 3	-1.09	0.592	1.14	0.417	1.35	0.111	-1.53	0.097	-0.03
1422251_at	Neurl	neuralized-like homolog (Drosophila)	1.37	0.576	-1.03	0.71	1.06	0.901	-1.4	0.473	0
1445989_at	---	Transcribed locus	1.63	0.406	1.33	0.638	-2.23	0.431	-1	0.992	-0.07
1432614_at	Wdr37	WD repeat domain 37	1.1	0.674	1.63	0.354	-1.5	0.572	-2.96	0.108	-0.43
1459661_at	AW492955	expressed sequence AW492955	1.34	0.035	-1.22	0.61	1.24	0.354	-1.53	0.538	-0.04
1416232_at	Olig2	oligodendrocyte transcription factor 2	-1.29	0.728	-1.07	0.944	1.69	0.204	2.09	0.064	0.36
1436598_at	---	---	-1.5	0.493	1.44	0.375	1.3	0.517	-1.75	0.106	-0.13
1425024_at	E430018J23Rik	RIKEN cDNA E430018J23 gene	1.25	0.545	1.24	0.247	-1.09	0.62	-1.99	0.078	-0.15
1418362_at	Zfp42	zinc finger protein 42	-1.68	0.11	1.71	0.229	1.1	0.773	-1.77	0.11	-0.16
1445341_at	---	---	2.02	0.101	-1.41	0.064	-1.48	0.181	1.33	0.49	0.12
1420221_at	4930461P20Rik	RIKEN cDNA 4930461P20 gene	1.26	0.713	1.16	0.646	-1.01	0.946	-1.11	0.878	0.07
1451154_a_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.42	0.259	-1.03	0.828	1.01	0.87	-1.52	0.269	-0.03
1447945_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	-1.11	0.914	2.17	0.152	-2.97	0.113	1.01	0.942	-0.22
1430613_at	1520402A15Rik	RIKEN cDNA 1520402A15 gene	-1.19	0.645	1.07	0.869	1.49	0.127	-1.09	0.111	0.07
1442147_at	Phka2	Phosphorylase kinase alpha 2	1.34	0.631	1.13	0.824	-1.07	0.924	-1.19	0.441	0.05
1429528_at	Rae1	RAE1 RNA export 1 homolog (S. pombe)	-1.01	0.978	-1.06	0.67	1.47	0.108	1.06	0.832	0.11
1456278_x_at	Gpr172b	G protein-coupled receptor 172B	-1.01	0.946	1.89	0.17	-1.88	0.19	1.06	0.825	0.01
1454658_at	Ilvbl	ilvB (bacterial acetolactate synthase)-like	1.08	0.69	-1.1	0.732	1.41	0.304	-1.45	0.397	-0.01
1451345_at	Mtap	methylthioadenosine phosphorylase	1.04	0.792	-1.07	0.618	1.43	0.289	-1.15	0.616	0.06
1451274_at	Ogdh	oxoglutarate dehydrogenase (lipoamide)	-1.09	0.501	-1.09	0.171	1.57	0.062	1.33	0.071	0.18
1419154_at	Tmprss2	transmembrane protease, serine 2	-1.22	0.183	1.63	0.224	-1.05	0.722	4.15	0.036	0.88
1421969_a_at	Faah	fatty acid amide hydrolase	1.02	0.944	-1.36	0.07	1.65	0.075	-1.26	0.462	0.01

1444175_at	Arfgef1	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibite	1.32	0.661	1.38	0.247	-1.43	0.373	-1.9	0.418	-0.15
1438449_at	Cdc42bpa	Cdc42 binding protein kinase alpha	1.84	0.384	-1.4	0.609	-1.17	0.705	1.08	0.907	0.09
1419612_at	4632415L05Rik	RIKEN cDNA 4632415L05 gene	1.39	0.124	-1.03	0.832	1.04	0.472	-1.44	0.11	-0.01
1444884_at	Ppt1	palmitoyl-protein thioesterase 1	1.24	0.497	1.3	0.418	-1.16	0.817	-1.53	0.212	-0.04
1436376_s_at	Srbd1	S1 RNA binding domain 1	-1	0.992	-1.06	0.747	1.47	0.046	1.45	0.233	0.21
1457155_at	Aldh2	aldehyde dehydrogenase 2, mitochondrial	1.4	0.103	-1.41	0.153	1.3	0.006	-2.01	0.224	-0.18
1459898_at	Sbsn	suprabasin	1.18	0.534	-2.47	0.152	1.83	0.285	-1.43	0.093	-0.22
1457047_at	Snrp70	U1 small nuclear ribonucleoprotein polypeptide A	1.58	0.31	-1.05	0.88	-1.14	0.735	1.42	0.302	0.2
1421417_s_at	Elac1	elaC homolog 1 (E. coli)	1.02	0.923	-1.18	0.653	1.54	0.078	-1.35	0.018	0.01
1444724_at	Pcdh9	Protocadherin 9	1.51	0.532	1.04	0.878	-1.16	0.505	-1.07	0.854	0.08
1457952_at	Cd80	CD80 antigen	-1.41	0.091	-1	0.987	1.71	0.311	1.17	0.311	0.11
1434121_at	Lgi4	leucine-rich repeat LGI family, member 4	-1.15	0.797	1.86	0.15	-1.48	0.37	1.23	0.707	0.12
1426679_at	Zfp706	zinc finger protein 706	1	0.998	-1.14	0.275	1.53	0.061	-1.04	0.798	0.09
1441586_at	Tom1l2	Target of myb1-like 2 (chicken)	1.99	0.393	-1.67	0.394	-1.23	0.778	2.02	0.072	0.28
1449488_at	Pitx1	paired-like homeodomain transcription factor 1	1.38	0.528	-2.07	0.101	1.54	0.213	-1.33	0.66	-0.12
1448226_at	Rrm2	ribonucleotide reductase M2	-1.28	0.34	-1	0.99	1.63	0.039	5.99	0.156	1.33
1426821_at	Cog8	component of oligomeric golgi complex 8	-1	0.989	-1.05	0.777	1.46	0.044	1.01	0.913	0.1
1451648_a_at	Folr2	folate receptor 2 (fetal)	-1.21	0.166	1.51	0.02	1.07	0.734	-1.11	0.658	0.07
1455177_at	Ahi1	Abelson helper integration site	-1.18	0.371	1.66	0.359	-1.1	0.743	2.19	0.229	0.39
1423407_a_at	Fbln2	fibulin 2	1.45	0.071	-1.57	0.497	1.32	0.501	-1.05	0.794	0.04
1417265_s_at	Coq5	coenzyme Q5 homolog, methyltransferase (yeast)	-1.1	0.329	-1.17	0.001	1.65	0.099	1.18	0.439	0.14
1459069_at	Ppm1d	Protein phosphatase 1D magnesium-dependent, delta isoform	-1.42	0.568	1.37	0.351	1.34	0.32	-1.21	0.329	0.02
1431860_at	BC026513	cDNA sequence BC026513	1.29	0.786	1.45	0.416	-1.48	0.598	-1.47	0.494	-0.05
1443028_at	Larp6	La ribonucleoprotein domain family, member 6	1.45	0.399	1.13	0.721	-1.21	0.608	-1.67	0.24	-0.07
1433719_at	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	1.08	0.825	1.38	0.069	-1.05	0.805	-1.13	0.612	0.07
1439165_at	---	---	2.29	0.161	-1.88	0.381	-1.7	0.101	1.06	0.545	-0.06
1427201_at	Mustn1	musculoskeletal, embryonic nuclear protein 1	1.08	0.711	1.76	0.123	-1.75	0.093	-1.26	0.449	-0.04
1448930_at	3010026O09Rik	RIKEN cDNA 3010026O09 gene	-1.32	0.039	-1.34	0.118	1.91	0.213	1.67	0.083	0.23
1419584_at	Ttc28	tetratricopeptide repeat domain 28	-1.14	0.148	1.36	0.195	1.17	0.49	-1.34	0.368	0.01
1454820_at	BC037034	cDNA sequence BC037034	-1.18	0.459	1.27	0.376	1.29	0.168	-1.25	0.097	0.03
1447609_at	5730410E15Rik	RIKEN cDNA 5730410E15 gene	-1.1	0.77	2.01	0.247	-2.01	0.042	1.09	0.701	0
1436336_at	Ptrh1	peptidyl-tRNA hydrolase 1 homolog (S. cerevisiae)	1.14	0.212	1.39	0.608	-1.14	0.489	-1.05	0.771	0.09
1422283_at	Cd40lg	CD40 ligand	1.49	0.53	-1.09	0.853	1.01	0.985	-1.22	0.724	0.05
1439665_at	Gpr23	G protein-coupled receptor 23	1.17	0.191	1.62	0.466	-1.6	0.364	-1.61	0.315	-0.11
1420519_a_at	Eral1	Era (G-protein)-like 1 (E. coli)	-1.08	0.773	1.09	0.607	1.4	0.329	-1.21	0.074	0.05
1419717_at	Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.57	0.225	1.01	0.978	-1.2	0.353	-1.08	0.849	0.07
1424435_a_at	Gart	phosphoribosylglycinamide formyltransferase	-1.48	0.417	-1.03	0.896	1.76	0.109	1.02	0.97	0.07
1455735_at	Ap1s3	adaptor-related protein complex AP-1, sigma 3	1.23	0.37	1.28	0.475	-1.1	0.546	-1.52	0.3	-0.03
1435258_at	Tmem141	transmembrane protein 141	1.27	0.42	1.32	0.324	-1.21	0.569	-1.04	0.836	0.08
1450238_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.33	0.231	-1.16	0.646	1.22	0.719	-2.16	0.419	-0.19
1433956_at	Cdh5	cadherin 5	-1.18	0.669	1.38	0.283	1.18	0.694	-1.14	0.579	0.06
1419296_at	Arhgap4	Rho GTPase activating protein 4	-1.01	0.532	1	0.994	1.42	0.04	-2.07	0.084	-0.16
1425216_at	Ffar2	free fatty acid receptor 2	-1.33	0.162	1.57	0.408	1.09	0.545	-2.08	0.061	-0.19
1439476_at	Dsg2	desmoglein 2	1.26	0.082	-1.17	0.218	1.3	0.156	-1.66	0.313	-0.07
1420619_a_at	Aes	amino-terminal enhancer of split	1.38	0.352	1.16	0.44	-1.15	0.471	-1.03	0.912	0.09
1451793_at	Klhl24	kelch-like 24 (Drosophila)	1.25	0.251	-1.16	0.585	1.3	0.501	-1.46	0.058	-0.02
1421302_a_at	Gna15	guanine nucleotide binding protein, alpha 15	1.09	0.863	1.35	0.371	-1.02	0.875	-1.02	0.938	0.1
1426098_a_at	Cast	calpastatin	-1.01	0.806	-1.1	0.27	1.52	0.155	1.44	0.38	0.21
1431933_a_at	Dcp1a	decapping enzyme	1.65	0.318	-1.97	0.169	1.25	0.669	-2.14	0.418	-0.3
1454974_at	Ntn1	netrin 1	1.05	0.374	-1.01	0.926	1.37	0.105	-1.14	0.707	0.07
1442255_at	5033414D02Rik	RIKEN cDNA 5033414D02 gene	1.22	0.338	1.27	0.388	-1.08	0.595	-1.56	0.264	-0.04
1420903_at	St6galnac3	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	1.11	0.415	1.49	0.366	-1.23	0.242	-1.02	0.947	0.09
1432472_a_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	1.06	0.542	-1.19	0.04	1.51	0.174	-1.1	0.73	0.07

1426261_s_at	Ugt1a2 /// Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A2 /// UDP glucuronosyltransf	-1.04	0.671	-1.12	0.431	1.56	0.156	1.87	0.065	0.32
1422623_x_at	Rpl41	Ribosomal protein L41	-1.09	0.613	1.45	0.079	1.05	0.756	-1.13	0.226	0.07
1418450_at	Islr	immunoglobulin superfamily containing leucine-rich repeat	1.38	0.173	1.06	0.834	-1.02	0.931	-1.37	0.417	0.01
1421581_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	-1.25	0.54	1.54	0.103	1.07	0.594	-1.03	0.946	0.08
1446831_at	D5Ertd521e	DNA segment, Chr 5, ERATO Doi 521, expressed	1.76	0.334	-1.37	0.481	-1.08	0.769	1.27	0.496	0.14
1426281_at	Catsper1	cation channel of sperm 1	-1.09	0.663	1.04	0.926	1.46	0.231	-1.38	0.285	0.01
1443486_at	Cog7	Component of oligomeric golgi complex 7	-1.06	0.86	1.27	0.19	1.21	0.177	-1.2	0.564	0.05
1417171_at	Itk	IL2-inducible T-cell kinase	-1.69	0.399	1.65	0.108	1.17	0.695	-2.83	0.087	-0.42
1432233_at	1110020C17Rik	RIKEN cDNA 1110020C17 gene	1.74	0.06	1	0.993	-1.49	0.142	-1.06	0.902	0.05
1456504_at	Zfp182	zinc finger protein 182	1.45	0.064	1.14	0.688	-1.21	0.005	-1.26	0.455	0.03
1436881_x_at	Afp	alpha fetoprotein	1.05	0.957	-1.12	0.825	1.47	0.406	-1.35	0.667	0.01
1418528_a_at	Dad1	defender against cell death 1	1.17	0.48	1.37	0.003	-1.14	0.215	-1.2	0.448	0.05
1450445_at	Phex	phosphate regulating gene with homologies to endopeptidases on the X chromos	1.74	0.492	-1.11	0.741	-1.28	0.463	1.34	0.579	0.17
1427037_at	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	-1.11	0.817	-1.02	0.972	1.53	0.417	1.28	0.655	0.17
1416559_at	1500003O22Rik	RIKEN cDNA 1500003O22 gene	1.4	0.211	1.13	0.479	-1.14	0.202	-1.03	0.858	0.09
1421156_a_at	Dsc2	desmocollin 2	-1.06	0.938	1.06	0.768	1.41	0.373	-1.97	0.072	-0.14
1459226_at	---	Transcribed locus	1.45	0.093	-1.04	0.903	1.01	0.966	-1.17	0.11	0.06
1442076_at	Cobl	cordon-bleu	-1.29	0.662	1.26	0.49	1.38	0.574	-1.31	0.24	0.01
1427591_at	Clcn1	chloride channel 1	1.05	0.836	-1.9	0.445	1.84	0.26	-1.07	0.915	-0.02
1433350_at	4930553P13Rik	RIKEN cDNA 4930553P13 gene	-1.16	0.485	1.65	0.478	-1.1	0.605	1.2	0.119	0.15
1455137_at	Rapgef5	Rap guanine nucleotide exchange factor (GEF) 5	1.15	0.347	1.35	0.041	-1.09	0.601	-1.59	0.371	-0.04
1457499_at	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	1.36	0.781	1.16	0.774	-1.11	0.675	-2.2	0.003	-0.2
1447363_s_at	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	-1.29	0.054	1.69	0.384	-1.05	0.743	2.62	0.148	0.49
1437603_at	BC050777	cDNA sequence BC050777	1.44	0.231	1.14	0.364	-1.2	0.507	-1.05	0.826	0.08
1430559_at	Nt5c3l	5'-nucleotidase, cytosolic III-like	1.64	0.66	1.16	0.789	-1.61	0.26	-1.88	0.316	-0.17
1447130_at	D8Wsu26e	DNA segment, Chr 8, Wayne State University 26, expressed	2.13	0.322	-1.16	0.805	-2.35	0.064	1.15	0.779	-0.06
1448278_at	Xab2	XPA binding protein 2	1.12	0.605	-1.04	0.009	1.34	0.01	-1.39	0.009	0.01
1432489_a_at	2410187C16Rik	RIKEN cDNA 2410187C16 gene	-1.22	0.247	-1.01	0.956	1.61	0.177	1.18	0.487	0.14
1448364_at	Ccng2	cyclin G2	-1.03	0.907	1.05	0.836	1.39	0.205	-1.39	0.174	0.01
1442218_at	Map3k9	mitogen-activated protein kinase kinase kinase 9	-1.3	0.518	1.28	0.61	1.38	0.332	-1.85	0.287	-0.12
1430582_at	Shprh	SNF2 histone linker PHD RING helicase	-1.01	0.978	1.38	0.264	1.06	0.902	-1.61	0.021	-0.05
1436685_at	LOC544888	hypothetical LOC544888	1.22	0.58	-1.48	0.347	1.52	0.262	-1.79	0.112	-0.13
1450042_at	Arx	aristaless related homeobox gene (Drosophila)	-1.03	0.965	1.22	0.257	1.23	0.672	-1.36	0.234	0.02
1436670_x_at	1700019G17Rik	RIKEN cDNA 1700019G17 gene	-1.03	0.856	1.26	0.019	1.19	0.215	-1.62	0.007	-0.05
1431441_at	1700106J16Rik	RIKEN cDNA 1700106J16 gene	1.22	0.587	1.33	0.414	-1.15	0.218	-1.01	0.889	0.1
1423959_at	Ropn1l	ropporin 1-like	-1.08	0.826	1.34	0	1.15	0.688	-1.42	0.479	0
1424903_at	Jarid1d	jumonji, AT rich interactive domain 1D (Rbp2 like)	-1.19	0.825	1.83	0.231	-1.33	0.542	1.85	0.173	0.29
1449208_at	Papolb	poly (A) polymerase beta (testis specific)	1.67	0.288	-1.44	0.215	1.06	0.918	-1.55	0.309	-0.07
1421260_a_at	Srm	spermidine synthase	-1.07	0.543	-1.01	0.894	1.5	0.136	1.56	0.076	0.25
1438860_a_at	Slc44a2	solute carrier family 44, member 2	1.03	0.908	-1	0.995	1.39	0.591	-2.09	0.097	-0.17
1422375_a_at	Art1	ADP-ribosyltransferase 1	-1.15	0.485	-1.09	0.579	1.64	0.212	1.08	0.495	0.12
1457899_at	Kalrn	kalirin, RhoGEF kinase	-1.04	0.882	1.44	0.028	1.02	0.949	-1.05	0.914	0.09
1419530_at	Il12b	interleukin 12b	1.19	0.682	1.6	0.201	-1.58	0.006	-1.24	0.627	-0.01
1445302_at	Igsf6	immunoglobulin superfamily, member 6	1.11	0.403	1.56	0.374	-1.31	0.295	-1.32	0.421	0.01
1448452_at	Irf8	interferon regulatory factor 8	1.03	0.914	1.59	0.104	-1.25	0.476	-1.44	0.392	-0.02
1417125_at	Ahcy	S-adenosylhomocysteine hydrolase	-1.07	0.695	-1.19	0.428	1.65	0.044	1.2	0.381	0.15
1450681_at	Zfp143	zinc finger protein 143	-1.02	0.969	1.27	0.373	1.17	0.137	-1.2	0.493	0.06
1452578_at	Runx1	runt related transcription factor 1	1.32	0.644	-1.13	0.667	1.22	0.559	-1.23	0.713	0.05
1433264_at	---	---	1.22	0.709	-1.35	0.564	1.47	0.386	-2.65	0.043	-0.33
1451433_at	Mfsd3	major facilitator superfamily domain containing 3	1.1	0.75	-1.05	0.662	1.38	0.235	-1.27	0.277	0.04
1423428_at	Ror2	receptor tyrosine kinase-like orphan receptor 2	1.43	0.321	-1.2	0.431	1.17	0.613	-1.2	0.465	0.05
1458998_at	Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	-1.13	0.767	1.28	0.592	1.26	0.304	-1.58	0.521	-0.04
1445258_at	Fgf9	Fibroblast growth factor 9	-1.56	0.16	1.61	0.287	1.18	0.291	-1.11	0.042	0.03

1439199_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.67	0.098	1.39	0.562	1.44	0.063	-1.65	0.27	-0.12
1431223_at	2700054A10Rik	RIKEN cDNA 2700054A10 gene	1.31	0.406	1.18	0.695	-1.06	0.895	-1.27	0.4	0.04
1455535_at	A730017D01Rik	RIKEN cDNA A730017D01 gene	1.63	0.158	-1.17	0.472	-1.07	0.799	2.06	0.288	0.37
1446934_at	---	---	1.27	0.337	1.56	0.171	-1.66	0.22	-1.3	0.399	-0.04
1420763_at	Klk4	kallikrein 4 (prostase, enamel matrix, prostate)	-1.04	0.909	1.97	0.381	-2.05	0.059	1.11	0.684	0
1422101_at	Tnfrsf23	tumor necrosis factor receptor superfamily, member 23	-1.07	0.894	1.44	0.216	1.05	0.901	-1.33	0.484	0.02
1436011_at	Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)	1.03	0.845	1.45	0.383	-1.06	0.598	-1.37	0.214	0.01
1434684_at	Rin3	Ras and Rab interactor 3	-1.08	0.727	1.11	0.266	1.39	0.075	-1.37	0.321	0.01
1417128_at	Plekho1	pleckstrin homology domain containing, family O member 1	1.01	0.97	1.49	0.148	-1.07	0.693	-1.85	0.144	-0.11
1433869_at	Zxdc	ZXD family zinc finger C	1.12	0.209	-1.1	0.741	1.39	0.056	-1.3	0.408	0.03
1433566_at	Rasl10b	RAS-like, family 10, member B	-1.02	0.96	-1	0.977	1.45	0.199	1.3	0.55	0.18
1423258_at	Syt9	synaptotagmin IX	1.15	0.544	1.37	0.309	-1.1	0.655	-1.17	0.809	0.06
1447042_at	Zbtb34	zinc finger and BTB domain containing 34	1.15	0.831	-1.8	0.336	1.73	0.283	-1.66	0.369	-0.15
1450311_at	Slc8a3	solute carrier family 8 (sodium/calcium exchanger), member 3	-2	0.461	1.54	0.246	1.39	0.409	-2.29	0.351	-0.34
1422235_at	Htr7	5-hydroxytryptamine (serotonin) receptor 7	-1.12	0.611	1.23	0.364	1.31	0.591	-1.48	0.486	-0.02
1430868_at	5830403M04Rik	RIKEN cDNA 5830403M04 gene	1.17	0.682	1.34	0.348	-1.09	0.872	-2.48	0.162	-0.26
1457291_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	1.44	0.613	1	0.997	-1.01	0.978	-3.11	0.136	-0.42
1437361_at	A430060F13Rik	RIKEN cDNA A430060F13 gene	-1.06	0.792	1.71	0.289	-1.28	0.185	1.04	0.946	0.1
1423747_a_at	Pdk1	pyruvate dehydrogenase kinase, isoenzyme 1	-1.16	0.472	1.06	0.798	1.51	0.059	-1.74	0.135	-0.08
1454994_at	Klhl20	kelch-like 20 (Drosophila)	-1.11	0.324	1.28	0.129	1.26	0.331	-1.12	0.47	0.08
1438087_at	Tpmt	thiopurine methyltransferase	1.17	0.183	1.32	0.058	-1.07	0.766	-1.35	0.231	0.02
1443021_at	Mthfs	5, 10-methenyltetrahydrofolate synthetase	-1.25	0.191	1.6	0.27	1.04	0.805	-1.21	0.618	0.04
1431859_at	4930414F18Rik	RIKEN cDNA 4930414F18 gene	1.38	0.333	1.36	0.51	-1.43	0.581	-2.74	0.056	-0.36
1441947_x_at	BC033915	cDNA sequence BC033915	1.13	0.513	-1.25	0.352	1.5	0.012	-1.16	0.308	0.06
1427834_at	Spi16	serine protease inhibitor 16	-1.49	0.542	1.59	0.312	1.17	0.726	-1.39	0.633	-0.03
1429438_at	Bcor	Bcl6 interacting corepressor	1.15	0.266	1.39	0.071	-1.11	0.653	-1.36	0.316	0.02
1427795_s_at	---	Mus musculus, clone IMAGE:5068294	-1.26	0.708	1.79	0.276	-1.18	0.726	1.47	0.625	0.21
1442822_at	Camk4	Calcium/calmodulin-dependent protein kinase IV	1.79	0.404	1.36	0.396	-3.61	0.021	-1.18	0.831	-0.41
1446869_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420455A1	1.19	0.823	1.25	0.56	-1.01	0.986	-1.12	0.885	0.08
1424937_at	2310076L09Rik	RIKEN cDNA 2310076L09 gene	-1.33	0.044	-1.66	0.164	2.08	0.098	1.28	0.677	0.09
1446427_at	B230118G17Rik	RIKEN cDNA B230118G17 gene	-1.06	0.84	1.39	0.532	1.1	0.474	-1.16	0.746	0.07
1415903_at	Slc38a1	solute carrier family 38, member 1	-1.14	0.541	1.29	0.089	1.27	0.5	-1.53	0.215	-0.03
1421550_a_at	Trim34 /// LOC4342	tripartite motif protein 34 /// similar to Tripartite motif protein 34 /// similar to Tripar	-1.02	0.841	1.06	0.744	1.39	0.363	-2.23	0.049	-0.2
1439043_at	Tra2a	transformer 2 alpha homolog (Drosophila)	1.57	0.512	1.3	0.585	-1.79	0.144	-1.34	0.415	-0.06
1451289_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	1.42	0.671	-1.15	0.736	1.15	0.276	-2.18	0.282	-0.19
1452008_at	9130422G05Rik	RIKEN cDNA 9130422G05 gene	1.62	0.109	1.04	0.795	-1.29	0.209	-1.02	0.855	0.09
1424714_at	Aldoc	aldolase 3, C isoform	1.01	0.985	-1.98	0.415	1.92	0.118	-1.45	0.327	-0.13
1433244_at	4930573G07Rik	RIKEN cDNA 4930573G07 gene	-1.48	0.366	1.2	0.645	1.56	0.13	-1.92	0.152	-0.16
1443568_x_at	---	---	1.09	0.899	1.57	0.489	-1.29	0.66	-1.11	0.827	0.06
1444596_at	Pax7	paired box gene 7	1.11	0.634	-1.16	0.692	1.46	0.376	-1.63	0.573	-0.06
1449490_at	Mbd4	methyl-CpG binding domain protein 4	1.44	0.324	-1.01	0.978	1	0.991	-1.01	0.982	0.11
1433390_at	A230105L22Rik	RIKEN cDNA A230105L22 gene	1	0.984	-1.43	0.347	1.73	0.062	-1.22	0.299	0.02
1429772_at	Plxna2	plexin A2	1.86	0.171	-1.02	0.956	-1.69	0.159	1.06	0.795	0.05
1439562_at	F730047E07Rik	RIKEN cDNA F730047E07 gene	-1.22	0.621	-1.08	0.842	1.68	0.15	2.22	0.25	0.4
1419465_at	Nkd2	naked cuticle 2 homolog (Drosophila)	-1.85	0.472	1.58	0.188	1.32	0.223	-1.03	0.966	0
1430112_at	Wdr66	WD repeat domain 66	1.49	0.531	-1.45	0.437	1.25	0.419	-2.02	0.118	-0.18
1440880_at	Mppe1	metallophosphoesterase 1	-1.12	0.465	1.12	0.407	1.42	0.006	-1.08	0.199	0.08
1429397_a_at	4921509E07Rik	RIKEN cDNA 4921509E07 gene	-2.21	0.229	1.05	0.931	1.93	0.322	-2.26	0.212	-0.37
1449286_at	Ntng1	netrin G1	-1.12	0.83	1.11	0.728	1.43	0.504	-1.05	0.874	0.09
1426629_at	Dhx8	DEAH (Asp-Glu-Ala-His) box polypeptide 8	-1.01	0.838	-1.24	0.167	1.64	0.011	1.03	0.758	0.11
1451167_at	Ccdc101	coiled-coil domain containing 101	-1.02	0.853	-1.07	0.435	1.53	0.066	1.11	0.478	0.13
1451194_at	Aldob	aldolase 2, B isoform	-1.15	0.073	-1.29	0.371	1.8	0.428	2.78	0.4	0.53
1456045_at	1700106N22Rik	RIKEN cDNA 1700106N22 gene	1.07	0.533	-1.07	0.79	1.43	0.035	-1.29	0.424	0.04

1446502_at	---	---	2.46	0.008	-2.31	0.323	-1.84	0.208	1.22	0.675	-0.12
1435305_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-2.02	0.544	1.09	0.898	1.85	0.225	-1.49	0.278	-0.14
1449074_at	1700019N12Rik	RIKEN cDNA 1700019N12 gene	-1.15	0.861	1.41	0.576	1.16	0.718	-1.02	0.975	0.1
1438694_at	Csn1s2a	casein alpha s2-like A	2.05	0.243	-1.71	0.353	-1.25	0.625	2	0.312	0.27
1435272_at	Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	1.08	0.622	1.41	0.114	-1.06	0.769	-1.35	0.284	0.02
1419212_at	Icosl	icos ligand	1.27	0.298	1.23	0.512	-1.07	0.71	-1.9	0.181	-0.12
1454030_at	Saps3	SAPS domain family, member 3	1.64	0.439	1.02	0.968	-1.28	0.4	-1.21	0.593	0.04
1439645_at	Adra2b	adrenergic receptor, alpha 2b	-1.05	0.899	1.11	0.652	1.37	0.434	-1.51	0.557	-0.02
1423276_at	Ildr1	immunoglobulin-like domain containing receptor 1	-1.09	0.192	1.03	0.968	1.49	0.002	-1.56	0.564	-0.03
1430623_s_at	5830411E10Rik	RIKEN cDNA 5830411E10 gene	-1.29	0.498	1.25	0.521	1.42	0.203	-1.68	0.062	-0.08
1451352_s_at	Mta3	metastasis associated 3	1.03	0.894	-1.13	0.322	1.52	0.006	-1.09	0.717	0.08
1427605_at	Hoxb3	homeo box B3	1.03	0.787	1.51	0.451	-1.12	0.362	-1.74	0.073	-0.08
1429672_at	5830407E08Rik	RIKEN cDNA 5830407E08 gene	-1.17	0.756	1.57	0.366	1.01	0.97	-2.48	0.053	-0.27
1442138_at	Gpr62	G protein-coupled receptor 62	1.18	0.802	-1.59	0.126	1.63	0.303	-2.19	0.291	-0.24
1448727_at	Tle6	transducin-like enhancer of split 6, homolog of Drosophila E(spl)	1.81	0.294	-1.29	0.683	-1.17	0.385	1.46	0.248	0.2
1418474_at	1500005A01Rik	RIKEN cDNA 1500005A01 gene	-1.37	0.166	-1.08	0.798	1.79	0.014	1.52	0.184	0.21
1447900_x_at	Entpd4	ectonucleoside triphosphate diphosphohydrolase 4	-1.13	0.746	1.31	0.263	1.24	0.348	-1.05	0.855	0.09
1448678_at	3110048E14Rik	RIKEN cDNA 3110048E14 gene	1.22	0.437	1.36	0.056	-1.17	0.495	-1.42	0.131	0
1443301_at	C230086A09Rik	RIKEN cDNA C230086A09 gene	-2.5	0.103	1.23	0.764	1.81	0.38	-5.49	0.191	-1.24
1435229_at	Gramd1b	GRAM domain containing 1B	1.07	0.827	1.44	0.306	-1.08	0.487	-1.04	0.855	0.1
1432395_at	1700039E15Rik	RIKEN cDNA 1700039E15 gene	2	0.343	-2.33	0.098	1.01	0.92	-1.96	0.356	-0.32
1454587_at	9330199C07Rik	RIKEN cDNA 9330199C07 gene	-2.91	0.003	2.06	0.039	1.04	0.915	-1.29	0.731	-0.28
1455658_at	Cggbp1	CGG triplet repeat binding protein 1	-1.09	0.383	-1.04	0.609	1.56	0.163	1.29	0.214	0.18
1445154_at	3300002I08Rik	RIKEN cDNA 3300002I08 gene	-1	0.978	1.21	0.504	1.24	0.31	-1.14	0.593	0.08
1429743_at	6720468P15Rik	RIKEN cDNA 6720468P15 gene	-1.65	0.417	1.12	0.804	1.71	0.069	-2.11	0.184	-0.23
1416332_at	Cirbp	cold inducible RNA binding protein	-1	0.992	1.14	0.692	1.3	0.472	-1.18	0.583	0.06
1426818_at	Arrdc4	arrestin domain containing 4	1.31	0.016	1.35	0.351	-1.28	0.361	-1.2	0.49	0.04
1444553_at	Pms1	Postmeiotic segregation increased 1 (S. cerevisiae)	-1.29	0.281	1.81	0.144	-1.16	0.756	1.96	0.091	0.33
1422164_at	Pou3f4	POU domain, class 3, transcription factor 4	-1.63	0.553	1.63	0.107	1.2	0.67	-1.01	0.99	0.05
1460634_at	Ralgds	ral guanine nucleotide dissociation stimulator	1.41	0.081	-1.04	0.765	1.06	0.793	-1.25	0.45	0.05
1438228_at	4930452B06Rik	RIKEN cDNA 4930452B06 gene	1.31	0.12	-1.82	0.055	1.58	0.1	-1.31	0.634	-0.06
1446685_at	LOC436089	Similar to matrilin 1, cartilage matrix protein	-1.98	0.225	2.19	0.032	-1.34	0.053	1.14	0.794	0
1426412_at	Neurod1	neurogenic differentiation 1	2.4	0.429	-1.76	0.222	-2.09	0.123	1.19	0.748	-0.07
1459488_at	3110050K21Rik	RIKEN cDNA 3110050K21 gene	1.29	0.577	1.51	0.313	-1.55	0.076	-1.12	0.759	0.03
1451650_at	Ddo	D-aspartate oxidase	-1.03	0.852	1.12	0.461	1.35	0.414	-1.37	0.421	0.02
1445332_at	---	Transcribed locus	-1.2	0.647	1.48	0.447	1.13	0.824	-2.36	0.299	-0.24
1459801_at	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	-1.18	0.773	-2.71	0.226	2.23	0.044	1.43	0.701	-0.06
1449674_s_at	Pdcd6ip	programmed cell death 6 interacting protein	-1.03	0.811	-1.09	0.323	1.55	0.002	1.22	0.018	0.16
1424421_at	Flad1	RFad1, flavin adenine dinucleotide synthetase, homolog (yeast)	1.12	0.151	-1.05	0.41	1.36	0.095	-1.03	0.763	0.1
1444441_at	---	PREDICTED: Mus musculus hypothetical protein LOC629847 (LOC629847), mR	-2.19	0.268	1.05	0.932	1.93	0.082	-1.43	0.616	-0.16
1453788_at	---	---	-3.44	0.22	1.55	0.466	1.6	0.289	-1.43	0.245	-0.43
1431831_at	2210009G21Rik	RIKEN cDNA 2210009G21 gene	1.01	0.971	1.5	0.002	-1.07	0.819	-1.13	0.666	0.08
1427427_at	Ryr3	ryanodine receptor 3	1.19	0.785	1.32	0.658	-1.07	0.908	-1.44	0.609	0
1456558_s_at	C87977	expressed sequence C87977	1.45	0.214	-1.41	0.649	1.28	0.728	-1.32	0.71	0
1448128_at	Ppgb	protective protein for beta-galactosidase	-1.09	0.183	1.26	0.033	1.27	0.103	-1.37	0.237	0.02
1451851_a_at	Csn3	casein kappa	-1	0.997	1.37	0.6	1.08	0.797	-1.14	0.761	0.08
1445769_at	LOC546862	Hypothetical LOC546862	1.34	0.715	-1.12	0.802	1.22	0.617	-1.18	0.449	0.06
1421488_at	Rabgap1l	RAB GTPase activating protein 1-like	1.2	0.768	-1.03	0.954	1.28	0.601	-1.53	0.425	-0.02
1454784_at	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	-1.16	0.807	1.54	0.249	1.04	0.736	-1.26	0.609	0.04
1452165_at	Prlpk	prolactin-like protein K	-1.14	0.551	-1.54	0.674	1.92	0.399	1	0.982	0.06
1420542_at	ORF28	open reading frame 28	1.18	0.711	-1.05	0.913	1.32	0.384	-1.74	0.163	-0.07
1454746_at	Plekhm1	pleckstrin homology domain containing, family M (with RUN domain) member 1	-1.13	0.23	1.24	0.095	1.32	0.175	-1.58	0.053	-0.04
1450990_at	Gpc3	glypican 3	1.47	0.148	-1.11	0.636	1.08	0.869	-1.36	0.72	0.02

1444851_at	Zfp532	Zinc finger protein 532	1.15	0.76	1.58	0.474	-1.4	0.126	-1.07	0.786	0.07
1459953_at	AW011752	Expressed sequence AW011752	1.88	0.016	-1.16	0.483	-1.43	0.035	1.03	0.904	0.08
1418402_at	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)	1.19	0.48	1.26	0.206	-1	0.988	-1.4	0.381	0.01
1454572_at	2810414N06Rik	RIKEN cDNA 2810414N06 gene	1.09	0.603	-1.07	0.677	1.42	0.061	-1.08	0.742	0.09
1445017_at	Cnot2	CCR4-NOT transcription complex, subunit 2	-1.64	0.455	1.44	0.218	1.39	0.576	-1.26	0.478	-0.02
1439708_at	Myom3	myomesin family, member 3	-1.59	0.376	1.58	0.581	1.24	0.283	-2.19	0.303	-0.24
1455694_at	Nbeal2	neurobeachin-like 2	-1.45	0.274	1.1	0.831	1.65	0.003	-1.04	0.874	0.07
1439982_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730006I1	-2.37	0.043	1.78	0.347	1.25	0.699	-1.36	0.439	-0.18
1424643_at	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	1.08	0.158	-1.05	0.704	1.42	0.151	-1.34	0.436	0.03
1460322_at	Chst3	carbohydrate (chondroitin 6/keratan) sulfotransferase 3	1.25	0.728	-1.32	0.072	1.44	0.573	-1.1	0.853	0.07
1420896_at	Snap23	synaptosomal-associated protein 23	-1.25	0.36	-1.05	0.806	1.7	0.253	1.22	0.397	0.15
1450926_at	Atp6v1g1 /// LOC62	ATPase, H+ transporting, lysosomal V1 subunit G1 /// similar to vacuolar H+ ATP	1.15	0.839	-1.44	0.668	1.61	0.264	-1.85	0.265	-0.13
1422502_at	Parp1	poly (ADP-ribose) polymerase family, member 1	-1.1	0.462	1.01	0.795	1.53	0.085	-1.25	0.082	0.05
1422427_a_at	Svs2	seminal vesicle protein, secretion 2	-1.03	0.929	1.38	0.584	1.09	0.603	-1.5	0.535	-0.01
1446614_at	---	---	1.22	0.628	1.5	0.002	-1.36	0.136	-1.09	0.824	0.07
1432606_at	2610012C04Rik	RIKEN cDNA 2610012C04 gene	-1.28	0.53	1.16	0.712	1.51	0.448	-2.35	0.008	-0.24
1423493_a_at	Nfix	nuclear factor I/X	-1.03	0.865	-1.4	0.092	1.77	0.067	1.98	0.092	0.33
1455917_at	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	1.95	0.433	-1.61	0.163	-1.13	0.738	1.07	0.92	0.07
1449268_at	Gfpt1	glutamine fructose-6-phosphate transaminase 1	-1.78	0.327	1.74	0.097	1.15	0.651	-1.07	0.501	0.01
1456977_at	---	---	-1.04	0.821	1.59	0.554	-1.11	0.852	2.49	0.255	0.48
1448057_at	---	---	-1	0.992	1.08	0.698	1.37	0.182	-1.39	0.329	0.01
1426198_at	---	Anti-human CD37 antibody WR17 gamma heavy chain variable region	-1.22	0.151	1.1	0.875	1.53	0.345	-4.96	0.216	-0.89
1419142_at	Ctsr	cathepsin R	1.61	0.09	1.31	0.376	-1.88	0.059	-1.45	0.451	-0.1
1453059_at	2310046A06Rik ///	RIKEN cDNA 2310046A06 gene /// RIKEN cDNA 2810047F03 gene	-1.03	0.759	1.26	0.625	1.22	0.601	-1.14	0.82	0.08
1426399_at	Vwa1	von Willebrand factor A domain containing 1	1.47	0.091	-1.14	0.746	1.11	0.419	-1.37	0.057	0.02
1422042_at	Gje1	gap junction membrane channel protein epsilon 1	1.55	0.647	-1.76	0.251	1.33	0.449	-2.35	0.279	-0.31
1417745_at	Cpn1	carboxypeptidase N, polypeptide 1	-1.19	0.423	1.05	0.43	1.56	0.264	-1.25	0.593	0.04
1430254_at	4921517D22Rik	RIKEN cDNA 4921517D22 gene	-1.77	0.404	1.29	0.564	1.59	0.25	-1.7	0.156	-0.15
1439916_at	LOC545182	hypothetical protein LOC545182	1.71	0.351	-1.05	0.861	-1.26	0.142	1.32	0.101	0.18
1428614_at	Ldhd	lactate dehydrogenase D	-1.12	0.328	1.22	0.297	1.34	0.299	-1.34	0.303	0.02
1432553_at	1700069L16Rik	RIKEN cDNA 1700069L16 gene	1.38	0.619	1.14	0.797	-1.07	0.827	-1.79	0.436	-0.09
1443482_at	1700124P09Rik	RIKEN cDNA 1700124P09 gene	1.49	0.55	1.06	0.906	-1.11	0.779	-1.07	0.881	0.09
1438832_x_at	Dhx30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	1.41	0.087	-1.15	0.569	1.18	0.654	-2.16	0.106	-0.18
1424399_at	Uck1	uridine-cytidine kinase 1	-1.08	0.73	-1.05	0.55	1.58	0.086	1.4	0.015	0.21
1455629_at	Drd1a	dopamine receptor D1A	1.82	0.397	-2.72	0.12	1.27	0.614	-1.44	0.483	-0.27
1455040_s_at	1110062M06Rik	RIKEN cDNA 1110062M06 gene	1.17	0.012	1.32	0.357	-1.05	0.822	-1.21	0.489	0.06
1417785_at	Pla1a	phospholipase A1 member A	-1.09	0.233	-1.1	0.471	1.63	0.055	1.82	0.289	0.31
1427872_at	Ptafr	platelet-activating factor receptor	1.17	0.535	1.49	0.446	-1.26	0.598	-1.2	0.537	0.05
1429210_at	Col23a1	procollagen, type XXIII, alpha 1	1.23	0.737	1.34	0.354	-1.14	0.582	-1.54	0.694	-0.03
1424340_at	Lrrc48	leucine rich repeat containing 48	1.03	0.916	1.58	0.087	-1.19	0.421	-1.29	0.699	0.03
1437949_x_at	Zfp313	zinc finger protein 313	-1.16	0.725	1.46	0.256	1.13	0.672	-1.05	0.902	0.1
1453461_at	Fxc1	fractured callus expressed transcript 1	1.02	0.917	1.77	0.139	-1.49	0.016	-2.49	0.032	-0.3
1449922_at	4933425L06Rik	RIKEN cDNA 4933425L06 gene	-1.08	0.721	-1.37	0.253	1.79	0.217	2.24	0.061	0.4
1435714_x_at	Il17d	interleukin 17D	1.99	0.31	-1.65	0.38	-1.16	0.553	1.21	0.668	0.09
1419980_at	Gba2	glucosidase beta 2	-1.01	0.976	1.69	0.336	-1.28	0.088	1.65	0.086	0.26
1448745_s_at	Lor	loricrin	1.79	0.146	-1.86	0.247	1.12	0.602	-1.81	0.206	-0.19
1451267_at	Sharpin	SHANK-associated RH domain interacting protein	1.02	0.931	-1	0.965	1.44	0.076	-1.33	0.085	0.03
1417440_at	Arid1a /// LOC6759	AT rich interactive domain 1A (Swi1 like) /// similar to AT rich interactive domain 1	-1.02	0.861	1.12	0.419	1.35	0.263	-1.17	0.478	0.07
1458141_at	---	---	-2.47	0.139	2.26	0.137	-1.27	0.483	2.55	0.004	0.27
1456255_at	AI314180	expressed sequence AI314180	1.17	0.438	-1.23	0.803	1.47	0.509	-1.13	0.693	0.07
1425545_x_at	H2-D1	histocompatibility 2, D region locus 1	1.37	0.19	-1.01	0.916	1.1	0.071	-1.2	0.191	0.06
1440517_x_at	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	1.35	0.008	-1.16	0.087	1.24	0.455	-1.41	0.103	0
1416611_at	Scamp2	secretory carrier membrane protein 2	-1.01	0.912	1.13	0.097	1.33	0.009	-1.22	0.266	0.06

1430198_at	3110009F21Rik	RIKEN cDNA 3110009F21 gene	-1.38	0.339	1.12	0.62	1.62	0.102	-1.48	0.174	-0.03
1454012_a_at	Parp6	poly (ADP-ribose) polymerase family, member 6	-1.52	0.445	1.66	0.153	1.14	0.748	-1.9	0.105	-0.16
1422211_a_at	B3gnt3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	-1.21	0.456	-1.01	0.986	1.64	0.122	1.01	0.991	0.11
1428329_a_at	Ift80	intraflagellar transport 80 homolog (Chlamydomonas)	-1.02	0.833	-1.01	0.966	1.48	0.364	1.36	0.529	0.2
1454407_at	4930435N07Rik	RIKEN cDNA 4930435N07 gene	1.38	0.63	-1.02	0.942	1.1	0.831	-2.07	0.386	-0.15
1447792_x_at	Gpr174	G protein-coupled receptor 174	-3.65	0.062	1.83	0.139	1.35	0.306	-1.94	0.214	-0.6
1447950_at	A730011C13Rik	RIKEN cDNA A730011C13 gene	1.11	0.622	-1.28	0.367	1.57	0.018	-1.05	0.737	0.09
1450501_at	Itga2	integrin alpha 2	1.39	0.463	-1.4	0.413	1.35	0.334	-1.1	0.798	0.06
1447427_at	---	PREDICTED: Mus musculus similar to developmentally regulated repeat element	-1.69	0.271	1.7	0.183	1.16	0.583	-1.53	0.541	-0.09
1443826_x_at	Men1	multiple endocrine neoplasia 1	1.45	0.555	1.37	0.548	-1.57	0.164	-1.67	0.461	-0.11
1453296_at	Tmem103	transmembrane protein 103	-1.02	0.966	1.41	0.485	1.06	0.886	-1.07	0.698	0.1
1457396_at	---	---	1.06	0.936	-1.1	0.721	1.48	0.25	-1.39	0.124	0.01
1420373_at	Foxj2	forkhead box J2	1.15	0.765	-1.47	0.558	1.62	0.438	-1.01	0.99	0.08
1434370_s_at	Faf1	Fas-associated factor 1	-1.23	0.151	-1.11	0.472	1.74	0.203	1.44	0.346	0.21
1442819_at	Rhbdl2	rhomboid, veinlet-like 2 (Drosophila)	-1.11	0.633	1.5	0.239	1.06	0.795	-1.51	0.067	-0.02
1442664_at	Mbnl3	Muscleblind-like 3 (Drosophila)	1.18	0.683	1.44	0.305	-1.19	0.288	-1.16	0.71	0.07
1459028_at	Utp20	UTP20, small subunit (SSU) processome component, homolog (yeast)	1.68	0.527	1.07	0.828	-1.41	0.566	-1.94	0.178	-0.15
1439650_at	Rtn4	reticulon 4	1.67	0.025	1.14	0.711	-1.55	0.022	-1.3	0.442	-0.01
1433536_at	Lrp11	low density lipoprotein receptor-related protein 11	-1.12	0.707	1.12	0.794	1.44	0.084	-1.65	0.262	-0.05
1416051_at	C2	complement component 2 (within H-2S)	-1.18	0.347	1.25	0.016	1.36	0.629	-1.65	0.084	-0.06
1419583_at	Cbx4	chromobox homolog 4 (Drosophila Pc class)	1.08	0.468	-1.03	0.871	1.41	0.012	-1.58	0.152	-0.03
1430410_at	1810019N24Rik	RIKEN cDNA 1810019N24 gene	1.17	0.689	1.65	0.325	-1.56	0.365	-1.34	0.591	-0.02
1454441_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	1.09	0.466	-1.24	0.6	1.56	0.443	-1.62	0.128	-0.05
1440682_at	Odz4	Odd Oz/ten-m homolog 4 (Drosophila)	-2.28	0.264	2.55	0.174	-2.15	0.112	2.14	0.166	0.07
1417070_at	Cyp4v3	cytochrome P450, family 4, subfamily v, polypeptide 3	1.65	0.234	-1.41	0.125	1.1	0.543	-1.24	0.49	0.02
1435465_at	Kbtbd11 /// LOC632	kelch repeat and BTB (POZ) domain containing 11 /// similar to Protein KIAA0711	-1.1	0.503	1.42	0.429	1.13	0.367	-1.8	0.252	-0.09
1441726_at	Clasp2	CLIP associating protein 2	-1.01	0.989	1.81	0.333	-1.53	0.052	1.37	0.346	0.16
1426278_at	Ifi27	interferon, alpha-inducible protein 27	-1.29	0.359	1.52	0.002	1.16	0.743	-2.45	0.076	-0.26
1425335_at	Cd8a /// LOC63614	CD8 antigen, alpha chain /// similar to T-cell surface glycoprotein CD8 alpha chai	-1.55	0.011	1.22	0.683	1.59	0.272	-1.94	0.183	-0.17
1459903_at	Sema7a	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaph	1.03	0.719	-1.25	0.667	1.63	0.178	-1.6	0.161	-0.05
1416371_at	Apod	apolipoprotein D	1.04	0.919	1.48	0.341	-1.06	0.724	-1.61	0.107	-0.04
1428074_at	Tmem158	transmembrane protein 158	1.27	0.451	-1.23	0.548	1.37	0.04	-1.51	0.068	-0.02
1438196_at	Gpd1l	glycerol-3-phosphate dehydrogenase 1-like	1.07	0.653	-1.08	0.749	1.46	0.187	-1.39	0.207	0.02
1438068_at	---	Transcribed locus, strongly similar to XP_579813.1 PREDICTED: hypothetical pr	-1.09	0.796	-1.07	0.89	1.61	0.06	1.91	0.217	0.34
1448768_at	Mog	myelin oligodendrocyte glycoprotein	1.38	0.6	-1.05	0.812	1.12	0.35	-3.07	0.237	-0.4
1422909_at	Smc6	structural maintenance of chromosomes 6	-1.84	0.038	1.69	0.06	1.22	0.406	-1.03	0.794	0.01
1443913_at	Vps33a	Vacuolar protein sorting 33A (yeast)	1.36	0.227	-1.23	0.463	1.28	0.533	-1.26	0.444	0.04
1428559_at	Fvt1	follicular lymphoma variant translocation 1	1.45	0.128	-1.22	0.187	1.19	0.41	-1.05	0.872	0.09
1419706_a_at	Akap12	A kinase (PRKA) anchor protein (gravin) 12	1.46	0.245	1.23	0.522	-1.28	0.354	-1.8	0.243	-0.1
1440807_at	Magi2	Membrane associated guanylate kinase, WW and PDZ domain containing 2	1.67	0.106	1.09	0.908	-1.43	0.151	-1.95	0.361	-0.16
1449859_at	Golt1b	golgi transport 1 homolog B (S. cerevisiae)	2.01	0.425	-1.95	0.184	-1.07	0.886	1.18	0.418	0.04
1444352_at	Zfp287	zinc finger protein 287	1.7	0.083	-1.31	0.607	1	0.999	-1.62	0.393	-0.06
1440461_at	0910001A06Rik	RIKEN cDNA 0910001A06 gene	1.45	0.283	1.12	0.248	-1.13	0.695	-1.79	0.121	-0.09
1426392_a_at	Actr3	ARP3 actin-related protein 3 homolog (yeast)	-1.19	0.131	1.46	0.008	1.16	0.443	-1.36	0.098	0.02
1416378_at	Pnkp	polynucleotide kinase 3'- phosphatase	1.07	0.816	-1.07	0.422	1.46	0.258	-1.08	0.555	0.09
1416551_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	-1.16	0.242	-1.26	0.202	1.81	0.234	1.11	0.575	0.12
1427681_s_at	V2r13	vomeronasal 2, receptor, 13	-1.17	0.581	1.11	0.79	1.51	0.421	-1.84	0.42	-0.1
1421435_at	Grid2	glutamate receptor, ionotropic, delta 2	-1.45	0.381	1.48	0.459	1.29	0.298	-1.06	0.838	0.07
1427521_a_at	9930023K05Rik	RIKEN cDNA 9930023K05 gene	-1.21	0.476	1.06	0.654	1.58	0.16	-1.14	0.775	0.07
1439181_at	BC043301	cDNA sequence BC043301	1.28	0.572	1.5	0.37	-1.46	0.102	-1.43	0.324	-0.03
1449598_at	Denr	Density-regulated protein	1.74	0.358	-1.69	0.394	1.13	0.759	-2.89	0.15	-0.43
1426921_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	-1.04	0.353	-1.04	0.783	1.55	0.19	1.11	0.626	0.14
1436890_at	Uap1l1	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	-1.27	0.043	1.61	0.015	1.07	0.688	-1.48	0.06	-0.02

1418309_at	Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	-1.55	0.577	1.79	0.068	1.03	0.955	-1.24	0.692	0.01
1433744_at	AI841794	expressed sequence AI841794	-1.13	0.427	1.1	0.898	1.48	0.114	-1.19	0.482	0.07
1442832_at	Ankrd52	ankyrin repeat domain 52	1.3	0.447	1.27	0.293	-1.12	0.645	-1.6	0.257	-0.04
1423204_at	Tm9sf4	transmembrane 9 superfamily protein member 4	-1.06	0.793	1.23	0.333	1.29	0.369	-1.02	0.888	0.11
1426102_at	Cyp2j13	cytochrome P450, family 2, subfamily j, polypeptide 13	1.5	0.494	-1.12	0.808	1.07	0.807	-2.74	0.092	-0.32
1435578_s_at	Dab1	disabled homolog 1 (Drosophila)	1.21	0.225	1.46	0.546	-1.26	0.431	-2.55	0.001	-0.29
1456273_x_at	Tpmt	thiopurine methyltransferase	1.26	0.322	1.3	0.279	-1.1	0.44	-1.46	0.245	0
1418373_at	Pgam2	phosphoglycerate mutase 2	-1.2	0.125	-1.88	0.163	2.1	0.2	1.57	0.203	0.15
1433532_a_at	Mbp	myelin basic protein	-1.22	0.606	-2.73	0.031	2.28	0.058	1.74	0.063	0.02
1442268_a_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230001K	2.33	0.389	-1.75	0.198	-1.76	0.043	1.05	0.949	-0.03
1445018_at	Pskh1	Protein serine kinase H1	1.58	0.367	-2.14	0.044	1.42	0.327	-2.13	0.149	-0.32
1455962_at	Hhat	hedgehog acyltransferase	1.1	0.816	-1.04	0.943	1.4	0.033	-1.5	0.363	-0.01
1430074_x_at	8430426H19Rik	RIKEN cDNA 8430426H19 gene	1.13	0.584	-1.03	0.903	1.36	0.272	-1.76	0.21	-0.07
1458741_at	Phgdhl1	Phosphoglycerate dehydrogenase like 1	1.69	0.137	1.07	0.837	-1.42	0.248	-1.14	0.781	0.05
1440438_at	Wasf1	WASP family 1	2.04	0.567	-1.85	0.162	-1.13	0.845	1.04	0.958	0.03
1437229_at	Efhb	EF hand domain family, member B	1.29	0.226	-1.24	0.727	1.36	0.265	-3	0.033	-0.4
1441257_x_at	Wdr45l	Wdr45 like	1.69	0.613	1.22	0.398	-1.77	0.373	-2.11	0.121	-0.25
1447657_s_at	Synpo2l	synaptopodin 2-like	-2.29	0.146	1.04	0.821	1.99	0.144	-1.13	0.842	-0.1
1449132_at	Opn1sw	opsin 1 (cone pigments), short-wave-sensitive (color blindness, tritan)	-1.17	0.667	1.71	0.417	-1.11	0.769	1.88	0.338	0.33
1445615_at	---	---	-1.03	0.935	1.25	0.53	1.24	0.235	-1.8	0.153	-0.08
1433368_x_at	8430401P03Rik	RIKEN cDNA 8430401P03 gene	1.18	0.565	1.66	0.341	-1.6	0.007	-1.32	0.304	-0.02
1417676_a_at	Ptpro	protein tyrosine phosphatase, receptor type, O	1.03	0.528	1.5	0.283	-1.07	0.77	-1.88	0.146	-0.11
1416231_at	Vac14	Vac14 homolog (S. cerevisiae)	-1.28	0.087	-1.06	0.737	1.74	0.05	1.04	0.847	0.11
1430734_at	Cyb5r3	cytochrome b5 reductase 3	1.8	0.193	-1.12	0.76	-1.28	0.672	1.23	0.295	0.16
1448977_at	Tcfap2c	transcription factor AP-2, gamma	-1.42	0.037	1.83	0.391	-1.07	0.745	1.31	0.581	0.16
1447916_at	---	---	-1.38	0.072	1.04	0.947	1.7	0.403	-1.45	0.466	-0.02
1460661_at	Edg3	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	-1	0.997	1.13	0.448	1.34	0.712	-2.55	0.432	-0.27
1438522_at	1700054H16Rik	RIKEN cDNA 1700054H16 gene	-1.35	0.404	1.8	0.133	-1.08	0.786	1.32	0.557	0.17
1426929_at	Brunol4	bruno-like 4, RNA binding protein (Drosophila)	1.33	0.454	1.29	0.364	-1.18	0.51	-1.08	0.812	0.09
1460297_at	Nphs2	nephrosis 2 homolog, podocin (human)	1.91	0.269	1.09	0.89	-2.1	0.081	-1	0.98	-0.03
1434027_at	Dscr1l2	Down syndrome critical region gene 1-like 2	-1.02	0.73	1.2	0.554	1.29	0.224	-1.35	0.105	0.03
1451713_a_at	Fcer2a	Fc receptor, IgE, low affinity II, alpha polypeptide	1.15	0.6	1.67	0.417	-1.54	0.396	-5.86	0.321	-1.15
1442055_at	---	Transcribed locus	-2.11	0.276	1.5	0.559	1.5	0.468	-2.02	0.233	-0.28
1438385_s_at	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	-1	0.976	-1.03	0.793	1.5	0.058	1.2	0.597	0.17
1437197_at	Sorbs2	sorbin and SH3 domain containing 2	1.13	0.483	-1.1	0.477	1.43	0.083	-1.21	0.464	0.06
1426466_s_at	Rps6kl1	ribosomal protein S6 kinase-like 1	1.52	0.042	1.01	0.97	-1.07	0.369	-1.05	0.909	0.1
1446657_at	---	---	1.29	0.554	-1.01	0.978	1.19	0.44	-1.46	0.423	0
1427758_x_at	Igh-4 /// Igh-6 /// Igh	immunoglobulin heavy chain 4 (serum IgG1) /// immunoglobulin heavy chain 6 (he	1.56	0.398	-1.14	0.104	1.03	0.927	-2.04	0.361	-0.15
1416407_at	Pea15	phosphoprotein enriched in astrocytes 15	1.23	0.433	1.4	0.124	-1.2	0.316	-1.15	0.739	0.07
1424083_at	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	-1.07	0.908	-1.16	0.61	1.67	0.242	1.25	0.46	0.17
1435535_at	Depdc5	DEP domain containing 5	1.21	0.008	-1.23	0.545	1.45	0.007	-1.11	0.609	0.08
1421835_at	Mtap7	microtubule-associated protein 7	1.1	0.766	-1.42	0.184	1.67	0.061	-1.34	0.12	0
1432203_at	4930563P21Rik	RIKEN cDNA 4930563P21 gene	1.56	0.557	1.09	0.804	-1.22	0.698	-1.13	0.828	0.07
1442400_at	Prickle1	Prickle like 1 (Drosophila)	-1.14	0.76	1.41	0.15	1.19	0.596	-1.1	0.781	0.09
1432566_at	1700129I15Rik	RIKEN cDNA 1700129I15 gene	1.94	0.219	1.04	0.937	-2.02	0.097	-1.23	0.669	-0.07
1445429_at	Prune	Prune homolog (Drosophila)	-1.27	0.373	1.92	0.035	-1.31	0.576	1.22	0.143	0.14
1448886_at	Gata3	GATA binding protein 3	-1.21	0.251	1.14	0.313	1.51	0.547	-2.01	0.216	-0.14
1456084_x_at	Fmod	fibromodulin	1.11	0.704	-1.35	0.708	1.62	0.517	-1.72	0.342	-0.09
1423007_a_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	-1.17	0.514	1.41	0.073	1.21	0.665	-1.21	0.395	0.06
1432359_at	4930435F05Rik	RIKEN cDNA 4930435F05 gene	-1.54	0.274	-1.18	0.754	1.97	0.096	1.26	0.635	0.13
1460733_at	AA407659	expressed sequence AA407659	-1.01	0.969	1.04	0.687	1.43	0.008	-1.5	0.083	-0.01
1435061_at	Nudt10	nudix (nucleoside diphosphate linked moiety X)-type motif 10	1.91	0.03	-2.09	0.189	1.09	0.789	-2.32	0.261	-0.36
1449388_at	Thbs4	thrombospondin 4	1.67	0.131	-1.67	0.243	1.21	0.74	-2.15	0.177	-0.24

1457698_at	AI314831	expressed sequence AI314831	-1.8	0.638	2.03	0.314	-1.13	0.264	1.34	0.07	0.11
1443991_at	Dock1	dedicator of cyto-kinesis 1	1.18	0.747	-1.04	0.936	1.32	0.6	-1.24	0.685	0.06
1418122_at	Myh11	myosin, heavy polypeptide 11, smooth muscle	1.87	0.37	-1.03	0.671	-1.59	0.358	1.32	0.616	0.14
1429415_at	Prkcbp1	protein kinase C binding protein 1	-1	0.993	1.12	0.181	1.36	0.177	-1	0.999	0.12
1421872_at	Rab24	RAB24, member RAS oncogene family	-1.17	0.04	1.06	0.354	1.56	0.058	-1.17	0.262	0.07
1426318_at	Serpinb1b	serine (or cysteine) peptidase inhibitor, clade B, member 1b	-1.1	0.76	1.91	0.313	-1.54	0.064	1.23	0.642	0.13
1451019_at	Ctsf	cathepsin F	-1.04	0.718	-1.18	0.228	1.66	0.113	4.14	0.212	0.9
1448751_at	Ap3m2	adaptor-related protein complex 3, mu 2 subunit	-1.07	0.797	1.09	0.485	1.45	0.066	-1.55	0.234	-0.02
1449430_a_at	Treh	trehalase (brush-border membrane glycoprotein)	1.13	0.13	1.5	0.389	-1.19	0.663	-1.46	0.673	-0.01
1424169_at	Tax1bp3	Tax1 (human T-cell leukemia virus type I) binding protein 3	1.4	0.034	1.28	0.196	-1.25	0.196	-1.38	0.277	0.01
1449740_s_at	Dsg2	desmoglein 2	1.2	0.14	-1.22	0.054	1.45	0.079	-1.96	0.092	-0.13
1442228_at	D630036G22Rik	RIKEN cDNA D630036G22 gene	-3.81	0.012	-1.25	0.459	2.41	0.25	1.62	0.285	-0.26
1436109_at	AI317395	expressed sequence AI317395	1.05	0.437	-1.11	0.304	1.52	0.1	-1.3	0.639	0.04
1418685_at	Tirap	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	1.2	0.315	1.35	0.26	-1.08	0.686	-1.09	0.579	0.09
1458610_at	---	---	-1.82	0.427	1.8	0.101	1.12	0.699	-1.25	0.057	-0.04
1447001_at	C87114	expressed sequence C87114	1.74	0.319	-1.06	0.944	-1.27	0.756	1.17	0.676	0.15
1454526_at	9430014F16Rik	RIKEN cDNA 9430014F16 gene	-1.08	0.918	1.52	0.091	1.02	0.967	-1.52	0.379	-0.01
1442857_at	Astn2	Astrotactin 2	-2.01	0.044	1.87	0.344	1.11	0.808	-1.29	0.285	-0.08
1429871_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	-1.04	0.958	-1.43	0.488	1.81	0.091	3.32	0.268	0.67
1418354_at	Cog1	component of oligomeric golgi complex 1	-1.31	0.153	1.19	0.48	1.52	0.231	-1.22	0.384	0.05
1439654_at	LOC319225 /// LOC	hypothetical LOC319225 /// hypothetical protein LOC633385	1.22	0.509	1.38	0.528	-1.15	0.577	-2.29	0.011	-0.21
1427529_at	Fzd9	frizzled homolog 9 (Drosophila)	-1.13	0.799	1.46	0.364	1.13	0.773	-2.44	0.073	-0.24
1453175_at	Zbtb25	zinc finger and BTB domain containing 25	-1	0.978	1.45	0.114	1.03	0.796	-1.23	0.119	0.06
1425380_at	Rasgrp4	RAS guanyl releasing protein 4	-1.21	0.066	1.15	0.781	1.5	0.551	-1.13	0.888	0.08
1438484_at	Gm237	gene model 237, (NCBI)	-1.75	0.213	1.62	0.356	1.28	0.534	-1.33	0.481	-0.04
1417178_at	Gipc2	GIPC PDZ domain containing family, member 2	-1.07	0.338	1.46	0.06	1.07	0.599	-1.05	0.862	0.11
1436144_at	Rpl31 /// LOC43268	ribosomal protein L31 /// similar to ribosomal protein L31 /// similar to ribosomal p	1.55	0.494	1.38	0.532	-1.85	0.312	-1.81	0.372	-0.18
1428671_at	2200002D01Rik	RIKEN cDNA 2200002D01 gene	1.37	0.173	1.41	0.129	-1.44	0.136	-1.14	0.38	0.05
1454122_at	1810011H11Rik	RIKEN cDNA 1810011H11 gene	-2.03	0.08	1.37	0.466	1.61	0.311	-1.39	0.192	-0.11
1445531_at	Csmd1	CUB and Sushi multiple domains 1	1.37	0.622	-1.4	0.542	1.39	0.184	-1.58	0.204	-0.05
1451759_at	Masp2	mannan-binding lectin serine peptidase 2	-1.22	0.76	1.11	0.149	1.54	0.227	-1.47	0.007	-0.01
1432970_at	4933423K11Rik	RIKEN cDNA 4933423K11 gene	1.71	0.388	1.28	0.544	-2.07	0.041	-1.19	0.506	-0.07
1450175_a_at	Ctsm	cathepsin M	2.7	0.055	-4.26	0.072	-1.83	0.022	2.2	0.064	-0.3
1421600_a_at	Trim26	tripartite motif protein 26	1.36	0.113	-1.29	0.421	1.34	0.43	-1.5	0.243	-0.02
1418884_x_at	Tuba1	tubulin, alpha 1	1.04	0.777	1.52	0.019	-1.09	0.395	-1.61	0.165	-0.03
1460353_at	Tmem48	transmembrane protein 48	-1.01	0.902	-1.07	0.795	1.56	0.128	2.02	0.201	0.37
1430449_at	C330002I19Rik	RIKEN cDNA C330002I19 gene	-1.08	0.505	-2.29	0.195	2.11	0.311	1.37	0.079	0.03
1430467_at	4921511H03Rik	RIKEN cDNA 4921511H03 gene	-1.3	0.784	1.75	0.346	-1.05	0.899	1.52	0.436	0.23
1433702_at	D19Wsu12e	DNA segment, Chr 19, Wayne State University 12, expressed	-1.09	0.71	1.32	0.114	1.24	0.09	-1.03	0.772	0.11
1422811_at	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	1.24	0.351	-1.15	0.606	1.36	0.198	-1.25	0.545	0.05
1442016_at	D630004N19Rik	RIKEN cDNA D630004N19 gene	2.07	0.236	-1.47	0.46	-1.37	0.119	1.25	0.12	0.12
1443960_at	---	---	-1.04	0.255	1.49	0.219	1.03	0.808	-1.03	0.712	0.11
1437560_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-1.29	0.07	1.74	0.416	-1.04	0.819	1.02	0.94	0.11
1448014_s_at	Usp24	ubiquitin specific peptidase 24	1.16	0.462	-1.11	0.456	1.41	0.064	-1.12	0.285	0.09
1458203_at	Spire1	Spire homolog 1 (Drosophila)	-1.22	0.611	1.92	0.425	-1.35	0.006	3.44	0.184	0.7
1444359_at	2500002G23Rik	RIKEN cDNA 2500002G23 gene	1.36	0.597	-1.46	0.422	1.43	0.394	-1.75	0.43	-0.1
1459935_at	AA517562	EST AA517562	1.29	0.641	1.82	0.191	-2.69	0.001	-1.28	0.294	-0.22
1446808_at	---	---	-1.41	0.577	1.09	0.812	1.68	0.129	-1.31	0.094	0.01
1421296_at	Tnfrsf10b	tumor necrosis factor receptor superfamily, member 10b	1.43	0.607	-1.11	0.667	1.15	0.687	-1.32	0.703	0.04
1421886_at	Sos1	Son of sevenless homolog 1 (Drosophila)	1.74	0.424	-1.41	0.175	1.03	0.839	-1.38	0.298	-0.01
1431517_at	4933417C20Rik	RIKEN cDNA 4933417C20 gene	2.22	0.333	-2	0.502	-1.31	0.558	1.42	0.338	0.08
1455516_at	---	Transcribed locus	-1.1	0.708	-1.09	0.877	1.65	0.513	1.16	0.555	0.15
1420602_a_at	Esx1	extraembryonic, spermatogenesis, homeobox 1	-2.42	0.197	2.17	0.072	-1.11	0.841	2.18	0.414	0.2

1459486_at	AU022240	expressed sequence AU022240	1.11	0.205	-1.1	0.443	1.47	0.508	-2.02	0.363	-0.14
1430927_at	Ceacam18	CEA-related cell adhesion molecule 1	-1.98	0.233	1.45	0.006	1.52	0.202	-1.03	0.928	-0.01
1452240_at	Brunol4	bruno-like 4, RNA binding protein (Drosophila)	-1.16	0.807	1.66	0.166	-1.05	0.783	1.16	0.731	0.15
1429113_at	2900092E17Rik ///	RIKEN cDNA 2900092E17 gene /// RIKEN cDNA 1500031I19 gene	1.57	0.247	1.25	0.59	-1.51	0.272	-1.06	0.904	0.06
1458904_at	Fzd6	Frizzled homolog 6 (Drosophila)	-1.39	0.458	1.69	0.182	1.08	0.867	-1.14	0.808	0.06
1445364_at	---	---	1.55	0.485	-1.19	0.387	1.09	0.722	-1.04	0.889	0.1
1421680_at	A030005L19Rik	RIKEN cDNA A030005L19 gene	1.84	0.391	-1.09	0.908	-1.38	0.544	1.02	0.905	0.1
1458936_at	---	---	-1.07	0.007	1.46	0.587	1.08	0.832	-1.64	0.202	-0.04
1444234_at	---	---	1.75	0.176	-1.11	0.768	-1.22	0.429	1.43	0.177	0.22
1450582_at	H2-Q5	histocompatibility 2, Q region locus 5	1.75	0.53	1.11	0.839	-1.61	0.419	-2.28	0.317	-0.26
1443071_at	AI839979	Expressed sequence AI839979	-2.2	0.014	1.96	0.188	1.06	0.663	-1.01	0.985	-0.05
1416685_s_at	Fbl	fibrillarin	-1.04	0.771	-1.08	0.332	1.59	0.14	1.06	0.582	0.13
1433701_at	Mpped1	metallophosphoesterase domain containing 1	-1.5	0.266	1.71	0.111	1.11	0.52	-2.39	0.23	-0.27
1458109_at	Hapln1	Hyaluronan and proteoglycan link protein 1	1.52	0.313	1.55	0.28	-2.4	0.273	-1.99	0.128	-0.33
1419069_at	Rabgef1	RAB guanine nucleotide exchange factor (GEF) 1	1.73	0.034	-1.28	0.084	-1.02	0.935	2.22	0.261	0.41
1424824_at	9630044O09Rik	RIKEN cDNA 9630044O09 gene	1.19	0.657	-1.2	0.738	1.46	0.351	-1.82	0.203	-0.09
1458344_at	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	-1.26	0.776	-2.05	0.151	2.2	0.047	1.84	0.214	0.18
1451986_s_at	Lrrk1	leucine-rich repeat kinase 1	1.28	0.19	1.22	0.01	-1.02	0.924	-1.3	0.35	0.05
1459232_at	---	---	1.52	0.596	1.08	0.864	-1.13	0.578	-1.15	0.815	0.08
1451183_at	Myohd1	myosin head domain containing 1	-1.28	0.018	-1.25	0.236	1.9	0.099	1.29	0.399	0.16
1421981_at	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	1.38	0.043	-1.7	0.035	1.51	0.276	-2.01	0.15	-0.21
1457566_at	A830058L05Rik	RIKEN cDNA A830058L05 gene	1.04	0.844	1.64	0.192	-1.25	0.601	-1.48	0.24	-0.01
1452354_at	2810459M11Rik	RIKEN cDNA 2810459M11 gene	1.05	0.833	-1.09	0.49	1.51	0.051	-1.03	0.943	0.11
1453487_at	Dhdh	dihydrodiol dehydrogenase (dimeric)	1.47	0.149	-1.2	0.296	1.17	0.465	-1.39	0.36	0.02
1448320_at	Stim1	stromal interaction molecule 1	1.28	0.059	-1.08	0.713	1.28	0.244	-1.14	0.404	0.08
1456030_at	Klf13	Kruppel-like factor 13	1.54	0.045	-1.19	0.739	1.1	0.767	-1.12	0.383	0.08
1449195_s_at	Cxcl16	chemokine (C-X-C motif) ligand 16	1.05	0.73	1.79	0.003	-1.55	0.003	-1.57	0.081	-0.07
1430812_at	4930511A02Rik	RIKEN cDNA 4930511A02 gene	-1.45	0.466	-1.17	0.71	1.94	0.342	1.4	0.694	0.18
1439863_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1.39	0.76	1.31	0.376	-1.28	0.32	-1.81	0.053	-0.1
1454148_at	4930443B20Rik	RIKEN cDNA 4930443B20 gene	1.47	0.274	-1.38	0.107	1.29	0.063	-1.06	0.543	0.08
1451588_at	1810022C23Rik	RIKEN cDNA 1810022C23 gene	-1.27	0.238	1.61	0.324	1.09	0.775	-1.07	0.86	0.09
1434083_a_at	Elmod1	ELMO domain containing 1	1.31	0.238	-1.29	0.618	1.4	0.177	-1.87	0.11	-0.11
1456536_at	Thap6	THAP domain containing 6	-1.12	0.843	1.01	0.983	1.58	0.317	-1.54	0.341	-0.02
1455684_at	Map3k9	mitogen-activated protein kinase kinase kinase 9	-1.35	0.047	1.47	0.268	1.27	0.113	-1.32	0.454	0.02
1425233_at	2210407C18Rik	RIKEN cDNA 2210407C18 gene	-1.91	0.2	2.12	0.13	-1.19	0.612	1.27	0.407	0.07
1419199_at	Cbx8	chromobox homolog 8 (Drosophila Pc class)	2.19	0.073	-1.34	0.481	-1.84	0.072	1.39	0.523	0.1
1419783_at	---	---	1.3	0.662	1.43	0.586	-1.34	0.626	-1.04	0.929	0.09
1450483_at	Gja12	gap junction membrane channel protein alpha 12	1.02	0.951	1.51	0.469	-1.05	0.762	-1.88	0.463	-0.1
1446012_at	Dtnb	Dystrobrevin, beta	1.16	0.166	1.34	0.494	-1.02	0.888	-1.32	0.275	0.04
1437639_at	3321401G04Rik	RIKEN cDNA 3321401G04 gene	-1.08	0.767	1.06	0.907	1.5	0.3	-2.93	0.079	-0.36
1452553_at	---	Mus musculus, clone IMAGE:5068294	1.4	0.109	1.39	0.587	-1.44	0.29	-2.43	0.156	-0.27
1443410_at	Grm5	Glutamate receptor, metabotropic 5	1.76	0.505	1.05	0.944	-1.48	0.52	-1.26	0.535	0.02
1450621_a_at	Hbb-y	hemoglobin Y, beta-like embryonic chain	1.23	0.193	1.44	0.553	-1.23	0.235	-1.28	0.424	0.04
1455192_at	A230078I05Rik	RIKEN cDNA A230078I05 gene	1	0.997	1.57	0.064	-1.1	0.681	-1.18	0.2	0.07
1447166_at	E230002P03Rik	RIKEN cDNA E230002P03 gene	1.14	0.514	1.41	0.585	-1.07	0.862	-1.91	0.205	-0.11
1450208_a_at	Elmo1	engulfment and cell motility 1, ced-12 homolog (C. elegans)	-2.75	0.127	1.53	0.501	1.59	0.158	-2.21	0.302	-0.46
1445207_at	D230050A05	Hypothetical protein LOC208426	1.08	0.938	1.59	0.256	-1.22	0.526	-1.46	0.319	0
1450918_s_at	Src	Rous sarcoma oncogene	-1.06	0.749	1.81	0.125	-1.38	0.025	1.15	0.51	0.13
1453964_at	1700021A07Rik	RIKEN cDNA 1700021A07 gene	-1.36	0.478	1.63	0.173	1.12	0.589	-1.17	0.324	0.05
1444035_at	Mesdc2	mesoderm development candiate 2	-1.09	0.877	1.13	0.807	1.44	0.211	-1.21	0.649	0.07
1443144_at	Prkcb1	protein kinase C, beta 1	1.36	0.748	-1.06	0.868	1.18	0.355	-1.71	0.226	-0.06
1447097_at	BC052688	cDNA sequence BC052688	-1.93	0.388	1.79	0.08	1.18	0.672	-1.1	0.846	-0.02
1444545_at	Epb4.1	Erythrocyte protein band 4.1	-1.13	0.732	1.71	0.345	-1.13	0.837	1.51	0.608	0.24

1420797_at	Otog	otogelin	-1	1	1.61	0.292	-1.14	0.674	1.28	0.595	0.19
1453812_at	Jakmip2	janus kinase and microtubule interacting protein 2	1.23	0.712	-1.42	0.685	1.56	0.25	-1.13	0.853	0.06
1453527_a_at	Neurl	neuralized-like homolog (Drosophila)	-1.06	0.924	-1.75	0.426	1.98	0.316	1.07	0.923	0.06
1428123_at	2610528K11Rik	RIKEN cDNA 2610528K11 gene	-1.02	0.659	-1.49	0.453	1.84	0.165	1.34	0.661	0.17
1445991_at	Lhfp	Lipoma HMGIC fusion partner	1.78	0.477	1.17	0.779	-1.87	0.299	-3.2	0.249	-0.53
1455946_x_at	Tmsb10	thymosin, beta 10	1.13	0.554	-1.41	0.139	1.65	0.337	-1.54	0.091	-0.04
1459694_at	AI428898	expressed sequence AI428898	-1.13	0.484	1.09	0.815	1.52	0.108	-1.59	0.187	-0.03
1445058_at	Fras1	Fraser syndrome 1 homolog (human)	1.16	0.305	1.35	0.344	-1.03	0.879	-1.84	0.549	-0.09
1432508_at	1700113I22Rik	RIKEN cDNA 1700113I22 gene	2.21	0.077	1.03	0.912	-4.06	0.217	-1.31	0.628	-0.53
1441066_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130061K	-2.03	0.004	2.59	0.092	-2.47	0.034	1.02	0.97	-0.22
1433914_at	AI747699	expressed sequence AI747699	1.09	0.503	1.55	0.049	-1.18	0.332	-1.27	0.304	0.05
1425900_at	Hkdc1	hexokinase domain containing 1	1.8	0.255	-1.46	0.645	1	0.981	-1.26	0.725	0.02
1433947_at	Rab37	RAB37, member of RAS oncogene family	1.79	0.29	-1.75	0.327	1.12	0.267	-1.34	0.015	-0.04
1421544_at	Dnahc11	dynein, axonemal, heavy chain 11	1.68	0.216	-1.72	0.367	1.22	0.368	-1.07	0.838	0.03
1434496_at	Plk3	polo-like kinase 3 (Drosophila)	1.4	0.526	-1.48	0.408	1.41	0.151	-1.1	0.739	0.06
1449852_a_at	Ehd4	EH-domain containing 4	1.14	0.016	1.48	0.014	-1.16	0.219	-1.05	0.773	0.11
1416454_s_at	Acta2	actin, alpha 2, smooth muscle, aorta	1.27	0.147	1.32	0.062	-1.11	0.524	-1.35	0.37	0.03
1437076_at	A930017M01Rik	RIKEN cDNA A930017M01 gene	-1.65	0.443	1.6	0.352	1.29	0.39	-1.05	0.837	0.05
1421594_a_at	Sytl2	synaptotagmin-like 2	1.06	0.485	1.69	0.174	-1.36	0.171	-1.41	0.375	0
1419932_s_at	---	---	-1.12	0.646	1.56	0.102	1.04	0.698	-1.46	0.458	0
1452232_at	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransfe	-1	0.949	1.39	0.092	1.1	0.482	-1.52	0.166	-0.01
1443345_at	1700047E16Rik	RIKEN cDNA 1700047E16 gene	1.21	0.169	1.31	0.729	-1.03	0.933	-1.79	0.452	-0.07
1418395_at	1300013J15Rik	RIKEN cDNA 1300013J15 gene	-1.06	0.282	-1.01	0.968	1.56	0.193	1.9	0.248	0.35
1456387_at	Nol4	nucleolar protein 4	1.9	0.406	-1.42	0.613	-1.13	0.815	1.15	0.539	0.12
AFFX-PyruCarbMur	Pcx	pyruvate carboxylase	-1.12	0.449	-1.03	0.825	1.64	0.33	2.05	0.064	0.38
1443834_at	---	Transcribed locus	-1.13	0.3	-1.78	0.194	2.05	0.194	2.07	0.092	0.3
1435909_at	C030034I22Rik	RIKEN cDNA C030034I22 gene	1.08	0.83	-1.09	0.65	1.49	0.015	-2.22	0.08	-0.18
1455520_at	LOC629605	hypothetical protein LOC629605	-1	0.991	1.19	0.295	1.3	0.136	-1.11	0.383	0.1
1419433_at	Nthl1	nth (endonuclease III)-like 1 (E.coli)	1.28	0.316	1.22	0.089	-1	0.979	-1.32	0.267	0.04
1457664_x_at	C2	Complement component 2 (within H-2S)	-1.04	0.681	1.19	0.066	1.34	0.459	-1.52	0.02	-0.01
1416723_at	Tcf4	transcription factor 4	1.05	0.745	1.66	0.016	-1.27	0.117	-1.31	0.362	0.03
1444599_at	---	---	1.5	0.51	1.32	0.208	-1.5	0.107	-1.18	0.745	0.04
1458753_at	Gm941	gene model 941, (NCBI)	-1.74	0.279	1.72	0.42	1.2	0.615	-1.93	0.318	-0.19
1418661_at	Abhd2	abhydrolase domain containing 2	-1.39	0.285	1.31	0.467	1.46	0.065	-1.09	0.537	0.07
1422941_at	Wnt16	wingless-related MMTV integration site 16	1.49	0.654	1.27	0.646	-1.37	0.397	-1.94	0.191	-0.14
1427810_at	Tyms	thymidylate synthase	1.08	0.861	1.66	0.134	-1.34	0.486	-1.3	0.463	0.03
1424826_s_at	Mtss1	metastasis suppressor 1	-1.05	0.728	1.02	0.893	1.52	0.102	-1.13	0.514	0.09
1453454_at	1700012E03Rik	RIKEN cDNA 1700012E03 gene	-2.06	0.199	1.54	0.408	1.46	0.287	-1.37	0.379	-0.11
1453335_a_at	Spata3	spermatogenesis associated 3	1.89	0.181	-1.14	0.86	-1.38	0.707	1.16	0.846	0.13
1427140_at	Pvt1	plasmacytoma variant translocation 1	-1.08	0.733	-1.29	0.433	1.79	0.329	1.78	0.086	0.3
1422198_a_at	Shmt1	serine hydroxymethyl transferase 1 (soluble)	1.16	0.673	-1.24	0.492	1.53	0.563	-1.37	0.355	0.02
1436485_s_at	Whrn	whirlin	1.14	0.513	-1.65	0.584	1.75	0.276	-2.56	0.05	-0.33
1416990_at	Rxrb	retinoid X receptor beta	1.51	0.004	-1.08	0.68	1.06	0.787	-1.19	0.08	0.07
1440812_at	---	Transcribed locus	1.35	0.482	1.33	0.682	-1.23	0.75	-2.31	0.361	-0.22
1438853_x_at	Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	1.01	0.952	-1.03	0.485	1.52	0.039	-1.59	0.106	-0.02
1437155_a_at	Wwtr1	WW domain containing transcription regulator 1	1.37	0.204	1.51	0.257	-1.61	0.103	-1.58	0.212	-0.08
1425345_at	Ccdc28a	coiled-coil domain containing 28A	-1.11	0.792	1.55	0.068	1.05	0.881	-1.28	0.563	0.05
1446893_at	LOC434228	hypothetical gene supported by AK035124	-1.51	0.51	2.02	0.017	-1.23	0.547	1.07	0.879	0.09
1451518_at	Zfp709	zinc finger protein 709	-1.03	0.884	1.01	0.97	1.51	0.162	-1.25	0.322	0.06
1456091_at	Sec22c	SEC22 vesicle trafficking protein-like C (S. cerevisiae)	1.27	0.399	-1.52	0.122	1.57	0.102	-1.01	0.97	0.08
1455223_at	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	1.05	0.961	1.91	0.279	-1.84	0.227	-1.81	0.296	-0.17
1417804_at	Rasgrp2	RAS, guanyl releasing protein 2	-1.06	0.819	1.19	0.211	1.35	0.325	-2.35	0.008	-0.21
1445399_at	Klrb1d	killer cell lectin-like receptor subfamily B member 1D	1.61	0.59	1.52	0.086	-2.72	0.003	-1.17	0.562	-0.19

1423423_at	Pdia3	protein disulfide isomerase associated 3	-1.26	0.484	1.02	0.92	1.68	0.114	-1.4	0.048	0.01
AFFX-PheX-5_at	---	---	1.57	0.527	-1.14	0.433	1.05	0.894	-1.92	0.531	-0.11
1446023_at	Ostf1	Osteoclast stimulating factor 1	1.07	0.824	-1.01	0.989	1.43	0.029	-1.47	0.332	0.01
1452348_s_at	Ifi203 /// Ifi204 /// LC	interferon activated gene 203 /// interferon activated gene 204 /// similar to interfe	-1	0.986	1.15	0.392	1.35	0.416	-2.22	0.072	-0.18
1424177_at	Tmem38a	transmembrane protein 38a	-1.08	0.788	1.1	0.783	1.47	0.067	-2.06	0.411	-0.14
1442870_at	---	CDNA, clone:Y2G0105B03, strand:unspecified	-1.03	0.903	1.35	0.436	1.17	0.691	-1.28	0.278	0.06
1418539_a_at	Ptpre	protein tyrosine phosphatase, receptor type, E	1.27	0.232	1.38	0.165	-1.18	0.19	-1.2	0.395	0.07
1438926_at	---	Transcribed locus, strongly similar to NP_063918.1 ribosomal protein L36a [Mus	2.52	0.3	-2.39	0.152	-1.79	0.311	1.18	0.761	-0.12
1458052_at	---	Transcribed locus	1.12	0.812	1.56	0.147	-1.2	0.416	-1.28	0.67	0.05
1452876_x_at	2610044O15Rik	RIKEN cDNA 2610044O15 gene	1.21	0.501	1.31	0.255	-1.01	0.957	-1.44	0.279	0.01
1416205_at	Glb1	galactosidase, beta 1	-1.01	0.582	-1	0.958	1.52	0.02	1.04	0.847	0.14
1458941_at	D130016B08Rik	RIKEN cDNA D130016B08 gene	-1.03	0.685	1.82	0.058	-1.42	0.173	1.3	0.093	0.17
1435887_at	Serpina11	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsi	1.95	0.062	1.02	0.923	-1.88	0.292	-1.52	0.423	-0.11
1425904_at	Satb2	special AT-rich sequence binding protein 2	-1.24	0.517	1.56	0.096	1.13	0.815	-1.11	0.876	0.09
1417263_at	Ptgs2	prostaglandin-endoperoxide synthase 2	-1.13	0.73	1.43	0.607	1.19	0.692	-1.56	0.449	-0.02
1419571_at	Slc28a3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	-1.83	0.433	1.86	0.226	1.1	0.771	-1.75	0.306	-0.16
1435676_at	Cep164	centrosomal protein 164	-1.01	0.928	-1.02	0.92	1.54	0.13	1.89	0.134	0.35
1456010_x_at	Hes5	hairy and enhancer of split 5 (Drosophila)	-1.04	0.933	1.18	0.683	1.36	0.454	-3.18	0.104	-0.42
1435941_at	Rhbdl3	rhomboid, veinlet-like 3 (Drosophila)	1.1	0.823	-1.28	0.35	1.63	0.248	-1.55	0.097	-0.03
1429576_at	1700060E18Rik	RIKEN cDNA 1700060E18 gene	1.02	0.945	-1.49	0.521	1.81	0.175	-1.83	0.021	-0.12
1426225_at	Rbp4	retinol binding protein 4, plasma	1.75	0.59	-1.26	0.347	-1.04	0.869	2.2	0.462	0.41
1426370_at	Mlstd2	male sterility domain containing 2	-1.2	0.332	1.45	0.379	1.22	0.726	-1.19	0.415	0.07
1431968_at	Spata16	spermatogenesis associated 16	-1.87	0.51	1.8	0.078	1.16	0.759	-1.83	0.476	-0.18
1417765_a_at	Amy1	amylase 1, salivary	-1.26	0.37	-1.1	0.286	1.81	0.37	1.7	0.406	0.29
1440664_at	Cecr5	cat eye syndrome chromosome region, candidate 5 homolog (human)	-2.17	0.312	1.68	0.557	1.36	0.593	-1.15	0.564	-0.07
1431159_at	2900006F19Rik	RIKEN cDNA 2900006F19 gene	-1.17	0.341	1.25	0.627	1.4	0.301	-1.33	0.438	0.04
1421241_at	Ngfr	nerve growth factor receptor (TNFR superfamily, member 16)	1.1	0.87	-1.07	0.765	1.48	0.09	-1.11	0.829	0.1
1432704_at	5730405A17Rik	RIKEN cDNA 5730405A17 gene	-1.69	0.281	1.34	0.178	1.57	0.335	-1.31	0.658	-0.02
1456595_x_at	Gh	growth hormone	1.09	0.752	-1.07	0.773	1.48	0.104	-1.14	0.192	0.09
1421013_at	Pitpnb	phosphatidylinositol transfer protein, beta	-1.03	0.88	-1.17	0.684	1.69	0.301	1.3	0.504	0.19
1423578_at	Col11a2	procollagen, type XI, alpha 2	1.32	0.619	-1.61	0.199	1.56	0.422	-1.01	0.978	0.07
1438933_x_at	Rasgrp2	RAS, guanyl releasing protein 2	-1.06	0.653	1.25	0.128	1.31	0.287	-1.31	0.125	0.05
1422842_at	Xrn2	5'-3' exoribonuclease 2	1.23	0.548	-1.11	0.817	1.37	0.487	-1.4	0.546	0.02
1424408_at	Lims2	LIM and senescent cell antigen like domains 2	1.22	0.322	-1.04	0.844	1.32	0.343	-1.43	0.17	0.02
1446539_at	Inpp4b	Inositol polyphosphate-4-phosphatase, type II	1.15	0.749	1.47	0.63	-1.13	0.825	-1.9	0.18	-0.1
1448747_at	Fbxo32	F-box only protein 32	1.5	0.351	1.07	0.926	-1.07	0.561	-1.32	0.551	0.04
1434998_at	Iqgap1	IQ motif containing GTPase activating protein 1	1.14	0.12	1.54	0.003	-1.21	0.064	-1.19	0.583	0.07
1416411_at	Gstm2	glutathione S-transferase, mu 2	-1.07	0.725	1.48	0.112	1.1	0.663	-1.23	0.345	0.07
1425336_x_at	H2-K1	histocompatibility 2, K1, K region	1.37	0.31	-1.05	0.665	1.18	0.244	-1.35	0.143	0.04
1426299_at	9130017C17Rik	RIKEN cDNA 9130017C17 gene	-1.57	0.494	1.36	0.714	1.51	0.23	-1.59	0.302	-0.07
AFFX-r2-Bs-dap-5_a	---	---	1.5	0.574	-1.13	0.694	1.13	0.789	-1.6	0.52	-0.03
1441908_x_at	Cd93	CD93 antigen	-2.91	0.233	-1.57	0.539	2.53	0.068	1.79	0.315	-0.04
1431115_at	Tgif2	TGFB-induced factor 2	-1.03	0.609	1.18	0.726	1.35	0.529	-2	0.375	-0.12
1440192_at	1810054D07Rik	RIKEN cDNA 1810054D07 gene	1.34	0.022	-1.03	0.777	1.19	0.541	-1.08	0.75	0.11
1437002_at	C030011O14Rik	RIKEN cDNA C030011O14 gene	1.47	0.124	1.08	0.719	-1.04	0.894	-1.09	0.873	0.1
1443884_at	Thada	thyroid adenoma associated	1.46	0.047	-1.54	0.263	1.39	0.307	-1.07	0.654	0.06
1419241_a_at	Aire	autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal d	-1.21	0.759	1.38	0.581	1.3	0.57	-1.82	0.237	-0.09
1436445_at	Gm996	gene model 996, (NCBI)	1.44	0.285	1.39	0.381	-1.47	0.005	-2.23	0.324	-0.22
1422222_at	Ivl	involucrin	1.69	0.592	-1.22	0.257	-1	0.974	1.04	0.802	0.13
1440217_at	LOC434197	similar to hypothetical protein FLJ39743	1.09	0.677	-1.16	0.336	1.56	0.476	-1.5	0.241	0
1443931_at	Ccnb2-ps	Cyclin B2, pseudogene	1.71	0.373	1.07	0.751	-1.36	0.218	-1.59	0.337	-0.04
1423489_at	Mmd	monocyte to macrophage differentiation-associated	1.42	0.085	-1.24	0.144	1.28	0.118	-1.02	0.86	0.11
1449975_a_at	Park2	parkin	-1.06	0.887	1.54	0.329	1.03	0.949	-1.91	0.375	-0.1

1453264_at	Marveld3	MARVEL (membrane-associating) domain containing 3	1.25	0.011	1.51	0.385	-1.34	0.217	-1.76	0.206	-0.08
1438757_at	C130069I09Rik	RIKEN cDNA C130069I09 gene	1.4	0.419	1.16	0.73	-1.06	0.811	-1.25	0.413	0.06
1447135_at	Ptprt	Protein tyrosine phosphatase, receptor type, T	1.41	0.631	-1.09	0.399	1.18	0.699	-2.28	0.246	-0.2
1421866_at	Nr3c1	nuclear receptor subfamily 3, group C, member 1	1.12	0.804	-1.05	0.927	1.43	0.534	-1.31	0.705	0.05
1457834_at	Yy1	YY1 transcription factor	1.07	0.487	-1	0.992	1.44	0.264	-1.2	0.562	0.08
1432236_a_at	Suv39h1	suppressor of variegation 3-9 homolog 1 (Drosophila)	-1.06	0.91	-1.39	0.416	1.84	0.306	2.48	0.322	0.47
1419078_at	Nin	ninein	-1.14	0.18	1.36	0.269	1.28	0.165	-1.06	0.267	0.11
1416797_at	Nck2	non-catalytic region of tyrosine kinase adaptor protein 2	-1.04	0.718	1.32	0.487	1.23	0.626	-1.56	0.215	-0.01
1457270_at	B230343A10Rik	RIKEN cDNA B230343A10 gene	-1.19	0.486	1.68	0.096	-1.01	0.943	1.03	0.742	0.13
1451541_at	Bcs1l	BCS1-like (yeast)	-1.11	0.333	-1.04	0.678	1.65	0	1.02	0.897	0.13
1450585_at	Tas2r119	taste receptor, type 2, member 119	1.45	0.733	-1.07	0.892	1.13	0.757	-2.09	0.247	-0.15
1430403_at	Usp32	ubiquitin specific peptidase 32	1.67	0.094	-1.16	0.712	-1.02	0.892	2.75	0.22	0.56
1451255_at	Lsr	lipolysis stimulated lipoprotein receptor	1.31	0.017	1.23	0.354	-1.03	0.807	-1.44	0.573	0.02
1430751_at	---	---	1.22	0.6	1.43	0.331	-1.17	0.682	-1.56	0.465	-0.02
1444886_at	Appbp2	Amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1.41	0.291	1.37	0.245	-1.37	0.296	-1.91	0.119	-0.12
1428862_at	Ttc17	tetratricopeptide repeat domain 17	-1.07	0.648	1.04	0.813	1.54	0.047	-1.35	0.067	0.04
1459103_at	Hira	Histone cell cycle regulation defective homolog A (S. cerevisiae)	1.79	0.402	-1.88	0.513	1.19	0.347	-1.39	0.727	-0.07
1444741_at	---	---	1.26	0.63	1.4	0.573	-1.17	0.516	-1.92	0.146	-0.11
1428276_at	Abhd13	abhydrolase domain containing 13	1.3	0.415	-1.06	0.835	1.27	0.288	-1.23	0.646	0.07
1448228_at	Lox	lysyl oxidase	1.72	0.343	-1.12	0.821	-1.12	0.742	1.76	0.074	0.31
1427038_at	Penk1	preproenkephalin 1	1.66	0.343	-1.16	0.216	-1.01	0.978	1.49	0.153	0.25
1420852_a_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	1.05	0.901	-1.03	0.926	1.49	0.321	-1.24	0.565	0.07
1434437_x_at	Rrm2	ribonucleotide reductase M2	-1.1	0.723	-1.14	0.504	1.73	0.094	3.69	0.128	0.79
1447422_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.19	0.428	1.67	0.427	-1	0.998	1.7	0.237	0.3
1458481_at	Gm614	gene model 614, (NCBI)	-1.62	0.289	2.11	0.399	-1.28	0.669	1.84	0.078	0.26
1439505_at	Clic5	chloride intracellular channel 5	1	0.99	1.77	0.03	-1.35	0.192	-1.59	0.126	-0.04
1440884_s_at	A530047J11Rik	RIKEN cDNA A530047J11 gene	1.23	0.827	1.42	0.596	-1.15	0.613	-1.34	0.094	0.04
1437568_at	Mmp16	matrix metallopeptidase 16	1.4	0.622	1.41	0.483	-1.42	0.324	-1.17	0.514	0.05
1436259_at	Asb2	Ankyrin repeat and SOCS box-containing protein 2	-1.02	0.98	1.46	0.475	1.07	0.884	-1.13	0.598	0.09
1419721_at	Gpr109a	G protein-coupled receptor 109A	-1.08	0.777	1.62	0.337	-1.03	0.918	1.62	0.217	0.28
1455935_at	2410131K14Rik	RIKEN cDNA 2410131K14 gene	-1.21	0.113	1.23	0.2	1.46	0.023	-1.28	0.164	0.05
1437214_at	Lrrtm4	leucine rich repeat transmembrane neuronal 4	2.06	0.289	-2.13	0.234	-1.01	0.986	3.06	0.298	0.49
1430552_a_at	Sbf1	SET binding factor 1	1.07	0.922	-1	0.981	1.45	0.132	-1.05	0.896	0.12
1418418_a_at	Prlpc1	prolactin-like protein C 1	-1.06	0.667	1.72	0.437	-1.17	0.415	1.17	0.614	0.16
1431739_at	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	2.28	0.203	-1.38	0.362	-1.97	0.115	1.79	0.236	0.18
1456818_at	Stk32a	serine/threonine kinase 32A	-1.15	0.709	1.11	0.828	1.54	0.29	-1.16	0.821	0.08
1439055_at	LOC217066	hypothetical LOC217066	-1.09	0.761	1.64	0.472	-1.04	0.802	1.71	0.458	0.3
1453916_at	4933431K23Rik	RIKEN cDNA 4933431K23 gene	1.01	0.989	1.66	0.323	-1.18	0.677	-2.74	0.199	-0.31
1452853_at	Carkl	carbohydrate kinase-like	-1.15	0.697	1.11	0.608	1.54	0.38	-2.4	0.058	-0.23
1450538_s_at	Mcpt9 /// Cma2	mast cell protease 9 /// chymase 2, mast cell	-2.09	0.069	1.19	0.683	1.85	0.113	-1.53	0.636	-0.15
1445502_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930047H	1.78	0.365	-1.03	0.936	-1.31	0.412	2.99	0.283	0.61
1437031_at	Acsl6	Acyl-CoA synthetase long-chain family member 6	1.95	0.535	-1.4	0.461	-1.17	0.69	1.92	0.066	0.32
1454330_at	4933415J04Rik	RIKEN cDNA 4933415J04 gene	1.16	0.838	-2.07	0.362	1.87	0.319	-1.46	0.294	-0.13
1426951_at	Crim1	cysteine rich transmembrane BMP regulator 1 (chordin like)	1.57	0.339	1.12	0.684	-1.22	0.428	-1.49	0.535	0
1456046_at	Cd93	CD93 antigen	1.23	0.356	1.36	0.163	-1.08	0.628	-1.11	0.226	0.1
1455383_at	C730043O17	hypothetical protein C730043O17	-1.93	0.287	1.79	0.093	1.21	0.5	-1.05	0.904	0
1445784_at	4933435A13Rik	RIKEN cDNA 4933435A13 gene	2.17	0.221	-2.76	0.293	-1.02	0.954	1.1	0.77	-0.13
1429654_at	Dppa2	developmental pluripotency associated 2	1.69	0.411	1.33	0.641	-2.02	0.212	-1.27	0.299	-0.07
1447233_at	D330027H18Rik	RIKEN cDNA D330027H18 gene	1.44	0.506	-1.2	0.31	1.24	0.583	-1.17	0.698	0.08
1427034_at	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	1.42	0.396	-1.87	0.142	1.57	0.013	-1.12	0.696	0
1444211_at	Endogl1	Endonuclease G-like 1	-1.54	0.374	1.81	0.438	1.06	0.852	-1.07	0.628	0.07
1418831_at	Pkp3	plakophilin 3	-1.14	0.05	1.36	0.346	1.28	0.217	-1.81	0.162	-0.08
1443146_at	Atad2	ATPase family, AAA domain containing 2	2	0.365	-1.57	0.178	-1.13	0.742	1.27	0.462	0.14

1437922_at	D10Ertd322e /// LO	DNA segment, Chr 10, ERATO Doi 322, expressed /// similar to mitochondrial rib	1.16	0.46	1.97	0.217	-2.61	0.316	-1.02	0.968	-0.12
1426103_a_at	Esr2	estrogen receptor 2 (beta)	1.98	0.365	-1.48	0.401	-1.16	0.589	2.12	0.06	0.36
1422054_a_at	Skil	SKI-like	-1.1	0.768	1.51	0.401	1.1	0.69	-1.19	0.256	0.08
1437787_at	Lrrtm2	Leucine rich repeat transmembrane neuronal 2	1.5	0.673	-1.68	0.371	1.43	0.541	-1.3	0.572	-0.01
1424092_at	Epb4.1	erythrocyte protein band 4.1	-1.05	0.776	-1.06	0.679	1.62	0.246	2.98	0.235	0.62
1445854_at	C230004F18Rik	RIKEN cDNA C230004F18 gene	-1.61	0.069	1.05	0.931	1.85	0.148	-1.19	0.634	0.02
1455926_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.42	0.087	1.32	0.254	-1.3	0.282	-1.24	0.723	0.05
1417839_at	Cldn5	claudin 5	-1.05	0.885	1.36	0.294	1.21	0.293	-1.33	0.078	0.05
1457892_at	---	Transcribed locus	1.69	0.579	-1.22	0.804	1.02	0.964	-1.13	0.855	0.09
1436295_at	Hcrtr1	hypocretin (orexin) receptor 1	-1	0.994	1.59	0.462	-1.07	0.866	2.08	0.086	0.4
1440612_at	---	---	-1.22	0.029	1.77	0.262	-1.08	0.841	1	0.996	0.12
1448170_at	Siah2	seven in absentia 2	1.18	0.489	-1.06	0.742	1.4	0.519	-1.1	0.425	0.1
1427408_a_at	Thrap3	thyroid hormone receptor associated protein 3	1.02	0.899	-1.19	0.694	1.66	0.316	-1.04	0.941	0.11
1450305_at	4930591A17Rik	RIKEN cDNA 4930591A17 gene	-1.8	0.397	1.02	0.958	1.95	0.087	-1.03	0.935	0.03
1422972_s_at	Gcn5l2	GCN5 general control of amino acid synthesis-like 2 (yeast)	1.1	0.84	-1.07	0.668	1.48	0.114	-1.05	0.855	0.12
1460731_at	Slc35c2	solute carrier family 35, member C2	1.27	0.466	-1.05	0.748	1.3	0.505	-2.03	0.195	-0.13
1437513_a_at	Serinc1	serine incorporator 1	1.14	0.753	-1.15	0.729	1.51	0.263	-1.01	0.974	0.12
1421177_at	Thap2	THAP domain containing, apoptosis associated protein 2	1.5	0.447	1.29	0.512	-1.36	0.248	-1.11	0.543	0.08
1425953_at	Dync1li1	Dynein cytoplasmic 1 light intermediate chain 1	1.77	0.088	-1.31	0.399	-1.01	0.976	1.45	0.098	0.22
1450754_at	LOC669637	similar to calcium channel, voltage-dependent, alpha 2/delta subunit 2	-1.1	0.79	1.59	0.392	1.02	0.963	-1.38	0.461	0.03
1456676_a_at	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	-1.19	0.489	-1.34	0.072	1.94	0.146	1	0.994	0.1
1432272_a_at	Ercc4	excision repair cross-complementing rodent repair deficiency, complementation g	1.42	0.45	-1.18	0.73	1.25	0.632	-1.67	0.519	-0.04
1436647_at	Ttbk2	tau tubulin kinase 2	1.18	0.441	-1.09	0.777	1.43	0.15	-1.29	0.454	0.06
1420429_at	Pcdhb3	protocadherin beta 3	1.26	0.383	1.38	0.501	-1.13	0.6	-1.18	0.515	0.08
1448117_at	Kitl	kit ligand	-1.08	0.681	1.83	0.156	-1.31	0.291	1.28	0.309	0.18
1433883_at	Tpm4	tropomyosin 4	1.33	0.232	1.36	0.01	-1.2	0.019	-1.19	0.077	0.08
1428039_at	2310040A13Rik	RIKEN cDNA 2310040A13 gene	1.46	0.475	-1.02	0.958	1.08	0.61	-1.13	0.783	0.1
1456777_at	Mgam	maltase-glucoamylase	-1.03	0.901	-1.17	0.21	1.69	0.341	1.29	0.609	0.2
1447357_at	---	---	1.1	0.865	1.53	0.47	-1.12	0.707	-1.19	0.583	0.08
1418888_a_at	Sepx1	selenoprotein X 1	1.04	0.746	-1.2	0.101	1.65	0.318	-1.03	0.763	0.11
1439701_at	9330121K16Rik	RIKEN cDNA 9330121K16 gene	-2.66	0.42	2.17	0.259	-1.02	0.964	1.45	0.564	-0.02
1460532_at	2900011F02Rik	RIKEN cDNA 2900011F02 gene	1.45	0.62	1.51	0.283	-1.77	0.476	-3.46	0.051	-0.57
1450766_at	Pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma	-1.26	0.317	1.66	0.416	1.07	0.775	-1.41	0.26	0.02
1452435_at	Wdr22	WD repeat domain 22	-1.06	0.71	1.32	0.186	1.26	0.186	-1.25	0.207	0.07
1421577_at	Evx2	even skipped homeotic gene 2 homolog	-1.15	0.609	1.15	0.782	1.51	0.424	-2.13	0.274	-0.16
1417018_at	Efemp2	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	1.42	0.015	-1.01	0.974	1.11	0.511	-1.16	0.571	0.09
1455120_at	Gloxd1	glyoxalase domain containing 1	1.07	0.759	2.03	0.389	-2.38	0.061	-1.39	0.38	-0.17
1416852_a_at	Ncdn	neurochondrin	1.08	0.5	-1.01	0.908	1.45	0.009	-1.46	0.106	0.02
1449769_at	---	---	-2.68	0.225	1.61	0.466	1.54	0.362	-1.51	0.557	-0.26
1421509_at	Sorcs1	VPS10 domain receptor protein SORCS 1	-1.47	0.486	1.54	0.519	1.31	0.589	-1.37	0.346	0
1449363_at	Atf3	activating transcription factor 3	1.09	0.227	1.62	0.039	-1.23	0.659	-1.15	0.59	0.08
1435840_x_at	LOC625360	similar to 2-cell-stage, variable group, member 3	1.6	0.571	1.34	0.572	-1.71	0.199	-1.7	0.377	-0.12
1459475_at	D10Ertd761e	DNA segment, Chr 10, ERATO Doi 761, expressed	1.41	0.063	-1.54	0.674	1.47	0.088	-1.49	0.274	-0.04
1422616_s_at	Wdr54	WD repeat domain 54	1.19	0.632	-1.51	0.328	1.67	0.167	-1.73	0.268	-0.1
1420646_at	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	-1.2	0.052	1.12	0.656	1.58	0.119	-1.02	0.939	0.12
1448663_s_at	Mvd	mevalonate (diphospho) decarboxylase	1.01	0.956	1.68	0.094	-1.19	0.619	-1.9	0.094	-0.1
1447177_at	---	---	1.28	0.568	1.37	0.4	-1.14	0.555	-1.92	0.278	-0.1
1424510_at	Nudt6	nudix (nucleoside diphosphate linked moiety X)-type motif 6	1.04	0.471	-1.01	0.939	1.49	0.064	-1.15	0.418	0.09
1458283_at	4931406P16Rik	RIKEN cDNA 4931406P16 gene	-1.01	0.984	1.22	0.656	1.31	0.514	-1.23	0.437	0.07
1455106_a_at	Ckb	creatine kinase, brain	1.01	0.729	1.56	0.083	-1.05	0.805	-1.23	0.253	0.07
1434559_at	Stx3	syntaxin 3	1.12	0.454	1.73	0.204	-1.48	0.017	-1.02	0.956	0.09
1432405_a_at	Plcz1	phospholipase C, zeta 1	1.61	0.52	-1	0.995	-1.08	0.889	2.87	0.296	0.6
1421855_at	Fgl2	fibrinogen-like protein 2	-1.08	0.833	1.64	0.03	-1.05	0.832	1.72	0.132	0.31

1418074_at	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	-1.02	0.952	1.49	0.194	1.06	0.801	-1.27	0.305	0.06
1425147_at	2410075B13Rik	RIKEN cDNA 2410075B13 gene	-1.01	0.947	1.44	0.259	1.1	0.807	-1.43	0.258	0.02
1423635_at	Bmp2	bone morphogenetic protein 2	1.76	0.108	-1.18	0.289	-1.09	0.704	1.15	0.752	0.16
1442934_at	C81608	expressed sequence C81608	1.26	0.769	-1.02	0.925	1.29	0.588	-1.19	0.676	0.08
1437432_a_at	Trim12	tripartite motif protein 12	1.2	0.579	1.38	0.255	-1.05	0.742	-2.72	0.031	-0.3
1433151_at	4933415B22Rik	RIKEN cDNA 4933415B22 gene	1.01	0.964	1.68	0.212	-1.2	0.489	-2.62	0.261	-0.28
1449968_s_at	Acot9 /// Acot10	acyl-CoA thioesterase 9 /// acyl-CoA thioesterase 10	1.02	0.868	1.59	0.019	-1.09	0.542	-1.17	0.412	0.09
1449078_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.2	0.262	1.75	0.032	-1.06	0.671	2.05	0.207	0.39
1417481_at	Ramp1	receptor (calcitonin) activity modifying protein 1	1.03	0.877	1.7	0.077	-1.25	0.239	-1.72	0.032	-0.06
1444816_at	---	---	-1.08	0.916	1.24	0.486	1.36	0.38	-1.04	0.951	0.12
1440005_at	C730009D12	hypothetical protein C730009D12	1.75	0.595	-1.23	0.223	-1.03	0.941	1.51	0.337	0.25
1429465_at	1700010M22Rik	RIKEN cDNA 1700010M22 gene	1.04	0.941	1.9	0.085	-1.72	0.125	-1.74	0.141	-0.13
1452630_at	Treml1	triggering receptor expressed on myeloid cells-like 1	-1.37	0.191	-1.08	0.47	1.87	0.206	2.15	0.344	0.39
1420637_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	1.08	0.838	-1.25	0.344	1.66	0.209	-1.01	0.974	0.12
1415885_at	Chgb	chromogranin B	-1.12	0.628	1.44	0.414	1.2	0.533	-1.13	0.872	0.1
1456208_at	A530057A03Rik	RIKEN cDNA A530057A03 gene	-1.74	0.331	1.58	0.083	1.38	0.41	-1.27	0.665	-0.01
1450033_a_at	Stat1	signal transducer and activator of transcription 1	-1.02	0.889	1.03	0.804	1.53	0.158	-1.19	0.308	0.08
1440674_at	Edil3	EGF-like repeats and discoidin I-like domains 3	1	0.999	1.68	0.39	-1.18	0.738	-1.13	0.801	0.09
1458459_a_at	E230029C05Rik ///	RIKEN cDNA E230029C05 gene /// expressed sequence AI452102 /// hypothetica	1.36	0.416	1.38	0.311	-1.26	0.317	-1.18	0.757	0.07
1423582_at	Dmrt1	doublesex and mab-3 related transcription factor 1	1.3	0.757	1.25	0.546	-1.02	0.929	-1.07	0.926	0.11
1438200_at	Sulf1	sulfatase 1	1.4	0.021	1.21	0.6	-1.09	0.821	-1.6	0.347	-0.02
1460030_at	Hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	-1.15	0.804	1.3	0.55	1.37	0.3	-1.61	0.537	-0.02
1456897_at	Stambpl1	Stam binding protein like 1	1.37	0.492	1.2	0.579	-1.03	0.897	-1.88	0.177	-0.09
1436686_at	Zfp706	zinc finger protein 706	1.38	0.387	-1.06	0.818	1.21	0.732	-1.25	0.38	0.07
1417832_at	Smc1a	structural maintenance of chromosomes 1A	1.6	0.684	1.04	0.947	-1.12	0.78	-1.03	0.971	0.12
1437653_at	Irgq	immunity-related GTPase family, Q	1.15	0.779	-1.26	0.623	1.59	0.428	-2.23	0.295	-0.19
1416396_at	---	---	-1.96	0.202	1.99	0.265	1.04	0.802	-1.05	0.723	0
1453232_at	Calr3	calreticulin 3	-1.07	0.892	1.07	0.891	1.52	0.253	-1.04	0.947	0.12
1439179_a_at	5830405N20Rik	RIKEN cDNA 5830405N20 gene	1.29	0.527	-1.26	0.721	1.45	0.391	-3.1	0.054	-0.4
1444576_at	Numa1	Nuclear mitotic apparatus protein 1	-1.01	0.993	1.75	0.063	-1.27	0.572	1.92	0.252	0.35
1456826_at	Taok2	TAO kinase 2	1.48	0.351	-1.34	0.472	1.3	0.496	-1.34	0.03	0.03
1438436_at	6330407J23Rik	RIKEN cDNA 6330407J23 gene	1.72	0.392	-1.58	0.248	1.18	0.783	-2.24	0.451	-0.23
1419123_a_at	Pdgfc	platelet-derived growth factor, C polypeptide	-1.17	0.236	1.7	0.22	-1.02	0.935	1.53	0.22	0.26
1436558_at	Josd3	Josephin domain containing 3	1.46	0.132	-1.05	0.792	1.13	0.512	-1.03	0.623	0.13
1434797_at	6720469N11Rik	RIKEN cDNA 6720469N11 gene	-1.06	0.859	1.46	0.125	1.13	0.628	-1.09	0.457	0.11
1431885_a_at	Mus81	MUS81 endonuclease homolog (yeast)	1.46	0.162	-1.09	0.47	1.16	0.551	-1.42	0.185	0.03
1460330_at	Anxa3	annexin A3	1.2	0.393	1.49	0.033	-1.19	0.206	-1.41	0.024	0.02
1423867_at	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	1.57	0.464	-1.37	0.56	1.24	0.719	-2	0.568	-0.14
1422729_at	Pcdhb10	protocadherin beta 10	1.05	0.392	1.93	0.267	-1.79	0.115	-1.23	0.414	-0.01
1443617_at	Sec15l2	SEC15-like 2 (S. cerevisiae)	1.76	0.144	-1.14	0.682	-1.11	0.863	1.27	0.722	0.2
1452482_at	Erbb3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	1.42	0.472	-1.59	0.594	1.48	0.592	-1.16	0.318	0.04
1423483_s_at	Taf1c	TATA box binding protein (Tbp)-associated factor, RNA polymerase I, C	1.21	0.208	1.34	0.029	-1.02	0.881	-1.12	0.267	0.1
1427189_at	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	-1.18	0.013	-1.28	0.262	1.91	0.017	1.46	0.288	0.23
1443304_at	Mtl5	metallothionein-like 5, testis-specific (tesmin)	1.19	0.819	-1.23	0.718	1.53	0.467	-1.61	0.563	-0.03
1433413_at	Nrxn1	neurexin I	-2.33	0.393	1.22	0.749	1.89	0.2	-1.62	0.469	-0.21
1457149_at	Ttc22	tetratricopeptide repeat domain 22	1.72	0.301	-1.75	0.368	1.24	0.579	-1.04	0.863	0.04
1433446_at	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	-1.14	0.488	1.47	0.157	1.19	0.271	-1.45	0.179	0.02
1433335_at	4930405G09Rik	RIKEN cDNA 4930405G09 gene	1.45	0.561	1.24	0.684	-1.17	0.539	-1.22	0.686	0.07
1427838_at	Tubb2a	tubulin, beta 2a	1.81	0.384	1.05	0.491	-1.47	0.14	-1.29	0.333	0.03
1423571_at	Edg1	endothelial differentiation sphingolipid G-protein-coupled receptor 1	-1.07	0.712	1	0.995	1.6	0.038	-2.46	0.057	-0.23
1439376_x_at	---	---	1.6	0.146	1.28	0.395	-1.5	0.04	-1.23	0.551	0.03
1427316_s_at	AA881470	EST AA881470	-1	0.925	1.01	0.975	1.54	0.056	-1.41	0.275	0.03
1422262_a_at	Lhx6	LIM homeobox protein 6	1.2	0.757	1.4	0.426	-1.07	0.769	-1.36	0.567	0.04

1432523_at	Hipk2	homeodomain interacting protein kinase 2	1.31	0.633	1.33	0.625	-1.1	0.828	-1.03	0.907	0.12
1439357_at	Il17re	interleukin 17 receptor E	-1.11	0.707	1.07	0.876	1.57	0.004	-1.45	0.355	0.02
1435915_at	Jmjd4	jumonji domain containing 4	1.27	0.302	-1.16	0.677	1.41	0.278	-1.29	0.638	0.06
1434147_at	4631403P03Rik	RIKEN cDNA 4631403P03 gene	-1.08	0.847	1.71	0.171	-1.1	0.65	1.15	0.171	0.17
1426825_at	Fmnl3	formin-like 3	-1.1	0.072	1.37	0.152	1.26	0.146	-1.73	0.123	-0.05
1455900_x_at	Tgm2	transglutaminase 2, C polypeptide	-1.08	0.306	1.61	0.07	1.01	0.954	-1.38	0.152	0.04
1440631_at	---	---	1.26	0.417	1.36	0.233	-1.08	0.812	-1.04	0.832	0.12
1454258_at	1110008E08Rik	RIKEN cDNA 1110008E08 gene	-1.2	0.279	-1.36	0.53	1.97	0.07	1.1	0.706	0.13
1454167_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	1.95	0.004	-2.79	0.116	1.23	0.336	-1.53	0.387	-0.28
1423814_at	Ddx41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	1.46	0.088	-1.21	0.323	1.25	0.202	-1.41	0.1	0.02
1455552_at	Snapc4	small nuclear RNA activating complex, polypeptide 4	-1.37	0.185	1.7	0.068	1.11	0.312	-1.77	0.05	-0.08
1434991_at	Fbxw17	F-box and WD-40 domain protein 17	-1.22	0.241	1.49	0.339	1.23	0.165	-1.14	0.592	0.09
1417270_at	Wdr12	WD repeat domain 12	1.23	0.488	1.32	0.363	-1	0.989	-1.27	0.316	0.07
1454335_at	9130214F15Rik	RIKEN cDNA 9130214F15 gene	-2.55	0.29	2.29	0.084	-1.16	0.734	1.47	0.343	0.01
1430591_at	Ddc	dopa decarboxylase	1.83	0.505	-1.24	0.696	-1.1	0.838	1.16	0.521	0.16
1445401_at	Shrm	Shroom	1.74	0.541	-1.08	0.739	-1.14	0.776	2.53	0.17	0.51
1429653_at	Gse1	genetic suppressor element 1	-1.11	0.667	-1.3	0.338	1.87	0.014	1.71	0.306	0.29
1444867_at	C76751	expressed sequence C76751	1.27	0.398	1.27	0.484	-1	0.991	-2.14	0.325	-0.15
1451085_at	C030006K11Rik	RIKEN cDNA C030006K11 gene	1.02	0.874	-1.18	0.444	1.68	0.113	-1.05	0.756	0.12
1427767_a_at	Cftr	cystic fibrosis transmembrane conductance regulator homolog	-1.21	0.203	2.26	0.371	-2.18	0.032	1.07	0.859	-0.01
1426543_x_at	Endod1	endonuclease domain containing 1	-1	0.995	1.74	0.223	-1.25	0.282	3.42	0.242	0.73
1423170_at	Taf7	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.75	0.043	-1.55	0.066	1.15	0.564	-1.02	0.891	0.08
1440346_at	Jmjd3	Jumonji domain containing 3	1.41	0.429	-1.28	0.539	1.35	0.554	-1.13	0.788	0.09
1459936_at	---	Transcribed locus	-1.03	0.631	1.65	0.419	-1.07	0.615	1.13	0.25	0.17
1459584_at	Vps24	vacuolar protein sorting 24 (yeast)	2.19	0.16	-1.47	0.002	-1.48	0.346	1.64	0.278	0.22
1421651_at	Ankrd22	ankyrin repeat domain 22	1.32	0.302	1.44	0.39	-1.26	0.574	-1.63	0.561	-0.04
1459763_at	Adipoq	Adiponectin, C1Q and collagen domain containing	1.91	0.298	-1.67	0.376	1.04	0.945	-1.97	0.263	-0.17
1441164_at	Pip5k2b	Phosphatidylinositol-4-phosphate 5-kinase, type II, beta	1.23	0.429	1.58	0.348	-1.37	0.23	-1.82	0.197	-0.09
1446631_at	9430083I22	hypothetical protein 9430083I22	-2.18	0.323	-1.2	0.725	2.25	0.016	1.11	0.88	0
1441087_at	2810011L19Rik	RIKEN cDNA 2810011L19 gene	-1.12	0.916	2.11	0.183	-1.85	0.072	1.73	0.382	0.22
1454137_s_at	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	-1.54	0.187	1.06	0.505	1.83	0.19	-1.13	0.888	0.06
1437961_x_at	AA407659	Expressed sequence AA407659	-1.04	0.815	-1.76	0.378	2.02	0.149	1.23	0.802	0.11
1431052_at	Arhgap12	Rho GTPase activating protein 12	1.07	0.861	-1.46	0.641	1.79	0.315	-2.75	0.277	-0.34
1419344_at	Tcte1	t-complex-associated testis expressed 1	-1	0.991	-1.33	0.281	1.79	0.026	1.31	0.266	0.19
1433742_at	Ankrd15	ankyrin repeat domain 15	-1	0.973	1.01	0.94	1.54	0.077	-1.75	0.18	-0.05
1439706_at	A330106F07Rik	RIKEN cDNA A330106F07 gene	-1.55	0.107	1.94	0.046	-1.04	0.913	1.54	0.406	0.22
1443645_at	1700026B20Rik	RIKEN cDNA 1700026B20 gene	-1.05	0.874	1.22	0.654	1.38	0.636	-1.35	0.411	0.05
1449969_at	Tmod4	tropomodulin 4	1.36	0.723	-1.97	0.262	1.68	0.27	-1.42	0.112	-0.09
1451657_a_at	Cova1	cytosolic ovarian carcinoma antigen 1	1.5	0.261	1.17	0.68	-1.13	0.629	-1.59	0.09	-0.02
1421902_at	Ixl	intersex-like (Drosophila)	1.65	0.509	-1.01	0.974	-1.1	0.877	1.5	0.501	0.26
1452832_s_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	-1.01	0.861	1.2	0.284	1.35	0.109	-1.24	0.445	0.08
1445011_at	---	---	1.22	0.036	-1.05	0.929	1.38	0.464	-1.13	0.734	0.1
1425890_at	Ly6i	lymphocyte antigen 6 complex, locus I	-1.21	0.761	-1.35	0.578	1.98	0.09	1.35	0.398	0.19
1457795_at	Scamp4	Secretory carrier membrane protein 4	-2.34	0.229	1.16	0.578	1.96	0.088	-1.01	0.969	-0.06
1447972_at	---	Transcribed locus	-1.45	0.507	1.12	0.799	1.74	0.383	-1.38	0.342	0.01
1456903_at	Ptx3	pentraxin related gene	2.29	0.053	-1.84	0.222	-1.4	0.548	1.36	0.677	0.1
1431456_at	4931439C15Rik	RIKEN cDNA 4931439C15 gene	1.04	0.962	-1.72	0.362	1.93	0.195	-1.64	0.524	-0.1
1445514_at	Vhlh	von Hippel-Lindau syndrome homolog	1.19	0.486	1.65	0.079	-1.42	0.158	-1.32	0.2	0.03
1452424_at	Gpr23	G protein-coupled receptor 23	1.41	0.392	1.41	0.499	-1.37	0.462	-1.21	0.694	0.06
1425281_a_at	Tsc22d3	TSC22 domain family 3	1.34	0.435	-1.11	0.565	1.31	0.182	-1.83	0.083	-0.07
1443327_at	D130043K22Rik	RIKEN cDNA D130043K22 gene	-1.05	0.854	1.14	0.721	1.45	0.048	-1.7	0.211	-0.04
1421605_a_at	Aqp9	aquaporin 9	-1.98	0.276	-1.03	0.938	2.07	0.243	2.58	0.191	0.41
1433804_at	Jak1	Janus kinase 1	-1.01	0.959	1.28	0.441	1.29	0.379	-1.17	0.728	0.09

1448982_at	Klk6	kallikrein 6	-1.83	0.293	1.68	0.273	1.33	0.622	-2.83	0.208	-0.41
1440124_at	B230334C09Rik	RIKEN cDNA B230334C09 gene	-1.09	0.831	1.2	0.729	1.44	0.366	-1.06	0.715	0.12
1421216_a_at	Ids	iduronate 2-sulfatase	1.44	0.425	-1.62	0.439	1.49	0.343	-1.21	0.29	0.03
1419468_at	Clec14a	C-type lectin domain family 14, member a	1.39	0.26	1.39	0.3	-1.29	0.119	-1.26	0.506	0.06
1459400_at	A630038E17Rik	RIKEN cDNA A630038E17 gene	1.54	0.496	1.09	0.866	-1.09	0.714	-1.39	0.37	0.04
1421333_a_at	Mynn	myoneurin	-1.06	0.664	-1.23	0.58	1.8	0.096	1.12	0.731	0.16
1455743_at	Olfml2a	olfactomedin-like 2A	-1.47	0.613	1.87	0.109	-1	0.989	1.66	0.199	0.27
1444948_at	---	---	1.84	0.388	1.03	0.951	-1.47	0.337	-2.44	0.28	-0.26
1421210_at	C2ta	class II transactivator	-1.09	0.652	1.17	0.466	1.46	0.368	-1.64	0.228	-0.02
1415786_at	Pgc	progastricsin (pepsinogen C)	2	0.057	-1.24	0.588	-1.34	0.453	1.29	0.575	0.18
1425978_at	Myocd	myocardin	1.76	0.3	1.15	0.765	-1.55	0.008	-1.41	0.498	-0.01
1440695_at	Zfp40	Zinc finger protein 40	1.31	0.188	1.63	0.207	-1.63	0.086	-1.39	0.133	-0.02
1448507_at	Efhd1	EF hand domain containing 1	1.1	0.313	-1.25	0.301	1.65	0.114	-1.49	0.068	0
1454650_at	Trim35	tripartite motif-containing 35	-1.1	0.021	1.49	0.027	1.16	0.421	-1.61	0.138	-0.02
1426864_a_at	Ncam1	neural cell adhesion molecule 1	-1.09	0.854	2.18	0.126	-2.18	0.078	3.47	0.138	0.6
1460494_at	Ttll10	tubulin tyrosine ligase-like family, member 10	1.64	0.603	1.51	0.608	-2.52	0.008	-1.95	0.462	-0.33
1459831_s_at	Tmco5	transmembrane and coiled-coil domains 5	1.63	0.478	1.32	0.658	-1.64	0.177	-3.78	0.023	-0.62
1450316_at	Pcdhb13	protocadherin beta 13	-1.1	0.778	-1.26	0.556	1.85	0.175	1.08	0.764	0.14
1441306_at	6820408C15Rik	RIKEN cDNA 6820408C15 gene	1.39	0.562	1.2	0.838	-1.03	0.928	-1.39	0.421	0.04
1416250_at	Btg2	B-cell translocation gene 2, anti-proliferative	-1.21	0.359	1.83	0.301	-1.11	0.739	1.15	0.5	0.16
1421356_at	Tex9	testis expressed gene 9	2.24	0.233	-1.12	0.875	-2.38	0.025	1.05	0.913	-0.05
1419393_at	Abcg5	ATP-binding cassette, sub-family G (WHITE), member 5	1.57	0.339	-1.63	0.055	1.37	0.428	-1.09	0.726	0.06
1434639_at	Kbtbd9	kelch repeat and BTB (POZ) domain containing 9	1.41	0.286	-1.09	0.701	1.23	0.689	-1.24	0.498	0.08
1438308_at	2310026E23Rik	RIKEN cDNA 2310026E23 gene	1.06	0.891	-1.02	0.966	1.51	0.215	-2.3	0.095	-0.19
1419550_a_at	Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	1.21	0.33	1.68	0.013	-1.52	0.264	-1.41	0.132	-0.01
1458888_at	---	CDNA clone IMAGE:5250818	1.82	0.087	-1.53	0.456	1.08	0.719	-1.7	0.249	-0.08
1417413_at	Cuzd1	CUB and zona pellucida-like domains 1	-1.08	0.907	2.1	0.048	-1.89	0.146	1.29	0.702	0.11
1455628_at	6430543G08Rik	RIKEN cDNA 6430543G08 gene	1.69	0.423	-1.14	0.613	-1.01	0.979	1.29	0.666	0.21
1425656_a_at	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2	1.22	0.502	-1.05	0.782	1.39	0.309	-1.43	0.271	0.03
1450138_a_at	Serpinb6a	serine (or cysteine) peptidase inhibitor, clade B, member 6a	1.03	0.589	1.66	0.004	-1.15	0.509	-1.2	0.592	0.08
1458516_at	Nckap1l	NCK associated protein 1 like	2.2	0.003	-2.99	0.052	1.02	0.963	-1.15	0.739	-0.23
1454634_at	Fuk	fucokinase	-1.04	0.9	1.31	0.24	1.28	0.331	-1.15	0.037	0.1
1452533_at	Ryr3	ryanodine receptor 3	1.4	0.549	1.49	0.601	-1.51	0.266	-1.3	0.632	0.02
1459832_s_at	Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	-1.1	0.702	1.01	0.856	1.64	0.005	-1.15	0.046	0.1
1444821_at	D8Ertd82e	DNA segment, Chr 8, ERATO Doi 82, expressed	-1.57	0.39	2.22	0.195	-1.43	0.65	1.41	0.619	0.16
1442746_at	---	---	-1.49	0.114	2.13	0.347	-1.32	0.58	1.44	0.637	0.19
1429024_at	1110018J23Rik	RIKEN cDNA 1110018J23 gene	-1.02	0.959	1.31	0.293	1.27	0.434	-1.74	0.256	-0.05
1444139_at	Ddit4l	DNA-damage-inducible transcript 4-like	-1.07	0.832	-1.07	0.848	1.68	0.083	1.15	0.38	0.17
1436419_a_at	1700097N02Rik	RIKEN cDNA 1700097N02 gene	-1.01	0.99	1.65	0.376	-1.09	0.638	2	0.381	0.39
1423703_at	Ppan	peter pan homolog (Drosophila)	1.07	0.471	-1.35	0.235	1.74	0.116	-1.04	0.675	0.11
1450210_at	Bmp15	bone morphogenetic protein 15	2	0.394	-1.88	0.355	1.03	0.957	-2.14	0.396	-0.25
1434573_at	Traf3ip3	TRAF3 interacting protein 3	-1.29	0.79	1.11	0.747	1.67	0.168	-2.65	0.034	-0.29
1429275_at	9530059J11Rik	RIKEN cDNA 9530059J11 gene	-1.13	0.299	1.29	0.052	1.38	0.04	-1.83	0.145	-0.07
1425778_at	C230043N17Rik	RIKEN cDNA C230043N17 gene	1.64	0.022	1.13	0.331	-1.26	0.429	-1.79	0.029	-0.07
1455445_at	Cbln3	cerebellin 3 precursor protein	1.37	0.442	1.33	0.76	-1.16	0.684	-1.38	0.662	0.04
1460412_at	1600015H20Rik	RIKEN cDNA 1600015H20 gene	1.24	0.099	1.69	0.182	-1.61	0.432	-1.18	0.578	0.04
1442860_at	Dgkb	diacylglycerol kinase, beta	-1.22	0.577	1.11	0.857	1.63	0.214	-1.15	0.715	0.09
1444062_at	2900056L01Rik	RIKEN cDNA 2900056L01 gene	-1.03	0.949	-1.92	0.204	2.07	0.288	1.48	0.138	0.15
1446907_at	C87679	expressed sequence C87679	1.79	0.236	-2.45	0.334	1.36	0.525	-1.32	0.739	-0.16
1435131_at	Zfp13	zinc finger protein 13	-1.17	0.36	1.36	0.607	1.35	0.473	-2.79	0.43	-0.31
1431606_a_at	Angel2	angel homolog 2 (Drosophila)	1.44	0.263	-1.18	0.599	1.27	0.524	-1.23	0.597	0.08
1426554_a_at	Pgam1 /// LOC668(	phosphoglycerate mutase 1 /// similar to Phosphoglycerate mutase 1 (Phosphogl	-1.06	0.427	1.05	0.501	1.56	0.001	-1.06	0.546	0.12
1419327_at	2210010A19Rik	RIKEN cDNA 2210010A19 gene	1.08	0.86	-1.14	0.769	1.61	0.501	-2.64	0.159	-0.27

1442013_at	4930532D21Rik	RIKEN cDNA 4930532D21 gene	1.66	0.465	1.18	0.741	-1.39	0.416	-3.38	0.032	-0.48
1436384_at	Rps10 /// LOC6217	ribosomal protein S10 /// similar to ribosomal protein S10 /// similar to ribosomal p	1.16	0.791	-1.1	0.795	1.5	0.037	-1.22	0.272	0.08
1452843_at	Il6st	interleukin 6 signal transducer	1.19	0.251	1.41	0.119	-1.04	0.713	-1.53	0.115	0.01
1420126_at	AA522020	expressed sequence AA522020	1.65	0.56	-1.13	0.844	1.02	0.96	-1.36	0.246	0.05
1442274_at	Zdhhc15	zinc finger, DHHC domain containing 15	-1.24	0.543	1.83	0.345	-1.07	0.87	1.3	0.402	0.2
1423313_at	Pde7a	phosphodiesterase 7A	-1.16	0.506	1.56	0.454	1.14	0.52	-1.48	0.072	0.02
1425145_at	Il1rl1	interleukin 1 receptor-like 1	2.18	0.119	-1.26	0.72	-1.71	0.137	6.04	0.21	1.32
1459810_at	1110008F13Rik	RIKEN cDNA 1110008F13 gene	-1.3	0.145	1.85	0.062	-1.06	0.843	1.24	0.657	0.18
1438410_at	Prtg	protogenin homolog (Gallus gallus)	1.59	0.362	1.21	0.756	-1.32	0.635	-1.38	0.038	0.03
1439320_at	BC030477	cDNA sequence BC030477	-1.13	0.43	1.78	0.249	-1.12	0.399	1	0.975	0.14
1430912_a_at	Tectb	tectorin beta	1.37	0.624	-1.29	0.614	1.42	0.33	-1.15	0.832	0.09
1423527_at	4921510H08Rik	RIKEN cDNA 4921510H08 gene	1.9	0.29	-1.23	0.634	-1.17	0.425	1.3	0.398	0.2
1458059_at	---	---	1.27	0.213	1.35	0.139	-1.06	0.777	-1.2	0.567	0.09
1451838_a_at	Mtac2d1	membrane targeting (tandem) C2 domain containing 1	1.77	0.398	-1.23	0.369	-1.02	0.895	1.38	0.523	0.22
1422567_at	Niban	niban protein	1.15	0.603	1.51	0.337	-1.11	0.645	-1.13	0.588	0.11
1437845_x_at	Pofut2	protein O-fucosyltransferase 2	-1	0.941	1.21	0.005	1.35	0.061	-1.06	0.715	0.13
1425198_at	Ptpn2	protein tyrosine phosphatase, non-receptor type 2	1.17	0.653	1.51	0.401	-1.12	0.664	-1.39	0.38	0.04
1450436_s_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	1.47	0.237	-1.02	0.948	1.11	0.566	-1.75	0.003	-0.05
1431283_at	---	---	-1.04	0.815	1.34	0.427	1.26	0.583	-1.73	0.587	-0.04
1456700_x_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.2	0.504	1.51	0.019	-1.17	0.203	-1.26	0.506	0.07
1446782_at	Lins2	lines homolog 2 (Drosophila)	-1.01	0.968	1.53	0.207	1.04	0.931	-1.06	0.942	0.13
1433306_at	4930456K20Rik	RIKEN cDNA 4930456K20 gene	-1.36	0.758	1.5	0.46	1.33	0.581	-1.11	0.877	0.09
1418263_at	Ddx25	DEAD (Asp-Glu-Ala-Asp) box polypeptide 25	1.07	0.881	-1.03	0.947	1.52	0.419	-2.65	0.133	-0.27
1441770_at	Ppat	phosphoribosyl pyrophosphate amidotransferase	-1.06	0.95	1.67	0.318	-1.05	0.874	1.36	0.507	0.23
1437691_at	Anxa2	annexin A2	-1.65	0.499	2.41	0.351	-1.82	0.313	1.34	0.335	0.07
1428420_a_at	1200009I06Rik	RIKEN cDNA 1200009I06 gene	-1.31	0.194	1.77	0.08	1.03	0.852	-1.29	0.132	0.05
1444650_at	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	1.54	0.254	-1.97	0.14	1.52	0.518	-3.41	0.051	-0.58
1430430_at	6130401L20Rik	RIKEN cDNA 6130401L20 gene	-1.29	0.43	2.02	0.228	-1.29	0.463	1.6	0.24	0.26
1460039_at	Clec1a	C-type lectin domain family 1, member a	1.8	0.122	1.1	0.754	-1.51	0.092	-1.27	0.729	0.03
1432717_at	1810015A16Rik	RIKEN cDNA 1810015A16 gene	1.44	0.538	1.13	0.731	-1	0.97	-2.43	0.236	-0.22
1445270_at	---	Transcribed locus	1.57	0.003	-1.08	0.859	1.06	0.499	-1.88	0.228	-0.08
1430988_at	2810407C02Rik	RIKEN cDNA 2810407C02 gene	1.03	0.904	1.63	0.414	-1.1	0.87	-1.85	0.455	-0.07
1430143_at	4930426D05Rik	RIKEN cDNA 4930426D05 gene	1.16	0.379	-1.01	0.982	1.41	0.664	-2.9	0.038	-0.33
1446368_at	9130221J18Rik	RIKEN cDNA 9130221J18 gene	-1.24	0.233	1.63	0.229	1.13	0.742	-1.24	0.641	0.07
1450183_a_at	Sh2b3	SH2B adaptor protein 3	1.16	0.423	-1.03	0.939	1.44	0.367	-1.75	0.357	-0.05
1434626_at	Rpusd3	RNA pseudouridylate synthase domain containing 3	-1.13	0.475	-1.17	0.36	1.83	0.095	1.16	0.293	0.17
1433950_at	Igsf21	immunoglobin superfamily, member 21	1.76	0.252	1.19	0.416	-1.59	0.332	-1.14	0.755	0.05
1441619_at	Zfp14	zinc finger protein 14	1.05	0.819	1.81	0.523	-1.41	0	-1.3	0.172	0.04
1418587_at	Traf3	Tnf receptor-associated factor 3	1.11	0.44	-1.01	0.933	1.47	0.187	-1.48	0.243	0.02
1416491_at	Numbl	numb-like	1.56	0.461	-1.18	0.836	1.16	0.582	-1.12	0.557	0.11
1444945_at	AU024605	expressed sequence AU024605	-1.73	0.168	1.04	0.889	1.95	0.042	-2.05	0.043	-0.2
1415973_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.21	0.418	1.49	0.017	-1.15	0.157	-1.34	0.461	0.05
1453438_x_at	Gsdm2	gasdermin 2	-1.99	0.344	1.46	0.498	1.61	0.387	-1.07	0.908	0
1455084_x_at	Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)	-1.16	0.453	-1.03	0.763	1.73	0.125	1.11	0.631	0.16
1455595_at	Ugt2b36	UDP glucuronosyltransferase 2 family, polypeptide B36	1.9	0.556	-1.14	0.105	-1.25	0.362	1.95	0.222	0.36
1453142_at	4921507P07Rik	RIKEN cDNA 4921507P07 gene	1.81	0.394	-1.12	0.864	-1.15	0.772	1.1	0.894	0.16
1441011_at	---	Transcribed locus	1.48	0.427	1.14	0.447	-1.06	0.805	-1.73	0.507	-0.04
1416487_a_at	Yap1	yes-associated protein 1	1.36	0.05	-1.42	0.445	1.51	0.4	-2.5	0.376	-0.26
1431204_at	4930578N16Rik	RIKEN cDNA 4930578N16 gene	1.03	0.934	1.62	0.443	-1.1	0.545	-1.56	0.146	0
1458271_at	---	12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530	-1.91	0.497	2.55	0.224	-2.01	0.195	1.68	0.449	0.08
1451239_a_at	Slc26a1	solute carrier family 26 (sulfate transporter), member 1	-1.32	0.149	-1.09	0.61	1.9	0.159	2.66	0.147	0.54
1424362_at	Ppapdc3	phosphatidic acid phosphatase type 2 domain containing 3	1.47	0.294	1.31	0.607	-1.27	0.63	-1.17	0.593	0.08
1451180_a_at	Nt5c3l	5'-nucleotidase, cytosolic III-like	1.62	0.043	1.1	0.641	-1.17	0.468	-1.6	0.1	-0.01

1428336_at	Agpat4	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransf	-1.18	0.497	1.87	0.023	-1.17	0.277	1.98	0.216	0.37
1445049_at	C80893	expressed sequence C80893	-1.15	0.878	1.79	0.215	-1.09	0.835	1.23	0.022	0.19
1445420_at	Mef2c	Myocyte enhancer factor 2C	1.5	0.039	1.28	0.682	-1.26	0.302	-2.05	0.28	-0.13
1450782_at	Wnt4	wingless-related MMTV integration site 4	-1.18	0	1.29	0.535	1.43	0.028	-1.44	0.099	0.03
1456051_at	Drd1a	dopamine receptor D1A	1.13	0.747	1.51	0.412	-1.07	0.836	-1.3	0.126	0.07
1426934_at	Nhsl1	NHS-like 1	1.25	0.082	-1.1	0.596	1.41	0.317	-1.6	0.299	-0.01
1459674_at	Prkcb1	Protein kinase C, beta 1	-2.03	0.228	1.42	0.556	1.67	0.218	-1.72	0.189	-0.17
1421917_at	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	1.18	0.496	1.64	0.017	-1.33	0.144	-1.52	0.406	-0.01
1418142_at	Kcnj8	potassium inwardly-rectifying channel, subfamily J, member 8	-1.08	0.664	1.79	0.181	-1.17	0.475	1.19	0.157	0.18
1422398_at	Hist1h1e	histone 1, H1e	-2.04	0.492	2.2	0.331	-1.13	0.497	1.27	0.601	0.08
1421175_at	Myt1l	myelin transcription factor 1-like	-1.34	0.756	2.01	0.388	-1.22	0.696	1.08	0.895	0.13
1435553_at	Pdzd2	PDZ domain containing 2	-1.13	0.112	1.95	0.167	-1.34	0.321	1.13	0.633	0.15
1451155_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.47	0.475	-1.32	0.62	1.34	0.223	-2.13	0.145	-0.16
1438241_at	Rgma	RGM domain family, member A	-1.59	0.097	1.51	0.017	1.43	0.268	-1.14	0.135	0.05
1440402_at	4831426I19Rik	RIKEN cDNA 4831426I19 gene	-1.27	0.738	1.1	0.899	1.68	0.098	-1.09	0.739	0.11
1439571_at	E230008J23Rik	RIKEN cDNA E230008J23 gene	1.14	0.694	1.51	0.132	-1.08	0.662	-1.36	0.204	0.05
1429334_at	2300002O18Rik	RIKEN cDNA 2300002O18 gene	2.44	0.431	-2.44	0.265	-1.38	0.604	1.83	0.483	0.11
1444646_at	8430420F16Rik	RIKEN cDNA 8430420F16 gene	-1.25	0.148	2.13	0.304	-1.55	0.032	1.23	0.803	0.14
1453349_at	Casz1	castor homolog 1, zinc finger (Drosophila)	-1.63	0.101	1.53	0.291	1.43	0.05	-1.27	0.425	0.02
1418145_at	Tfip11	tuftelin interacting protein 11	1.03	0.882	-1.11	0.201	1.64	0.019	-1.28	0.072	0.07
1426502_s_at	Gpt1	glutamic pyruvic transaminase 1, soluble	1.72	0.033	-1.15	0.549	-1.02	0.914	1.16	0.59	0.18
1454048_a_at	4931408A02Rik ///	RIKEN cDNA 4931408A02 gene /// similar to Protein C21orf63 homolog precurso	-1.04	0.875	1.58	0.187	1.04	0.749	-1.16	0.442	0.1
1439819_at	AU015263	expressed sequence AU015263	1.42	0.543	1.37	0.321	-1.28	0.369	-1.58	0.317	-0.01
1425957_x_at	1700021K02Rik	RIKEN cDNA 1700021K02 gene	-2	0.486	-2.87	0.176	2.73	0.035	1.41	0.51	-0.18
1458633_at	---	---	1.48	0.305	1.12	0.497	-1.02	0.947	-1.77	0.21	-0.05
1441005_at	2610304G08Rik	RIKEN cDNA 2610304G08 gene	-1.36	0.354	1.88	0.109	-1.04	0.801	1.02	0.85	0.13
1418393_a_at	Itga7	integrin alpha 7	1.45	0.119	1.32	0.207	-1.24	0.178	-1.24	0.667	0.07
1431101_a_at	Srd5a1	steroid 5 alpha-reductase 1	1.44	0.393	-1.56	0.168	1.5	0.506	-1.06	0.42	0.08
1418643_at	Tspan13	tetraspanin 13	1.16	0.3	1.71	0.018	-1.41	0.005	-1.44	0.216	0
1457404_at	Nfkbiz	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.02	0.882	1.63	0.081	-1.08	0.714	-1.41	0.285	0.04
1439374_x_at	Rps10 /// LOC6217	ribosomal protein S10 /// similar to ribosomal protein S10 /// similar to ribosomal p	-1.35	0.148	1.8	0.001	1.04	0.954	-3.84	0.04	-0.59
1432035_at	4933427J07Rik	RIKEN cDNA 4933427J07 gene	-1.86	0.431	-1.46	0.623	2.36	0.043	1.24	0.523	0.07
1429802_at	Dhrs10	dehydrogenase/reductase (SDR family) member 10	2.05	0.024	-1.24	0.104	-1.39	0.461	3.4	0.002	0.7
1424468_s_at	Phldb1	pleckstrin homology-like domain, family B, member 1	1.08	0.471	1.79	0.085	-1.4	0.142	-1.14	0.681	0.08
1425453_x_at	Klra12	killer cell lectin-like receptor subfamily A, member 12	1.42	0.67	-1.24	0.657	1.35	0.512	-1.17	0.84	0.09
1458446_at	3222401L13Rik	RIKEN cDNA 3222401L13 gene	1.67	0.003	-1.04	0.939	-1.05	0.82	1.29	0.051	0.22
1431890_a_at	Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosoph	-1.18	0.227	2.04	0.009	-1.45	0.027	1.78	0.143	0.3
1450807_at	---	---	-1.05	0.538	1.32	0.481	1.31	0.573	-1.7	0.482	-0.03
1440984_at	Baz2b	bromodomain adjacent to zinc finger domain, 2B	1.28	0.388	-1.02	0.939	1.32	0.394	-1.09	0.706	0.12
1435997_at	Spag8	sperm associated antigen 8	-1.72	0.376	1.43	0.442	1.57	0.295	-1.69	0.484	-0.1
1432874_at	4632404M16Rik	RIKEN cDNA 4632404M16 gene	-1.07	0.913	1.13	0.86	1.52	0.487	-1.18	0.768	0.1
1426196_at	Igh-1a	Immunoglobulin heavy chain 1a (serum IgG2a)	-1.02	0.968	1.67	0.415	-1.07	0.844	1.55	0.124	0.28
1420914_at	---	---	1.17	0.408	-1.09	0.738	1.49	0.138	-1.14	0.511	0.11
1453638_at	9030420J04Rik	RIKEN cDNA 9030420J04 gene	-1.16	0.422	1.08	0.794	1.64	0.273	-1.83	0.024	-0.07
1443590_at	---	---	-1.88	0.285	1.36	0.394	1.69	0.188	-1.24	0.626	-0.02
1431285_at	Mgrn1	mahogunin, ring finger 1	1.17	0.75	-1.32	0.444	1.65	0.296	-1.43	0.304	0.02
1455299_at	1700110N18Rik	RIKEN cDNA 1700110N18 gene	1.65	0.394	1.26	0.559	-1.5	0.04	-1.53	0.304	-0.03
1416853_at	Ncdn	neurochondrin	1.16	0.505	-1	0.989	1.42	0.118	-1.08	0.208	0.13
1450358_at	Arl4d	ADP-ribosylation factor-like 4D	1.04	0.912	-1.16	0.796	1.68	0.37	-1.23	0.435	0.08
1445626_at	Lgals3	Lectin, galactose binding, soluble 3	-1.42	0.588	1.8	0.13	1.08	0.817	-1.11	0.673	0.09
1445463_at	Npepps	aminopeptidase puromycin sensitive	-1.37	0.493	1.23	0.607	1.62	0.174	-1.24	0.694	0.06
1427700_x_at	Krt6a	keratin 6A	-1.73	0.305	2.15	0.164	-1.17	0.814	1.53	0.537	0.19
1425416_s_at	Psrc1	proline/serine-rich coiled-coil 1	-1.72	0.6	-1.43	0.46	2.3	0.034	5.42	0.104	1.14

1429372_at	Sox11	SRY-box containing gene 11	2.16	0.359	-1.28	0.578	-1.55	0.29	1.06	0.898	0.1
1425646_at	BC016495	cDNA sequence BC016495	-1.16	0.615	1.27	0.431	1.45	0.352	-1.18	0.572	0.09
1431414_at	2610312K03Rik	RIKEN cDNA 2610312K03 gene	1.63	0.566	-1.76	0.475	1.39	0.131	-1.15	0.798	0.03
1439503_at	Zfp28	zinc finger protein 28	-1.06	0.359	1.57	0.116	1.06	0.596	-1.58	0.277	0
1460739_at	D11Bwg0280e	DNA segment, Chr 11, Brigham & Women's Genetics 0280e expressed	1.07	0.75	-1.12	0.648	1.62	0.226	-1.36	0.368	0.05
1426092_a_at	Trim34	tripartite motif protein 34	1.26	0.741	-1.15	0.814	1.46	0.044	-2.93	0.123	-0.34
1441039_at	4930532J02Rik	RIKEN cDNA 4930532J02 gene	1.64	0.023	-1.18	0.604	1.09	0.726	-1.62	0.593	-0.02
1435850_at	---	Transcribed locus	-1.03	0.954	1.35	0.669	1.27	0.647	-1.2	0.705	0.1
1430926_at	Ttc18	tetratricopeptide repeat domain 18	1.57	0.036	-1.68	0.352	1.42	0.373	-1.41	0.474	-0.03
1447968_at	9330158F14Rik	RIKEN cDNA 9330158F14 gene	1.09	0.885	1.5	0.422	-1.01	0.981	-1.03	0.957	0.14
1440759_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1	0.992	1.91	0.061	-1.49	0.193	-1.24	0.425	0.05
1448274_at	C1qbp	complement component 1, q subcomponent binding protein	-1.15	0.316	-1.01	0.787	1.72	0.038	1.23	0.103	0.2
1426872_at	Fcgbp	Fc fragment of IgG binding protein	1.42	0.066	-1.16	0.344	1.3	0.238	-1.65	0.524	-0.02
1453449_at	---	---	-2.44	0.412	1.73	0.255	1.45	0.434	-3.91	0.131	-0.79
1433050_at	5730478J17Rik	RIKEN cDNA 5730478J17 gene	1.09	0.855	-1.75	0.135	1.92	0.306	-1.48	0.426	-0.05
1457687_at	Bcl2	B-cell leukemia/lymphoma 2	-1.07	0.771	1.21	0.267	1.44	0.19	-1.1	0.839	0.12
1448933_at	Pcdhb17	protocadherin beta 17	1.17	0.358	1.64	0.274	-1.28	0.268	-1.1	0.455	0.11
1438950_x_at	Ric8	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	-3.16	0.05	2.07	0.319	1.2	0.503	-2.12	0.11	-0.5
1422438_at	Ephx1	epoxide hydrolase 1, microsomal	1.37	0.168	-1.14	0.125	1.34	0.056	-1.93	0.181	-0.09
1420567_at	Prkcn	protein kinase C, nu	1.24	0.73	-1.78	0.32	1.78	0.598	-2.42	0.551	-0.29
1426617_a_at	Ttyh1	tweety homolog 1 (Drosophila)	1.89	0.547	1.3	0.558	-2.5	0.084	-1.5	0.517	-0.2
1437380_x_at	Pgd	phosphogluconate dehydrogenase	-1.12	0.368	1.38	0.012	1.31	0.103	-1.42	0.001	0.04
1424943_at	BC013476	cDNA sequence BC013476	-1.17	0.627	-2.65	0.084	2.35	0.064	1.16	0.804	-0.08
1458455_at	Abra	actin-binding Rho activating protein	1.23	0.589	1.71	0.258	-1.55	0.263	-1.21	0.796	0.05
1421198_at	Itgav	integrin alpha V	1.56	0.006	-1.91	0.502	1.5	0.553	-1.55	0.234	-0.1
1416863_at	Abhd8	abhydrolase domain containing 8	1.3	0.527	1.3	0.509	-1.01	0.834	-1.35	0.107	0.06
1457165_at	---	---	1.61	0.563	-1.11	0.322	1.07	0.662	-1.24	0.733	0.08
1432975_at	2310038E17Rik	RIKEN cDNA 2310038E17 gene	-1.2	0.666	1.66	0.223	1.09	0.85	-1.29	0.425	0.07
1440808_x_at	E430002D04Rik	RIKEN cDNA E430002D04 gene	-1.37	0.448	-1.52	0.303	2.2	0.014	1.58	0.175	0.22
1440925_at	---	---	1.33	0.456	1.28	0.427	-1.03	0.952	-1.68	0.287	-0.02
1427172_at	Ofd1	oral-facial-digital syndrome 1 gene homolog (human)	-1.08	0.825	1.06	0.774	1.6	0.107	-1.02	0.921	0.14
1448069_at	Tm4sf1	transmembrane 4 superfamily member 1	-1.23	0.424	1.93	0.364	-1.18	0.121	1.02	0.973	0.13
1417079_s_at	Lgals2	lectin, galactose-binding, soluble 2	-1.93	0.174	-1.11	0.847	2.17	0.185	1.37	0.41	0.13
1420824_at	Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	-1.16	0.459	1.25	0.248	1.47	0.041	-1.47	0.349	0.02
1442659_at	Pcdh9	protocadherin 9	1.92	0.212	-1.1	0.687	-1.31	0.249	1.31	0.342	0.2
1429450_at	1700026J04Rik	RIKEN cDNA 1700026J04 gene	1.35	0.182	-1.04	0.933	1.28	0.704	-1.16	0.783	0.11
1449787_at	---	---	1.21	0.61	-1.14	0.816	1.51	0.504	-1.66	0.449	-0.02
1422874_at	Acrbp	proacrosin binding protein	1.33	0.286	1.61	0.151	-1.54	0.41	-1.15	0.574	0.06
1458081_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330025C	1.45	0.651	1.42	0.513	-1.38	0.696	-1.07	0.92	0.1
1416560_at	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-1.29	0.346	1.83	0.237	-1.02	0.92	1.87	0.521	0.35
1430130_at	Vwce	von Willebrand factor C and EGF domains	1.12	0.347	-1.24	0.39	1.67	0.318	-3.01	0.232	-0.37
1450928_at	Id4	inhibitor of DNA binding 4	-1.15	0.614	1.77	0.13	-1.04	0.832	1.11	0.481	0.17
1439961_x_at	---	Transcribed locus	1.31	0.334	-1.85	0.142	1.74	0.206	-1.61	0.126	-0.1
1445002_at	---	---	2.09	0.045	-1.16	0.772	-1.55	0.04	1.08	0.887	0.11
1425399_at	9630055N22Rik	RIKEN cDNA 9630055N22 gene	1.11	0.741	-1.39	0.541	1.76	0.214	-1.32	0.45	0.04
1453679_at	1700100I10Rik	RIKEN cDNA 1700100I10 gene	1.01	0.985	-1.01	0.986	1.6	0.397	-2.02	0.278	-0.11
1438586_at	Tbx22	T-box 22	1.12	0.895	-1.2	0.81	1.63	0.362	-1.38	0.389	0.05
1421332_at	Hs3st3b1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1.5	0.219	-1	0.996	1.1	0.679	-1.3	0.45	0.07
1427420_at	Nkx6-2	NK6 transcription factor related, locus 2 (Drosophila)	1.87	0.015	-1.34	0.566	-1.02	0.963	1.9	0.202	0.35
1447335_x_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	-1.13	0.693	2.01	0.496	-1.42	0.509	1.18	0.665	0.16
1419293_at	Dscam	Down syndrome cell adhesion molecule	2.12	0.161	-2.89	0.02	1.13	0.794	-1.17	0.714	-0.2
1439041_at	Slc39a10	solute carrier family 39 (zinc transporter), member 10	-1.05	0.87	1.31	0.589	1.33	0.344	-1.23	0.546	0.09
1422123_s_at	Ceacam1 /// Ceaca	CEA-related cell adhesion molecule 1 /// CEA-related cell adhesion molecule 2	1.5	0.451	-1.16	0.475	1.24	0.514	-1.12	0.745	0.11

1444056_at	2900006B13Rik	RIKEN cDNA 2900006B13 gene	1.6	0.398	-1.09	0.772	1.08	0.646	-1.12	0.492	0.12
1438627_x_at	Pgd	phosphogluconate dehydrogenase	-1.1	0.679	1.32	0.009	1.36	0.099	-1.26	0.293	0.08
1437135_at	Fbxw10	F-box and WD-40 domain protein 10	1.63	0.322	-1.44	0.411	1.27	0.154	-1.39	0.509	0.02
1418030_at	Slco3a1	solute carrier organic anion transporter family, member 3a1	1.36	0.294	1.44	0.581	-1.26	0.039	-1.1	0.737	0.11
1416998_at	Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	-1.13	0.355	-1.01	0.942	1.72	0.004	1.12	0.074	0.18
1442837_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	1.56	0.553	1.71	0.557	-3.06	0.001	-2.78	0.36	-0.64
1444065_at	Cyb5d2	Cytochrome b5 domain containing 2	1.53	0.054	1.24	0.648	-1.21	0.667	-1	0.995	0.14
1425234_at	Col20a1	collagen, type XX, alpha 1	1.1	0.786	1.59	0.19	-1.11	0.489	-1.17	0.473	0.1
1452151_at	BC021523	cDNA sequence BC021523	-1.01	0.93	1.23	0.286	1.38	0.044	-1.07	0.528	0.13
1459667_at	Arhgap17	Rho GTPase activating protein 17	1.14	0.541	1.51	0.009	-1.06	0.799	-1.19	0.239	0.1
1448168_a_at	Spt1	salivary protein 1	-2.82	0.328	2.61	0.052	-1.57	0.466	1.98	0.232	0.05
1428059_at	Cd247	CD247 antigen	1.16	0.179	1.71	0.293	-1.38	0.314	-1.42	0.303	0.02
1456233_at	---	Transcribed locus	1.99	0.178	1.07	0.909	-1.84	0.202	-1.06	0.924	0.04
1428977_at	Chst8	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 8	1.2	0.564	1.63	0.444	-1.3	0.162	-1.02	0.979	0.13
1417551_at	Cln3	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	1.18	0.296	-1.04	0.534	1.46	0.123	-1.01	0.97	0.15
1444419_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	-1.07	0.564	1.6	0.29	1.06	0.821	-1.25	0.364	0.09
1458322_x_at	E230008N13Rik	RIKEN cDNA E230008N13 gene	1.5	0.258	1.15	0.661	-1.06	0.713	-1.38	0.378	0.05
1441246_s_at	Dpysl5	dihydropyrimidinase-like 5	-1.42	0.558	1.12	0.8	1.78	0.301	-2.19	0.45	-0.18
1432692_at	4930517G19Rik	RIKEN cDNA 4930517G19 gene	1.91	0.038	-2.07	0.185	1.21	0.643	-1.18	0.488	-0.03
1425113_x_at	---	PREDICTED: Mus musculus hypothetical protein LOC621686 (LOC621686), mR	-1.58	0.107	1.76	0.001	1.2	0.308	-1.14	0.401	0.06
1432095_at	4921534H16Rik	RIKEN cDNA 4921534H16 gene	1.14	0.776	1.57	0.443	-1.12	0.828	-1.13	0.682	0.12
1434644_at	Tbl1x	transducin (beta)-like 1 X-linked	1.48	0.337	-1.12	0.723	1.23	0.566	-1.01	0.982	0.15
1454247_a_at	Gpa33	glycoprotein A33 (transmembrane)	1.63	0.041	1.21	0.713	-1.29	0.408	-1.21	0.711	0.08
1432341_at	1700022A22Rik	RIKEN cDNA 1700022A22 gene	-1.31	0.668	1.17	0.75	1.67	0.415	-1.24	0.44	0.07
1451258_at	Psca	prostate stem cell antigen	1	0.997	-1.41	0.222	1.89	0.391	-1.49	0.455	0
1452804_at	1700010A17Rik	RIKEN cDNA 1700010A17 gene	-1.63	0.424	1.94	0.181	1.05	0.882	-1.11	0.589	0.06
1421169_at	Zfp46	zinc finger protein 46	-2.7	0.261	1.96	0.221	1.28	0.29	-1.99	0.26	-0.36
1417954_at	Sst	somatostatin	1.37	0.603	-1.24	0.164	1.43	0.186	-2.14	0.029	-0.15
1444275_at	Ust	Uronyl-2-sulfotransferase	1.74	0.446	1.41	0.549	-2.22	0.05	-1.18	0.048	-0.06
1428340_s_at	Atp13a2	ATPase type 13A2	-1	0.991	1.44	0.001	1.17	0.126	-1.16	0.494	0.11
1437277_x_at	Tgm2	transglutaminase 2, C polypeptide	-1.1	0.172	1.59	0.078	1.11	0.294	-1.04	0.759	0.14
1443771_x_at	Smad7	MAD homolog 7 (Drosophila)	-1.75	0.265	1.4	0.485	1.63	0.107	-2.01	0.109	-0.18
1429631_at	Sirt6	sirtuin 6 (silent mating type information regulation 2, homolog) 6 (S. cerevisiae)	-1.37	0.169	2.12	0.043	-1.31	0.132	1.51	0.339	0.23
1451301_at	Tmod2	tropomodulin 2	1.06	0.837	-1.05	0.606	1.59	0.316	-1.36	0.433	0.06
1440663_at	Xpo4	Exportin 4	2.55	0.053	-2.19	0.236	-1.67	0.085	2.04	0.265	0.18
1433216_at	9430024C03Rik	RIKEN cDNA 9430024C03 gene	-1.28	0.719	1.03	0.947	1.8	0.339	-1.89	0.231	-0.09
1435326_at	AW112037	expressed sequence AW112037	1.1	0.36	1.58	0.137	-1.08	0.488	-1.71	0.106	-0.03
1435500_at	Rab26	RAB26, member RAS oncogene family	1.13	0.313	-1.08	0.458	1.56	0.177	-1.35	0.101	0.06
1434655_at	Foxk1	forkhead box K1	1.3	0.207	-1.07	0.84	1.38	0.153	-1.5	0.216	0.02
1437814_at	Dnajc5g	DnaJ (Hsp40) homolog, subfamily C, member 5 gamma	1.26	0.343	-1.11	0.847	1.45	0.351	-1.43	0.607	0.04
1422999_at	Map3k14	mitogen-activated protein kinase kinase kinase 14	-1.45	0.133	1.75	0.421	1.17	0.616	-1.2	0.424	0.07
1457837_at	BC033606 /// LOC6	cDNA sequence BC033606 /// similar to phospholipase B	1.65	0.419	-1.53	0.312	1.3	0.173	-1.59	0.555	-0.04
1423077_at	Snx9	sorting nexin 9	1.02	0.886	-1.28	0.221	1.81	0.033	-1.39	0.151	0.04
1435285_at	Mpped2	metallophosphoesterase domain containing 2	1.12	0.812	1.66	0.131	-1.21	0.523	-1.23	0.574	0.09
1442292_at	Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	1.6	0.224	1.12	0.755	-1.13	0.539	-2.1	0.103	-0.13
1438633_x_at	Lasp1	LIM and SH3 protein 1	-1.06	0.119	1.19	0.463	1.48	0.034	-1.47	0.17	0.03
1454499_at	4933431C10Rik	RIKEN cDNA 4933431C10 gene	2.18	0.2	-1.61	0.232	-1.25	0.637	1.85	0.047	0.29
1429135_at	1110059M19Rik	RIKEN cDNA 1110059M19 gene	-2.03	0.464	1.95	0.198	1.17	0.761	-1.49	0.518	-0.1
1436634_at	Robo3	roundabout homolog 3 (Drosophila)	-1.5	0.349	2.12	0.301	-1.22	0.706	1.83	0.458	0.31
1434623_at	Uba52 /// LOC3833	ubiquitin A-52 residue ribosomal protein fusion product 1 /// similar to ubiquitin A-	-1.56	0.608	1.5	0.111	1.47	0.122	-1.17	0.649	0.06
1428934_at	Cmtm2b	CKLF-like MARVEL transmembrane domain containing 2B	2.19	0.405	-1.83	0.456	-1.14	0.595	1.37	0.494	0.15
1434811_at	Cage1	cancer antigen 1	1.32	0.462	1.55	0.39	-1.33	0.576	-1.73	0.451	-0.05
1452425_at	Tnfrsf14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediat	1.69	0.317	-1	0.993	-1.08	0.889	3.12	0.185	0.68

1425119_at	---	---	1.78	0.566	1.14	0.822	-1.45	0.311	-1.28	0.555	0.05
1434327_at	---	---	2.33	0.267	-1.71	0.184	-1.44	0.166	1.13	0.601	0.08
1419503_at	Stc2	stanniocalcin 2	1.1	0.792	1.53	0.261	-1.01	0.958	-1.02	0.965	0.15
1453703_at	Dnah17	dynein, axonemal, heavy polypeptide 17	-1.65	0.496	-1.72	0.459	2.42	0.164	1.1	0.867	0.04
1439892_at	Brsk1	BR serine/threonine kinase 1	1.63	0.582	-1.09	0.624	1.06	0.891	-1.29	0.467	0.08
1459719_at	Depdc6	DEP domain containing 6	1.19	0.691	-1.06	0.906	1.49	0.132	-1.74	0.203	-0.03
1442927_at	Ptk2b	PTK2 protein tyrosine kinase 2 beta	1.23	0.321	-1.32	0.598	1.62	0.274	-1.24	0.713	0.07
1431710_at	Cmtm2a	CKLF-like MARVEL transmembrane domain containing 2A	1.35	0.243	1.43	0.381	-1.2	0.543	-2.53	0.185	-0.24
1449341_a_at	Stom	stomatin	-1.27	0.152	-1.15	0.692	1.96	0.278	3.53	0.245	0.77
1427802_a_at	Tcrg	T-cell receptor gamma chain	-2.21	0.258	1.94	0.42	1.22	0.654	-2.66	0.021	-0.43
1437847_x_at	Rbmx	RNA binding motif protein, X chromosome	2.07	0.197	-3.22	0.152	1.23	0.526	-1.21	0.229	-0.28
1428723_at	2310047M10Rik	RIKEN cDNA 2310047M10 gene	1.08	0.687	-1.04	0.762	1.58	0.023	-1.23	0.247	0.1
1454889_x_at	Tmcc3	transmembrane and coiled coil domains 3	1.58	0.131	1.12	0.355	-1.1	0.429	-1.28	0.329	0.08
1424724_a_at	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed	1.5	0.468	-1.42	0.03	1.41	0.167	-1.17	0.224	0.08
1427336_at	Aldh8a1	aldehyde dehydrogenase 8 family, member A1	-1.08	0.591	-1.03	0.871	1.71	0.092	1.33	0.492	0.23
1419589_at	Cd93	CD93 antigen	1.29	0.096	1.47	0.042	-1.16	0.07	-1.15	0.527	0.11
1443084_at	Ctso	cathepsin O	1.59	0.013	1.08	0.14	-1.06	0.755	-1.58	0.346	0.01
1447888_x_at	Msh2	mutS homolog 2 (E. coli)	1.4	0.434	1.63	0.394	-1.72	0.4	-1.83	0.204	-0.13
1453879_at	1700016H13Rik	RIKEN cDNA 1700016H13 gene	-1.34	0.529	1.7	0.311	1.17	0.752	-1.92	0.221	-0.1
1439938_at	Stk38	serine/threonine kinase 38	1.46	0.109	-1.03	0.923	1.18	0.543	-1.43	0.165	0.05
1438641_x_at	1500016O10Rik	RIKEN cDNA 1500016O10 gene	-1.34	0.384	1.18	0.747	1.68	0.021	-1.1	0.871	0.11
1453327_at	Krt24	keratin 24	-1.61	0.222	2.45	0.217	-1.85	0.147	1.01	0.968	0
1449952_s_at	Tmprss8	transmembrane protease, serine 8 (intestinal)	1.09	0.744	-1.57	0.019	1.89	0.179	-2.13	0.117	-0.18
1450228_a_at	Pip5k1c	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	1.03	0.815	-1.59	0.292	1.96	0.285	-1.06	0.938	0.08
1435275_at	Cox6b2	cytochrome c oxidase subunit VIb polypeptide 2	1.74	0.106	-1.01	0.979	-1.13	0.406	8.53	0.192	2.03
1458100_at	C87482	expressed sequence C87482	1.34	0.685	1.5	0.453	-1.29	0.547	-1.19	0.694	0.09
1433006_at	5430430B14Rik	RIKEN cDNA 5430430B14 gene	1.07	0.755	-1.03	0.974	1.57	0.027	-1	0.987	0.15
1447443_at	Spock2	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	-1.05	0.956	1.36	0.412	1.3	0.453	-1.43	0.55	0.05
1448280_at	Syp	synaptophysin	-1.36	0.242	1.5	0.126	1.38	0.249	-1.14	0.543	0.1
1454020_at	4930554H23Rik	RIKEN cDNA 4930554H23 gene	-1.13	0.658	1.11	0.868	1.63	0.309	-2.19	0.39	-0.15
1443478_at	C86695	expressed sequence C86695	1.93	0.36	-1.87	0.419	1.16	0.759	-1.46	0.513	-0.06
1419677_at	Masp1	mannan-binding lectin serine peptidase 1	1.89	0.541	-1.05	0.435	-1.29	0.075	1.57	0.081	0.28
1446369_at	Armc1	armadillo repeat containing 1	1.35	0.093	-1.35	0.577	1.52	0.284	-1.06	0.908	0.12
1453655_at	2900005J15Rik	RIKEN cDNA 2900005J15 gene	-1.48	0.594	2	0.28	-1.06	0.686	1.31	0.416	0.19
1450878_at	Sri	sorcin	-1.02	0.794	1.29	0.205	1.34	0.436	-1.36	0.249	0.06
1428283_at	Cyp2s1	cytochrome P450, family 2, subfamily s, polypeptide 1	-1.12	0.337	-1.21	0.663	1.9	0.031	2	0.051	0.39
1428064_at	Centd2	centaurin, delta 2	-1.07	0.445	1.31	0.031	1.38	0.086	-1.26	0.238	0.09
1448825_at	Pdk2	pyruvate dehydrogenase kinase, isoenzyme 2	1.06	0.814	-1.05	0.834	1.6	0.106	-1.1	0.657	0.13
1437661_at	AU021092	expressed sequence AU021092	1.04	0.835	1.72	0.356	-1.16	0.144	-1.69	0.065	-0.02
1434774_at	Rhbdf2	rhomboid 5 homolog 2 (Drosophila)	1.62	0.353	1.07	0.911	-1.08	0.732	-1.24	0.367	0.09
1444859_at	---	---	2.29	0.355	-2.21	0.357	-1.14	0.298	1.42	0.615	0.09
1446292_at	Spata5	Spermatogenesis associated 5	-1.92	0.288	1.83	0.28	1.27	0.583	-1.63	0.546	-0.11
1448342_at	Mapk10	mitogen activated protein kinase 10	-1.09	0.782	1.44	0.374	1.26	0.381	-1.68	0.157	-0.02
1435710_at	AI661384	expressed sequence AI661384	-1.18	0.813	-1.07	0.896	1.84	0.162	1.05	0.903	0.16
1423015_at	Kirrel1	kin of IRRE like 1 (Drosophila)	1.31	0.272	1.45	0.406	-1.16	0.496	-1.29	0.367	0.08
1446721_at	---	---	1.55	0.598	1.15	0.732	-1.08	0.885	-1.27	0.307	0.09
1454924_at	Fut10	fucosyltransferase 10	1.73	0.494	1.08	0.913	-1.22	0.168	-1.02	0.975	0.14
1425039_at	Itgbl1	integrin, beta-like 1	2.03	0.079	-1.56	0.184	-1.05	0.844	1.11	0.628	0.13
1425575_at	Epha3	Eph receptor A3	1.78	0.05	1.15	0.813	-1.45	0.464	-1.14	0.757	0.08
1448984_at	Ercc4	excision repair cross-complementing rodent repair deficiency, complementation g	-1.3	0.201	1.2	0.404	1.65	0.071	-1.09	0.49	0.12
1437805_at	---	---	-1.14	0.835	1.79	0.204	-1.05	0.797	1.31	0.623	0.23
1423830_a_at	Mier2	mesoderm induction early response 1, family member 2	1.33	0.704	1.46	0.482	-1.2	0.642	-1.06	0.803	0.13
1456819_at	G630049C14Rik	RIKEN cDNA G630049C14 gene	1.69	0.326	-1.13	0.553	1.04	0.895	-1.22	0.435	0.1

1421249_at	LOC674308	similar to solute carrier family 39 (zinc transporter), member 9	1.72	0.392	1.22	0.203	-1.48	0.47	-3.31	0.139	-0.46
1458572_at	Chmp5	chromatin modifying protein 5	-1.35	0.716	1.67	0.355	1.21	0.606	-1	0.996	0.13
1431262_at	LOC544988 /// LOC	hypothetical protein LOC544988 /// similar to Spetex-2H protein /// similar to Spet	-1.03	0.951	1.65	0.468	1.01	0.981	-1.05	0.945	0.14
1443958_at	9030203C11Rik	RIKEN cDNA 9030203C11 gene	1.59	0.271	1.13	0.646	-1.1	0.641	-1.53	0.081	0.02
1442179_at	9430053O09Rik	RIKEN cDNA 9430053O09 gene	1.65	0.285	-2.23	0.313	1.53	0.222	-1.29	0.688	-0.09
1439205_at	Nfatc2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	-1.01	0.946	1.37	0.564	1.26	0.427	-1.23	0.537	0.1
1439641_at	LOC553090	hypothetical LOC553090	1.67	0.114	1.08	0.821	-1.14	0.469	-1.6	0.025	0
1438722_at	2610014I16Rik	RIKEN cDNA 2610014I16 gene	1.65	0.235	1.45	0.429	-1.9	0.005	-2.21	0.367	-0.25
1441060_at	2900052L18Rik	RIKEN cDNA 2900052L18 gene	-1.05	0.863	1.35	0.549	1.32	0.553	-1.36	0.317	0.07
1422027_a_at	Ets1	E26 avian leukemia oncogene 1, 5' domain	1.07	0.822	-1.16	0.707	1.7	0.088	-1.86	0.154	-0.06
1434526_at	Abhd7	abhydrolase domain containing 7	-1.49	0.488	1.71	0.179	1.24	0.486	-1.81	0.396	-0.09
1442377_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.09	0.453	1.38	0.637	1.33	0.565	-2.11	0.374	-0.12
1427428_at	Clec4g	C-type lectin domain family 4, member g	1.79	0.506	1.28	0.136	-1.82	0.022	-1.59	0.236	-0.08
1441350_at	---	---	1.93	0.21	-1.16	0.814	-1.2	0.676	1.17	0.546	0.18
1426744_at	Srebf2	sterol regulatory element binding factor 2	-1.09	0.791	1.13	0.686	1.58	0.07	-1.73	0.216	-0.03
1421518_at	Kcns1	K+ voltage-gated channel, subfamily S, 1	1.81	0.444	-1.01	0.971	-1.2	0.699	1.49	0.402	0.27
1422674_s_at	Crygb /// Crygc	crystallin, gamma B /// crystallin, gamma C	2.34	0.288	-1.37	0.035	-1.77	0.062	1.24	0.615	0.11
1431311_at	4430401P03Rik	RIKEN cDNA 4430401P03 gene	-1.86	0.207	1.47	0.113	1.62	0.186	-1.01	0.916	0.05
1417574_at	Cxcl12	chemokine (C-X-C motif) ligand 12	-1.06	0.622	1.11	0.359	1.57	0.109	-1.21	0.71	0.1
1420989_at	4933411K20Rik	RIKEN cDNA 4933411K20 gene	1.39	0.599	-1.04	0.928	1.28	0.572	-1.57	0.254	0.01
1429701_at	2410003J06Rik	RIKEN cDNA 2410003J06 gene	-1.06	0.875	-1.34	0.525	1.94	0.169	11.14	0.2	2.67
1425311_at	4930432F04Rik	RIKEN cDNA 4930432F04 gene	-1.03	0.872	1.31	0.336	1.35	0.216	-1.12	0.61	0.13
1447737_at	Prkra	protein kinase, interferon inducible double stranded RNA dependent activator	-1.13	0.852	1.15	0.408	1.59	0.371	-2.27	0.182	-0.16
1449549_at	Efnb2	ephrin B2	1.49	0.3	-1.43	0.371	1.44	0.527	-1.03	0.808	0.12
1426058_a_at	Kcnk3	potassium channel, subfamily K, member 3	-1.06	0.87	1.35	0.675	1.34	0.205	-1.3	0.58	0.08
1442866_at	Rcsd1	RCSD domain containing 1	1.75	0.114	-1.17	0.709	1.02	0.93	-2.71	0.08	-0.28
1416249_at	Nadk	NAD kinase	1.17	0.627	-1.02	0.909	1.48	0.336	-1.14	0.695	0.12
1431244_s_at	Dnmbp	dynamin binding protein	1.79	0.42	-2.06	0.334	1.36	0.4	-1.78	0.112	-0.17
1435924_at	Tfb1m	transcription factor B1, mitochondrial	-1.13	0.31	1.31	0.454	1.44	0.101	-1.17	0.619	0.11
1416383_a_at	Pcx	pyruvate carboxylase	-1.1	0.553	-1.08	0.673	1.79	0.238	3.07	0.161	0.67
1449900_at	Galc	galactosylceramidase	1.58	0.35	-1.12	0.844	1.17	0.762	-1.7	0.216	-0.02
1428578_s_at	Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	1.84	0.312	-2.17	0.475	1.33	0.266	-1.48	0.314	-0.12
1442721_at	---	Transcribed locus	1.27	0.819	1.46	0.454	-1.1	0.767	-1.58	0.539	0.01
1447069_at	Rnf43	Ring finger protein 43	1.98	0.558	-1.47	0.325	-1.03	0.854	1.03	0.945	0.13
1437527_x_at	Mcl1	myeloid cell leukemia sequence 1	-1.02	0.868	1.58	0.002	1.07	0.426	-1.36	0.13	0.07
1416822_at	Es2el	expressed sequence 2 embryonic lethal	1.43	0.207	-1.18	0.228	1.35	0.401	-1.65	0.294	-0.01
1427855_at	---	---	1.56	0.024	-1.21	0.757	1.25	0.511	-1.33	0.424	0.07
1445954_at	C81354	expressed sequence C81354	-1.54	0.002	1.79	0.375	1.19	0.288	-1.57	0.368	-0.03
1425869_a_at	Psen2	presenilin 2	1.1	0.521	-1.17	0.257	1.68	0.106	-1.13	0.351	0.12
1430667_at	Pcdh10	protocadherin 10	1.27	0.525	1.47	0.604	-1.12	0.792	-1.01	0.989	0.15
1432502_at	1700028N14Rik	RIKEN cDNA 1700028N14 gene	1.06	0.947	1.78	0.412	-1.27	0.726	-2.97	0.05	-0.35
1460373_a_at	Setd4	SET domain containing 4	1.42	0.206	1.26	0.312	-1.05	0.59	-1.46	0.248	0.04
1440400_at	---	---	1.65	0.368	-1.13	0.818	1.1	0.849	-1.07	0.829	0.14
1419420_at	St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	1.52	0.186	-1.75	0.135	1.54	0.06	-1.26	0.376	0.01
1454362_at	8030431A06Rik	RIKEN cDNA 8030431A06 gene	1.37	0.597	1.57	0.232	-1.44	0.06	-1.22	0.645	0.07
1441460_at	Fgfr1op2	FGFR1 oncogene partner 2	1.89	0.118	1.17	0.777	-1.74	0.074	-1.01	0.977	0.08
1435409_at	---	Transcribed locus	1.07	0.792	1.77	0.002	-1.25	0.214	-1.19	0.566	0.1
1421727_at	Eya1	eyes absent 1 homolog (Drosophila)	1.08	0.874	-1.75	0.096	1.98	0.31	-1.73	0.319	-0.1
1449082_at	Mfap5	microfibrillar associated protein 5	1.26	0.33	1.87	0.346	-2.01	0.018	-2.49	0.04	-0.34
1454120_a_at	Pcgf6	polycomb group ring finger 6	-1.56	0.222	1.61	0.337	1.38	0.143	-1.08	0.787	0.09
1446701_at	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	-1.4	0.471	1.9	0.359	1.02	0.967	-1.33	0.628	0.05
1439168_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	1.52	0.404	1.26	0.38	-1.18	0.681	-1.33	0.419	0.07
1441173_at	4930451G09Rik	RIKEN cDNA 4930451G09 gene	1.1	0.707	1.62	0.042	-1.09	0.736	-1.23	0.576	0.1

1437578_at	Clca1 /// Clca2	chloride channel calcium activated 1 /// chloride channel calcium activated 2	-1.46	0.407	1.47	0.396	1.48	0.285	-2.01	0.491	-0.13
1446106_at	1700109G14Rik	RIKEN cDNA 1700109G14 gene	1.54	0.041	1.27	0.441	-1.22	0.479	-1.43	0.48	0.04
1421898_a_at	Mr1	major histocompatibility complex, class I-related	1.55	0.603	-1.37	0.592	1.36	0.564	-1.22	0.541	0.08
1455469_at	Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	1.56	0.045	1.25	0.499	-1.21	0.716	-1.26	0.457	0.09
1424181_at	6-Sep	septin 6	-1.02	0.949	1.06	0.488	1.59	0.244	-1.73	0.24	-0.02
1415957_a_at	Nnp1	novel nuclear protein 1	1.18	0.649	-1.04	0.859	1.5	0.139	-1.09	0.755	0.14
1430768_at	9530018H14Rik	RIKEN cDNA 9530018H14 gene	1.56	0.233	1.29	0.552	-1.27	0.603	-1.18	0.811	0.1
1425302_at	BC024997	cDNA sequence BC024997	-1.28	0.511	-1.08	0.874	1.93	0.046	1.44	0.564	0.25
1448023_at	Kalrn	kalirin, RhoGEF kinase	-1.18	0.706	1.87	0.393	-1.08	0.685	1.04	0.909	0.16
1445691_at	Chn1	chimerin (chimaerin) 1	-1.04	0.882	1.16	0.756	1.51	0.209	-2.21	0.011	-0.14
1445098_at	AU022706	expressed sequence AU022706	1.44	0.484	1.58	0.312	-1.62	0.067	-4.3	0.083	-0.72
1460584_at	Hisppd2a	histidine acid phosphatase domain containing 2A	-1.17	0.205	1.21	0.182	1.57	0.136	-1.11	0.109	0.12
1421131_a_at	Zfp111	zinc finger protein 111	1.37	0.462	1.72	0.213	-1.8	0.004	-1.06	0.876	0.05
1422330_at	Glp1r	glucagon-like peptide 1 receptor	1.54	0.073	-1.21	0.559	1.28	0.651	-2.52	0.321	-0.23
1427227_at	Gabrg1	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 1	1.22	0.788	1.88	0.458	-1.86	0.471	-1.56	0.557	-0.08
1449685_s_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	1.32	0.299	-1.21	0.542	1.5	0.253	-1.57	0.13	0.01
1439078_at	Klhl4	kelch-like 4 (Drosophila)	1.24	0.241	1.61	0.261	-1.25	0.212	-1.3	0.411	0.07
1457861_at	A230009B12Rik	RIKEN cDNA A230009B12 gene	1.54	0.568	-2.06	0.292	1.61	0.118	-1.02	0.961	0.02
1419090_x_at	Klk1b26	kallikrein 1-related petidase b26	1.12	0.879	1.53	0.528	-1.01	0.976	-1.92	0.125	-0.07
1445903_at	---	---	1.41	0.538	1.63	0.475	-1.67	0.319	-1.18	0.347	0.05
1451535_at	Il31ra	interleukin 31 receptor A	-1.54	0.174	-1.01	0.976	2.01	0.033	1.8	0.098	0.31
1438994_at	Hyal5	hyaluronoglucosaminidase 5	1.51	0.033	1.16	0.856	-1.03	0.945	-2.41	0.295	-0.19
1434927_at	Hspb7	heat shock protein family, member 7 (cardiovascular)	-1.21	0.143	-1.11	0.767	1.91	0.369	1.02	0.941	0.15
1427350_a_at	Gtpbp6	GTP binding protein 6 (putative)	1.79	0.03	-1.23	0.342	1.04	0.884	-1.74	0.211	-0.04
1426967_at	Axin1	axin 1	-1.21	0.757	1.2	0.592	1.61	0.06	-1.12	0.682	0.12
1449698_at	C330027C09Rik	RIKEN cDNA C330027C09 gene	-1.41	0.494	2.15	0.292	-1.27	0.582	1.75	0.231	0.3
1441519_at	Nid1	nidogen 1	1.23	0.302	1.59	0.583	-1.22	0.254	-1.12	0.751	0.12
1457792_at	Lmbr1l	Limb region 1 like	1.39	0.704	-1.51	0.367	1.59	0.504	-1.5	0.517	-0.01
1416656_at	Clic1	chloride intracellular channel 1	-1.19	0.029	1.35	0.087	1.45	0.124	-1.4	0.241	0.05
1437404_at	Mast4	microtubule associated serine/threonine kinase family member 4	-1.03	0.821	1.26	0.275	1.41	0.27	-1.26	0.5	0.09
1434874_x_at	Centb1	centaurin, beta 1	-1.26	0.148	1.67	0.288	1.18	0.447	-1.47	0.289	0.03
1460107_at	1700129I04Rik	RIKEN cDNA 1700129I04 gene	-1	0.997	1.58	0.347	1.07	0.797	-1.45	0.511	0.05
1421690_s_at	Agrp	agouti related protein	1.44	0.518	-1.92	0.461	1.68	0.156	-1.38	0.331	-0.04
1418053_at	Sncb	synuclein, beta	-1.4	0.032	2.11	0.036	-1.22	0.35	1.4	0.115	0.22
1419619_at	Krt80	keratin 80	1.21	0.462	-1.29	0.416	1.66	0.002	-1.45	0.323	0.03
1422776_at	Serpinb8	serine (or cysteine) peptdiase inhibitor, clade B, member 8	1.39	0.106	1.38	0.066	-1.15	0.575	-2.27	0.039	-0.16
1453889_at	4930461C15Rik	RIKEN cDNA 4930461C15 gene	-1.56	0.079	1.67	0.568	1.33	0.642	-1.03	0.617	0.1
1445647_at	AI447881	expressed sequence AI447881	-1.34	0.244	1.34	0.071	1.55	0.313	-1.64	0.049	-0.02
1430584_s_at	Car3	carbonic anhydrase 3	-1.25	0.767	-1.55	0.609	2.19	0.495	1.25	0.707	0.16
1434848_at	---	Transcribed locus	1.19	0.596	1.53	0.29	-1.08	0.761	-1.18	0.479	0.11
1431738_at	4921531P14Rik	RIKEN cDNA 4921531P14 gene	-1.05	0.828	1.03	0.956	1.66	0.326	-1.02	0.943	0.16
1442768_at	E130112L23Rik	RIKEN cDNA E130112L23 gene	1.19	0.764	1.62	0.426	-1.2	0.59	-1.12	0.68	0.12
1434473_at	Slc16a5	solute carrier family 16 (monocarboxylic acid transporters), member 5	-1.14	0.646	1.32	0.227	1.45	0.236	-2.07	0.043	-0.11
1421862_a_at	Vamp1	vesicle-associated membrane protein 1	-1.01	0.986	1.5	0.361	1.15	0.767	-2.77	0.251	-0.28
1430652_at	9030612E09Rik	RIKEN cDNA 9030612E09 gene	1.57	0.501	-1.42	0.533	1.37	0.238	-1.13	0.653	0.1
1421018_at	1110018J18Rik	RIKEN cDNA 1110018J18 gene	1.52	0.339	-1.14	0.573	1.25	0.582	-1.62	0.067	0
1443757_x_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	-1.24	0.538	1.94	0.125	-1.11	0.719	1.07	0.753	0.16
1457996_at	Tnfaip8	Tumor necrosis factor, alpha-induced protein 8	-1.01	0.986	1.49	0.406	1.16	0.546	-1.14	0.508	0.13
1418905_at	Nubp1	nucleotide binding protein 1	-1.03	0.703	1.03	0.781	1.64	0.103	-1.21	0.311	0.11
1433714_at	Sult4a1	sulfotransferase family 4A, member 1	1.5	0.282	1.49	0.537	-1.51	0.425	-1.04	0.922	0.11
1425561_at	Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	-1.16	0.637	1.24	0.353	1.54	0.055	-1.09	0.757	0.13
1420663_at	Zbtb7b	Vzinc finger and BTB domain containing 7B	-1.02	0.942	1.28	0.481	1.38	0.378	-1.4	0.284	0.06
1431183_at	1700066M21Rik	RIKEN cDNA 1700066M21 gene	1.29	0.499	-1.18	0.598	1.51	0.085	-1.1	0.862	0.13

1418438_at	Fabp2	fatty acid binding protein 2, intestinal	2.94	0.087	-2.38	0.026	-3.52	0.197	1.39	0.618	-0.39
1429891_at	Capsl	calcyphosine-like	1.04	0.957	1.64	0.266	-1.04	0.895	-1.9	0.359	-0.06
1439884_at	Nudt16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	1.35	0.055	-1	0.999	1.3	0.068	-1.38	0.376	0.07
1432844_at	Phactr4	phosphatase and actin regulator 4	1.85	0.53	-1.36	0.54	1.06	0.839	-1.91	0.34	-0.09
1441912_x_at	C2	complement component 2 (within H-2S)	-1.16	0.428	1.27	0.059	1.51	0.35	-1.47	0.085	0.04
1443064_at	9130004C02Rik	RIKEN cDNA 9130004C02 gene	1.64	0.303	1.07	0.86	-1.07	0.883	-1.51	0.489	0.03
1440004_at	Sufu	Suppressor of fused homolog (Drosophila)	2.21	0.165	-1.22	0.4	-1.62	0.08	1.23	0.289	0.15
1446262_at	Acad10	Acyl-Coenzyme A dehydrogenase family, member 10	1.57	0.312	1.18	0.42	-1.11	0.577	-1.07	0.705	0.14
1453995_a_at	Htf9c	HpaII tiny fragments locus 9c	1.12	0.595	-1.01	0.976	1.54	0.369	-1.17	0.706	0.12
1448015_at	2310047C04Rik	RIKEN cDNA 2310047C04 gene	2.71	0.194	-2.17	0.44	-2.08	0.438	1.34	0.499	-0.05
1454098_at	Olfr112	olfactory receptor 112	-1.05	0.948	-1	0.998	1.69	0.057	1.67	0.364	0.33
1458319_at	Gpr177	G protein-coupled receptor 177	-1.33	0.09	1.19	0.743	1.71	0.181	-2.21	0.321	-0.16
1447397_at	1700129I04Rik	RIKEN cDNA 1700129I04 gene	1.52	0.499	1.24	0.425	-1.13	0.54	-1.28	0.655	0.09
1450359_at	Fut1	fucosyltransferase 1	-1.05	0.667	1.57	0.463	1.12	0.661	-1.79	0.166	-0.04
1440863_at	---	---	1.45	0.07	1.26	0.651	-1.06	0.822	-1.18	0.041	0.12
1429758_at	1700017B05Rik ///	RIKEN cDNA 1700017B05 gene /// hypothetical protein LOC640563	-1.06	0.03	-1.15	0.166	1.84	0.122	1.49	0.046	0.28
1416639_at	Slc2a5	solute carrier family 2 (facilitated glucose transporter), member 5	1.03	0.883	1.68	0.533	-1.07	0.738	-4.19	0.016	-0.64
1450321_at	Zfp354c	zinc finger protein 354C	-1.29	0.696	1.6	0.429	1.28	0.535	-1.16	0.841	0.11
1442707_at	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	-2	0.07	1.85	0.536	1.3	0.252	-1.64	0.414	-0.12
1417310_at	Tob2	transducer of ERBB2, 2	1.24	0.588	-1.45	0.028	1.73	0.098	-1.13	0.67	0.1
1416561_at	Gad1	glutamic acid decarboxylase 1	1.31	0.476	-1.07	0.868	1.41	0.119	-3.38	0.062	-0.43
1456165_at	4921521F21Rik	RIKEN cDNA 4921521F21 gene	1.34	0.059	1.64	0.061	-1.48	0.482	-2.48	0.352	-0.25
1427752_a_at	Tcrb-V13 /// LOC66	T-cell receptor beta, variable 13 /// similar to T-cell receptor beta chain V region P	1.56	0.436	-1.17	0.722	1.24	0.703	-8.22	0.081	-1.65
1443139_at	---	---	1.78	0.077	-1.22	0.741	1.05	0.939	-1.7	0.371	-0.02
1432374_a_at	D5Wsu178e	DNA segment, Chr 5, Wayne State University 178, expressed	-1.32	0.406	1.17	0.509	1.73	0	-1.12	0.726	0.11
1432831_at	6230424H07Rik	RIKEN cDNA 6230424H07 gene	1.31	0.672	-1.14	0.805	1.47	0.261	-1.07	0.679	0.14
1444967_at	Dag1	Dystroglycan 1	2.21	0.492	-1.53	0.466	-1.27	0.667	2.03	0.138	0.36
1435504_at	---	Transcribed locus	-1.4	0.241	1.85	0.375	1.09	0.123	-1.1	0.801	0.11
1460048_at	Zdhhc13	Zinc finger, DHHC domain containing 13	1.29	0.495	1.64	0.437	-1.38	0.256	-1.18	0.291	0.09
1443676_at	Slc4a4	Solute carrier family 4 (anion exchanger), member 4	-1.15	0.211	2.23	0.015	-1.8	0.417	1.2	0.631	0.12
1447891_at	Tacc2	Transforming, acidic coiled-coil containing protein 2	-1.33	0.46	2.36	0.218	-1.83	0.268	3.1	0.014	0.57
1430311_at	Marcks	Myristoylated alanine rich protein kinase C substrate	1.84	0.141	1.04	0.88	-1.29	0.3	-1.15	0.272	0.11
1426575_at	Tmem23	transmembrane protein 23	1.32	0.226	-1.12	0.649	1.45	0.373	-1.17	0.701	0.12
1431781_at	Ypel1	yippee-like 1 (Drosophila)	-1.54	0.582	1.81	0.335	1.2	0.601	-1.1	0.77	0.09
1430870_at	4930442P19Rik	RIKEN cDNA 4930442P19 gene	1.61	0.209	-2.12	0.152	1.58	0.003	-1.05	0.933	0
1435195_at	Vash1	vasohibin 1	1.14	0.583	1.76	0.03	-1.32	0.067	-1.2	0.272	0.1
1433059_at	4930439G18Rik	RIKEN cDNA 4930439G18 gene	-1.35	0.6	1.14	0.853	1.77	0.012	-2.16	0.202	-0.15
1456571_at	Dcps	decapping enzyme, scavenger	1.16	0.698	-1.03	0.9	1.53	0.231	-1.11	0.683	0.14
1449210_at	Igf2bp1	insulin-like growth factor 2 mRNA binding protein 1	1.4	0.6	1.45	0.323	-1.24	0.666	-1.16	0.387	0.11
1446866_at	A530089I17Rik	RIKEN cDNA A530089I17 gene	1.04	0.95	1.88	0.232	-1.36	0.258	-1.51	0.481	0.01
1454326_at	1700017H01Rik	RIKEN cDNA 1700017H01 gene	-1.08	0.916	1.81	0.349	-1.08	0.783	1.6	0.54	0.31
1437886_at	Klhl6	kelch-like 6 (Drosophila)	-1	0.988	1.19	0.233	1.48	0.129	-2.07	0.042	-0.1
1451337_at	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	-1.16	0.138	-1.23	0.147	1.99	0.028	2.78	0.134	0.59
1438392_at	Cd247	CD247 antigen	1.06	0.678	1.81	0.194	-1.26	0.455	-2.32	0.163	-0.18
1441915_s_at	2310076L09Rik	RIKEN cDNA 2310076L09 gene	-1.03	0.941	-1.77	0.184	2.13	0.069	1.8	0.002	0.28
1423832_at	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	-1.07	0.687	1.13	0.458	1.59	0.087	-1.39	0.029	0.07
1460148_at	---	Transcribed locus	-1.05	0.801	1.65	0.443	1.05	0.917	-1.48	0.38	0.04
1423353_at	Crispld1	cysteine-rich secretory protein LCCL domain containing 1	-1.4	0.207	1.52	0.556	1.42	0.448	-1.31	0.257	0.06
1437140_at	4930412F15Rik	RIKEN cDNA 4930412F15 gene	1.9	0.255	-1.32	0.621	1	0.993	-3.46	0.017	-0.47
1432879_at	6820402A03Rik	RIKEN cDNA 6820402A03 gene	-1.06	0.704	2.06	0.453	-1.53	0.385	1	1	0.12
1422233_at	Elk4	ELK4, member of ETS oncogene family	-1.18	0.271	1.94	0.402	-1.14	0.74	1.13	0.869	0.19
1437860_at	Prkce	protein kinase C, epsilon	1.86	0.285	1.01	0.986	-1.26	0.665	-2.07	0.517	-0.12
1447870_x_at	1110002E22Rik	RIKEN cDNA 1110002E22 gene	-1.2	0.779	1.63	0.4	1.2	0.784	-1.48	0.114	0.04

1452792_at	Dzip1	DAZ interacting protein 1	-1.04	0.895	1.67	0.153	1.03	0.567	-1.46	0.246	0.05
1429918_at	Arhgap20	Rho GTPase activating protein 20	1.27	0.046	1.84	0.214	-1.83	0.105	-1.7	0.074	-0.1
1449541_x_at	1700010I14Rik	RIKEN cDNA 1700010I14 gene	-1.37	0.637	1.62	0.349	1.31	0.06	-1.08	0.711	0.12
1420991_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	1.57	0.348	-2.05	0.242	1.61	0.039	-1.15	0.511	-0.01
1432404_at	4930505A04Rik	RIKEN cDNA 4930505A04 gene	1.96	0.479	-1.03	0.943	-1.36	0.398	1.79	0.402	0.34
1437118_at	Usp7	ubiquitin specific peptidase 7	-1.1	0.626	-1.5	0.255	2.09	0.066	1.77	0.25	0.31
1433651_at	Wtip	WT1-interacting protein	1.42	0.063	1.34	0.052	-1.11	0.525	-1.28	0.229	0.09
1433833_at	Fndc3b	fibronectin type III domain containing 3B	-1.07	0.518	1.83	0.205	-1.11	0.498	1.14	0.618	0.2
1425566_at	Rest /// LOC665152	RE1-silencing transcription factor /// hypothetical protein LOC665152 /// hypotheti	1.61	0.339	1.11	0.851	-1.06	0.899	-1.14	0.845	0.13
1440113_at	Mta1	metastasis associated 1	1.43	0.34	1.37	0.628	-1.15	0.201	-1.1	0.815	0.14
1442431_at	---	Transcribed locus	1.23	0.546	1.51	0.383	-1.09	0.854	-1.67	0.359	0
1432655_at	3222402N08Rik	RIKEN cDNA 3222402N08 gene	1.38	0.323	1.56	0.359	-1.38	0.487	-1.06	0.894	0.13
1432240_at	4930533L02Rik	RIKEN cDNA 4930533L02 gene	1.81	0.43	-1.98	0.061	1.35	0.541	-1.9	0.418	-0.18
1430948_at	4921525B02Rik	RIKEN cDNA 4921525B02 gene	1.6	0.281	-1.05	0.824	1.1	0.618	-1.03	0.908	0.16
1458955_at	Eef1g	Eukaryotic translation elongation factor 1 gamma	-1.31	0.569	1.76	0.277	1.14	0.812	-1.54	0.629	0.01
1427803_at	---	---	2.48	0.075	-1.86	0.342	-1.54	0.109	1.32	0.158	0.1
1422125_at	Htr2b	5-hydroxytryptamine (serotonin) receptor 2B	-1.17	0.778	1.78	0.385	1.03	0.906	-2.42	0.336	-0.19
1424502_at	Oit1	oncoprotein induced transcript 1	1.84	0.217	1.12	0.824	-1.4	0.292	-1.36	0.649	0.05
1439703_at	Cd200r1	CD200 receptor 1	-1.79	0.391	1.98	0.123	1.13	0.65	-1.29	0.441	0.01
1417824_at	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	-1.77	0.231	1.14	0.386	1.96	0.222	-1.58	0.32	-0.06
1417556_at	Fabp1	fatty acid binding protein 1, liver	2.56	0.169	-1.55	0.306	-2.16	0.042	1.83	0.554	0.17
1430407_at	3110035C09Rik	RIKEN cDNA 3110035C09 gene	1.95	0.254	-1.49	0.157	1.04	0.843	-1.73	0.449	-0.06
1438614_x_at	Osbpl9	Oxysterol binding protein-like 9	1.66	0.268	1.51	0.354	-2.01	0.02	-1.23	0.396	-0.02
1455522_at	Arhgef15	Rho guanine nucleotide exchange factor (GEF) 15	-1.02	0.938	1.57	0.177	1.11	0.662	-1.16	0.677	0.13
1460180_at	Hexb	hexosaminidase B	-1.03	0.517	1.6	0	1.1	0.346	-1.58	0.212	0.02
1458705_at	1700031C06Rik	RIKEN cDNA 1700031C06 gene	1.11	0.716	-1.36	0.481	1.82	0.096	-1.15	0.808	0.1
1431777_a_at	Hmgn3	high mobility group nucleosomal binding domain 3	-1.17	0.139	1.67	0.019	1.15	0.47	-1.38	0.098	0.07
1445197_x_at	C79595	expressed sequence C79595	2.22	0.208	-1.23	0.826	-1.59	0.407	1.21	0.259	0.15
1447208_at	---	Transcribed locus	-1.17	0.871	-1.21	0.697	1.99	0.042	1.66	0.582	0.32
1450831_at	Pou3f2	POU domain, class 3, transcription factor 2	1.64	0.559	-1.15	0.676	1.16	0.375	-2.35	0.466	-0.18
1424022_at	1700012B18Rik	RIKEN cDNA 1700012B18 gene	1.51	0.555	-1.01	0.957	1.17	0.313	-1	0.957	0.17
1417076_at	Fabp9	fatty acid binding protein 9, testis	1.77	0.008	1.1	0.88	-1.25	0.649	-1.67	0.215	-0.01
1428021_at	Mccc2	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	1.2	0.527	-1.3	0.275	1.7	0.33	-1.36	0.517	0.06
1430228_at	Dtl	denticleless homolog (Drosophila)	-1.81	0.339	-1.58	0.389	2.49	0.035	3.73	0.189	0.7
1418328_at	Cpt1b	carnitine palmitoyltransferase 1b, muscle	-1.02	0.927	1.09	0.832	1.61	0.287	-1.19	0.479	0.12
1449520_at	Ttc28	tetratricopeptide repeat domain 28	-1.01	0.795	1.44	0.236	1.24	0.199	-1.2	0.472	0.12
1453617_at	Zranb3	zinc finger, RAN-binding domain containing 3	1.37	0.389	-1.41	0.3	1.59	0.233	-1.4	0.371	0.04
1456670_at	A930007A09Rik	RIKEN cDNA A930007A09 gene	1.8	0.098	1.07	0.883	-1.25	0.472	-1.13	0.811	0.12
1422087_at	Mycl1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avia	-1.63	0.255	1.44	0.224	1.62	0.291	-1.62	0.25	-0.05
1422640_at	Pcdhb9	protocadherin beta 9	1.74	0.029	1.11	0.862	-1.22	0.446	-1.17	0.155	0.11
1460245_at	Klrd1	killer cell lectin-like receptor, subfamily D, member 1	1.93	0.004	1.11	0.706	-1.59	0.114	-1.62	0.311	-0.04
1430993_at	Ubap2l	ubiquitin associated protein 2-like	1.57	0.155	-1.04	0.826	1.14	0.348	-1.12	0.87	0.14
1427651_x_at	H2-D1	histocompatibility 2, D region locus 1	-1.17	0.186	1.19	0.605	1.62	0.245	-3.97	0.079	-0.58
1460503_at	Zpbp2	zona pellucida binding protein 2	2.5	0.004	-1.8	0.195	-1.64	0.276	1.05	0.932	0.03
1422256_at	Sstr2	somatostatin receptor 2	1.69	0.211	-1.23	0.636	1.16	0.32	-1.09	0.929	0.14
1454052_at	Hormad2	HORMA domain containing 2	-2.15	0.424	2.14	0.332	1.07	0.45	-1.16	0.6	-0.03
1417561_at	Apoc1	apolipoprotein C-I	1.85	0.542	-1.12	0.594	-1.08	0.652	2.73	0.076	0.6
1456198_at	1810007D17Rik	RIKEN cDNA 1810007D17 gene	2.36	0.09	-1.37	0.62	-1.72	0.179	1.03	0.967	0.08
1444512_at	Arhgap29	Rho GTPase activating protein 29	-1.45	0.523	1.12	0.858	1.86	0.361	-1.27	0.673	0.07
1457600_x_at	Nkd2	Naked cuticle 2 homolog (Drosophila)	1.8	0.369	-1.3	0.658	1.1	0.756	-1.29	0.201	0.08
1443371_at	4930473A06Rik	RIKEN cDNA 4930473A06 gene	1.16	0.832	1.7	0.287	-1.24	0.29	-1.39	0.541	0.06
1439215_at	Atp2c1	ATPase, Ca++-sequestering	1.89	0.208	1.26	0.218	-1.93	0.015	-1.22	0.648	0
1427183_at	Efemp1	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	1.27	0.223	1.56	0.003	-1.19	0.417	-1.11	0.777	0.13

1428750_at	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2	1.02	0.951	1.66	0.105	-1.01	0.965	-1.06	0.713	0.15
1430259_at	Tnfrsf11a	tumor necrosis factor receptor superfamily, member 11a	-1.51	0.263	2.12	0.197	-1.13	0.681	1.07	0.785	0.14
1446924_at	---	Transcribed locus	-1.11	0.815	1.34	0.703	1.44	0.4	-1.93	0.171	-0.07
1453121_at	Tekt4	tektin 4	1.92	0.496	-1.84	0.378	1.21	0.554	-1.56	0.358	-0.07
1418595_at	S3-12	plasma membrane associated protein, S3-12	-1.18	0.656	-2.23	0.145	2.38	0.394	1.64	0.028	0.15
1446587_at	2310042E16Rik	RIKEN cDNA 2310042E16 gene	1.22	0.827	1.6	0.488	-1.17	0.486	-1.04	0.939	0.15
1453129_a_at	Rgs12	regulator of G-protein signaling 12	-1.2	0.294	1.85	0.08	-1.01	0.969	2.91	0.236	0.64
1443113_at	Jmjd2b	Jumonji domain containing 2B	-1.4	0.018	1.88	0.207	1.08	0.803	-1.55	0.269	0
1448091_at	D15Ertd50e	DNA segment, Chr 15, ERATO Doi 50, expressed	2.55	0.315	-2.29	0.225	-1.46	0.596	2.12	0.019	0.23
1419023_x_at	Eno1	enolase 1, alpha non-neuron	1.02	0.842	-1.12	0.391	1.76	0.005	-1.19	0.133	0.12
1425924_at	Mdfi	MyoD family inhibitor	-1.99	0.152	1.6	0.09	1.58	0.39	-1.07	0.855	0.03
1421057_at	Dnase1l3	deoxyribonuclease 1-like 3	-1.33	0.49	1.07	0.751	1.86	0.227	-1.2	0.522	0.1
1431275_at	Chaf1b	chromatin assembly factor 1, subunit B (p60)	-1.19	0.608	1.65	0.338	1.19	0.358	-1.15	0.521	0.12
1425851_a_at	Amigo1	adhesion molecule with Ig like domain 1	-1.18	0.185	-1.26	0.211	2.03	0.019	1.56	0.122	0.29
1423928_at	Phgdhl1	phosphoglycerate dehydrogenase like 1	1.15	0.56	-1.06	0.618	1.58	0.037	-1.33	0.245	0.09
1448130_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	1.22	0.383	1.57	0.036	-1.13	0.317	-1.01	0.985	0.16
1441123_at	ORF34	open reading frame 34	-1.73	0.471	2	0.32	1.1	0.843	-1.63	0.419	-0.07
1444399_at	5830411E10Rik	RIKEN cDNA 5830411E10 gene	1.36	0.423	-1.52	0.209	1.66	0.356	-2.76	0.015	-0.31
1436743_at	Igsf4d	immunoglobulin superfamily, member 4	1.27	0.635	1.61	0.461	-1.24	0.112	-1.19	0.663	0.11
1459158_at	---	---	-1.34	0.545	2.04	0.087	-1.13	0.467	1.29	0.738	0.22
1420150_at	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1	1.2	0.605	1.48	0.043	-1	0.985	-1.24	0.44	0.11
1449670_x_at	Gpr137b	G protein-coupled receptor 137B	-1.01	0.969	1.33	0.206	1.36	0.233	-1.31	0.474	0.09
1443896_at	Tbc1d5	TBC1 domain family, member 5	-1.04	0.797	1.31	0.027	1.4	0.081	-1.09	0.66	0.15
1454656_at	Spata13	spermatogenesis associated 13	-1.02	0.457	-1	0.994	1.7	0.02	1.2	0.083	0.22
1433065_at	6330510M09Rik	RIKEN cDNA 6330510M09 gene	1.37	0.348	1.63	0.104	-1.48	0.16	-1.49	0.139	0.01
1454875_a_at	Rbbp4	retinoblastoma binding protein 4	-1.18	0.61	-1.28	0.403	2.05	0.245	1.21	0.759	0.2
1417643_at	Tsga2	testis specific gene A2	1.55	0.251	1.32	0.486	-1.23	0.406	-2.58	0.314	-0.24
1417716_at	Got2	glutamate oxaloacetate transaminase 2, mitochondrial	-1.04	0.923	-1.06	0.777	1.77	0.073	1.57	0.322	0.31
1431954_x_at	4930431C11Rik	RIKEN cDNA 4930431C11 gene	1.17	0.819	-1.27	0.261	1.72	0.08	-1.08	0.789	0.13
1459868_x_at	Il11ra1 /// Il11ra2 ///	interleukin 11 receptor, alpha chain 1 /// interleukin 11 receptor, alpha chain 2 /// s	-1.53	0.241	1.8	0.019	1.23	0.456	-1.4	0.149	0.02
1448089_at	D4Ertd58e	DNA segment, Chr 4, ERATO Doi 58, expressed	1.3	0.735	1.71	0.365	-1.49	0.42	-3.25	0.002	-0.43
1454310_at	5830490A12Rik	RIKEN cDNA 5830490A12 gene	-1.23	0.649	1.4	0.184	1.47	0.203	-2.11	0.269	-0.12
1430817_at	Samd7	sterile alpha motif domain containing 7	-1.04	0.899	1.5	0.319	1.22	0.588	-1.72	0.457	-0.01
1449429_at	Fkbp1b	FK506 binding protein 1b	1.92	0.329	-1.51	0.222	1.1	0.551	-1.25	0.026	0.07
1459969_x_at	---	Transcribed locus	-1.17	0.339	1.89	0.232	-1.07	0.886	2.13	0.301	0.45
1429157_at	4930507C10Rik	RIKEN cDNA 4930507C10 gene	1.03	0.743	2.1	0.078	-1.83	0.245	-3.54	0.121	-0.56
1451911_a_at	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	1.62	0.23	-1.31	0.102	1.31	0.282	-1.11	0.698	0.12
1436231_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	-2.93	0.146	1.83	0.29	1.51	0.016	-2.23	0.119	-0.45
1428386_at	Acsl3	acyl-CoA synthetase long-chain family member 3	-1.43	0.318	1.69	0.164	1.29	0.268	-1.14	0.756	0.1
1426132_at	---	---	-1.53	0.597	-1.25	0.718	2.23	0.204	1.67	0.129	0.28
1453368_at	2310003H01Rik	RIKEN cDNA 2310003H01 gene	1.02	0.759	-1.04	0.924	1.7	0.014	-1.02	0.861	0.16
1432779_at	1700037N05Rik	RIKEN cDNA 1700037N05 gene	1.22	0.425	1.83	0.356	-1.59	0.342	-1.44	0.282	0.01
1425982_a_at	Wrn	Werner syndrome homolog (human)	-1.08	0.856	-1.19	0.782	1.91	0.42	2.81	0.358	0.61
1421314_at	Cttn	cortactin	1.62	0.442	-1.07	0.897	1.13	0.584	-3.7	0.238	-0.51
1425597_a_at	Qk	quaking	1.33	0.691	1.57	0.378	-1.28	0.587	-1.48	0.409	0.04
1455494_at	Col1a1	procollagen, type I, alpha 1	1.28	0.042	1.92	0.124	-2.06	0.009	-1.82	0.012	-0.17
1433288_at	1520401O13Rik	RIKEN cDNA 1520401O13 gene	-1.16	0.737	1.93	0.129	-1.12	0.861	1.13	0.845	0.19
1440490_at	Mpp6	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	2.05	0.144	-1.52	0.063	-1.02	0.945	1.15	0.379	0.16
1444809_at	Marveld3	MARVEL (membrane-associating) domain containing 3	-1.19	0.775	2.08	0.093	-1.3	0.533	1.25	0.615	0.21
1438556_a_at	Tmod3	tropomodulin 3	1.39	0.447	-1.04	0.904	1.34	0.512	-1.41	0.551	0.07
1423541_at	4930511I11Rik	RIKEN cDNA 4930511I11 gene	-1.22	0.344	2.43	0.183	-2.28	0.104	1.17	0.371	0.02
1422331_at	Pou3f3	POU domain, class 3, transcription factor 3	2.71	0.04	-2.29	0.005	-1.86	0.243	1.09	0.644	-0.09
1458061_at	LOC402769	hypothetical LOC402769	1.87	0.31	-1.42	0.551	1.11	0.885	-1.27	0.774	0.07

1449325_at	Fads2	fatty acid desaturase 2	-1	1	-1.54	0.324	2.04	0.277	1.82	0.372	0.33
1447500_at	Cutl2	cut-like 2 (Drosophila)	-1.44	0.122	1.43	0.525	1.56	0.041	-2.81	0.01	-0.31
1423981_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), men	1.25	0.416	1.51	0.591	-1.08	0.756	-1.03	0.896	0.16
1422750_a_at	Zmynd10	zinc finger, MYND domain containing 10	1.12	0.482	-1.04	0.734	1.61	0.126	-1.41	0.545	0.07
1456346_at	Dnm1	Dynamin 1	1.58	0.208	1.24	0.732	-1.16	0.528	-1.2	0.494	0.12
1443700_at	Bcl9l	B-cell CLL/lymphoma 9-like	1.7	0.021	1.45	0.336	-1.87	0.189	-3.48	0.305	-0.55
1425368_a_at	Numb	numb gene homolog (Drosophila)	1.14	0.615	-1.19	0.743	1.7	0.162	-2.42	0.021	-0.19
1450506_a_at	Isg20l1	interferon stimulated exonuclease gene 20-like 1	1.17	0.396	-1.01	0.937	1.52	0.124	-1.03	0.902	0.17
1438270_at	AI846148	expressed sequence AI846148	1.02	0.951	1.88	0.018	-1.27	0.431	-1.19	0.384	0.11
1426185_at	Cacna2d2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.57	0.038	1.12	0.653	-1	0.996	-1.21	0.791	0.12
1446042_at	---	PREDICTED: Mus musculus similar to preferentially expressed antigen in melanc	-1.03	0.974	1.53	0.384	1.19	0.682	-1.79	0.463	-0.03
1431780_at	1700021K14Rik	RIKEN cDNA 1700021K14 gene	-1.16	0.734	-2.06	0.412	2.34	0.135	1.53	0.231	0.16
1455848_at	Tmprss11a	transmembrane protease, serine 11a	-1.2	0.345	1.33	0.742	1.53	0.264	-2.95	0.256	-0.32
1428891_at	---	---	-1.05	0.805	1.61	0.273	1.13	0.406	-1.77	0.227	-0.02
1418161_at	Jph3	junctophilin 3	-1.23	0.383	1.24	0.547	1.63	0.404	-1.05	0.859	0.15
1422938_at	Bcl2	B-cell leukemia/lymphoma 2	-1.36	0.611	1.64	0.09	1.32	0.519	-1.12	0.74	0.12
1446563_at	---	---	1.41	0.725	-1.43	0.477	1.58	0.273	-1.27	0.69	0.07
1460565_at	Slc41a1	solute carrier family 41, member 1	-1.12	0.068	1.55	0.066	1.25	0.296	-1.04	0.918	0.16
1437153_at	MGC91195 /// Oogi	similar to Oogenesin 2 /// oogenesin 2	1.26	0.557	1.52	0.094	-1.1	0.737	-1.46	0.398	0.05
1431836_x_at	5430432N15Rik	RIKEN cDNA 5430432N15 gene	2.04	0.518	-1.1	0.874	-1.35	0.086	1.63	0.146	0.31
1428713_s_at	4833427B12Rik	RIKEN cDNA 4833427B12 gene	-1.58	0.656	-1.76	0.421	2.49	0.13	1.89	0.254	0.26
1448764_a_at	Fabp1	fatty acid binding protein 1, liver	2.49	0.175	-1.34	0.352	-2.21	0.035	1.72	0.606	0.17
1430437_a_at	1300018I17Rik	RIKEN cDNA 1300018I17 gene	1.38	0.634	1.4	0.371	-1.1	0.788	-1.23	0.803	0.11
1442283_at	Phgdhl1	Phosphoglycerate dehydrogenase like 1	-1.21	0.328	1.57	0.289	1.29	0.534	-1.4	0.383	0.06
1421932_at	Cbx5	chromobox homolog 5 (Drosophila HP1a)	-1.02	0.973	1.3	0.652	1.41	0.173	-1.53	0.171	0.04
1425392_a_at	Nr1i3	nuclear receptor subfamily 1, group I, member 3	1.92	0.399	-1.29	0.166	1	0.991	-1.43	0.6	0.05
1434522_at	Wdr4	WD repeat domain 4	-1.33	0.292	1.27	0.67	1.67	0.432	-1.27	0.659	0.09
1430733_at	4932441P12Rik	RIKEN cDNA 4932441P12 gene	1.21	0.783	-1.1	0.729	1.58	0.57	-1.6	0.369	0.02
1435615_at	Zfp365	zinc finger protein 365	1.48	0.344	1.32	0.433	-1.12	0.746	-1.44	0.651	0.06
1421327_at	Mtap2 /// A730034C	microtubule-associated protein 2 /// hypothetical protein A730034C02	1.19	0.653	-1.19	0.66	1.66	0.03	-1.64	0.226	0
1447307_at	---	Transcribed locus	-1.57	0.523	1.23	0.591	1.82	0.187	-2.43	0.074	-0.24
1449633_s_at	Nt5c3l	5'-nucleotidase, cytosolic III-like	1.45	0.166	1.39	0.432	-1.17	0.401	-1.62	0.198	0.01
1430336_at	Gucy2g	guanylate cyclase 2g	-1.34	0.064	-1.04	0.899	1.98	0.067	1.01	0.972	0.16
1440666_at	4933430I17Rik	RIKEN cDNA 4933430I17 gene	-1.23	0.692	-1.03	0.961	1.91	0.168	1.35	0.564	0.25
1436902_x_at	Tmsb10	thymosin, beta 10	1.38	0.077	1.57	0.04	-1.34	0.004	-1.84	0.122	-0.06
1420372_at	Sntb2	syntrophin, basic 2	1.5	0.456	1.25	0.366	-1.06	0.869	-1.08	0.646	0.15
1460475_at	3110056J03Rik	RIKEN cDNA 3110056J03 gene	-1.02	0.971	1.28	0.545	1.43	0.263	-1.95	0.071	-0.06
1422342_at	Nmbr	neuromedin B receptor	1.54	0.565	-1.28	0.109	1.38	0.312	-1.2	0.415	0.11
1433504_at	Pygb	brain glycogen phosphorylase	-1.05	0.729	1.51	0.017	1.24	0.289	-1.32	0.333	0.09
1449866_at	Syt2	synaptotagmin II	-1.03	0.878	1.41	0.21	1.31	0.532	-2.19	0.227	-0.12
1420913_at	Slco2a1	solute carrier organic anion transporter family, member 2a1	1.49	0.051	-1.03	0.617	1.23	0.312	-1.52	0.115	0.04
1424764_at	Sez6l	seizure related 6 homolog like	-1.32	0.675	1.85	0.153	1.08	0.82	-1.17	0.547	0.11
1443552_at	E230008N13Rik	RIKEN cDNA E230008N13 gene	-1.14	0.841	1.61	0.393	1.21	0.225	-1.17	0.338	0.13
1416514_a_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	1.32	0.009	1.6	0.004	-1.29	0.299	-2.54	0.123	-0.23
1445559_at	Rp9h	Retinitis pigmentosa 9 homolog (human)	1.49	0.462	1.6	0.252	-1.65	0.166	-1.27	0.684	0.04
1432873_at	4932702M13Rik	RIKEN cDNA 4932702M13 gene	1.37	0.268	1.37	0.203	-1.05	0.529	-1.16	0.593	0.13
1418647_at	---	---	-1.08	0.133	1.39	0.201	1.39	0.105	-1.53	0.018	0.04
1435598_at	---	Transcribed locus	1.88	0.089	-1.32	0.574	1.06	0.762	-1.05	0.931	0.14
1433199_at	B230114A03Rik	RIKEN cDNA B230114A03 gene	2.05	0.324	-2	0.349	1.14	0.392	-1.01	0.955	0.05
1436147_at	Snx19	Sorting nexin 19	1.07	0.873	-1.63	0.101	2.02	0.053	-1.78	0.267	-0.08
1421298_a_at	Hipk1	homeodomain interacting protein kinase 1	-1.09	0.69	-1.29	0.738	2	0.05	2.44	0.158	0.52
1454082_a_at	Giyd2	GIY-YIG domain containing 2	-1.01	0.938	1.14	0.546	1.57	0.07	-1.18	0.41	0.13
1421701_at	V2r16	vomeronasal 2, receptor, 16	-2.22	0.162	1.65	0.323	1.6	0.102	-3.15	0.321	-0.53

1447084_at	Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.64	0.124	-1.24	0.321	1.26	0.688	-1.23	0.527	0.11
1444088_at	---	---	1.66	0.545	1.23	0.785	-1.24	0.507	-8.46	0.023	-1.7
1448883_at	Lgmn	legumain	-1.35	0.064	1.87	0.017	1.08	0.547	-1.11	0.661	0.12
1441801_at	Kctd4	potassium channel tetramerisation domain containing 4	-1.99	0.048	2.64	0.22	-1.81	0.353	1.62	0.039	0.12
1443706_at	C1galt1c1	C1GALT1-specific chaperone 1	2.14	0.264	-1.38	0.506	-1.2	0.662	1.38	0.073	0.23
1443206_at	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	2.4	0.063	-1.28	0.413	-1.93	0.052	1.18	0.374	0.09
1424768_at	Cald1	caldesmon 1	1.65	0.354	-1.03	0.914	1.08	0.843	-1.47	0.376	0.06
1432366_at	4930447K03Rik	RIKEN cDNA 4930447K03 gene	-1.3	0.345	-1.23	0.745	2.11	0.205	1.67	0.353	0.32
1428047_s_at	Zfa /// Zfx	zinc finger protein, autosomal /// zinc finger protein X-linked	1.61	0.067	-1.03	0.941	1.12	0.781	-1.15	0.602	0.14
1430619_a_at	Mvk /// LOC637711	mevalonate kinase /// similar to mevalonate kinase	-1.05	0.894	1.73	0.376	1.02	0.952	-1.22	0.641	0.12
1416001_a_at	Cotl1	coactosin-like 1 (Dictyostelium)	-1.45	0.068	1.35	0.015	1.66	0.063	-1.67	0.117	-0.03
1430767_a_at	4930543E12Rik	RIKEN cDNA 4930543E12 gene	1.32	0.528	1.47	0.218	-1.09	0.787	-1.84	0.201	-0.04
1438667_at	5730410E15Rik	RIKEN cDNA 5730410E15 gene	1.2	0.48	1.54	0.388	-1.04	0.859	-1.88	0.252	-0.04
1457311_at	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	1.13	0.838	-1.06	0.882	1.63	0.309	-1.16	0.639	0.13
1451553_at	Art5	ADP-ribosyltransferase 5	1.14	0.824	-1.41	0.488	1.86	0.259	-1.16	0.803	0.1
1431866_at	4930425K24Rik	RIKEN cDNA 4930425K24 gene	1.46	0.652	1.68	0.412	-1.77	0.119	-1.15	0.017	0.05
1436718_at	Nxph1	neurexophilin 1	-1.5	0.605	-1.38	0.294	2.31	0.074	2.12	0.182	0.39
1454007_a_at	Zfp142	zinc finger protein 142	1.72	0.337	-1.58	0.134	1.35	0.445	-1.3	0.436	0.05
1458755_at	---	Transcribed locus	-1.05	0.939	1.26	0.396	1.49	0.539	-1.28	0.492	0.11
1441811_x_at	0610011I04Rik	RIKEN cDNA 0610011I04 gene	1.03	0.791	1.69	0.209	-1.02	0.896	-1.39	0.048	0.08
1437626_at	Zfp36l2	zinc finger protein 36, C3H type-like 2	1.11	0.226	-1.03	0.895	1.62	0.023	-1.47	0.295	0.06
1423726_at	Vat1	vesicle amine transport protein 1 homolog (T californica)	-1.21	0.728	1.77	0.074	1.11	0.697	-1.14	0.723	0.13
1456937_at	Cdh26	cadherin-like 26	1.54	0.513	-1.02	0.924	1.18	0.613	-1.6	0.47	0.03
1447999_x_at	LOC14433 /// LOC3	similar to glyceraldehyde-3-phosphate dehydrogenase /// similar to glyceraldehyd	-1.33	0.343	1.2	0.132	1.75	0.083	-1.47	0.294	0.04
1459941_at	4933402J24Rik	RIKEN cDNA 4933402J24 gene	1.62	0.512	1.3	0.803	-1.27	0.475	-1.67	0.309	-0.01
1454094_at	4930471E19Rik	RIKEN cDNA 4930471E19 gene	-1.18	0.835	1.72	0.471	1.13	0.763	-1.12	0.842	0.14
1437842_at	Plcxd1	phosphatidylinositol-specific phospholipase C, X domain containing 1	1.63	0.079	-1.04	0.934	1.12	0.706	-1.33	0.465	0.09
1444355_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	-1.3	0.733	2.45	0.001	-2.04	0.037	1.14	0.57	0.06
1446422_at	3-Mar	Membrane-associated ring finger (C3HC4) 3	-1.21	0.648	2.06	0.22	-1.22	0.307	3.89	0.167	0.88
1455649_at	Ttc9	tetratricopeptide repeat domain 9	-1.87	0.226	1.88	0.338	1.29	0.344	-1.49	0.218	-0.05
1439702_at	---	---	1.54	0.374	1.3	0.446	-1.15	0.717	-1.11	0.796	0.14
1422043_at	Tsc1	tuberous sclerosis 1	-2.83	0.036	1.29	0.673	2.06	0.074	-1.19	0.509	-0.17
1453022_at	Gpihbp1	GPI-anchored HDL-binding protein 1	1.31	0.235	1.47	0.152	-1.08	0.665	-1.53	0.096	0.04
1455718_at	Spata21	spermatogenesis associated 21	-2.31	0.284	-1.38	0.644	2.55	0.104	2.2	0.041	0.26
1450534_x_at	LOC56628	MHC (A.CA/J(H-2K-f) class I antigen	-1.07	0.827	1.03	0.622	1.74	0.102	-1.43	0.264	0.07
1446415_at	Hebp2	heme binding protein 2	-1.25	0.762	1.51	0.355	1.4	0.594	-1.23	0.339	0.11
1447587_at	G630024C07Rik	RIKEN cDNA G630024C07 gene	-1.29	0.357	1.79	0.344	1.14	0.661	-1.1	0.791	0.14
1443439_at	Acss1	Acyl-CoA synthetase short-chain family member 1	1.22	0.701	1.94	0.146	-1.82	0.004	-1.2	0.457	0.03
1452940_x_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	1.99	0.336	-1.01	0.983	-1.39	0.188	1.33	0.147	0.23
1419654_at	Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	-1	0.988	1.59	0.195	1.13	0.53	-1.28	0.262	0.11
1421010_at	Mobp	myelin-associated oligodendrocytic basic protein	1.2	0.078	1.74	0.465	-1.31	0.493	-1.67	0.131	-0.01
1420979_at	Pak1	p21 (CDKN1A)-activated kinase 1	-1.06	0.535	1.88	0.058	-1.13	0.499	1.06	0.801	0.19
1453759_at	Nsun2	NOL1/NOP2/Sun domain family 2	2.05	0.044	-1.61	0.592	1.04	0.828	-1.21	0.511	0.07
1437259_at	---	---	-1.05	0.847	1.41	0.276	1.35	0.352	-1.58	0.272	0.03
1450916_at	Stau2	staufen (RNA binding protein) homolog 2 (Drosophila)	1.23	0.248	1.59	0.526	-1.12	0.551	-1.12	0.62	0.15
1435879_at	Akt3	thymoma viral proto-oncogene 3	1.18	0.403	1.79	0.125	-1.34	0.07	-1.39	0.057	0.06
1432623_at	Supv3l1	suppressor of var1, 3-like 1 (S. cerevisiae)	-1.33	0.24	2.02	0.035	-1.06	0.712	1.27	0.353	0.22
1444658_at	---	---	2.06	0.003	-2.63	0.043	1.27	0.415	-1.4	0.207	-0.18
1456398_at	Tug1	taurine upregulated gene 1	1.49	0.446	-1.21	0.595	1.4	0.535	-1.57	0.487	0.03
1443227_at	Bzw2	basic leucine zipper and W2 domains 2	-1.04	0.882	1.66	0.172	1.1	0.716	-1.35	0.312	0.09
1459759_s_at	1700065I17Rik	RIKEN cDNA 1700065I17 gene	1.41	0.619	-1.18	0.811	1.46	0.474	-3.17	0.247	-0.37
1422194_at	Scn5a	sodium channel, voltage-gated, type V, alpha	-1.59	0.534	1.28	0.65	1.81	0.256	-4.01	0.204	-0.63
1429807_at	1700011H22Rik	RIKEN cDNA 1700011H22 gene	2.26	0.355	-1.32	0.583	-1.43	0.288	1.55	0.464	0.27

1452351_at	C030027K23Rik ///	RIKEN cDNA C030027K23 gene /// poly (ADP-ribose) polymerase family, membe	-1.02	0.848	1.25	0.076	1.49	0.233	-1.1	0.826	0.15
1415899_at	Junb	Jun-B oncogene	-1.03	0.379	1.66	0.036	1.09	0.836	-1.25	0.491	0.12
1458377_at	Crsp7	cofactor required for Sp1 transcriptional activation, subunit 7	1.71	0.285	-1.1	0.874	1.1	0.537	-1.1	0.702	0.15
1456719_at	---	2 cells egg cDNA, RIKEN full-length enriched library, clone:B020004L17 product:	2	0.514	-1.28	0.596	-1.07	0.881	1.16	0.422	0.2
1452308_a_at	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	-1.44	0.443	1.55	0.397	1.47	0.382	-1.93	0.144	-0.09
1438837_at	Chrna9	Cholinergic receptor, nicotinic, alpha polypeptide 9	-1.3	0.342	1.59	0.532	1.35	0.422	-2.15	0.316	-0.13
1460460_a_at	Gorasp2	golgi reassembly stacking protein 2	1.29	0.555	-1.02	0.948	1.45	0.458	-1.08	0.878	0.16
1432537_at	4930465A12Rik	RIKEN cDNA 4930465A12 gene	-1.28	0.781	1.41	0.455	1.52	0.354	-2.3	0.086	-0.16
1426329_s_at	Baalc	brain and acute leukemia, cytoplasmic	-1.06	0.924	-1.08	0.837	1.84	0.058	1.14	0.807	0.21
1460482_at	3110047P20Rik	RIKEN cDNA 3110047P20 gene	-3	0.012	2.61	0.154	-1.3	0.278	3.99	0.039	0.58
1452588_at	Zfp688	zinc finger protein 688	1.69	0.1	-1.3	0.321	1.25	0.015	-1.58	0.233	0.02
1453996_a_at	Cts3	cathepsin 3	-1.67	0.526	1.83	0.192	1.28	0.69	-1.62	0.243	-0.04
1445208_at	Exdl2	exonuclease 3''-5'' domain-like 2	1.04	0.781	1.88	0.025	-1.27	0.252	-1.41	0.727	0.06
1456053_at	---	Transcribed locus	1.15	0.792	-2.78	0.151	2.21	0.101	-1.33	0.599	-0.19
1425967_a_at	Mcpt4	mast cell protease 4	-1.18	0.667	-1	0.992	1.87	0.28	1.01	0.974	0.17
1421547_at	Cd180	CD180 antigen	-1.39	0.193	1.74	0.135	1.26	0.703	-1.56	0.217	0.01
1438634_x_at	Lasp1	LIM and SH3 protein 1	-1.01	0.876	1.3	0.197	1.43	0.054	-1.37	0.221	0.09
1458675_at	---	---	2.38	0.206	-2	0.277	-1.19	0.496	1.01	0.994	0.05
1427004_at	Fbxo2	F-box only protein 2	1.01	0.976	1.72	0.033	-1.01	0.955	-1.24	0.819	0.12
1431601_at	Rtdr1	rhabdoid tumor deletion region gene 1	1.27	0.283	-1.05	0.774	1.49	0.321	-1.25	0.504	0.12
1444083_at	Ttn	titin	-2.89	0.284	-1.06	0.852	2.43	0.172	1.19	0.738	-0.08
1460062_at	Plekhh2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	1.59	0.039	1.34	0.53	-1.26	0.508	-1.55	0.071	0.03
1441317_x_at	Jakmip1	janus kinase and microtubule interacting protein 1	1.99	0.039	-2.29	0.264	1.29	0.555	-2.17	0.077	-0.3
1435276_a_at	Dgcr2	DiGeorge syndrome critical region gene 2	-1.06	0.769	-1.13	0.522	1.89	0.274	1.25	0.513	0.24
1447787_x_at	Gja7	gap junction membrane channel protein alpha 7	1.9	0.348	1.06	0.722	-1.32	0.196	-2.01	0.325	-0.09
1427437_at	2610203C20Rik	RIKEN cDNA 2610203C20 gene	1.92	0.375	1.23	0.288	-1.76	0.236	-1.64	0.5	-0.06
1420978_at	Nrf1	nuclear respiratory factor 1	2.14	0.081	-1.11	0.727	-1.48	0.355	2.27	0.163	0.46
1449556_at	H2-T23 /// C92002	histocompatibility 2, T region locus 23 /// RIKEN cDNA C920025E04 gene /// simi	1.55	0.073	-1.12	0.106	1.28	0.152	-1.29	0.213	0.1
1421817_at	Gsr	glutathione reductase 1	-1.12	0.147	-1.02	0.667	1.85	0.125	1.35	0.453	0.26
1450646_at	Cyp51	cytochrome P450, family 51	1.1	0.464	1.64	0.111	-1.02	0.921	-1.38	0.416	0.09
1434767_at	C79407	expressed sequence C79407	-1.54	0.121	2.19	0.115	-1.13	0.675	2.96	0.203	0.62
1440318_at	Wdr35	WD repeat domain 35	-1	0.982	-1.45	0.317	2.04	0.363	1.06	0.85	0.16
1436583_at	2600005O03Rik	RIKEN cDNA 2600005O03 gene	1.76	0.49	-1.04	0.882	-1	1	1.86	0.315	0.39
1422638_s_at	Rassf5	Ras association (RalGDS/AF-6) domain family 5	-1.05	0.7	1.24	0.048	1.53	0.028	-1.75	0.154	-0.01
1446133_at	D2Ertd295e	DNA segment, Chr 2, ERATO Doi 295, expressed	1.45	0.455	1.47	0.405	-1.25	0.521	-1.13	0.859	0.14
1436669_at	1700019G17Rik	RIKEN cDNA 1700019G17 gene	-1.1	0.774	1.63	0.07	1.19	0.324	-1.5	0.04	0.05
1449419_at	Dock8	dedicator of cytokinesis 8	1.15	0.535	-1.14	0.303	1.69	0.035	-1.3	0.411	0.1
1419615_at	Trpv6	transient receptor potential cation channel, subfamily V, member 6	1.9	0.155	-1.05	0.856	-1.15	0.314	1.19	0.688	0.22
1426706_s_at	Xylb	xylulokinase homolog (H. influenzae)	-1.11	0.609	-1.11	0.582	1.92	0.032	1.69	0.404	0.35
1459847_x_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	1.26	0.746	1.82	0.016	-1.56	0.023	-1.23	0.504	0.07
1438358_x_at	Pfdn5 /// LOC4348	prefoldin 5 /// prefoldin 5 pseudogene	2.05	0.552	-1.37	0.224	-1.06	0.846	1.01	0.939	0.16
1459141_at	1810008I18Rik	RIKEN cDNA 1810008I18 gene	1.6	0.388	1.36	0.3	-1.31	0.529	-2.16	0.26	-0.13
1434245_a_at	Cybasc3	cytochrome b, ascorbate dependent 3	-1.04	0.796	1.02	0.846	1.74	0.279	-1.91	0.111	-0.05
1435549_at	Trpm4	transient receptor potential cation channel, subfamily M, member 4	1.45	0.177	1.33	0.44	-1.06	0.72	-1.19	0.587	0.13
AFFX-ThrX-5_at	---	---	1.84	0.451	-1.16	0.705	1.02	0.976	-2.36	0.561	-0.16
1429935_at	Lcn12	lipocalin 12	2.14	0.445	1.08	0.892	-1.96	0.206	-2.42	0.328	-0.29
1439146_s_at	Lck	lymphocyte protein tyrosine kinase	-1.09	0.871	1.03	0.85	1.78	0.098	-2.04	0.308	-0.08
1429036_at	Otop3	otopetrin 3	1.67	0.357	1.07	0.923	-1.01	0.975	-1.26	0.452	0.12
1448800_at	Rtn4ip1	reticulon 4 interacting protein 1	-1.01	0.962	-1.19	0.101	1.9	0.062	1.37	0.316	0.27
1417761_at	Apoa4	apolipoprotein A-IV	1.43	0.619	1.33	0.541	-1.03	0.778	-2.1	0.092	-0.09
1419825_at	Nrxn3	Neurexin III	1.65	0.276	1.33	0.609	-1.33	0.665	-1.01	0.987	0.16
1459803_x_at	2810408A11Rik	RIKEN cDNA 2810408A11 gene	1.24	0.765	-4.9	0.097	2.29	0.207	-1.84	0.476	-0.81
1445143_at	Vash1	vasohibin 1	1.54	0.313	1.77	0.052	-2.36	0.021	-2.05	0.295	-0.28

1444398_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	1.52	0.025	-1.24	0.732	1.4	0.389	-2.32	0.119	-0.16
1453002_at	Sox11	SRY-box containing gene 11	2.45	0.022	-1.43	0.485	-1.73	0.117	1.1	0.824	0.1
1432008_at	Tmem86b	transmembrane protein 86B	1.79	0.309	-1.03	0.935	-1.03	0.939	1.38	0.361	0.28
1440146_at	Vps13a	vacuolar protein sorting 13A (yeast)	1.47	0.31	1.3	0.305	-1.04	0.857	-1.09	0.77	0.16
1435290_x_at	H2-Aa	histocompatibility 2, class II antigen A, alpha	1.67	0.115	1.18	0.435	-1.13	0.47	-1.41	0.135	0.08
1453057_at	Tmem162	transmembrane protein 162	1.32	0.711	1.67	0.461	-1.36	0.493	-1.39	0.546	0.06
1456673_at	AL022943	expressed sequence AL022943	-1.16	0.505	1.68	0.298	1.19	0.31	-1.16	0.719	0.14
1423287_at	Cbln1	cerebellin 1 precursor protein	1.71	0.164	1.08	0.889	-1.06	0.874	-1.53	0.54	0.05
1423543_at	Swap70	SWA-70 protein	1.11	0.677	-1.21	0.49	1.79	0.235	-1.55	0.208	0.04
1425426_a_at	Mef2a	myocyte enhancer factor 2A	1.18	0.803	-1.41	0.496	1.85	0.425	-1.89	0.255	-0.07
1422659_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	-1.23	0.214	1.64	0.009	1.28	0.261	-1.14	0.656	0.14
1451015_at	Tkt	transketolase	-1.42	0.009	-1.02	0.891	2.05	0.07	1.04	0.885	0.16
1428305_at	Pcsk2	proprotein convertase subtilisin/kexin type 2	1.3	0.705	1.76	0.471	-1.49	0.132	-1.78	0.274	-0.05
1436799_at	D230005D02Rik	RIKEN cDNA D230005D02 gene	1.53	0.475	1.31	0.744	-1.12	0.713	-4.6	0.051	-0.72
1453575_at	1200003I10Rik	RIKEN cDNA 1200003I10 gene	-1.33	0.56	1.81	0.447	1.18	0.512	-1.24	0.677	0.1
1451792_a_at	Pja1	praja1, RING-H2 motif containing	1.22	0.697	-1.52	0.361	1.85	0.225	-1.21	0.735	0.09
1450295_s_at	Pvr	poliovirus receptor	1.31	0.612	-1.28	0.768	1.64	0.509	-2.21	0.366	-0.13
1445886_at	Elk3	ELK3, member of ETS oncogene family	2.31	0.005	-1.26	0.768	-1.59	0.022	1.33	0.491	0.2
1437931_at	Tlr12	toll-like receptor 12	1.8	0.002	-1.14	0.642	1.05	0.901	-1	0.998	0.18
1430861_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	-1.07	0.94	1.71	0.327	1.09	0.861	-1.05	0.92	0.17
1449416_at	Fzd4	frizzled homolog 4 (Drosophila)	1.74	0.423	-1.49	0.446	1.33	0.612	-1.11	0.885	0.11
1448914_a_at	Csf1	colony stimulating factor 1 (macrophage)	1.32	0.064	-1.09	0.844	1.5	0.051	-1.26	0.332	0.12
1458300_at	Akr7a5	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	-1.15	0.755	1.56	0.478	1.31	0.548	-1.91	0.33	-0.05
1418958_at	Amac1	acyl-malonyl condensing enzyme 1	-1.13	0.608	1.04	0.909	1.82	0.074	-1.5	0.167	0.06
1427668_at	Siglec1	sialic acid binding Ig-like lectin 1, sialoadhesin	-1.44	0.64	1.27	0.606	1.78	0.107	-1.48	0.245	0.03
1433468_at	6430527G18Rik	RIKEN cDNA 6430527G18 gene	1.1	0.36	-1	0.981	1.63	0.096	-1.96	0.141	-0.06
1458819_at	Garnl3	GTPase activating RANGAP domain-like 3	1.24	0.815	1.85	0.121	-1.56	0.079	-1.47	0.114	0.02
1431319_at	Ulk4	unc-51-like kinase 4 (C. elegans)	-1.02	0.967	-1.01	0.964	1.76	0.339	1.76	0.079	0.37
1459718_x_at	Klf6	Kruppel-like factor 6	-1.07	0.909	1.75	0.032	1.05	0.513	-1.54	0.301	0.05
1436169_at	C730029A08Rik	RIKEN cDNA C730029A08 gene	-1.01	0.935	-1.21	0.169	1.92	0.203	4.68	0.159	1.1
1445408_at	LOC432611	similar to dynein, axonemal, intermediate polypeptide 2	1.53	0.692	-1.3	0.61	1.44	0.526	-1.48	0.444	0.05
1442122_at	AI451458	expressed sequence AI451458	-1.22	0.4	1.54	0.276	1.39	0.438	-2.03	0.148	-0.08
1455304_at	Unc13c	unc-13 homolog C (C. elegans)	-1.53	0.011	1.91	0.073	1.17	0.771	-2.6	0.009	-0.26
1458986_at	4930534H18Rik	RIKEN cDNA 4930534H18 gene	2.32	0.303	-2.32	0.194	-1.01	0.984	1.87	0.343	0.22
1427146_at	AI790298	expressed sequence AI790298	1.62	0.109	1.4	0.661	-1.38	0.619	-3.19	0.116	-0.39
1428733_at	Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polype	-1.12	0.694	1.31	0.018	1.53	0.067	-1.1	0.6	0.16
1447238_at	---	---	-1.03	0.977	1.22	0.727	1.55	0.271	-3.45	0.034	-0.43
1424332_at	Rab40c	Rab40c, member RAS oncogene family	1.35	0.595	-1.06	0.897	1.45	0.486	-1.3	0.605	0.11
1445503_at	Gm715 /// LOC671	gene model 715, (NCBI) /// similar to CG4768-PA	1.51	0.058	-1.15	0.744	1.36	0.384	-1.03	0.888	0.17
1431174_at	A930036K24Rik	RIKEN cDNA A930036K24 gene	-1.59	0.407	2.1	0.032	1.01	0.949	-1.02	0.966	0.13
1431974_at	4930443G12Rik	RIKEN cDNA 4930443G12 gene	2.02	0.448	-1.1	0.802	-1.23	0.398	1.78	0.186	0.37
1420703_at	Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	-1.05	0.903	1.3	0.24	1.49	0.036	-1.07	0.815	0.17
1457275_at	Dmn	desmuslin	1.49	0.378	1.54	0.518	-1.41	0.22	-1.34	0.127	0.07
1429088_at	Lbh	limb-bud and heart	1.5	0.282	1.4	0.071	-1.18	0.502	-1.3	0.607	0.1
1458658_at	---	---	1.88	0.15	-1.6	0.046	1.24	0.382	-1.26	0.724	0.07
1435936_at	Slc13a5	Solute carrier family 13 (sodium-dependent citrate transporter), member 5	-1.45	0.296	2.38	0.176	-1.49	0.177	1.11	0.792	0.14
1447528_at	---	---	-1.12	0.917	1.79	0.241	1.06	0.926	-1.95	0.034	-0.05
1421425_a_at	Dscr1l1	Down syndrome critical region gene 1-like 1	1.03	0.848	2.08	0.029	-1.57	0.136	-1.05	0.907	0.12
1424978_at	Odf4	outer dense fiber of sperm tails 4	-1.05	0.919	-1.06	0.879	1.85	0.229	1.21	0.783	0.24
1438377_x_at	Slc13a3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-1.19	0.482	2.03	0.175	-1.15	0.347	2.6	0.058	0.57
1433132_at	Edaradd	EDAR (ectodysplasin-A receptor)-associated death domain	-1.82	0.546	1.97	0.233	1.23	0.596	-1.02	0.936	0.09
1454238_a_at	1700010H22Rik	RIKEN cDNA 1700010H22 gene	1.21	0.644	2.25	0.113	-3.5	0.333	-2.02	0.087	-0.52
1417184_s_at	Hbb-b1 /// Hbb-b2	hemoglobin, beta adult major chain /// hemoglobin, beta adult minor chain	1.29	0.16	1.71	0.034	-1.35	0.039	-1.22	0.068	0.11

1422936_at	Mas1	MAS1 oncogene	-2.46	0.025	1.69	0.276	1.65	0.244	-2.84	0.255	-0.49
1439247_at	Dock10 /// LOC630	dedicator of cytokinesis 10 /// similar to Dedicator of cytokinesis protein 10 (Protei	1.61	0.054	1.27	0.703	-1.15	0.584	-1.58	0.407	0.04
1415906_at	Tmsb4x	thymosin, beta 4, X chromosome	1.14	0.166	1.81	0.004	-1.26	0.009	-1.33	0.017	0.09
1442853_at	Mapk8ip3	Mitogen-activated protein kinase 8 interacting protein 3	1.22	0.235	1.77	0.122	-1.33	0.3	-1.42	0.352	0.06
1436659_at	Dcamkl1	Double cortin and calcium/calmodulin-dependent protein kinase-like 1	1.44	0.357	-1.08	0.836	1.38	0.282	-1.78	0.391	-0.01
1449284_at	1700008P20Rik	RIKEN cDNA 1700008P20 gene	1.83	0.587	1.01	0.981	-1.11	0.433	-1.58	0.423	0.04
1431539_at	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	1.92	0.128	-2.17	0.076	1.36	0.15	-1.08	0.818	0.01
1425431_at	Krtap16-10 /// Krtap	keratin associated protein 16-10 /// keratin associated protein 16-3 /// keratin assc	-1.16	0.807	2.3	0.102	-1.73	0.129	1.8	0.332	0.31
1431649_at	1700108M19Rik	RIKEN cDNA 1700108M19 gene	2.54	0.036	-2.05	0.076	-1.4	0.574	2.93	0.163	0.5
1450767_at	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	-1.48	0.223	1.75	0.302	1.32	0.449	-2.4	0.029	-0.2
1422695_at	Ttyh1 /// Taf1	tweety homolog 1 (Drosophila) /// TAF1 RNA polymerase II, TATA box binding pr	-1.3	0.693	1.46	0.415	1.52	0.414	-1.59	0.351	0.02
1443240_at	Gpc3	Glypican 3	-1.02	0.98	1.22	0.743	1.55	0.315	-1.43	0.517	0.08
1443850_at	---	Transcribed locus	2.53	0.06	-1.62	0.39	-1.65	0.302	2.66	0.181	0.48
1449530_at	Trps1	trichorhinophalangeal syndrome I (human)	1.33	0.283	1.72	0.079	-1.42	0.208	-1.89	0.157	-0.07
1419892_at	1110021J02Rik	RIKEN cDNA 1110021J02 gene	-1.67	0.4	-1.09	0.303	2.23	0.042	1.77	0.362	0.31
1450064_at	---	---	1.61	0.42	1.43	0.434	-1.4	0.18	-1.09	0.862	0.14
1441159_at	Med12l	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like	1.9	0.583	-1.03	0.932	-1.14	0.131	1.34	0.316	0.27
1427996_at	BC028528	cDNA sequence BC028528	1.36	0.013	1.44	0.182	-1.05	0.65	-2.24	0.095	-0.12
1431233_at	Cnnm4	cyclin M4	1.31	0.73	-1.51	0.391	1.77	0.443	-1.28	0.573	0.07
1446061_at	BC042698	CDNA sequence BC042698	1.85	0.571	-1.14	0.603	1.03	0.836	-1.36	0.719	0.09
1431236_at	Stk32b	serine/threonine kinase 32B	-1.13	0.572	1.71	0.062	1.15	0.68	-1.17	0.486	0.14
1445009_at	Slc9a8	Solute carrier family 9 (sodium/hydrogen exchanger), member 8	1.9	0.334	-1.21	0.708	1.03	0.907	-1.18	0.651	0.13
1430266_at	1700003D09Rik	RIKEN cDNA 1700003D09 gene	1.08	0.77	1.69	0.285	-1.02	0.979	-1.33	0.565	0.1
1432983_at	1700026H06Rik	RIKEN cDNA 1700026H06 gene	-1.74	0.596	1.39	0.509	1.79	0.189	-2.05	0.408	-0.15
1437409_s_at	Gpr126	G protein-coupled receptor 126	1.37	0.303	1.88	0.016	-2	0.01	-2	0.091	-0.19
1419616_at	Bmpr2	bone morphogenic protein receptor, type II (serine/threonine kinase)	-1.01	0.959	1.91	0.217	-1.17	0.392	1.03	0.927	0.19
1450253_a_at	Map3k4	mitogen activated protein kinase kinase kinase 4	1.29	0.595	-1.03	0.929	1.49	0.259	-1.09	0.753	0.16
1434255_at	Pacs2	phosphofurin acidic cluster sorting protein 2	1.56	0.203	1.44	0.509	-1.34	0.349	-1.07	0.662	0.15
1447162_at	---	---	1.62	0.302	1.29	0.046	-1.19	0.403	-1.04	0.663	0.17
1435672_at	3830612M24	hypothetical protein 3830612M24	-1.17	0.333	1.58	0.002	1.32	0.06	-1.57	0.191	0.04
1420748_a_at	Adat1	adenosine deaminase, tRNA-specific 1	1.62	0.231	1.31	0.091	-1.21	0.18	-1.17	0.513	0.14
1431669_at	4930583I09Rik	RIKEN cDNA 4930583I09 gene	-1.57	0.067	2.46	0.007	-1.52	0.239	1.37	0.537	0.19
1446600_at	---	---	-1.07	0.714	1.09	0.874	1.73	0.236	-1.07	0.896	0.17
1433785_at	Mobp	myelin-associated oligodendrocytic basic protein	-1.32	0.782	-1.21	0.762	2.17	0.335	1.95	0.071	0.4
1423280_at	Stmn2	stathmin-like 2	1.35	0.132	1.51	0.176	-1.11	0.604	-2.07	0.102	-0.08
1424004_x_at	4930444A02Rik	RIKEN cDNA 4930444A02 gene	1.05	0.484	1.73	0.086	-1.03	0.91	-1.54	0.228	0.05
1429072_at	1110001D15Rik	RIKEN cDNA 1110001D15 gene	1.51	0.526	-1.15	0.444	1.38	0.464	-1.99	0.092	-0.06
1427527_a_at	Pthlh	parathyroid hormone-like peptide	1.45	0.486	1.62	0.178	-1.45	0.549	-1.51	0.299	0.03
1439223_at	Tmod2	tropomodulin 2	1.31	0.754	1.54	0.556	-1.1	0.664	-1.24	0.738	0.13
1430388_a_at	Sulf2	sulfatase 2	1.27	0.024	-1.3	0.332	1.72	0.017	-1.29	0.52	0.1
1458064_at	Rnf34	Ring finger protein 34	-1.01	0.966	1.71	0.434	1.06	0.897	-1.07	0.788	0.17
1416011_x_at	Ehd1	EH-domain containing 1	-1.15	0.601	1.23	0.099	1.66	0.093	-1.13	0.621	0.15
1421134_at	Areg	amphiregulin	1.26	0.726	1.7	0.615	-1.25	0.455	-1.11	0.297	0.15
1456055_x_at	Pold1	polymerase (DNA directed), delta 1, catalytic subunit	-1.03	0.887	1.79	0.08	1	0.99	-1.23	0.079	0.13
1417522_at	Fbxo32	F-box only protein 32	-1.04	0.891	1.28	0.553	1.51	0.026	-2.23	0.205	-0.12
1428995_at	Oplah	5-oxoprolinase (ATP-hydrolysing)	-1.78	0.493	1.46	0.358	1.74	0.115	-1.38	0.592	0.01
1421006_at	Col4a6	procollagen, type IV, alpha 6	-1.12	0.693	1.2	0.78	1.67	0.113	-1.5	0.577	0.06
1427635_at	Kif5c	kinesin family member 5C	-1.57	0.375	1.57	0.501	1.56	0.469	-1.74	0.502	-0.04
1440085_at	Eda2r	ectodysplasin A2 isoform receptor	1.95	0.137	-1.13	0.444	-1.08	0.82	1.02	0.924	0.19
1420102_at	---	---	1.33	0.419	1.85	0.085	-1.71	0.045	-1.2	0.807	0.07
1459399_at	Slc31a2	Solute carrier family 31, member 2	-2.11	0.424	1.42	0.496	1.88	0.118	-2.44	0.314	-0.31
1422781_at	Tlr3	toll-like receptor 3	1.13	0.792	1.7	0.206	-1.07	0.458	-1.54	0.25	0.06
1431633_x_at	4930526L06Rik	RIKEN cDNA 4930526L06 gene	1.85	0.162	1.25	0.579	-1.51	0.399	-1.46	0.67	0.03

1440298_at	Treml2	triggering receptor expressed on myeloid cells-like 2	-1.97	0.083	1.73	0.292	1.53	0.191	-2.09	0.004	-0.2
1432889_at	4930466I24Rik	RIKEN cDNA 4930466I24 gene	-1.09	0.914	-1.14	0.813	1.97	0.105	1.01	0.95	0.19
1436225_at	Trpm2	transient receptor potential cation channel, subfamily M, member 2	-1.3	0.128	1.55	0.117	1.45	0.222	-1.05	0.886	0.16
1417741_at	Pygl	liver glycogen phosphorylase	-1.27	0.196	-1.22	0.058	2.15	0.094	1.41	0.467	0.27
1448250_at	9030425E11Rik	RIKEN cDNA 9030425E11 gene	1.12	0.383	1.68	0.092	-1.03	0.63	-1.13	0.716	0.16
1423537_at	Gap43	growth associated protein 43	1.19	0.783	1.59	0.059	-1.02	0.92	-2.01	0.372	-0.06
1431813_at	Myo18b	myosin XVIIIb	1.03	0.878	1.95	0.243	-1.27	0.702	-1.75	0.477	-0.01
1427612_at	Defb9	defensin beta 9	-2.12	0.022	-2.01	0.124	2.8	0.011	1.43	0.541	0.02
1443176_at	Sfmbt2	Scm-like with four mbt domains 2	-1.09	0.706	1.26	0.594	1.59	0.244	-1.35	0.455	0.1
1425581_s_at	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransfe	1.1	0.834	-1.01	0.954	1.68	0.253	-1.03	0.922	0.18
1418682_at	Tenr	testis nuclear RNA binding protein	1.12	0.629	1.8	0.24	-1.18	0.632	-1.98	0.436	-0.06
1437369_at	---	---	1.19	0.79	1.68	0.424	-1.11	0.652	-1.45	0.536	0.08
1426294_at	Hapln1	hyaluronan and proteoglycan link protein 1	2.08	0.198	-1.09	0.84	-1.3	0.513	1.19	0.619	0.22
1441758_at	Rhot1	ras homolog gene family, member T1	1.54	0.528	-1.32	0.566	1.47	0.391	-1.63	0.593	0.01
1446910_at	Sema5a	Sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmem	1.33	0.669	1.46	0.038	-1.02	0.946	-1.23	0.526	0.13
1421431_at	Ptrf	polymerase I and transcript release factor	-1.48	0.036	1.66	0.333	1.44	0.363	-1.18	0.646	0.11
1425925_at	Fcamr	Fc receptor, IgA, IgM, high affinity	1.17	0.807	-1.2	0.75	1.77	0.257	-1.42	0.564	0.08
1420743_a_at	Ppp3cc	protein phosphatase 3, catalytic subunit, gamma isoform	-1.15	0.569	1.62	0.001	1.28	0.203	-1.7	0.304	0.01
1458958_at	Nope	neighbor of Punc E11	-1.76	0.482	2.4	0.04	-1.24	0.588	2.42	0.012	0.45
1445323_at	Greb1	gene regulated by estrogen in breast cancer protein	1.83	0.312	-1.57	0.375	1.3	0.487	-1.31	0.638	0.06
1432514_at	1700066J24Rik	RIKEN cDNA 1700066J24 gene	1.17	0.818	1.63	0.4	-1.03	0.943	-1.29	0.337	0.12
1438116_x_at	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	-1.07	0.32	1.15	0.116	1.69	0.085	-1.66	0.172	0.03
1458764_at	---	---	-1.85	0.37	1.04	0.925	2.19	0.26	-1.6	0.23	-0.05
1441919_x_at	Crat	carnitine acetyltransferase	-1.29	0.086	-1.33	0.582	2.25	0.148	2.74	0.056	0.59
1458476_at	Eif2c3	eukaryotic translation initiation factor 2C, 3	1.35	0.235	1.61	0.29	-1.23	0.426	-1.48	0.04	0.06
1449245_at	Grin2c	glutamate receptor, ionotropic, NMDA2C (epsilon 3)	1.08	0.035	-1.65	0.374	2.09	0.254	-1.19	0.779	0.08
1417711_at	0610012D09Rik	RIKEN cDNA 0610012D09 gene	-1.44	0.361	1.83	0.354	1.25	0.533	-1.26	0.646	0.1
1459503_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-3.15	0.084	1.58	0.534	1.88	0.167	-1.18	0.707	-0.22
1450850_at	Vil2	villin 2	-1.02	0.681	1.19	0.301	1.61	0.031	-1.62	0.066	0.04
1450313_at	Tas1r2	taste receptor, type 1, member 2	-1.38	0.291	1.62	0.505	1.43	0.169	-1.54	0.002	0.03
1425405_a_at	Adar	adenosine deaminase, RNA-specific	1.28	0.494	-1.01	0.924	1.51	0.203	-1.27	0.216	0.13
1436058_at	Rsad2	radical S-adenosyl methionine domain containing 2	-1.06	0.797	-1.33	0.122	2.08	0.398	2.12	0.27	0.45
1447730_at	Sp2	Sp2 transcription factor	1.44	0.134	-1.56	0.113	1.7	0.482	-3.52	0.246	-0.49
1453504_at	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.95	0.27	-1.5	0.505	1.16	0.721	-1.86	0.39	-0.06
1420884_at	Sln	sarcolipin	1.08	0.81	1.89	0.449	-1.25	0.475	-1	0.994	0.18
1417603_at	Per2	period homolog 2 (Drosophila)	1.34	0.428	1.45	0.494	-1.01	0.95	-1.75	0.573	0.01
1433042_at	---	---	-1.24	0.354	1.25	0.726	1.72	0.348	-1.13	0.745	0.15
1454357_at	3110067C02Rik	RIKEN cDNA 3110067C02 gene	1.81	0.208	-1.62	0.253	1.35	0.16	-1.48	0.543	0.02
1456284_at	Gm905	gene model 905, (NCBI)	-1.32	0.005	1.34	0.586	1.68	0.213	-1.47	0.618	0.06
1425320_at	A830023I12Rik	RIKEN cDNA A830023I12 gene	1.9	0.117	1	0.999	-1.14	0.352	-1.14	0.557	0.16
1422434_a_at	2210010C04Rik	RIKEN cDNA 2210010C04 gene	1.74	0.313	-2.15	0.256	1.57	0.383	-1.57	0.683	-0.1
1423719_at	U46068	cDNA sequence U46068	1.08	0.837	-1.55	0.274	2.05	0.24	-2.73	0.027	-0.29
1457744_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	-1	1	1.8	0.104	-1.02	0.953	1.03	0.93	0.2
1457200_at	Serpinb9d	serine (or cysteine) peptidase inhibitor, clade B, member 9d	1.29	0.141	1.73	0.381	-1.32	0.338	-1.04	0.896	0.17
1447603_x_at	1700027J05Rik	RIKEN cDNA 1700027J05 gene	-1.25	0.683	2.14	0.136	-1.2	0.714	1.03	0.972	0.18
1424481_s_at	Armcx5	armadillo repeat containing, X-linked 5	-1.02	0.821	1.4	0.301	1.41	0.168	-1.49	0.11	0.07
1458727_at	Ptplb	Protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	2.31	0.154	-1.64	0.511	-1.16	0.833	1.08	0.829	0.15
1459330_at	Rpl31	Ribosomal protein L31	2.38	0.108	-1.52	0.475	-1.34	0.451	1.08	0.92	0.15
1419476_at	Adamdec1	ADAM-like, decysin 1	1	0.99	1.99	0.047	-1.27	0.057	-1.14	0.711	0.15
1429990_at	Hyal4	hyaluronoglucosaminidase 4	-1.21	0.307	-1.16	0.614	2.09	0.174	1.06	0.913	0.19
1415835_at	Csh2	chorionic somatomammotropin hormone 2	1.94	0.565	1.13	0.799	-1.41	0.571	-2.05	0.239	-0.1
1431828_a_at	Synj2	synaptojanin 2	1.1	0.602	-1.07	0.591	1.74	0.474	-1.98	0.416	-0.05
1449781_at	---	---	-3.16	0.365	1.21	0.826	2.25	0.22	-1	0.999	-0.17

1417379_at	Iqgap1	IQ motif containing GTPase activating protein 1	1.3	0.482	1.51	0.011	-1.03	0.825	-1.37	0.261	0.1
1446514_at	Dpp10	Dipeptidylpeptidase 10	1.11	0.591	2.02	0.21	-1.55	0.526	-1.43	0.629	0.04
1430308_at	5730409N16Rik	RIKEN cDNA 5730409N16 gene	1.12	0.685	-1.32	0.378	1.91	0.24	-1.45	0.603	0.06
1417036_at	Sac3d1	SAC3 domain containing 1	1.68	0.274	-1.27	0.682	1.32	0.404	-1.1	0.853	0.16
1429286_at	1190003M12Rik	RIKEN cDNA 1190003M12 gene	2.4	0.058	-1.54	0.382	-1.36	0.234	1.17	0.376	0.17
1449997_at	Tpm3	tropomyosin 3, gamma	1.51	0.397	-1.25	0.619	1.47	0.103	-1.74	0.233	0
1416340_a_at	Man2b1	mannosidase 2, alpha B1	-1.06	0.562	1.09	0.013	1.74	0	-1	0.989	0.19
1427503_at	AI324046	expressed sequence AI324046	1.09	0.758	-2.26	0.019	2.25	0.012	-3.7	0.161	-0.65
1437906_x_at	Txnl1	thioredoxin-like 1	2.23	0.462	1.15	0.797	-2.47	0.012	-1.94	0.322	-0.26
1439894_at	A730056I06Rik	RIKEN cDNA A730056I06 gene	-1.27	0.264	-1.78	0.279	2.44	0.024	1.43	0.173	0.2
1442301_at	AW060742	expressed sequence AW060742	1.94	0.045	-1.41	0.536	1.14	0.725	-1.45	0.343	0.05
1437895_at	Tmem16h	transmembrane protein 16H	-1.48	0.725	1.29	0.577	1.82	0.197	-1.25	0.753	0.1
1435098_at	LOC213332	similar to Na+ dependent glucose transporter 1	2.22	0.061	-2.17	0.355	1.1	0.611	-1.82	0.359	-0.16
1422596_at	C030019F02Rik	RIKEN cDNA C030019F02 gene	2.07	0.307	-1.33	0.458	-1.04	0.913	2.15	0.204	0.46
1436134_at	Scn2b	sodium channel, voltage-gated, type II, beta	1.38	0.158	1.68	0.118	-1.36	0.146	-1.47	0.186	0.05
1439130_at	Atg4d	autophagy-related 4D (yeast)	2.24	0.105	-1.16	0.842	-1.46	0.446	1.07	0.893	0.17
1443190_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930036L	-1.08	0.924	1.52	0.495	1.34	0.56	-1.4	0.279	0.1
1417230_at	Ralgps2	Ral GEF with PH domain and SH3 binding motif 2	1.23	0.271	-1.16	0.462	1.7	0.237	-2.44	0.038	-0.17
1441255_at	Cdh3	cadherin 3	1.24	0.716	-1.44	0.506	1.85	0.099	-1.77	0.029	-0.03
1440611_at	6230409E13Rik	RIKEN cDNA 6230409E13 gene	-1.58	0.176	1.01	0.923	2.14	0.017	-1.47	0.57	0.03
1439491_at	Lrrc38	leucine rich repeat containing 38	1.39	0.124	1.44	0.218	-1.04	0.657	-1.63	0.014	0.04
1437692_x_at	Anxa2	annexin A2	-1.19	0.118	2.29	0.04	-1.51	0.218	1.01	0.968	0.15
1437863_at	Bche	butyrylcholinesterase	1.81	0.337	-1.39	0.307	1.27	0.341	-2.36	0.082	-0.17
1436127_at	Crhbp	corticotropin releasing hormone binding protein	-1.08	0.931	-1.37	0.496	2.13	0.085	1.5	0.283	0.3
1445955_at	2400010G15Rik	RIKEN cDNA 2400010G15 gene	1.96	0.035	-1.33	0.455	1.08	0.753	-1.32	0.373	0.1
1420506_a_at	Stxbp1	syntaxin binding protein 1	-1.13	0.773	1.17	0.78	1.73	0.213	-1.16	0.625	0.15
1424581_at	Stac2	SH3 and cysteine rich domain 2	-1.36	0.308	1.85	0.173	1.2	0.605	-1.37	0.115	0.08
1439237_a_at	Ssh1	slingshot homolog 1 (Drosophila)	-1.77	0.379	-1.23	0.244	2.41	0.001	1.04	0.791	0.11
1443208_at	Gpr137b	G protein-coupled receptor 137B	1.3	0.424	1.74	0.152	-1.33	0.323	-1.03	0.952	0.17
1436262_x_at	Otud5	OTU domain containing 5	-1.79	0.636	2.52	0.007	-1.4	0.583	1.83	0.127	0.29
1455772_at	Pgr	progesterone receptor	1.14	0.754	-1.05	0.586	1.7	0.086	-1.38	0.518	0.1
1416516_at	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	-1.17	0.478	1.01	0.986	1.92	0.434	-1.45	0.386	0.08
1432229_a_at	Cdyl2	chromodomain protein, Y chromosome-like 2	1.16	0.539	1.73	0.187	-1.11	0.715	-2.05	0.03	-0.07
1415797_at	Ddr1	discoidin domain receptor family, member 1	-1.13	0.276	1.41	0.424	1.49	0.092	-1.26	0.438	0.13
1443479_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	1.16	0.554	-1.48	0.436	1.96	0.093	-2.97	0.236	-0.33
1420927_at	St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	-1.1	0.87	1.56	0.421	1.32	0.5	-1.63	0.513	0.04
1440396_at	Mpp6	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	2.21	0.097	-1.14	0.71	-1.42	0.029	1.53	0.299	0.3
1452962_at	Tmem25	transmembrane protein 25	-1.11	0.764	1.02	0.923	1.88	0.054	-1.04	0.929	0.18
1454134_at	5730412P04Rik	RIKEN cDNA 5730412P04 gene	-1.35	0.647	-1.09	0.913	2.13	0.035	1.81	0.193	0.38
1415954_at	Try4 /// Prss1 /// 18	trypsin 4 /// protease, serine, 1 (trypsin 1) /// RIKEN cDNA 1810049H19 gene /// tr	1.12	0.85	1.73	0.358	-1.06	0.887	-2.53	0.286	-0.19
1440080_at	Srpk2	Serine/arginine-rich protein specific kinase 2	-1.15	0.646	1.88	0.074	1.04	0.809	-1.41	0.319	0.09
1447095_at	C86942	expressed sequence C86942	1.39	0.386	-1.44	0.647	1.71	0.327	-1.06	0.594	0.15
1436346_at	Cd109	CD109 antigen	-1.74	0.323	2.23	0.154	-1.01	0.976	1.1	0.662	0.15
1419534_at	Olr1	oxidized low density lipoprotein (lectin-like) receptor 1	-1.24	0.565	2	0.046	-1.02	0.938	1.03	0.957	0.2
1420389_at	Pax3	paired box gene 3	-1.02	0.98	1.07	0.927	1.75	0.205	-1.2	0.314	0.15
1417314_at	Cfb	complement factor B	-1.02	0.528	1.04	0.713	1.78	0.204	-1.55	0.363	0.06
1419754_at	Myo5a	myosin Va	-1.5	0.063	1.76	0.229	1.37	0.196	-1.37	0.288	0.07
1445557_at	0610040B10Rik	RIKEN cDNA 0610040B10 gene	1.36	0.345	1.55	0.512	-1.12	0.784	-1.43	0.331	0.09
1440783_at	4930529M08Rik	RIKEN cDNA 4930529M08 gene	1.85	0.405	1.22	0.677	-1.39	0.422	-2.17	0.368	-0.12
1423410_at	Meig1	meiosis expressed gene 1	1.59	0.524	1.21	0.696	-1	0.997	-1.28	0.665	0.13
1432549_s_at	1700112M01Rik	RIKEN cDNA 1700112M01 gene	-1.07	0.597	2.44	0.046	-2.33	0.379	3.83	0.042	0.72
1431909_at	Zc3hav1	zinc finger CCCH type, antiviral 1	2.23	0.483	-1.38	0.388	-1.19	0.693	1.27	0.369	0.23
1417061_at	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	-1.24	0.015	1.23	0.121	1.76	0.211	-1.12	0.754	0.16

1423355_at	Snap29	synaptosomal-associated protein	1.1	0.391	-1.05	0.856	1.75	0.243	-1.15	0.761	0.16
1448408_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	-1.11	0.388	1.27	0.035	1.63	0.1	-1.63	0.257	0.04
1456028_x_at	Marcks	Myristoylated alanine rich protein kinase C substrate	1.26	0.543	1.56	0.053	-1.02	0.923	-1.41	0.373	0.1
1432941_at	5730408A14Rik	RIKEN cDNA 5730408A14 gene	-1.78	0.381	2.86	0.187	-2.62	0.05	2.48	0.104	0.23
1419696_at	Cd4	CD4 antigen	1.3	0.346	-1	0.999	1.5	0.393	-1.29	0.682	0.13
1428571_at	Col9a1	procollagen, type IX, alpha 1	1.63	0.483	1.2	0.649	-1.03	0.944	-2.26	0.15	-0.12
1421409_at	Msi1	Musashi homolog 1(Drosophila)	-1.41	0.45	1.03	0.939	2.06	0.247	-1.87	0.325	-0.05
1433456_at	AU022751	expressed sequence AU022751	1.99	0.122	-1.07	0.916	-1.15	0.412	1.5	0.037	0.32
1443564_at	---	---	1.3	0.546	-1.08	0.763	1.58	0.241	-2.62	0.174	-0.21
1450846_at	Bzw1	basic leucine zipper and W2 domains 1	1.12	0.752	-1.14	0.745	1.81	0.363	-1.37	0.6	0.1
1441589_at	Scap1	Src family associated phosphoprotein 1	1.46	0.391	1.54	0.514	-1.24	0.3	-2.52	0.08	-0.19
1417282_at	Mmp23	matrix metallopeptidase 23	-1.1	0.418	1.43	0.449	1.46	0.134	-1.18	0.342	0.15
1426938_at	Nova1 /// LOC6648	neuro-oncological ventral antigen 1 /// similar to neuro-oncological ventral antigen	1.06	0.916	1.78	0.263	-1.04	0.892	-1	0.988	0.2
1441627_at	Ebf1	Early B-cell factor 1	1.9	0.34	1.04	0.939	-1.16	0.743	-2.47	0.14	-0.17
1437097_at	Zbed3	zinc finger, BED domain containing 3	-1.8	0.298	1.51	0.454	1.74	0.321	-1.02	0.932	0.11
1420243_at	Zfhx1a	zinc finger homeobox 1a	1.21	0.847	-1.32	0.257	1.84	0.335	-1.26	0.59	0.12
1438962_s_at	Ddx31	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 31	-1.04	0.928	1.26	0.469	1.58	0.041	-1.7	0.329	0.03
1449713_at	Cbx7	Chromobox homolog 7	1.41	0.269	1.47	0.051	-1.08	0.727	-1.36	0.231	0.11
1427195_at	---	Mus musculus, clone IMAGE:3983419, mRNA	-1.09	0.681	2.05	0.021	-1.19	0.162	1.25	0.098	0.25
1425675_s_at	Ceacam1	CEA-related cell adhesion molecule 1	1.87	0.053	-1.18	0.195	1.08	0.8	-1.21	0.491	0.14
1442544_at	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	-1.87	0.197	1.81	0.025	1.46	0.211	-1.82	0.148	-0.11
1441851_x_at	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	-1.26	0.785	1.64	0.414	1.37	0.452	-1.32	0.292	0.11
1448231_at	Fkbp5	FK506 binding protein 5	-1.12	0.888	1.07	0.907	1.84	0.337	-1.32	0.174	0.12
1440782_at	Scap1	src family associated phosphoprotein 1	-1.03	0.891	1.65	0.383	1.18	0.708	-1.83	0.158	-0.01
1425393_a_at	Map2k7	mitogen activated protein kinase kinase 7	1.56	0.076	-1.43	0.509	1.55	0.289	-2.15	0.315	-0.12
1422566_at	Tcfeb	transcription factor EB	-1.05	0.873	1.47	0.127	1.38	0.218	-1.54	0.251	0.07
1445206_at	Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	2.11	0.138	1.37	0.632	-3.04	0	-1.18	0.541	-0.19
1427417_at	Scml4	sex comb on midleg-like 4 (Drosophila)	-1.15	0.757	1.23	0.624	1.7	0.102	-2.77	0.131	-0.24
1455837_at	Trim36	tripartite motif-containing 36	-2.13	0.142	1.77	0.458	1.57	0.328	-1.15	0.6	0.01
1452555_at	LOC667141 /// LOC	hypothetical protein LOC667141 /// hypothetical protein LOC671961 /// hypothetic	-1.82	0.596	2.63	0.108	-1.6	0.513	1.55	0.545	0.19
1421797_a_at	Snx12	sorting nexin 12	-1	0.977	1.38	0.324	1.43	0.205	-1.24	0.229	0.14
1445065_at	Atp11c	Atpase, class VI, type 11C	1.53	0.306	-1.19	0.713	1.43	0.673	-1.41	0.747	0.09
1419221_a_at	Rgs14	regulator of G-protein signaling 14	-1.15	0.136	1.16	0.424	1.78	0.074	-1.32	0.359	0.12
1447389_at	AI662168	expressed sequence AI662168	1.98	0.185	-1.02	0.96	-1.17	0.541	1.22	0.788	0.25
1451374_x_at	Cklf	chemokine-like factor	1.1	0.738	1.88	0.056	-1.2	0.243	-1.29	0.407	0.12
1416266_at	Pdyn	prodynorphin	-1.53	0.35	1.08	0.879	2.08	0.039	-1.72	0.443	-0.02
1441434_at	2810426N06Rik	RIKEN cDNA 2810426N06 gene	-1.68	0.249	2.35	0.092	-1.16	0.586	1.48	0.535	0.25
1421668_x_at	Speer3	spermatogenesis associated glutamate (E)-rich protein 3	-3.4	0.076	2.02	0.175	1.49	0.336	-1.37	0.68	-0.31
1458780_at	D8Ertd620e	DNA segment, Chr 8, ERATO Doi 620, expressed	-2.65	0.169	1.28	0.562	2.16	0.041	-1.19	0.845	-0.1
1454589_at	9430006E15Rik	RIKEN cDNA 9430006E15 gene	1.79	0.12	1.08	0.778	-1.05	0.802	-1.23	0.305	0.14
1454897_at	6330509M05Rik	RIKEN cDNA 6330509M05 gene	-1.25	0.711	1.84	0.26	1.17	0.617	-2.59	0.054	-0.21
1436557_at	Krt73	keratin 73	-2.09	0.222	1.85	0.34	1.49	0.156	-1.27	0.67	-0.01
1454832_at	Phactr1	phosphatase and actin regulator 1	-1.03	0.843	2.12	0.179	-1.37	0.297	1.02	0.917	0.18
1432561_at	4930569F06Rik	RIKEN cDNA 4930569F06 gene	1.6	0.008	1.61	0.421	-1.65	0.428	-1.06	0.754	0.12
1452029_a_at	Purg	purine-rich element binding protein G	1.44	0.67	1.72	0.23	-1.53	0.227	-1.2	0.628	0.11
1434090_at	4930429A22Rik	RIKEN cDNA 4930429A22 gene	1.34	0.385	-1.46	0.258	1.79	0.311	-1.24	0.599	0.11
1430135_at	Dnase2a	deoxyribonuclease II alpha	1.57	0.117	1.26	0.166	-1.02	0.705	-1.12	0.662	0.17
1432584_at	1110004M10Rik	RIKEN cDNA 1110004M10 gene	1.85	0.525	-1.07	0.667	1.03	0.968	-1.19	0.804	0.15
1420610_at	Prkacb	protein kinase, cAMP dependent, catalytic, beta	1.19	0.374	-1.05	0.907	1.67	0.139	-2.15	0.382	-0.08
1422455_s_at	Nsf	N-ethylmaleimide sensitive fusion protein	-1.15	0.226	1.16	0.566	1.78	0.132	-1.07	0.739	0.18
1420233_at	---	---	-1.34	0.211	1.78	0.041	1.29	0.179	-1.1	0.401	0.16
1437318_at	Pak3	p21 (CDKN1A)-activated kinase 3	1.95	0.234	-1.06	0.882	-1.08	0.861	1.19	0.737	0.25
1447260_at	H2-Bl /// 2410017I1	histocompatibility 2, blastocyst /// RIKEN cDNA 2410017I17 gene /// similar to MH	-1.45	0.431	2.11	0.066	1.01	0.89	-1.17	0.35	0.13

1445522_at	Atp8b4	ATPase, class I, type 8B, member 4	-1.23	0.656	1.03	0.959	1.97	0.118	-1.19	0.496	0.15
1424041_s_at	C1s	complement component 1, s subcomponent	1.64	0.196	1.22	0.265	-1.04	0.893	-1.42	0.346	0.1
1440210_at	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	-1.9	0.593	2.19	0.364	1.1	0.767	-1.17	0.829	0.06
1427419_x_at	Ccr9	chemokine (C-C motif) receptor 9	1.83	0.316	1.23	0.753	-1.33	0.455	-4.26	0.041	-0.63
1434349_at	Vars2l	valyl-tRNA synthetase 2-like	1.29	0.403	-1.02	0.952	1.55	0.137	-1.31	0.359	0.13
1416002_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	-1.32	0.289	1.17	0.318	1.89	0.009	-1.32	0.308	0.1
1452684_at	Akt1s1	AKT1 substrate 1 (proline-rich)	-1.05	0.936	-1.19	0.531	2.02	0.18	1.24	0.452	0.26
1421913_at	Mrpl19	mitochondrial ribosomal protein L19	1.31	0.363	-1.2	0.545	1.68	0.206	-1.05	0.725	0.18
1443266_at	Npc2	Niemann Pick type C2	2	0.181	1.17	0.729	-1.53	0.08	-1.39	0.512	0.06
1445482_at	---	Transcribed locus	1.22	0.712	1.61	0.384	-1	0.992	-1.67	0.5	0.04
1449337_at	Tdo2	tryptophan 2,3-dioxygenase	1.47	0.736	-1.24	0.195	1.54	0.019	-1.19	0.428	0.15
1437165_a_at	Pcolce	procollagen C-endopeptidase enhancer protein	1.23	0.494	1.64	0.011	-1.05	0.853	-1.01	0.935	0.2
1433230_at	5730415C11Rik	RIKEN cDNA 5730415C11 gene	1.47	0.257	1.6	0.466	-1.33	0.452	-1.05	0.919	0.17
1452564_at	Ofa	oncofetal antigen	1.49	0.419	1.78	0.265	-1.8	0.383	-1.2	0.59	0.07
1424383_at	Tmem51	transmembrane protein 51	-1.25	0.13	1.82	0.026	1.2	0.202	-1.41	0.275	0.09
1444152_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	2.01	0.231	1.12	0.828	-1.43	0.087	-1.81	0.186	-0.03
1441640_at	Socs5	Suppressor of cytokine signaling 5	1.12	0.61	2.02	0.33	-1.46	0.018	-1.89	0.331	-0.05
1438629_x_at	Grn	granulin	-1.04	0.705	1.3	0.12	1.56	0.001	-1	0.982	0.2
1459290_at	C030015D19Rik	RIKEN cDNA C030015D19 gene	-1.36	0.715	1.57	0.407	1.52	0.22	-1.21	0.746	0.13
1430454_x_at	Bcl2l2	Bcl2-like 2	1.8	0.082	1.09	0.873	-1.07	0.91	-2.33	0.002	-0.13
1459693_x_at	Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polyp	1.65	0.36	1.26	0.483	-1.09	0.819	-2.34	0.327	-0.13
1437299_at	Nalp4f	NACHT, leucine rich repeat and PYD containing 4F	1.99	0.004	-1.2	0.538	1.01	0.99	-1.45	0.621	0.09
1425721_at	Phip	pleckstrin homology domain interacting protein	2.01	0.18	-1.39	0.386	1.1	0.759	-1.56	0.089	0.04
1450237_at	Dnase2b	deoxyribonuclease II beta	2.18	0.447	1.04	0.736	-1.63	0.337	-1.29	0.695	0.07
1459911_at	Cdr2l	cerebellar degeneration-related protein 2-like	1.92	0.197	-1.02	0.974	-1.08	0.51	1.12	0.805	0.23
1433105_at	5830438M01Rik	RIKEN cDNA 5830438M01 gene	1.1	0.893	-1.75	0.294	2.16	0.167	-1.41	0.581	0.02
1417870_x_at	Ctsz	cathepsin Z	-1.01	0.708	1.27	0.103	1.57	0.021	-1.53	0.249	0.07
1420940_x_at	Rgs5	regulator of G-protein signaling 5	-1.04	0.495	1.5	0.241	1.37	0.014	-1.05	0.893	0.2
1422390_at	V1rc5	vomeronasal 1 receptor, C5	-1.09	0.894	-1.29	0.161	2.14	0.245	1.17	0.829	0.23
1437673_at	---	Transcribed locus	1.21	0.474	1.97	0.283	-1.53	0.203	-2.68	0.031	-0.26
1446561_at	Pax8	paired box gene 8	1.21	0.797	-1.31	0.388	1.86	0.024	-1.2	0.371	0.14
1417543_at	Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	1.37	0.283	-1.04	0.927	1.5	0.257	-1.63	0.274	0.05
1439588_at	Slco5a1	solute carrier organic anion transporter family, member 5A1	-1.11	0.09	1.76	0.237	1.17	0.208	-1.29	0.46	0.13
1451419_at	Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	1	0.993	-1.28	0.645	2.05	0.02	-1.04	0.94	0.18
1451158_at	Trip12	thyroid hormone receptor interactor 12	1.32	0.097	-1.08	0.9	1.59	0.405	-1.57	0.473	0.06
1442795_x_at	1700016G05Rik	RIKEN cDNA 1700016G05 gene	-1.05	0.959	1.35	0.584	1.53	0.148	-1.41	0.675	0.1
1425387_at	Akr1c20	aldo-keto reductase family 1, member C20	2	0.055	-1.17	0.226	-1.02	0.965	1.27	0.696	0.27
1443709_at	Ypel2	Yippee-like 2 (Drosophila)	-1.32	0.172	1.44	0.44	1.64	0.183	-1.44	0.499	0.08
1434674_at	Lyst	lysosomal trafficking regulator	1.12	0.575	-1.05	0.681	1.75	0.032	-1.59	0.186	0.06
1455909_at	9530002K18Rik	RIKEN cDNA 9530002K18 gene	-1.56	0.296	2.08	0.079	1.12	0.811	-2.02	0.156	-0.1
1459382_at	Dock2	Dedicator of cyto-kinesis 2	-1.17	0.794	1.85	0.465	1.12	0.6	-1.82	0.114	0
1451836_at	BC022651	cDNA sequence BC022651	-1.21	0.584	-1.88	0.37	2.47	0.161	1.11	0.834	0.12
1445187_at	9430070O13Rik	RIKEN cDNA 9430070O13 gene	-1.28	0.723	2.6	0.132	-2.17	0.177	1.04	0.95	0.05
1427369_at	Nalp6	NACHT, leucine rich repeat and PYD containing 6	1.02	0.623	-1.09	0.598	1.89	0.062	-1.34	0.204	0.12
1456179_at	---	---	1.61	0.343	-1.01	0.981	1.24	0.632	-1.28	0.317	0.14
1431691_a_at	Rab31	RAB31, member RAS oncogene family	-1	0.998	1.44	0.386	1.4	0.452	-1.26	0.381	0.15
1453492_at	Tmem67	transmembrane protein 67	-2.16	0.14	1.19	0.662	2.19	0.323	-1.16	0.715	0.01
1440721_at	5930433N17Rik	RIKEN cDNA 5930433N17 gene	1.18	0.482	1.99	0.068	-1.51	0.073	-1.93	0.13	-0.07
1436607_a_at	C330002I19Rik /// L	RIKEN cDNA C330002I19 gene /// similar to kinase D-interacting substance 220	1.32	0.579	-1.41	0.501	1.81	0.34	-1.01	0.955	0.18
1453646_at	3110005L21Rik	RIKEN cDNA 3110005L21 gene	1.28	0.712	1.56	0.433	-1.01	0.986	-1.33	0.758	0.13
1416040_at	Lipf	lipase, gastric	-2.48	0.333	1.11	0.832	2.33	0.126	-2.04	0.257	-0.27
1450906_at	Plxnc1	plexin C1	-1.86	0.062	1.91	0.136	1.39	0.337	-1.32	0.455	0.03
1441508_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930026H04 product	1.32	0.554	1.87	0.327	-1.54	0.27	-1.19	0.675	0.11

1416876_at	Parvg	parvin, gamma	-1.47	0.608	1.25	0.64	1.91	0.213	-1.52	0.509	0.04
1421607_at	Vgll1	vestigial like 1 homolog (Drosophila)	-1.49	0.489	2.76	0.023	-2.48	0.199	1.32	0.673	0.03
1445829_at	8030491N06Rik	RIKEN cDNA 8030491N06 gene	1.65	0.343	1.23	0.728	-1.04	0.936	-1.12	0.814	0.18
1429867_at	4933424C08Rik	RIKEN cDNA 4933424C08 gene	-1	0.961	-1.09	0.82	1.93	0.001	1.09	0.773	0.23
1440275_at	Runx3	runt related transcription factor 3	1.13	0.475	-1.04	0.947	1.75	0.03	-1.48	0.238	0.09
1457659_x_at	Odf1	outer dense fiber of sperm tails 1	1.86	0.376	1.14	0.69	-1.19	0.661	-3.2	0.072	-0.35
1431583_at	0610038L08Rik	RIKEN cDNA 0610038L08 gene	1.2	0.485	1.77	0.381	-1.14	0.582	-2.39	0.05	-0.14
1430671_a_at	0610010K06Rik	RIKEN cDNA 0610010K06 gene	1.62	0.44	-1.56	0.406	1.58	0.533	-1.71	0.365	-0.02
1440585_at	Stx6	Syntaxin 6	1.25	0.225	2.06	0.197	-1.88	0.039	-1.63	0.428	-0.05
1417755_at	Topors	topoisomerase I binding, arginine/serine-rich	1.67	0.192	-1.46	0.152	1.49	0.193	-1.25	0.63	0.11
1431821_a_at	Eps8l1	EPS8-like 1	1.1	0.685	1.77	0.37	-1.03	0.872	-1.19	0.696	0.16
1420790_x_at	Klra16	killer cell lectin-like receptor, subfamily A, member 16	1.25	0.751	2.06	0.237	-1.89	0.275	-1.34	0.58	0.02
1431547_at	4930435F18Rik	RIKEN cDNA 4930435F18 gene	-2.57	0.025	1.95	0.178	1.51	0.488	-1.2	0.783	-0.08
1453694_at	4631402N15Rik	RIKEN cDNA 4631402N15 gene	1.67	0.545	-1.15	0.522	1.31	0.432	-1.17	0.355	0.16
1426506_at	Evi2a /// Evi2b	ecotropic viral integration site 2a /// ecotropic viral integration site 2b	1.11	0.629	-1.13	0.761	1.85	0.164	-1.67	0.03	0.04
1447903_x_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1.08	0.739	1.82	0.082	-1.07	0.704	-1.16	0.596	0.17
1434809_at	Arhgap28	Rho GTPase activating protein 28	-1.05	0.824	1.8	0.122	1.09	0.587	-1.76	0.075	0.02
1459030_at	---	---	-1.12	0.802	-1.33	0.215	2.2	0.178	1.07	0.839	0.21
1436591_at	BC023744	cDNA sequence BC023744	-1.05	0.644	1.83	0.108	1.06	0.627	-1.04	0.814	0.2
1423089_at	Tmod3	tropomodulin 3	1.36	0.442	-1.02	0.955	1.51	0.373	-2.1	0.332	-0.06
1441759_at	Cd82	CD82 antigen	-1.22	0.21	1.22	0.498	1.81	0.288	-1.17	0.56	0.16
1444986_at	---	---	1.34	0.521	1.64	0.441	-1.15	0.431	-1.21	0.492	0.15
1448171_at	Siah2	seven in absentia 2	-1.02	0.774	1.04	0.424	1.83	0.215	-1.08	0.407	0.19
1429022_at	Adcyap1r1	adenylate cyclase activating polypeptide 1 receptor 1	1.19	0.439	-1.39	0.587	1.94	0.259	-1.82	0.495	-0.02
1419538_at	Flt3	FMS-like tyrosine kinase 3	1.48	0.119	1.38	0.692	-1.01	0.971	-2.07	0.125	-0.06
1426562_a_at	Olfm1	olfactomedin 1	1.51	0.033	-1.23	0.654	1.52	0.088	-1.49	0.372	0.08
1435408_at	2700092H06Rik	RIKEN cDNA 2700092H06 gene	1.45	0.396	1.43	0.499	-1.03	0.928	-1.82	0.241	0.01
1446766_at	AU022746	expressed sequence AU022746	-1.85	0.434	2.03	0.059	1.28	0.46	-1.74	0.303	-0.07
1441264_x_at	A930005H10Rik	RIKEN cDNA A930005H10 gene	1.54	0.184	-1.07	0.572	1.37	0.151	-2.58	0.023	-0.18
1430116_at	6030422M01Rik	RIKEN cDNA 6030422M01 gene	-1	0.993	1.43	0.166	1.43	0.136	-1.12	0.517	0.18
1426772_x_at	Tcrb-J /// Tcrb-V13	T-cell receptor beta, joining region /// T-cell receptor beta, variable 13 /// similar to	1.53	0.4	1.33	0.499	-1.01	0.883	-3.27	0.037	-0.35
1421760_at	Ptcra	pre T-cell antigen receptor alpha	-1.25	0.705	2.5	0.161	-1.8	0.131	1.2	0.746	0.16
1433202_at	6030400A10Rik	RIKEN cDNA 6030400A10 gene	1.16	0.856	2.15	0.024	-1.85	0.145	-1.1	0.808	0.09
1426008_a_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	1.45	0.081	-1.13	0.477	1.52	0.13	-1.32	0.288	0.13
1437956_at	BB220380	expressed sequence BB220380	-1.29	0.057	2.03	0.007	1.05	0.637	-1.1	0.677	0.17
1419086_at	Fgfbp1	fibroblast growth factor binding protein 1	1.2	0.718	1.89	0.272	-1.31	0.386	-1.95	0.315	-0.04
1453949_s_at	Lypla1	lysophospholipase 1	1.24	0.536	-1.16	0.662	1.76	0.229	-1.04	0.914	0.2
1457934_at	Rbm12	RNA binding motif protein 12	2.38	0.12	-1.85	0.198	-1.08	0.474	1.15	0.548	0.15
1425637_at	---	---	1.73	0.267	1.6	0.419	-1.89	0.245	-1.42	0.426	0
1424626_at	2010003K11Rik	RIKEN cDNA 2010003K11 gene	-1.24	0.299	2.13	0.018	-1.09	0.77	1.02	0.815	0.21
1455067_at	Psd4	pleckstrin and Sec7 domain containing 4	-1.51	0.358	2.09	0.003	1.11	0.38	-1.62	0.072	0.02
1451023_at	Hcn3	hyperpolarization-activated, cyclic nucleotide-gated K+ 3	1.37	0.33	-1.26	0.007	1.7	0.027	-1.15	0.648	0.16
1455761_at	---	---	1.43	0.103	1.49	0.337	-1.06	0.8	-1.28	0.055	0.14
1440878_at	Runx1	runt related transcription factor 1	1.41	0.632	1.79	0.318	-1.52	0.016	-1.24	0.153	0.11
1453489_at	1700020O03Rik	RIKEN cDNA 1700020O03 gene	1.62	0.158	1.41	0.407	-1.21	0.202	-1.04	0.864	0.2
1434727_at	2900042E01Rik	RIKEN cDNA 2900042E01 gene	1.59	0.422	1.29	0.083	-1.02	0.936	-1.73	0.392	0.03
1423305_at	Extl1	exostoses (multiple)-like 1	-1.49	0.184	2.07	0.011	1.12	0.646	-1.68	0.076	0
1458145_at	Rora	RAR-related orphan receptor alpha	1.49	0.131	-1.11	0.859	1.47	0.221	-1.05	0.795	0.2
1458680_at	Hephl1	Hephaestin-like 1	1.61	0.249	1.42	0.637	-1.2	0.656	-2.17	0.037	-0.09
1425391_a_at	Osbpl5	oxysterol binding protein-like 5	1.06	0.607	1.91	0.301	-1.12	0.286	-1.49	0.38	0.09
1447857_at	---	---	-1.64	0.626	2.31	0.373	-1.06	0.874	1.45	0.414	0.27
1458863_at	6330415G19Rik	RIKEN cDNA 6330415G19 gene	1.69	0.295	-1	0.998	1.18	0.609	-1.24	0.342	0.15
1458021_at	Snx15	Sorting nexin 15	2.17	0.072	-1.1	0.728	-1.27	0.262	1.42	0.437	0.3

1423310_at	Tpbg	trophoblast glycoprotein	1.75	0.469	1.64	0.343	-2.09	0.042	-2.74	0.108	-0.36
1448826_at	Myh6	myosin, heavy polypeptide 6, cardiac muscle, alpha	1.05	0.719	-1.65	0.395	2.21	0.153	-1.14	0.804	0.12
1438702_at	---	---	1.53	0.466	1.39	0.18	-1.07	0.747	-1.07	0.887	0.2
1428012_at	C8a	complement component 8, alpha polypeptide	1.83	0.037	1.34	0.576	-1.44	0.554	-3.12	0.447	-0.35
1435752_s_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	1.34	0.031	1.58	0.092	-1.06	0.781	-1.04	0.339	0.21
1451737_at	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	-1.09	0.415	-1.46	0.135	2.26	0.092	1.62	0.219	0.33
1459599_at	---	---	1.15	0.039	2.24	0.418	-2.13	0.01	-1.52	0.653	-0.06
1440202_at	LOC622175	similar to gonadotropin inducible ovarian transcription factor 2	1.8	0.051	-1.03	0.919	1.1	0.756	-1.38	0.099	0.12
1443418_at	Prps2	Phosphoribosyl pyrophosphate synthetase 2	1.44	0.586	1.88	0.365	-1.83	0.197	-1.16	0.849	0.08
1455724_at	---	2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, cl	1.2	0.655	1.82	0	-1.18	0.338	-1.06	0.708	0.19
1455125_at	Centb1	centaurin, beta 1	-1.14	0.829	1.75	0.272	1.24	0.454	-1.53	0.102	0.08
1454306_at	LOC672445	similar to RIKEN cDNA 1190002C06 gene	1.78	0.565	1.5	0.564	-1.71	0.168	-1.72	0.529	-0.04
1435375_at	BC052328	cDNA sequence BC052328	1.47	0.298	1.58	0.08	-1.23	0.299	-1.31	0.533	0.13
1452379_at	Auts2	autism susceptibility candidate 2	1.31	0.294	-1.25	0.764	1.76	0.095	-1.6	0.049	0.06
1420670_at	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	1.33	0.605	1.62	0.443	-1.09	0.84	-2.38	0.183	-0.13
1460514_s_at	Ascl2	achaete-scute complex homolog-like 2 (Drosophila)	1.25	0.464	-1.11	0.713	1.71	0.089	-1.01	0.989	0.21
1430002_at	Iqcf1	IQ motif containing F1	2.33	0.092	-2.1	0.412	1.06	0.795	-2.42	0.183	-0.28
1450823_at	Og9x	OG9 homeobox gene	-1.24	0.801	2.3	0.328	-1.31	0.489	1.1	0.858	0.21
1419836_at	---	---	-1.14	0.796	-1.07	0.854	2.06	0.376	2.34	0.264	0.55
1445808_at	---	---	1.03	0.935	2.24	0.018	-1.66	0.251	-2.44	0.127	-0.21
1442792_x_at	4930471M23Rik	RIKEN cDNA 4930471M23 gene	-1.1	0.865	1.57	0.224	1.39	0.556	-1.32	0.441	0.14
1439663_at	Ptch1	Patched homolog 1	1.41	0.296	1.84	0.186	-1.6	0.034	-1.27	0.741	0.1
1432305_at	4930542C16Rik	RIKEN cDNA 4930542C16 gene	-2.44	0.495	1.57	0.406	1.89	0.303	-1.56	0.469	-0.13
1429396_at	Atg16l2	autophagy related 16 like 2 (S. cerevisiae)	-1.02	0.803	1.75	0.049	1.14	0.245	-2.17	0.036	-0.07
1460279_a_at	Gtf2i /// LOC66900	general transcription factor II I /// similar to General transcription factor II-I (GTFII-	1.23	0.542	-1.1	0.701	1.73	0.171	-1.09	0.843	0.19
1447257_at	Taok3	TAO kinase 3	1.12	0.581	2.05	0.125	-1.42	0.097	-1.47	0.002	0.07
1417411_at	Nap1l5	nucleosome assembly protein 1-like 5	-1.17	0.452	1.67	0.406	1.35	0.36	-2.07	0.13	-0.06
1447810_x_at	Plekhb2	pleckstrin homology domain containing, family B (evectins) member 2	-1.11	0.875	1.97	0.112	1.01	0.974	-1.61	0.525	0.06
1450235_at	Fgd3	FYVE, RhoGEF and PH domain containing 3	1.62	0.427	-2.38	0.043	1.83	0.067	-1.26	0.216	-0.05
1458117_at	Garnl1	GTPase activating RANGAP domain-like 1	1.78	0.352	1.46	0.421	-1.57	0.005	-1.02	0.973	0.16
1455795_at	Sart2	squamous cell carcinoma antigen recognized by T cells 2	1.36	0.282	1.91	0.006	-1.63	0.027	-1.25	0.55	0.09
1443518_at	Sgce	sarcoglycan, epsilon	-1.19	0.278	2.23	0.043	-1.24	0.268	1.11	0.844	0.23
1428393_at	Nrn1	neuritin 1	1.74	0.348	-1.2	0.12	1.3	0.149	-1.2	0.207	0.16
1418731_at	Rnf12	ring finger protein 12	1.14	0.879	1.8	0.039	-1.07	0.891	-1.23	0.678	0.16
1416318_at	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	-1.58	0.019	2.03	0.458	1.22	0.605	-1.98	0.002	-0.08
1418403_at	Adam19	a disintegrin and metallopeptidase domain 19 (meltrin beta)	1.67	0.512	-1.7	0.216	1.62	0.037	-1.22	0.214	0.09
1421257_at	Pigb	phosphatidylinositol glycan anchor biosynthesis, class B	1.67	0.233	1.47	0.283	-1.35	0.378	-1.25	0.204	0.13
1446527_at	Agtr1b	angiotensin II receptor, type 1b	-2.71	0.014	2.74	0.234	-1.3	0.388	1.07	0.889	-0.05
1454869_at	Wdr40b	WD repeat domain 40B	-1.03	0.859	1.01	0.99	1.91	0.248	-1.29	0.662	0.15
1443010_at	Fbxw11	F-box and WD-40 domain protein 11	1.1	0.303	2.03	0.092	-1.32	0.032	-1.31	0.456	0.12
1445764_at	---	PREDICTED: Mus musculus hypothetical protein LOC628151 (LOC628151), mR	1.02	0.959	2.03	0.348	-1.2	0.793	-1.11	0.774	0.19
1417550_a_at	Gsg1	germ cell-specific gene 1	1.77	0.265	-1.09	0.889	1.19	0.573	-2.2	0.197	-0.08
1451766_at	Cdh11	cadherin 11	-1.16	0.83	-1.47	0.457	2.34	0.021	1.72	0.263	0.36
1443504_at	E330022O07	hypothetical protein E330022O07	-1.44	0.627	2.71	0.097	-2.1	0.171	1.29	0.633	0.11
1422990_at	Met	met proto-oncogene	1.3	0.479	-1.07	0.888	1.65	0.424	-1.11	0.864	0.19
1415822_at	Scd2	stearoyl-Coenzyme A desaturase 2	-1.09	0.722	1.9	0.016	1.07	0.615	-1.51	0.035	0.09
1439157_at	D330012D11Rik	RIKEN cDNA D330012D11 gene	1.81	0.199	-1.22	0.59	1.25	0.604	-1.42	0.601	0.11
1433508_at	Klf6	Kruppel-like factor 6	1.08	0.535	1.95	0.014	-1.16	0.462	-1.24	0.334	0.16
1451852_at	Tcstv3	2-cell-stage, variable group, member 3	-1.85	0.393	1.93	0.264	1.41	0.414	-3.16	0.001	-0.42
1460658_at	Ap1g1	Adaptor protein complex AP-1, gamma 1 subunit	1.64	0.4	1.33	0.014	-1.09	0.574	-1.36	0.655	0.13
1426699_at	AU040320	expressed sequence AU040320	1.25	0.506	-1.35	0.588	1.89	0.239	-1.84	0.362	-0.01
1416326_at	Crip1	cysteine-rich protein 1 (intestinal)	1.36	0.098	1.69	0.07	-1.21	0.112	-2.02	0.129	-0.04
1420025_s_at	LOC637741	hypothetical protein LOC637741	-1.27	0.711	1.75	0.238	1.35	0.489	-1.92	0.201	-0.02

1422762_at	Kif17	kinesin family member 17	-2.61	0.063	1.32	0.713	2.18	0.005	-2.79	0.245	-0.48
1424976_at	Rhov	ras homolog gene family, member V	-1.18	0.473	1.55	0.322	1.49	0.436	-1.1	0.891	0.19
1446032_at	---	---	1.08	0.815	2.02	0.294	-1.28	0.66	-1.27	0.709	0.14
1428355_at	Osbp2	oxysterol binding protein 2	-1.06	0.435	1.63	0.395	1.31	0.678	-1.29	0.206	0.15
1460298_at	4930483J18Rik	RIKEN cDNA 4930483J18 gene	1.54	0.016	1.38	0.696	-1.04	0.935	-1.64	0.452	0.06
1419624_a_at	1700010I14Rik	RIKEN cDNA 1700010I14 gene	-1.54	0.072	2.09	0.096	1.15	0.626	-1.12	0.484	0.14
1452296_at	Slit3	slit homolog 3 (Drosophila)	2.12	0.461	-1.24	0.538	-1.05	0.885	1.25	0.516	0.27
1446222_at	---	---	1.28	0.562	1.89	0.037	-1.39	0.321	-1.25	0.353	0.13
1418096_at	Dok3	docking protein 3	-1.19	0.319	1.22	0.221	1.83	0.136	-1.17	0.532	0.17
1450881_s_at	Gpr137b	G protein-coupled receptor 137B	-1.04	0.848	1.7	0.073	1.23	0.03	-1.52	0.301	0.09
1421353_at	Pde7b	phosphodiesterase 7B	-1.25	0.662	2.17	0.169	-1.08	0.782	1.25	0.675	0.27
1429579_at	6330407I18Rik	RIKEN cDNA 6330407I18 gene	1.65	0.045	1.57	0.074	-1.5	0.198	-1.5	0.287	0.06
1421120_at	Myo6	myosin VI	2.24	0.067	-1.54	0.154	1	0.99	-3.35	0.239	-0.41
1436449_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930025C	-1.05	0.863	-1.03	0.759	1.96	0.148	1.08	0.525	0.24
1428895_at	3222401M22Rik	RIKEN cDNA 3222401M22 gene	1.39	0.424	1.53	0.376	-1.03	0.91	-2.78	0.088	-0.22
1421310_at	4921517D21Rik	RIKEN cDNA 4921517D21 gene	-1.1	0.726	1.67	0.068	1.31	0.077	-1.64	0.231	0.06
1444455_at	Cacna1a	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.98	0.413	2.61	0.345	-1.28	0.589	1.54	0.111	0.22
1459337_at	Alg6	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase	-1.64	0.352	2.51	0.268	-1.3	0.424	1.11	0.674	0.17
1458845_at	D4Ertd264e	DNA segment, Chr 4, ERATO Doi 264, expressed	-1.82	0.381	1.18	0.789	2.17	0.098	-2.26	0.373	-0.19
1455699_at	---	Transcribed locus	-1.51	0.205	2.51	0.153	-1.39	0.08	1.65	0.209	0.32
1457495_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	-1.13	0.884	1.33	0.341	1.68	0.261	-2.26	0.147	-0.1
1436039_at	---	Transcribed locus	1.05	0.529	-1.22	0.251	2.02	0.056	-1.4	0.379	0.11
1419208_at	Map3k8	mitogen activated protein kinase kinase kinase 8	-1.05	0.859	1.44	0.18	1.5	0.105	-1.44	0.421	0.11
1443370_at	Ascc3	Activating signal cointegrator 1 complex subunit 3	-1.2	0.701	2.15	0.262	-1.1	0.842	1.38	0.465	0.31
1453488_at	4930458D05Rik	RIKEN cDNA 4930458D05 gene	1.45	0.581	1.64	0.407	-1.24	0.548	-1.56	0.584	0.07
1435343_at	Dock10 /// LOC630	dedicator of cytokinesis 10 /// similar to Dedicator of cytokinesis protein 10 (Protei	1.52	0.162	1.47	0.017	-1.09	0.462	-1.88	0.146	0
1421157_at	Fzd3	frizzled homolog 3 (Drosophila)	1.59	0.663	1.67	0.11	-1.56	0.051	-1.42	0.723	0.07
1439731_at	E130309F12Rik	RIKEN cDNA E130309F12 gene	-1.1	0.87	2.4	0.137	-1.7	0.264	1.07	0.876	0.17
1440520_a_at	1700051A21Rik	RIKEN cDNA 1700051A21 gene	2.3	0.201	-1.34	0.55	-1.17	0.718	1.1	0.866	0.22
1445876_at	---	---	-1.06	0.729	1.47	0.581	1.49	0.457	-1.55	0.474	0.09
1435747_at	Fgf14	fibroblast growth factor 14	2.41	0.012	-1.83	0.259	-1.07	0.899	1.96	0.407	0.37
1433251_at	Hsp90aa1 /// LOC6	heat shock protein 90kDa alpha (cytosolic), class A member 1 /// similar to heat s	1.84	0.195	1.31	0.526	-1.34	0.547	-1.35	0.729	0.11
1426199_x_at	---	Anti-human CD37 antibody WR17 gamma heavy chain variable region	1.13	0.58	-1.17	0.465	1.91	0.323	-1.09	0.911	0.2
1440363_at	---	Transcribed locus	1.75	0.634	-1.02	0.976	1.17	0.724	-1.51	0.185	0.1
1420841_at	Ptprf	protein tyrosine phosphatase, receptor type, F	1.34	0.604	-1.08	0.789	1.63	0.181	-1.18	0.723	0.18
1454387_at	Panx3	pannexin 3	-1.71	0.415	2.29	0.406	1.03	0.86	-1.35	0.228	0.06
1444892_at	Nup160	nucleoporin 160	1.48	0.418	1.63	0.334	-1.27	0.654	-1.57	0.065	0.07
1418680_at	Serpind1	serine (or cysteine) peptidase inhibitor, clade D, member 1	2.03	0.342	-1.03	0.689	-1.11	0.528	1.71	0.116	0.4
1433716_x_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	-1.04	0.972	2.12	0.034	-1.23	0.624	1	0.994	0.21
1445500_at	Adam17	A disintegrin and metallopeptidase domain 17	1.34	0.757	1.79	0.209	-1.31	0.04	-1.39	0.295	0.11
1421805_at	---	---	1.83	0.456	-1.94	0.217	1.55	0.309	-1.83	0.369	-0.1
1454101_at	4933401P06Rik	RIKEN cDNA 4933401P06 gene	1.47	0.227	-1.21	0.431	1.6	0.168	-2.38	0.388	-0.13
1423514_at	Gykl1	glycerol kinase-like 1	1.55	0.411	2.01	0.425	-2.95	0.13	-1.93	0.227	-0.33
1422783_a_at	Krt6a	keratin 6A	-1.05	0.943	2.19	0.034	-1.32	0.384	1.16	0.551	0.24
1422607_at	Etv1	ets variant gene 1	-1.17	0.403	2.06	0.155	-1.02	0.943	1.58	0.442	0.36
1424791_a_at	Bcam	basal cell adhesion molecule	1.21	0.458	1.7	0.481	-1	0.98	-1.05	0.772	0.21
1423842_a_at	Rnf41	ring finger protein 41	-1.31	0.101	1.08	0.866	2.06	0.031	-1.39	0.096	0.11
1445816_at	---	---	1.11	0.368	1.85	0.005	-1.06	0.762	-1.3	0.712	0.15
1437492_at	Mkx	mohawk	1.44	0.408	-1.01	0.992	1.47	0.089	-1	0.991	0.22
1431280_at	AI597468	expressed sequence AI597468	-1.98	0.232	2.5	0.129	-1.11	0.807	1.22	0.436	0.16
1427722_at	9830102E05Rik	RIKEN cDNA 9830102E05 gene	-3.04	0.384	2.89	0.295	-1.46	0.454	2.24	0.22	0.16
1425908_at	Gnb1	guanine nucleotide binding protein, beta 1	2.17	0.557	-1.03	0.956	-1.31	0.55	1.06	0.929	0.22
1418555_x_at	Spic	Spi-C transcription factor (Spi-1/PU.1 related)	1.47	0.411	1.46	0.374	-1.02	0.935	-1.03	0.916	0.22

1445158_at	Sypl	synaptophysin-like protein	1.61	0.605	1.31	0.529	-1.01	0.967	-1.2	0.786	0.18
1442460_at	---	---	-1.12	0.898	1.87	0.031	1.15	0.617	-1.43	0.453	0.12
1453875_at	Slc7a15	solute carrier family 7 (cationic amino acid transporter, y+ system), member 15	1.68	0.589	-1.08	0.732	1.31	0.559	-1.18	0.426	0.18
1426937_at	6330406I15Rik	RIKEN cDNA 6330406I15 gene	1.7	0.592	1.22	0.407	-1.02	0.908	-1.05	0.747	0.22
1437185_s_at	Tmsb10	thymosin, beta 10	1.4	0.112	1.71	0.008	-1.24	0.005	-1.39	0.092	0.12
1456235_at	BB165335	expressed sequence BB165335	1.39	0.719	1.68	0.348	-1.19	0.591	-2.05	0.082	-0.04
1439879_at	Zfp568	Zinc finger protein 568	1.41	0.17	2.01	0.096	-2.07	0.053	-1.17	0.715	0.05
1460112_at	---	Transcribed locus	1.64	0.301	-1.08	0.817	1.34	0.025	-1.75	0.363	0.04
1452541_at	Epb4.1l2	erythrocyte protein band 4.1-like 2	1.33	0.056	-1.05	0.935	1.63	0.39	-1.02	0.966	0.22
1439797_at	Ppard	peroxisome proliferator activator receptor delta	-1.13	0.058	2.07	0.113	-1.05	0.796	1.12	0.667	0.25
1437828_s_at	Wdr46	WD repeat domain 46	-1.01	0.916	1.39	0.047	1.53	0.149	-1.13	0.261	0.19
1456047_at	Pla2g4b	phospholipase A2, group IVB (cytosolic)	-1.13	0.794	1.18	0.703	1.85	0.013	-1.95	0.022	-0.01
1440623_at	Gpr26	G protein-coupled receptor 26	-6.33	0.149	2.24	0.043	1.51	0.435	-1.24	0.053	-0.95
1460518_at	E130119H09Rik	RIKEN cDNA E130119H09 gene	1.75	0.564	-3.22	0.138	1.85	0.128	-1.08	0.86	-0.17
1454356_at	1810021M19Rik	RIKEN cDNA 1810021M19 gene	-1.21	0.167	-1.28	0.529	2.3	0.002	1.38	0.301	0.3
1435992_at	Iqca	IQ motif containing with AAA domain	1.47	0.247	-1.04	0.928	1.48	0.21	-1.2	0.622	0.18
1451658_a_at	Polr3c	polymerase (RNA) III (DNA directed) polypeptide C	1.03	0.936	-1.04	0.91	1.92	0.2	-1.01	0.983	0.23
1443419_at	D5Ertd525e	DNA segment, Chr 5, ERATO Doi 525, expressed	1.28	0.658	1.66	0.421	-1.03	0.762	-1.22	0.622	0.17
1445725_at	---	---	1.01	0.958	2.21	0.295	-1.44	0.458	-1.36	0.344	0.11
1430422_at	1700020A23Rik	RIKEN cDNA 1700020A23 gene	1.9	0.309	1.32	0.512	-1.44	0.315	-1.77	0.015	0
1459193_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	-1.25	0.457	2.16	0.234	-1.04	0.855	2.21	0.073	0.52
1457530_at	---	Transcribed locus	1.98	0.082	-1.14	0.744	1.05	0.864	-1.61	0.316	0.07
1450085_at	---	---	1.99	0.333	-1.01	0.974	-1.07	0.776	1.23	0.725	0.28
1423134_at	BC003324	cDNA sequence BC003324	-1.21	0.364	1.22	0.172	1.87	0.261	-1.27	0.314	0.15
1440164_x_at	Cd8a	CD8 antigen, alpha chain	-1.39	0.61	1.84	0.24	1.36	0.341	-1.07	0.37	0.18
1426379_at	Eif4b	eukaryotic translation initiation factor 4B	1.38	0.119	-1.01	0.962	1.55	0.174	-1.05	0.807	0.22
1437149_at	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1.16	0.084	-1.02	0.878	1.78	0.009	-1.1	0.652	0.2
1423518_at	Csk	c-src tyrosine kinase	-1.03	0.829	1.13	0.468	1.82	0.1	-1.34	0.323	0.14
1424875_at	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (human)	1.31	0.559	-1.02	0.928	1.63	0.281	-1.25	0.597	0.17
1422422_at	Defcr4	defensin related cryptdin 4	-2.38	0.401	2.8	0.075	-1.43	0.427	1.2	0.502	0.05
1420904_at	Il17ra	interleukin 17 receptor A	-1.24	0.269	1.22	0.509	1.89	0.111	-1.76	0.157	0.03
1424987_at	5430435G22Rik	RIKEN cDNA 5430435G22 gene	1.52	0.022	1.7	0.007	-1.44	0.018	-1.37	0.162	0.1
1436547_at	Dgke	diacylglycerol kinase, epsilon	-1.65	0.273	2.25	0.131	1.06	0.775	-1.01	0.97	0.16
1439657_at	LOC319980	hypothetical LOC319980	2.15	0.426	1.03	0.951	-1.36	0.165	-1.04	0.936	0.2
1425325_at	Ms4a4b	membrane-spanning 4-domains, subfamily A, member 4B	1.53	0.566	1.42	0.447	-1.03	0.937	-1.57	0.445	0.09
1453810_at	Aftph	aftiphilin	1.39	0.352	1.63	0.019	-1.11	0.784	-1.78	0.117	0.03
1451743_at	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	1.24	0.121	-1.06	0.791	1.74	0.301	-1.03	0.938	0.22
1421002_at	Angptl2	angiopoietin-like 2	1.41	0.536	-1.04	0.943	1.55	0.317	-1.3	0.519	0.15
1424865_at	Pyy	peptide YY	2.02	0.329	-1.45	0.302	1.21	0.585	-1.13	0.67	0.16
1444537_at	AI429363	expressed sequence AI429363	1.02	0.95	2	0.304	-1.11	0.542	-1.34	0.298	0.14
1421775_at	Fcer1a	Fc receptor, IgE, high affinity I, alpha polypeptide	-3.08	0.02	-2.27	0.093	3.16	0.103	1.91	0.425	-0.07
1438334_at	Dock2	Dedicator of cyto-kinesis 2	1.79	0.034	-1.01	0.973	1.14	0.637	-1.67	0.19	0.06
1441356_at	Shc2	src homology 2 domain-containing transforming protein C2	-1.06	0.903	1.87	0.383	1.11	0.803	-1.27	0.376	0.16
1457116_at	Rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	-1.12	0.495	2.2	0.048	-1.2	0.509	1.1	0.731	0.25
1423488_at	Mmd	monocyte to macrophage differentiation-associated	1.38	0.272	-1.32	0.007	1.79	0.049	-1.12	0.11	0.18
1427404_x_at	LOC433182	similar to enolase 1, alpha non-neuron	1.02	0.876	-1.09	0.431	1.99	0.008	-1.16	0.317	0.19
1443106_at	4930562C15Rik	RIKEN cDNA 4930562C15 gene	2.1	0.249	-1.18	0.448	-1.02	0.976	1.11	0.809	0.25
1421297_a_at	Cacna1c	calcium channel, voltage-dependent, L type, alpha 1C subunit	-1.53	0.459	2.48	0.382	-1.26	0.27	1.25	0.647	0.23
1426298_at	Irx2	Iroquois related homeobox 2 (Drosophila)	1.04	0.88	2.16	0.153	-1.38	0.319	-1.16	0.676	0.17
1429880_at	4921531C22Rik	RIKEN cDNA 4921531C22 gene	1.86	0.337	-1.17	0.733	1.21	0.727	-1.37	0.453	0.13
1435318_at	E130218I03Rik	RIKEN cDNA E130218I03 gene	-1.23	0.081	1.01	0.956	2.1	0.198	-1.88	0.227	0
1439054_at	Zfp36l2	zinc finger protein 36, C3H type-like 2	1.12	0.559	-1	0.985	1.81	0.394	-1.46	0.564	0.12
1457577_at	---	---	-1.01	0.986	2.36	0.078	-1.74	0.242	1.63	0.596	0.31

1455882_x_at	Vwc2	von Willebrand factor C domain containing 2	-3.35	0.461	-1.35	0.451	2.89	0.008	1.13	0.798	-0.17
1432776_at	9430087J23Rik	RIKEN cDNA 9430087J23 gene	1.53	0.384	-1.14	0.793	1.52	0.252	-1.79	0.065	0.03
1430884_at	4930568G15Rik	RIKEN cDNA 4930568G15 gene	1.06	0.899	2.23	0.218	-1.56	0.192	-1.49	0.489	0.06
1434730_at	AI854517	expressed sequence AI854517	-1.31	0.132	1.92	0.247	1.25	0.656	-1.44	0.319	0.11
1448499_a_at	Ephx2	epoxide hydrolase 2, cytoplasmic	-1.03	0.665	-1.61	0.083	2.34	0.332	1.05	0.635	0.19
1432414_at	---	---	2.26	0.169	-1.93	0.021	1.15	0.677	-1.24	0.792	0.06
1426573_at	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	-1.08	0.846	1.59	0.269	1.42	0.007	-1.33	0.456	0.15
1420992_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	-1.04	0.839	1.6	0.293	1.37	0.108	-1.14	0.292	0.2
1424613_at	Gprc5b	G protein-coupled receptor, family C, group 5, member B	1.21	0.198	1.75	0.505	-1.03	0.887	-2.82	0.078	-0.22
1431171_at	D730001G18Rik	RIKEN cDNA D730001G18 gene	1.29	0.572	2.18	0.036	-2.15	0.004	-1	0.998	0.08
1458334_at	Wnt7a	wingless-related MMTV integration site 7A	1.02	0.976	2.21	0.266	-1.4	0.549	-2.14	0.23	-0.08
1457023_at	5830411G16Rik	RIKEN cDNA 5830411G16 gene	1.67	0.453	-1.39	0.424	1.55	0.259	-1.9	0.212	-0.02
1434359_at	6330500D04Rik	RIKEN cDNA 6330500D04 gene	-1.2	0.708	1.12	0.548	1.99	0.014	-2.26	0.053	-0.09
1460524_at	6430711C07Rik	RIKEN cDNA 6430711C07 gene	1.51	0.244	1.8	0.484	-1.61	0.333	-1.75	0.222	-0.01
1456066_a_at	Rpo1-4	RNA polymerase 1-4	-1.18	0.661	1.61	0.09	1.47	0.337	-1.25	0.182	0.17
1438982_s_at	2810417J12Rik	RIKEN cDNA 2810417J12 gene	-1.49	0.172	2.56	0.182	-1.41	0.162	1.59	0.211	0.31
1436282_at	4732440D04Rik	RIKEN cDNA 4732440D04 gene	1.18	0.432	1.93	0.187	-1.21	0.097	-1.03	0.092	0.22
1454942_at	Niban	niban protein	1.3	0.593	1.77	0.001	-1.16	0.463	-1.11	0.793	0.2
1444792_at	---	---	-1.35	0.073	2.24	0.04	-1.04	0.95	2.88	0.016	0.68
1421153_at	Loxl4	lysyl oxidase-like 4	1.17	0.786	2.04	0.293	-1.37	0.361	-1.15	0.709	0.17
1445744_at	Tmem56	Transmembrane protein 56	2.48	0.036	-1.18	0.452	-1.63	0.053	1.59	0.458	0.31
1459424_at	D3Ertd108e	DNA segment, Chr 3, ERATO Doi 108, expressed	2.49	0.4	-1.31	0.517	-1.47	0.167	2.8	0.013	0.63
1421414_a_at	Sema6a	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.09	0.765	1.34	0.319	1.68	0.431	-2.04	0.366	-0.03
1450773_at	Kcnd2	potassium voltage-gated channel, Shal-related family, member 2	1.68	0.329	1.45	0.575	-1.23	0.189	-1.8	0.119	0.02
1419057_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	-1.16	0.164	1.83	0.154	1.24	0.306	-1.28	0.258	0.16
1458243_at	---	---	-2.33	0.272	2.36	0.063	1.15	0.804	-1.66	0.133	-0.12
1428861_at	4631422O05Rik ///	RIKEN cDNA 4631422O05 gene /// similar to downregulated in ovarian cancer 1 i	1.04	0.448	2.11	0.022	-1.26	0.306	-1.89	0.179	0
1421536_at	Gabrq	gamma-aminobutyric acid (GABA-A) receptor, subunit theta	-1.77	0.408	2.27	0.268	1.1	0.812	-1.56	0.41	0.01
1421303_at	Zfpn1a1	zinc finger protein, subfamily 1A, 1 (Ikaros)	-1.16	0.646	1.01	0.963	2.07	0.016	-1.29	0.709	0.16
1438784_at	---	---	-1.33	0.533	2.17	0.382	1.02	0.967	-3.2	0.066	-0.33
1422098_at	Acvr1b	activin A receptor, type 1B	2.2	0.244	-1.83	0.272	1.19	0.621	-3.67	0.163	-0.53
1422725_at	Mak	male germ cell-associated kinase	1.99	0.318	-1	0.996	-1.04	0.838	1.18	0.505	0.28
1450456_at	Il21r	interleukin 21 receptor	1.89	0.432	-1.7	0.292	1.46	0.099	-1.79	0.201	-0.03
1436648_at	Nanos1	nanos homolog 1 (Drosophila)	2.26	0.401	-1.35	0.353	-1.06	0.906	1.37	0.471	0.3
1419380_at	Zfp423	zinc finger protein 423	2.19	0.253	-1.05	0.946	-1.25	0.615	1.42	0.436	0.33
1450393_a_at	Scamp4	secretory carrier membrane protein 4	-1.17	0.146	1.12	0.484	1.97	0.022	-1.05	0.791	0.22
1429561_at	Brf2	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-like	1.32	0.264	-1.04	0.81	1.67	0.029	-1.09	0.512	0.21
1443494_at	Polr3b	polymerase (RNA) III (DNA directed) polypeptide B	1.6	0.305	-1.29	0.663	1.57	0.391	-2.15	0.304	-0.07
1458600_at	---	Transcribed locus	2.87	0.391	-1.25	0.413	-3.62	0.04	1.29	0.643	-0.18
1437417_s_at	Gpc6	glypican 6	1.63	0.262	1.34	0.575	-1.02	0.92	-1.02	0.918	0.23
1430834_at	---	---	2.11	0.141	-1.4	0.447	1.13	0.789	-1.91	0.03	-0.02
1430672_at	5033418A18Rik	RIKEN cDNA 5033418A18 gene	1.32	0.433	1.85	0.248	-1.28	0.259	-1.39	0.304	0.12
1445192_at	D8Ertd575e	DNA segment, Chr 8, ERATO Doi 575, expressed	2.33	0.021	-1.03	0.964	-1.54	0.444	1.02	0.94	0.19
1432058_at	4930474H20Rik	RIKEN cDNA 4930474H20 gene	-1	0.998	-1.78	0.394	2.39	0.095	1.14	0.282	0.19
1419049_at	Pcnx	pecanex homolog (Drosophila)	1.2	0.403	-1.54	0.408	2.09	0.081	-1.25	0.755	0.13
1436627_at	D17Ertd663e	DNA segment, Chr 17, ERATO Doi 663, expressed	1.25	0.687	1.92	0.136	-1.3	0.14	-1.05	0.822	0.21
1428066_at	Ccdc120	coiled-coil domain containing 120	-1.01	0.983	1.78	0.362	1.18	0.351	-1.09	0.762	0.21
1421009_at	Rsad2	radical S-adenosyl methionine domain containing 2	-1.25	0.209	-1.18	0.48	2.3	0.374	2.67	0.248	0.63
1460049_s_at	1500015O10Rik	RIKEN cDNA 1500015O10 gene	2.22	0.031	1.19	0.557	-1.83	0.019	-1.7	0.181	-0.03
1451795_at	Tom1l2	target of myb1-like 2 (chicken)	1.96	0.065	-1.14	0.717	1.11	0.876	-1.84	0.59	0.02
1453948_at	4930529K09Rik	RIKEN cDNA 4930529K09 gene	1.99	0.323	1.09	0.9	-1.14	0.801	-1.68	0.158	0.06
1444222_x_at	---	Transcribed locus	1.34	0.731	1.63	0.173	-1.02	0.81	-1.25	0.505	0.17
1456004_x_at	Iapp	islet amyloid polypeptide	-1.37	0.396	1.62	0.209	1.61	0.176	-2.06	0.128	-0.05

1441616_at	---	---	2.12	0.331	1.11	0.701	-1.38	0.455	-1.37	0.61	0.12
1428432_at	2310047A01Rik	RIKEN cDNA 2310047A01 gene	1.96	0.032	1.1	0.564	-1.11	0.501	-1.21	0.649	0.18
1450539_at	Krtap5-1	keratin associated protein 5-1	-1.05	0.95	-1.05	0.835	2.04	0.209	4.62	0.282	1.14
1438203_at	Scarf2	scavenger receptor class F, member 2	1.88	0.324	-1.99	0.1	1.57	0.413	-1.19	0.764	0.07
1440161_at	Mmp16	Matrix metallopeptidase 16	1.71	0.03	1.46	0.549	-1.27	0.66	-1	0.997	0.22
1437445_at	Trpm1	transient receptor potential cation channel, subfamily M, member 1	2.1	0.296	1.12	0.596	-1.37	0.173	-2.78	0.496	-0.23
1420005_s_at	Bmp15	bone morphogenetic protein 15	1.96	0.056	1.11	0.788	-1.13	0.727	-1.78	0.054	0.04
1427687_at	Pcdha10	protocadherin alpha 10	1.27	0.77	2.06	0.311	-1.61	0.131	-1.48	0.605	0.06
1420417_at	Sema3a	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.58	0.345	-1.39	0.43	1.66	0.17	-1.32	0.276	0.13
1454476_at	4933428L12Rik	RIKEN cDNA 4933428L12 gene	2.44	0.049	-1.62	0.398	-1.11	0.818	2.99	0.188	0.67
1456983_at	Trps1	Trichorhinophalangeal syndrome I (human)	1.02	0.967	2.06	0.22	-1.15	0.683	-1.4	0.263	0.14
1446154_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	2.11	0.357	-1.32	0.211	1.09	0.871	-1.6	0.339	0.07
1456288_at	Slfn5	schlafen 5	1.57	0.487	1.5	0.236	-1.12	0.778	-1.53	0.499	0.1
1433056_at	4931407J08Rik	RIKEN cDNA 4931407J08 gene	-1.46	0.331	2.19	0.102	1.08	0.846	-1.83	0.499	0
1422113_at	Slc5a5	solute carrier family 5 (sodium iodide symporter), member 5	-1.28	0.647	1.63	0.35	1.55	0.22	-1.84	0.375	0.02
1429014_at	D1Ertd161e	DNA segment, Chr 1, ERATO Doi 161, expressed	-1.08	0.64	1.92	0.272	1.11	0.364	-1.31	0.691	0.16
1450695_at	Ahr	aryl-hydrocarbon receptor	1.31	0.705	1.65	0.213	-1	0.997	-1.25	0.342	0.18
1433933_s_at	Slco2b1	solute carrier organic anion transporter family, member 2b1	1.38	0.35	-1.02	0.896	1.6	0.074	-1.23	0.564	0.18
1423602_at	Traf1	Tnf receptor-associated factor 1	1.72	0.274	1.39	0.429	-1.16	0.492	-2.07	0.089	-0.03
1442588_at	---	Mus musculus, clone IMAGE:1533345, mRNA	-1.45	0.225	2.47	0.045	-1.25	0.22	2.29	0.017	0.52
1436922_at	Ppil5	peptidylprolyl isomerase (cyclophilin) like 5	-1.02	0.957	-1.19	0.795	2.14	0.128	4.92	0.236	1.21
1426037_a_at	Rgs16	regulator of G-protein signaling 16	2.62	0.161	-1.54	0.57	-1.44	0.183	1.61	0.175	0.31
1426565_at	Igf1r	insulin-like growth factor I receptor	-1.16	0.691	-1.17	0.598	2.25	0.018	1.1	0.6	0.25
1432592_at	Pappa	pregnancy-associated plasma protein A	1.03	0.912	1.98	0.245	-1.05	0.893	-2.77	0.209	-0.2
1457820_at	---	---	-2.27	0.303	1.73	0.355	1.79	0.189	-1.41	0.202	-0.04
1441084_at	BE686333	expressed sequence BE686333	2.01	0.209	-1.19	0.747	1.11	0.446	-1.64	0.21	0.07
1443908_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430069K	-1.24	0.298	1.01	0.943	2.15	0.27	-2.11	0.275	-0.05
1429414_at	4933400E14Rik	RIKEN cDNA 4933400E14 gene	1.75	0.471	1.33	0.252	-1.13	0.237	-1.8	0.33	0.04
1432349_a_at	Sync	syncoilin	-1.36	0.684	2.14	0.28	1.09	0.841	-1.23	0.406	0.16
1457777_at	Gsdm1	gasdermin 1	2.44	0.117	-1.22	0.487	-1.42	0.546	2.03	0.243	0.46
1446312_at	---	---	1.07	0.864	1.93	0.055	-1.04	0.886	-1.41	0.082	0.14
1449012_s_at	Fndc4	fibronectin type III domain containing 4	1.58	0.031	1.53	0.016	-1.16	0.56	-1.3	0.443	0.16
1445149_at	Pvr	Poliovirus receptor	1.05	0.918	2.22	0.075	-1.43	0.456	-1.18	0.113	0.16
1457136_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	-1.19	0.741	-1.24	0.69	2.32	0.236	1.12	0.684	0.25
1443043_at	Otop2	otopetrin 2	-1.2	0.71	1.69	0.398	1.45	0.248	-1.9	0.508	0.01
1425047_a_at	4921517L17Rik	RIKEN cDNA 4921517L17 gene	1.62	0.075	1.39	0.391	-1.04	0.686	-1.35	0.396	0.15
1424960_at	Epn3	epsin 3	2.08	0.189	-1.23	0.227	1.08	0.802	-1.01	0.924	0.23
1448669_at	Dkk3	dickkopf homolog 3 (Xenopus laevis)	-1.04	0.867	2.11	0.104	-1.11	0.657	1.27	0.415	0.31
1426867_at	Dmrt2	doublesex and mab-3 related transcription factor 2	-1.04	0.859	-1.41	0.57	2.3	0.004	1.63	0.102	0.37
1421383_at	Ccdc82	coiled-coil domain containing 82	-1.47	0.513	2.41	0.138	-1.13	0.626	1.19	0.676	0.25
1419412_at	Xcl1	chemokine (C motif) ligand 1	-1.01	0.978	1.67	0.349	1.31	0.431	-1.13	0.639	0.21
1446826_at	Xpo7	exportin 7	2.6	0.154	-2.01	0.202	-1.14	0.75	4.7	0.23	1.04
1456307_s_at	Adcy7	adenylate cyclase 7	1.43	0.301	1.7	0.053	-1.19	0.186	-1.64	0.186	0.08
1450108_at	Kif1a	kinesin family member 1A	1.39	0.054	-1.21	0.506	1.75	0.019	-1.02	0.948	0.23
1448074_at	Rln1	Relaxin 1	-1.58	0.413	2.33	0.3	1.01	0.99	-1.19	0.725	0.14
1423002_at	Pag1	phosphoprotein associated with glycosphingolipid microdomains 1	1.77	0.063	-1.36	0.172	1.47	0.283	-1.82	0.035	0.01
1452367_at	Coro2a	coronin, actin binding protein 2A	-1.22	0.621	1.56	0.045	1.59	0.025	-1.91	0.112	0.01
1450603_s_at	V1ra3 /// V1ra4	vomeronasal 1 receptor, A3 /// vomeronasal 1 receptor, A4	-1.85	0.361	1.98	0.288	1.46	0.547	-1.12	0.84	0.11
1419771_at	---	PREDICTED: Mus musculus similar to dachsous 2 isoform 2 (LOC627094), mRN	2.26	0.35	-1.39	0.613	-1	0.997	1.01	0.985	0.22
1432339_at	4933432I03Rik	RIKEN cDNA 4933432I03 gene	-1.67	0.132	-1.49	0.549	2.7	0.01	2.69	0.016	0.56
1437595_at	E030010A14Rik	RIKEN cDNA E030010A14 gene	1.31	0.384	-1.56	0.447	2.03	0.174	-2.04	0.299	-0.07
1419157_at	Sox4 /// LOC67227	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	1.42	0.55	-1.28	0.677	1.78	0.391	-2.81	0.249	-0.22
1427341_at	E130103I17Rik	RIKEN cDNA E130103I17 gene	-1.08	0.673	1.86	0.047	1.18	0.441	-1.25	0.495	0.18

1437025_at	Cd28	CD28 antigen	2.58	0.133	-4.45	0.108	1.17	0.617	-1.56	0.3	-0.56
1418448_at	Rras	Harvey rat sarcoma oncogene, subgroup R	1.5	0.002	1.53	0.001	-1.05	0.184	-1.33	0.339	0.16
1443827_x_at	BC004044	cDNA sequence BC004044	-1.07	0.303	1.63	0.104	1.41	0.165	-1.38	0.021	0.15
1420469_at	4933411G06Rik	RIKEN cDNA 4933411G06 gene	1.54	0.295	-1.4	0.502	1.73	0.395	-1.44	0.54	0.11
1435245_at	Gls2	glutaminase 2 (liver, mitochondrial)	2.08	0.581	-1.01	0.954	-1.1	0.806	3.29	0.049	0.81
1452453_a_at	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	1.07	0.443	2.29	0.259	-1.61	0.397	-1.62	0.508	0.03
1429775_a_at	Gpr137b /// LOC66	G protein-coupled receptor 137B /// similar to transmembrane 7 superfamily mem	-1.11	0.588	1.43	0.194	1.65	0.029	-1.41	0.431	0.14
1447358_at	C87198	expressed sequence C87198	-1.03	0.922	2.48	0.112	-1.9	0.313	2.02	0.039	0.4
1448529_at	Thbd	thrombomodulin	1.42	0.139	1.57	0.053	-1	0.974	-1.19	0.285	0.2
1438306_at	Rnf180	ring finger protein 180	1.17	0.626	1.9	0.194	-1.09	0.768	-1.02	0.891	0.24
1423172_at	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	-1.05	0.729	2.13	0.13	-1.11	0.711	1.18	0.669	0.29
1446311_at	Mbc2	membrane bound C2 domain containing protein	1.67	0.362	-1.1	0.7	1.4	0.4	-1.12	0.837	0.22
1447205_x_at	Rps12 /// LOC4328	ribosomal protein S12 /// similar to ribosomal protein S12 /// similar to ribosomal p	-1.49	0.393	1.25	0.467	2.07	0.15	-1.36	0.069	0.12
1425630_at	Sin3b	transcriptional regulator, SIN3B (yeast)	1.71	0.119	1.33	0.372	-1.06	0.843	-1.22	0.312	0.19
1429133_at	4930519N16Rik	RIKEN cDNA 4930519N16 gene	1.51	0.347	-1.19	0.795	1.63	0.146	-1.27	0.538	0.17
1427052_at	Acacb	acetyl-Coenzyme A carboxylase beta	-1.02	0.928	1.14	0.135	1.86	0.226	-1.13	0.842	0.21
1436742_a_at	Gm1967	gene model 1967, (NCBI)	1.51	0.247	-3.25	0.179	2.17	0.091	-3.04	0.2	-0.65
1415828_a_at	D3Ucla1	DNA segment, Chr 3, University of California at Los Angeles 1	1.19	0.506	-1.08	0.781	1.87	0.091	-1.26	0.315	0.18
1436658_at	B130024G19Rik	RIKEN cDNA B130024G19 gene	1.74	0.174	-1.01	0.982	1.26	0.561	-2.12	0.102	-0.03
1431612_at	1700007J10Rik	RIKEN cDNA 1700007J10 gene	1.56	0.701	1.75	0.53	-1.48	0.301	-2.36	0.305	-0.13
1451045_at	Syt13	synaptotagmin XIII	1.63	0.54	-1.04	0.909	1.4	0.21	-1.02	0.947	0.24
1454013_at	1810062O18Rik	RIKEN cDNA 1810062O18 gene	1.07	0.71	2.03	0.005	-1.12	0.467	-1.6	0.044	0.1
1448750_at	Hand1	heart and neural crest derivatives expressed transcript 1	1.12	0.906	2.04	0.181	-1.22	0.566	-1.78	0.344	0.04
1459416_at	Bcl7a	B-cell CLL/lymphoma 7A	2.07	0.082	1.22	0.676	-1.44	0.486	-1.29	0.557	0.14
1418499_a_at	Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	1.13	0.353	1.89	0.093	-1.03	0.924	-1.14	0.841	0.21
1445524_at	Ddc	Dopa decarboxylase	1.9	0.273	1.37	0.262	-1.4	0.625	-1.85	0.376	0.01
1443774_at	Zfp406	zinc finger protein 406	2.16	0.214	1.2	0.694	-1.6	0.503	-1.51	0.195	0.06
1429875_at	1700034J05Rik /// I	RIKEN cDNA 1700034J05 gene /// hypothetical protein LOC635035	1.34	0.619	2.29	0.228	-2.73	0.039	-1.41	0.331	-0.13
1450212_at	Fmnl1	formin-like 1	-1.04	0.935	-1.02	0.963	2.05	0.114	1.16	0.499	0.29
1458654_at	---	Transcribed locus	-1.62	0.19	1.8	0.401	1.57	0.039	-2.39	0.276	-0.16
1430218_at	4933424M12Rik	RIKEN cDNA 4933424M12 gene	1.03	0.952	2.34	0.178	-1.61	0.169	-3.59	0.086	-0.46
1418153_at	Lama1	laminin, alpha 1	-1.18	0.525	1.26	0.321	1.89	0.111	-2.07	0.241	-0.02
1445639_at	9130014G24Rik	RIKEN cDNA 9130014G24 gene	-1.21	0.795	2.14	0.213	1.03	0.82	-1.23	0.64	0.18
1453205_at	Dydc1	DPY30 domain containing 1	-1.1	0.731	1.93	0.306	1.15	0.762	-1.04	0.947	0.24
1459996_at	Cacna1a	Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	-1.28	0.264	1.61	0.368	1.61	0.068	-1.65	0.372	0.07
1436236_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	-1.39	0.178	2.04	0	1.24	0.314	-2.1	0.326	-0.05
1432454_at	2410137M14Rik	RIKEN cDNA 2410137M14 gene	1.75	0.396	-1.01	0.99	1.25	0.237	-1.54	0.324	0.12
1437855_at	Mtap4	microtubule-associated protein 4	1.06	0.915	2.46	0.067	-2.09	0.015	-1.57	0.559	-0.03
1453244_at	5830416P10Rik	RIKEN cDNA 5830416P10 gene	-1.42	0.205	1.25	0.586	2.05	0.354	-2.14	0.097	-0.07
1435635_at	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1.31	0.588	-1.34	0.622	1.94	0.377	-1.29	0.687	0.16
1446712_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	1.01	0.982	-1.12	0.757	2.09	0.015	-1.39	0.36	0.15
1459555_at	---	---	1.73	0.42	-1.39	0.558	1.55	0.403	-1.28	0.723	0.15
1455714_at	Gm691	gene model 691, (NCBI)	-1.65	0.08	2.26	0.307	1.13	0.545	-1.11	0.847	0.16
1456448_at	2610301B20Rik	RIKEN cDNA 2610301B20 gene	1.94	0.279	1.29	0.527	-1.29	0.334	-1.08	0.674	0.22
1419511_at	Msh4	mutS homolog 4 (E. coli)	-1.03	0.943	2.08	0.217	-1.05	0.859	1.17	0.6	0.29
1442788_at	2600003E23Rik	RIKEN cDNA 2600003E23 gene	-1.06	0.95	1.12	0.686	1.94	0.495	-1.79	0.55	0.05
1451001_at	1700019N19Rik	RIKEN cDNA 1700019N19 gene	2.11	0.056	-1.27	0.564	1.11	0.807	-1.57	0.53	0.09
1438022_at	Rab11fip3	RAB11 family interacting protein 3 (class II)	-1.13	0.524	1.69	0.038	1.43	0.393	-1.67	0.221	0.08
1419052_at	Ovol1	OVO homolog-like 1 (Drosophila)	-1.01	0.98	2.38	0.005	-1.58	0.343	1.19	0.7	0.25
1458905_x_at	2610002D18Rik	RIKEN cDNA 2610002D18 gene	-1.18	0.667	2.29	0.112	-1.16	0.783	1.09	0.776	0.26
1438232_at	Foxp2	forkhead box P2	2.6	0.111	-1.22	0.202	-1.73	0.007	1.05	0.946	0.18
1444009_at	Rassf4	Ras association (RalGDS/AF-6) domain family 4	1.99	0.25	-1.07	0.853	1.08	0.803	-1.03	0.951	0.24
1437669_x_at	Ccrl1	Chemokine (C-C motif) receptor-like 1	1.36	0.578	1.75	0.15	-1.11	0.569	-2.68	0.01	-0.17

1416612_at	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	1.66	0.211	-1.09	0.814	1.43	0.223	-1.37	0.395	0.16
1433360_at	1700023B13Rik	RIKEN cDNA 1700023B13 gene	1.23	0.686	1.99	0.172	-1.26	0.519	-1.25	0.679	0.18
1420738_at	Mzf1	myeloid zinc finger 1	2.67	0.447	-2.71	0.283	-1.04	0.92	1.65	0.098	0.14
1450016_at	Ccng1	cyclin G1	1.27	0.406	-1.05	0.697	1.79	0.21	-1.01	0.978	0.25
1459611_at	Mpp3	membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	-1.34	0.617	1.89	0.549	1.38	0.419	-1.96	0.313	-0.01
1451832_at	---	---	1.53	0.538	1.67	0.247	-1.24	0.606	-1.52	0.49	0.11
1449033_at	Tnfrsf11b	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	1.79	0.078	1.46	0.216	-1.32	0.366	-1.42	0.115	0.13
1453319_at	Ccar1	cell division cycle and apoptosis regulator 1	2.37	0.247	1.17	0.719	-2.16	0.084	-1.05	0.941	0.08
1430142_at	Tgm5	transglutaminase 5	1.49	0.329	-1.17	0.743	1.66	0.448	-1.01	0.979	0.24
1420684_at	Acox3	acyl-Coenzyme A oxidase 3, pristanoyl	1.42	0.356	-1.22	0.459	1.77	0.162	-1.24	0.551	0.18
1459529_at	E230016K23Rik	RIKEN cDNA E230016K23 gene	-2.02	0.132	2.32	0.151	1.2	0.579	-2.18	0.278	-0.17
1454224_at	2010300F17Rik	RIKEN cDNA 2010300F17 gene	-1.03	0.959	1.19	0.667	1.85	0.462	-2.44	0.34	-0.11
1447035_at	A230091C14Rik	RIKEN cDNA A230091C14 gene	1.37	0.64	-1.81	0.399	2.09	0.042	-1.04	0.957	0.15
1446681_at	BB086117	expressed sequence BB086117	2.29	0.003	-1.5	0.466	1.05	0.928	-2.03	0.368	-0.05
1459706_at	Exoc4	Exocyst complex component 4	2.6	0.181	-1.48	0.693	-1.35	0.415	1.11	0.834	0.22
1445119_at	D7Ertd661e	DNA segment, Chr 7, ERATO Doi 661, expressed	-1.25	0.7	2.29	0.314	-1.09	0.793	1.95	0.124	0.48
1457719_at	---	Transcribed locus	-1.04	0.834	2.44	0.188	-1.64	0.026	1	0.995	0.19
1442747_at	---	---	2.67	0.084	-1.37	0.262	-1.63	0.493	1.79	0.203	0.36
1431998_at	4930432L08Rik	RIKEN cDNA 4930432L08 gene	1.62	0.282	1.7	0.299	-1.45	0.548	-1.03	0.959	0.21
1458330_x_at	Cnnm3	Cyclin M3	1.18	0.38	-1	0.953	1.84	0.095	-2.11	0.243	-0.02
1445294_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.7	0.431	1.37	0.091	-1.07	0.734	-1.11	0.875	0.22
1437894_at	Prox1	prospero-related homeobox 1	1.78	0.13	1.32	0.251	-1.08	0.759	-1.02	0.914	0.25
1443540_at	Map3k1 /// LOC670	mitogen activated protein kinase kinase kinase 1 /// similar to Mitogen-activated p	1.15	0.706	2	0.144	-1.15	0.625	-1.27	0.269	0.18
1446992_at	Ccdc64	Coiled-coil domain containing 64	1.32	0.007	1.75	0.362	-1.06	0.856	-2.75	0.123	-0.19
1451373_at	Ugt3a1 /// LOC666	UDP glycosyltransferases 3 family, polypeptide A1 /// similar to UDP glycosyltrans	-1.11	0.069	-1.15	0.075	2.24	0.072	1.83	0.228	0.45
1440550_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.72	0.47	-1.35	0.548	1.56	0.196	-1.42	0.595	0.13
1432588_at	5830468K08Rik	RIKEN cDNA 5830468K08 gene	1.79	0.16	1.34	0.409	-1.12	0.825	-1.19	0.754	0.2
1417748_x_at	Foxm1	forkhead box M1	-1.43	0.673	2.83	0.136	-2.03	0.183	3.02	0.164	0.6
1422496_at	Hmgn1	high mobility group nucleosomal binding domain 1	-2.06	0.362	1.12	0.773	2.42	0.04	-1.26	0.822	0.05
1421150_at	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	-1.09	0.193	1.32	0.612	1.78	0.274	-1.23	0.673	0.19
1424755_at	Hip1	huntingtin interacting protein 1	2.18	0.186	-1.1	0.882	-1.07	0.847	1.46	0.401	0.37
1444373_at	Tiam1	T-cell lymphoma invasion and metastasis 1	1.32	0.631	1.76	0.408	-1.06	0.829	-1.96	0.125	0.01
1441631_at	Ddx24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	1.57	0.078	1.55	0.354	-1.12	0.576	-1.5	0.083	0.13
1444613_at	---	Transcribed locus	1.37	0.163	-1.21	0.185	1.82	0.326	-1.58	0.414	0.1
1429671_at	2410018M08Rik	RIKEN cDNA 2410018M08 gene	1.27	0.685	-1.06	0.878	1.8	0.078	-1.12	0.838	0.22
1432333_a_at	1700027D21Rik	RIKEN cDNA 1700027D21 gene	-1.95	0.396	2.29	0.231	1.22	0.479	-1.04	0.891	0.13
1448075_at	AA408251	expressed sequence AA408251	-1.26	0.489	2.42	0.372	-1.23	0.699	1.05	0.912	0.24
1424439_at	1810065E05Rik	RIKEN cDNA 1810065E05 gene	1.4	0.329	1.73	0.375	-1.13	0.82	-1.27	0.699	0.19
1439434_x_at	Sh2d5	SH2 domain containing 5	2.31	0.017	-1.21	0.701	-1.13	0.672	2.36	0.281	0.59
1453441_at	4921522P10Rik	RIKEN cDNA 4921522P10 gene	1.12	0.416	-1.04	0.781	1.94	0.053	-1.38	0.567	0.16
1446115_at	---	---	-1.03	0.949	1.36	0.417	1.69	0.325	-1.28	0.786	0.19
1440399_at	Usp32	Ubiquitin specific peptidase 32	-1.03	0.949	1.21	0.726	1.84	0.237	-1.28	0.561	0.19
1431326_a_at	Tmod2	tropomodulin 2	1.71	0.1	1.33	0.587	-1.02	0.903	-4	0.142	-0.49
1444739_at	Pole4	Polymerase (DNA-directed), epsilon 4 (p12 subunit)	-1.06	0.928	1.81	0.042	1.27	0.616	-1.69	0.477	0.08
1420176_x_at	Igll1	immunoglobulin lambda-like polypeptide 1	1.9	0.3	-1.47	0.681	1.44	0.147	-1.7	0.468	0.04
1419080_at	Gdnf	glial cell line derived neurotrophic factor	-1.02	0.964	1.39	0.564	1.66	0.225	-1.02	0.839	0.25
1415904_at	Lpl	lipoprotein lipase	-1.54	0.259	2.19	0.006	1.19	0.513	-1.19	0.408	0.16
1445864_at	---	Transcribed locus	2.17	0.123	-1.5	0.583	1.19	0.639	-1.11	0.561	0.19
1460206_at	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	1.46	0.562	1.67	0.396	-1.12	0.622	-1.49	0.506	0.13
1425906_a_at	Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	2.5	0.087	-3.63	0.331	1.25	0.508	-2.7	0.172	-0.64
1448996_at	Rom1	rod outer segment membrane protein 1	-1.02	0.914	-1.11	0.858	2.15	0.148	1.17	0.687	0.3
1423378_at	Adam23	a disintegrin and metallopeptidase domain 23	-1.11	0.5	1.84	0.315	1.28	0.405	-1.75	0.266	0.07
1445967_at	AU022331	expressed sequence AU022331	1.04	0.904	2.25	0.036	-1.34	0.415	-1.01	0.984	0.23

1441156_at	Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (Arabidopsis thaliana)	1.48	0.669	-1	0.992	1.56	0.431	-1.17	0.343	0.22
1456751_x_at	A530021J07	hypothetical protein A530021J07	-3.55	0.004	2.52	0.053	1.23	0.698	-1.98	0.222	-0.44
1417219_s_at	Tmsb10	thymosin, beta 10	1.44	0.139	1.69	0.11	-1.11	0.44	-1.87	0.116	0.04
1432937_at	5430439C14Rik	RIKEN cDNA 5430439C14 gene	-1	0.99	1.38	0.242	1.66	0.091	-1.21	0.738	0.21
1431817_at	Adh6-ps1	alcohol dehydrogenase 6 (class V), pseudogene 1	1.51	0.301	-1.32	0.152	1.77	0.259	-1.04	0.942	0.23
1453144_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	1.57	0.06	1.78	0.164	-1.48	0.12	-2.31	0.061	-0.11
1416097_at	Lrrc4	leucine rich repeat containing 4	1.73	0.399	1.69	0.299	-1.62	0.557	-2.21	0.35	-0.1
1422723_at	Stra6	stimulated by retinoic acid gene 6	-1.3	0.305	1.63	0.008	1.64	0.347	-1.27	0.736	0.17
1421814_at	Msn	moesin	1.32	0.186	1.78	0.028	-1.08	0.485	-1.32	0.396	0.18
1457186_at	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	1.79	0.318	1.51	0.398	-1.37	0.188	-2.08	0.263	-0.04
1458487_at	Klf3 /// C230096K1(	Kruppel-like factor 3 (basic) /// RIKEN cDNA C230096K16 gene	1.56	0.588	-1.37	0.421	1.74	0.126	-1.01	0.972	0.23
1459428_at	C76662	expressed sequence C76662	2.62	0.366	-1.37	0.429	-1.44	0.081	1.76	0.488	0.39
1418699_s_at	Fech	ferrochelatase	-1.01	0.898	-1.12	0.214	2.15	0.283	3.6	0.193	0.91
1420085_at	Fgf4	fibroblast growth factor 4	1.52	0.552	-1.18	0.678	1.67	0.277	-1.6	0.138	0.1
1436482_a_at	Sdc3	syndecan 3	1.17	0.079	1.96	0.218	-1.09	0.736	-1.09	0.703	0.23
1431315_at	Hyls1	hydrolethalus syndrome 1	-1	0.994	2.05	0.127	-1.01	0.989	1.88	0.182	0.48
1448468_a_at	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1	1.05	0.869	2.14	0.222	-1.18	0.688	-1.71	0.108	0.08
1435596_at	A530088I07Rik	RIKEN cDNA A530088I07 gene	2.07	0.178	1.05	0.782	-1.09	0.729	-1.05	0.877	0.25
1418426_at	Gtf2a1lf	general transcription factor II A, 1-like factor	2.06	0.067	-1.18	0.729	1.13	0.768	-3.36	0.015	-0.34
1458966_at	C80278	expressed sequence C80278	2.25	0.329	1.05	0.736	-1.36	0.237	-1.11	0.854	0.21
1431786_s_at	1190003J15Rik	RIKEN cDNA 1190003J15 gene	1.9	0.017	-1.23	0.129	1.33	0.279	-2.16	0.006	-0.04
1424507_at	Rin1	Ras and Rab interactor 1	1.45	0.117	-1.01	0.975	1.6	0.115	-1.08	0.566	0.24
1445435_at	Gm732	gene model 732, (NCBI)	-1.4	0.565	2.13	0.241	1.19	0.722	-1.12	0.79	0.2
1438389_x_at	Acly	ATP citrate lyase	1.38	0.423	2.28	0.109	-2.62	0.015	-1.65	0.428	-0.15
1439612_at	Cacna1b	calcium channel, voltage-dependent, N type, alpha 1B subunit	-1.58	0.398	1.51	0.412	1.9	0.011	-1.94	0.188	-0.03
1441999_at	---	Transcribed locus	1.56	0.636	-1.24	0.648	1.67	0.062	-1.09	0.193	0.23
1446137_at	Gbas	Glioblastoma amplified sequence	1.77	0.334	1.65	0.619	-1.58	0.456	-1.06	0.817	0.19
1437422_at	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmeml	1.24	0.392	2.25	0.148	-1.8	0.019	-1.49	0.287	0.05
1427175_at	AI428936	expressed sequence AI428936	-1.14	0.635	2.39	0.236	-1.27	0.297	1.31	0.597	0.32
1439407_x_at	Tagln2 /// LOC6724	transgelin 2 /// similar to transgelin 2	1.16	0.224	2.25	0.271	-1.55	0.082	-1.88	0.428	-0.01
1421376_at	Traf6	Tnf receptor-associated factor 6	-1.37	0.512	1.66	0.286	1.66	0.159	-1.4	0.105	0.14
1416956_at	Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	-1.63	0.158	1.75	0.029	1.69	0.022	-1.54	0.064	0.07
1425221_at	E030025L21Rik	RIKEN cDNA E030025L21 gene	2.54	0.484	-2.48	0.374	1.11	0.776	-2.22	0.032	-0.26
1435137_s_at	1200015M12Rik ///	RIKEN cDNA 1200015M12 gene /// RIKEN cDNA 1200016E24 gene /// RIKEN cI	1.86	0.37	1.23	0.308	-1.04	0.839	-1.41	0.406	0.16
1424534_at	Mmd2	monocyte to macrophage differentiation-associated 2	1.03	0.924	2.3	0.01	-1.38	0.164	-1.42	0.626	0.13
1417380_at	Iqgap1	IQ motif containing GTPase activating protein 1	1.39	0.327	1.71	0.045	-1.05	0.79	-1.56	0.224	0.12
1440545_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.6	0.522	-1.59	0.367	2.8	0.007	1.24	0.587	0.21
1438858_x_at	H2-Aa	Histocompatibility 2, class II antigen A, alpha	2.08	0.232	1.24	0.572	-1.36	0.187	-1.69	0.184	0.07
1432505_at	1700009J07Rik	RIKEN cDNA 1700009J07 gene	2.17	0.424	1.22	0.493	-1.49	0.395	-1.66	0.458	0.06
1460009_at	---	Transcribed locus	-1.05	0.805	2.05	0.014	1.06	0.702	-1.83	0.108	0.05
1431706_at	Ranbp5	RAN binding protein 5	2.25	0.094	1.02	0.966	-1.27	0.531	-1.05	0.875	0.24
1426658_x_at	Phgdh /// LOC6730	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.58	0.148	1.52	0.575	1.91	0.097	-1.09	0.404	0.19
1423233_at	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	1.46	0.088	1.68	0.204	-1.09	0.543	-1.08	0.767	0.24
1441098_at	Pnldc1	poly(A)-specific ribonuclease (PARN)-like domain containing 1	-1.03	0.96	-1.31	0.332	2.32	0.233	3.24	0.095	0.81
1425775_at	MGC29393	hypothetical gene MGC29393	2.19	0.309	1.24	0.638	-1.59	0.152	-1.09	0.812	0.19
1432466_a_at	Apoe	apolipoprotein E	1.46	0.234	-1.2	0.465	1.76	0.074	-1.27	0.276	0.19
1446555_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.66	0.117	2.41	0.025	1.04	0.912	-1.09	0.788	0.18
1440814_x_at	Hs3st2	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	-1.48	0.696	1.08	0.861	2.3	0.134	-1.06	0.889	0.21
1418790_at	Fezf2	Fez family zinc finger 2	1.93	0.371	-1.26	0.44	1.33	0.531	-2	0.08	0
1454125_a_at	4930563E19Rik	RIKEN cDNA 4930563E19 gene	2.56	0.484	-2.03	0.041	1	0.998	-1.74	0.402	-0.05
1422947_at	Hist2h4 /// Hist1h4f	histone 2, H4 /// histone 1, H4f /// histone 1, H4m /// histone 1, H4a /// histone 1, H	1.63	0.553	1.49	0.352	-1.06	0.893	-1.86	0.379	0.05
1427799_x_at	Igk-V28 /// Igk-V8 ///	immunoglobulin kappa chain variable 28 (V28) /// immunoglobulin kappa chain va	1.39	0.575	-1.98	0.058	2.17	0.002	-1.38	0.482	0.05
1420894_at	Tgfbr1	transforming growth factor, beta receptor I	1.73	0.167	-1.02	0.942	1.35	0.518	-1.05	0.936	0.25

1453998_at	Smap1	stromal membrane-associated protein 1	-1.02	0.942	2.14	0.185	-1.06	0.875	1.22	0.684	0.32
1452494_s_at	Slco1b2	solute carrier organic anion transporter family, member 1b2	2.37	0.56	-1.39	0.038	-1.03	0.965	2.59	0.073	0.64
1428141_at	Gga2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	-1.04	0.743	1.3	0.057	1.8	0.327	-1.66	0.028	0.1
1433043_at	Cspg2	chondroitin sulfate proteoglycan 2	-2.24	0.22	1.94	0.322	1.68	0.154	-1.39	0.02	0
1455088_at	LOC381936 /// LOC	similar to Ser/Thr protein kinase PAR-1A /// similar to serine/threonine kinase /// s	1.11	0.827	-1.84	0.396	2.41	0.103	-1.61	0.031	0.02
1447777_x_at	---	---	-1.14	0.543	1.8	0.201	1.39	0.179	-2.33	0.264	-0.07
1453988_a_at	Ide	insulin degrading enzyme	-1.05	0.887	-1.07	0.87	2.18	0.403	1.08	0.866	0.29
1449683_x_at	Tubb2b	tubulin, beta 2b	1.7	0.421	-1.26	0.725	1.58	0.307	-1.08	0.794	0.23
1427401_at	Chrna5	cholinergic receptor, nicotinic, alpha polypeptide 5	1.75	0.374	1.56	0.068	-1.32	0.544	-1.34	0.594	0.16
1431971_at	---	---	-1.28	0.074	-1.07	0.896	2.35	0.056	2.61	0.19	0.65
1444270_at	Rshl3	radial spokehead-like 3	2.09	0.223	-1.04	0.916	1.01	0.962	-1.71	0.563	0.09
1425783_at	Mtac2d1	membrane targeting (tandem) C2 domain containing 1	-2.31	0.096	2.62	0.013	1.02	0.853	-1.59	0.388	-0.07
1435453_at	A930011O12Rik	RIKEN cDNA A930011O12 gene	1.64	0.492	1.53	0.346	-1.12	0.781	-1.2	0.713	0.21
1440180_x_at	Zbtb3	zinc finger and BTB domain containing 3	-1.44	0.256	1.85	0.281	1.52	0.2	-1.18	0.695	0.19
1416714_at	Irf8	interferon regulatory factor 8	1.34	0.097	1.76	0.005	-1.04	0.81	-1.88	0.109	0.05
1452339_at	Adamts7	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	2.93	0.086	-1.47	0.453	-2.17	0.059	1.39	0.692	0.17
1452738_at	Stoml1	stomatin-like 1	-1.02	0.66	1.22	0.512	1.86	0.159	-1.18	0.67	0.22
1439212_at	6820429M01	hypothetical protein 6820429M01	-1.12	0.851	1.61	0.18	1.57	0.536	-1.82	0.167	0.06
1420823_at	Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	1.09	0.888	2	0.248	-1.03	0.872	-1.88	0.397	0.05
1446424_at	Dnahc12	dynein, axonemal, heavy chain 12	-1.08	0.91	2.06	0.117	1.09	0.794	-1.15	0.647	0.23
1442291_at	Edg4	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor 4	1.24	0.723	2.26	0.149	-1.75	0.283	-3.4	0.056	-0.41
1445479_at	---	---	-1.82	0.351	1.52	0.368	2	0.05	-1.6	0.564	0.03
1437096_at	Ttc29	tetratricopeptide repeat domain 29	2.49	0.378	-1.89	0.1	1.05	0.831	-1.17	0.786	0.12
1416178_a_at	Plekhb1	pleckstrin homology domain containing, family B (evectins) member 1	1.44	0.112	1.65	0.067	-1.02	0.889	-1.15	0.644	0.23
1438696_at	Edn3	endothelin 3	1.21	0.609	2.14	0.015	-1.39	0.426	-1.45	0.25	0.13
1440687_at	---	6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430439N1	1.24	0.188	-1.03	0.951	1.86	0.087	-1.21	0.814	0.22
1433949_x_at	Pla2g1b	phospholipase A2, group IB, pancreas	1.56	0.446	1.7	0.509	-1.24	0.606	-1.79	0.02	0.06
1442693_at	LOC667823	similar to tripartite motif protein TRIM5	-1.12	0.801	1.7	0.134	1.48	0.236	-1.64	0.308	0.1
1432265_at	4930445B16Rik	RIKEN cDNA 4930445B16 gene	-1.32	0.167	2.33	0.146	-1.02	0.919	1.18	0.269	0.29
1438594_at	---	PREDICTED: Mus musculus similar to poly(A) binding protein, cytoplasmic 1 (LO	1.46	0.508	-1.65	0.425	2	0.14	-1.27	0.682	0.14
1422224_at	Tcp10a /// Tcp10b /	t-complex protein 10a /// t-complex protein 10b /// t-complex protein 10c	1.12	0.826	-1.29	0.108	2.18	0.196	-1.13	0.82	0.22
1433426_at	1700111A04Rik	RIKEN cDNA 1700111A04 gene	1.37	0.467	2.01	0.049	-1.43	0.423	-2.14	0.087	-0.05
1444064_at	Samhd1	SAM domain and HD domain, 1	1.79	0.542	1.37	0.206	-1.1	0.53	-1.79	0.097	0.07
1420148_at	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1.24	0.73	-3.46	0.355	2.54	0.448	-1.1	0.569	-0.19
1427659_at	---	Mus musculus, clone IMAGE:4006890	-1.29	0.446	2	0.508	1.3	0.57	-1.32	0.308	0.17
1458788_at	Evi2a	Ecotropic viral integration site 2a	1.53	0.146	1.94	0.265	-1.65	0.078	-1.43	0.047	0.1
1421056_at	Dnase1l3	deoxyribonuclease 1-like 3	-1.23	0.51	1.19	0.715	2.08	0.298	-1.23	0.641	0.2
1437571_at	Hic2	hypermethylated in cancer 2	2.22	0.432	-1.12	0.744	-1.04	0.932	1.7	0.329	0.44
1415958_at	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	-1.03	0.256	-1.16	0.7	2.24	0.123	5.93	0.126	1.5
1446338_at	---	---	1.79	0.449	-2.02	0.493	1.8	0.331	-1.95	0.395	-0.1
1447197_at	C86544	expressed sequence C86544	-1.69	0.313	1.03	0.949	2.46	0.033	-1.85	0.19	-0.01
1419173_at	Acy1	aminoacylase 1	1.42	0.267	-1.15	0.53	1.79	0.064	-1.01	0.971	0.26
1429765_at	1500005K14Rik	RIKEN cDNA 1500005K14 gene	-1.09	0.859	1.38	0.563	1.78	0.061	-1.01	0.953	0.27
1421008_at	Rsad2	radical S-adenosyl methionine domain containing 2	-1.1	0.543	-1.49	0.326	2.5	0.253	3.87	0.231	0.95
1440803_x_at	Tacr3	tachykinin receptor 3	1.27	0.453	2.1	0.101	-1.39	0.529	-3.99	0.224	-0.51
1420076_at	Atp8b1	ATPase, class I, type 8B, member 1	1.96	0.163	1.2	0.727	-1.08	0.792	-1.6	0.516	0.12
1448471_a_at	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	1.32	0.214	1.93	0.026	-1.2	0.073	-1.09	0.526	0.24
1425834_a_at	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	1.28	0.527	-1.02	0.964	1.83	0.437	-1.5	0.125	0.15
1449276_at	1700029P11Rik	RIKEN cDNA 1700029P11 gene	1.14	0.778	2.52	0.41	-2.34	0.288	-3.27	0.158	-0.49
1440555_at	Rragd	Ras-related GTP binding D	-1.39	0.014	2.11	0.047	1.25	0.462	-1.55	0.379	0.11
1436913_at	Cdc14a	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	-1.13	0.123	2.14	0.026	1.06	0.765	-1.23	0.034	0.21
1447559_at	AI834762	expressed sequence AI834762	2.07	0.478	-1.07	0.855	1.08	0.616	-1.08	0.765	0.25
1424010_at	Mfap4	microfibrillar-associated protein 4	1.53	0.453	-1.07	0.776	1.62	0.477	-3.91	0.43	-0.46

1452508_x_at	2610009E16Rik	RIKEN cDNA 2610009E16 gene	1.99	0.115	-1.27	0.394	1.3	0.442	-1.23	0.713	0.2
1454522_at	4930573G07Rik	RIKEN cDNA 4930573G07 gene	1.05	0.868	2.23	0.111	-1.24	0.575	-1.14	0.63	0.23
1454419_at	4930537H20Rik	RIKEN cDNA 4930537H20 gene	-1.09	0.523	2.28	0.2	-1.13	0.7	1.34	0.398	0.35
1440731_at	AI413759	expressed sequence AI413759	-1.11	0.793	1.87	0.055	1.32	0.093	-1.17	0.618	0.23
1443704_at	Adcy8	Adenylate cyclase 8	1.52	0.585	1.6	0.33	-1.03	0.938	-1.09	0.892	0.25
1422081_at	Ky	kyphoscoliosis peptidase	-1.6	0.621	1.83	0.298	1.63	0.315	-1.56	0.364	0.08
1445627_at	Osbpl9	Oxysterol binding protein-like 9	2.38	0.127	-1.45	0.463	1.01	0.967	-1.65	0.288	0.07
1459781_x_at	Trp53	transformation related protein 53	1.27	0.38	2.2	0.34	-1.62	0.505	-2.29	0.371	-0.11
1437139_at	Glra1	glycine receptor, alpha 1 subunit	2.37	0.12	-1.22	0.592	-1.11	0.807	1.57	0.357	0.4
1439423_x_at	U46068	cDNA sequence U46068	1.78	0.007	-1.17	0.785	1.46	0.533	-1.96	0.375	0.03
1445988_at	Il17d	Interleukin 17D	-1.73	0.069	-1.24	0.61	2.7	0.025	1.46	0.172	0.3
1432908_at	2810410P21Rik	RIKEN cDNA 2810410P21 gene	2.23	0.032	1.51	0.341	-2.89	0.021	-3.5	0.107	-0.66
1430120_at	4930519G04Rik	RIKEN cDNA 4930519G04 gene	-1.15	0.843	1.83	0.382	1.38	0.475	-1.76	0.476	0.08
1421461_at	Mpl	myeloproliferative leukemia virus oncogene	-3.4	0.019	-1.51	0.413	3.13	0.137	2.95	0.244	0.29
1449402_at	Chst7	carbohydrate (N-acetylglucosamino) sulfotransferase 7	-1.02	0.958	1.47	0.077	1.64	0.173	-1.09	0.768	0.25
1447136_at	Mastl	Microtubule associated serine/threonine kinase-like	3.28	0.134	-3.47	0.08	-1.91	0.195	3.11	0.004	0.25
1443096_at	4921526F01Rik	RIKEN cDNA 4921526F01 gene	1.27	0.417	1.92	0.257	-1.11	0.708	-2.31	0.387	-0.06
1442201_at	---	Transcribed locus	1.88	0.049	1.43	0.18	-1.29	0.228	-1.38	0.435	0.16
1458320_at	4932431H17Rik ///	RIKEN cDNA 4932431H17 gene /// similar to RIKEN cDNA 4932431H17 gene	1.78	0.185	-1.27	0.72	1.53	0.495	-1.3	0.609	0.18
1454334_at	2810409C01Rik	RIKEN cDNA 2810409C01 gene	2.27	0.194	-1.06	0.927	-1.14	0.673	1.22	0.773	0.32
1458877_at	---	Transcribed locus	2.21	0.16	-1.06	0.912	-1.06	0.865	2.48	0.03	0.64
1457339_at	Ccm2	Cerebral cavernous malformation 2 homolog (human)	1.81	0.053	1.71	0.255	-1.76	0.194	-1.45	0.54	0.08
1460015_at	Sohlh1	spermatogenesis and oogenesis specific basic helix-loop-helix 1	-1.57	0.002	2	0.415	1.45	0.383	-1.35	0.491	0.14
1427713_x_at	Pou2f2	POU domain, class 2, transcription factor 2	1.61	0.236	-1.31	0.525	1.72	0.129	-1.55	0.231	0.12
1423886_at	Lamc1	laminin, gamma 1	-1.14	0.86	1.43	0.577	1.79	0.183	-2.12	0.332	-0.01
1445771_at	---	---	1.35	0.434	-1.03	0.959	1.78	0.119	-1.63	0.649	0.12
1427778_at	Defb8	defensin beta 8	1.44	0.461	2.28	0.079	-2.71	0.088	-2.54	0.206	-0.38
1454379_at	5730405O12Rik	RIKEN cDNA 5730405O12 gene	-1.82	0.066	-2.44	0.433	3.14	0.011	1.28	0.31	0.04
1450562_at	Ly6f	lymphocyte antigen 6 complex, locus F	1.34	0.62	1.81	0.404	-1.05	0.86	-1.01	0.985	0.27
1432383_a_at	Armc9	armadillo repeat containing 9	2.6	0.151	-1.5	0.267	-1.21	0.412	1.7	0.487	0.4
1419566_at	Fank1	fibronectin type 3 and ankyrin repeat domains 1	-1.37	0.711	2.03	0.37	1.34	0.355	-1.26	0.746	0.18
1439428_x_at	Gmds	GDP-mannose 4, 6-dehydratase	-1.06	0.679	2.02	0.028	1.13	0.294	-1.18	0.063	0.23
1419758_at	Abcb1a	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	-1.18	0.334	1.34	0.39	1.91	0.098	-1.57	0.446	0.13
1446739_at	St6gal1	Beta galactoside alpha 2,6 sialyltransferase 1	2.21	0.25	1.28	0.394	-1.64	0.029	-2.41	0.18	-0.14
1416893_at	3110001A13Rik	RIKEN cDNA 3110001A13 gene	1.19	0.694	-1.38	0.224	2.18	0.266	-1.26	0.617	0.18
1449215_at	Slc22a21	solute carrier family 22 (organic cation transporter), member 21	-1.06	0.858	-1.04	0.895	2.2	0.107	1.51	0.207	0.4
1428809_at	1810010H24Rik ///	RIKEN cDNA 1810010H24 gene /// hypothetical protein LOC671668 /// hypothetic	-1.59	0.122	2.28	0.14	1.19	0.489	-1.53	0.469	0.09
1426114_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	1.79	0.345	-1.06	0.867	1.36	0.58	-1.13	0.831	0.24
1453816_at	5730427N09Rik	RIKEN cDNA 5730427N09 gene	-1.47	0.099	2.07	0.233	1.35	0.353	-1.08	0.406	0.22
1421641_at	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	-1.79	0.03	1.05	0.857	2.49	0.073	-1.55	0.066	0.05
1447003_at	Ccpg1	Cell cycle progression 1	1.14	0.745	1.99	0.128	-1.02	0.911	-1.39	0.17	0.18
1455553_at	5330401P04Rik	RIKEN cDNA 5330401P04 gene	1.24	0.836	1.92	0.062	-1.06	0.805	-2.07	0.114	0.01
1446273_at	Csmd1	CUB and Sushi multiple domains 1	-1.2	0.143	1.59	0.369	1.68	0.299	-1.42	0.311	0.16
1433939_at	A730046J16	hypothetical protein A730046J16	1.46	0.101	1.7	0.413	-1.06	0.804	-1.92	0.162	0.05
1431609_a_at	Acp5	acid phosphatase 5, tartrate resistant	-1.07	0.541	1.04	0.5	2.12	0.167	-1.44	0.049	0.16
1441854_at	Pole	Polymerase (DNA directed), epsilon	-1.94	0.192	-1.17	0.839	2.74	0.209	2.78	0.184	0.6
1425816_at	Zfp287	zinc finger protein 287	1.31	0.387	-1.09	0.434	1.87	0.052	-2.65	0.266	-0.14
1439856_at	Acvr2b	activin receptor IIB	1.59	0.083	1.62	0.076	-1.11	0.68	-2.73	0.208	-0.16
1459547_at	---	Transcribed locus	2.16	0.081	-2.17	0.015	1.49	0.354	-1.32	0.713	0.04
1447182_at	C77815	expressed sequence C77815	1.65	0.555	-1.05	0.899	1.5	0.382	-1.17	0.527	0.23
1446901_at	AU022077	expressed sequence AU022077	1.48	0.312	-1.26	0.777	1.84	0.248	-1.2	0.681	0.21
1448735_at	Cp	ceruloplasmin	1.57	0.271	1.69	0.08	-1.17	0.086	-1.43	0.223	0.16
1444801_at	2900041M22Rik	RIKEN cDNA 2900041M22 gene	-1.69	0.339	1.41	0.316	2.1	0.22	-1.18	0.863	0.16

1450424_a_at	Il18bp	interleukin 18 binding protein	-1.44	0.156	2.01	0.024	1.4	0.013	-1.28	0.066	0.17
1429604_at	1810011H11Rik	RIKEN cDNA 1810011H11 gene	-1.45	0.653	-1.22	0.696	2.6	0.252	1.28	0.762	0.3
1449097_at	Txnrd2	thioredoxin reductase 2	-1	0.983	-1.05	0.794	2.16	0.007	3.19	0.173	0.82
1426389_at	Camk1d	calcium/calmodulin-dependent protein kinase ID	2.07	0.054	1.13	0.592	-1.1	0.544	-1.53	0.265	0.14
1454110_at	4930408K08Rik	RIKEN cDNA 4930408K08 gene	2.88	0.074	-2.5	0.225	-1.2	0.536	1.53	0.192	0.18
1447616_at	---	Transcribed locus	1.8	0.388	1.54	0.268	-1.3	0.616	-1.54	0.123	0.12
1440458_at	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	-1.33	0.628	1.76	0.229	1.6	0.041	-1.25	0.494	0.19
1422023_at	Bsn	bassoon	2.43	0.024	1.03	0.93	-1.51	0.443	-1.11	0.9	0.21
1435210_s_at	Snph	syntaphilin	1.68	0.603	-1.44	0.456	1.74	0.158	-3.33	0.186	-0.34
1419873_s_at	Csf1r	colony stimulating factor 1 receptor	1.54	0.048	1.58	0.006	-1.01	0.943	-1.36	0.426	0.19
1446594_at	---	---	-1.77	0.455	-1.06	0.896	2.61	0.257	2.7	0.06	0.62
1422097_at	4933434I20Rik	RIKEN cDNA 4933434I20 gene	1.17	0.836	2.33	0.266	-1.61	0.146	-3.19	0.049	-0.33
1426869_at	Boc	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) b	1.17	0.153	1.99	0.319	-1.05	0.838	-1.19	0.571	0.23
1446744_at	Sorbs2	sorbin and SH3 domain containing 2	-4.25	0.016	2.36	0.011	1.52	0.363	-1.63	0.339	-0.5
1436563_at	4932441J04Rik	RIKEN cDNA 4932441J04 gene	1.14	0.736	-2.2	0.249	2.52	0.061	-1.21	0.695	0.06
1443936_at	Olfr976	Olfactory receptor 976	2.22	0.227	-1.34	0.66	1.16	0.746	-1.74	0.252	0.07
1420109_at	Pip5k2a	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	2.16	0.127	1.66	0.387	-3.29	0.031	-1.96	0.103	-0.36
1439713_at	Itga1	integrin alpha 1	2.1	0.37	1.31	0.539	-1.41	0.448	-1.14	0.776	0.21
1439682_at	---	---	-1.19	0.822	-1.27	0.7	2.49	0.014	1.08	0.859	0.28
1431587_at	Ccdc7	coiled-coil domain containing 7	1.33	0.492	1.97	0.511	-1.21	0.57	-1.36	0.411	0.18
1433733_a_at	Cry1	cryptochrome 1 (photolyase-like)	1.65	0.425	-1.15	0.478	1.6	0.047	-1.74	0.1	0.09
1445118_at	---	---	2.31	0.513	1.44	0.547	-2.66	0.245	-1.22	0.269	-0.03
1418411_at	Fbxl8	F-box and leucine-rich repeat protein 8	2.01	0.157	-1.02	0.915	1.13	0.597	-1.43	0.406	0.17
1459904_at	BC030870	cDNA sequence BC030870	1.39	0.574	1.85	0.219	-1.13	0.648	-1.35	0.294	0.19
1458062_at	Mapk10	Mitogen activated protein kinase 10	-1.77	0.452	1.7	0.359	1.86	0.06	-1.35	0.637	0.11
1431250_at	9030624G23Rik ///	RIKEN cDNA 9030624G23 gene /// similar to development- and differentiation-en	2.16	0.295	-1.18	0.651	1.12	0.672	-1.1	0.725	0.25
1453925_at	4930429F24Rik	RIKEN cDNA 4930429F24 gene	2.47	0.022	1.06	0.926	-1.67	0.265	-1.55	0.343	0.08
1426315_a_at	6330416G13Rik	RIKEN cDNA 6330416G13 gene	-1.51	0.127	2.08	0.061	1.39	0.09	-1.19	0.25	0.19
1453992_at	Zpbp	zona pellucida binding protein	1.27	0.416	1.95	0.348	-1.11	0.824	-1.78	0.06	0.08
1427673_a_at	Sema3e	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	2.08	0.072	-1.08	0.888	1.12	0.703	-1.13	0.725	0.25
1436604_at	Ttll3	tubulin tyrosine ligase-like family, member 3	2.08	0.037	-1	0.989	1.05	0.807	-1.19	0.497	0.23
1438654_x_at	Mmd2	monocyte to macrophage differentiation-associated 2	-1.65	0.307	2.49	0.007	1.04	0.861	-1.96	0.352	-0.02
1457666_s_at	Ifi202b	interferon activated gene 202B	-1.47	0.449	2.18	0.144	1.27	0.336	-1.59	0.479	0.1
1453871_at	Slc6a11	solute carrier family 6 (neurotransmitter transporter, GABA), member 11	2.16	0.325	-1.13	0.653	1.08	0.801	-1.25	0.688	0.22
1432698_at	2900024I21Rik	RIKEN cDNA 2900024I21 gene	1.77	0.405	1.58	0.458	-1.27	0.482	-1.44	0.41	0.16
1418424_at	Tnfaip6	tumor necrosis factor alpha induced protein 6	2.2	0.2	1.07	0.695	-1.17	0.686	-1.54	0.187	0.14
1452657_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1.51	0.108	1.73	0.054	-1.12	0.263	-1.42	0.147	0.17
1438524_x_at	Pnrc1	proline-rich nuclear receptor coactivator 1	3.21	0.126	-2.82	0.018	-1.76	0.302	1.42	0.631	0.01
1419683_at	Trp53rk	Trp53 regulating kinase	2.98	0.104	-2.25	0.017	-1.4	0.558	1.04	0.897	0.09
1432026_a_at	Herc5	hect domain and RLD 5	1.99	0.104	1.3	0.472	-1.18	0.362	-1.03	0.885	0.27
1438193_at	Nrxn3	neurexin III	1.01	0.991	2.42	0.058	-1.41	0.573	-2.06	0.271	-0.01
1435688_at	Chd9	Chromodomain helicase DNA binding protein 9	2.04	0.271	-2.17	0.011	1.64	0.223	-1.12	0.861	0.1
1416950_at	Tnfaip8	tumor necrosis factor, alpha-induced protein 8	-1.12	0.431	1.75	0.021	1.5	0.085	-1.32	0.286	0.2
1442370_at	---	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830028	2.34	0.341	-1	0.996	-1.25	0.587	1.2	0.775	0.32
1458938_at	---	---	-1.18	0.755	2.25	0.097	1.03	0.917	-1.06	0.905	0.26
1455004_at	D2Wsu81e	DNA segment, Chr 2, Wayne State University 81, expressed	1.88	0.439	-1.13	0.839	1.38	0.597	-1.3	0.107	0.21
1446574_at	Ncor1	Nuclear receptor co-repressor 1	-1.55	0.273	1.16	0.334	2.34	0.093	-2.26	0.139	-0.08
1439207_at	Pnma5	paraneoplastic antigen family 5	1.86	0.059	-1.71	0.339	1.69	0.275	-1.3	0.175	0.14
1432192_at	4930483K19Rik	RIKEN cDNA 4930483K19 gene	-1.23	0.67	1.86	0.46	1.47	0.169	-1.82	0.352	0.07
1449991_at	Cd244 /// LOC6770	CD244 natural killer cell receptor 2B4 /// similar to Natural killer cell receptor 2B4	1.77	0.597	-1.03	0.944	1.4	0.547	-1.34	0.01	0.2
1450206_at	Dlc1	deleted in liver cancer 1	1.19	0.869	-1.2	0.63	2.12	0.351	-1.66	0.056	0.11
1449126_at	Zfp90	zinc finger protein 90	1.19	0.522	2.19	0.027	-1.32	0.238	-1.34	0.404	0.18
1439694_at	Fbxw16	F-box and WD-40 domain protein 16	-1.32	0.354	1.9	0.17	1.49	0.303	-1.37	0.706	0.17

1459469_at	C78516	expressed sequence C78516	1.96	0.313	1.57	0.078	-1.63	0.09	-1.62	0.372	0.07
1458734_at	C78128	expressed sequence C78128	1.12	0.911	-2.17	0.212	2.56	0.017	-1.18	0.776	0.08
1421579_at	Hoxa9	homeo box A9	-1.3	0.015	2.4	0.219	-1.02	0.968	1.57	0.391	0.41
1457484_at	D930050J11	hypothetical D930050J11	1.74	0.391	1.45	0.156	-1.05	0.881	-1.45	0.392	0.17
1431396_at	Iqgap1	IQ motif containing GTPase activating protein 1	-1.15	0.738	1.47	0.089	1.81	0.266	-1.75	0.405	0.09
1425245_a_at	Rgs11	regulator of G-protein signaling 11	1.14	0.226	2.1	0.287	-1.1	0.347	-1.26	0.305	0.22
1459393_at	Tcfap2b	Transcription factor AP-2 beta	-1.25	0.298	2.04	0.214	1.3	0.505	-1.34	0.45	0.19
1449105_at	Sh2d2a	SH2 domain protein 2A	-1.12	0.645	1.45	0.545	1.8	0.238	-1.33	0.416	0.2
1450143_at	Rasgrp1	RAS guanyl releasing protein 1	1.42	0.005	-1.44	0.269	2.03	0.202	-3.45	0.383	-0.36
1425436_x_at	Klra3	killer cell lectin-like receptor, subfamily A, member 3	-1.14	0.208	2.64	0.091	-1.59	0.248	2.75	0.354	0.67
1417618_at	Itih2	inter-alpha trypsin inhibitor, heavy chain 2	2.18	0.574	-1.05	0.449	1.02	0.961	-1.22	0.779	0.23
1425106_a_at	Wars	tryptophanyl-tRNA synthetase	1.57	0.092	-1.04	0.886	1.62	0.334	-1.01	0.982	0.29
1444686_at	A930016P21Rik	RIKEN cDNA A930016P21 gene	1.07	0.875	-1.3	0.474	2.31	0.054	-3.84	0.204	-0.44
1443971_x_at	Mpp7	Membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	2.98	0.446	-2.03	0.449	-1.46	0.039	1.4	0.677	0.22
1439951_at	---	---	-1.04	0.961	1.66	0.351	1.53	0.28	-1.44	0.014	0.18
1416985_at	Sirpa	signal-regulatory protein alpha	-1.13	0.159	1.88	0.01	1.39	0.107	-1.02	0.909	0.28
1447000_at	---	---	-1.54	0.275	1.09	0.856	2.41	0.012	-1.69	0.057	0.07
1438479_at	Zfp213	zinc finger protein 213	-1.06	0.703	1.41	0.688	1.8	0.015	-1.36	0.698	0.2
1419171_at	Tmem157	transmembrane protein 157	1.42	0.114	2.02	0.166	-1.41	0.171	-1.54	0.285	0.12
1452870_at	---	---	-1.03	0.769	2.19	0.008	-1.01	0.839	1.03	0.855	0.3
1444988_at	---	---	1.98	0.323	1.42	0.486	-1.32	0.54	-1.25	0.724	0.21
1442433_at	---	---	-1.1	0.81	1.68	0.339	1.57	0.185	-1.05	0.846	0.27
1457497_at	Syt1	Synaptotagmin I	1.17	0.879	2.02	0.122	-1.03	0.947	-1.62	0.295	0.13
1444710_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230020K	1.96	0.136	1.37	0.096	-1.2	0.534	-1.4	0.505	0.18
1457519_at	---	Transcribed locus	2.24	0.422	1.2	0.58	-1.39	0.437	-1.12	0.776	0.23
1419216_at	Azi1	5-azacytidine induced gene 1	-1.4	0.731	1.44	0.482	2.01	0.048	-1.26	0.532	0.19
1434641_x_at	Sez6l2	seizure related 6 homolog like 2	1.52	0.337	-1.15	0.794	1.77	0.131	-1.02	0.929	0.28
1459991_at	Myo9a	myosin IXa	1.02	0.959	2.53	0.056	-1.64	0.053	-1.07	0.69	0.21
1456487_at	Adcy1	adenylate cyclase 1	-1.16	0.013	1.85	0.358	1.45	0.058	-1.3	0.165	0.21
1453472_a_at	Slamf7	SLAM family member 7	-1.16	0.83	2.1	0.338	1.2	0.421	-1.46	0.381	0.17
1439690_at	5133401N09Rik	RIKEN cDNA 5133401N09 gene	1.83	0.326	1.54	0.51	-1.26	0.315	-1.7	0.052	0.1
1428005_at	Mosc1	MOCO sulphurase C-terminal domain containing 1	1.68	0.032	-1.27	0.051	1.7	0.176	-1.11	0.846	0.25
1445424_at	---	---	2.23	0.473	1.1	0.741	-1.2	0.76	-1.18	0.67	0.24
1424178_at	Tmem38a	transmembrane protein 38a	2.35	0.312	-2.27	0.194	1.37	0.723	-1.01	0.957	0.11
1435071_at	Zfyve1	zinc finger, FYVE domain containing 1	1.09	0.824	-1.09	0.772	2.16	0.179	-1.3	0.39	0.21
1421421_at	Angptl1	angiopoietin-like 1	1.5	0.309	1.99	0.098	-1.49	0.121	-2.44	0.349	-0.11
1448301_s_at	Serpinb1a	serine (or cysteine) peptidase inhibitor, clade B, member 1a	-1.25	0.204	2.26	0.47	1.11	0.693	-1.89	0.017	0.05
1427380_at	Klk1b3	kallikrein 1-related peptidase b3	1.49	0.511	-1.58	0.387	2.04	0.191	-2.18	0.256	-0.06
1441721_at	---	---	-1.16	0.81	-1.61	0	2.67	0.026	2.46	0.098	0.59
1450092_at	Ighmbp2	immunoglobulin mu binding protein 2	-1.15	0.776	1.34	0.396	1.95	0.315	-2.04	0.215	0.03
1449449_at	Ptges	prostaglandin E synthase	-1.7	0.209	2.32	0.212	1.25	0.399	-1.28	0.156	0.15
1459262_at	Mterfd1	MTERF domain containing 1	2.54	0.093	-1.1	0.771	-1.4	0.308	1.05	0.951	0.27
1448554_s_at	Myh6 /// LOC67189	myosin, heavy polypeptide 6, cardiac muscle, alpha /// similar to myosin, heavy p	-1.5	0.319	1.09	0.766	2.41	0.266	-1.1	0.598	0.22
1422476_at	Ifi30	interferon gamma inducible protein 30	-1.15	0.203	1.76	0	1.54	0.033	-1.26	0.342	0.22
1433765_at	Ube2o	ubiquitin-conjugating enzyme E2O	-1.02	0.734	-1.05	0.74	2.24	0.22	3.21	0.267	0.84
1426316_at	6330416G13Rik	RIKEN cDNA 6330416G13 gene	-1.14	0.704	1.96	0.141	1.33	0.178	-1.02	0.875	0.28
1417277_at	Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	-1.27	0.1	2.3	0.001	1.08	0.815	-1.48	0.374	0.16
1447755_at	Srpk2	Serine/arginine-rich protein specific kinase 2	1.32	0	2.03	0.418	-1.22	0.297	-2.14	0.553	0
1433000_at	---	---	1.86	0.223	1.36	0.304	-1.05	0.923	-1.86	0.298	0.08
1433453_a_at	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	-1.1	0.13	1.19	0.529	2.06	0.081	-1.76	0.3	0.1
1426177_a_at	Nkx1-2	NK1 transcription factor related, locus 2 (Drosophila)	-1.83	0.168	1.48	0.319	2.14	0.332	-1.15	0.672	0.16
1429349_at	Hmgb4	high-mobility group box 4	2.96	0.399	-2.67	0.202	-1.2	0.378	1.02	0.695	0.03
1453116_at	Zfp689	zinc finger protein 689	-1.33	0.627	1.29	0.372	2.12	0.229	-1.65	0.342	0.11

1443754_x_at	Lsamp	Limbic system-associated membrane protein	2.56	0.508	1.23	0.593	-2.69	0.274	-1.9	0.409	-0.2
1423501_at	Max	Max protein	-3.16	0.239	2.23	0.131	1.62	0.11	-1.35	0.597	-0.17
1446420_at	Plxna2	Plexin A2	2.06	0.254	1.42	0.186	-1.45	0.095	-1.52	0.302	0.13
1447586_at	Cspg2	chondroitin sulfate proteoglycan 2	-1.38	0.389	2.67	0.242	-1.29	0.234	1.09	0.607	0.27
1453913_a_at	Tap2	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	-1.22	0.33	1.22	0.196	2.13	0.008	-1.33	0.33	0.2
AFFX-TrpnX-3_at	---	---	1.75	0.155	1.43	0.369	-1.01	0.957	-1.42	0.461	0.19
1433454_at	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	-1.08	0.932	1.41	0.415	1.83	0.259	-1.95	0.169	0.05
1454152_a_at	Gprk2l	G protein-coupled receptor kinase 2, groucho gene related (Drosophila)	2.45	0.102	-2.99	0.062	1.38	0.269	-1.53	0.49	-0.17
1423634_at	Gsdm1	gasdermin 1	1.93	0.245	1.33	0.447	-1.09	0.844	-1.77	0.053	0.1
1435124_at	LOC328644	hypothetical gene supported by AK045595	1.82	0.228	-1.35	0.556	1.61	0.194	-2.69	0.273	-0.15
1416297_s_at	Pap	pancreatitis-associated protein	-1.9	0.2	1.31	0.523	2.34	0.058	-1.21	0.374	0.13
1443634_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	1.59	0.241	-1	0.993	1.59	0.247	-2.57	0.422	-0.1
1440862_at	Gpr178	G protein-coupled receptor 178	-1.01	0.978	1.76	0.258	1.42	0.301	-1.23	0.626	0.24
1442333_a_at	Scn9a /// LOC6718	sodium channel, voltage-gated, type IX, alpha /// similar to sodium channel 25	-1.14	0.879	2.01	0.045	1.29	0.606	-1.49	0.479	0.17
1451623_at	Mrpl15	mitochondrial ribosomal protein L15	2.08	0.069	-1.03	0.897	1.13	0.516	-1.94	0.324	0.06
1454231_a_at	Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	-1.05	0.894	2.06	0.238	1.17	0.621	-1.81	0.147	0.09
1443508_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	2.33	0.014	1.28	0.59	-1.77	0.161	-1.17	0.64	0.17
1432722_at	4933408K01Rik	RIKEN cDNA 4933408K01 gene	1.68	0.459	2	0.147	-2.02	0.179	-3.03	0.189	-0.34
1451733_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.35	0.318	-1.34	0.036	2.08	0.166	-1	0.998	0.27
1451944_a_at	Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11	-1.05	0.924	2	0.102	1.23	0.677	-1.64	0.161	0.13
1448443_at	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1	-1.39	0.435	1.33	0.516	2.13	0.017	-1.75	0.197	0.08
1457796_at	Ubr1	Ubiquitin protein ligase E3 component n-recognin 1	1.77	0.145	1.73	0.189	-1.47	0.105	-1.56	0.241	0.12
1456513_at	Ebf3	Early B-cell factor 3	1.21	0.796	2	0.214	-1.03	0.957	-2.4	0.08	-0.06
1424913_at	2310044G17Rik	RIKEN cDNA 2310044G17 gene	1.8	0.354	-1.07	0.793	1.44	0.338	-1.11	0.679	0.27
1418724_at	Cfi	complement component factor i	2.41	0.233	-1.1	0.319	-1.16	0.077	1.91	0.004	0.52
1419466_at	Nkd2	naked cuticle 2 homolog (Drosophila)	-1.53	0.623	2.04	0.248	1.49	0.298	-1.15	0.75	0.21
1418994_at	2410116G06Rik	RIKEN cDNA 2410116G06 gene	1.42	0.455	-1.18	0.777	1.91	0.086	-1.47	0.324	0.17
1448754_at	Rbp1	retinol binding protein 1, cellular	1.3	0.212	2.29	0.113	-1.68	0.027	-1.17	0.261	0.18
1438100_at	B230208H17Rik	RIKEN cDNA B230208H17 gene	1.6	0.27	1.8	0.182	-1.26	0.497	-1.19	0.672	0.24
1427473_at	Gstm3	glutathione S-transferase, mu 3	-1.14	0.647	1.99	0.169	1.32	0.143	-1.13	0.499	0.26
1447617_at	Cdk2	cyclin-dependent kinase 2	1.8	0.511	-1.15	0.282	1.52	0.324	-1	0.992	0.29
1444704_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	1.63	0.242	1.86	0.343	-1.44	0.286	-1.17	0.783	0.22
1427318_s_at	Dysf /// Fer1l3	dysferlin /// fer-1-like 3, myoferlin (C. elegans)	1.22	0.347	1.97	0.233	-1.01	0.966	-1.54	0.222	0.16
1439793_at	Gja3	gap junction membrane channel protein alpha 3	-1.67	0.306	2.34	0.138	1.25	0.631	-2.39	0.232	-0.12
1427723_at	Gdf11	growth differentiation factor 11	-1.37	0.528	2.34	0.262	1.12	0.833	-1.99	0.141	0.03
1434593_at	Eif5a2	eukaryotic translation initiation factor 5A2	-1.02	0.954	2.29	0.046	-1.09	0.664	2.12	0.291	0.58
1437672_at	Irs3	insulin receptor substrate 3	1.93	0.025	-1.17	0.349	1.41	0.05	-1.43	0.26	0.18
1425511_at	Mark1	MAP/microtubule affinity-regulating kinase 1	2.2	0.074	1.23	0.769	-1.31	0.719	-2.47	0.232	-0.09
1416953_at	Ctgf	connective tissue growth factor	1.19	0.323	2.04	0.001	-1.03	0.866	-1.42	0.455	0.19
1434795_at	Disp1	dispatched homolog 1 (Drosophila)	-1	0.996	1.76	0.067	1.43	0.191	-1.2	0.229	0.25
1450148_at	Mcoln3	mucolipin 3	-1.22	0.185	1.94	0.169	1.44	0.066	-2.74	0.015	-0.15
1458489_at	---	Transcribed locus	2.84	0.031	-1.17	0.786	-1.99	0.005	1.26	0.421	0.23
1443900_at	Chd8	chromodomain helicase DNA binding protein 8	1.37	0.163	1.85	0.353	-1.03	0.875	-1.22	0.737	0.24
1446669_at	Ebf1	Early B-cell factor 1	1.47	0.499	1.91	0.246	-1.22	0.593	-2.6	0.119	-0.11
1437054_x_at	Prm1	protamine 1	-1.83	0.562	2.17	0.392	1.48	0.291	-1.14	0.815	0.17
1444252_at	---	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130003J	1.47	0.502	1.97	0.219	-1.33	0.176	-1.08	0.881	0.26
1441647_at	Fyn	Fyn proto-oncogene	2.17	0.151	1.23	0.317	-1.26	0.632	-1.37	0.622	0.19
1435123_at	C030014M07Rik ///	RIKEN cDNA C030014M07 gene /// similar to RIKEN cDNA C920006C10	1.03	0.969	2.38	0.111	-1.26	0.225	-1.42	0.333	0.18
1442810_x_at	Scn9a /// LOC6718	sodium channel, voltage-gated, type IX, alpha /// similar to sodium channel 25	2.11	0.014	-3.12	0.261	1.77	0.051	-3.75	0.143	-0.75
1440811_x_at	Cd8a	CD8 antigen, alpha chain	-1.98	0.111	1.44	0.37	2.26	0.339	-1.42	0.37	0.07
1447806_s_at	Srpk3	serine/arginine-rich protein specific kinase 3	-1.04	0.911	1.26	0.517	1.98	0.182	-2.24	0.101	-0.01
1437540_at	---	---	-1.06	0.64	1.61	0.168	1.65	0.099	-2.62	0.056	-0.11
1443061_at	---	Transcribed locus	-1.1	0.726	2.23	0.234	1.06	0.876	-1	0.993	0.3

1428912_at	Ttll4	tubulin tyrosine ligase-like family, member 4	-1.96	0.385	2.68	0.031	1.02	0.972	-1.42	0.397	0.08
1436418_at	1600027N09Rik	RIKEN cDNA 1600027N09 gene	-1.36	0.591	1.16	0.822	2.31	0.132	-1.35	0.532	0.19
1429223_a_at	Hfe2	hemochromatosis type 2 (juvenile) (human homolog)	1.11	0.807	-1.01	0.917	2.1	0.135	-2.28	0.449	-0.02
1436504_x_at	Apoa4	apolipoprotein A-IV	2.19	0.22	1.27	0.529	-1.35	0.254	-1.68	0.439	0.11
1452468_s_at	Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	1.24	0.625	-1.13	0.851	2.07	0.273	-1.04	0.859	0.29
1419527_at	Comp	cartilage oligomeric matrix protein	1.57	0.027	-1.03	0.916	1.67	0.158	-1.49	0.049	0.18
1418608_at	Calml3	calmodulin-like 3	1.28	0.493	-1.32	0.552	2.17	0.04	-1.15	0.785	0.24
1420413_at	Slc7a11	solute carrier family 7 (cationic amino acid transporter, y+ system), member 11	-1.68	0.391	2.09	0.058	1.53	0.115	-1.21	0.562	0.18
1460426_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	1.67	0.178	-1.53	0.042	1.88	0.17	-1.46	0.22	0.14
1457387_at	Repin1	Replication initiator 1	2.13	0.465	-1.31	0.598	1.32	0.322	-1.48	0.536	0.16
1416121_at	Lox	lysyl oxidase	1.29	0.554	2.32	0.121	-1.67	0.208	-1.18	0.719	0.19
1448510_at	Efna1	ephrin A1	-1.12	0.659	2.22	0.171	1.09	0.791	-1.76	0.516	0.11
1445213_at	Cyld	cylindromatosis (turban tumor syndrome)	2.13	0.235	1.51	0.598	-1.74	0.082	-1.36	0.508	0.13
1459113_at	Nfasc	Neurofascin	1.27	0.53	1.99	0.208	-1.06	0.825	-1	0.99	0.3
1419848_x_at	Tlr7	toll-like receptor 7	-1.65	0.428	1.65	0.295	1.97	0.14	-1.81	0.041	0.04
1429947_a_at	Zbp1	Z-DNA binding protein 1	-1.04	0.946	1.31	0.081	1.95	0.065	-1.62	0.346	0.15
1420433_at	Taf7l	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.7	0.186	1.45	0.514	2.18	0.205	-1.85	0.094	0.02
1439242_at	Mocs3	molybdenum cofactor synthesis 3	1.04	0.652	-2.19	0.127	2.72	0.022	-1.41	0.551	0.04
1415965_at	Scd1	stearoyl-Coenzyme A desaturase 1	-1.36	0.41	1.05	0.935	2.43	0.045	-2.18	0.243	-0.02
1449347_a_at	Xlr4b /// Xlr4a /// Xlr	X-linked lymphocyte-regulated 4B /// X-linked lymphocyte-regulated 4A /// X-linke	1.14	0.762	-1.09	0.808	2.16	0.353	-1.77	0.157	0.11
1453899_at	---	---	-1.02	0.938	2.36	0.181	-1.13	0.611	1.72	0.554	0.48
1449182_at	Retn	resistin	-3.67	0.094	-1.21	0.642	3.12	0.354	4.7	0.138	0.74
1454180_at	Armc2	armadillo repeat containing 2	2.42	0.27	-1.08	0.8	-1.14	0.126	1.2	0.732	0.35
1441781_at	AI317158	expressed sequence AI317158	-1.19	0.763	-1.37	0.167	2.65	0.074	1.37	0.318	0.37
1435551_at	Fhod3	formin homology 2 domain containing 3	-1.06	0.425	1.53	0.287	1.75	0.117	-1.2	0.653	0.26
1433256_at	A930011E06Rik	RIKEN cDNA A930011E06 gene	-2.22	0.027	2.61	0.057	1.16	0.692	-1.63	0.49	-0.02
1436168_at	C730029A08Rik	RIKEN cDNA C730029A08 gene	-1.17	0.082	-1.24	0.219	2.56	0.107	3.46	0.135	0.9
1422221_at	Hand2	heart and neural crest derivatives expressed transcript 2	-1.64	0.2	2.28	0.328	1.34	0.647	-1.22	0.69	0.19
1455270_at	---	---	-1.61	0.499	2.32	0.071	1.28	0.024	-1.88	0.019	0.03
1457859_at	Arl15	ADP-ribosylation factor-like 15	2.12	0.135	1.24	0.605	-1.15	0.701	-1.2	0.799	0.25
1447567_at	D130007H15Rik	RIKEN cDNA D130007H15 gene	1.93	0.331	-1.16	0.619	1.44	0.194	-1.19	0.778	0.25
1431944_at	4930484H19Rik	RIKEN cDNA 4930484H19 gene	2.18	0.509	-2.48	0.026	1.64	0.261	-3.39	0.001	-0.51
1430570_at	Kynu	kynureninase (L-kynurenine hydrolase)	-1	0.997	1.12	0.518	2.11	0.241	-1.64	0.169	0.15
1429974_at	Tbx18	T-box18	-2.8	0.091	2.71	0.03	1.16	0.83	-1.78	0.417	-0.18
1443243_at	---	---	1.32	0.715	-2.14	0.497	2.44	0.025	-1.44	0.707	0.05
1435622_at	Hs3st3a1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	-1	0.994	1.53	0.591	1.7	0.103	-2.18	0.17	0.01
1429571_a_at	Spaca1	sperm acrosome associated 1	-1.47	0.324	2.53	0.011	1.03	0.95	-1.65	0.311	0.11
1419396_at	Arid3a	AT rich interactive domain 3A (Bright like)	-1.05	0.862	1.84	0.047	1.44	0.087	-1.2	0.174	0.26
1446018_at	C79240	expressed sequence C79240	-1.02	0.856	2.15	0.037	1.11	0.799	-1.32	0.354	0.23
1418557_s_at	Tssk3	testis-specific serine kinase 3	-1.14	0.827	2.66	0.036	-1.43	0.641	1.9	0.15	0.5
1424233_at	Meox2	mesenchyme homeobox 2	1.44	0.606	1.97	0.307	-1.22	0.185	-2.34	0.307	-0.04
1435033_at	Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4	-1.04	0.93	1.81	0.136	1.47	0.051	-1.06	0.835	0.29
1430648_at	Scn2b	sodium channel, voltage-gated, type II, beta	1.76	0.056	1.52	0.282	-1.05	0.674	-1.94	0.152	0.07
1439637_at	Kif7	kinesin family member 7	1.81	0.292	1.79	0.273	-1.59	0.222	-1.2	0.047	0.2
1456392_at	Negr1	neuronal growth regulator 1	1.31	0.511	2.4	0.124	-1.92	0.103	-1.05	0.933	0.18
1421201_a_at	Tro	trophinin	1.19	0.54	2.54	0.172	-1.97	0.1	-1.04	0.96	0.18
1444452_at	D930002L09Rik	RIKEN cDNA D930002L09 gene	3.08	0.038	-1.71	0.496	-1.76	0.335	1.91	0.3	0.38
1453876_at	LOC621121 /// LOC	hypothetical LOC621121 /// hypothetical protein LOC631862 /// RIKEN cDNA 17(	-2.16	0.03	2.46	0.399	1.31	0.558	-2.07	0.587	-0.12
1453597_at	4933425O20Rik	RIKEN cDNA 4933425O20 gene	1.38	0.187	-1.14	0.605	1.98	0.044	-1.39	0.185	0.21
1447243_at	BC040756	cDNA sequence BC040756	2.66	0.003	-1.83	0.299	1.03	0.932	-1.97	0.555	-0.03
1426143_at	Trdn	triadin	1.59	0.523	-1.89	0.469	2.12	0.542	-1.21	0.71	0.15
1449529_s_at	Prlpe	prolactin-like protein E	2.75	0.35	1.07	0.892	-2.39	0.182	-1.11	0.76	0.08
1447457_at	Pkig	Protein kinase inhibitor, gamma	2.84	0.017	-2.26	0.346	-1.04	0.957	1	0.996	0.14

1446708_at	Hif3a	hypoxia inducible factor 3, alpha subunit	-1.44	0.424	2.33	0.398	1.22	0.553	-1.65	0.13	0.11
1421178_at	Mgat4c	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isc	2.03	0.259	-1.82	0.453	1.66	0.032	-1.51	0.527	0.09
1447763_at	---	---	2.67	0.03	-1.11	0.844	-1.48	0.342	1	0.996	0.27
1449316_at	Cyp4f15	cytochrome P450, family 4, subfamily f, polypeptide 15	2.01	0.339	-1.33	0.013	1.48	0.386	-1.48	0.359	0.17
1442612_at	C730036E19Rik	RIKEN cDNA C730036E19 gene	2.4	0.159	-1.12	0.165	-1.05	0.826	3.93	0.168	1.04
1425849_at	Chrnb4	cholinergic receptor, nicotinic, beta polypeptide 4	1.91	0.22	-2.07	0.208	1.85	0.038	-1.28	0.657	0.1
1425081_at	Zfp286	zinc finger protein 286	1.96	0.052	1.5	0.55	-1.27	0.511	-1.16	0.734	0.26
1453535_at	Olfr78	olfactory receptor 78	-1.12	0.898	1.58	0.289	1.78	0.273	-1.85	0.307	0.1
1452687_at	Dus2l	dihydrouridine synthase 2-like (SMM1, S. cerevisiae)	2.21	0.169	-1.34	0.183	1.28	0.53	-1.25	0.527	0.23
1457426_at	1700048O20Rik	RIKEN cDNA 1700048O20 gene	-1.89	0.556	1.34	0.402	2.38	0.195	-2.1	0.014	-0.07
1444294_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930551A22 pr	2.1	0.22	1.31	0.731	-1.19	0.604	-2.74	0.1	-0.13
1444257_at	Prr11	proline rich 11	-2.78	0.205	2.9	0.005	-1.01	0.958	3.6	0.143	0.68
1445368_at	---	---	-1.51	0.53	2.34	0.107	1.25	0.158	-1.23	0.594	0.21
1429178_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	1.58	0.233	-1.18	0.479	1.82	0.29	-1.11	0.72	0.28
1429718_at	Slitrk5	SLIT and NTRK-like family, member 5	1.88	0.247	-1.11	0.825	1.47	0.232	-1.21	0.597	0.26
1421183_at	Tex12	testis expressed gene 12	2.11	0.454	1.49	0.258	-1.53	0.483	-1.07	0.829	0.25
1426396_at	Cd247	CD247 antigen	1.96	0.208	1.46	0.466	-1.2	0.12	-1.95	0.23	0.07
1443047_at	Pdzrn3	PDZ domain containing RING finger 3	2.01	0.472	1.28	0.56	-1.04	0.953	-1.49	0.242	0.19
1432720_at	4833412K13Rik	RIKEN cDNA 4833412K13 gene	2.21	0.183	1.51	0.467	-1.88	0.151	-1.39	0.45	0.11
1460301_at	V1rd2	vomeronasal 1 receptor, D2	-2.43	0.239	1.98	0.149	1.87	0.085	-1.34	0.434	0.02
1449296_a_at	Cnp1	cyclic nucleotide phosphodiesterase 1	1.17	0.737	-1.04	0.907	2.12	0.143	-1.38	0.431	0.22
1435427_x_at	BC037112	cDNA sequence BC037112	1.46	0.552	-1.38	0.221	2.07	0.045	-1.26	0.611	0.22
1418216_at	Ggtla1	gamma-glutamyltransferase-like activity 1	1.23	0.07	2.1	0.129	-1.08	0.724	-1.42	0.279	0.21
1417150_at	Slc6a4	solute carrier family 6 (neurotransmitter transporter, serotonin), member 4	-1.02	0.939	-1.03	0.917	2.31	0.117	2.33	0.405	0.65
1446845_at	LOC272350	similar to RIKEN cDNA 1110067D22	2.89	0.363	-1.57	0.269	-1.37	0.486	1.95	0.319	0.47
1424100_s_at	Cend1	cell cycle exit and neuronal differentiation 1	-3.95	0.048	2.49	0.207	1.52	0.319	-1.07	0.912	-0.25
1418832_at	Pkp3	plakophilin 3	1.35	0.591	-1.12	0.454	2.01	0.33	-1.14	0.779	0.28
1456226_x_at	Ddr1	discoidin domain receptor family, member 1	-1.14	0.363	1.68	0.174	1.71	0.105	-2.06	0.041	0.05
1446999_at	---	---	2.07	0.212	1.51	0.239	-1.45	0.253	-1.28	0.579	0.21
1445486_at	Lrrc49	Leucine rich repeat containing 49	-1.18	0.677	1.16	0.655	2.26	0.054	-1.27	0.149	0.24
1447722_at	---	Transcribed locus	2.44	0.469	-1	0.999	-1.22	0.758	1.04	0.955	0.31
1432637_at	LOC675539 /// LOC	similar to Hippocalcin-like protein 1 (Visinin-like protein 3) (VILIP-3) (Neural visinii	1.41	0.428	2.17	0.028	-1.46	0.46	-2.68	0.236	-0.14
1423381_at	4921521F21Rik	RIKEN cDNA 4921521F21 gene	-1.08	0.073	1.72	0.102	1.61	0.03	-1.67	0.15	0.15
1447779_x_at	Bat1a	HLA-B-associated transcript 1A	1.34	0.564	2.31	0.227	-1.64	0.445	-1.29	0.588	0.18
1453683_a_at	Cep55	centrosomal protein 55	1.79	0.021	1.64	0.112	-1.2	0.595	-1.15	0.71	0.27
1442496_at	Cdkl3	Cyclin-dependent kinase-like 3	1.54	0.056	1.88	0.214	-1.17	0.56	-1.39	0.337	0.21
1459838_s_at	Btbd11	BTB (POZ) domain containing 11	-1.03	0.901	-1.12	0.739	2.4	0.183	1.03	0.951	0.32
1432493_at	1700020M10Rik	RIKEN cDNA 1700020M10 gene	2.72	0.02	-1.36	0.558	-1.24	0.526	1.76	0.152	0.47
1426334_a_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	1.46	0.564	-1.56	0.32	2.16	0.236	-1.14	0.621	0.23
1458485_at	Fbxl7	F-box and leucine-rich repeat protein 7	-1.13	0.894	1.76	0.088	1.62	0.198	-1.18	0.142	0.27
1435971_at	Rims3	regulating synaptic membrane exocytosis 3	-1.06	0.694	1.74	0.063	1.59	0.357	-1.3	0.601	0.24
1447949_at	---	---	2.33	0.348	-2.16	0.168	1.48	0.52	-3.05	0.331	-0.35
1449569_at	Thpo	thrombopoietin	-1.29	0.489	1.07	0.807	2.43	0.039	-1.39	0.432	0.2
1426542_at	Endod1	endonuclease domain containing 1	-1	0.993	2.46	0.1	-1.22	0.425	3.41	0.201	0.91
1436987_at	5430433G21Rik	RIKEN cDNA 5430433G21 gene	2.17	0.086	1.24	0.577	-1.16	0.655	-1.81	0.488	0.11
1431329_at	Nphp4	nephronophthisis 4 (juvenile) homolog (human)	1.26	0.773	2.4	0.182	-1.62	0.431	-1.6	0.522	0.11
1431217_at	Lrrc27	leucine rich repeat containing 27	-1.7	0.256	2.56	0.158	1.12	0.803	-1.02	0.968	0.24
1445124_at	A930009L07Rik	RIKEN cDNA A930009L07 gene	-1.88	0.09	2.89	0.158	-1.17	0.731	1.11	0.837	0.24
1417216_at	Pim2	proviral integration site 2	-1.25	0.02	-1.04	0.811	2.52	0.215	1.45	0.315	0.42
1447501_at	---	Transcribed locus	2.05	0.367	-1.04	0.922	1.27	0.285	-2.48	0.299	-0.05
1456524_at	Nrg1	neuregulin 1	-1.2	0.707	1.6	0.595	1.85	0.149	-2	0.031	0.06
1420910_at	Ppap2c	phosphatidic acid phosphatase type 2c	-1.57	0.513	2.76	0.015	-1.13	0.629	2.28	0.091	0.58
1457427_at	Ajap1	Adherens junction associated protein 1	-2.54	0.383	2.91	0.035	-1.02	0.973	1.61	0.277	0.24

1455457_at	Cyp2c50 /// Cyp2c5	cytochrome P450, family 2, subfamily c, polypeptide 50 /// cytochrome P450	2.98	0.382	-1.68	0.043	-1.4	0.067	1	0.987	0.22
1437927_at	Dlgh2	discs, large homolog 2 (Drosophila)	-1.01	0.985	1.21	0.619	2.09	0.198	-4.33	0.027	-0.51
1449421_a_at	Kcne2	potassium voltage-gated channel, Isk-related subfamily, gene 2	2.5	0.46	1.24	0.515	-1.83	0.017	-1.42	0.16	0.12
1455973_at	RP23-219P13.3	hypothetical protein LOC626870	-1.02	0.93	1.24	0.778	2.07	0.049	-1.77	0.36	0.13
1436748_at	1110014K08Rik	RIKEN cDNA 1110014K08 gene	2.72	0.054	-1.22	0.674	-1.33	0.262	1.04	0.954	0.3
1418980_a_at	Cnp1	cyclic nucleotide phosphodiesterase 1	1.85	0.053	-1.04	0.354	1.47	0.204	-1.31	0.417	0.24
1444281_at	Camk2d	Calcium/calmodulin-dependent protein kinase II, delta	2.1	0.196	1.3	0.761	-1.12	0.791	-1.28	0.556	0.25
1458152_at	Etfdh	electron transferring flavoprotein, dehydrogenase	2	0.204	-1.72	0.113	1.71	0.375	-1.67	0.543	0.08
1459017_at	---	---	3.17	0.009	-1.72	0.392	-1.85	0.412	1.59	0.588	0.3
1435138_at	Tmem28	transmembrane protein 28	-1.44	0.622	1.7	0.284	1.9	0.28	-1.36	0.571	0.2
1451483_s_at	1700054N08Rik	RIKEN cDNA 1700054N08 gene	-1.86	0.34	2.21	0.242	1.54	0.177	-1.01	0.976	0.22
1432909_at	4933424H11Rik	RIKEN cDNA 4933424H11 gene	-2	0.47	-1.05	0.949	2.84	0.026	1.93	0.201	0.43
1450554_at	Defb2	defensin beta 2	2.54	0.118	1.04	0.942	-1.41	0.172	-1.45	0.124	0.18
1440946_at	Zfp483	Zinc finger protein 483	2.25	0.158	-1.47	0.4	1.37	0.446	-1.87	0.063	0.07
1439644_at	Ebf1	Early B-cell factor 1	2.33	0.431	1.07	0.851	-1.12	0.727	-1.91	0.195	0.09
1430534_at	Rnase6	ribonuclease, RNase A family, 6	1.89	0.156	1.55	0.092	-1.18	0.433	-1.96	0.118	0.08
1460555_at	6330500D04Rik	RIKEN cDNA 6330500D04 gene	-1.22	0.404	1.72	0.229	1.75	0.039	-2.1	0.098	0.04
1445951_at	C86345	expressed sequence C86345	-1.6	0.599	1.86	0.149	1.81	0.305	-1.04	0.962	0.26
1430025_at	Ppp3cc	protein phosphatase 3, catalytic subunit, gamma isoform	-1.05	0.903	1.37	0.046	1.97	0.004	-1.31	0.502	0.25
1445175_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	1.84	0.209	1.58	0.311	-1.14	0.607	-1.44	0.383	0.21
1425308_at	Trim31	tripartite motif-containing 31	-1.36	0.735	2.07	0.215	1.49	0.435	-1.08	0.805	0.28
1440889_at	BC006965	cDNA sequence BC006965	-2.14	0.454	2.91	0.046	-1.08	0.845	1.46	0.344	0.29
1430855_at	Col20a1	collagen, type XX, alpha 1	2.33	0.176	1.1	0.874	-1.14	0.76	-1.45	0.565	0.21
1440726_at	A230062I15Rik	RIKEN cDNA A230062I15 gene	2.86	0.066	-4.02	0.135	1.19	0.677	-1.24	0.355	-0.3
1458530_at	Zfp532	Zinc finger protein 532	1.92	0.526	1.47	0.153	-1.09	0.475	-1.17	0.58	0.28
1422741_a_at	Bbx	bobby sox homolog (Drosophila)	-1.84	0.387	2.69	0.078	1.06	0.908	-1.98	0.285	-0.02
1439510_at	Sgol1	shugoshin-like 1 (S. pombe)	-1.03	0.972	-1.18	0.462	2.49	0.047	10.93	0.185	2.8
1420049_at	C78859	expressed sequence C78859	1.45	0.06	2.22	0.073	-1.59	0.472	-1.35	0.19	0.19
1445510_at	C79601	expressed sequence C79601	2.44	0.16	-1.33	0.574	1.11	0.829	-2.21	0.328	0
1437116_at	Letmd1	LETM1 domain containing 1	-1.44	0.687	1.57	0.543	2.04	0.09	-3.38	0.184	-0.3
1452300_at	2410005O16Rik	RIKEN cDNA 2410005O16 gene	2.02	0.204	1.32	0.34	-1.04	0.903	-1.08	0.745	0.31
1419700_a_at	Prom1	prominin 1	-1.06	0.728	2.47	0.026	-1.11	0.473	2.38	0.423	0.67
1441834_x_at	Tia1	Cytotoxic granule-associated RNA binding protein 1	1.89	0.246	1.73	0.309	-1.45	0.397	-1.17	0.618	0.25
1450259_a_at	Stat5a	signal transducer and activator of transcription 5A	1.37	0.477	-1.09	0.798	2.02	0.179	-1.04	0.926	0.32
1449468_at	St6galnac5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	2.54	0.016	1.41	0.493	-2.75	0.03	-4.36	0.004	-0.79
1440367_at	Pgs1	Phosphatidylglycerophosphate synthase 1	2.18	0.475	-1.08	0.895	1.21	0.423	-1.23	0.656	0.27
1430759_at	4930523C07Rik	RIKEN cDNA 4930523C07 gene	1.53	0.106	-1.54	0.422	2.14	0.16	-2.23	0.215	-0.03
1435438_at	Sox8	SRY-box containing gene 8	2.2	0.043	-1.02	0.975	1.12	0.85	-1.77	0.39	0.14
1443004_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730045N	1.2	0.539	2.31	0.236	-1.25	0.695	-2.12	0.305	0.04
1449606_at	---	---	2.22	0.058	1.34	0.379	-1.32	0.539	-1.12	0.818	0.28
1454534_at	Ing1	inhibitor of growth family, member 1	1.8	0.365	1.53	0.089	-1.02	0.908	-1.41	0.464	0.23
1442380_at	Lcn4	lipocalin 4	-1.38	0.734	1.8	0.236	1.79	0.189	-1.07	0.883	0.28
1451824_at	Btn1a1	butyrophilin, subfamily 1, member A1	1.35	0.619	1.98	0.11	-1.01	0.972	-1.11	0.827	0.3
1422303_a_at	Tnfrsf18	tumor necrosis factor receptor superfamily, member 18	-1.23	0.582	2.22	0.113	1.29	0.266	-1.54	0.19	0.18
1460283_at	Mefv	Mediterranean fever	-1.64	0.22	1.56	0.073	2.15	0.156	-1.66	0.022	0.1
1424144_at	Cdt1	chromatin licensing and DNA replication factor 1	-1.19	0.481	-1.26	0.113	2.69	0.016	2.05	0.169	0.57
1418483_a_at	Ggta1	glycoprotein galactosyltransferase alpha 1, 3	1.37	0.114	2.18	0.009	-1.3	0.074	-1.28	0.321	0.24
1422078_at	Akt3	thymoma viral proto-oncogene 3	-1.03	0.959	2.08	0.294	1.27	0.621	-1.36	0.532	0.24
1432286_at	Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	2.33	0.488	-1.61	0.195	1.37	0.591	-2.76	0.319	-0.17
1443125_at	Trip12	thyroid hormone receptor interactor 12	2.62	0.125	-1.44	0.495	1.01	0.983	-2.12	0.473	0.02
1430132_at	Krt28	keratin 28	2.01	0.052	-1.25	0.694	1.52	0.332	-1.47	0.334	0.2
1420905_at	Il17ra	interleukin 17 receptor A	-1.15	0.444	1.58	0.058	1.88	0.059	-1.71	0.074	0.15
1442566_at	C78878	expressed sequence C78878	2.4	0.458	1.27	0.683	-1.51	0.408	-1.21	0.75	0.24

1427331_at	Adora1	adenosine A1 receptor	-1.37	0.091	1.73	0.256	1.87	0.313	-2.04	0.127	0.05
1451477_at	1700029I01Rik	RIKEN cDNA 1700029I01 gene	-2.43	0.104	2.07	0.066	1.85	0.061	-1.86	0.261	-0.09
1417370_at	Tff3	trefoil factor 3, intestinal	-2.74	0.377	3.21	0.339	-1.33	0.374	1.45	0.431	0.15
1447117_at	Ctnna2	Catenin (cadherin associated protein), alpha 2	-1.02	0.954	1.36	0.506	1.99	0.193	-1.34	0.604	0.25
1450633_at	Calm4	calmodulin 4	1.37	0.543	2.09	0.375	-1.14	0.557	-1.06	0.906	0.31
1419119_at	Hcst	hematopoietic cell signal transducer	2.19	0.062	-1.2	0.53	1.31	0.254	-1.28	0.542	0.25
1427452_at	Rpl7	ribosomal protein L7	1.49	0.104	1.86	0.043	-1.02	0.934	-1.02	0.964	0.33
1450709_at	Defcr5	defensin related cryptdin 5	3.1	0.099	-1.98	0.168	-1.37	0.591	1.27	0.649	0.25
1426127_x_at	Klra18	killer cell lectin-like receptor, subfamily A, member 18	1.2	0.803	2.59	0.181	-1.86	0.078	-1.71	0.095	0.06
1456029_a_at	Ttc7b	tetratricopeptide repeat domain 7B	-1.19	0.75	-1.16	0.422	2.63	0.225	1.51	0.114	0.45
1420504_at	Slc6a14	solute carrier family 6 (neurotransmitter transporter), member 14	1.62	0.356	1.88	0.464	-1.19	0.169	-1.08	0.92	0.31
1432079_at	4933436N17Rik	RIKEN cDNA 4933436N17 gene	2.74	0.451	1.23	0.759	-2.72	0.059	-1.08	0.882	0.04
1457458_at	BC057627	cDNA sequence BC057627	2.86	0.039	-1.06	0.845	-1.89	0.173	1.15	0.649	0.26
1429012_at	Arhgef6	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	1.25	0.075	2.14	0.119	-1.07	0.669	-1.57	0.227	0.19
1458774_at	D10Ertd584e	DNA segment, Chr 10, ERATO Doi 584, expressed	2.56	0.427	-1	0.979	-1.28	0.734	3.62	0.031	0.97
1420463_at	Clnk	cytokine-dependent hematopoietic cell linker	-1.07	0.937	2.62	0.028	-1.28	0.721	1.19	0.495	0.36
1454095_at	4930579H20Rik	RIKEN cDNA 4930579H20 gene	2.64	0.142	-1.81	0.433	1.14	0.797	-1.13	0.785	0.21
1432141_x_at	Gsdm2	gasdermin 2	1.99	0.357	1.5	0.188	-1.19	0.718	-1.92	0.355	0.1
1447058_at	A530058N18Rik	RIKEN cDNA A530058N18 gene	2.05	0.476	1.33	0.185	-1.04	0.631	-1.66	0.339	0.17
1416784_at	Pgk2	phosphoglycerate kinase 2	1.5	0.635	2.22	0.109	-1.63	0.404	-1.45	0.53	0.16
1449916_at	Pbx4	pre-B-cell leukemia transcription factor 4	2.94	0.378	-2.84	0.052	1.05	0.901	-1.16	0.295	0
1455123_at	St18	suppression of tumorigenicity 18	2.19	0.275	-1.16	0.762	1.29	0.6	-1.57	0.25	0.19
1426471_at	Zfp52	zinc finger protein 52	-1.07	0.637	1.59	0.272	1.82	0.181	-1.81	0.148	0.13
1430654_at	Nsun3	NOL1/NOP2/Sun domain family 3	-1.16	0.322	1.34	0.604	2.14	0.184	-1.5	0.224	0.21
1419732_at	Rtn4r	reticulon 4 receptor	1.39	0.485	1.96	0.229	-1	0.979	-1.48	0.054	0.22
1445222_at	Cd22	CD22 antigen	2.33	0.394	-1.27	0.702	1.22	0.592	-1.53	0.267	0.19
1425359_at	Mall	mal, T-cell differentiation protein-like	1.49	0.552	-1.05	0.923	1.91	0.28	-1.05	0.944	0.32
1438792_at	1200007D18Rik	RIKEN cDNA 1200007D18 gene	1.16	0.877	2.46	0.122	-1.38	0.251	-1.3	0.616	0.23
1450383_at	Ldlr	low density lipoprotein receptor	-1.06	0.876	1.15	0.795	2.25	0.449	-2.18	0.541	0.04
1447079_at	---	---	-1.19	0.489	2.01	0.214	1.49	0.306	-1.32	0.711	0.25
1441193_at	---	---	-1.55	0.343	2.13	0.284	1.57	0.321	-1.03	0.958	0.28
1436473_at	Zfp248	zinc finger protein 248	-1.4	0.027	2.6	0.259	1.04	0.801	-1.93	0.307	0.08
1437811_x_at	Cotl1	Coactosin-like 1 (Dictyostelium)	-1.33	0.175	1.38	0.214	2.22	0.07	-1.34	0.346	0.23
1451595_a_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	1	0.995	2.89	0	-2.17	0.211	-1.03	0.865	0.17
1443842_at	Arfgef2 /// LOC670	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-inhibite	-1.9	0.335	2.38	0.17	1.45	0.49	-1.85	0.621	0.02
1448092_x_at	Serpina4-ps1	serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1	3.63	0.251	-75.16	0.135	-1.42	0.347	1.6	0.325	-17.84
1448064_at	Ranbp9	RAN binding protein 9	2.9	0.003	-2.01	0.353	-1.05	0.893	1.49	0.363	0.33
1429637_at	2210419I08Rik	RIKEN cDNA 2210419I08 gene	-1.05	0.738	2.71	0.019	-1.44	0.144	1.11	0.531	0.33
1426731_at	Des	desmin	-1.04	0.491	2.22	0.134	1.18	0.571	-1.27	0.325	0.27
1441439_at	Ucn3	urocortin 3	2.34	0.463	-1.21	0.762	1.19	0.723	-1.48	0.345	0.21
1449531_at	Leprel2	leprecan-like 2	1.3	0.055	2.15	0.101	-1.1	0.698	-1.15	0.639	0.3
1436063_at	Loxl1	lysyl oxidase-like 1	2.2	0.17	1.61	0.452	-1.85	0.314	-1.09	0.641	0.22
1444283_at	Gimap7	GTPase, IMAP family member 7	1.13	0.677	-1.79	0.457	2.67	0.214	-1.56	0.297	0.11
1431254_at	Kbtbd11 /// LOC632	kelch repeat and BTB (POZ) domain containing 11 /// similar to Protein KIAA0711	1.07	0.86	-1.17	0.679	2.43	0.117	-1.39	0.467	0.24
1442611_at	4930592C13Rik	RIKEN cDNA 4930592C13 gene	2.32	0.415	1.06	0.852	-1.02	0.953	-2.15	0.422	0.05
1427366_at	Krtap3-1	keratin associated protein 3-1	1.16	0.884	2.54	0.009	-1.5	0.657	-1.4	0.636	0.2
1421622_a_at	Rapgef4	Rap guanine nucleotide exchange factor (GEF) 4	2.29	0.039	-1.37	0.25	1.35	0.399	-1.98	0.079	0.07
1434777_at	Mycl1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avia	2.05	0.492	1.5	0.251	-1.23	0.475	-1.75	0.449	0.14
1430761_at	0610039K10Rik	RIKEN cDNA 0610039K10 gene	1.81	0.323	1.98	0.384	-1.72	0.332	-2	0.191	0.02
1441400_at	1810029B16Rik	RIKEN cDNA 1810029B16 gene	1.13	0.882	2.35	0.381	-1.12	0.834	-1.19	0.382	0.29
1434616_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	2.22	0.467	1.41	0.435	-1.36	0.631	-1.56	0.581	0.18
1439052_at	5430433G21Rik	RIKEN cDNA 5430433G21 gene	1.86	0.449	-1.56	0.258	1.87	0.199	-2.1	0.459	0.02
1430843_at	Gadl1	glutamate decarboxylase-like 1	2.88	0.088	1.02	0.9	-2.11	0.169	-1.34	0.31	0.11

1430155_at	4933427E11Rik	RIKEN cDNA 4933427E11 gene	-1.08	0.837	1.44	0.409	2	0.094	-1.31	0.103	0.26
1432596_at	4930599N24Rik	RIKEN cDNA 4930599N24 gene	-1.36	0.652	-2.86	0.07	3.29	0.062	1.36	0.255	0.11
1444362_at	Neurod2	neurogenic differentiation 2	2.47	0.475	-1.51	0.317	1.25	0.603	-1.1	0.845	0.28
1444368_at	---	---	-1.84	0.201	2.57	0.015	1.26	0.31	-1.31	0.556	0.17
1442846_at	Pbx1	Pre B-cell leukemia transcription factor 1	-1.09	0.803	2.87	0.034	-1.69	0.279	1.25	0.689	0.33
1437063_at	Fem1a	feminization 1 homolog a (C. elegans)	2.23	0.081	-1.03	0.933	1.18	0.407	-1.83	0.229	0.14
1444020_at	Cspg3	chondroitin sulfate proteoglycan 3	-1.13	0.747	1.44	0.505	2.06	0.06	-1.1	0.912	0.32
1416818_at	Parva	parvin, alpha	1.44	0.43	-1.09	0.765	2.02	0.38	-1	0.994	0.34
1422070_at	Adh4	alcohol dehydrogenase 4 (class II), pi polypeptide	2.49	0.474	-1.19	0.251	1.05	0.92	-1	0.996	0.34
1428568_at	B230217C12Rik	RIKEN cDNA B230217C12 gene	1.04	0.884	2.43	0.121	-1.1	0.671	-1.38	0.487	0.25
1431419_at	2610524G07Rik	RIKEN cDNA 2610524G07 gene	1.17	0.787	-1.11	0.83	2.32	0.049	-1.49	0.315	0.22
1447499_s_at	Omt2a /// Omt2b ///	oocyte maturation, alpha /// oocyte maturation, beta /// similar to oocyte maturatio	1.22	0.522	-1.42	0.327	2.45	0.03	-1.95	0.071	0.08
1431385_a_at	Mbtps1	membrane-bound transcription factor peptidase, site 1	1.32	0.221	-1.43	0.58	2.37	0.465	-1.45	0.547	0.2
1440245_at	Ccdc88	coiled-coil domain containing 88	-1.51	0.137	1.75	0.274	1.98	0.131	-1.33	0.372	0.22
1443783_x_at	H2-Aa	Histocompatibility 2, class II antigen A, alpha	1.76	0.026	1.64	0.131	-1.01	0.979	-1.81	0.214	0.14
1417721_s_at	Laptm5 /// LOC669	lysosomal-associated protein transmembrane 5 /// similar to Lysosomal-associate	1.54	0.291	-1.01	0.958	1.86	0.165	-1.05	0.934	0.34
1419336_at	Lcn5	lipocalin 5	1.41	0.333	2.01	0.31	-1.03	0.907	-1.07	0.774	0.33
1432358_at	1110008I14Rik	RIKEN cDNA 1110008I14 gene	-1.14	0.578	-1.39	0.281	2.8	0.385	1.6	0.405	0.46
1446286_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	2.52	0.067	1.39	0.063	-2.09	0.117	-2.24	0.276	-0.1
1460488_at	Zbtb4	zinc finger and BTB domain containing 4	1.3	0.057	2.2	0.351	-1.12	0.747	-1.3	0.238	0.27
1456024_at	Gtf3c1	general transcription factor III C 1	1.41	0.349	-2.08	0.375	2.5	0.248	-1.3	0.75	0.13
1426228_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	-1.29	0.517	2.9	0.302	-1.39	0.182	1.21	0.273	0.36
1447334_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	1.59	0.502	-1.09	0.879	1.89	0.376	-1.17	0.339	0.31
1423660_at	Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	1.01	0.908	-1.15	0.596	2.51	0.266	-1.44	0.307	0.23
1454468_at	5430434N17Rik	RIKEN cDNA 5430434N17 gene	2.56	0.529	1.01	0.975	-1.21	0.783	-1.21	0.563	0.29
1447745_at	Aqp4	aquaporin 4	1.05	0.645	-1.13	0.636	2.47	0.275	-1.25	0.731	0.28
1460469_at	Tnfrsf9	tumor necrosis factor receptor superfamily, member 9	2.35	0.231	1.35	0.529	-1.43	0.216	-1.02	0.911	0.31
1432646_a_at	LOC640370 /// LOC	hypothetical LOC640370 /// hypothetical protein LOC667653 /// hypothetical prote	-1.25	0.006	-1.88	0.44	3.07	0.344	1.21	0.664	0.29
1444370_at	C77058	expressed sequence C77058	1.3	0.367	-1.2	0.641	2.26	0.171	-1.12	0.504	0.31
1429738_at	Myt1l	myelin transcription factor 1-like	1.15	0.044	2.65	0.107	-1.67	0.288	-1.06	0.879	0.27
1426601_at	Slc37a1	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	-1.17	0.011	2.21	0.183	1.34	0.078	-1.61	0.16	0.19
1425395_at	Adam26a	a disintegrin and metallopeptidase domain 26A (testase 3)	1.62	0.366	-1.36	0.21	2.04	0.075	-1.36	0.157	0.24
1427478_at	Usp12	ubiquitin specific peptidase 12	1.94	0.329	-1.28	0.722	1.68	0.535	-3.12	0.264	-0.19
1441706_at	Dscaml1	Down syndrome cell adhesion molecule-like 1	1.43	0.199	-1.22	0.833	2.16	0.052	-2.39	0.091	-0.01
1441699_at	Atp8b2	Atpase, class I, type 8B, member 2	2.21	0.389	1.36	0.648	-1.18	0.748	-1.61	0.456	0.19
1442479_at	---	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830040	1.97	0.426	-1.03	0.96	1.47	0.465	-1.96	0.351	0.11
1460255_at	Tnfsf13b	tumor necrosis factor (ligand) superfamily, member 13b	2.21	0.217	1.31	0.67	-1.14	0.459	-1	0.979	0.35
1458668_at	Tpd52	Tumor protein D52	-1.12	0.661	1.5	0.43	2.02	0.337	-1.18	0.798	0.3
1419022_a_at	Eno1 /// LOC43318	enolase 1, alpha non-neuron /// similar to enolase 1, alpha non-neuron /// similar t	1	0.993	-1.33	0.266	2.66	0.001	-1.21	0.274	0.28
1419727_at	Daf2	decay accelerating factor 2	1.96	0.156	-1	0.994	1.46	0.358	-1.41	0.134	0.25
1433388_at	2900022M07Rik	RIKEN cDNA 2900022M07 gene	2.45	0.46	1.06	0.477	-1.11	0.849	-1.03	0.962	0.34
1422531_at	Syt5	synaptotagmin V	-1.2	0.663	2.15	0.069	1.43	0.206	-2.07	0.54	0.08
1422733_at	Fjx1	four jointed box 1 (Drosophila)	-1.05	0.788	1.18	0.529	2.28	0.044	-1.08	0.756	0.33
1422923_at	Fgf3	fibroblast growth factor 3	2.58	0.2	-1.26	0.664	1.04	0.757	-1.31	0.534	0.26
1442619_at	Klf15	Kruppel-like factor 15	-1.7	0.356	1.8	0.352	2.03	0.054	-2.41	0.129	-0.07
1429756_at	4931428F04Rik	RIKEN cDNA 4931428F04 gene	2.16	0.544	-1.11	0.752	1.36	0.502	-1.21	0.779	0.3
1422388_at	V1rc8	vomeronasal 1 receptor, C8	2.26	0.169	1.22	0.787	-1.07	0.843	-1.25	0.655	0.29
1420925_at	Tub	tubby candidate gene	2.54	0.036	-1.35	0.666	1.14	0.559	-1.89	0.1	0.11
1441201_at	Utx	Ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1.46	0.028	2.28	0.182	-1.47	0.343	-1.67	0.388	0.15
1429818_at	2410012M07Rik	RIKEN cDNA 2410012M07 gene	-1.06	0.757	2.22	0.145	1.26	0.608	-1.26	0.601	0.29
1459034_at	Wdr19	WD repeat domain 19	-1.11	0.842	1.53	0.354	2	0.186	-1.24	0.727	0.29
1436838_x_at	Cotl1	coactosin-like 1 (Dictyostelium)	-1.09	0.041	1.63	0.003	1.87	0.17	-1.56	0.149	0.22
1420164_at	D7Ertd183e	DNA segment, Chr 7, ERATO Doi 183, expressed	1.14	0.853	2.72	0.06	-1.76	0.335	-4.21	0.127	-0.53

1447525_at	Ift172	Intraflagellar transport 172 homolog (Chlamydomonas)	1.54	0.535	2.41	0.16	-2.11	0.261	-2.04	0.357	-0.05
1427688_a_at	Ptprs	protein tyrosine phosphatase, receptor type, S	-1.08	0.778	1.62	0.181	1.89	0.294	-1.31	0.47	0.28
1421092_at	Serpina12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsi	2.42	0.027	-1.2	0.599	1.18	0.801	-1.38	0.56	0.25
1427629_at	Ptprj	protein tyrosine phosphatase, receptor type, J	-1.21	0.612	2	0.04	1.61	0.357	-2.31	0.189	0.02
1432381_a_at	Fsip1 /// LOC64045	fibrous sheath-interacting protein 1 /// similar to fibrous sheath-interacting protein	2.38	0.453	-1.17	0.603	1.2	0.661	-2.96	0.384	-0.14
1442530_at	---	---	1.76	0.545	-1.55	0.405	2.03	0.082	-2.11	0.434	0.03
1430506_at	8430406P12Rik	RIKEN cDNA 8430406P12 gene	1.49	0.012	2.24	0.222	-1.43	0.006	-2.17	0.048	0.03
1446366_at	Trpc4	transient receptor potential cation channel, subfamily C, member 4	1.83	0.044	-1.01	0.991	1.61	0.441	-1.2	0.801	0.31
1444510_at	---	Transcribed locus	-1.1	0.577	2.95	0.34	-1.75	0.167	1.27	0.62	0.34
1432262_at	4930504E06Rik	RIKEN cDNA 4930504E06 gene	1.12	0.9	-1.19	0.827	2.48	0.369	-1.05	0.945	0.34
1442493_at	---	Transcribed locus	-1.01	0.979	-1.2	0.475	2.61	0.161	1.15	0.882	0.39
1431309_at	Ttll10	tubulin tyrosine ligase-like family, member 10	1.5	0.347	2.2	0.263	-1.36	0.126	-1.57	0.58	0.19
1449563_at	Cntn1	contactin 1	1.89	0.151	1.59	0.237	-1.05	0.836	-2.03	0.071	0.1
1417021_a_at	Spo11 /// LOC6759	sporulation protein, meiosis-specific, SPO11 homolog (S. cerevisiae) /// similar to	-1.05	0.936	1.78	0.327	1.71	0.156	-1.02	0.832	0.35
1453614_a_at	Nfe2l3	nuclear factor, erythroid derived 2, like 3	1.76	0.105	1.76	0.022	-1.09	0.874	-2.13	0.317	0.08
1458726_at	C87033	expressed sequence C87033	-1.94	0.071	2.62	0.17	1.3	0.362	-2.87	0.065	-0.22
1457048_at	Gpr103	G protein-coupled receptor 103	3.08	0.011	-2.56	0.109	-1.02	0.96	1.01	0.986	0.13
1454411_at	4933406F09Rik	RIKEN cDNA 4933406F09 gene	1.99	0.072	-1.61	0.481	1.83	0.279	-2.02	0.521	0.05
1420648_at	Trim12	tripartite motif protein 12	1.99	0.225	1.69	0.385	-1.3	0.339	-1.83	0.163	0.14
1456376_at	Mmp24	Matrix metallopeptidase 24	2.84	0.028	-1.48	0.562	-1.07	0.609	1.59	0.052	0.47
1436037_at	Cerkl	ceramide kinase-like	1.53	0.192	1.92	0.008	-1.01	0.975	-1.03	0.883	0.35
1432217_a_at	Wdr16	WD repeat domain 16	1.98	0.149	-1.04	0.952	1.51	0.323	-2.65	0.203	-0.05
1455969_at	Nudt15	nudix (nucleoside diphosphate linked moiety X)-type motif 15	-1.15	0.489	1.8	0.235	1.78	0.058	-1.19	0.577	0.31
1440526_at	D130029J02Rik	RIKEN cDNA D130029J02 gene	2.58	0.139	1.04	0.898	-1.19	0.249	-1.23	0.041	0.3
1433097_at	4930473M17Rik	RIKEN cDNA 4930473M17 gene	1.49	0.459	-1.12	0.809	2.07	0.063	-2.22	0.518	0.06
1451597_at	Tmprss11d	transmembrane protease, serine 11d	-1.04	0.809	2.48	0.148	1.02	0.971	-1.76	0.301	0.17
1457365_at	---	---	-1.65	0.31	2.41	0.023	1.44	0.421	-2.32	0.212	-0.03
1454548_at	1700039M15Rik	RIKEN cDNA 1700039M15 gene	-1.34	0.549	2.51	0.139	1.2	0.418	-1.06	0.939	0.33
1425112_at	Ankrd27	ankyrin repeat domain 27 (VPS9 domain)	2.52	0.162	1.4	0.619	-1.83	0.143	-1.34	0.764	0.18
1449808_at	---	Transcribed locus	-1.86	0.311	3.47	0.04	-2.19	0.175	1.01	0.991	0.11
1433155_at	B230204H03Rik	RIKEN cDNA B230204H03 gene	-1.59	0.455	2.49	0.039	1.34	0.535	-1.82	0.48	0.11
1460613_x_at	Gh	growth hormone	1.39	0.668	-1.28	0.528	2.3	0.169	-1.17	0.326	0.31
1415935_at	Smoc2	SPARC related modular calcium binding 2	1.32	0.02	2.26	0.003	-1.13	0.767	-1.05	0.789	0.35
1430395_at	Ankrd45	ankyrin repeat domain 45	1.61	0.322	-1.17	0.757	2	0.32	-1.19	0.705	0.31
1440406_at	Gpatc3	G patch domain containing 3	-1.42	0.531	2.29	0.23	1.47	0.038	-1.18	0.562	0.29
1449568_at	Klb	klotho beta	1.26	0.836	-1.26	0.03	2.42	0.385	-1.09	0.911	0.33
1439692_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	1.97	0.519	1.64	0.44	-1.17	0.605	-2.05	0.035	0.1
1440435_at	Ky	kyphoscoliosis peptidase	1.11	0.785	2.41	0.215	-1.05	0.866	-1.56	0.111	0.23
1445889_at	Sorl1	Sortilin-related receptor, LDLR class A repeats-containing	-1.62	0.492	2.43	0.074	1.42	0.279	-1.08	0.675	0.29
1448327_at	Actn2	actinin alpha 2	1.77	0.412	-1.13	0.815	1.81	0.142	-3.43	0.006	-0.24
1440147_at	Lgi2	leucine-rich repeat LGI family, member 2	-1.04	0.808	2.61	0.054	-1.11	0.668	1.64	0.277	0.53
1441889_x_at	Racgap1	Rac GTPase-activating protein 1	1.96	0.325	2	0.181	-1.96	0.395	-4.45	0.008	-0.61
1425151_a_at	Noxo1	NADPH oxidase organizer 1	2.46	0.386	-1.58	0.366	1.38	0.191	-1.67	0.252	0.15
1421452_at	Cdon	cell adhesion molecule-related/down-regulated by oncogenes	-1.6	0.599	2.09	0.348	1.76	0.21	-2.68	0.445	-0.11
1453439_at	5430427O21Rik	RIKEN cDNA 5430427O21 gene	-1.31	0.024	2.61	0.004	1.1	0.806	-1.75	0.13	0.16
1432037_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	2.74	0.48	1.27	0.683	-2.15	0.083	-1.35	0.56	0.13
1438052_at	A130071D04Rik	RIKEN cDNA A130071D04 gene	2.56	0.105	1.1	0.77	-1.21	0.48	-1.97	0.216	0.12
1446612_at	9330118A15Rik	RIKEN cDNA 9330118A15 gene	1.95	0.094	-1.13	0.825	1.64	0.196	-1.76	0.064	0.18
1434227_at	Krtdap	keratinocyte differentiation associated protein	-1.6	0.274	1.54	0.307	2.32	0.17	-1.37	0.707	0.22
1432586_at	5730596P11Rik	RIKEN cDNA 5730596P11 gene	2.88	0.312	-1.2	0.793	-1.31	0.523	3.59	0.029	0.99
1436916_at	Tmem108	transmembrane protein 108	-1.01	0.968	2.8	0.057	-1.45	0.277	1.02	0.976	0.34
1433424_at	---	---	-1.08	0.908	1.79	0.426	1.77	0.373	-1.13	0.845	0.34
1460472_at	Cdk3	cyclin-dependent kinase 3	2.34	0.117	1.32	0.576	-1.21	0.715	-2.28	0.227	0.04

1429076_a_at	Gdpd2	glycerophosphodiester phosphodiesterase domain containing 2	2.33	0.315	-1.71	0.33	1.57	0.264	-1.7	0.318	0.12
1422187_at	Gabrg3	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 3	-2.22	0.071	1.77	0.124	2.27	0.128	-1.26	0.764	0.14
1430351_at	Spata18	spermatogenesis associated 18	2.3	0.14	-1.55	0.019	1.54	0.121	-1.06	0.907	0.31
1433328_at	1700095A21Rik	RIKEN cDNA 1700095A21 gene	-1.81	0.298	2.37	0.065	1.57	0.263	-2.01	0.336	0.03
1451478_at	Angptl7	angiopoietin-like 7	-1.79	0.172	1.51	0.554	2.42	0.195	-1.39	0.524	0.19
1439051_a_at	Mark4	MAP/microtubule affinity-regulating kinase 4	1.66	0.261	-2.09	0.357	2.35	0.061	-1.04	0.943	0.22
1431203_at	Sdccag8	serologically defined colon cancer antigen 8	2.08	0.103	-1.09	0.778	1.5	0.364	-1.43	0.23	0.26
1421777_at	Olfr73	olfactory receptor 73	2.91	0.17	-1.48	0.544	-1.09	0.806	1.18	0.676	0.38
1428841_at	Vmd2	vitelliform macular dystrophy 2 homolog (human)	2.14	0.361	-1.02	0.86	1.38	0.08	-1.15	0.82	0.34
1420039_s_at	Cbx7	chromobox homolog 7	1.43	0.535	-3.11	0.158	2.74	0.11	-1.18	0.68	-0.03
1437656_at	Arhgef4	Rho guanine nucleotide exchange factor (GEF) 4	1.33	0.717	2.27	0.387	-1.11	0.808	-1.3	0.212	0.3
1443523_at	---	---	1.98	0.532	-1.22	0.64	1.7	0.367	-1.05	0.929	0.35
1442341_at	Kalrn	kalirin, RhoGEF kinase	1.5	0.6	2.57	0.11	-2.31	0.098	-5.17	0.152	-0.85
1456920_at	---	---	-1.76	0.393	2.31	0.319	1.62	0.02	-1.14	0.355	0.26
1453297_at	4933417O08Rik	RIKEN cDNA 4933417O08 gene	-1.83	0.642	2.17	0.175	1.79	0.214	-1.63	0.517	0.12
1457263_at	Serpina3k	Serine (or cysteine) peptidase inhibitor, clade A, member 3K	2.89	0.461	-1.53	0.29	-1.05	0.856	1.15	0.725	0.37
1433162_at	6230414M07Rik	RIKEN cDNA 6230414M07 gene	-1.05	0.904	2.56	0.003	-1.01	0.981	1.13	0.392	0.41
1432288_at	5830468F06Rik	RIKEN cDNA 5830468F06 gene	-1.04	0.815	1.39	0.307	2.15	0.156	-1.31	0.607	0.3
1439390_at	1300018I17Rik	RIKEN cDNA 1300018I17 gene	2.66	0.281	-1.03	0.957	-1.15	0.849	1.13	0.78	0.4
1421681_at	Nrg4	neuregulin 4	-1.12	0.644	2.27	0.056	1.35	0.401	-1.5	0.38	0.25
1438936_s_at	Ang1	angiogenin, ribonuclease A family, member 1	3.03	0.438	-1.1	0.601	-1.76	0.002	1.46	0.212	0.41
1422582_at	Lep	leptin	-1.14	0.391	-1.2	0.712	2.8	0.448	1.31	0.283	0.44
1459918_at	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	2.33	0.25	1.4	0.192	-1.28	0.233	-1.21	0.518	0.31
1432724_at	4930445G23Rik	RIKEN cDNA 4930445G23 gene	-1.31	0.554	2.51	0.306	1.23	0.693	-1.13	0.749	0.33
1425621_at	Trim35	tripartite motif-containing 35	1.09	0.721	-1.43	0.498	2.73	0.139	-1.8	0.055	0.15
1452647_a_at	Dph2	DPH2 homolog (S. cerevisiae)	-1.06	0.777	2.25	0.016	1.31	0.068	-1.48	0.007	0.26
1429835_at	2310033E01Rik	RIKEN cDNA 2310033E01 gene	-1.23	0.716	-1.88	0.176	3.17	0.204	2.62	0.329	0.67
1459914_at	2810402A17Rik	RIKEN cDNA 2810402A17 gene	1.36	0.514	-1.13	0.368	2.27	0.182	-1.57	0.351	0.23
1430699_at	Gpr165	G protein-coupled receptor 165	1.57	0.673	2.1	0.036	-1.18	0.752	-1.19	0.684	0.32
1426849_at	Sec24b	SEC24 related gene family, member B (S. cerevisiae)	1.23	0.631	-1.35	0.607	2.54	0.194	-1.44	0.424	0.25
1443584_at	1110028C15Rik	RIKEN cDNA 1110028C15 gene	2.15	0.416	1.81	0.181	-1.79	0.144	-1.48	0.546	0.17
1459691_at	---	---	1.48	0.26	2.59	0.092	-2.27	0.009	-2.22	0.174	-0.1
1457599_at	2310047H23Rik	RIKEN cDNA 2310047H23 gene	2.3	0.075	-1.2	0.534	1.38	0.321	-1.1	0.832	0.35
1417033_at	Ube2g2	ubiquitin-conjugating enzyme E2G 2	1.86	0.342	-1.2	0.662	1.83	0.382	-1.05	0.942	0.36
1421352_at	Tlr6	toll-like receptor 6	-1.19	0.78	1.84	0.114	1.83	0.177	-1.37	0.17	0.28
1425232_x_at	Arr3	arrestin 3, retinal	1.18	0.848	2.76	0.042	-1.72	0.189	-1.45	0.443	0.19
1456811_at	Cxxc4	CXXC finger 4	2.11	0.281	1.85	0.249	-1.77	0.273	-1.55	0.404	0.16
1418290_a_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	1.23	0.758	-1.04	0.933	2.33	0.365	-1.34	0.605	0.3
1422039_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	-1.15	0.579	2.33	0.248	1.33	0.356	-1.2	0.818	0.33
1430807_at	Klhl22	kelch-like 22 (Drosophila)	3.17	0.369	-1.91	0.264	-1.2	0.756	2.6	0.249	0.67
1439602_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-1.11	0.812	2.79	0.263	-1.2	0.757	1.95	0.352	0.61
1446605_at	Srgap3	SLIT-ROBO Rho GTPase activating protein 3	1.04	0.959	2.88	0.356	-1.65	0.08	-1.22	0.741	0.26
1447476_at	Abcc10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	2.14	0.162	-1.27	0.107	1.6	0.275	-1.34	0.213	0.28
1457420_at	Lmtk3	lemur tyrosine kinase 3	2.39	0.003	1.2	0.514	-1.07	0.839	-1.5	0.475	0.26
1420751_at	Krtap6-1	keratin associated protein 6-1	1.69	0.07	-1.54	0.41	2.19	0.262	-2.19	0.331	0.04
1434920_a_at	Evl	Ena-vasodilator stimulated phosphoprotein	1.05	0.449	2.62	0.034	-1.15	0.585	-1.92	0.131	0.15
1440386_at	Glce	glucuronyl C5-epimerase	1.04	0.867	-1.44	0.609	2.79	0.045	-1.24	0.639	0.29
1442449_at	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	-1.17	0.729	1.02	0.956	2.66	0.11	-1.22	0.006	0.32
1431676_x_at	Gtf2i	general transcription factor II I	1.99	0.112	-1.08	0.893	1.62	0.509	-1.49	0.58	0.26
1445077_at	---	---	1.92	0.385	1.67	0.413	-1.06	0.868	-2.67	0.28	-0.03
1428183_at	Ankrd23	ankyrin repeat domain 23	1.69	0.046	-1.06	0.831	1.9	0.424	-1.4	0.555	0.28
1438154_x_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	-1.48	0.368	1.46	0.37	2.4	0.206	-1.49	0.255	0.22
1442913_at	---	12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:I	-1.29	0.495	1.78	0.291	1.98	0.243	-2.37	0.16	0.03

1444878_at	Dock10	Dedicator of cytokinesis 10	2.23	0.093	1.66	0.325	-1.55	0.252	-1.75	0.12	0.15
1450441_at	Lrrc50	leucine rich repeat containing 50	-1.02	0.93	1.35	0.565	2.21	0.115	-1.97	0.155	0.14
1423214_at	Plxnc1	plexin C1	-1.04	0.929	1.3	0.594	2.28	0.171	-2.01	0.175	0.13
1426926_at	Plcg2	phospholipase C, gamma 2	-1.2	0.063	1.63	0.053	2.08	0.052	-1.5	0.263	0.25
1418464_at	Matn4	matrilin 4	-1.57	0.349	2.84	0.246	1.07	0.897	-1.16	0.103	0.29
1416200_at	9230117N10Rik	RIKEN cDNA 9230117N10 gene	1.67	0.245	2.21	0.071	-1.5	0.002	-1.14	0.123	0.31
1444143_at	B230342M21Rik	RIKEN cDNA B230342M21 gene	2.15	0.21	-1.13	0.694	1.5	0.081	-1.52	0.407	0.25
1434347_s_at	---	---	1.2	0.589	2.82	0.145	-1.91	0.39	-1.18	0.53	0.23
1444835_at	BC030499	cDNA sequence BC030499	-2.05	0.521	1.48	0.524	2.58	0.125	-1.43	0.477	0.14
1422724_at	Mak	male germ cell-associated kinase	-1.04	0.963	2.36	0.166	1.22	0.488	-1.74	0.227	0.2
1459023_at	---	---	-1.32	0.697	2.46	0.065	1.33	0.642	-1.37	0.717	0.28
1445407_at	---	---	3.13	0.011	1.09	0.905	-2.98	0.075	-1.3	0.461	-0.01
1437199_at	Dusp5	dual specificity phosphatase 5	2.36	0.088	-2.01	0.473	1.69	0.393	-1.47	0.387	0.14
1426131_at	1700036D21Rik	RIKEN cDNA 1700036D21 gene	-1.01	0.979	1.45	0.404	2.11	0.107	-1.78	0.295	0.19
1439808_at	A130090K04Rik	RIKEN cDNA A130090K04 gene	-1.28	0.219	2.05	0.177	1.73	0.162	-1.83	0.083	0.17
1440735_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	2.99	0.404	-1.37	0.407	-1.2	0.223	1.19	0.497	0.4
1459905_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	-1.44	0.536	1.78	0.184	2.09	0.046	-1.41	0.57	0.25
1457874_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930550J05 prc	1.3	0.711	2.5	0.381	-1.31	0.654	-1.26	0.781	0.31
1428975_at	Susd3	sushi domain containing 3	-1.08	0.906	1.33	0.647	2.32	0.055	-1.94	0.129	0.15
1436957_at	Gabra3	Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	-1.19	0.805	1.33	0.267	2.39	0.205	-1.69	0.415	0.21
1446695_at	Xrn1	5'-3' exoribonuclease 1	1.49	0.572	2.62	0.239	-2.2	0.139	-1.93	0.201	0
1429562_at	5031415C07Rik	RIKEN cDNA 5031415C07 gene	-1.25	0.107	-1.16	0.84	2.9	0.007	1.06	0.889	0.39
1417621_at	Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	-1.15	0.632	1.22	0.27	2.48	0.212	-1.02	0.938	0.38
1448555_at	D15Ertd682e	DNA segment, Chr 15, ERATO Doi 682, expressed	-1.12	0.382	2.57	0.082	1.1	0.335	-1.05	0.86	0.38
1451013_at	Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	-1.66	0.193	1.86	0.445	2.1	0.089	-2.22	0.406	0.02
1441745_at	Falz	Fetal Alzheimer antigen	2.09	0.389	1.71	0.143	-1.31	0.385	-2.78	0.223	-0.07
1438350_at	Gpr64	G protein-coupled receptor 64	2.18	0.177	-1.06	0.903	1.45	0.34	-1.41	0.073	0.29
1441932_at	Ptprd	Protein tyrosine phosphatase, receptor type, D	1.91	0.334	2.13	0.297	-1.88	0.427	-2.78	0.299	-0.15
1436965_at	Emilin3	elastin microfibril interfacer 3	3.04	0.393	-1.27	0.051	-1.35	0.523	1.98	0.314	0.6
1438577_at	---	Transcribed locus	1.43	0.409	2.38	0.278	-1.29	0.128	-1.76	0.195	0.19
1430729_at	Myg1	melanocyte proliferating gene 1	1.14	0.898	2.64	0.111	-1.24	0.69	-1.67	0.308	0.22
1453543_at	4930556H04Rik	RIKEN cDNA 4930556H04 gene	1.81	0.252	1.95	0.402	-1.23	0.616	-1.17	0.476	0.34
1426179_a_at	Twsg1	twisted gastrulation homolog 1 (Drosophila)	1.25	0.716	-1.29	0.658	2.55	0.422	-1.26	0.563	0.31
1441218_at	ttc21a	Tetratricopeptide repeat domain 21A	-1.55	0.623	2.59	0.253	1.35	0.006	-1.25	0.73	0.28
1434762_at	Tmem142b	transmembrane protein 142B	-1.65	0.624	2.9	0.134	1.07	0.54	-1.42	0.357	0.23
1440207_at	Agpat7	Nacylglycerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransfe	2.14	0.323	-1.83	0.294	1.9	0.056	-1.29	0.682	0.23
1443326_at	---	---	2.85	0.247	-1.41	0.552	1.03	0.943	-1.07	0.855	0.35
1441146_at	C76132	expressed sequence C76132	-1.97	0.115	2.79	0.103	1.29	0.731	-1.02	0.96	0.27
1420078_at	---	Transcribed locus, moderately similar to XP_218017.3 PREDICTED: similar to pu	2.7	0.279	1.28	0.775	-1.65	0.236	-1.18	0.653	0.29
1422564_at	Actl6b	actin-like 6B	3.06	0.356	1.06	0.548	-2.16	0.051	-1.89	0.268	0.02
1419406_a_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	2.15	0.133	-1.51	0.206	1.77	0.314	-1.4	0.008	0.25
1422114_at	Erf	Ets2 repressor factor	1.46	0.715	2.15	0.175	-1.03	0.923	-1.89	0.373	0.17
1456074_at	Sdro	orphan short chain dehydrogenase/reductase	2.92	0.019	-1.36	0.005	-1.08	0.71	1.95	0.011	0.61
1448734_at	Cp	ceruloplasmin	2.31	0.136	1.33	0.247	-1.06	0.777	-1.44	0.122	0.29
1453555_at	3830408D07Rik	RIKEN cDNA 3830408D07 gene	2.4	0.188	1.58	0.535	-1.62	0.068	-1.04	0.928	0.33
1428550_at	1810015A11Rik	RIKEN cDNA 1810015A11 gene	-1.5	0.014	2.17	0.274	1.76	0.034	-1.01	0.954	0.35
1457699_at	E330009J07Rik	RIKEN cDNA E330009J07 gene	1.42	0.48	2.36	0.014	-1.23	0.255	-1.06	0.908	0.37
1438217_at	A2bp1	ataxin 2 binding protein 1	-1.24	0.714	2.77	0.005	1.03	0.909	-1.35	0.64	0.3
1419651_at	2610200G18Rik	RIKEN cDNA 2610200G18 gene	-1.04	0.68	1.53	0.058	2.12	0.068	-1.05	0.842	0.39
1442501_at	Nrxn1	neurexin I	-1.14	0.8	3.14	0.143	-1.71	0.024	1.01	0.971	0.33
1444834_at	Ppp1r12a	Protein phosphatase 1, regulatory (inhibitor) subunit 12A	-1.12	0.775	-1.55	0.481	3.06	0.063	2	0.08	0.6
1428932_at	ttc21a	tetratricopeptide repeat domain 21A	-1.03	0.972	1.64	0.425	1.99	0.154	-1.08	0.885	0.38
1431102_at	Cep350	centrosomal protein 350	2.36	0.166	-1.03	0.973	1.27	0.677	-1.35	0.634	0.31

1458876_at	Enah	Enabled homolog (Drosophila)	1.41	0.394	2.76	0.036	-2.29	0.025	-1.38	0.344	0.13
1447348_at	Waspip	Wiskott-Aldrich syndrome protein interacting protein	1.17	0.315	2.6	0.041	-1.19	0.304	-1.9	0.077	0.17
1441599_at	2900075B16Rik	RIKEN cDNA 2900075B16 gene	2.42	0.388	1.28	0.732	-1.1	0.787	-1.18	0.818	0.36
1431741_a_at	4930408O21Rik	RIKEN cDNA 4930408O21 gene	1.59	0.673	-1.01	0.979	2.04	0.356	-1.04	0.941	0.39
1420256_x_at	Prph1	Peripherin 1	2.24	0.262	1.61	0.172	-1.31	0.438	-1.24	0.58	0.32
1453558_at	4930504H06Rik	RIKEN cDNA 4930504H06 gene	-1.21	0.659	2.73	0.043	1.06	0.858	-1.07	0.903	0.38
1441951_x_at	2010109A12Rik	RIKEN cDNA 2010109A12 gene	3.08	0.139	-1.47	0.686	-1.17	0.728	1.04	0.95	0.37
1451946_a_at	Cabyr	calcium-binding tyrosine-(Y)-phosphorylation regulated (fibrousheathin 2)	2.07	0.515	-1.58	0.306	1.92	0.113	-1.8	0.057	0.15
1438845_at	Ihpk1	inositol hexaphosphate kinase 1	-2.58	0.378	3.51	0.067	-1.38	0.578	1.24	0.685	0.2
1449285_at	Cst9	cystatin 9	2.11	0.082	-1.04	0.949	1.55	0.49	-1.73	0.329	0.22
1440284_at	---	Transcribed locus, weakly similar to XP_576460.1 PREDICTED: similar to hypoth	-1.25	0.374	1.94	0.003	1.88	0.273	-2.18	0.103	0.1
1431348_at	Ppifos	peptidylprolyl isomerase F, opposite strand transcription unit	-1.21	0.818	2.27	0.023	1.53	0.472	-1.59	0.316	0.25
1435331_at	AI447904	expressed sequence AI447904	2.17	0.214	1.56	0.154	-1.12	0.511	-3.77	0.042	-0.29
1417346_at	Pycard	PYD and CARD domain containing	-1	0.97	1.95	0.001	1.68	0.065	-1.23	0.319	0.35
1458165_at	Ipo7	importin 7	1.03	0.971	2.83	0.104	-1.31	0.601	-1.05	0.87	0.37
1442475_at	D14Ertd574e	DNA segment, Chr 14, ERATO Doi 574, expressed	2.46	0.346	1.61	0.423	-1.79	0.164	-2.45	0.006	-0.04
1420311_s_at	---	---	-1.46	0.619	3.03	0.17	-1.1	0.826	1.18	0.773	0.41
1446919_at	BC062115	CDNA sequence BC062115	1.79	0.437	1.9	0.072	-1.07	0.883	-2.62	0.454	0
1417484_at	Ibsp	integrin binding sialoprotein	-1	1	1.47	0.497	2.15	0.21	-1.24	0.527	0.35
1424341_s_at	Pcdha4 /// Pcdha6	protocadherin alpha 4 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protoc	2.8	0.113	-1.08	0.864	-1.11	0.741	1.09	0.822	0.43
1417198_at	Wwc2	WW, C2 and coiled-coil domain containing 2	2.52	0.365	-3.87	0.325	1.85	0.391	-2.15	0.256	-0.41
1431088_at	Foxp4	forkhead box P4	1.76	0.172	-1.23	0.633	2.05	0.101	-1.33	0.471	0.31
1451314_a_at	Vcam1	vascular cell adhesion molecule 1	1.04	0.899	2.91	0.032	-1.48	0.112	-1.07	0.679	0.35
1449394_at	Slco1b2	solute carrier organic anion transporter family, member 1b2	3.28	0.5	-1.34	0.029	-1.65	0.42	1.38	0.72	0.42
1448616_at	Dvl2	dishevelled 2, dsh homolog (Drosophila)	2.28	0.453	-1.88	0.134	1.82	0.347	-4.62	0.269	-0.6
1417679_at	Gfi1	growth factor independent 1	-1.4	0.379	2.76	0.115	1.16	0.569	-1.3	0.378	0.3
1450154_at	Folh1	folate hydrolase	-1.19	0.454	-1.96	0.281	3.28	0.004	1.37	0.614	0.38
1438379_x_at	2310007F21Rik	RIKEN cDNA 2310007F21 gene	1.79	0.041	1.9	0.164	-1.05	0.83	-1.04	0.764	0.4
1455879_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	1.91	0.327	-1.19	0.718	1.88	0.297	-1.74	0.426	0.22
1444913_at	Hhat	Hedgehog acyltransferase	-1.13	0.829	1.81	0.218	1.94	0.209	-1.33	0.524	0.32
1450019_at	Cx3cr1	chemokine (C-X3-C) receptor 1	3.14	0.291	-3	0.209	1.16	0.622	-1.21	0.752	0.02
1430106_at	1700126L10Rik	RIKEN cDNA 1700126L10 gene	2.61	0.131	-1.12	0.727	1.13	0.706	-2.44	0.061	0.05
1417859_at	Gas7	growth arrest specific 7	1.62	0.263	-1.03	0.858	2.05	0.001	-1.58	0.165	0.26
1438184_a_at	Ankrd5	ankyrin repeat domain 5	-1.04	0.589	2.29	0.232	1.39	0.393	-1.74	0.344	0.22
1458196_at	Gnpnat1	Glucosamine-phosphate N-acetyltransferase 1	2.34	0.473	1.48	0.521	-1.21	0.523	-1.63	0.49	0.24
1447510_at	C530014P21Rik	RIKEN cDNA C530014P21 gene	-1.13	0.74	3.23	0.133	-1.9	0.066	2.02	0.011	0.55
1455683_a_at	Tbc1d8	TBC1 domain family, member 8	2.39	0.172	-1.08	0.814	1.33	0.351	-1.41	0.161	0.31
1458026_at	---	---	1.64	0.026	2.53	0.147	-2.12	0.075	-1.3	0.689	0.19
1439891_at	Zfp703	Zinc finger protein 703	1.16	0.728	-1.04	0.869	2.53	0.126	-1.25	0.654	0.35
1419480_at	Sell	selectin, lymphocyte	-1.22	0.696	1.84	0.289	1.99	0.214	-2.31	0.054	0.08
1446942_at	---	---	-1.79	0.09	-1.3	0.566	3.32	0.118	1.37	0.681	0.4
1418061_at	Ltbp2	latent transforming growth factor beta binding protein 2	2.44	0.006	1.3	0.445	-1.09	0.687	-1.04	0.912	0.4
1439911_at	---	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:95300	-1.02	0.934	2.78	0.013	-1.12	0.697	1.4	0.616	0.51
1424487_x_at	Txnrd1	thioredoxin reductase 1	1.84	0.371	-1.32	0.693	2.06	0.376	-1.25	0.759	0.33
1431943_at	2210011K15Rik	RIKEN cDNA 2210011K15 gene	-1.04	0.877	2.28	0.303	1.41	0.621	-1.07	0.911	0.39
1452755_at	---	---	-2.61	0.119	-1.54	0.654	3.62	0.012	1.17	0.561	0.16
1451598_at	Pax4	paired box gene 4	2.84	0.039	-1.68	0.307	1.22	0.681	-4.15	0.165	-0.44
1446455_at	---	Transcribed locus	2.48	0.226	1.34	0.676	-1.2	0.503	-1.59	0.212	0.26
1418798_s_at	Srpk3	serine/arginine-rich protein specific kinase 3	-1.97	0.161	2.63	0.011	1.52	0.149	-2.19	0.058	0
1424962_at	Tm4sf4	transmembrane 4 superfamily member 4	2.44	0.469	1.36	0.101	-1.16	0.619	-3	0.009	-0.09
1418686_at	Oas1c	2'-5' oligoadenylate synthetase 1C	2.78	0.072	-1.23	0.693	1.07	0.616	-1.6	0.023	0.25
1418990_at	Ms4a4d	membrane-spanning 4-domains, subfamily A, member 4D	2.26	0.258	1.73	0.022	-1.48	0.041	-1.45	0.275	0.26
1438942_x_at	Tgm2	transglutaminase 2, C polypeptide	-1.07	0.912	2.49	0.07	1.24	0.532	-3.05	0.133	-0.1

1427176_s_at	AI428936	expressed sequence AI428936	-1.3	0.312	3.04	0.197	-1.16	0.397	1.01	0.981	0.4
1458209_at	Kndc1	Kinase non-catalytic C-lobe domain (KIND) containing 1	2.92	0	-1	0.988	-1.33	0.036	2.3	0.332	0.72
1443131_at	Ran	RAN, member RAS oncogene family	-1.05	0.962	3.1	0.182	-1.6	0.562	1.68	0.153	0.53
1441007_at	A330102I10Rik	RIKEN cDNA A330102I10 gene	2.04	0.183	-1.1	0.815	1.72	0.274	-2.11	0.339	0.14
1460150_at	---	Transcribed locus	3.05	0.089	-1.84	0.15	1.08	0.759	-1.28	0.485	0.25
1452015_at	6330416G13Rik	RIKEN cDNA 6330416G13 gene	-1.11	0.725	2.08	0.077	1.7	0.137	-1.21	0.361	0.37
1429551_at	4930579G22Rik	RIKEN cDNA 4930579G22 gene	-1.19	0.409	2.79	0.11	1.05	0.741	-2.7	0.15	-0.01
1441994_at	Pcdhb16	protocadherin beta 16	2.52	0.031	1.49	0.021	-1.47	0.087	-1.46	0.303	0.27
1443977_at	E130014H10Rik	RIKEN cDNA E130014H10 gene	-1	0.992	2.88	0.005	-1.23	0.333	1.4	0.152	0.51
1438469_at	Bcorl1	BCL6 co-repressor-like 1	-1.04	0.958	2.87	0.03	-1.17	0.605	3.31	0.158	0.99
1449820_at	Cort	cortistatin	-1.88	0.061	1.18	0.812	2.97	0.069	-1.49	0.486	0.2
1445196_at	C79595	expressed sequence C79595	2.49	0.498	1.32	0.565	-1.14	0.771	-1.46	0.135	0.3
1439850_at	BC066028	cDNA sequence BC066028	2.82	0.054	-1.41	0.605	1.16	0.804	-2.11	0.465	0.12
1429755_a_at	4933406F09Rik	RIKEN cDNA 4933406F09 gene	2.27	0.379	-1.07	0.803	1.5	0.282	-1.03	0.961	0.41
1430495_at	Impa1	inositol (myo)-1(or 4)-monophosphatase 1	2.33	0.025	1.78	0.286	-1.7	0.227	-1.3	0.599	0.28
1422129_at	Apc2	adenomatosis polyposis coli 2	1.75	0.539	-1.19	0.823	2.1	0.174	-1.62	0.321	0.26
1441974_at	---	Transcribed locus	1.8	0.511	2.13	0.07	-1.31	0.63	-2.15	0.187	0.12
1441303_at	---	---	-1.45	0.657	2.24	0.28	1.78	0.37	-1.52	0.16	0.26
1420353_at	Lta	lymphotoxin A	1.82	0.374	-2.23	0.126	2.43	0.228	-3.69	0.056	-0.42
1450446_a_at	Socs1	suppressor of cytokine signaling 1	2.85	0.104	-1.78	0.347	1.3	0.589	-1.09	0.581	0.32
1427779_a_at	Cd4	CD4 antigen	2.55	0.365	1.2	0.657	-1.04	0.909	-4.49	0.416	-0.45
1455885_at	6530401C20Rik	RIKEN cDNA 6530401C20 gene	-1.05	0.862	2.71	0.082	1.04	0.726	-1.06	0.8	0.41
1459134_at	Cdc91l1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	2.65	0.077	1.17	0.73	-1.13	0.768	-1.02	0.974	0.42
1451885_at	LOC574530	metallothionein 1K	-1.73	0.057	2.69	0.238	1.44	0.592	-1.37	0.611	0.26
1429440_at	1810041L15Rik	RIKEN cDNA 1810041L15 gene	-1.42	0.402	1.95	0.436	2.06	0.035	-1.06	0.769	0.38
1442440_at	Neud4	Neuronal d4 domain family member	2.14	0.112	1.57	0.463	-1	0.991	-3.03	0.006	-0.08
1441896_x_at	Obfc1	Oligonucleotide/oligosaccharide-binding fold containing 1	1.68	0.354	2.1	0.076	-1.07	0.77	-1.86	0.014	0.21
1440756_at	---	---	2.71	0.242	-1.89	0.307	1.47	0.227	-1.8	0.474	0.12
1429029_at	4933405A16Rik	RIKEN cDNA 4933405A16 gene	-1.16	0.21	-1.06	0.695	2.91	0.065	2.21	0.23	0.73
1431810_a_at	Tmco4	transmembrane and coiled-coil domains 4	-1.08	0.053	1.38	0.34	2.41	0.04	-1.41	0.509	0.33
1419667_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	1.26	0.291	2.53	0.063	-1.08	0.826	-1.57	0.005	0.29
1425576_at	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	1.44	0.436	-1.16	0.759	2.41	0.267	-1.01	0.977	0.42
1438616_x_at	Svs5	seminal vesicle secretion 5	-1.93	0.313	1.5	0.389	2.7	0.003	-1.17	0.784	0.28
1454469_at	5430434N17Rik	RIKEN cDNA 5430434N17 gene	2.84	0.188	-1.18	0.814	1.04	0.937	-2.42	0.316	0.07
1422515_at	Svs7	seminal vesicle protein, secretion 7	-1.21	0.443	1.19	0.646	2.71	0.007	-1.07	0.862	0.4
1429592_at	Lhfpl3	lipoma HMGIC fusion partner-like 3	2.74	0.028	-1.01	0.974	1.01	0.987	-1.3	0.641	0.36
1451603_at	Rtbdn	retbindin	2.28	0.407	-2.5	0.293	2.05	0.244	-1.37	0.341	0.11
1432857_at	6430500D05Rik	RIKEN cDNA 6430500D05 gene	-1.98	0.469	1.1	0.622	3.13	0.003	-1.81	0.232	0.11
1442287_at	---	Transcribed locus	3.13	0.265	-1.57	0.201	-1.03	0.942	2.48	0.243	0.75
1437621_x_at	Phgdh /// LOC6687	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.21	0.099	2.2	0.048	1.71	0.065	-1.48	0.326	0.31
1459367_at	Trpc5	Transient receptor potential cation channel, subfamily C, member 5	2.65	0.437	1.41	0.488	-1.48	0.325	-1.27	0.251	0.33
1459346_at	Tsen2	tRNA splicing endonuclease 2 homolog (SEN2, S. cerevisiae)	1.82	0.213	2.28	0.034	-1.55	0.043	-1.13	0.342	0.35
1452205_x_at	Tcrb-J /// Tcrb-V13	T-cell receptor beta, joining region /// T-cell receptor beta, variable 13 /// similar to	2.59	0.067	1.19	0.594	-1.05	0.534	-3.28	0.055	-0.13
1457096_at	6430520M22Rik	RIKEN cDNA 6430520M22 gene	-1.23	0.618	-1.13	0.595	3.05	0.299	1.16	0.243	0.46
1430567_at	Spink5	serine peptidase inhibitor, Kazal type 5	1.86	0.481	-1.13	0.629	1.99	0.044	-1.56	0.626	0.29
1442448_at	1810064F22Rik	RIKEN cDNA 1810064F22 gene	-1.05	0.879	2.99	0.193	-1.25	0.274	1.28	0.784	0.49
1449385_at	Hsd17b9	hydroxysteroid (17-beta) dehydrogenase 9	3.31	0.068	-1.77	0.005	-1.15	0.341	1.34	0.613	0.43
1421214_at	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	1.24	0.613	-1.28	0.448	2.72	0.106	-1.39	0.411	0.33
1441286_at	LOC328483	similar to T-cell receptor alpha chain V region CTL-F3 precursor	2.38	0.465	-1.04	0.737	1.41	0.233	-1.13	0.403	0.4
1447803_x_at	Capg	Capping protein (actin filament), gelsolin-like	1.86	0.239	2.03	0.06	-1.17	0.54	-1.43	0.122	0.32
1422061_at	Akr1c20	aldo-keto reductase family 1, member C20	2.95	0.03	-1.32	0.057	1.04	0.938	-1.15	0.584	0.38
1426597_s_at	C79267	expressed sequence C79267	2.58	0.08	-1.01	0.977	1.18	0.472	-1.25	0.528	0.38
1459754_x_at	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange prot	-3.05	0.139	-1.53	0.371	3.77	0.001	4.71	0.001	0.97

1423673_at	Ldoc1l	leucine zipper, down-regulated in cancer 1-like	-1.08	0.465	2.26	0.043	1.57	0.184	-1.32	0.154	0.36
1451930_at	Efna5	Ephrin A5	1.01	0.973	3.11	0.115	-1.58	0.054	-1.14	0.812	0.35
1443015_at	Rhoh	Ras homolog gene family, member H	2.36	0.101	1.61	0.428	-1.27	0.691	-1.57	0.112	0.28
1431320_a_at	Myo5a	myosin Va	-1.18	0.381	2.56	0.039	1.35	0.37	-1.26	0.325	0.37
1430626_at	Zfp398	zinc finger protein 398	1.5	0.033	2.37	0.021	-1.12	0.642	-1.06	0.744	0.42
1448511_at	Ptprcap	protein tyrosine phosphatase, receptor type, C polypeptide-associated protein	1.9	0.338	-1.07	0.887	1.93	0.284	-2.04	0.154	0.18
1448664_a_at	Speg	SPEG complex locus	-1.88	0.009	2.78	0.178	1.45	0.109	-1.95	0.079	0.1
1454282_at	1700084C06Rik	RIKEN cDNA 1700084C06 gene	1.6	0.644	2.38	0.121	-1.28	0.636	-1.45	0.115	0.32
1449227_at	Ch25h	cholesterol 25-hydroxylase	2.45	0.272	-1.27	0.123	1.54	0.045	-1.97	0.073	0.18
1422851_at	Hmga2	high mobility group AT-hook 2	2.16	0.059	1.95	0.304	-1.51	0.122	-1.43	0.581	0.29
1438883_at	Fgf5	fibroblast growth factor 5	2.53	0.365	1.37	0.45	-1.15	0.498	-1.72	0.008	0.26
1422678_at	Dgat2	diacylglycerol O-acyltransferase 2	-1.17	0.232	-1.12	0.577	3.03	0.247	2.25	0.018	0.75
1451488_at	1110028A07Rik	RIKEN cDNA 1110028A07 gene	-1.04	0.827	1.4	0.594	2.42	0.142	-1.5	0.47	0.32
1421125_at	Strbp	spermatid perinuclear RNA binding protein	-3.3	0.009	3.13	0.001	1.34	0.461	-1.02	0.981	0.04
1445216_at	---	---	-1.29	0.692	1.43	0.388	2.58	0.031	-1.88	0.256	0.21
1419192_at	Il4i1	interleukin 4 induced 1	1.1	0.694	-1.76	0.217	3.11	0.238	-2.52	0.063	-0.02
1419160_at	Golga3	golgi autoantigen, golgin subfamily a, 3	-1.41	0.128	3.09	0.021	-1.02	0.973	1.05	0.92	0.43
1443197_at	Wnt9b	wingless-type MMTV integration site 9B	1.2	0.786	3.2	0.232	-2.66	0.187	-1.12	0.479	0.16
1421988_at	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	-2.18	0.325	2.19	0.269	2.13	0.116	-1.62	0.408	0.13
1425417_x_at	Klra8 /// Klra21 /// L	killer cell lectin-like receptor, subfamily A, member 8 /// killer cell lectin-like recept	2.84	0.107	1.58	0.494	-2.76	0.043	-1.86	0.101	-0.05
1419128_at	Itgax	integrin alpha X	2.04	0.049	1.74	0.238	-1	0.991	-1.08	0.809	0.43
1426169_a_at	Lat2	linker for activation of T cells family, member 2	2	0.39	-1.91	0.142	2.26	0.046	-1.68	0.143	0.17
1446364_at	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	1.39	0.518	-1.73	0.138	2.82	0.019	-1.23	0.705	0.31
1441115_at	D18Ertd232e	DNA segment, Chr 18, ERATO Doi 232, expressed	2.1	0.477	1.75	0.374	-1.06	0.799	-1.47	0.388	0.33
1455802_x_at	Agr2	anterior gradient 2 (Xenopus laevis)	1.91	0.399	2.24	0.226	-1.55	0.177	-1.95	0.272	0.16
1423619_at	Rasd1	RAS, dexamethasone-induced 1	-2.24	0.252	1.1	0.827	3.25	0.194	-1.35	0.55	0.19
1450291_s_at	Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	-1.06	0.874	2.36	0.02	1.49	0.249	-2.7	0.062	0.02
1457920_at	C130026L21Rik	RIKEN cDNA C130026L21 gene	2.43	0.221	-1.54	0.332	1.72	0.201	-1.31	0.643	0.33
1456847_at	Cd160	CD160 antigen	1.12	0.877	2.9	0.16	-1.29	0.266	-1.63	0.103	0.28
1429953_at	2210011C24Rik	RIKEN cDNA 2210011C24 gene	1.06	0.391	2.85	0.201	-1.11	0.519	-2.36	0.081	0.11
1441762_at	Bcl11b	B-cell leukemia/lymphoma 11B	1.1	0.754	2.99	0.166	-1.4	0.559	-1.25	0.767	0.36
1423771_at	Prkcdbp	protein kinase C, delta binding protein	1.27	0.262	2.64	0.142	-1.11	0.417	-1.18	0.431	0.4
1438732_at	6430511F03	hypothetical protein 6430511F03	2.47	0.082	1.4	0.548	-1.06	0.891	-2.37	0.185	0.11
1456292_a_at	Vim	vimentin	1.67	0.026	2.21	0.01	-1.08	0.618	-1.61	0.391	0.3
1447889_x_at	Gm50	gene model 50, (NCBI)	-1.7	0.001	2.53	0.063	1.69	0.388	-1.67	0.523	0.21
1430484_at	8430428J23Rik	RIKEN cDNA 8430428J23 gene	1.96	0.178	-1.01	0.987	1.87	0.456	-1.01	0.986	0.45
1447272_s_at	Atp10a	ATPase, class V, type 10A	-1.11	0.907	2.11	0.45	1.81	0.116	-1.12	0.404	0.42
1419020_at	Gif	gastric intrinsic factor	2.47	0.457	1.44	0.609	-1.11	0.789	-1.36	0.554	0.36
1458336_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	2.95	0.173	1.15	0.333	-1.38	0.477	-1.11	0.849	0.4
1421755_at	Gpr132	G protein-coupled receptor 132	-1.29	0.68	2.07	0.305	1.98	0.066	-1.76	0.216	0.25
1438118_x_at	Vim	vimentin	1.79	0.001	2.08	0.012	-1.04	0.687	-1.54	0.271	0.32
1424127_at	Eya2	eyes absent 2 homolog (Drosophila)	-1.13	0.626	2.82	0.087	1.11	0.782	-1.63	0.299	0.29
1437017_at	AI480653	expressed sequence AI480653	-1.24	0.374	2.55	0.039	1.46	0.013	-1.46	0.18	0.33
1457728_at	Pgls	6-phosphogluconolactonase	1.16	0.805	-1.35	0.564	2.92	0.315	-1.96	0.059	0.2
1418921_at	Igsf4b	immunoglobulin superfamily, member 4B	-1.81	0.581	1.06	0.919	3.22	0.065	-2.38	0.028	0.02
1423858_a_at	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	1.78	0.188	-1.5	0.052	2.38	0.174	-1.86	0.138	0.2
1451304_at	Tmem143	transmembrane protein 143	-1.32	0.357	1.18	0.636	2.89	0.208	-2.09	0.273	0.17
1453295_at	Asxl2	additional sex combs like 2 (Drosophila)	2.49	0.441	-1.23	0.538	1.53	0.43	-1.14	0.798	0.41
1459934_at	Usp42	ubiquitin specific peptidase 42	-2.25	0.462	1.94	0.096	2.45	0.066	-1.07	0.862	0.27
1441456_at	Mmp24	matrix metallopeptidase 24	1.72	0.077	-1.52	0.511	2.45	0.153	-2	0.364	0.16
1460516_at	3110006I21Rik	RIKEN cDNA 3110006I21 gene	1.06	0.702	2.85	0.066	-1.08	0.786	-1.73	0.385	0.27
1437998_at	Ap1s2	Adaptor-related protein complex 1, sigma 2 subunit	3	0.284	1.39	0.546	-2.27	0.289	-2.49	0.449	-0.09
1415824_at	Scd2	stearoyl-Coenzyme A desaturase 2	-1.2	0.622	-1.22	0.687	3.2	0.411	1.2	0.775	0.49

1455382_at	Zwint	ZW10 interactor	2.81	0.022	1.08	0.838	-1.05	0.859	-1.23	0.474	0.4
1418787_at	Mbl2	mannose binding lectin (C)	2.66	0.324	-1.28	0.07	1.41	0.274	-1.09	0.911	0.42
1441581_at	Asb10	ankyrin repeat and SOCS box-containing protein 10	2.2	0.031	-1.01	0.866	1.66	0.445	-1.11	0.382	0.43
1445447_at	---	---	-2.7	0.223	2.67	0.179	1.81	0.24	-1.02	0.981	0.19
1420777_a_at	4933400A11Rik	RIKEN cDNA 4933400A11 gene	1.21	0.271	3.28	0.03	-2.8	0.161	-1.81	0.274	-0.03
1443044_at	A830091E24	hypothetical A830091E24	-1.19	0.674	1.84	0.2	2.17	0.424	-1.56	0.355	0.32
1438827_at	Gls	Glutaminase	2.79	0.29	-1.07	0.901	1.13	0.757	-4.47	0.003	-0.4
1437703_at	LOC382156	similar to F-box- and WD40-repeat-containing protein	-1.16	0.698	3.08	0.072	-1.09	0.75	1.58	0.369	0.6
1427531_a_at	Slc22a18	solute carrier family 22 (organic cation transporter), member 18	-1.1	0.726	-1.19	0.415	3.11	0.127	1.74	0.276	0.64
1442019_at	B230343A10Rik	RIKEN cDNA B230343A10 gene	1.68	0.135	-1.28	0.677	2.4	0.42	-3.51	0.311	-0.18
1437675_at	Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	-1.14	0.814	3.21	0.347	-1.3	0.264	1.32	0.209	0.52
1460550_at	Mtmr11	myotubularin related protein 11	1.03	0.531	2.94	0.187	-1.12	0.435	-1.15	0.46	0.42
1450882_s_at	Gpr137b /// LOC66	G protein-coupled receptor 137B /// similar to transmembrane 7 superfamily mem	-1.21	0.161	2.34	0.017	1.7	0.004	-1.36	0.346	0.37
1420079_at	LOC195691 /// LOC	similar to putative pheromone receptor (Go-VN5) /// similar to putative pheromone	2.7	0.049	-1.05	0.815	1.21	0.544	-1.05	0.894	0.45
1451910_a_at	Cd6	CD6 antigen	2.74	0.36	1.17	0.682	-1.05	0.879	-1.64	0.437	0.3
1453426_a_at	Wdfy1	WD repeat and FYVE domain containing 1	1.81	0.014	-1.31	0.719	2.29	0.261	-1.01	0.983	0.44
1444116_at	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	2.02	0.518	2.33	0.28	-1.96	0.118	-1.1	0.92	0.32
1457733_at	---	Transcribed locus	2.34	0.22	1.59	0.271	-1.07	0.886	-1.15	0.637	0.43
1440178_x_at	Zap70	zeta-chain (TCR) associated protein kinase	1.64	0.393	-1.09	0.712	2.32	0.001	-1.41	0.327	0.36
1432028_at	Rab11fip2	RAB11 family interacting protein 2 (class I)	2.91	0.22	1.18	0.746	-1.26	0.615	-2.05	0.316	0.19
1428356_at	Osbp2	oxysterol binding protein 2	-1.35	0.574	2.49	0.01	1.66	0.34	-1.11	0.848	0.42
1421456_at	P2ry1	purinergic receptor P2Y, G-protein coupled 1	-1.02	0.894	-2.07	0.267	3.42	0.147	5.6	0.274	1.48
1427454_at	Hoxc6	homeo box C6	2.59	0.205	1.6	0.287	-1.44	0.646	-1.51	0.242	0.31
1459105_at	---	---	2.4	0.499	1.76	0.575	-1.36	0.546	-1.04	0.883	0.44
1420420_at	Hao1	hydroxyacid oxidase 1, liver	3.45	0.207	-1.53	0.034	-1.26	0.568	2.03	0	0.67
1434982_at	Rnf182	Ring finger protein 182	2.55	0.255	1.45	0.605	-1.11	0.735	-1.15	0.818	0.43
1443349_at	Dock10	Dedicator of cytokinesis 10	1.12	0.748	3.12	0.053	-1.54	0.012	-1.69	0.199	0.25
1420255_at	---	---	1.26	0.178	3.17	0.349	-2.16	0.074	-3.47	0.044	-0.3
1450254_at	Tert	telomerase reverse transcriptase	2.97	0.334	1.04	0.945	-1.12	0.77	-2.8	0.084	0.02
1431872_at	4930449A18Rik	RIKEN cDNA 4930449A18 gene	3.15	0.3	-1.83	0.327	1.21	0.48	-1.47	0.242	0.26
1427845_at	Fgfr4	fibroblast growth factor receptor 4	3.37	0.034	-1.03	0.948	-1.79	0.508	1.47	0.221	0.51
1432274_at	4930543N07Rik	RIKEN cDNA 4930543N07 gene	1.07	0.871	3.07	0.017	-1.31	0.544	-1.08	0.61	0.44
1455736_at	Mybpc2	myosin binding protein C, fast-type	-1.1	0.886	1.44	0.608	2.56	0.264	-1.09	0.875	0.45
1454114_a_at	4933425K02Rik	RIKEN cDNA 4933425K02 gene	-1.62	0.002	2.46	0.277	1.83	0.01	-1.35	0.525	0.33
1415804_at	Cx3cl1	chemokine (C-X3-C motif) ligand 1	1.64	0.496	-2.43	0.225	2.86	0.109	-1.63	0.357	0.11
1458996_at	Itga5	integrin alpha 5 (fibronectin receptor alpha)	2.4	0.37	1.95	0.253	-1.79	0.345	-1.76	0.51	0.2
1417787_at	Dkkl1	dickkopf-like 1	-1.19	0.684	-1.74	0.322	3.49	0.088	3.38	0.049	0.98
1454103_at	Dnhd3	dynein heavy chain domain 3	-1.06	0.89	3.35	0.031	-1.6	0.405	1.41	0.494	0.52
1431317_at	2410018L13Rik	RIKEN cDNA 2410018L13 gene	2.2	0.434	1.88	0.347	-1.2	0.82	-1.06	0.874	0.46
1436066_at	Kalrn	kalirin, RhoGEF kinase	2.83	0.137	-1.19	0.799	1.24	0.73	-3.3	0.108	-0.1
1420831_at	Qscn6	quiescin Q6	-1.03	0.945	1.74	0.432	2.21	0.275	-1.3	0.633	0.41
1438768_at	LOC665225 /// LOC	hypothetical protein LOC665225 /// hypothetical protein LOC669601 /// hypothetic	-1.08	0.668	3.31	0.007	-1.47	0.201	1.35	0.659	0.53
1422249_s_at	Zfa /// Zfx	zinc finger protein, autosomal /// zinc finger protein X-linked	-1.67	0.625	2.4	0.096	1.93	0.502	-1.27	0.805	0.35
1445707_at	Zdhhc6 /// LOC669	zinc finger, DHHC domain containing 6 /// similar to Probable palmitoyltransferase	2.35	0.018	-1.1	0.747	1.67	0.423	-1.29	0.173	0.41
1444039_at	Disp2	dispatched homolog 2 (Drosophila)	-1.14	0.31	2.02	0.028	2.03	0.004	-1.48	0.372	0.36
1456774_at	Ppp1r13l	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	-1.18	0.588	3.14	0.173	-1.06	0.594	2.65	0.329	0.89
1428722_at	Ckmt2	creatine kinase, mitochondrial 2	2.09	0.003	-1.33	0.589	2.09	0.154	-1.67	0.479	0.3
1438687_at	Lax1	lymphocyte transmembrane adaptor 1	-1.13	0.784	2.27	0.028	1.78	0.221	-1.8	0.208	0.28
1457436_at	Tbc1d7	TBC1 domain family, member 7	2.64	0.017	-1.46	0.361	1.61	0.154	-1.07	0.903	0.43
1417207_at	Dvl2	dishevelled 2, dsh homolog (Drosophila)	-1.06	0.786	2.89	0.136	1.1	0.643	-1.12	0.409	0.45
1444582_at	Dcun1d5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	1.65	0.317	2.44	0.301	-1.19	0.544	-1.3	0.444	0.4
1449909_at	2010005H15Rik	RIKEN cDNA 2010005H15 gene	-1.16	0.83	1.21	0.788	2.87	0.042	-1.22	0.751	0.42
1448530_at	Gmpr	guanosine monophosphate reductase	-1.24	0.009	3.23	0.042	-1.11	0.432	1.26	0.549	0.54

1447731_at	Peg3	paternally expressed 3	2.77	0.005	1.23	0.729	-1.06	0.906	-1.03	0.831	0.48
1427377_x_at	Hsd3b3	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 3	-1.17	0.225	-2.12	0.015	3.62	0.232	1.86	0.214	0.55
1430520_at	Cpne8	copine VIII	1.17	0.333	3.19	0.158	-1.73	0.065	-1.44	0.163	0.3
1440595_at	Epb4.1l3	erythrocyte protein band 4.1-like 3	1.93	0.267	2.32	0.256	-1.42	0.577	-1.12	0.856	0.43
1434572_at	Hdac9	histone deacetylase 9	-1.29	0.815	1.9	0.179	2.27	0.272	-1.52	0.329	0.34
1456114_at	Cds1	CDP-diacylglycerol synthase 1	-1.01	0.478	2.84	0.159	1.11	0.646	-1.99	0.359	0.24
1448162_at	Vcam1	vascular cell adhesion molecule 1	1.96	0.099	2.15	0.024	-1.2	0.304	-1.02	0.953	0.47
1422231_a_at	Tnfrsf25	tumor necrosis factor receptor superfamily, member 25	1.13	0.908	2.94	0.03	-1.13	0.753	-3.25	0.03	-0.08
1449269_at	F5	coagulation factor V	-1.4	0.233	-1.13	0.084	3.36	0.091	1.96	0.416	0.7
1422804_at	Serpinb6b	serine (or cysteine) peptidase inhibitor, clade B, member 6b	1.21	0.248	3.09	0.012	-1.51	0.007	-1.3	0.242	0.37
1441669_at	Centb2	centaurin, beta 2	3.04	0.065	1.43	0.383	-2.02	0.026	-1.23	0.419	0.31
1432344_a_at	Aplp2	amyloid beta (A4) precursor-like protein 2	-1.08	0.83	-1.62	0.314	3.42	0.345	2.05	0.347	0.69
1420579_s_at	Cftr	cystic fibrosis transmembrane conductance regulator homolog	-1.3	0.204	3.57	0.076	-1.61	0.036	1.16	0.765	0.46
1425086_a_at	Slamf6	SLAM family member 6	-1.26	0.202	1.26	0.429	2.91	0.118	-2.38	0.107	0.13
1421789_s_at	Arf3	ADP-ribosylation factor 3	2.23	0.255	-1.52	0.329	2.08	0.388	-1.4	0.456	0.35
1444095_a_at	---	---	1.95	0.338	2.22	0.198	-1.27	0.611	-1.11	0.818	0.45
1432308_at	1700058C13Rik	RIKEN cDNA 1700058C13 gene	-2.07	0.218	2.87	0.043	1.61	0.22	-1.03	0.957	0.35
1421791_at	Ang3	angiogenin, ribonuclease A family, member 3	2.34	0.167	-1.2	0.672	1.8	0.421	-1.58	0.544	0.34
1455393_at	---	---	3.05	0.063	1.29	0.261	-1.59	0.109	-1.27	0.271	0.37
1421471_at	Npy1r	neuropeptide Y receptor Y1	2.42	0.23	-1.03	0.956	1.58	0.064	-1.45	0.24	0.38
1425386_at	4833422F24Rik	RIKEN cDNA 4833422F24 gene	2	0.424	2.33	0.322	-1.56	0.421	-1.08	0.666	0.42
1431047_at	Chd6	chromodomain helicase DNA binding protein 6	1.69	0.473	2.61	0.037	-1.48	0.554	-2.93	0.424	-0.03
1459553_at	---	---	-1.67	0.402	3.34	0.129	1.04	0.931	-1.34	0.345	0.34
1422300_at	Nog	noggin	2.51	0.303	1.48	0.418	-1.01	0.968	-1.02	0.924	0.49
1440413_at	A830006F12Rik	RIKEN cDNA A830006F12 gene	1.21	0.776	-1.01	0.985	2.78	0.17	-2.04	0.3	0.23
1417399_at	Gas6	growth arrest specific 6	-1.22	0.159	3.07	0.062	1.09	0.765	-1.15	0.634	0.45
1453873_at	4933421H06Rik	RIKEN cDNA 4933421H06 gene	-1.56	0.597	3.96	0.021	-2.63	0.045	1.34	0.672	0.28
1456534_at	Man1a2	Mannosidase, alpha, class 1A, member 2	3.21	0.107	-1.06	0.919	-1.2	0.06	1.6	0.278	0.64
1457779_at	1110046J04Rik	RIKEN cDNA 1110046J04 gene	2.59	0.067	1.62	0.313	-1.29	0.374	-1.72	0.295	0.3
1433220_at	6720482G16Rik	RIKEN cDNA 6720482G16 gene	2.35	0.363	-1.06	0.891	1.69	0.08	-2.64	0.273	0.09
1418532_at	Fzd2	frizzled homolog 2 (Drosophila)	1.9	0.363	2.21	0.152	-1.13	0.717	-1.88	0.416	0.27
1430229_at	6330416L11Rik	RIKEN cDNA 6330416L11 gene	-2.09	0.358	3.18	0.08	1.34	0.25	-1.43	0.282	0.25
1422353_at	Pou4f3	POU domain, class 4, transcription factor 3	-1.43	0.26	1.87	0.364	2.42	0.321	-1.52	0.586	0.34
1418989_at	Ctse	cathepsin E	-1.14	0.41	-1.08	0.848	3.19	0.095	4.37	0.079	1.34
1416468_at	Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	3.43	0.012	-1.19	0.42	-1.37	0.004	4.4	0.161	1.32
1419004_s_at	Bcl2a1a /// Bcl2a1b	B-cell leukemia/lymphoma 2 related protein A1a /// B-cell leukemia/lymphoma 2 r	1.41	0.162	2.65	0.093	-1.05	0.821	-1.84	0.099	0.29
1448239_at	Hmox1	heme oxygenase (decycling) 1	-1.47	0.265	2.99	0.007	1.33	0.131	-1.25	0.642	0.4
1446578_at	---	---	3.12	0.005	1.48	0.561	-2.52	0.025	-1.36	0.526	0.18
1421173_at	Irf4	interferon regulatory factor 4	-1.64	0.379	1.02	0.929	3.38	0.278	-1.21	0.542	0.39
1453579_at	Phf12	PHD finger protein 12	2.4	0.052	1.88	0.072	-1.36	0.403	-1.2	0.711	0.43
1446570_at	Maml2	Mastermind like 2 (Drosophila)	1.08	0.885	3.35	0.008	-1.74	0.12	-2.47	0.098	0.06
1447621_s_at	2610307O08Rik	RIKEN cDNA 2610307O08 gene	2.17	0.088	1.86	0.139	-1.02	0.892	-1.88	0.162	0.28
1453789_at	4933440N22Rik	RIKEN cDNA 4933440N22 gene	1.46	0.191	-2.29	0.078	3.12	0.006	-3.23	0.007	-0.24
1441088_at	Zfpn1a3	zinc finger protein, subfamily 1A, 3 (Aiolos)	-1.11	0.648	1.27	0.509	2.84	0.252	-1.02	0.941	0.5
1446085_at	Socs2	Suppressor of cytokine signaling 2	-1.63	0.266	3.79	0.034	-1.64	0.038	1.19	0.54	0.43
1427155_at	Fchsd1	FCH and double SH3 domains 1	-1.07	0.878	2.96	0.128	1.13	0.605	-1.94	0.169	0.27
1419033_at	---	---	-1.4	0.084	2.42	0.015	1.89	0.059	-1.24	0.072	0.42
1425984_at	Col5a3	procollagen, type V, alpha 3	-1.23	0.279	1.83	0.158	2.38	0.112	-1.45	0.15	0.38
1422022_at	Zfp319	zinc finger protein 319	2.44	0.191	-1.76	0.219	2.02	0.248	-2.13	0.325	0.14
1417495_x_at	Cp	ceruloplasmin	2.98	0.106	1.21	0.31	-1.19	0.422	-1.3	0.061	0.42
1441207_at	9630041N07Rik	RIKEN cDNA 9630041N07 gene	3.87	0.009	-1.37	0.171	-2.35	0.063	1.05	0.702	0.3
1424898_at	Slc10a1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	3.63	0.429	-1.39	0.108	-1.46	0.561	1.77	0.374	0.64
1459872_x_at	H2-DMa	histocompatibility 2, class II, locus DMa	2.93	0.402	-1.22	0.681	1.28	0.504	-2.06	0.123	0.23

1430517_at	4930544O15Rik	RIKEN cDNA 4930544O15 gene	2.81	0.032	-1.31	0.424	1.46	0.493	-1.68	0.586	0.32
1427755_at	Mcpt-ps1	mast cell protease, pseudogene 1	2.75	0	-1.2	0.82	1.46	0.398	-2.07	0.425	0.23
1448541_at	Kns2	kinesin 2	2.59	0.214	-1.56	0.432	1.81	0.404	-1.26	0.736	0.4
1422924_at	Tnfsf9	tumor necrosis factor (ligand) superfamily, member 9	1.05	0.945	3.11	0.035	-1.12	0.413	-1.21	0.571	0.46
1429965_at	Lonrf2	LON peptidase N-terminal domain and ring finger 2	1.02	0.885	3.13	0.273	-1.11	0.27	-1.05	0.747	0.5
1435211_at	Ttc12 /// LOC64038	tetratricopeptide repeat domain 12 /// similar to tetratricopeptide repeat domain 12	-1.36	0.046	3.34	0.058	-1.03	0.923	1.11	0.878	0.52
1425797_a_at	Syk	spleen tyrosine kinase	-1.11	0.703	1.17	0.711	2.98	0.121	-1.67	0.53	0.34
1431323_at	Lztfl1	leucine zipper transcription factor-like 1	3.15	0.02	1.03	0.93	-1.14	0.626	-1.3	0.075	0.44
1423443_at	Slc4a8	solute carrier family 4 (anion exchanger), member 8	1.05	0.604	-1.22	0.684	3.19	0.039	-1.52	0.109	0.37
1438511_a_at	1190002H23Rik	RIKEN cDNA 1190002H23 gene	-1.38	0.634	3.49	0.132	-1.18	0.439	3.38	0.172	1.08
1430841_at	3300002P13Rik	RIKEN cDNA 3300002P13 gene	-1.73	0.363	1.4	0.324	3.08	0.058	-1.29	0.602	0.37
1432674_at	2300010F08Rik	RIKEN cDNA 2300010F08 gene	1.87	0.234	-1.98	0.339	2.69	0.111	-2.38	0.095	0.05
1440087_at	---	---	1.3	0.492	2.82	0.171	-1.05	0.825	-1.19	0.749	0.47
1419830_at	---	---	-2.14	0.435	4.03	0.071	-1.7	0.324	1.95	0.033	0.53
1439947_at	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1	-1.58	0.175	-1.09	0.736	3.54	0.115	1.63	0.076	0.62
1424957_at	Ahdc1	AT hook, DNA binding motif, containing 1	2.52	0.421	2.03	0.257	-1.84	0.105	-1.02	0.943	0.42
1426251_at	Cpz	carboxypeptidase Z	2.82	0.046	-1.26	0.463	1.48	0.263	-1.34	0.34	0.42
1449273_at	Cyfip2	cytoplasmic FMR1 interacting protein 2	1.24	0.044	-1.08	0.757	2.93	0.108	-1.31	0.388	0.44
1418383_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	-1.1	0.735	1.73	0.446	2.46	0.129	-3.24	0.157	-0.04
1427288_at	Apba2	amyloid beta (A4) precursor protein-binding, family A, member 2	-1.04	0.859	2.72	0.281	1.42	0.46	-1.2	0.425	0.47
1417276_at	Tulp2	tubby-like protein 2	-1.13	0.674	3.14	0.104	1.08	0.807	-2.34	0.359	0.19
1459910_at	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	1.42	0.497	-1.21	0.767	2.86	0.026	-1.5	0.394	0.39
1419810_x_at	Arhgap9	Rho GTPase activating protein 9	-1.81	0.198	2.54	0.078	2.02	0.003	-1.83	0.105	0.23
1417441_at	Dnajc12	DnaJ (Hsp40) homolog, subfamily C, member 12	-1.25	0.071	3.16	0.129	1.16	0.51	-1.08	0.575	0.49
1460710_at	Adora2a	adenosine A2a receptor	-2.64	0.007	1.18	0.739	3.55	0.016	-1.12	0.789	0.24
1457683_at	Grik2	glutamate receptor, ionotropic, kainate 2 (beta 2)	-1.7	0.488	-1.32	0.713	3.77	0.096	1.4	0.683	0.54
1422726_x_at	Speer4a	spermatogenesis associated glutamate (E)-rich protein 4a	1.5	0.003	-2	0.13	3.12	0.014	-1.98	0.357	0.16
1421637_at	Slc5a4a	solute carrier family 5, member 4a	-1	1	2.38	0.16	1.74	0.152	-1.55	0.301	0.39
1418829_a_at	Eno2	enolase 2, gamma neuronal	2.78	0.088	1.39	0.61	-1.04	0.914	-1.32	0.259	0.45
1444418_at	Itpr2	Inositol 1,4,5-triphosphate receptor 2	-1.71	0.083	3.35	0.014	1.19	0.35	-1.87	0.193	0.24
1431928_at	Ttn	titin	3.07	0.071	-1.33	0.414	1.3	0.567	-2.15	0.239	0.22
1447215_at	Wdr66	WD repeat domain 66	3	0.018	-1.1	0.751	1.22	0.382	-1.11	0.741	0.5
1420191_s_at	D16Bwg1494e	DNA segment, Chr 16, Brigham & Women's Genetics 1494 expressed	1.21	0.467	-1.48	0.547	3.24	0.055	-1.02	0.755	0.49
1421813_a_at	Psap	prosaposin	-1.54	0.29	1.05	0.896	3.43	0.018	-2.08	0.075	0.22
1445123_at	---	PREDICTED: Mus musculus similar to ubiquitin A-52 residue ribosomal protein fu	4.19	0.155	-3.84	0.145	-1.46	0.246	1.29	0.449	0.04
1446877_at	C87490	Expressed sequence C87490	3.42	0.101	-2.27	0.121	1.27	0.374	-1.09	0.902	0.33
1460236_at	Klk10	kallikrein 10	3.37	0.089	-2.01	0.054	1.27	0.528	-2.36	0.352	0.07
1421170_a_at	Plcb1	phospholipase C, beta 1	1.4	0.096	2.9	0.344	-1.19	0.24	-1.37	0.509	0.43
1454714_x_at	Phgdh /// LOC6687	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.42	0.078	1.76	0.245	2.68	0.19	-1.19	0.38	0.46
1449502_at	Dazl	deleted in azoospermia-like	-1.58	0.45	2.81	0.211	1.7	0.381	-1.62	0.353	0.33
1446449_at	Klhl21	kelch-like 21 (Drosophila)	2.97	0.427	-1.78	0.267	1.61	0.109	-1.63	0.186	0.29
1436672_at	5830428H23Rik	RIKEN cDNA 5830428H23 gene	1.64	0.175	2.76	0.001	-1.35	0.06	-1.34	0.353	0.43
1426085_a_at	Pxn	paxillin	1.55	0.581	-1.04	0.968	2.64	0.304	-1.18	0.816	0.49
1454575_at	5730422E09Rik	RIKEN cDNA 5730422E09 gene	2.91	0.046	1.41	0.461	-1.21	0.646	-1.54	0.271	0.39
1438020_at	Hapln1	hyaluronan and proteoglycan link protein 1	3.58	0.066	1.01	0.975	-1.77	0.215	-2.01	0.325	0.2
1434754_at	Garnl4	GTPase activating RANGAP domain-like 4	-1.07	0.397	1.62	0.031	2.6	0.029	-1.08	0.708	0.52
1446650_at	---	---	-1.08	0.874	3.16	0.1	1.07	0.701	-1.76	0.454	0.35
1439361_at	Myo9a	Myosin IXa	1.59	0.51	2.79	0.066	-1.28	0.505	-1.21	0.646	0.47
1457862_at	---	---	1.51	0.485	3.04	0.076	-1.64	0.412	-3.23	0.214	-0.08
1427746_x_at	H2-K1	histocompatibility 2, K1, K region	1.55	0.161	-1.11	0.256	2.71	0.003	-1.6	0.14	0.39
1422828_at	Cd3d	CD3 antigen, delta polypeptide	2.64	0.301	-1.02	0.981	1.55	0.222	-2.14	0.23	0.26
1458146_at	D030011O10Rik	RIKEN cDNA D030011O10 gene	3.33	0.406	1	0.997	-1.21	0.68	-1.1	0.881	0.51
1457545_at	9530036O11Rik	RIKEN cDNA 9530036O11 gene	3.27	0.002	1.22	0.75	-1.48	0.108	-1.96	0.443	0.26

1457553_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	4.41	0.104	-3.24	0.156	-2.26	0.057	1.32	0.162	0.06
1419907_s_at	Fcrla	Fc receptor-like A	-2.07	0.224	1.35	0.417	3.34	0.344	-2.32	0.097	0.07
1443699_at	Ptprk	protein tyrosine phosphatase, receptor type, K	3.14	0.286	1.19	0.694	-1.2	0.591	-1.41	0.517	0.43
1433315_at	4930486A15Rik	RIKEN cDNA 4930486A15 gene	-2.31	0.321	3.77	0.193	-1.04	0.933	1.79	0.176	0.55
1445450_x_at	A530021J07	hypothetical protein A530021J07	2.8	0.074	1.75	0.215	-1.59	0.41	-2.42	0.085	0.13
1459229_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	-1.84	0.157	1.75	0.265	2.88	0.009	-1.21	0.503	0.4
1450334_at	Il21	interleukin 21	-1.18	0.654	3.49	0.002	-1.18	0.779	1.62	0.214	0.69
1445583_x_at	---	PREDICTED: Mus musculus hypothetical protein LOC621058 (LOC621058), mR	-1.08	0.932	2.88	0.123	1.38	0.45	-1.48	0.292	0.43
1421285_at	Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	2.88	0.03	-1.03	0.909	1.34	0.458	-1.09	0.719	0.52
1452485_at	Phospho1	phosphatase, orphan 1	-1.08	0.877	2.33	0.321	1.93	0.196	-1.36	0.566	0.45
1429419_at	2310007A19Rik	RIKEN cDNA 2310007A19 gene	1.91	0.546	2.53	0.031	-1.33	0.397	-1.23	0.85	0.47
1438074_at	2210010C17Rik	RIKEN cDNA 2210010C17 gene	-1.12	0.77	3.21	0.169	1.1	0.778	-1.39	0.249	0.45
1436690_at	Lrba	LPS-responsive beige-like anchor	-1.05	0.847	2.53	0.168	1.71	0.237	-1.33	0.704	0.47
1454268_a_at	Cyba	cytochrome b-245, alpha polypeptide	-1.06	0.77	2.33	0	1.93	0.069	-1.38	0.188	0.45
1425569_a_at	Slamf1	signaling lymphocytic activation molecule family member 1	-1.57	0.385	3.02	0.143	1.55	0.446	-1.7	0.324	0.32
1425084_at	Gimap7	GTPase, IMAP family member 7	-1.03	0.936	1.21	0.208	3.03	0.116	-1.46	0.402	0.44
1456835_at	LOC624549	Hypothetical protein LOC624549	1.26	0.401	3.11	0.219	-1.19	0.474	-1.43	0.073	0.44
1450443_at	Ptbp1	polypyrimidine tract binding protein 1	-1.08	0.419	2.81	0.046	1.48	0.473	-2.56	0.006	0.16
1417494_a_at	Cp	ceruloplasmin	3.4	0.097	1.06	0.629	-1.31	0.173	-1.22	0.418	0.48
1432528_at	1700021P04Rik	RIKEN cDNA 1700021P04 gene	3.4	0.074	-1.47	0.49	1.13	0.544	-1.07	0.718	0.5
1452592_at	Mgst2	microsomal glutathione S-transferase 2	-1.35	0.182	3.43	0	1.04	0.814	-1.55	0.028	0.39
1439836_at	Asb15	ankyrin repeat and SOCS box-containing protein 15	-1.27	0.525	1.33	0.46	3.1	0.335	-1.35	0.302	0.45
1457783_at	Rab12	RAB12, member RAS oncogene family	2.33	0.152	2.16	0.013	-1.37	0.152	-1.78	0.22	0.33
1437248_at	2700049A03Rik	RIKEN cDNA 2700049A03 gene	2.41	0.202	1.88	0.274	-1.07	0.748	-1.1	0.629	0.53
1456732_at	Gpd1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	1.06	0.948	3.48	0.166	-1.47	0.213	-1.71	0.43	0.34
1437792_at	1700013D24Rik	RIKEN cDNA 1700013D24 gene	1.8	0.23	2.79	0.088	-1.56	0.172	-1.11	0.899	0.48
1450068_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	1.42	0.553	-1.25	0.308	3.01	0.255	-1.01	0.975	0.54
1446146_at	Gja7	Gap junction membrane channel protein alpha 7	2.16	0.315	2.15	0.338	-1.09	0.881	-1.71	0.365	0.38
1447251_x_at	2610301F02Rik	RIKEN cDNA 2610301F02 gene	3.06	0.016	-1.07	0.823	1.24	0.649	-1.07	0.903	0.54
1451580_a_at	Ttr	transthyretin	-1.08	0.896	-1.27	0.343	3.53	0.183	4.3	0.312	1.37
1430686_at	4833418N02Rik	RIKEN cDNA 4833418N02 gene	1.31	0.38	3.45	0.01	-2.09	0.368	-1.14	0.266	0.38
1429563_x_at	5031415C07Rik	RIKEN cDNA 5031415C07 gene	-1.32	0.257	1.02	0.925	3.47	0.029	-1.25	0.486	0.48
1426619_at	Gm1313	gene model 1313, (NCBI)	2.47	0.046	-1.61	0.255	2.16	0.108	-5.08	0.245	-0.51
1445283_at	---	---	-2.82	0.437	3.35	0.121	1.56	0.201	-1.4	0.57	0.17
1425928_at	Xkr6	X Kell blood group precursor related family member 6 homolog	2.61	0.095	1.74	0.364	-1.1	0.673	-1.59	0.345	0.42
1447564_x_at	Piwil4	piwi-like homolog 4 (Drosophila)	-1.39	0.594	3.68	0.116	-1.16	0.597	1.16	0.768	0.57
1435095_at	C030009O12Rik	RIKEN cDNA C030009O12 gene	3.35	0.127	-1.37	0.535	1.18	0.553	-1.41	0.103	0.44
1437195_x_at	Mapk10	mitogen activated protein kinase 10	2.5	0.045	1.97	0.102	-1.25	0.688	-1.65	0.371	0.39
1425513_at	Map2k7	mitogen activated protein kinase kinase 7	2.73	0.015	1.86	0.161	-1.48	0.208	-1.02	0.967	0.52
1453150_at	5830406J20Rik	RIKEN cDNA 5830406J20 gene	1.26	0.183	-2.22	0.294	3.56	0.023	-1.35	0.611	0.31
1458206_at	---	---	-1.49	0.518	3.5	0.009	1.1	0.674	-2.24	0.137	0.22
1444718_at	Treml2	triggering receptor expressed on myeloid cells-like 2	3.16	0.37	-2.03	0.114	1.62	0.28	-2.26	0.094	0.12
1420122_at	AA517858	expressed sequence AA517858	2.52	0.196	-1.47	0.399	2.07	0.084	-1.15	0.866	0.5
1418451_at	Gng2	guanine nucleotide binding protein (G protein), gamma 2 subunit	3.02	0.017	-1.05	0.915	1.31	0.426	-1.55	0.189	0.43
1436403_at	BC025575	cDNA sequence BC025575	-1.12	0.78	1.86	0.177	2.54	0.051	-1.18	0.494	0.52
1453058_at	Wdr5b	WD repeat domain 5B	1.13	0.208	3.23	0.052	-1.07	0.658	-1.06	0.69	0.55
1432428_at	Ankrd55	ankyrin repeat domain 55	-1.45	0.033	2.21	0.322	2.39	0.187	-1.08	0.848	0.52
1427479_at	Eif1a /// MGC10753	eukaryotic translation initiation factor 1A /// similar to Eukaryotic translation initiati	2.91	0.464	1.45	0.472	-1.06	0.894	-2.56	0.216	0.18
1431764_at	2310067P03Rik	RIKEN cDNA 2310067P03 gene	3.13	0.132	1.62	0.386	-1.81	0.401	-2.22	0.213	0.18
1454171_x_at	9530053H05Rik	RIKEN cDNA 9530053H05 gene	-1.3	0.511	1.88	0.108	2.66	0.041	-1.73	0.181	0.38
1437536_at	Fkrp	fukutin related protein	-1.55	0.61	1.06	0.901	3.6	0.259	-2.41	0.337	0.18
1415893_at	Sgpl1	sphingosine phosphate lyase 1	1.14	0.806	-1.22	0.767	3.35	0.278	-1.44	0.695	0.46
1455592_at	Vangl2	vang-like 2 (van gogh, Drosophila)	-1.52	0.029	3.92	0	-1.36	0.105	1	0.973	0.51

1456841_at	---	PREDICTED: Mus musculus similar to Kinesin-like protein KIF2C (Mitotic centron	-1.21	0.483	-1.38	0.583	3.76	0.084	1.6	0.406	0.69
1454445_at	5430430K15Rik	RIKEN cDNA 5430430K15 gene	-1.09	0.885	2.8	0.151	1.6	0.395	-1.45	0.172	0.46
1444954_at	Cdkl4	Cyclin-dependent kinase-like 4	4.08	0.426	-1.93	0.117	-1.37	0.543	1.27	0.595	0.51
1445768_at	LOC625662	similar to Ankyrin repeat domain protein 11 (Ankyrin repeat-containing cofactor 1)	-1.96	0.053	3.27	0.017	1.55	0.137	-3.37	0.075	-0.13
1431056_a_at	Lpl /// LOC669888	lipoprotein lipase /// similar to Lipoprotein lipase precursor (LPL)	-1.49	0.248	3.15	0.014	1.52	0.254	-1.1	0.47	0.52
1457013_at	Garnl1	GTPase activating RANGAP domain-like 1	3.05	0.057	-1.02	0.973	1.32	0.395	-1.74	0.224	0.4
1428043_a_at	Cmah	cytidine monophospho-N-acetylneuraminic acid hydroxylase	1.46	0.363	-1.22	0.677	3.06	0.069	-1.47	0.555	0.46
1454632_at	6330442E10Rik	RIKEN cDNA 6330442E10 gene	-1.16	0.655	2.36	0.322	2.12	0.066	-1.63	0.128	0.42
1427343_at	Rasd2	RASD family, member 2	3.93	0.286	-2.19	0.299	-1.04	0.932	2.07	0.236	0.69
1458474_at	---	---	2.79	0.199	1.74	0.261	-1.21	0.651	-1.18	0.43	0.54
1433996_at	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	-1.01	0.989	3.5	0.04	-1.14	0.743	1.61	0.238	0.74
1436111_at	E030011K20Rik	RIKEN cDNA E030011K20 gene	-2.71	0.019	3.89	0.122	1.1	0.687	-1.27	0.555	0.25
1446017_at	---	Transcribed locus	3.01	0.325	2.02	0.268	-2.96	0.262	-1.74	0.198	0.08
1426157_a_at	Cd209b	CD209b antigen	-3.5	0.413	2.51	0.146	2.58	0.189	-4.04	0.019	-0.61
1453577_at	2610018I03Rik	RIKEN cDNA 2610018I03 gene	3.3	0.004	-1.04	0.83	1.11	0.769	-1.18	0.388	0.55
1459064_at	Dlgh2	Discs, large homolog 2 (Drosophila)	3.15	0.456	1.33	0.72	-1.13	0.813	-1.85	0.352	0.38
1430634_a_at	Pfkp	phosphofructokinase, platelet	1.68	0.226	-1.31	0.459	2.93	0.089	-1.02	0.968	0.57
1421106_at	Jag1	jagged 1	-1.31	0.698	3.15	0.01	1.46	0.078	-1.15	0.441	0.54
1447996_at	AI848149	expressed sequence AI848149	1.18	0.745	-1.28	0.561	3.42	0.012	-1.01	0.989	0.58
1442941_at	C77027	expressed sequence C77027	2.42	0.349	2.38	0.155	-1.68	0.124	-1.02	0.973	0.52
1419676_at	Mx2	myxovirus (influenza virus) resistance 2	2.22	0.389	2.4	0.234	-1.3	0.629	-1.84	0.075	0.37
1448256_at	Gosr1	golgi SNAP receptor complex member 1	3.11	0.282	-1.34	0.571	1.54	0.622	-1.07	0.876	0.56
1443210_at	---	---	-1.61	0.054	4.47	0.027	-3.27	0.086	1.69	0.5	0.32
1450513_at	Cd33	CD33 antigen	-1.82	0.17	3.53	0.008	1.32	0.504	-1.31	0.166	0.43
1442136_at	Ankib1	ankyrin repeat and IBR domain containing 1	-1.33	0.557	3.61	0.028	1.04	0.916	-1.15	0.794	0.54
1440940_at	Cacnb1	Calcium channel, voltage-dependent, beta 1 subunit	3.29	0.119	-1.93	0.244	1.6	0.044	-1.15	0.558	0.45
1425293_a_at	Zcchc18	zinc finger, CCHC domain containing 18	1.53	0.163	-1.78	0.15	3.32	0.269	-1.02	0.951	0.51
1447111_at	---	---	2.01	0.288	2.54	0.266	-1.16	0.249	-2.27	0.391	0.28
1420391_at	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	3.47	0.071	-1.48	0.453	1.27	0.487	-2.04	0.396	0.31
1456197_x_at	---	Transcribed locus	3.73	0.034	-2.4	0.271	1.28	0.669	-1.49	0.619	0.28
1427725_a_at	Pou2f2	POU domain, class 2, transcription factor 2	-2.28	0.178	1.36	0.596	3.63	0.078	-1.58	0.233	0.28
1428019_at	4932425I24Rik	RIKEN cDNA 4932425I24 gene	2.96	0.026	-1.19	0.522	1.63	0.548	-2.33	0.043	0.27
1431999_at	Polr3f	polymerase (RNA) III (DNA directed) polypeptide F	4.04	0.027	-1.56	0.573	-1.33	0.329	1.95	0.229	0.77
1432866_at	6030442K20Rik	RIKEN cDNA 6030442K20 gene	-1.41	0.659	2.32	0.039	2.41	0.066	-1.15	0.591	0.54
1417359_at	Mfap2	microfibrillar-associated protein 2	-1.03	0.626	3.53	0.102	-1.06	0.482	1.06	0.95	0.62
1419337_at	1700080E11Rik	RIKEN cDNA 1700080E11 gene	3.94	0.001	-1.18	0.72	-1.53	0.374	1.14	0.898	0.59
1455622_at	Podxl2	podocalyxin-like 2	4.24	0.007	-1.31	0.734	-2.25	0.197	1.32	0.116	0.5
1428379_at	Slc17a6	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), m	2	0.451	2.97	0.232	-2.09	0.18	-1.27	0.265	0.4
1453980_at	5330434G04Rik	RIKEN cDNA 5330434G04 gene	1.52	0.256	-1.11	0.813	3.03	0.009	-1.01	0.969	0.61
1431715_a_at	Lig3	ligase III, DNA, ATP-dependent	-1.02	0.945	1.3	0.231	3.18	0.408	-1.37	0.73	0.52
1424948_x_at	H2-D1 /// H2-K1 ///	histocompatibility 2, D region locus 1 /// histocompatibility 2, K1, K region /// MHC	1.46	0.219	-1.15	0.646	3.13	0.001	-1.47	0.394	0.49
1439851_at	---	Transcribed locus	1.18	0.544	3.3	0.198	-1.02	0.943	-1.97	0.176	0.37
1448560_at	Bid	BH3 interacting domain death agonist	1.05	0.916	-1.03	0.918	3.44	0.078	-1.07	0.805	0.6
1458080_at	Setx	senataxin	-1.26	0.764	2.45	0.144	2.23	0.054	-2.75	0.209	0.17
1431463_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	3.22	0.322	-1.14	0.71	1.39	0.435	-1.04	0.956	0.61
1417049_at	Rhd	Rh blood group, D antigen	-1.3	0.709	-2.39	0.034	4.3	0.015	8.96	0.138	2.39
1427682_a_at	Egr2	early growth response 2	3.57	0.443	1.27	0.661	-1.56	0.228	-1.79	0.123	0.37
1430435_at	Aff3	AF4/FMR2 family, member 3	-1.94	0.385	1.73	0.131	3.25	0.027	-2.05	0.014	0.25
1425291_at	Foxj1	forkhead box J1	3.36	0.031	-1.71	0.293	1.55	0.03	-1.27	0.763	0.48
1436086_at	4921526F01Rik	RIKEN cDNA 4921526F01 gene	4.18	0.018	-1.38	0.551	-1.68	0.17	2.27	0.26	0.85
1440876_at	Rp9h	Retinitis pigmentosa 9 homolog (human)	3.41	0.02	1.29	0.62	-1.24	0.279	-1.09	0.769	0.59
1422051_a_at	Gabbr1	gamma-aminobutyric acid (GABA-B) receptor, 1	2.98	0.071	1.62	0.38	-1.1	0.814	-1.32	0.609	0.55
1460089_at	Per3	Period homolog 3 (Drosophila)	3.57	0.032	-1.05	0.863	-1	0.992	1.77	0.298	0.82

1451769_s_at	Pcdha4 /// Pcdha6	protocadherin alpha 4 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protoc	3.32	0.219	1.52	0.225	-1.45	0.265	-1.36	0.593	0.5
1446076_at	---	Transcribed locus	-1.83	0.325	4.22	0.163	-1.32	0.452	1.96	0.126	0.76
1447303_at	---	---	3.41	0.003	-1.09	0.872	1.2	0.686	-1.51	0.516	0.5
1449902_at	1110058A15Rik	RIKEN cDNA 1110058A15 gene	3.52	0.129	-1.27	0.327	1.23	0.117	-1.3	0.488	0.54
1445121_at	1110007J02Rik	RIKEN cDNA 1110007J02 gene	1.67	0.219	2.99	0.172	-1.15	0.565	-1.71	0.417	0.45
1456888_at	Pfkfb4	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	1.18	0.209	3.43	0.086	-1.07	0.133	-1.08	0.668	0.62
1453850_at	1500002I01Rik	RIKEN cDNA 1500002I01 gene	-1.01	0.965	2.54	0	2.01	0.028	-1.12	0.487	0.61
1425805_a_at	Usp12	ubiquitin specific peptidase 12	1.15	0.845	-2.51	0.465	4	0.384	-1.71	0.642	0.23
1447293_x_at	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	-1.04	0.948	1.33	0.543	3.26	0.003	-2.59	0.293	0.24
1453820_at	A930005F02Rik ///	RIKEN cDNA A930005F02 gene /// suppressor of hairy wing homolog 4 (Drosoph	3.8	0.041	1.13	0.457	-1.6	0.26	-1.36	0.71	0.49
1420200_at	---	---	3.41	0.031	1.33	0.671	-1.22	0.771	-2.19	0.084	0.33
1454288_at	5830468K08Rik	RIKEN cDNA 5830468K08 gene	1.11	0.616	3.64	0.01	-1.23	0.573	-1.45	0.138	0.52
1426927_at	Ap3b2	adaptor-related protein complex 3, beta 2 subunit	-1.04	0.952	3.07	0.156	1.55	0.245	-1.45	0.233	0.53
1446121_at	Dmt2	Dorso-medial telencephalon gene 2	1.6	0.449	3.35	0.178	-1.59	0.191	-1.29	0.74	0.52
1430853_a_at	3110045G13Rik	RIKEN cDNA 3110045G13 gene	-2.96	0.427	1.33	0.519	3.91	0.132	-1.17	0.736	0.28
1419463_at	Clca2	chloride channel calcium activated 2	3.1	0.046	-1.28	0.688	1.71	0.406	-1.09	0.875	0.61
1446809_at	B830045N13Rik	RIKEN cDNA B830045N13 gene	3.08	0.419	1.65	0.151	-1.15	0.755	-2.34	0.234	0.31
1456471_x_at	Phgdh /// LOC3829	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.47	0.033	3.39	0.032	1.53	0.304	-1.04	0.808	0.61
1438698_at	4632425D07Rik	RIKEN cDNA 4632425D07 gene	1.38	0.774	3.57	0.14	-1.49	0.225	-1.13	0.453	0.58
1428435_at	Muc2	mucin 2	-1.03	0.819	2.78	0.229	1.88	0.343	-1.1	0.888	0.63
1430881_at	7630403G23Rik	RIKEN cDNA 7630403G23 gene	3.61	0.122	1.31	0.651	-1.39	0.43	-1.03	0.962	0.63
1451463_at	Arhgap8	Rho GTPase activating protein 8	-1.07	0.637	1.03	0.951	3.68	0.063	-1.14	0.808	0.63
1422651_at	Adipoq	adiponectin, C1Q and collagen domain containing	-2.05	0.298	-1.13	0.77	4.28	0.392	10.48	0.193	2.9
1436800_at	Fstl5	follistatin-like 5	1.25	0.581	3.73	0.055	-1.48	0.343	-2.6	0.386	0.23
1440877_at	Frs2	Fibroblast growth factor receptor substrate 2	3.09	0.21	2.11	0.385	-2.18	0.162	-1.53	0.065	0.37
1453178_at	Iqch	IQ motif containing H	3.47	0.083	-1.17	0.766	1.35	0.231	-1.08	0.91	0.64
1450248_at	Adam11	a disintegrin and metallopeptidase domain 11	-2.54	0.108	3.92	0.072	1.36	0.187	-2.26	0.036	0.12
1432220_at	4933430L12Rik	RIKEN cDNA 4933430L12 gene	3.41	0.152	-1.24	0.685	1.45	0.461	-2.55	0.007	0.27
1446715_at	Abca13 /// LOC672	ATP-binding cassette, sub-family A (ABC1), member 13 /// similar to ATP binding	-1.19	0.37	-1.03	0.922	3.87	0.239	2.06	0.507	0.93
1447145_at	---	---	1.17	0.838	3.92	0.152	-1.7	0.486	-1.61	0.464	0.44
1451578_at	Ccdc65	coiled-coil domain containing 65	2.88	0.078	-1.09	0.82	1.89	0.029	-2.84	0.527	0.21
1437659_at	Als2cr11	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 11 (hum	-1.17	0.866	3.18	0.267	1.66	0.417	-1.38	0.671	0.57
1457168_at	AI225934	expressed sequence AI225934	4.67	0.03	-1.77	0.275	-2.17	0.167	1.15	0.343	0.47
1441008_at	Dym	dymeclin	4.32	0.25	-2.2	0.282	-1.09	0.755	1.94	0.473	0.74
1431496_at	B230104F01Rik	RIKEN cDNA B230104F01 gene	2.63	0.293	2.54	0.214	-1.86	0.269	-1.76	0.433	0.39
1424482_at	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	-2.26	0.22	4.4	0.081	-1.15	0.586	1.89	0.005	0.72
1430323_at	1700049E17Rik ///	RIKEN cDNA 1700049E17 gene /// hypothetical protein LOC624112 /// similar to	4.01	0.109	1.07	0.842	-1.57	0.423	-1.35	0.571	0.54
1429417_at	4833446K15Rik	RIKEN cDNA 4833446K15 gene	3.62	0.368	1.53	0.379	-1.76	0.053	-1.17	0.821	0.56
1437477_at	Lrrfip1	leucine rich repeat (in FLII) interacting protein 1	3.53	0.01	1.36	0.291	-1.21	0.608	-1.08	0.884	0.65
1430620_at	4930588N13Rik	RIKEN cDNA 4930588N13 gene	2.59	0.382	2.23	0.191	-1.1	0.688	-1.39	0.428	0.58
1429919_at	Ankrd48	ankyrin repeat domain 48	3.05	0.456	-1.05	0.936	1.73	0.383	-1.91	0.032	0.45
1449736_at	Pip5k2a	Phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	3.91	0.013	1.16	0.62	-1.5	0.517	-3.1	0.168	0.12
1429439_at	Ercc8	excision repaiross-complementing rodent repair deficiency, complementation gro	1.81	0.457	3.18	0.076	-1.34	0.595	-1.27	0.72	0.6
1443597_at	Crsp2	cofactor required for Sp1 transcriptional activation, subunit 2	2	0.114	-1.4	0.402	3.04	0.158	-1.8	0.329	0.46
1446518_at	Rock1	Rho-associated coiled-coil forming kinase 1	-1.17	0.625	4.01	0.048	-1.12	0.686	1.29	0.475	0.75
1431845_at	2810016G10Rik	RIKEN cDNA 2810016G10 gene	2.8	0.033	2.23	0.024	-1.36	0.666	-2.15	0.277	0.38
1444803_at	Zfpm2	Zinc finger protein, multitype 2	3.14	0.078	2.02	0.238	-1.6	0.288	-2.83	0.144	0.18
1443691_at	2410089E03Rik	RIKEN cDNA 2410089E03 gene	2.28	0.154	-1	0.989	2.51	0.073	-1.08	0.858	0.67
1457603_at	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A	1.91	0.516	3.01	0.292	-1.15	0.754	-3.02	0.015	0.19
1433177_at	5830411G16Rik	RIKEN cDNA 5830411G16 gene	1.75	0.464	3.31	0.195	-1.37	0.548	-2.05	0.165	0.41
1425219_x_at	Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polype	1.91	0.327	3.09	0.097	-1.24	0.433	-1.6	0.33	0.54
1453724_a_at	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1	4.01	0.385	-1.35	0.408	1.07	0.898	-1.09	0.555	0.66
1457857_at	---	---	2.79	0.009	-1.47	0.4	2.35	0.057	-1.34	0.729	0.58

1438601_at	Pkmyt1	protein kinase, membrane associated tyrosine/threonine 1	-1.49	0.274	3.91	0.195	1.25	0.596	-1.34	0.691	0.58
1447196_at	MGC58416	hypothetical protein LOC622866	1.68	0.553	3.44	0.039	-1.4	0.55	-1.63	0.15	0.52
1435839_at	---	Transcribed locus	-1.5	0.089	4.22	0.1	-1.04	0.909	1.46	0.376	0.78
1425502_x_at	---	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library,	3.93	0.023	-1.45	0.534	1.23	0.778	-1.55	0.266	0.54
1435113_x_at	Stmn3	stathmin-like 3	2.66	0.208	2.26	0.125	-1.07	0.859	-2.39	0.321	0.37
1455431_at	Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	-1.02	0.91	3.85	0.03	1.03	0.781	-1.38	0.614	0.62
1438282_at	Syt1	synaptotagmin I	3.92	0.027	1.09	0.803	-1.18	0.609	-1.39	0.556	0.61
1447508_at	---	Transcribed locus	3.46	0.396	2.15	0.202	-3.89	0.155	-1.01	0.986	0.18
1419021_at	Mcf2	mcf.2 transforming sequence	3.3	0.106	1.85	0.134	-1.39	0.548	-1.16	0.831	0.65
1460256_at	Car3	carbonic anhydrase 3	-2.11	0.264	-2.31	0.267	4.97	0.349	3.25	0.167	0.95
1419410_at	Batf	basic leucine zipper transcription factor, ATF-like	-1.79	0.631	4.13	0.02	1.19	0.42	-1.05	0.645	0.62
1460131_at	Rnf170	Ring finger protein 170	2.59	0.056	2.48	0.34	-1.22	0.41	-1.31	0.322	0.63
1425995_s_at	Wt1	Wilms tumor homolog	-1.34	0.217	3.62	0.027	1.54	0.454	-1.25	0.445	0.64
1444751_at	Pou6f1	POU domain, class 6, transcription factor 1	1.04	0.723	3.92	0.058	-1.05	0.846	-1.85	0.434	0.51
1442074_at	Clec2g	C-type lectin domain family 2, member g	1.74	0.429	-1.07	0.916	3.24	0.323	-1.15	0.703	0.69
1448290_at	Pap	pancreatitis-associated protein	-1.02	0.949	2.85	0.404	2.1	0.263	-1.97	0.504	0.49
1419621_at	Ankrd2	ankyrin repeat domain 2 (stretch responsive muscle)	-2.03	0.16	4.01	0.013	1.43	0.449	-1.2	0.317	0.55
1418987_at	Pla2g2d	phospholipase A2, group IID	1.18	0.581	-1.04	0.836	3.81	0.226	-2.22	0.148	0.43
1421618_at	Myo1f	myosin IF	-1.21	0.327	2.48	0.223	2.65	0.062	-1.62	0.146	0.57
1441855_x_at	Cxcl1	chemokine (C-X-C motif) ligand 1	-1.51	0.043	4.04	0.091	1.24	0.481	-1.1	0.794	0.67
1423466_at	Ccr7	chemokine (C-C motif) receptor 7	2.44	0.202	2.82	0.136	-1.45	0.215	-4.21	0.059	-0.1
1447747_x_at	Adal	Adenosine deaminase-like	4.34	0.008	-1.11	0.855	-1.4	0.413	1.13	0.542	0.74
1424187_at	Ccdc80	coiled-coil domain containing 80	3.57	0.139	1.69	0.307	-1.43	0.477	-1.81	0.27	0.51
1441197_at	9530059O14Rik	RIKEN cDNA 9530059O14 gene	3.95	0.059	-1.16	0.724	1.17	0.75	-1.96	0.122	0.5
1427424_at	Galnt6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	-1.34	0.633	1.62	0.322	3.62	0.063	-1.54	0.264	0.59
1452968_at	Cthrc1	collagen triple helix repeat containing 1	2.93	0.007	2.09	0.388	-1.03	0.948	-1.98	0.239	0.5
1424950_at	Sox9	SRY-box containing gene 9	4.13	0.007	1.23	0.558	-1.55	0.275	-1.16	0.838	0.66
1447008_at	---	---	1.89	0.347	3.53	0.047	-1.69	0.562	-1.4	0.69	0.58
1458214_at	A730012O14Rik	RIKEN cDNA A730012O14 gene	1.95	0.417	-1.9	0.002	3.54	0.032	-1.39	0.415	0.55
1456388_at	Atp11a	ATPase, class VI, type 11A	1.1	0.652	4	0.1	-1.08	0.434	-1.25	0.421	0.69
1435393_at	---	CDNA, clone:Y0G0149N04, strand:unspecified	-1.83	0.079	4.95	0.163	-1.84	0.237	1.5	0.396	0.69
1428595_at	Slc6a19	solute carrier family 6 (neurotransmitter transporter), member 19	-1.18	0.173	3.41	0.006	1.78	0.216	-3.62	0.038	0.1
1426657_s_at	Phgdh /// LOC6664	3-phosphoglycerate dehydrogenase /// similar to 3-phosphoglycerate dehydrogen	-1.42	0.31	2.81	0.351	2.54	0.066	-1.21	0.181	0.68
1419622_at	Ugt2b5	UDP glucuronosyltransferase 2 family, polypeptide B5	4.29	0.293	-1.3	0.121	-1	0.998	2.1	0.524	1.02
1455770_at	---	Transcribed locus	4.02	0.124	-1.07	0.59	1.12	0.828	-1.04	0.909	0.76
1438617_at	Serpina7	Serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitryps	1.54	0.673	3.61	0.032	-1.08	0.75	-1.93	0.539	0.53
1420518_a_at	Igsf9	immunoglobulin superfamily, member 9	-1.74	0.062	3.35	0.177	2.15	0.028	-1.87	0.316	0.47
1424524_at	1200002N14Rik	RIKEN cDNA 1200002N14 gene	1.12	0.76	4.3	0.058	-1.53	0.017	-1.24	0.26	0.66
1457961_at	---	---	-1.4	0.369	4.16	0.015	1.21	0.14	-1.14	0.234	0.71
1447163_x_at	---	---	1.09	0.732	4.45	0.003	-1.81	0.318	-1.25	0.637	0.62
1440973_at	LOC552874	hypothetical LOC552874	1.2	0.452	3.95	0.012	-1.04	0.872	-1.02	0.889	0.77
1420280_x_at	Col9a3	procollagen, type IX, alpha 3	1.38	0.735	3.9	0.003	-1.2	0.782	-2.06	0.409	0.5
1435014_at	Rab39b	RAB39B, member RAS oncogene family	-1.61	0.282	4.77	0.003	-1.39	0.314	1.31	0.586	0.77
1439768_x_at	Sema4f	sema domain, immunoglobulin domain (Ig), TM domain, and short cytoplasmic do	1.87	0.288	3.56	0.017	-1.46	0.181	-1.29	0.296	0.67
1452894_at	Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	3.4	0.042	-1.03	0.95	1.74	0.195	-1.92	0.148	0.55
1460250_at	Sostdc1	sclerostin domain containing 1	-1.04	0.733	-3.08	0.038	4.84	0.038	1.09	0.854	0.45
1419801_x_at	---	Transcribed locus	-3.39	0.075	4.45	0	1.41	0.445	-3.85	0.012	-0.34
1460258_at	Lect1	leukocyte cell derived chemotaxin 1	4.52	0.004	-1.29	0.43	-1.16	0.845	1.49	0.437	0.89
1441093_at	---	---	-1.39	0.368	1.88	0.105	3.57	0.219	-1.52	0.463	0.64
1444203_at	---	PREDICTED: Mus musculus similar to HYPOTHETICAL PROTEIN ORF-1137 (L	-1.07	0.927	1.92	0.438	3.31	0.081	-3.05	0.242	0.28
1449453_at	Bst1	bone marrow stromal cell antigen 1	-1.15	0.432	3.4	0.267	1.91	0.035	-1.96	0.012	0.55
1452503_a_at	Brwd1	bromodomain and WD repeat domain containing 1	3.43	0.073	2.02	0.31	-1.34	0.387	-2.46	0.148	0.41
1446252_at	---	Adult retina cDNA, RIKEN full-length enriched library, clone:A930029I05 product:	-1.17	0.731	4.59	0.18	-1.33	0.443	1.4	0.532	0.87

1455408_at	Pla2g4f	phospholipase A2, group IVF	4.17	0.426	1.24	0.824	-1.27	0.251	-1.24	0.743	0.73
1422364_at	Olfr68	olfactory receptor 68	4.18	0.022	1.1	0.749	-1.1	0.872	-1.31	0.277	0.72
1443110_at	Gtf2e1	general transcription factor II E, polypeptide 1 (alpha subunit)	3.96	0.237	-1.3	0.576	1.48	0.543	-1.23	0.669	0.73
1426888_at	Ehmt2	euchromatic histone lysine N-methyltransferase 2	1.51	0.626	-1.22	0.725	3.9	0.162	-1.13	0.844	0.76
1442865_at	Dgkk	diacylglycerol kinase kappa	4.39	0.011	1.2	0.63	-1.59	0.426	-1.36	0.689	0.66
1420816_at	Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polyp	3.71	0.342	-1.09	0.929	1.61	0.666	-2.04	0.561	0.55
1459438_at	---	---	4.08	0.18	-1.17	0.752	1.3	0.482	-1.15	0.776	0.77
1438101_at	Fzd3	Frizzled homolog 3 (Drosophila)	1.49	0.23	3.85	0.361	-1.11	0.829	-1.31	0.403	0.73
1450133_at	Ugt2a3	UDP glucuronosyltransferase 2 family, polypeptide A3	4.87	0.443	-1.38	0.123	-1.44	0.419	1.14	0.552	0.8
1450545_a_at	Dntt	deoxynucleotidyltransferase, terminal	3.82	0.011	1.66	0.064	-1.17	0.836	-1.58	0.272	0.68
1442771_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	-1.35	0.467	4.86	0.129	-1.35	0.257	1.1	0.442	0.82
1447998_at	AI324046	expressed sequence AI324046	1.66	0.477	-1.1	0.893	3.79	0.009	-1.03	0.941	0.83
1439579_at	LOC433408	hypothetical LOC433408	3.61	0.003	-1.12	0.732	1.89	0.289	-1.99	0.022	0.6
1446265_at	Dnm3	dynamin 3	4.6	0.132	-1.02	0.928	-1.23	0.649	3.72	0.215	1.52
1422934_x_at	Defcr-rs7	defensin related cryptdin, related sequence 7	3.12	0.28	2.58	0.102	-1.43	0.299	-1.31	0.097	0.74
1432618_at	3110037L02Rik	RIKEN cDNA 3110037L02 gene	-1.06	0.86	4.03	0.25	1.44	0.178	-1.19	0.673	0.8
1436087_at	Dpp10	dipeptidylpeptidase 10	4.56	0.093	1.27	0.626	-1.68	0.38	-1.29	0.354	0.71
1442947_x_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330042P	3.34	0.159	2.21	0.152	-1.14	0.738	-1.84	0.104	0.64
1435641_at	9530018I07Rik	RIKEN cDNA 9530018I07 gene	-1.43	0.072	4.54	0.003	1.2	0.19	-1.59	0.236	0.68
1432425_at	4930418G15Rik	RIKEN cDNA 4930418G15 gene	3.83	0.111	1.79	0.389	-1.23	0.402	-1.45	0.342	0.74
1449156_at	Ly9	lymphocyte antigen 9	-1.07	0.864	2.71	0.05	2.8	0.1	-2.25	0.114	0.55
1419875_at	---	Transcribed locus	4.24	0.1	1.29	0.6	-1.08	0.907	-2.28	0.238	0.54
1451204_at	Scara5	scavenger receptor class A, member 5 (putative)	-1.09	0.413	4.73	0.137	-1.2	0.453	1.53	0.447	0.99
1451780_at	Blnk	B-cell linker	-1.12	0.142	1.67	0.131	3.93	0.196	-1.76	0.172	0.68
1454184_a_at	Ikbkb	inhibitor of kappaB kinase beta	2.47	0.206	-1.11	0.9	3.11	0.407	-2.44	0.426	0.51
1419627_s_at	Clec4n	C-type lectin domain family 4, member n	1.58	0.575	4.08	0	-1.21	0.552	-1.03	0.919	0.86
1430887_s_at	1700112E06Rik	RIKEN cDNA 1700112E06 gene	-1	0.987	4.48	0.001	1.05	0.795	-1.05	0.732	0.87
1451557_at	Tat	tyrosine aminotransferase	3.59	0.401	-1.19	0.203	2.09	0.452	-1	0.995	0.87
1438665_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	-1.62	0.334	3.6	0.093	2.31	0.066	-2.06	0.062	0.56
1425837_a_at	Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	-1.36	0.77	4.81	0.005	-1	0.969	6.06	0.212	2.13
1438007_at	AI851790	expressed sequence AI851790	-1.29	0.629	4.86	0.001	-1.1	0.812	2.05	0.055	1.13
1454339_at	4930551I15Rik	RIKEN cDNA 4930551I15 gene	4.85	0.098	-2.24	0.372	1.25	0.685	-2.3	0.122	0.39
1437079_at	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	4.96	0.008	-1.57	0.128	-1.03	0.958	1.22	0.749	0.89
1459643_at	---	Transcribed locus	3.95	0.061	1.85	0.302	-1.31	0.368	-1.33	0.17	0.79
1429948_x_at	Crygf	crystallin, gamma F	1.53	0.127	4.64	0.086	-2.48	0.117	-2.96	0.047	0.19
1452004_at	Calca	calcitonin/calcitonin-related polypeptide, alpha	5.21	0.097	-1.35	0.504	-1.59	0.246	1.01	0.965	0.82
1424270_at	Dcamkl1	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	4.2	0.008	-1.16	0.832	1.61	0.05	-2.61	0.132	0.51
1458813_at	Scn5a	sodium channel, voltage-gated, type V, alpha	-1.27	0.53	4.38	0.157	1.51	0.031	-1.07	0.788	0.89
1417470_at	Apobec3	apolipoprotein B editing complex 3	-1.05	0.706	3.19	0.011	2.54	0.211	-1.13	0.696	0.89
1419626_at	LOC382006	similar to ADAM 25 precursor (A disintegrin and metalloproteinase domain 25) (T	3.92	0.035	-4.31	0.179	2.55	0.018	-1.86	0.383	0.08
1460553_at	1700025K23Rik	RIKEN cDNA 1700025K23 gene	-1.36	0.147	4.87	0.006	1.11	0.725	-1.52	0.111	0.78
1427631_x_at	Mup3	major urinary protein 3	4.46	0.48	1.41	0.109	-1.18	0.751	-1.21	0.793	0.87
1423547_at	Lyzs	lysozyme	3.58	0.154	2.37	0.016	-1.28	0.002	-1.45	0.093	0.81
1433285_at	9330179C17Rik	RIKEN cDNA 9330179C17 gene	-1.11	0.686	2.41	0.169	3.43	0.051	-2.82	0.271	0.48
1455240_x_at	LOC666185 /// LOC	hypothetical protein LOC666185 /// hypothetical protein LOC666222 /// hypothetic	2	0.498	4.03	0.098	-1.37	0.226	-1.92	0.024	0.69
1417396_at	Podxl	podocalyxin-like	1.18	0.593	-1.48	0.244	4.91	0.325	-1.21	0.792	0.85
1441216_at	5330418N22Rik	RIKEN cDNA 5330418N22 gene	3.8	0.068	2.01	0.066	-1	0.994	-1.17	0.188	0.91
1429629_at	Ezh1	enhancer of zeste homolog 1 (Drosophila)	3.97	0.007	2.18	0.224	-1.44	0.392	-1.23	0.464	0.87
1451583_a_at	BC025076	cDNA sequence BC025076	-1.23	0.549	4.51	0.2	1.52	0.128	-1.41	0.325	0.85
1450180_a_at	Rara	retinoic acid receptor, alpha	4.58	0.163	-2.62	0.256	1.9	0.134	-1.33	0.196	0.63
1436996_x_at	Lzp-s	P lysozyme structural	3.96	0.183	2.19	0.025	-1.32	0.007	-1.48	0.014	0.84
1450266_at	Scn10a	sodium channel, voltage-gated, type X, alpha	-1.95	0.391	4.35	0.128	2.04	0.211	-1.17	0.798	0.82
1459003_at	Fhl1	four and a half LIM domains 1	3.75	0.037	2.2	0.056	-1.04	0.877	-1.86	0.161	0.76

1451963_at	---	Anti-HLA class II antibody gamma F3.3 heavy chain variable region	1.58	0.002	-1.08	0.75	4.4	0.151	-1.84	0.473	0.77
1418037_at	C4bp	complement component 4 binding protein	4.86	0.479	1.26	0.409	-1.13	0.812	-1.06	0.905	0.98
1437060_at	Olfm4	olfactomedin 4	-1.1	0.139	-1.04	0.957	5.15	0.282	2.76	0.297	1.44
1427459_at	Cpn2	carboxypeptidase N, polypeptide 2	5.47	0.446	1.01	0.933	-1.76	0.151	-1.15	0.879	0.89
1441284_at	---	Transcribed locus	1.41	0.361	4.92	0.148	-1.37	0.459	-1.28	0.462	0.92
1455645_at	8030451F13Rik	RIKEN cDNA 8030451F13 gene	1.38	0.406	-1.11	0.864	4.77	0.317	-1.36	0.585	0.92
1425763_x_at	Igh-VJ558 /// LOC2	immunoglobulin heavy chain (J558 family) /// similar to immunoglobulin heavy cha	5.23	0.001	-1.22	0.544	1.02	0.968	-2.05	0.039	0.75
1449242_s_at	Hrg	histidine-rich glycoprotein	5.44	0.422	-1	0.971	-1.45	0.53	1.81	0.019	1.2
1448012_at	C76336	expressed sequence C76336	3.15	0.104	3.19	0.179	-1.06	0.892	-1.2	0.8	1.02
1429387_at	Grap	GRB2-related adaptor protein	4.66	0.054	1.85	0.051	-1.27	0.363	-2.3	0.082	0.73
1418613_at	Kcnj1	potassium inwardly-rectifying channel, subfamily J, member 1	-1.05	0.656	2.44	0.019	3.94	0.324	-1.19	0.81	1.03
1456632_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	4.42	0.382	-1.24	0.62	2.13	0.429	-1.48	0.081	0.96
1419292_at	Htra3	HtrA serine peptidase 3	3.14	0.009	3.24	0.029	-1.02	0.938	-1.06	0.58	1.07
1444348_at	---	---	5.08	0.009	-1.63	0.259	1.7	0.192	-1.73	0.356	0.86
1459096_at	Atf7ip	Activating transcription factor 7 interacting protein	3.03	0.042	3.56	0.107	-1.23	0.552	-1.11	0.62	1.06
1447072_at	Gripap1	GRIP1 associated protein 1	1.56	0.433	5.13	0.132	-1.4	0.034	-1.87	0.298	0.85
1418190_at	Pon1	paraoxonase 1	5.78	0.402	-1.31	0.255	-1.16	0.664	2.99	0.335	1.58
1429309_at	Prdm16	PR domain containing 16	1.28	0.324	5.26	0.034	-1.13	0.288	-1.51	0.131	0.98
1439426_x_at	Lzp-s	P lysozyme structural	2.77	0.149	4.07	0.032	-1.62	0.003	-1.25	0.554	0.99
1422973_a_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	-1.5	0.329	-1.03	0.951	5.82	0.337	1.68	0.21	1.24
1423515_at	Scn8a	sodium channel, voltage-gated, type VIII, alpha	-1.28	0.527	5.78	0.021	-1.1	0.406	1.23	0.376	1.16
1421959_s_at	Adcy3	adenylate cyclase 3	2.45	0.238	4.13	0.34	-1.09	0.686	-1.46	0.457	1.01
1437996_s_at	1500012D20Rik	RIKEN cDNA 1500012D20 gene	6.01	0.021	1.01	0.961	-1.86	0.085	-1.01	0.986	1.04
1437094_x_at	Dnaic1	dynein, axonemal, intermediate chain 1	-1.52	0.003	5.6	0.13	1.31	0.413	-1.34	0.646	1.01
1421507_at	Olfr78	olfactory receptor 78	4.73	0.018	1.95	0.289	-1.08	0.643	-1.29	0.567	1.08
1425802_a_at	Fcrla	Fc receptor-like A	3.96	0.027	-1.37	0.435	3.01	0.29	-2.05	0.171	0.89
1419407_at	Hc	hemolytic complement	6.11	0.463	1.04	0.846	-1.75	0.014	-1.29	0.564	1.03
1420993_at	B3gnt5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	1.54	0.308	5.25	0.008	-1	0.984	-2.45	0.061	0.83
1422708_at	Pik3cg	phosphoinositide-3-kinase, catalytic, gamma polypeptide	4.29	0.056	2.57	0.349	-1.05	0.861	-1.25	0.391	1.14
1427762_x_at	Hist1h2bp	histone 1, H2bp	6.54	0.012	-1.73	0.13	-1.01	0.976	1.47	0.523	1.32
1419307_at	Tnfrsf13c	tumor necrosis factor receptor superfamily, member 13c	4.19	0.123	-1.42	0.299	3.23	0.32	-2.33	0.162	0.92
1418708_at	Apoc4	apolipoprotein C-IV	6.73	0.428	-1.24	0.138	-1.62	0.553	2.65	0.033	1.63
1423954_at	C3	complement component 3	5.74	0.329	-1.11	0.622	1.52	0.061	-1.53	0.28	1.16
1424273_at	Cyp2c70	cytochrome P450, family 2, subfamily c, polypeptide 70	6.32	0.402	-1	0.989	-1.09	0.788	1.17	0.731	1.35
1430324_x_at	1700049E17Rik ///	RIKEN cDNA 1700049E17 gene /// similar to Spetex-2C protein	4.7	0.053	2.63	0.303	-1.09	0.818	-1.89	0.315	1.09
1441836_x_at	1700006H03Rik	RIKEN cDNA 1700006H03 gene	-3.24	0.069	6.47	0.008	1.49	0.168	-1.2	0.692	0.88
1419133_at	Evpl	Envoplakin	-1.28	0.231	5.92	0.002	1.58	0.055	-1.22	0.708	1.25
1452651_a_at	Myl1	myosin, light polypeptide 1	-1.96	0.074	1.24	0.68	6.55	0.216	-1.54	0.337	1.07
1450118_a_at	Tnnt3	troponin T3, skeletal, fast	-2.75	0.424	-3.58	0.149	7.89	0.296	1.53	0.525	0.77
1428640_at	Hsf2bp	heat shock transcription factor 2 binding protein	1.55	0.06	6.09	0.042	-1.07	0.68	-1.11	0.824	1.37
1421653_a_at	Igh-VJ558 /// LOC2	immunoglobulin heavy chain (J558 family) /// similar to immunoglobulin heavy cha	6.95	0.014	-1.21	0.615	1.15	0.808	-1.53	0.054	1.34
1453588_at	Car3	carbonic anhydrase 3	-2.69	0.322	-1.6	0.598	7.99	0.373	1.08	0.93	1.2
1451600_s_at	LOC13909 /// Es31	esterase 31-like /// esterase 31	8.08	0.407	-2.13	0.024	-1.94	0.143	1.04	0.96	1.26
1448723_at	Rdh7	retinol dehydrogenase 7	7.38	0.395	-1.23	0.247	-1.11	0.771	1.67	0.532	1.68
1420464_s_at	Pira1 /// Pira11 /// P	paired-Ig-like receptor A1 /// paired-Ig-like receptor A11 /// paired-Ig-like receptor	-1.04	0.904	2.99	0.007	5.16	0.189	-1.01	0.951	1.52
1448997_at	Pscd1	pleckstrin homology, Sec7 and coiled-coil domains 1	5.49	0.209	-1.42	0.512	2.96	0.245	-2.16	0.472	1.22
1453194_at	4930432K21Rik	RIKEN cDNA 4930432K21 gene	3.28	0.258	5.15	0.031	-1.08	0.692	-2.05	0.413	1.32
1434237_at	Upk3b	uroplakin 3B	-1.11	0.916	-1.66	0.181	8.04	0.387	1.27	0.093	1.64
1440765_at	Fras1	Fraser syndrome 1 homolog (human)	-1.42	0.274	-1.09	0.662	7.97	0.184	1.77	0.124	1.81
1448394_at	Myl2	myosin, light polypeptide 2, regulatory, cardiac, slow	1.09	0.76	-1.77	0.366	8.24	0.189	-1.17	0	1.6
1423439_at	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	-1.28	0.336	-1.02	0.868	8.22	0.357	2.44	0.093	2.09
1427026_at	Myh4	myosin, heavy polypeptide 4, skeletal muscle	1.34	0.148	-1.41	0.609	8.16	0.382	-1.03	0.965	1.76
1448881_at	Hp	haptoglobin	8.6	0.435	-1.07	0.626	-1.19	0.081	2.43	0.424	2.19

1426452_a_at	Rab30	RAB30, member RAS oncogene family	8.68	0.075	-1.65	0.145	1.13	0.821	-1.22	0.576	1.74
1449984_at	Cxcl2	chemokine (C-X-C motif) ligand 2	-1.01	0.922	1.66	0.173	7.9	0.227	-1.13	0.832	1.85
1445359_at	Adcy1	adenylate cyclase 1	-2.76	0.023	11.83	0.143	1	0.999	-2.12	0.138	1.99
1418155_at	Myot	myotilin	-1.51	0.532	-1.32	0.674	12.58	0.248	1.14	0.649	2.72
1448854_s_at	Mug-ps1 /// Mug1 //	murinoglobulin, pseudogene 1 /// murinoglobulin 1 /// murinoglobulin 2 /// similar t	13.37	0.409	-1.38	0.122	1.53	0.019	-1.16	0.863	3.09
1420484_a_at	Vtn	vitronectin	15.87	0.411	-1.01	0.938	-2.39	0.029	2.02	0.083	3.62
1418457_at	Cxcl14	chemokine (C-X-C motif) ligand 14	1.99	0.186	15.88	0.091	-2.02	0.015	-1.15	0.534	3.68
1418239_at	Apof	apolipoprotein F	18.22	0.421	-1.17	0.221	1.14	0.443	-1.22	0.69	4.24
1457373_at	---	Transcribed locus	-1.44	0.627	20.99	0.021	1.52	0.272	-2.14	0.254	4.73
1447410_at	---	---	21.64	0.032	1.01	0.976	-1.16	0.717	-1.72	0.063	4.94
1425153_at	Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult	-2.07	0.437	-1.97	0.15	33.49	0.343	2.77	0.383	8.06
1416474_at	Nope	neighbor of Punc E11	-1.07	0.922	35.26	0.203	1.08	0.862	-1.84	0.191	8.36
1419059_at	Apcs	serum amyloid P-component	36.97	0.412	2.2	0.183	-1.96	0.452	-1.23	0.353	8.99
1423866_at	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	50.52	0.408	-1.34	0.19	-1.25	0.531	1.51	0.668	12.36
1417464_at	Tnnc2	troponin C2, fast	-1.41	0.69	-1.46	0.581	64.15	0.229	1.26	0.408	15.64
1423944_at	Hpxn	hemopexin	64.01	0.412	-1.13	0.507	-1.14	0.779	2.25	0.397	15.99
1415968_a_at	Kap	kidney androgen regulated protein	1.01	0.907	-13.81	0.126	1.11	0.728	1.26	0.606	-2.61
1426071_at	Tiaf2	TGF-beta1-induced anti-apoptotic factor 2	-3.26	0.377	1.06	0.917	1.01	0.972	2.1	0.365	0.23
1430563_at	Mcmdc1	minichromosome maintenance deficient domain containing 1	-3.03	0.047	1.02	0.915	1.03	0.955	1.3	0.56	0.08
1419728_at	Cxcl5	chemokine (C-X-C motif) ligand 5	1.05	0.955	-5.42	0.377	1.15	0.769	2.6	0.3	-0.15
1459711_at	Sdk1	sidekick homolog 1 (chicken)	1.03	0.88	1.02	0.971	-2.81	0.005	1.03	0.948	0.07
1421369_a_at	Mab21l1	mab-21-like 1 (C. elegans)	-2.94	0.102	1.02	0.983	1.06	0.836	1.01	0.992	0.04
1438849_at	---	---	-2.9	0.085	1.06	0.894	1.01	0.971	1.35	0.508	0.13
1430246_at	4933406C10Rik	RIKEN cDNA 4933406C10 gene	1.03	0.929	-2.54	0.113	1.03	0.955	1.49	0.455	0.25
1454026_a_at	Rgs3	regulator of G-protein signaling 3	-2.73	0.02	1.02	0.772	1.07	0.887	1.33	0.611	0.17
1421401_at	Kcnmb1	Potassium large conductance calcium-activated channel, subfamily M, beta mem	-3.52	0.176	1.1	0.887	1.07	0.739	1.4	0.656	0.01
1447598_x_at	Rpo1-4	RNA polymerase 1-4	1	0.995	-2.82	0.093	1.11	0.849	2.14	0.117	0.36
AFFX-18SRNAMur/	---	---	1.08	0.95	1.16	0.901	-4.4	0.451	4.09	0.35	0.48
1448595_a_at	Bex1	brain expressed gene 1	1.1	0.502	1.02	0.942	-2.84	0.001	1.01	0.979	0.07
1446659_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930044F	-2.19	0.046	1.02	0.977	1	0.997	1.37	0.143	0.3
1444276_at	Ict1	immature colon carcinoma transcript 1	-2.44	0.036	1.07	0.892	1	0.995	1.52	0.026	0.29
1417806_at	Popdc2	popeye domain containing 2	-2.39	0.075	1.06	0.894	1.01	0.956	4.1	0.216	0.94
1452089_at	Cacnb4	calcium channel, voltage-dependent, beta 4 subunit	1.08	0.489	-2.89	0.204	1.08	0.888	1.74	0.523	0.25
AFFX-18SRNAMur/	---	---	1.15	0.921	1.05	0.959	-3.31	0.46	2.05	0.547	0.24
1449860_at	Higd1b	HIG1 domain family, member 1B	1.05	0.852	1.02	0.97	-2.25	0.005	1.63	0.264	0.36
1425887_at	4930511J11Rik	RIKEN cDNA 4930511J11 gene	1.05	0.917	-2.68	0.051	1.09	0.703	1	0.997	0.11
1453093_at	Rasgef1c	RasGEF domain family, member 1C	-2.29	0.133	1.02	0.945	1.06	0.846	2.11	0.276	0.48
1460406_at	AI427122	expressed sequence AI427122	1.03	0.803	-2.21	0.1	1.04	0.851	2	0.248	0.47
1429804_at	Slc22a16	solute carrier family 22 (organic cation transporter), member 16	-3.47	0.033	1.06	0.67	1.18	0.272	1.8	0.359	0.14
1458443_at	Crtc1	CREB regulated transcription coactivator 1	-2.92	0.071	1.04	0.911	1.15	0.479	1.17	0.267	0.11
1425049_at	Oas1h	2'-5' oligoadenylate synthetase 1H	-3.56	0.385	1	0.989	1.25	0.763	1.3	0.56	0
1442799_x_at	Nudcd3	NudC domain containing 3	1.17	0.797	-3.01	0.016	1.03	0.843	1.08	0.698	0.07
1456410_at	AU045128	expressed sequence AU045128	-1.96	0.025	1	0.981	1.02	0.934	1.03	0.841	0.27
1419518_at	Tuba8	tubulin, alpha 8	-2.02	0.34	1	0.995	1.04	0.898	2.42	0.404	0.61
1420267_at	Npm1	Nucleophosmin 1	-2.05	0.508	1.04	0.958	1.01	0.974	1.76	0.293	0.44
1439477_at	Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	1.11	0.578	1.02	0.949	-2.36	0.024	1.08	0.493	0.21
1430831_at	4930404J24Rik	RIKEN cDNA 4930404J24 gene	-2.36	0.447	1.06	0.881	1.07	0.735	1.07	0.894	0.21
1456784_at	LOC623781	hypothetical protein LOC623781	-2.92	0.228	1.09	0.849	1.12	0.856	1.47	0.295	0.19
1427015_at	C230021P08Rik	Riken cDNA C230021P08 gene	1.02	0.926	-1.9	0.18	1	0.991	1.41	0.67	0.38
1417988_at	Resp18	regulated endocrine-specific protein 18	1.17	0.614	1.18	0.336	-4.9	0.037	1.04	0.789	-0.38
1420836_at	Slc25a30	solute carrier family 25, member 30	1.14	0.682	-3.58	0.047	1.14	0.391	1.31	0.219	0
1425946_at	Gstm7	glutathione S-transferase, mu 7	-2.08	0.001	1	0.99	1.08	0.83	1.04	0.837	0.26
1446874_at	---	---	-1.95	0.272	1.04	0.919	1.01	0.97	1.24	0.506	0.33

1425751_at	BC014805	cDNA sequence BC014805	-3.53	0.067	1.07	0.685	1.21	0.624	1.25	0.8	0
1450018_s_at	Slc25a30	solute carrier family 25, member 30	1.25	0.496	-3.54	0.057	1.03	0.847	1.11	0.573	-0.04
1452842_at	Hspb9	heat shock protein, alpha-crystallin-related, B9	-2.7	0.429	1.12	0.527	1.07	0.55	1.17	0.492	0.17
1445451_at	---	---	-2.33	0.104	1.05	0.828	1.08	0.557	1.9	0.102	0.43
1442736_at	Klhl11	kelch-like 11 (Drosophila)	1.1	0.892	-2.15	0.159	1.01	0.951	1.63	0.622	0.4
1431099_at	Hoxd8	homeo box D8	1.06	0.523	-2.21	0.024	1.07	0.8	1.4	0.459	0.33
1449958_a_at	Fgf14	fibroblast growth factor 14	-2.18	0.47	1.1	0.847	1.02	0.905	1.22	0.768	0.29
1442608_at	Layn	layilin	-2.06	0.074	1.08	0.885	1.01	0.954	1.12	0.867	0.29
1422273_at	Mmp1b	matrix metallopeptidase 1b (interstitial collagenase)	-2.98	0.112	1.17	0.565	1.08	0.837	1.13	0.45	0.1
1454102_at	5031425E22Rik	RIKEN cDNA 5031425E22 gene	1.06	0.684	1.04	0.942	-2.06	0.092	1.2	0.78	0.31
1452361_at	Rnf20	ring finger protein 20	1.08	0.879	-2.16	0.056	1.05	0.871	1.39	0.419	0.34
1423494_at	2310042E22Rik	RIKEN cDNA 2310042E22 gene	1.15	0.179	-2.37	0.279	1.02	0.972	1.13	0.56	0.23
1451551_at	Krt84	keratin 84	1.17	0.792	-2.76	0.015	1.06	0.891	2.21	0.331	0.42
1442353_at	Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	1.02	0.926	1.04	0.93	-1.88	0.202	1.07	0.855	0.31
1444150_at	Epb4.1	erythrocyte protein band 4.1	1.06	0.837	1.03	0.849	-1.98	0.176	3.11	0.161	0.8
1436998_at	Ankrd43	ankyrin repeat domain 43	1.07	0.787	-2.42	0.309	1.11	0.798	7.12	0.179	1.72
1452713_a_at	Wdr57	WD repeat domain 57 (U5 snRNP specific)	1.01	0.984	1.03	0.897	-1.81	0.029	1.29	0.527	0.38
1444261_at	---	---	1.32	0.562	1.04	0.954	-4.15	0.008	1.07	0.799	-0.18
1420334_at	Slc12a8	solute carrier family 12 (potassium/chloride transporters), member 8	1.2	0.635	1.02	0.974	-2.67	0.014	1.25	0.662	0.2
1458002_at	Mapk10	Mitogen activated protein kinase 10	1.21	0.801	-2.75	0.051	1.02	0.962	1.49	0.451	0.25
1443815_x_at	Slk	STE20-like kinase (yeast)	-3	0.006	1.12	0.814	1.15	0.516	1.19	0.825	0.11
1453469_at	1810073G21Rik	RIKEN cDNA 1810073G21 gene	-2.3	0.08	1.1	0.51	1.07	0.913	1.07	0.904	0.23
1432591_at	Pappa	pregnancy-associated plasma protein A	1.24	0.686	-2.78	0.022	1.01	0.961	1.01	0.98	0.12
1440527_at	---	Transcribed locus, strongly similar to NP_035188.1 platelet derived growth factor	-2.62	0.44	1.14	0.764	1.08	0.412	1.95	0.217	0.39
1458895_at	C80008	expressed sequence C80008	-2.38	0.274	1.1	0.686	1.09	0.79	1.58	0.178	0.35
1428459_at	Pramef12	PRAME family member 12	-1.98	0.172	1.07	0.776	1.03	0.959	1.62	0.565	0.44
1425641_at	---	---	-5.95	0.014	1.1	0.811	1.34	0.565	1.05	0.814	-0.62
1459670_at	Hnrpll	Heterogeneous nuclear ribonucleoprotein L-like	1.08	0.317	1.01	0.961	-1.93	0.11	1.49	0.278	0.41
1422287_at	Phxr2	per-hexamer repeat gene 2	-3.67	0.035	1.11	0.765	1.23	0.703	1.17	0.004	-0.04
1443303_at	4930521E07Rik	RIKEN cDNA 4930521E07 gene	1.02	0.943	1.03	0.928	-1.79	0.316	1.12	0.685	0.35
1420351_at	Tnfrsf4	tumor necrosis factor receptor superfamily, member 4	-2.16	0.01	1.07	0.828	1.08	0.647	1.09	0.761	0.27
1452807_s_at	1500016O10Rik	RIKEN cDNA 1500016O10 gene	-2.16	0.147	1.1	0.442	1.06	0.883	1.09	0.869	0.27
1460471_at	2410146L05Rik	RIKEN cDNA 2410146L05 gene	-1.66	0.259	1.01	0.98	1.01	0.961	1.45	0.295	0.45
1453517_at	Metapl1	methionine aminopeptidase-like 1	-2.83	0.051	1.06	0.922	1.21	0.601	1.82	0.383	0.32
1459388_at	Dcc	Deleted in colorectal carcinoma	1.02	0.943	-2.37	0.2	1.18	0.344	1.23	0.627	0.27
1418565_at	Serbp1	Serpine1 mRNA binding protein 1	1.03	0.922	1	0.987	-1.67	0.015	1.16	0.367	0.38
1433458_at	E330021D16Rik	RIKEN cDNA E330021D16 gene	1.02	0.871	-2.47	0.082	1.2	0.56	1.45	0.202	0.3
1458199_at	Ascc2	Activating signal cointegrator 1 complex subunit 2	-4.21	0.023	1.34	0.433	1.05	0.885	1.02	0.95	-0.2
1460538_at	Cdh10	cadherin 10	-1.74	0.068	1.03	0.925	1.03	0.952	1.9	0.079	0.55
1454381_at	5033428C03Rik	RIKEN cDNA 5033428C03 gene	-3.21	0.174	1.03	0.951	1.29	0.608	2.12	0.11	0.31
1456634_at	9830001H06Rik	RIKEN cDNA 9830001H06 gene	1.03	0.958	-1.69	0.085	1.01	0.957	1.55	0.213	0.47
1431482_at	2900012M01Rik	RIKEN cDNA 2900012M01 gene	1.11	0.702	-2.1	0.158	1.04	0.914	1.14	0.792	0.3
1433327_at	---	---	-3.1	0.261	1.04	0.913	1.27	0.616	1.01	0.982	0.06
1446904_at	Arhgef11	Rho guanine nucleotide exchange factor (GEF) 11	1.04	0.967	1.04	0.936	-1.78	0.028	1.13	0.855	0.36
1432867_at	9230112J17Rik	RIKEN cDNA 9230112J17 gene	-2.04	0.179	1.14	0.75	1	0.996	1.42	0.34	0.38
1446512_at	2610312B22Rik	RIKEN cDNA 2610312B22 gene	1.05	0.949	1.01	0.98	-1.74	0.024	1.06	0.88	0.35
1443124_at	---	---	1.08	0.271	-1.81	0.116	1.01	0.953	1.24	0.529	0.38
1445821_at	Il1rapl1	Interleukin 1 receptor accessory protein-like 1	-2.1	0.225	1.05	0.933	1.11	0.772	1.36	0.549	0.36
1421677_at	Fgf20	fibroblast growth factor 20	1.04	0.873	-3.14	0.13	1.28	0.249	1.38	0.568	0.14
1438244_at	Nfib	nuclear factor I/B	1.1	0.45	1.07	0.509	-2.14	0.005	1.15	0.422	0.3
1422258_at	Chrm3	cholinergic receptor, muscarinic 3, cardiac	-3.33	0.186	1.33	0.42	1.01	0.99	3.84	0.032	0.71
1456322_at	---	---	1.03	0.968	-1.92	0.113	1.09	0.856	2.55	0.216	0.69
1438258_at	Vldlr	very low density lipoprotein receptor	1.09	0.421	1.06	0.953	-2.02	0.013	1.35	0.612	0.37

1421418_a_at	Psg19	pregnancy specific glycoprotein 19	-3.06	0.324	1.02	0.829	1.3	0.47	1.57	0.289	0.21
1435197_at	Pou3f3	POU domain, class 3, transcription factor 3	1.03	0.81	-2.25	0.18	1.18	0.066	1.25	0.392	0.3
1459494_at	Rabep1	Rabaptin, RAB GTPase binding effector protein 1	1.09	0.818	1.06	0.817	-2	0.015	1.15	0.79	0.33
1448545_at	Sdc2	syndecan 2	1.1	0.13	1	0.933	-1.84	0.001	1.37	0.006	0.41
1436361_at	Vgll2	vestigial like 2 homolog (Drosophila)	-2.56	0.253	1.13	0.776	1.13	0.581	1.21	0.732	0.23
1457407_at	Robo1	roundabout homolog 1 (Drosophila)	1.01	0.99	-2.28	0.327	1.21	0.341	1.47	0.399	0.35
1425831_at	Zfp101	zinc finger protein 101	1.14	0.703	1	0.993	-1.97	0.087	1.59	0.074	0.44
1441074_at	Ewsr1	Ewing sarcoma breakpoint region 1	1.05	0.874	1.3	0.23	-3.26	0.092	2.2	0.02	0.32
1438190_x_at	Tpbpa	trophoblast specific protein alpha	-3.77	0.012	1.24	0.444	1.16	0.763	1.87	0.346	0.12
1459361_at	---	---	1.03	0.961	1.09	0.842	-1.84	0.053	1.73	0.217	0.5
1437804_at	Igfbp7	Insulin-like growth factor binding protein 7	-3.13	0.405	1.11	0.787	1.23	0.481	1.64	0.028	0.21
1422987_at	Ntn1	netrin 1	1.01	0.96	-2.3	0.096	1.21	0.732	1.01	0.985	0.23
1457170_at	Lrrc36	leucine rich repeat containing 36	1.07	0.703	-1.71	0.061	1	0.978	2.56	0.139	0.73
1431793_at	3732407C23Rik	RIKEN cDNA 3732407C23 gene	-2.01	0.474	1.06	0.885	1.1	0.802	1.05	0.797	0.3
1460217_at	Plfr	proliferin related protein	-1.73	0.284	1.04	0.906	1.04	0.927	1.37	0.683	0.43
1442036_a_at	LOC668580 /// LOC	hypothetical protein LOC668580 /// hypothetical protein LOC670695	-2.2	0.497	1.13	0.767	1.08	0.783	1.06	0.85	0.27
1443415_at	4931432P07Rik	RIKEN cDNA 4931432P07 gene	1.2	0.368	1.11	0.731	-2.83	0.046	1.08	0.901	0.14
1441420_at	Igsf9	immunoglobulin superfamily, member 9	-1.94	0.417	1.05	0.916	1.1	0.307	1.54	0.408	0.44
1441176_at	---	---	1.17	0.353	1	0.987	-2	0.172	1.6	0.212	0.44
1450419_at	Serhl	serine hydrolase-like	1.21	0.673	1.09	0.772	-2.68	0.237	2.25	0.071	0.47
1447622_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	1.03	0.965	1.11	0.867	-1.87	0.062	1.23	0.651	0.38
1441882_at	---	---	1.07	0.776	-1.75	0.455	1.03	0.959	1.16	0.728	0.38
1443868_at	Atp13a3	ATPase type 13A3	1	0.999	-2.09	0.069	1.2	0.59	1.49	0.284	0.4
1432711_at	4933425M03Rik	RIKEN cDNA 4933425M03 gene	-1.93	0.254	1.15	0.667	1.01	0.958	1.16	0.719	0.35
1430725_at	4933432I09Rik	RIKEN cDNA 4933432I09 gene	-1.63	0.123	1.06	0.851	1	0.984	1.02	0.891	0.36
1420872_at	Gucy1b3	guanylate cyclase 1, soluble, beta 3	1.18	0.078	1.03	0.641	-2.12	0.003	1.58	0.342	0.42
1452614_at	Gm566	gene model 566, (NCBI)	-2.14	0.161	1.2	0.688	1.03	0.966	2.4	0.035	0.62
1451577_at	Zbtb20	zinc finger and BTB domain containing 20	1.23	0.475	1.06	0.793	-2.51	0.024	1.45	0.172	0.31
1421445_at	Slc26a3	solute carrier family 26, member 3	1.36	0.042	-3.52	0.042	1.04	0.865	1.24	0.646	0.03
1437590_at	4833409A17Rik	RIKEN cDNA 4833409A17 gene	1.26	0.458	1.08	0.848	-2.9	0.149	4.03	0	0.87
1440597_at	---	---	1.24	0.375	1.11	0.882	-2.98	0.052	1.32	0.7	0.17
1459978_x_at	Ccnjl	cyclin J-like	-1.62	0.098	1.05	0.896	1.03	0.928	1.14	0.655	0.4
1422937_at	Fzd5	frizzled homolog 5 (Drosophila)	-3.11	0.087	1.29	0.71	1.08	0.844	1.22	0.704	0.12
1439478_at	Acot2	acyl-CoA thioesterase 2	1.05	0.658	-1.73	0.203	1.07	0.201	1.01	0.914	0.35
1441677_at	Smc4l1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	1	0.996	1.08	0.738	-1.62	0.014	1.16	0.707	0.4
1450146_at	Freq	frequenin homolog (Drosophila)	-1.77	0.346	1	0.994	1.13	0.805	1.09	0.801	0.36
1447882_x_at	Ddx54	DEAD (Asp-Glu-Ala-Asp) box polypeptide 54	1.04	0.91	-2	0.088	1.15	0.599	1.03	0.881	0.31
1446856_at	D3Wsu167e	DNA segment, Chr 3, Wayne State University 167, expressed	1.01	0.987	-1.7	0.129	1.09	0.857	1.22	0.653	0.41
1445740_at	---	Transcribed locus	-3.45	0.063	1.37	0.657	1.04	0.892	1.67	0.513	0.16
1433198_at	4930445B03Rik	RIKEN cDNA 4930445B03 gene	-1.53	0.306	1.04	0.928	1.01	0.99	1.15	0.639	0.42
1439458_x_at	Ceacam11	CEA-related cell adhesion molecule 11	1.14	0.846	-1.83	0.291	1.02	0.98	1.86	0.458	0.55
1443107_at	Tmem16f	Transmembrane protein 16F	1.2	0.258	1.18	0.655	-3.22	0.001	1.01	0.953	0.04
1454355_at	1810021M19Rik	RIKEN cDNA 1810021M19 gene	-1.76	0.055	1.04	0.89	1.09	0.879	3.57	0.132	0.98
1442435_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	1.08	0.852	1.07	0.902	-1.85	0.03	1.15	0.32	0.37
1430097_at	8430436C05Rik	RIKEN cDNA 8430436C05 gene	1.05	0.788	1.11	0.712	-1.86	0.029	1.04	0.917	0.34
1444960_at	Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	1.21	0.445	-3.17	0.029	1.18	0.176	1.18	0.699	0.1
1460489_at	1700097M23Rik	RIKEN cDNA 1700097M23 gene	-2.69	0.159	1.2	0.754	1.13	0.742	1.25	0.759	0.22
1439297_at	AI449441	expressed sequence AI449441	1.26	0.398	1.11	0.638	-2.98	0.302	4.01	0.087	0.85
1447654_at	---	---	1.1	0.7	-2.14	0.369	1.14	0.764	1.27	0.577	0.34
1448437_a_at	Gtpbp2	GTP binding protein 2	-1.56	0.441	1.04	0.764	1.02	0.861	2.78	0.235	0.82
1455568_at	2310015A05Rik	RIKEN cDNA 2310015A05 gene	-2.08	0.226	1.21	0.722	1.01	0.955	1.61	0.222	0.44
1445392_at	Tm7sf3	Transmembrane 7 superfamily member 3	1.01	0.926	1.25	0.499	-2.24	0.034	1.26	0.28	0.32
1438772_at	Zfp367	zinc finger protein 367	-1.79	0.371	1.14	0.678	1	0.981	2.06	0.359	0.6

1460328_at	Brd3	bromodomain containing 3	1.01	0.935	-1.67	0.002	1.1	0.497	1.04	0.647	0.37
1429951_at	Ssbp2	single-stranded DNA binding protein 2	1.1	0.15	1.01	0.969	-1.68	0.011	1.21	0.358	0.41
1445925_at	D15Ertd492e	DNA segment, Chr 15, ERATO Doi 492, expressed	1.27	0.775	-2.84	0.095	1.09	0.826	1.26	0.662	0.19
1459501_at	AU022194	expressed sequence AU022194	-3.26	0.11	1.11	0.861	1.3	0.365	1.07	0.797	0.05
1444982_at	Rhoj	Ras homolog gene family, member J	1.29	0.449	1.08	0.885	-2.99	0.001	1.41	0.071	0.2
1427716_at	1700036D21Rik	RIKEN cDNA 1700036D21 gene	-3.34	0.128	1.29	0.74	1.13	0.583	1.9	0.192	0.24
1436324_at	Stard9 /// LOC6688	START domain containing 9 /// similar to StAR-related lipid transfer protein 9 (StA	1.01	0.936	1.1	0.824	-1.66	0.082	1.03	0.947	0.37
1417805_at	Xpnpep2	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	1.05	0.909	-1.79	0.233	1.11	0.262	1.04	0.915	0.35
1436083_at	Lrp3	low density lipoprotein receptor-related protein 3	1.12	0.747	1.22	0.641	-2.71	0.016	1.74	0.229	0.34
1449553_at	2610200G18Rik	RIKEN cDNA 2610200G18 gene	1.02	0.497	-1.64	0.436	1.09	0.789	2.68	0.142	0.79
1430531_at	Bphl	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antig	-2.33	0.103	1.24	0.193	1.05	0.903	1.5	0.372	0.36
1444236_at	AW552393	expressed sequence AW552393	-1.79	0.093	1.12	0.762	1.04	0.734	1.01	0.938	0.34
1444678_at	---	---	1.02	0.906	1.26	0.595	-2.27	0.083	1.04	0.896	0.26
1432215_s_at	4930417O22Rik	RIKEN cDNA 4930417O22 gene	-2.09	0.226	1.07	0.804	1.17	0.676	2.65	0.007	0.7
1418420_at	Myod1	myogenic differentiation 1	-1.45	0.168	1.01	0.975	1.02	0.971	1.2	0.752	0.44
1423429_at	Rhox5	reproductive homeobox 5	-2.87	0.061	1.11	0.869	1.26	0.603	1.55	0.363	0.26
1436062_at	Arcn1	archain 1	1.04	0.479	1.03	0.668	-1.55	0.003	1.22	0.221	0.44
1447534_at	---	---	1	0.995	-1.51	0.188	1.06	0.778	1.34	0.441	0.47
1445806_at	Cog5	component of oligomeric golgi complex 5	1.08	0.813	-1.83	0.058	1.1	0.725	1.26	0.712	0.4
1422197_at	Kcna2	potassium voltage-gated channel, shaker-related subfamily, member 2	-3.44	0.006	1.2	0.709	1.24	0.616	1.22	0.251	0.05
1437003_at	---	---	1.05	0.491	1.06	0.827	-1.64	0.221	1.08	0.809	0.39
1427510_at	Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	1.05	0.83	-1.78	0.073	1.12	0.61	1.45	0.181	0.46
1456589_x_at	Allc	allantoicase	1.08	0.348	-1.66	0.313	1.05	0.938	2.67	0.036	0.78
1447726_at	C030002E08Rik	RIKEN cDNA C030002E08 gene	-3.48	0.006	1.26	0.666	1.18	0.749	1.86	0.137	0.21
1446191_at	Abi3	ABI gene family, member 3	1.15	0.706	-1.88	0.08	1.05	0.906	1.08	0.909	0.35
1439313_at	Lphn3	latrophilin 3	1.13	0.416	-1.79	0.213	1.04	0.722	1.24	0.477	0.41
1460208_at	Fbn1	fibrillin 1	1.06	0.856	1.14	0.497	-1.89	0.05	1.01	0.921	0.33
1417482_at	Tex19	testis expressed gene 19	1.1	0.761	-1.73	0.032	1.05	0.789	1.52	0.178	0.49
1443988_at	B330012G18Rik	RIKEN cDNA B330012G18 gene	1.18	0.806	1.1	0.783	-2.22	0.186	1.32	0.457	0.35
1459448_at	Cyb5r2	cytochrome b5 reductase 2	-2.9	0.048	1.27	0.653	1.12	0.833	1.13	0.814	0.15
1441557_at	Setd8	SET domain containing (lysine methyltransferase) 8	1.18	0.765	1.05	0.9	-1.98	0.322	2.68	0.257	0.73
1417654_at	Sdc4	syndecan 4	1.09	0.912	1.07	0.934	-1.75	0.523	1.25	0.602	0.41
1440175_at	Epn2	Epsin 2	1.08	0.615	1.11	0.86	-1.84	0.223	1.25	0.554	0.4
1456008_at	Lrrc8e	leucine rich repeat containing 8 family, member E	-1.73	0.197	1.12	0.799	1.04	0.835	1.04	0.644	0.37
1435979_a_at	Myo15b	myosin XVB	1.21	0.195	-1.89	0.077	1	0.995	1.28	0.442	0.4
1430157_at	1700095J03Rik	RIKEN cDNA 1700095J03 gene	-2.5	0.292	1.05	0.919	1.29	0.062	1.75	0.073	0.4
1425531_at	Znhit1	zinc finger, HIT domain containing 1	1.01	0.755	-1.48	0.032	1.05	0.853	1.28	0.164	0.47
1421007_at	Col4a6	procollagen, type IV, alpha 6	1.16	0.769	-2.43	0.245	1.17	0.472	1.77	0.001	0.42
1449216_at	Itgae	integrin, alpha E, epithelial-associated	1.06	0.714	-1.6	0.397	1.05	0.798	1.17	0.49	0.42
1428402_at	Zcchc3	zinc finger, CCHC domain containing 3	1.05	0.018	-1.97	0.051	1.18	0.073	1.49	0.43	0.44
1442350_at	---	0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632424N07	-1.64	0.488	1.07	0.911	1.06	0.425	1.19	0.615	0.42
1449244_at	Cdh2	cadherin 2	1.01	0.971	1.02	0.596	-1.4	0.691	1.61	0.324	0.56
1429026_at	Hexim2	hexamthylene bis-acetamide inducible 2	-1.46	0.288	1.04	0.756	1.01	0.956	1.63	0.107	0.56
1425272_at	Emp2	epithelial membrane protein 2	1.12	0.799	1.02	0.934	-1.65	0.299	1.2	0.516	0.42
1444525_at	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	1.07	0.665	1.09	0.162	-1.72	0.07	1.16	0.553	0.4
1450716_at	Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.03	0.884	1.03	0.778	-1.46	0.498	1.25	0.25	0.46
1440314_at	Trip12	Thyroid hormone receptor interactor 12	1.01	0.916	1.15	0.56	-1.71	0.131	1.06	0.798	0.38
1429957_at	2310002B14Rik	RIKEN cDNA 2310002B14 gene	1.12	0.814	1.03	0.938	-1.7	0.245	1.41	0.523	0.47
1429641_x_at	2310007F04Rik	RIKEN cDNA 2310007F04 gene	-1.83	0.231	1.04	0.895	1.16	0.69	1.17	0.668	0.39
1429530_a_at	Smpd4	sphingomyelin phosphodiesterase 4	1.13	0.636	-2.06	0.005	1.13	0.714	2.19	0.297	0.6
1440357_at	---	Transcribed locus	1.03	0.928	1.1	0.801	-1.65	0.068	1.21	0.401	0.42
1440034_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.07	0.686	1.06	0.886	-1.63	0.171	1.45	0.445	0.49
1447259_at	Ank3	ankyrin 3, epithelial	1.13	0.573	1.19	0.653	-2.38	0.043	1.79	0.248	0.43

1447396_at	LOC545253	Hypothetical protein LOC545253	1.09	0.6	1.25	0.654	-2.46	0.081	1.38	0.061	0.31
1459473_at	Pdss2	Prenyl (solanesyl) diphosphate synthase, subunit 2	1.08	0.903	1.04	0.941	-1.59	0.23	1.15	0.66	0.42
1432697_at	5830431M20Rik	RIKEN cDNA 5830431M20 gene	1.03	0.944	1.19	0.714	-1.9	0.142	1.27	0.029	0.4
1440194_at	2210011C24Rik	RIKEN cDNA 2210011C24 gene	-1.59	0.528	1.1	0.768	1.02	0.973	1.05	0.7	0.4
1450477_at	Htr2c	5-hydroxytryptamine (serotonin) receptor 2C	1.09	0.596	-1.64	0.157	1.05	0.791	1.11	0.892	0.4
1450796_at	Atoh7	atonal homolog 7 (Drosophila)	-1.48	0.484	1.05	0.886	1.03	0.886	2.4	0.065	0.75
1429911_at	Mcph1	microcephaly, primary autosomal recessive 1	-1.77	0.105	1.08	0.826	1.1	0.549	2.43	0.213	0.71
1456052_at	Cdkl3	cyclin-dependent kinase-like 3	1.1	0.823	-1.56	0.466	1.02	0.932	1.43	0.015	0.5
1425939_at	Rad50	RAD50 homolog (S. cerevisiae)	-3.36	0.215	1.29	0.583	1.17	0.753	1.03	0.957	0.03
1437035_x_at	Rnf14	ring finger protein 14	-1.55	0.219	1.11	0.523	1	0.965	1.15	0.613	0.43
1453192_at	3110032G18Rik	RIKEN cDNA 3110032G18 gene	1.1	0.891	1.24	0.476	-2.42	0.359	1.12	0.577	0.26
1438939_x_at	Ndn	necdin	-1.6	0.12	1.06	0.921	1.08	0.658	1.04	0.928	0.39
1436036_at	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	1.16	0.78	-1.77	0.068	1.03	0.925	1.51	0.37	0.48
1431787_at	3300002A11Rik	RIKEN cDNA 3300002A11 gene	1.15	0.788	-2.15	0.07	1.15	0.685	1.17	0.833	0.33
1431178_at	LOC640488	similar to murine ULBP-like transcript 1	-2.12	0.185	1.06	0.497	1.22	0.164	1.57	0.061	0.44
1443273_at	Epha3	Eph receptor A3	-1.5	0.537	1.07	0.879	1.02	0.963	1.42	0.252	0.5
1446357_at	BC020402	cDNA sequence BC020402	1.03	0.808	-2.49	0.037	1.33	0.178	1.13	0.717	0.25
1460127_at	Hnf4g	hepatocyte nuclear factor 4, gamma	1.12	0.547	-2.23	0.167	1.2	0.598	1.29	0.725	0.34
1425629_a_at	Nol6	nucleolar protein family 6 (RNA-associated)	-1.59	0.232	1.08	0.858	1.05	0.811	1.3	0.547	0.46
1425804_at	Hmx2	H6 homeo box 2	-1.98	0.365	1.02	0.963	1.23	0.62	1.23	0.609	0.38
1445468_at	---	PREDICTED: Mus musculus hypothetical protein LOC625847 (LOC625847), mR	1.05	0.85	-2.11	0.234	1.24	0.777	1.53	0.07	0.43
1430549_at	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like	1.01	0.901	1.06	0.658	-1.44	0.057	1.15	0.522	0.44
1438290_x_at	Sftpc	Surfactant associated protein C	1.19	0.838	-1.8	0.283	1.02	0.979	1.04	0.783	0.36
1451555_at	Nln	neurolysin (metallopeptidase M3 family)	1.05	0.727	1.01	0.947	-1.41	0.149	1.1	0.637	0.44
1441938_x_at	Cables1 /// LOC635	Cdk5 and Abl enzyme substrate 1 /// similar to Cdk5 and Abl enzyme substrate 1	-1.7	0.232	1.17	0.379	1.01	0.977	1.25	0.564	0.43
1444120_at	Bin1	bridging integrator 1	-1.84	0.296	1.04	0.9	1.18	0.665	1.03	0.845	0.36
1433438_x_at	Mela	melanoma antigen	1.06	0.807	-1.58	0.453	1.08	0.872	3.28	0.339	0.96
1415921_a_at	Tnfrsf19	tumor necrosis factor receptor superfamily, member 19	1.04	0.959	-1.51	0.509	1.07	0.914	1.86	0.154	0.61
1429590_at	Tacc1	transforming, acidic coiled-coil containing protein 1	1.04	0.844	1.05	0.711	-1.48	0.198	1.41	0.137	0.51
1440185_x_at	Uble1a	Ubiquitin-like 1 (sentrin) activating enzyme E1A	-1.9	0.117	1.15	0.665	1.1	0.731	1.06	0.797	0.35
1427647_at	BC022150	cDNA sequence BC022150	1.01	0.927	-1.5	0.391	1.09	0.673	1.49	0.383	0.53
1456350_at	Zfp451	zinc finger protein 451	1.13	0.366	1.05	0.824	-1.68	0.035	1.07	0.529	0.39
1418948_at	Fscn3	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratu	-2.54	0.16	1.38	0.464	1	0.999	1.29	0.345	0.28
1439986_at	Dgki	diacylglycerol kinase, iota	1.16	0.856	-4.1	0.021	1.37	0.346	1.4	0.247	-0.04
1441860_x_at	Ide	Insulin degrading enzyme	-1.64	0.075	1.06	0.243	1.1	0.184	1.18	0.47	0.43
1419964_s_at	Hdgf	hepatoma-derived growth factor	1	0.988	1.06	0.48	-1.4	0.054	2	0.138	0.66
1435975_at	AI115600	expressed sequence AI115600	-1.42	0.114	1.03	0.805	1.04	0.706	1.85	0.134	0.63
1430647_at	Ckap5	cytoskeleton associated protein 5	-3.37	0.032	1.26	0.681	1.22	0.691	1.76	0.187	0.22
1432642_at	4933411E06Rik	RIKEN cDNA 4933411E06 gene	1.01	0.988	1.32	0.665	-2.24	0.105	3.7	0.108	0.95
1442145_at	Atp13a3	ATPase type 13A3	1.07	0.263	-1.49	0.006	1.04	0.886	1.33	0.444	0.49
1455026_at	Sbno1	sno, strawberry notch homolog 1 (Drosophila)	1.03	0.84	1.01	0.97	-1.36	0.273	1.08	0.77	0.44
1440145_at	H60	Histocompatibility 60	-1.58	0.289	1.13	0.749	1.01	0.985	1.46	0.615	0.51
1418986_a_at	Uxt	ubiquitously expressed transcript	1.03	0.818	1.02	0.703	-1.37	0.034	1.12	0.453	0.45
1447561_at	---	Transcribed locus	1.12	0.72	-2.11	0.056	1.18	0.798	1.12	0.817	0.33
1429679_at	Lrrc17	leucine rich repeat containing 17	1.14	0.739	-1.67	0.416	1.04	0.849	1.66	0.106	0.54
1447578_at	1700084J12Rik	RIKEN cDNA 1700084J12 gene	-1.59	0.559	1	0.997	1.15	0.774	1.65	0.123	0.55
1441053_at	---	Transcribed locus	1.17	0.596	-2.09	0.124	1.13	0.841	1.03	0.967	0.31
1429443_at	Cpne4	copine IV	-1.5	0.035	1	0.997	1.11	0.85	2.46	0.402	0.77
1447484_x_at	2610002F03Rik	RIKEN cDNA 2610002F03 gene	1.07	0.937	1.03	0.804	-1.48	0.166	1.22	0.613	0.46
1458995_at	AA408296	Expressed sequence AA408296	1.03	0.937	-2.49	0.266	1.34	0.318	1.33	0.448	0.3
1455052_a_at	2410129H14Rik	RIKEN cDNA 2410129H14 gene	1.07	0.602	1.01	0.938	-1.43	0.003	1.75	0.137	0.6
1458549_at	LOC436015	LOC436015	1.13	0.67	1.06	0.818	-1.67	0.019	1.35	0.298	0.47
1435780_at	Psd	pleckstrin and Sec7 domain containing	1.31	0.424	-2.13	0.2	1	0.994	2.43	0.039	0.65

1442065_at	Arhgap17	Rho GTPase activating protein 17	1.07	0.905	-1.48	0.557	1.03	0.896	1.04	0.86	0.42
1430275_a_at	Aqr	aquarius	1.12	0.192	-2.41	0.002	1.24	0.59	1.26	0.671	0.31
1425105_at	Rbp3	retinol binding protein 3, interstitial	1.13	0.775	-1.85	0.197	1.11	0.818	1.12	0.811	0.38
1446446_at	Ranbp10	RAN binding protein 10	1.4	0.689	1.01	0.991	-2.65	0.134	4.88	0.22	1.16
1450442_at	Add2	adducin 2 (beta)	1.06	0.936	1.04	0.95	-1.46	0.402	2.01	0.157	0.66
1460528_at	4930413G21Rik ///	RIKEN cDNA 4930413G21 gene /// hypothetical protein LOC668574 /// hypotheti	1.06	0.815	1.01	0.953	-1.39	0.562	1.37	0.176	0.51
1416778_at	Sdpr	serum deprivation response	1.04	0.419	1.03	0.776	-1.39	0.01	1.01	0.98	0.42
1426702_at	4632419K20Rik	RIKEN cDNA 4632419K20 gene	1.21	0.534	1.05	0.909	-1.9	0.097	1.85	0.092	0.55
1418321_at	Dci	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A isomerase	1.12	0.564	-1.54	0.194	1.02	0.875	1.07	0.669	0.42
1452094_at	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha	1.05	0.742	1.05	0.636	-1.45	0.084	1.04	0.643	0.42
1458416_at	A330048O09Rik	RIKEN cDNA A330048O09 gene	1.08	0.86	1.07	0.913	-1.58	0.406	1.17	0.302	0.44
1452088_at	Zbed3	zinc finger, BED domain containing 3	1.15	0.732	1.08	0.831	-1.81	0.259	1.35	0.567	0.45
1457049_at	Atp6v1e1	VATPase, H+ transporting, lysosomal V1 subunit E1	1.09	0.775	1.14	0.677	-1.81	0.245	1.33	0.623	0.44
1457755_at	Gng8	guanine nucleotide binding protein (G protein), gamma 8 subunit	1.1	0.897	-3.22	0.041	1.38	0.203	1.58	0.433	0.21
1459985_at	Wdr61	WD repeat domain 61	-1.32	0.008	1.01	0.896	1.02	0.827	1.09	0.58	0.45
1419332_at	Egfl6	EGF-like-domain, multiple 6	1.19	0.486	1.15	0.819	-2.18	0.024	1.17	0.841	0.33
1417217_at	Magel2	melanoma antigen, family L, 2	1.28	0.236	1	0.999	-1.96	0.083	1.02	0.902	0.34
1427572_at	Lrrc51	Leucine rich repeat containing 51	1.18	0.578	-1.68	0.126	1.02	0.943	1.07	0.7	0.4
1460230_at	Syn2	synapsin II	1.01	0.946	-1.59	0.054	1.16	0.133	1.1	0.578	0.42
1424763_at	1700027N10Rik	RIKEN cDNA 1700027N10 gene	1.13	0.545	-1.72	0.253	1.08	0.803	2.04	0.298	0.63
1431132_x_at	0610007P22Rik	RIKEN cDNA 0610007P22 gene	-1.42	0.003	1.05	0.751	1.04	0.808	1.13	0.272	0.45
1420574_at	1700065I17Rik	RIKEN cDNA 1700065I17 gene	1.1	0.423	-1.47	0.102	1.02	0.908	1.33	0.463	0.49
1453761_at	Phf6	PHD finger protein 6	1.14	0.155	-2.6	0.024	1.27	0.645	1.13	0.785	0.24
1459216_at	Tdrd7	Tudor domain containing 7	1.06	0.924	1.42	0.499	-3.21	0.135	1.02	0.968	0.07
1418141_at	Dcx	doublecortin	-1.88	0.516	1.08	0.85	1.19	0.711	1.21	0.344	0.4
1429420_at	4931414P19Rik	RIKEN cDNA 4931414P19 gene	1.08	0.52	-1.44	0.065	1.03	0.874	1.31	0.419	0.49
1452011_a_at	Uxs1	UDP-glucuronate decarboxylase 1	1.03	0.863	1.16	0.359	-1.65	0.071	1.19	0.591	0.43
1431782_s_at	Ypel1	yippee-like 1 (Drosophila)	1.33	0.353	1.03	0.938	-2.3	0.122	1.29	0.603	0.34
1427068_x_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	1.03	0.914	-1.34	0.342	1.02	0.935	1.02	0.948	0.43
1423291_s_at	Hyou1	hypoxia up-regulated 1	-1.4	0.214	1.02	0.867	1.07	0.789	1.24	0.008	0.48
1419037_at	Csnk2a1	casein kinase 2, alpha 1 polypeptide	1.1	0.546	1.02	0.952	-1.46	0.137	1.19	0.438	0.46
1444324_at	E530001K10Rik	RIKEN cDNA E530001K10 gene	1.22	0.697	-1.75	0.058	1.01	0.987	1.16	0.562	0.41
1426286_at	Noc3l	nucleolar complex associated 3 homolog (S. cerevisiae)	1.01	0.887	-1.31	0.221	1.03	0.913	1.12	0.076	0.46
1451744_a_at	Zadh1	zinc binding alcohol dehydrogenase, domain containing 1	1.01	0.644	-1.31	0.019	1.03	0.795	1.06	0.713	0.45
1432664_at	4933404M09Rik	RIKEN cDNA 4933404M09 gene	-1.53	0.495	1.08	0.839	1.07	0.841	1.44	0.515	0.52
1454926_at	4930544G21Rik	RIKEN cDNA 4930544G21 gene	1.04	0.935	1.1	0.644	-1.5	0.416	1.09	0.827	0.43
1457050_at	1700129O19Rik	RIKEN cDNA 1700129O19 gene	1.02	0.965	1.18	0.646	-1.65	0.102	1.53	0.323	0.52
1437178_at	LOC631105	hypothetical LOC631105	1.2	0.666	-1.96	0.162	1.09	0.512	1.58	0.248	0.48
1426223_at	2810439F02Rik	RIKEN cDNA 2810439F02 gene	1.15	0.471	-1.77	0.058	1.1	0.851	1.37	0.248	0.46
1429285_at	Serpina9	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsi	1.34	0.19	-3.43	0.08	1.18	0.437	2.25	0.144	0.33
1439302_at	Ube1l2	ubiquitin-activating enzyme E1-like 2	1.14	0.186	1.02	0.95	-1.53	0.089	1.01	0.979	0.41
1436776_x_at	Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	1.06	0.656	-1.92	0.049	1.22	0.142	2.25	0.432	0.65
1457791_at	B830008H07Rik	RIKEN cDNA B830008H07 gene	1.02	0.661	-1.37	0.215	1.06	0.781	1.09	0.694	0.45
1460076_x_at	---	---	-2.31	0.061	1.26	0.584	1.11	0.706	1.75	0.101	0.45
1446451_at	---	---	-5.05	0.035	1.13	0.796	1.49	0.416	1.09	0.793	-0.34
1438349_at	BC043476	cDNA sequence BC043476	1	0.991	1.1	0.081	-1.42	0.017	1.06	0.555	0.44
1420168_at	AA517841	expressed sequence AA517841	1.17	0.758	-2.87	0.086	1.29	0.309	1.13	0.757	0.18
1445285_at	Hrh3	Histamine receptor H 3	1.12	0.308	-1.61	0.022	1.08	0.682	1.48	0.361	0.51
1429006_s_at	2610110G12Rik	RIKEN cDNA 2610110G12 gene	1.02	0.864	-1.39	0.192	1.07	0.738	1.2	0.531	0.48
1423013_at	Foxf1a	forkhead box F1a	-1.95	0.014	1.14	0.717	1.16	0.713	2.39	0.037	0.68
1447519_x_at	Tpx2	TPX2, microtubule-associated protein homolog (Xenopus laevis)	1.02	0.925	-1.3	0.246	1.02	0.936	1.25	0.481	0.5
1432122_at	Lrrc44	leucine rich repeat containing 44	1	0.981	-1.24	0.076	1	0.971	1.1	0.727	0.47
1458964_at	Il1rapl1	Interleukin 1 receptor accessory protein-like 1	1.16	0.722	-1.56	0.215	1.01	0.948	1.05	0.835	0.42

1456505_at	Braf	Braf transforming gene	1.27	0.237	1.01	0.976	-1.85	0.05	1.49	0.041	0.48
1440755_at	Nbr1	Neighbor of Brca1 gene 1	1.22	0.708	1.03	0.912	-1.77	0.026	1.42	0.313	0.47
1457256_x_at	Ptch2 /// LOC6744	patched homolog 2 /// similar to Protein patched homolog 2 (PTC2)	1.02	0.946	-1.32	0.347	1.04	0.844	1.74	0.518	0.62
1439516_at	2610201A13Rik	RIKEN cDNA 2610201A13 gene	-1.44	0.228	1.07	0.827	1.05	0.853	1.1	0.801	0.45
1437137_at	6430550H21Rik	RIKEN cDNA 6430550H21 gene	1.1	0.918	1.07	0.924	-1.56	0.395	1.12	0.787	0.43
1450651_at	Myo10	myosin X	1.06	0.872	-1.57	0.048	1.12	0.369	1.13	0.725	0.43
1455974_at	1110049F12Rik	RIKEN cDNA 1110049F12 gene	1.12	0.585	-3.41	0.204	1.41	0.311	1.36	0.673	0.12
1426684_at	Cnot6	CCR4-NOT transcription complex, subunit 6	-1.37	0.006	1.02	0.872	1.07	0.577	1.43	0.299	0.54
1431558_at	2310016D03Rik	RIKEN cDNA 2310016D03 gene	1.25	0.364	-2.22	0.137	1.12	0.825	1.08	0.892	0.31
1446432_at	B530045E10Rik	RIKEN cDNA B530045E10 gene	1.17	0.601	-1.6	0.282	1.03	0.96	1.81	0.248	0.6
1419187_at	1700012L04Rik /// I	RIKEN cDNA 1700012L04 gene /// similar to Histone H2A.x (H2a/x)	1.38	0.459	-3.1	0.113	1.12	0.783	3.04	0.251	0.61
1423581_at	Nmt2	N-myristoyltransferase 2	1.32	0.26	-2.03	0.06	1	0.964	1.02	0.936	0.33
1425907_s_at	Amot	angiomotin	-1.6	0.397	1.05	0.402	1.15	0.531	1.13	0.382	0.43
1457770_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	1.23	0.797	1.12	0.649	-2.09	0.184	1.12	0.784	0.34
1424816_at	Cecr5	cat eye syndrome chromosome region, candidate 5 homolog (human)	1.05	0.83	-1.87	0.111	1.24	0.34	1.13	0.705	0.39
1441539_at	---	---	1.04	0.858	1.01	0.985	-1.28	0.568	1.46	0.08	0.56
1430771_a_at	Msh5	mutS homolog 5 (E. coli)	1.03	0.929	-1.45	0.506	1.1	0.75	1.66	0.368	0.59
1450411_at	2900009I07Rik	RIKEN cDNA 2900009I07 gene	1.03	0.784	-1.37	0.353	1.06	0.705	1.29	0.388	0.5
1425846_a_at	Caln1	calneuron 1	-1.28	0.556	1.01	0.954	1.04	0.915	1.54	0.23	0.58
1450994_at	Rock1	Rho-associated coiled-coil containing protein kinase 1	1.03	0.888	1.04	0.501	-1.32	0.015	1.06	0.535	0.45
1460397_at	Armc6	armadillo repeat containing 6	-1.31	0.486	1.02	0.864	1.04	0.797	1.52	0.321	0.57
1436796_at	1110061A14Rik	RIKEN cDNA 1110061A14 gene	1.04	0.712	1.02	0.808	-1.31	0.129	1.06	0.816	0.46
1456022_at	Hipk2	homeodomain interacting protein kinase 2	1	0.956	-1.28	0.147	1.04	0.894	2.72	0.15	0.87
1458641_at	Braf	Braf transforming gene	1.02	0.877	-1.31	0.121	1.04	0.695	1.08	0.787	0.46
1443734_at	D5Wsu148e	DNA segment, Chr 5, Wayne State University 148, expressed	-1.73	0.366	1.22	0.696	1.03	0.693	1.15	0.669	0.42
1437001_at	Gsk3b	glycogen synthase kinase 3 beta	1.06	0.747	1.01	0.967	-1.3	0.118	1.27	0.103	0.51
1429145_at	Nhlrc2	NHL repeat containing 2	1.04	0.733	1.17	0.608	-1.6	0.027	1.05	0.856	0.41
1453049_at	6620401M08Rik	RIKEN cDNA 6620401M08 gene	1.18	0.201	1.04	0.703	-1.63	0.026	4.05	0.166	1.16
1441606_at	Nrg3	Neuregulin 3	1.22	0.501	-1.8	0.26	1.06	0.903	1.34	0.464	0.45
1427661_a_at	Tssc4	tumor-suppressing subchromosomal transferable fragment 4	1.07	0.77	-1.36	0.048	1.03	0.86	1.23	0.46	0.49
1455232_at	Cml2	camello-like 2	1.36	0.355	1.13	0.373	-2.88	0.023	1.89	0.514	0.37
1431249_at	---	---	-1.22	0.654	1.01	0.973	1.01	0.989	1.07	0.901	0.47
1427614_at	Pip	prolactin induced protein	1.37	0.307	-3.19	0.001	1.15	0.758	1.29	0.524	0.16
1428685_at	Syce1	synaptonemal complex central element protein 1	-2.48	0.402	1.08	0.909	1.35	0.653	1.07	0.938	0.26
1442317_at	Tcp1	T-complex protein 1	-1.32	0.256	1.04	0.912	1.04	0.759	1.07	0.731	0.46
1446385_at	9430083A17Rik	RIKEN cDNA 9430083A17 gene	1.1	0.77	-1.74	0.059	1.16	0.692	1.32	0.416	0.46
1459574_at	C86865	expressed sequence C86865	-2.61	0.233	1.1	0.802	1.35	0.392	1.72	0.325	0.39
1429412_at	Eny2	enhancer of yellow 2 homolog (Drosophila)	1.16	0.54	-1.58	0.075	1.04	0.667	1.32	0.378	0.49
1435773_at	4930547N16Rik	RIKEN cDNA 4930547N16 gene	1.16	0.767	-2.1	0.285	1.2	0.363	3.69	0.206	0.99
1426305_at	Upk1a	uroplakin 1A	1.05	0.827	-2.92	0.009	1.44	0.088	1.01	0.887	0.15
1434887_at	Freq	frequenin homolog (Drosophila)	1.12	0.379	-1.84	0.163	1.18	0.175	1.18	0.612	0.41
1426438_at	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	1.3	0.277	-4.09	0	1.3	0.682	3	0.161	0.38
1436928_s_at	Adcy3	adenylate cyclase 3	-1.46	0.536	1.1	0.718	1.06	0.806	1.04	0.66	0.43
1456957_at	---	---	-1.87	0.271	1.03	0.9	1.27	0.315	1.38	0.112	0.45
1445948_at	---	Transcribed locus	-3.31	0.441	1.45	0.476	1.08	0.547	1.79	0.325	0.25
1441703_at	2210018M03Rik	RIKEN cDNA 2210018M03 gene	-1.6	0.542	1.18	0.765	1.03	0.802	1.03	0.94	0.41
1431288_at	Car10	carbonic anhydrase 10	-1.55	0.048	1.03	0.892	1.17	0.625	1.13	0.518	0.44
1456623_at	Tpm1	tropomyosin 1, alpha	1.4	0.351	1.02	0.95	-2.37	0.124	1.72	0.144	0.44
1439564_at	1700090G07Rik	RIKEN cDNA 1700090G07 gene	-1.45	0.712	1.11	0.81	1.05	0.909	1.93	0.344	0.66
1441872_x_at	Phf17	PHD finger protein 17	1.15	0.529	-2.59	0.072	1.31	0.583	1.05	0.695	0.23
1437882_s_at	3110048L19Rik /// (	RIKEN cDNA 3110048L19 gene /// RIKEN cDNA 6330416L07 gene	-1.53	0.111	1.05	0.693	1.14	0.741	1.47	0.367	0.53
1432575_at	4930548F15Rik	RIKEN cDNA 4930548F15 gene	1.13	0.661	1.16	0.726	-1.79	0.166	1.11	0.879	0.4
1460520_at	Mocs1	molybdenum cofactor synthesis 1	1.03	0.948	-1.88	0.378	1.28	0.682	2.89	0.183	0.83

1423941_at	Camk2g	calcium/calmodulin-dependent protein kinase II gamma	1.01	0.817	-1.21	0.159	1.01	0.953	1.02	0.906	0.46
1445906_at	Zfp35	Zinc finger protein 35	-1.35	0.238	1.04	0.913	1.07	0.679	2.01	0.329	0.69
1446905_at	---	Transcribed locus	1.03	0.94	1.07	0.867	-1.33	0.148	1.03	0.964	0.45
1448856_a_at	Msra	methionine sulfoxide reductase A	-1.21	0.409	1	0.995	1.02	0.913	1.09	0.68	0.47
1441942_x_at	Snupn	snurportin 1	-1.24	0.604	1.02	0.939	1.01	0.949	1.12	0.742	0.48
1436080_at	AW011738	expressed sequence AW011738	1.09	0.84	1.07	0.544	-1.46	0.483	1.19	0.697	0.47
1458848_at	LOC624549	Hypothetical protein LOC624549	-2.15	0.091	1	0.99	1.38	0.422	1.33	0.592	0.39
1431332_a_at	Terf1	telomeric repeat binding factor 1	1.06	0.792	-1.29	0.463	1.01	0.947	1.35	0.447	0.53
1421574_at	Rap2a	RAS related protein 2a	1.15	0.848	1.04	0.88	-1.51	0.124	1.06	0.887	0.44
1443085_at	Sfrs2ip	Splicing factor, arginine/serine-rich 2, interacting protein	1.08	0.833	1.06	0.85	-1.41	0.326	1.43	0.062	0.54
1450517_at	Tal2	T-cell acute lymphocytic leukemia 2	-1.99	0.56	1.22	0.73	1.12	0.725	1.52	0.565	0.47
1420863_at	Dctn4	dynactin 4	1.15	0.763	-1.62	0.32	1.09	0.68	2.24	0.123	0.71
1434189_at	Stag1	stromal antigen 1	1.01	0.904	1.11	0.223	-1.36	0.072	1.14	0.477	0.47
1440336_at	Prmt6	protein arginine N-methyltransferase 6	-1.4	0.296	1.14	0.656	1	0.974	1.42	0.225	0.54
1418943_at	B230120H23Rik	RIKEN cDNA B230120H23 gene	1.05	0.845	-1.25	0.316	1	0.986	3.9	0.164	1.18
1429324_at	1700012A16Rik	RIKEN cDNA 1700012A16 gene	1.2	0.777	1.05	0.948	-1.64	0.15	1.08	0.734	0.42
1436784_x_at	Sf3b4 /// LOC63441	splicing factor 3b, subunit 4 /// similar to splicing factor 3b, subunit 4 (predicted) //	-1.62	0.042	1.01	0.958	1.23	0.413	1.4	0.188	0.51
1423160_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1.11	0.395	1.04	0.765	-1.41	0.006	1.01	0.945	0.44
1432048_at	6330565B04Rik	RIKEN cDNA 6330565B04 gene	1.09	0.87	1.04	0.907	-1.37	0.403	1.33	0.24	0.52
1430339_at	2610021K21Rik	RIKEN cDNA 2610021K21 gene	1.43	0.409	-3.2	0.011	1.12	0.448	1.67	0.279	0.25
1445544_x_at	Obfc1	oligonucleotide/oligosaccharide-binding fold containing 1	1.05	0.504	1.05	0.835	-1.33	0.147	1.55	0.183	0.58
1427835_at	Pou2f1	POU domain, class 2, transcription factor 1	1.03	0.955	-1.31	0.491	1.06	0.671	1.18	0.105	0.49
1439393_x_at	Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	1.03	0.936	1.01	0.943	-1.23	0.412	1.66	0.124	0.62
1429896_at	5830408B19Rik	RIKEN cDNA 5830408B19 gene	1.13	0.706	1.18	0.665	-1.84	0.045	1.13	0.578	0.4
1451079_at	Adpgk	ADP-dependent glucokinase	1.01	0.931	-1.19	0.466	1	0.994	1.16	0.724	0.5
1417862_at	A830059I20Rik	RIKEN cDNA A830059I20 gene	1.14	0.574	-1.39	0.52	1	0.999	1.18	0.594	0.48
1447185_at	9330158H04Rik	RIKEN cDNA 9330158H04 gene	1.13	0.79	-1.47	0.18	1.04	0.94	1.53	0.47	0.56
1416123_at	Ccnd2	cyclin D2	1.16	0.059	1.08	0.807	-1.62	0.177	1.34	0.482	0.49
1447804_x_at	BC031781	CDNA sequence BC031781	1.08	0.852	1.06	0.794	-1.4	0.103	1.25	0.538	0.5
1459690_at	---	---	-1.43	0.177	1.01	0.982	1.15	0.462	1.24	0.357	0.49
1433485_x_at	Gpr56	G protein-coupled receptor 56	1.01	0.962	-1.37	0.488	1.12	0.757	3.79	0.177	1.14
1432322_at	2310016E02Rik	RIKEN cDNA 2310016E02 gene	-1.2	0.656	1	0.999	1.02	0.881	1.37	0.501	0.55
1455310_at	Rbm16	RNA binding motif protein 16	1.06	0.579	1.04	0.673	-1.31	0.08	1.25	0.264	0.51
1428513_at	Calcoco1	calcium binding and coiled coil domain 1	1.06	0.824	-1.29	0.129	1.02	0.673	1.37	0.18	0.54
1415950_a_at	Pebp1	phosphatidylethanolamine binding protein 1	1.01	0.766	-1.18	0.404	1	0.998	1.06	0.221	0.47
1454018_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	-1.31	0.237	1.02	0.927	1.07	0.577	1.17	0.671	0.49
1417393_a_at	C1qdc2	C1q domain containing 2	1.09	0.39	-1.43	0.059	1.07	0.65	4.58	0.139	1.33
1449822_at	Atoh1	atonal homolog 1 (Drosophila)	-1.71	0.413	1.11	0.883	1.17	0.503	1.28	0.618	0.46
1425622_at	Edil3	EGF-like repeats and discoidin I-like domains 3	1.02	0.979	1.39	0.398	-2.21	0.001	1.13	0.765	0.33
1424141_at	Hectd1	HECT domain containing 1	1.01	0.95	-1.19	0.091	1.01	0.93	1.78	0.152	0.65
1458313_at	Cdc2l5	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	1.01	0.98	-1.34	0.56	1.1	0.836	1.32	0.259	0.52
1416805_at	1110032E23Rik	RIKEN cDNA 1110032E23 gene	1.17	0.548	-1.57	0.116	1.06	0.421	1.22	0.362	0.47
1419267_at	Nfyb	nuclear transcription factor-Y beta	1.03	0.813	1.07	0.433	-1.3	0.131	1.32	0.374	0.53
1425048_a_at	Hmgb1	high mobility group box 1	1.06	0.503	1	0.976	-1.26	0.144	1.37	0.041	0.54
1458450_at	Zfr	zinc finger RNA binding protein	1.3	0.157	1.03	0.859	-1.87	0.02	1.18	0.695	0.41
1450740_a_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	1.08	0.649	1.02	0.565	-1.3	0.005	1.16	0.077	0.49
1436247_at	Ints2	integrator complex subunit 2	-1.35	0.125	1.03	0.891	1.09	0.637	1.16	0.241	0.48
1433414_at	9530086P17Rik	RIKEN cDNA 9530086P17 gene	1.06	0.848	1.4	0.078	-2.45	0.109	1.91	0.012	0.48
1451840_at	Kcnip4	Kv channel interacting protein 4	-1.59	0.308	1.12	0.809	1.11	0.767	1.27	0.651	0.48
1458234_at	A730052K04Rik	RIKEN cDNA A730052K04 gene	1.25	0.1	1.17	0.794	-2.22	0.295	1.33	0.28	0.38
1454271_at	1810013D15Rik	RIKEN cDNA 1810013D15 gene	-1.5	0.461	1.13	0.745	1.08	0.758	1.49	0.23	0.55
1451240_a_at	Glo1	glyoxalase 1	1.03	0.02	1.06	0.291	-1.28	0.047	1.42	0.332	0.56
1456612_at	Il17d	Interleukin 17D	1.19	0.376	-2.17	0.014	1.22	0.62	1.71	0.354	0.49

1445016_at	---	---	1.07	0.882	-1.34	0.434	1.05	0.841	1.17	0.738	0.49
1446833_at	Dock9	Dedicator of cytokinesis 9	1.03	0.718	1.32	0.448	-1.96	0.103	1.62	0.269	0.51
1451653_a_at	4930430E16Rik	RIKEN cDNA 4930430E16 gene	-1.29	0.104	1.03	0.793	1.06	0.795	1.33	0.443	0.53
1427701_a_at	Six4	sine oculis-related homeobox 4 homolog (Drosophila)	1.08	0.462	1.06	0.704	-1.37	0.668	1.19	0.465	0.49
1423640_at	Synpr	synaptoporin	1.36	0.588	1.04	0.955	-2.12	0.096	2.45	0.031	0.68
1456697_x_at	Dmtf1	cyclin D binding myb-like transcription factor 1	1.05	0.918	1.14	0.816	-1.47	0.241	1.26	0.607	0.49
1448232_x_at	Tuba6 /// LOC6265	tubulin, alpha 6 /// similar to Tubulin alpha-6 chain (Alpha-tubulin 6)	-1.2	0.431	1.03	0.836	1.01	0.966	1.52	0.253	0.59
1458384_at	---	Transcribed locus	1.17	0.619	1.07	0.701	-1.59	0.006	1.48	0.435	0.53
1417345_at	2900064A13Rik	RIKEN cDNA 2900064A13 gene	1.29	0.611	-1.89	0.371	1.05	0.888	1.1	0.846	0.39
1432007_s_at	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	1.02	0.968	1.03	0.886	-1.22	0.493	1.28	0.538	0.53
1429509_at	2600001B17Rik	RIKEN cDNA 2600001B17 gene	1.06	0.613	-1.25	0.312	1.01	0.963	1.43	0.122	0.56
1452997_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	1.04	0.859	-1.22	0.125	1.01	0.884	1.01	0.977	0.46
1444333_at	---	---	-1.29	0.663	1.05	0.902	1.04	0.903	1.03	0.894	0.46
1438302_at	Zf	HCF-binding transcription factor Zhangfei	1.19	0.708	-1.48	0.431	1	0.993	1.15	0.402	0.47
1424344_s_at	Eif1a	eukaryotic translation initiation factor 1A	1.06	0.758	1.06	0.804	-1.33	0.095	1.02	0.796	0.45
1431642_at	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural gene Y-linked	1.08	0.782	1.01	0.981	-1.29	0.498	2.14	0.058	0.74
1425608_at	Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	1.04	0.895	1.06	0.703	-1.29	0.411	2.23	0.252	0.76
1447061_at	Hif3a	Hypoxia inducible factor 3, alpha subunit	1.12	0.902	-1.39	0.343	1.04	0.872	1.03	0.921	0.45
1439103_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	-1.16	0.565	1	0.992	1.01	0.912	1.1	0.453	0.49
1435072_at	Zfyve1	zinc finger, FYVE domain containing 1	1.02	0.276	-1.21	0.097	1.02	0.818	1.02	0.878	0.46
1419840_at	Krt72	keratin 72	1.11	0.837	1.24	0.677	-1.89	0.265	2.02	0.08	0.62
1422829_at	Drd4	dopamine receptor 4	1.38	0.413	1.13	0.79	-2.81	0.078	1.21	0.672	0.23
1435604_at	Trim37	tripartite motif protein 37	-1.45	0.166	1.03	0.925	1.16	0.631	1.08	0.697	0.45
1437217_at	Ankrd6	ankyrin repeat domain 6	1.06	0.917	-2.02	0.495	1.32	0.084	1.32	0.185	0.42
1423223_a_at	Prdx6	peroxiredoxin 6	1.02	0.33	-1.18	0.301	1	0.96	1.23	0.344	0.52
1428979_at	Mtf1	metal response element binding transcription factor 1	1.02	0.779	-1.17	0.373	1	0.998	1.06	0.756	0.48
1444664_at	Igsf4d	Immunoglobulin superfamily, member 4	1.01	0.98	-1.18	0.081	1.02	0.937	1.1	0.91	0.49
1420346_at	Asb12	ankyrin repeat and SOCS box-containing protein 12	1.19	0.29	1.15	0.805	-1.85	0.031	1.17	0.825	0.41
1452020_a_at	Siva	Cd27 binding protein (Hindu God of destruction)	1.01	0.951	1.17	0.211	-1.43	0.104	1.65	0.244	0.6
1450348_at	Slc19a3	solute carrier family 19 (sodium/hydrogen exchanger), member 3	1.05	0.845	-3.24	0.095	1.51	0.436	1.11	0.81	0.11
1432647_at	Egfr	epidermal growth factor receptor	-1.16	0.778	1.01	0.985	1.01	0.954	2.24	0.3	0.77
1448769_at	Slc35b1	solute carrier family 35, member B1	1.03	0.256	1.05	0.803	-1.25	0.073	1.52	0.014	0.59
1430551_s_at	Lipl3	lipase-like, ab-hydrolase domain containing 3	1.12	0.712	1.22	0.537	-1.88	0.07	1.17	0.809	0.41
1421506_at	Olfr78	olfactory receptor 78	-1.63	0.173	1.03	0.936	1.24	0.393	1.06	0.753	0.42
1423093_at	Incenp	inner centromere protein	1.11	0.8	1.01	0.981	-1.33	0.59	3.46	0.309	1.06
1425653_at	Atf7	activating transcription factor 7	-3.54	0.046	1.1	0.851	1.5	0.139	1.13	0.745	0.05
1416661_at	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)	1.05	0.884	-1.25	0.318	1.02	0.955	1.96	0.132	0.7
1424093_x_at	Cd151	CD151 antigen	1.04	0.795	1.05	0.694	-1.26	0.037	1.05	0.63	0.47
1426811_at	Ppp2r5b	protein phosphatase 2, regulatory subunit B (B56), beta isoform	1.13	0.469	-1.37	0.173	1.01	0.917	2.95	0.245	0.93
1452037_at	Mgat2	mannoside acetylglucosaminyltransferase 2	1.06	0.022	-1.31	0.318	1.05	0.612	1.09	0.461	0.47
1435911_s_at	Slc2a12	solute carrier family 2 (facilitated glucose transporter), member 12	1	0.957	-1.5	0.3	1.21	0.481	1.11	0.813	0.45
1417387_at	Med31	mediator of RNA polymerase II transcription, subunit 31 homolog (yeast)	1.03	0.575	1.07	0.552	-1.28	0.162	1.01	0.956	0.46
1417589_at	Galnt3 /// LOC6208	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.11	0.749	-1.7	0.442	1.18	0.602	1.11	0.747	0.42
1422655_at	Ptch2	patched homolog 2	-1.24	0.537	1.07	0.806	1.01	0.967	1.36	0.02	0.55
1431042_at	Paqr8	progestin and adipoQ receptor family member VIII	-1.4	0.561	1.15	0.634	1.02	0.926	1.2	0.599	0.49
1438339_at	Fancd2	Fanconi anemia, complementation group D2	1.13	0.887	-1.84	0.108	1.21	0.317	2.88	0.237	0.84
1428814_at	---	---	-1.32	0.411	1.09	0.807	1.04	0.926	1.3	0.174	0.53
1451093_at	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	-1.39	0.205	1.03	0.883	1.13	0.423	1	0.982	0.44
1443408_at	Plk1	Polo-like kinase 1 (Drosophila)	1.24	0.759	-2.13	0.204	1.17	0.518	1.35	0.392	0.41
1417717_a_at	Tyr	tyrosinase	-2.32	0.033	1.18	0.403	1.27	0.442	1.33	0.482	0.37
1436887_x_at	Grwd1	glutamate-rich WD repeat containing 1	-1.42	0.45	1.04	0.875	1.13	0.703	1.23	0.299	0.5
1430645_at	Cd200r3	CD200 receptor 3	1.26	0.253	-2.04	0.387	1.13	0.793	1.59	0.023	0.49
1453601_at	Zfp710	zinc finger protein 710	1.02	0.934	1.09	0.84	-1.3	0.302	1.38	0.215	0.55

1428849_at	Rps6kb1	ribosomal protein S6 kinase, polypeptide 1	1.04	0.755	-1.31	0.232	1.08	0.518	1.81	0.077	0.66
1428062_at	Cpa1	carboxypeptidase A1	1.14	0.639	1.13	0.626	-1.63	0.058	1	0.996	0.41
1460247_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	1.01	0.964	1.07	0.884	-1.26	0.221	1.6	0.047	0.61
1438967_x_at	Amhr2	anti-Mullerian hormone type 2 receptor	1	0.993	-1.2	0.567	1.04	0.644	1.11	0.643	0.49
1439781_at	D930048N14Rik	RIKEN cDNA D930048N14 gene	-1.37	0.172	1.09	0.798	1.07	0.826	1.22	0.085	0.5
1429451_at	2610301B20Rik	RIKEN cDNA 2610301B20 gene	-1.39	0.087	1.12	0.185	1.04	0.833	1.48	0.21	0.56
1428290_at	Mipep	mitochondrial intermediate peptidase	1.01	0.922	-1.23	0.241	1.06	0.638	1.08	0.675	0.48
1442129_at	1810058I24Rik	RIKEN cDNA 1810058I24 gene	1	0.995	-1.28	0.407	1.1	0.467	1.34	0.534	0.54
1449036_at	Rnf128	ring finger protein 128	1.01	0.918	-1.19	0.186	1.04	0.824	3.55	0.06	1.1
1433498_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	1.02	0.928	-1.21	0.261	1.04	0.815	1.29	0.087	0.54
1447647_at	Wnt7a	wingless-related MMTV integration site 7A	-1.27	0.514	1.01	0.968	1.09	0.876	1.87	0.443	0.67
1432290_at	1700040G22Rik	RIKEN cDNA 1700040G22 gene	1.01	0.975	1.21	0.743	-1.51	0.317	1.03	0.929	0.44
1435381_at	2610110G12Rik	RIKEN cDNA 2610110G12 gene	1.02	0.909	-1.42	0.121	1.16	0.667	1.47	0.199	0.56
1428535_at	9430020K01Rik	RIKEN cDNA 9430020K01 gene	1.1	0.814	1.04	0.648	-1.34	0.116	1.06	0.757	0.47
1440132_s_at	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	1.15	0.522	-1.57	0.504	1.1	0.412	1.86	0.24	0.64
1427297_at	Mrpl9	mitochondrial ribosomal protein L9	1.06	0.692	-1.22	0.22	1.01	0.958	1.05	0.803	0.47
1441949_x_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	1.19	0.663	-1.64	0.264	1.09	0.8	1.19	0.568	0.46
1416093_a_at	Mrpl20	mitochondrial ribosomal protein L20	1.06	0.51	1.05	0.738	-1.28	0.013	1.21	0.54	0.51
1450423_s_at	Bxdc1	brix domain containing 1	-1.22	0.04	1	0.983	1.07	0.758	1.02	0.91	0.47
1423624_at	Fancl	Fanconi anemia, complementation group L	-1.27	0.09	1.08	0.634	1.02	0.929	1.53	0.218	0.59
1420449_at	A230048G03Rik	RIKEN cDNA A230048G03 gene	-1.42	0.093	1.17	0.502	1.01	0.967	1.01	0.967	0.45
1434472_at	Dusp3	dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	1.04	0.83	1.1	0.564	-1.32	0.188	1.09	0.358	0.47
1449697_s_at	Mfn1	mitofusin 1	-1.2	0.224	1.02	0.878	1.04	0.661	1.34	0.048	0.55
1442596_at	Klhdc2	kelch domain containing 2	1.06	0.357	1.29	0.461	-1.86	0.014	1.54	0.207	0.51
1416082_at	Rab1	RAB1, member RAS oncogene family	1.01	0.809	1.02	0.833	-1.16	0.404	1.17	0.062	0.51
1421316_at	1110058A15Rik	RIKEN cDNA 1110058A15 gene	-1.49	0.201	1.09	0.792	1.13	0.582	1.26	0.197	0.5
1459516_at	Cul1	Cullin 1	-1.39	0.329	1.08	0.55	1.09	0.694	1.1	0.55	0.47
1423179_at	Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1	1.21	0.403	-1.55	0.239	1.04	0.864	1.01	0.954	0.43
1432074_at	4930517E11Rik	RIKEN cDNA 4930517E11 gene	-1.98	0.47	1.22	0.761	1.17	0.639	1.51	0.321	0.48
1436588_at	Rttn	rotatin	1.2	0.241	-1.55	0.519	1.05	0.768	1.08	0.632	0.44
1457817_at	Bcas3	Breast carcinoma amplified sequence 3	1.17	0.748	1.31	0.527	-2.4	0.104	2.13	0.157	0.55
1434208_at	2900057K09Rik	RIKEN cDNA 2900057K09 gene	1.07	0.711	-1.24	0.602	1.02	0.955	1.17	0.354	0.5
1450511_at	Musk	muscle, skeletal, receptor tyrosine kinase	-1.38	0.65	1.02	0.966	1.15	0.639	1.11	0.845	0.48
1439677_at	Epm2a	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	1.01	0.981	-1.22	0.668	1.07	0.768	1.48	0.072	0.58
1452444_at	Napb	N-ethylmaleimide sensitive fusion protein attachment protein beta	1.02	0.925	-1.4	0.291	1.16	0.745	2.8	0.072	0.89
1459590_at	---	Transcribed locus	-1.58	0.476	1.08	0.823	1.18	0.475	1.01	0.945	0.42
1423162_s_at	Spred1	sprouty protein with EVH-1 domain 1, related sequence	1.02	0.895	1.12	0.589	-1.32	0.127	1.04	0.686	0.47
1416436_a_at	2410003P15Rik	RIKEN cDNA 2410003P15 gene	1.01	0.839	-1.29	0.071	1.11	0.26	1.03	0.732	0.47
1459204_at	AU015449	expressed sequence AU015449	-1.53	0.539	1.06	0.736	1.19	0.657	1.06	0.936	0.44
1434956_at	LOC668047 /// LOC	similar to ring finger protein 170 /// similar to ring finger protein 170	1.15	0.127	1.05	0.642	-1.44	0.02	1.05	0.828	0.45
1422599_s_at	Zfp143	zinc finger protein 143	1.05	0.775	1.05	0.49	-1.24	0.24	1.06	0.54	0.48
1419893_at	D930048N14Rik	RIKEN cDNA D930048N14 gene	1.07	0.877	-1.84	0.096	1.29	0.61	1.41	0.376	0.48
1426463_at	Gphn	gephyrin	1.06	0.776	-1.19	0.473	1	0.986	1.09	0.478	0.49
1425003_at	Uroc1	urocanase domain containing 1	-1.7	0.179	1.15	0.725	1.16	0.533	1.04	0.952	0.41
1456280_at	Clspn	claspin homolog (Xenopus laevis)	-1.4	0.421	1.18	0.699	1.01	0.949	4.5	0.18	1.32
1448318_at	Adfp	adipose differentiation related protein	1.06	0.708	-1.31	0.185	1.08	0.612	1.02	0.911	0.46
1458927_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	1.1	0.727	-1.33	0.107	1.05	0.842	1.54	0.123	0.59
1428193_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	1.08	0.607	1.06	0.307	-1.32	0.128	1.35	0.154	0.54
1418490_at	Sdsl	serine dehydratase-like	-1.32	0.182	1.13	0.445	1.01	0.969	4.66	0.184	1.37
1445883_at	Ranbp2	RAN binding protein 2	1.03	0.952	-1.68	0.106	1.28	0.244	1.11	0.779	0.43
1423727_at	Cnih	cornichon homolog (Drosophila)	1.02	0.797	1.04	0.553	-1.18	0.04	1.11	0.462	0.5
1439606_at	---	Transcribed locus	1.04	0.74	-1.38	0.277	1.14	0.671	2.78	0.228	0.89
1423943_at	Dus1l	dihydrouridine synthase 1-like (S. cerevisiae)	1.01	0.844	-1.14	0.071	1.02	0.879	1.15	0.655	0.51

1457350_at	Per2	period homolog 2 (Drosophila)	1.03	0.955	-1.44	0.519	1.18	0.754	1.04	0.927	0.45
1422459_a_at	Psmd13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	1	0.96	1.07	0.514	-1.21	0.003	1.02	0.922	0.47
1421976_at	Mmp19	matrix metallopeptidase 19	-1.46	0.627	1.02	0.93	1.2	0.195	1.23	0.007	0.5
1439026_at	Trpm3	transient receptor potential cation channel, subfamily M, member 3	1.08	0.898	-1.83	0.335	1.28	0.642	1.54	0.532	0.52
1446652_at	Reps2	RALBP1 associated Eps domain containing protein 2	1.2	0.779	-1.95	0.113	1.19	0.725	1.04	0.757	0.37
1458149_at	---	---	1.21	0.786	1.06	0.859	-1.59	0.144	1.07	0.839	0.44
1445571_at	Tbk1	TANK-binding kinase 1	1.13	0.633	1.06	0.775	-1.4	0.189	1.09	0.759	0.47
1458277_at	Ccl25	Chemokine (C-C motif) ligand 25	1.06	0.762	-1.38	0.044	1.12	0.488	1.22	0.48	0.51
1434276_x_at	BC004004	cDNA sequence BC004004	-1.13	0.314	1.02	0.894	1	0.998	1.12	0.593	0.5
1426939_at	Tsr2	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	1.01	0.857	-1.12	0.36	1	0.995	1.12	0.35	0.5
1422379_x_at	V1rb9	vomeronasal 1 receptor, B9	1	1	1.02	0.914	-1.14	0.55	1.74	0.421	0.66
1432049_at	4930422I22Rik	RIKEN cDNA 4930422I22 gene	1.04	0.906	1.1	0.799	-1.32	0.545	1.37	0.498	0.55
1444101_at	Odf2	outer dense fiber of sperm tails 2	1.09	0.545	1.08	0.796	-1.34	0.047	1.35	0.159	0.54
1417732_at	Anxa8	annexin A8	-1.4	0.26	1.06	0.926	1.14	0.681	1.58	0.231	0.59
1457028_at	A430033K04Rik	RIKEN cDNA A430033K04 gene	1.06	0.732	-1.21	0.518	1.02	0.936	1.04	0.856	0.48
1422814_at	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	-1.67	0.385	1.16	0.657	1.15	0.689	3.86	0.152	1.12
1458559_at	A730028G07Rik	RIKEN cDNA A730028G07 gene	1.13	0.879	-1.43	0.505	1.09	0.849	1.05	0.785	0.46
1455819_at	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	1.1	0.294	1.06	0.488	-1.34	0.126	1.09	0.414	0.48
1443359_at	Odz4	Odd Oz/ten-m homolog 4 (Drosophila)	-1.23	0.443	1.07	0.879	1.03	0.949	1.01	0.988	0.47
1437332_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.14	0.888	-1.63	0.186	1.15	0.728	1.31	0.395	0.49
1437708_x_at	Vamp3	vesicle-associated membrane protein 3	1.02	0.658	1.12	0.431	-1.3	0.003	1.24	0.268	0.52
1456711_at	4932425I24Rik	RIKEN cDNA 4932425I24 gene	-1.76	0.043	1.1	0.82	1.24	0.389	1.12	0.692	0.43
1428145_at	Acaa2	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiol	1.01	0.94	-1.21	0.052	1.07	0.523	1.33	0.047	0.55
1450391_a_at	Mgll	monoglyceride lipase	1.31	0.137	-1.73	0.146	1.02	0.947	2.25	0.107	0.71
1439543_at	1110064A23Rik	RIKEN cDNA 1110064A23 gene	-1.19	0.644	1.07	0.851	1.01	0.963	1.19	0.684	0.52
1425931_a_at	Arntl2	aryl hydrocarbon receptor nuclear translocator-like 2	1.07	0.809	1.05	0.937	-1.27	0.645	1.51	0.394	0.59
1423164_at	LOC664862	similar to transmembrane 7 superfamily member 1	1.04	0.914	-1.4	0.071	1.16	0.186	1.01	0.972	0.45
1430586_at	2700007P21Rik	RIKEN cDNA 2700007P21 gene	-1.62	0.119	1.09	0.747	1.2	0.247	1.06	0.797	0.43
1458695_at	Zbtb10	Zinc finger and BTB domain containing 10	-1.5	0.393	1.12	0.845	1.13	0.623	1.05	0.767	0.45
1421267_a_at	Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1	0.989	-1.19	0.407	1.07	0.709	1.36	0.289	0.56
1438717_a_at	Osbpl6	oxysterol binding protein-like 6	-1.68	0.078	1.06	0.92	1.25	0.382	1.76	0.178	0.6
1418014_a_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	-1.1	0.617	1	0.967	1	0.979	1.31	0.125	0.55
1418035_a_at	Prim2	DNA primase, p58 subunit	1.02	0.946	-1.13	0.74	1.01	0.974	2.25	0.202	0.79
1424747_at	Kif1c	Kinesin family member 1C	1.04	0.892	-1.16	0.719	1.02	0.949	1.35	0.339	0.56
1424460_s_at	Aytl2	acyltransferase like 2	1.04	0.765	1.03	0.846	-1.18	0.104	1.44	0.393	0.58
1424151_at	Jtv1	JTV1 gene	-1.28	0.45	1.03	0.69	1.11	0.342	1.19	0.424	0.51
1436490_x_at	Ran /// LOC625094	RAN, member RAS oncogene family /// similar to RAN, member RAS oncogene f	1.34	0.681	1.23	0.311	-2.86	0.073	1.86	0.361	0.39
1432507_at	B430319H21Rik	RIKEN cDNA B430319H21 gene	1.13	0.897	1.15	0.793	-1.57	0.263	1.08	0.275	0.45
1437278_a_at	Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B	-1.18	0.184	1.04	0.689	1.03	0.709	1	0.974	0.47
1418991_at	Bak1	BCL2-antagonist/killer 1	-1.36	0.219	1.09	0.646	1.09	0.763	1.16	0.381	0.5
1435953_at	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1 homolo	1	0.989	1.04	0.6	-1.15	0.33	1.43	0.363	0.58
1435175_at	BC034090	cDNA sequence BC034090	1.08	0.788	-1.36	0.315	1.1	0.738	1.91	0.088	0.68
1451103_at	D14Ertd500e	DNA segment, Chr 14, ERATO Doi 500, expressed	1.01	0.917	-1.24	0.156	1.1	0.61	1.75	0.149	0.65
1446754_a_at	Vax2os1	Vax2 opposite strand transcript 1	1.15	0.751	-1.66	0.038	1.16	0.373	1.11	0.814	0.44
1455641_at	1600014C10Rik	RIKEN cDNA 1600014C10 gene	1.06	0.868	1.37	0.673	-2.05	0.11	1.29	0.335	0.42
1442639_at	---	---	-1.47	0.615	1.18	0.731	1.06	0.878	1.01	0.992	0.44
1429270_a_at	Syce2	synaptonemal complex central element protein 2	1.03	0.736	1.04	0.707	-1.18	0.052	3.1	0.211	1
1450720_at	Acp1	acid phosphatase 1, soluble	1.02	0.841	1.04	0.668	-1.16	0.465	2.06	0.234	0.74
1428232_at	Cpsf6	cleavage and polyadenylation specific factor 6	-1.19	0.319	1.06	0.495	1.02	0.723	1.01	0.94	0.48
1415725_at	Rrn3	RRN3 RNA polymerase I transcription factor homolog (yeast)	1	0.994	-1.19	0.316	1.08	0.479	1.18	0.201	0.52
1425050_at	Isoc1	isochorismatase domain containing 1	1	0.97	-1.2	0.359	1.08	0.59	1.14	0.128	0.51
1450119_at	Dst	dystonin	1.1	0.728	-1.43	0.246	1.12	0.716	1.88	0.429	0.67
1452434_s_at	Dgcr6	DiGeorge syndrome critical region gene 6	1.02	0.882	-1.11	0.375	1	0.974	1.01	0.847	0.48

1422841_at	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransf	-2.25	0.294	1.4	0.55	1.07	0.617	1.48	0.015	0.43
1419548_at	Kpna1	karyopherin (importin) alpha 1	1	0.982	1.01	0.918	-1.11	0.485	1.37	0.37	0.57
1434103_at	AA408278	expressed sequence AA408278	-1.27	0.058	1.06	0.645	1.08	0.535	1.02	0.864	0.47
1431142_s_at	Amid	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death	1.27	0.516	-1.94	0.013	1.14	0.48	1.53	0.232	0.5
1445161_at	---	---	1.18	0.226	1.01	0.968	-1.37	0.267	1.18	0.415	0.5
1438419_at	Rbm16	RNA binding motif protein 16	1.15	0.287	1.07	0.522	-1.42	0.176	1.14	0.503	0.48
1440385_at	9530051E23Rik	RIKEN cDNA 9530051E23 gene	1.28	0.576	1.06	0.914	-1.71	0.034	1.15	0.568	0.44
1456555_at	Ccdc67	coiled-coil domain containing 67	-1.12	0.641	1.02	0.964	1	0.979	1.09	0.741	0.5
1420161_at	AA409749	expressed sequence AA409749	1.03	0.825	1.04	0.931	-1.18	0.169	1.11	0.486	0.5
1416199_at	Kifc3	kinesin family member C3	1.08	0.6	-1.25	0.358	1.04	0.67	1.25	0.437	0.53
1426736_at	Gspt1	G1 to S phase transition 1	-1.24	0.096	1.03	0.64	1.08	0.399	1.24	0.244	0.53
1424778_at	D10Ucla1	DNA segment, Chr 10, University of California at Los Angeles 1	1.06	0.775	-1.24	0.364	1.05	0.85	1.04	0.89	0.48
1426594_at	Frmd4b	FERM domain containing 4B	-1.28	0.731	1.14	0.68	1	0.99	1.08	0.85	0.48
1460387_a_at	Siae	sialic acid acetylesterase	1.02	0.944	-1.19	0.356	1.06	0.842	1.11	0.425	0.5
1438737_at	Zic3	zinc finger protein of the cerebellum 3	1.15	0.508	1.42	0.556	-2.78	0.158	1.85	0.345	0.41
1442964_at	AU020772	Expressed sequence AU020772	1.02	0.94	1.09	0.769	-1.24	0.368	1.1	0.652	0.49
1451844_at	Prlr	prolactin receptor	-1.4	0.262	1	0.97	1.2	0.535	1.48	0.499	0.57
1453941_at	4930579P08Rik	RIKEN cDNA 4930579P08 gene	-1.97	0.109	1.35	0.109	1.07	0.885	1.82	0.266	0.57
1424716_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	1.38	0.24	-2.21	0.186	1.09	0.611	1.31	0.097	0.39
1449578_at	Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)	1.01	0.976	1.05	0.809	-1.16	0.659	1.55	0.263	0.61
1439050_at	---	---	1.01	0.932	-1.21	0.053	1.08	0.578	5.28	0.185	1.54
1441832_at	Hdac10	histone deacetylase 10	1.02	0.96	1.21	0.779	-1.43	0.636	1.02	0.967	0.45
1449778_at	---	---	-1.79	0.476	1.1	0.833	1.27	0.681	1.42	0.52	0.5
1448038_at	---	---	-1.23	0.142	1.02	0.717	1.09	0.708	1.31	0.036	0.55
1422158_at	Clstn2	calsyntenin 2	1.13	0.731	1.09	0.868	-1.43	0.178	2.14	0.145	0.73
1417719_at	Sap30	sin3 associated polypeptide	1	0.974	-1.28	0.064	1.14	0.437	1.29	0.459	0.54
1427887_at	2610304G08Rik	RIKEN cDNA 2610304G08 gene	-1.3	0.049	1.03	0.766	1.13	0.28	1.39	0.371	0.56
1458343_x_at	Med6	mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	1.04	0.871	1.04	0.822	-1.18	0.483	1.1	0.611	0.5
1435885_s_at	Itsn1	intersectin 1 (SH3 domain protein 1A)	1.05	0.663	1.08	0.672	-1.26	0.198	2.66	0.218	0.88
1438011_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	-1.31	0.308	1.02	0.834	1.14	0.398	3.46	0.161	1.08
1435819_at	4922503N01Rik	RIKEN cDNA 4922503N01 gene	1.06	0.909	1.08	0.859	-1.26	0.316	1.69	0.319	0.64
1452891_at	Ccdc51	coiled-coil domain containing 51	1.09	0.757	-1.21	0.184	1.01	0.95	1.06	0.739	0.49
1423344_at	Epor	erythropoietin receptor	-1.21	0.27	1.08	0.264	1.02	0.909	5.82	0.174	1.68
1416991_at	Mto1	mitochondrial translation optimization 1 homolog (S. cerevisiae)	1.07	0.219	-1.3	0.152	1.09	0.529	1.24	0.45	0.53
1448516_at	Tsn	translin	1.07	0.068	1.02	0.86	-1.19	0.148	1.37	0.051	0.57
1451967_x_at	Kpnb1	karyopherin (importin) beta 1	1.11	0.841	-1.29	0.051	1.04	0.923	1.4	0.051	0.57
1434381_at	BC060631	cDNA sequence BC060631	1.02	0.595	1.03	0.887	-1.14	0.501	1.05	0.717	0.49
1421078_at	Tcf23	transcription factor 23	-1.37	0.665	1.05	0.852	1.14	0.713	1.18	0.789	0.5
1435389_at	Reps2	RALBP1 associated Eps domain containing protein 2	1.31	0.059	1.05	0.732	-1.77	0.005	1.31	0.474	0.48
1438091_a_at	H2afz /// LOC6318	H2A histone family, member Z /// similar to H2A histone family, member Z /// simil	1.02	0.22	1.04	0.719	-1.15	0.214	1.34	0.19	0.56
1433816_at	Mcart1	mitochondrial carrier triple repeat 1	1.02	0.451	-1.1	0.481	1	0.994	2.22	0.138	0.79
1423807_a_at	Calm2	calmodulin 2	1.08	0.494	1.08	0.176	-1.29	0.005	1.05	0.49	0.48
1418727_at	Nup155	nucleoporin 155	1.13	0.57	-1.35	0.152	1.06	0.025	1.09	0.594	0.48
1421196_at	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	1.02	0.89	-1.67	0.316	1.31	0.378	1.11	0.799	0.44
1451064_a_at	Psat1	phosphoserine aminotransferase 1	-1.38	0.431	1.08	0.884	1.13	0.63	1.06	0.727	0.47
1455176_a_at	Syt11	synaptotagmin XI	1.11	0.454	-2.19	0.247	1.36	0.112	1.15	0.651	0.36
1416907_at	Tsn	translin	1.01	0.901	1.1	0.459	-1.21	0.378	1.23	0.276	0.53
1431036_a_at	Tmed2	transmembrane emp24 domain trafficking protein 2	1.01	0.945	1.04	0.785	-1.14	0.62	1.18	0.325	0.52
1417724_at	Thoc4	THO complex 4	1.02	0.949	1.1	0.71	-1.22	0.403	1.48	0.102	0.59
1443793_x_at	Ints1	integrator complex subunit 1	-1.32	0.25	1.05	0.79	1.12	0.371	1.21	0.379	0.52
1429033_at	Gcc1	golgi coiled coil 1	1	0.996	1.11	0.493	-1.21	0.342	1.05	0.547	0.49
1452517_at	Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	1.33	0.237	-2.55	0.121	1.21	0.469	1.24	0.756	0.31
1457252_x_at	Pld2	phospholipase D2	1.17	0.168	1.01	0.952	-1.34	0.098	1.04	0.935	0.47

1455588_at	BC034664	cDNA sequence BC034664	1.04	0.806	1.02	0.892	-1.15	0.412	1.91	0.143	0.7
1453189_at	Ube2i	ubiquitin-conjugating enzyme E2I	1.15	0.456	1.04	0.889	-1.35	0.29	1.36	0.141	0.55
1418437_a_at	Mlx	MAX-like protein X	1	0.976	1.14	0.292	-1.25	0.133	1	0.985	0.47
1434855_at	Amdhd2	amidohydrolase domain containing 2	-1.13	0.433	1.03	0.825	1.02	0.897	1.15	0.444	0.52
1421750_a_at	Vbp1	von Hippel-Lindau binding protein 1	1.01	0.922	1.01	0.846	-1.09	0.221	1.3	0.114	0.56
1438574_at	Gpr152	G protein-coupled receptor 152	-1.95	0.247	1.33	0.577	1.09	0.797	2.1	0.104	0.64
1420871_at	Gucy1b3	guanylate cyclase 1, soluble, beta 3	1.16	0.359	1.16	0.299	-1.61	0.117	1.47	0.4	0.54
1422653_at	Cep70	centrosomal protein 70	-1.29	0.112	1.09	0.757	1.07	0.734	2.67	0.158	0.88
1454479_at	---	---	1.08	0.917	1.1	0.874	-1.33	0.282	1.11	0.839	0.49
1425180_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	-1.65	0.156	1.31	0.679	1.02	0.921	1.4	0.527	0.52
1420591_at	Gpr84	G protein-coupled receptor 84	-3.01	0.277	1.42	0.604	1.18	0.666	1.5	0.403	0.27
1459913_at	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	-1.23	0.383	1.1	0.756	1.02	0.939	1.3	0.383	0.55
1443986_at	Cdc73	Vcell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S	-1.41	0.285	1.12	0.503	1.11	0.546	1.12	0.164	0.48
1417945_at	Pou5f1	POU domain, class 5, transcription factor 1	1.31	0.651	-1.76	0.06	1.06	0.861	1.29	0.279	0.48
1438913_x_at	Hdgfrp2	hepatoma-derived growth factor, related protein 2	-1.31	0.308	1.16	0.559	1.01	0.937	1.02	0.935	0.47
1434012_at	Ints5	integrator complex subunit 5	1.04	0.864	-1.16	0.07	1.04	0.817	1.27	0.255	0.55
1428875_at	Golph4	golgi phosphoprotein 4	1.07	0.386	1.12	0.196	-1.34	0.111	2.08	0.163	0.73
1417204_at	Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.07	0.174	1.08	0.465	-1.27	0.136	1.21	0.233	0.52
1445210_at	---	Transcribed locus	1.21	0.763	1.06	0.894	-1.49	0.047	1.23	0.464	0.5
1441943_x_at	Ciapin1	Cytokine induced apoptosis inhibitor 1	-1.87	0.049	1.12	0.711	1.28	0.113	1.22	0.465	0.44
1454717_at	Ankrd27	Ankyrin repeat domain 27 (VPS9 domain)	-1.16	0.252	1.07	0.551	1	0.985	1.1	0.459	0.51
1426018_a_at	Sox6	SRY-box containing gene 6	1.01	0.905	-1.09	0.785	1.01	0.977	5.63	0.243	1.64
1454591_at	Mast4	microtubule associated serine/threonine kinase family member 4	1.3	0.483	1.07	0.866	-1.77	0.104	1.08	0.873	0.42
1430598_at	Crem	cAMP responsive element modulator	1.27	0.567	1.09	0.74	-1.75	0.147	1.12	0.721	0.44
1431719_a_at	Srgap1	SLIT-ROBO Rho GTPase activating protein 1	-1.41	0.134	1.2	0.533	1.03	0.924	1.09	0.732	0.48
1435991_at	Nr3c2	nuclear receptor subfamily 3, group C, member 2	-1.28	0.083	1.01	0.97	1.15	0.409	1.66	0.035	0.63
1442163_at	Hace1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	1.14	0.438	1.04	0.831	-1.31	0.129	2.24	0.227	0.78
1460563_at	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	-1.18	0.429	1.08	0.588	1.02	0.842	1.02	0.732	0.48
1438151_x_at	Zdhhc14	zinc finger, DHHC domain containing 14	-1.49	0.054	1.24	0.217	1.03	0.844	1.34	0.289	0.53
1456607_at	Vcpip1	valosin containing protein (p97)/p47 complex interacting protein 1	1.13	0.449	1.02	0.491	-1.26	0.24	1.22	0.153	0.53
1423877_at	Chaf1b	chromatin assembly factor 1, subunit B (p60)	1.03	0.836	-1.43	0.394	1.21	0.5	2.47	0.159	0.82
1437378_x_at	Scarb1	scavenger receptor class B, member 1	-1.08	0.269	1	0.984	1.01	0.936	1.15	0.079	0.52
1428415_at	Rnf113a2	ring finger protein 113A2	1.05	0.807	-1.14	0.415	1.02	0.906	1.06	0.541	0.5
1418230_a_at	Lims1	LIM and senescent cell antigen-like domains 1	1.06	0.58	1.16	0.205	-1.38	0.04	1.22	0.025	0.51
1429101_at	Gja5	gap junction membrane channel protein alpha 5	-1.28	0.095	1.11	0.868	1.05	0.57	1.47	0.516	0.59
1440299_at	E330016A19Rik	RIKEN cDNA E330016A19 gene	-1.25	0.164	1.09	0.189	1.05	0.733	1.35	0.332	0.56
1420203_at	---	---	-2.67	0.434	1.18	0.685	1.39	0.416	1.12	0.876	0.25
1435869_s_at	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	1.01	0.941	1.03	0.775	-1.11	0.356	1.52	0.198	0.61
1428586_at	Tmem41b	transmembrane protein 41B	-1.33	0.496	1.13	0.594	1.06	0.793	1.1	0.757	0.49
1423457_at	Slc35a5	solute carrier family 35, member A5	-1.2	0.502	1.02	0.87	1.09	0.663	1.08	0.343	0.5
1417861_at	Ccnc	cyclin C	1.03	0.757	1.15	0.503	-1.29	0.122	1.04	0.634	0.48
1451453_at	Dapk2	death-associated kinase 2	1.11	0.503	1.02	0.918	-1.23	0.175	3.01	0.124	0.98
1420630_at	8430419L09Rik	RIKEN cDNA 8430419L09 gene	-1.2	0.249	1.09	0.612	1.02	0.838	2.95	0.092	0.97
1431937_at	Kif24	kinesin family member 24	1.07	0.937	1.13	0.503	-1.34	0.346	1.17	0.812	0.51
1440253_at	---	---	1.07	0.419	-1.19	0.202	1.03	0.672	1.09	0.197	0.5
1443946_s_at	---	---	1.11	0.903	-1.31	0.615	1.07	0.592	1.43	0.602	0.57
1426583_at	Atf2	activating transcription factor 2	1	0.998	-1.12	0.097	1.05	0.245	1.12	0.4	0.51
1433971_at	Camta1	calmodulin binding transcription activator 1	1	0.995	1.04	0.947	-1.1	0.578	1.88	0.145	0.7
1447940_a_at	Braf	Braf transforming gene	-1.19	0.599	1.04	0.911	1.07	0.838	1.12	0.647	0.51
1455484_at	2600009P04Rik	RIKEN cDNA 2600009P04 gene	1.07	0.748	-1.54	0.473	1.23	0.766	1.47	0.246	0.56
1426191_a_at	Bcl2l1	Bcl2-like 1	1.37	0.724	-1.83	0.48	1.03	0.94	3.39	0.245	0.99
1453135_at	Fndc5	fibronectin type III domain containing 5	1.03	0.943	1.04	0.763	-1.14	0.743	1.33	0.636	0.56
1427084_a_at	Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	1.02	0.916	1.03	0.873	-1.11	0.521	2.72	0.206	0.91

1419437_at	Sim2	single-minded homolog 2 (Drosophila)	1.13	0.64	-2.36	0.334	1.39	0.31	1.52	0.041	0.42
1437748_at	Fut11	fucosyltransferase 11	1.1	0.319	1	0.99	-1.18	0.295	1.06	0.312	0.5
1432539_a_at	Nup54	nucleoporin 54	1.13	0.874	-1.94	0.439	1.31	0.664	1.11	0.865	0.4
1417913_at	Gins4	GINS complex subunit 4 (Sld5 homolog)	1	0.997	-1.16	0.335	1.09	0.498	1.76	0.137	0.67
1436875_at	Dnm3	dynamin 3	1.21	0.441	1.11	0.893	-1.58	0.042	1.38	0.248	0.53
1423192_at	Pspc1	paraspeckle protein 1	-1.32	0.076	1.02	0.921	1.17	0.24	1.13	0.345	0.5
1421464_at	Bapx1	bagpipe homeobox gene 1 homolog (Drosophila)	1.04	0.646	1.29	0.71	-1.6	0.56	1.32	0.713	0.51
1418331_at	1110031I02Rik	RIKEN cDNA 1110031I02 gene	1.03	0.623	-1.24	0.168	1.11	0.272	1.31	0.223	0.55
1419102_at	Sin3a	transcriptional regulator, SIN3A (yeast)	1.01	0.925	-1.06	0.61	1	0.982	1	0.99	0.49
1429920_at	4933403M22Rik	RIKEN cDNA 4933403M22 gene	1.03	0.925	1.01	0.947	-1.11	0.831	1.61	0.322	0.64
1425514_at	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	1.19	0.645	-1.39	0.126	1.05	0.883	1.13	0.609	0.49
1452481_at	Plcb2	phospholipase C, beta 2	-1.68	0.617	1.14	0.765	1.22	0.466	1.04	0.737	0.43
1460639_a_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	-1.08	0.74	1.01	0.882	1.02	0.935	1.17	0.604	0.53
1435669_at	Zfp532	zinc finger protein 532	1.04	0.739	1.02	0.825	-1.12	0.6	1.22	0.201	0.54
1452298_a_at	Myo5b	myosin Vb	1.06	0.349	1.14	0.055	-1.33	0.204	1.53	0.092	0.6
1419234_at	Helb	helicase (DNA) B	-1.46	0.111	1.18	0.497	1.09	0.763	1.43	0.449	0.56
1456885_at	---	Transcribed locus	1.12	0.669	-1.44	0.363	1.13	0.516	2.12	0.004	0.73
1441572_at	C030036D22Rik	RIKEN cDNA C030036D22 gene	-1.33	0.329	1.14	0.776	1.06	0.721	1.16	0.836	0.51
1421061_at	Guca1a	guanylate cyclase activator 1a (retina)	1.06	0.875	1.19	0.597	-1.43	0.073	1.69	0.242	0.63
1417013_at	Hspb8	heat shock protein 8	1.06	0.827	1.04	0.79	-1.17	0.391	1.05	0.48	0.49
1426651_at	Mrpl44	mitochondrial ribosomal protein L44	-1.09	0.435	1.01	0.814	1.03	0.689	1.09	0.057	0.51
1433358_at	A230102O21Rik	RIKEN cDNA A230102O21 gene	-1.8	0.298	1.31	0.477	1.09	0.557	1.08	0.846	0.42
1460225_at	Mrp63	mitochondrial ribosomal protein 63	1.04	0.951	1.07	0.776	-1.18	0.325	1.16	0.372	0.52
1453854_at	Ptar1 /// LOC67629	protein prenyltransferase alpha subunit repeat containing 1 /// similar to protein pr	1.22	0.174	-1.5	0.168	1.07	0.791	1.79	0.336	0.64
1425833_a_at	Hpca	hippocalcin	1.33	0.255	1.04	0.921	-1.74	0.052	1.09	0.881	0.43
1433539_at	Commd3	COMM domain containing 3	1	0.989	1	0.966	-1.05	0.575	1.12	0.242	0.52
1431068_at	Rmnd5a	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	1.05	0.842	-1.71	0.428	1.32	0.265	1.31	0.098	0.49
1455813_at	MGC91194	similar to oogenesin	1.11	0.586	-1.19	0.711	1	0.977	2.8	0.012	0.93
1440813_s_at	Plxnb3	plexin B3	-2.37	0.118	1.23	0.667	1.3	0.46	1.41	0.315	0.39
1432447_a_at	2310005N01Rik	RIKEN cDNA 2310005N01 gene	1.09	0.393	-1.3	0.501	1.09	0.543	1.19	0.537	0.52
1421580_at	Cntnap1	contactin associated protein 1	1.29	0.729	1.08	0.655	-1.72	0.162	2.87	0.112	0.88
1422558_at	Gamt	guanidinoacetate methyltransferase	1.01	0.974	-1.11	0.63	1.04	0.767	1.25	0.344	0.55
1458328_x_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	1.23	0.357	1.43	0.198	-3.4	0.17	2.7	0.155	0.49
AFFX-18SRNAMur/2	---	---	1.39	0.817	1.28	0.833	-3.53	0.495	2.85	0.451	0.5
1458959_at	Aff4	AF4/FMR2 family, member 4	1.1	0.725	-1.38	0.535	1.13	0.668	1.02	0.974	0.47
1415848_at	Csh1	chorionic somatomammotropin hormone 1	-1.35	0.23	1.19	0.684	1.03	0.956	1.24	0.676	0.53
1424205_at	Smarca5 /// 923011	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.01	0.881	1.09	0.593	-1.18	0.467	1.61	0.167	0.64
1453649_at	C030039L03Rik	RIKEN cDNA C030039L03 gene	1.05	0.788	1.12	0.85	-1.27	0.302	1	0.996	0.47
1454845_x_at	Mchr1	melanin-concentrating hormone receptor 1	-1.68	0.44	1.08	0.821	1.29	0.19	1.37	0.396	0.51
1443816_s_at	BB220380	expressed sequence BB220380	-1.24	0.472	1.11	0.324	1.04	0.746	1.5	0.126	0.6
1426726_at	Ppp1r10	protein phosphatase 1, regulatory subunit 10	1.05	0.764	-1.22	0.587	1.09	0.348	1.27	0.071	0.55
1449048_s_at	Rab4a	RAB4A, member RAS oncogene family	-1.14	0.108	1.04	0.698	1.04	0.736	1.88	0.251	0.71
1434908_at	AI480556	expressed sequence AI480556	1.01	0.972	-1.15	0.117	1.08	0.637	1.22	0.275	0.54
AFFX-r2-Ec-bioB-M_	---	---	1.21	0.063	1.09	0.368	-1.52	0.09	1.03	0.91	0.45
1451131_at	Arl6ip1	ADP-ribosylation factor-like 6 interacting protein 1	1	0.985	-1.17	0.497	1.1	0.708	1.07	0.791	0.5
1456859_at	Lnp	limb and neural patterns	1.1	0.851	1.01	0.97	-1.17	0.598	1.03	0.889	0.49
1452560_a_at	Nfya	nuclear transcription factor-Y alpha	1.03	0.788	1.02	0.887	-1.1	0.621	1.13	0.344	0.52
1432573_at	4930506C02Rik	RIKEN cDNA 4930506C02 gene	-1.23	0.531	1	0.998	1.15	0.792	1.25	0.762	0.54
1455631_at	H13	histocompatibility 13	1.14	0.607	-1.58	0.156	1.19	0.464	1.19	0.027	0.48
1436955_at	Tssc1	tumor suppressing subtransferable candidate 1	1.09	0.699	1.02	0.883	-1.18	0.281	1.09	0.815	0.51
1438428_at	Jph1	Junctophilin 1	1.11	0.707	-1.38	0.455	1.13	0.04	1.28	0.208	0.53
1428247_at	Vps26b	vacuolar protein sorting 26 homolog B (yeast)	-1.19	0.226	1.02	0.871	1.1	0.668	1.23	0.139	0.54
1422254_a_at	Dyrk1b	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b	1.05	0.708	-1.12	0.576	1.02	0.95	1.48	0.426	0.61

1455467_at	C330043M08Rik	RIKEN cDNA C330043M08 gene	1.03	0.887	1.09	0.715	-1.2	0.126	1.72	0.006	0.66
1428275_at	Abhd13	abhydrolase domain containing 13	1.07	0.782	-1.32	0.019	1.13	0.409	1.01	0.968	0.47
1422715_s_at	Acp1 /// LOC63128	acid phosphatase 1, soluble /// similar to acid phosphatase 1, soluble /// similar to	1.1	0.627	1.07	0.661	-1.26	0.372	2.48	0.123	0.85
1421436_at	Grid2	glutamate receptor, ionotropic, delta 2	1.04	0.841	-1.49	0.323	1.25	0.399	1.02	0.931	0.45
1450282_at	Fgf4	fibroblast growth factor 4	-1.3	0.092	1.17	0.614	1.02	0.924	1.16	0.439	0.51
1450614_x_at	Ifna5	interferon alpha 5	-2.56	0.48	1.14	0.567	1.43	0.496	1.84	0.385	0.46
1433900_at	0610007L01Rik	RIKEN cDNA 0610007L01 gene	1.08	0.17	-1.22	0.096	1.06	0.026	1.29	0.028	0.55
1445632_at	Ogdh	oxoglutarate dehydrogenase (lipoamide)	1.07	0.854	1.01	0.991	-1.13	0.622	1.07	0.587	0.51
1440352_at	LOC625175	region containing RIKEN cDNA 1700028E10 gene; hypothetical protein A630054	1.02	0.952	1.26	0.671	-1.47	0.532	1.27	0.571	0.52
1457034_at	D14Abb1e	DNA segment, Chr 14, Abbott 1 expressed	1.09	0.794	1.17	0.141	-1.42	0.042	1.02	0.951	0.46
1419796_at	---	---	1.18	0.26	-1.45	0.385	1.09	0.384	2.19	0.319	0.75
1436471_at	Rab36	RAB36, member RAS oncogene family	-1.27	0.236	1.09	0.679	1.09	0.159	1.48	0.104	0.6
1418862_at	Echdc3	enoyl Coenzyme A hydratase domain containing 3	-1.22	0.297	1.01	0.956	1.14	0.041	1.15	0.103	0.52
1435814_at	Xpo7	exportin 7	1.07	0.842	1.06	0.764	-1.2	0.583	5.18	0.182	1.53
1420539_a_at	Chrdl2	chordin-like 2	-1.34	0.029	1.07	0.881	1.14	0.492	1.19	0.424	0.52
1446453_at	---	---	1.05	0.85	1.34	0.442	-1.74	0.04	1.05	0.819	0.42
1436572_at	Ccdc45	coiled-coil domain containing 45	1.02	0.708	1.25	0.457	-1.43	0.077	1.13	0.437	0.49
1419270_a_at	Dut	deoxyuridine triphosphatase	-1.12	0.664	1	0.98	1.07	0.783	2.35	0.235	0.83
1422494_s_at	Ccrk	cell cycle related kinase	-1.7	0.105	1.26	0.344	1.11	0.665	1.3	0.687	0.49
1448165_at	Casp2	caspase 2	1.01	0.95	1	0.99	-1.04	0.807	1.24	0.177	0.55
1417606_a_at	Calr	calreticulin	1.03	0.759	1.01	0.919	-1.08	0.383	1.14	0.403	0.53
1443763_at	Brca1	Breast cancer 1	1.08	0.779	1.02	0.969	-1.16	0.736	3.73	0.236	1.17
1452007_at	Sybl1	synaptobrevin like 1	-1.21	0.347	1.01	0.936	1.13	0.296	1.21	0.064	0.53
1453443_at	1110015O18Rik	RIKEN cDNA 1110015O18 gene	-3.35	0.049	1.56	0.315	1.11	0.848	1.54	0.008	0.21
1455306_at	BC037112	cDNA sequence BC037112	-1.21	0.095	1.01	0.913	1.13	0.545	1.12	0.444	0.51
1419275_at	Dazap1	DAZ associated protein 1	1.01	0.767	-1.12	0.258	1.06	0.79	1.21	0.472	0.54
1449653_at	---	Transcribed locus	-1.54	0.344	1.2	0.537	1.12	0.545	1.24	0.345	0.5
1443173_at	Ptn	pleiotrophin	1.14	0.319	1.13	0.683	-1.44	0.104	1.27	0.009	0.53
1460262_a_at	1700037H04Rik	RIKEN cDNA 1700037H04 gene	-1.05	0.803	1.01	0.912	1	0.985	2.41	0.191	0.84
1438162_x_at	LOC231885 /// LOC	hypothetical LOC231885 /// hypothetical protein LOC670882	1.06	0.954	-1.35	0.616	1.17	0.713	1.02	0.958	0.47
1433818_at	Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	1.08	0.475	-1.28	0.212	1.11	0.129	1.39	0.243	0.57
1416458_at	Arf2	ADP-ribosylation factor 2	1.03	0.61	1.13	0.157	-1.25	0.037	1.36	0.266	0.57
1429175_at	2810417M05Rik	RIKEN cDNA 2810417M05 gene	1.05	0.552	1.44	0.297	-2.09	0.013	2.29	0.104	0.67
1459280_at	D1Ertd185e	DNA segment, Chr 1, ERATO Doi 185, expressed	-1.72	0.199	1.17	0.222	1.22	0.273	1.34	0.44	0.5
1446175_at	1700095A21Rik	RIKEN cDNA 1700095A21 gene	-1.25	0.274	1.17	0.716	1	0.991	1.13	0.723	0.51
1453021_at	Stxbp5	syntaxin binding protein 5 (tomosyn)	-1.21	0.388	1.09	0.46	1.06	0.631	1.64	0.224	0.64
1452950_at	Mett5d1	methyltransferase 5 domain containing 1	-1.37	0.013	1.12	0.566	1.12	0.547	1.39	0.165	0.56
1460040_at	4933407H18Rik	RIKEN cDNA 4933407H18 gene	1	0.999	1.07	0.917	-1.11	0.741	1.63	0.401	0.65
1424718_at	Mapt	microtubule-associated protein tau	-1.18	0.195	1.05	0.916	1.07	0.782	2	0.063	0.74
1429837_at	1700016D18Rik	RIKEN cDNA 1700016D18 gene	-1.52	0.206	1.19	0.259	1.12	0.511	1.14	0.444	0.48
1445813_at	Wdr27	WD repeat domain 27	1.2	0.802	-1.69	0.206	1.18	0.48	1.13	0.719	0.45
1422833_at	Foxa2	forkhead box A2	1.25	0.435	-1.43	0.174	1.02	0.854	1.24	0.704	0.52
1424244_at	Rwdd4a	RWD domain containing 4A	1.04	0.632	-1.21	0.074	1.1	0.708	1.14	0.434	0.52
1420649_at	Atbf1	AT motif binding factor 1	1.05	0.821	-1.2	0.132	1.08	0.67	1.12	0.404	0.51
1420722_at	Elovl3	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 3	1.08	0.879	-3.05	0.031	1.56	0.487	1.15	0.307	0.19
1440656_at	Hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	1.15	0.579	1.02	0.953	-1.25	0.413	1.66	0.347	0.65
1436574_at	1700029I01Rik /// L	RIKEN cDNA 1700029I01 gene /// similar to zinc finger protein 665 /// similar to zi	-1.47	0.062	1.27	0.059	1.02	0.771	1.1	0.477	0.48
1447345_at	A430107O13Rik	RIKEN cDNA A430107O13 gene	1.47	0.66	1.02	0.901	-2.11	0.017	1.02	0.961	0.35
1427822_a_at	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2	-1.2	0.737	1.04	0.866	1.1	0.795	1.16	0.546	0.53
1425638_at	Centa2	centaurin, alpha 2	1.21	0.177	1.01	0.973	-1.33	0.176	1.2	0.74	0.52
1459894_at	Iqgap2	IQ motif containing GTPase activating protein 2	1.07	0.876	-1.22	0.301	1.08	0.824	1.14	0.532	0.52
1435312_at	Paqr7	Progestin and adipoQ receptor family member VII	1.09	0.846	-1.78	0.007	1.32	0.243	1.1	0.742	0.43
1449170_at	Piwil2	piwi-like homolog 2 (Drosophila)	-2.82	0.394	1.26	0.551	1.35	0.631	1.18	0.808	0.24

1422753_a_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	-1.33	0.228	1.05	0.599	1.17	0.613	1.27	0.576	0.54
1419403_at	BC017612	cDNA sequence BC017612	1.03	0.894	-1.07	0.674	1	0.99	1.19	0.498	0.54
1429917_at	9030625N01Rik	RIKEN cDNA 9030625N01 gene	-1.91	0.234	1.28	0.623	1.16	0.474	1.57	0.567	0.53
1456695_x_at	Anapc5	anaphase-promoting complex subunit 5	1	0.957	1.02	0.792	-1.05	0.697	1.23	0.085	0.55
1425448_x_at	Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	-1.27	0.286	1.05	0.491	1.13	0.587	1.03	0.354	0.49
1448743_at	Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	1.05	0.594	1.11	0.485	-1.24	0.106	4.92	0.201	1.46
1438759_x_at	---	---	1	0.99	-1.12	0.555	1.08	0.45	1.19	0.204	0.54
1417463_a_at	2400001E08Rik ///	RIKEN cDNA 2400001E08 gene /// hypothetical LOC433216	-1.14	0.447	1.07	0.199	1.03	0.746	1	0.99	0.49
1422787_at	Fkbpl	FK506 binding protein-like	1.12	0.416	-1.42	0.101	1.14	0.044	1.02	0.937	0.47
1421583_at	Creb1	cAMP responsive element binding protein 1	1.13	0.469	1	0.995	-1.19	0.665	2.14	0.263	0.77
1431930_x_at	Crls1	cardiolipin synthase 1	1.05	0.614	1.11	0.368	-1.23	0.364	1	0.946	0.48
1421967_at	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	1.11	0.918	1.09	0.881	-1.29	0.176	1.1	0.888	0.5
1424193_at	Pwp2h	PWP2 (periodic tryptophan protein) homolog, yeast	1.01	0.796	1.09	0.429	-1.15	0.495	1.16	0.526	0.53
1427917_s_at	Ssbp3	single-stranded DNA binding protein 3	1.02	0.823	-1.12	0.509	1.06	0.653	2.31	0.202	0.82
1434223_at	1810007P19Rik	RIKEN cDNA 1810007P19 gene	1.08	0.476	-1.22	0.752	1.07	0.76	1.17	0.679	0.52
1422721_at	Tnk1	tyrosine kinase, non-receptor, 1	-1.08	0.027	1.02	0.958	1.02	0.638	6.4	0.301	1.84
1440244_at	Erg	avian erythroblastosis virus E-26 (v-ets) oncogene related	1.05	0.809	1.06	0.558	-1.17	0.448	1.15	0.353	0.53
1424231_s_at	Exoc6	exocyst complex component 6	-1.2	0.299	1.03	0.734	1.1	0.658	1.61	0.174	0.64
1424149_at	Nsmce2	non-SMC element 2 homolog (MMS21, S. cerevisiae)	1.08	0.545	1.01	0.937	-1.13	0.455	1.07	0.493	0.51
1416343_a_at	Lamp2	lysosomal membrane glycoprotein 2	-1.17	0.391	1.04	0.547	1.08	0.704	1.09	0.199	0.51
1445132_at	Rnpep	Arginyl aminopeptidase (aminopeptidase B)	1.01	0.974	1.18	0.593	-1.27	0.356	1.59	0.2	0.63
1428900_s_at	Mett5d1	methyltransferase 5 domain containing 1	-1.18	0.008	1.11	0.38	1.02	0.801	1.41	0.346	0.59
1436689_a_at	Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	1.04	0.404	-1.22	0.029	1.11	0.266	1.13	0.387	0.52
1421761_a_at	Barx2	BarH-like homeobox 2	-1.07	0.547	1.01	0.947	1.03	0.873	1.04	0.83	0.5
1428311_at	Ccdc6	coiled-coil domain containing 6	-1.21	0.22	1.13	0.469	1.02	0.888	1.21	0.399	0.54
1452689_at	Zfp512	zinc finger protein 512	1.06	0.513	1.03	0.839	-1.13	0.324	1.11	0.169	0.52
1453525_at	9130413E14Rik	RIKEN cDNA 9130413E14 gene	1.05	0.84	1.19	0.662	-1.37	0.296	1.01	0.984	0.47
1447281_at	---	---	1.03	0.926	1.01	0.963	-1.07	0.705	2.23	0.002	0.8
1426683_at	Cnot6	CCR4-NOT transcription complex, subunit 6	1.02	0.534	1.13	0.453	-1.22	0.179	1.4	0.279	0.58
1460237_at	Trim8	tripartite motif protein 8	1.02	0.963	-1.14	0.463	1.07	0.626	1.13	0.613	0.52
1457705_at	5330421C15Rik	RIKEN cDNA 5330421C15 gene	1.21	0.693	1.28	0.527	-2.06	0.29	1.11	0.819	0.39
1439967_at	1700071A11Rik	RIKEN cDNA 1700071A11 gene	1.13	0.499	-1.68	0.069	1.25	0.065	1.81	0.275	0.63
1416862_at	Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	1	0.984	1.08	0.093	-1.12	0.335	1.57	0.346	0.63
1418195_at	Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.03	0.883	-1.09	0.678	1.03	0.889	1.26	0.39	0.56
1453533_at	4933403O08Rik	RIKEN cDNA 4933403O08 gene	-2.32	0.123	1.25	0.507	1.29	0.628	1.17	0.689	0.35
1423848_at	Mphosph6	M phase phosphoprotein 6	1.12	0.547	1	0.987	-1.17	0.367	1.8	0.01	0.69
1439867_at	Ubox5	U box domain containing 5	1.12	0.579	-1.45	0.438	1.17	0.419	1.25	0.613	0.52
1448972_at	Gria1	glutamate receptor, ionotropic, AMPA1 (alpha 1)	-2.31	0.402	1.32	0.548	1.22	0.201	1.04	0.961	0.32
1449070_x_at	Apcdd1	adenomatosis polyposis coli down-regulated 1	1.02	0.907	1.19	0.726	-1.31	0.305	1.05	0.785	0.49
1442645_at	Atp2b3	ATPase, Ca++ transporting, plasma membrane 3	-1.45	0.374	1.28	0.304	1.01	0.931	1.31	0.324	0.54
1438250_s_at	Taf9 /// LOC54560(	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor /// si	-1.26	0.12	1.09	0.578	1.09	0.478	1.06	0.707	0.5
1436777_at	---	---	1.05	0.724	1.2	0.779	-1.37	0.424	1.39	0.219	0.57
1431520_at	4933406J09Rik	RIKEN cDNA 4933406J09 gene	-1.2	0.009	1.13	0.792	1.02	0.923	1.19	0.471	0.53
1438173_x_at	Pmf1	Polyamine-modulated factor 1	1.1	0.804	-1.24	0.048	1.07	0.812	1.3	0.148	0.56
1422225_s_at	Tcp10a /// Tcp10b /	t-complex protein 10a /// t-complex protein 10b /// t-complex protein 10c	1.02	0.981	1.16	0.683	-1.25	0.35	1.07	0.704	0.5
1444383_at	1110014J01Rik	RIKEN cDNA 1110014J01 gene	1.16	0.681	-1.35	0.406	1.08	0.757	1.26	0.729	0.54
1439225_at	Lars2	leucyl-tRNA synthetase, mitochondrial	1.15	0.301	-2.24	0.105	1.38	0.49	1.04	0.931	0.33
1453082_at	2310022L06Rik	RIKEN cDNA 2310022L06 gene	-1.26	0.458	1.02	0.968	1.17	0.66	1.19	0.623	0.53
1435555_at	---	---	1.04	0.351	-1.14	0.543	1.06	0.793	1.07	0.291	0.51
1428413_at	5730405I09Rik	RIKEN cDNA 5730405I09 gene	1.02	0.921	1.2	0.265	-1.32	0.222	1.07	0.542	0.49
1435344_at	Tfdp2	transcription factor Dp 2	1.19	0.01	1.05	0.762	-1.34	0.197	4.34	0.123	1.31
1433917_x_at	D2Bwg1423e	DNA segment, Chr 2, Brigham & Women's Genetics 1423 expressed	-1.17	0.374	1.08	0.745	1.04	0.803	1.05	0.88	0.5
1431470_a_at	4933414I15Rik	RIKEN cDNA 4933414I15 gene	1.06	0.882	1.25	0.765	-1.5	0.175	1.04	0.918	0.46

1446328_at	---	Transcribed locus	1.15	0.613	-1.26	0.402	1.03	0.901	5.27	0.225	1.55
1453650_at	4930413F20Rik	RIKEN cDNA 4930413F20 gene	-1.56	0.247	1.01	0.944	1.32	0.299	1.15	0.588	0.48
1438550_x_at	Srr	serine racemase	1.11	0.417	-1.16	0.446	1.01	0.984	1.35	0.481	0.58
1421802_at	Ear1	eosinophil-associated, ribonuclease A family, member 1	1.13	0.889	1.21	0.776	-1.55	0.125	32.39	0.272	8.29
1428699_at	Sms	spermine synthase	1.02	0.919	1.1	0.739	-1.16	0.477	1.03	0.887	0.5
1435102_a_at	Stx18	syntaxin 18	-1.44	0.028	1.07	0.516	1.22	0.379	1.12	0.586	0.49
1426541_a_at	Endod1	endonuclease domain containing 1	1.19	0.783	1.05	0.907	-1.35	0.614	3.37	0.215	1.07
1449481_at	Slc25a13	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), m	1.18	0.338	-1.27	0.144	1.02	0.96	1.95	0.198	0.72
1427205_x_at	Ccdc46	coiled-coil domain containing 46	-1.16	0.425	1.11	0.665	1.01	0.945	1.02	0.939	0.49
1450866_a_at	Mrpl17	mitochondrial ribosomal protein L17	1.01	0.916	-1.12	0.032	1.08	0.599	1.03	0.929	0.5
1450350_a_at	Jundm2	Jun dimerization protein 2	1.09	0.441	1.09	0.767	-1.24	0.083	1.03	0.779	0.49
1451753_at	Plxna2	plexin A2	1.08	0.113	1.01	0.989	-1.11	0.22	1.04	0.908	0.5
1435701_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	1.02	0.945	1.06	0.68	-1.11	0.613	1.14	0.506	0.53
1418104_at	Nrip3	nuclear receptor interacting protein 3	1.01	0.953	-1.29	0.519	1.19	0.449	3.26	0.333	1.04
1417331_a_at	Arl6	ADP-ribosylation factor-like 6	1.01	0.925	1.02	0.86	-1.05	0.691	1.17	0.469	0.54
1452442_at	Usp13	Ubiquitin specific peptidase 13 (isopeptidase T-3)	1.32	0.719	-1.53	0.394	1.01	0.981	1	0.986	0.45
1417437_at	Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6	-1.18	0.188	1.02	0.816	1.11	0.418	1.23	0.41	0.55
1436793_at	St18	suppression of tumorigenicity 18	1.06	0.944	1.14	0.845	-1.27	0.494	1.41	0.49	0.58
1439849_at	---	Mus musculus, clone IMAGE:4222153, mRNA	-1.34	0.001	1.16	0.54	1.08	0.595	1.07	0.645	0.49
1416664_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	-1.62	0.093	1.12	0.805	1.25	0.193	3.09	0.223	0.96
1439342_at	Clpx	Caseinolytic peptidase X (E.coli)	1.11	0.66	1.37	0.511	-1.95	0.026	1.05	0.659	0.39
1425398_at	Hist1h2bc /// LOC6	histone 1, H2bc /// similar to Histone H2B F (H2B 291A) /// similar to Histone H2B	-1.81	0.336	1.15	0.771	1.28	0.567	1.86	0.512	0.62
1419746_at	Arhgap23	Rho GTPase activating protein 23	1.05	0.33	-1.25	0.368	1.13	0.632	1.4	0.371	0.58
1433807_at	6720463M24Rik	RIKEN cDNA 6720463M24 gene	-1.12	0.824	1.01	0.967	1.08	0.638	2.09	0.304	0.76
1423207_at	---	---	1.01	0.956	1.04	0.751	-1.06	0.533	1.02	0.907	0.5
1433579_at	Tmem30b	transmembrane protein 30B	1.03	0.756	-1.12	0.19	1.06	0.741	2.27	0.373	0.81
1421540_at	Tcam1	testicular cell adhesion molecule 1	1	0.995	1.26	0.621	-1.39	0.273	1.3	0.554	0.54
1426743_at	Dip3b	Dip3 beta	-1.22	0.095	1.09	0.563	1.07	0.624	1.01	0.981	0.49
1423900_at	Trip12	thyroid hormone receptor interactor 12	-1.11	0.583	1.07	0.547	1.02	0.893	1.22	0.374	0.55
1426054_at	Npy1r	neuropeptide Y receptor Y1	-1.81	0.168	1.08	0.785	1.36	0.457	1.1	0.353	0.43
1421158_at	Cgnl1	cingulin-like 1	1.06	0.91	-1.25	0.572	1.12	0.847	1.83	0.067	0.69
1452983_at	Cep57	centrosomal protein 57	1.03	0.849	-1.07	0.828	1.02	0.951	1.59	0.127	0.64
1436984_at	Abi2	abl-interactor 2	1.1	0.158	1.14	0.034	-1.35	0.001	1.15	0.151	0.51
1443463_at	Wnt5b	Wingless-related MMTV integration site 5B	1.12	0.81	1.25	0.674	-1.63	0.163	1.12	0.774	0.47
1417628_at	Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	1.05	0.804	1.05	0.669	-1.13	0.401	1	0.98	0.49
1422685_at	Exoc4	exocyst complex component 4	1	0.987	1.13	0.485	-1.17	0.259	1.11	0.391	0.52
1424389_at	Nupl1	nucleoporin like 1	1.03	0.865	-1.35	0.363	1.21	0.338	1.21	0.488	0.53
1423047_at	Tollip	toll interacting protein	-1.19	0.215	1.03	0.783	1.12	0.4	1.27	0.359	0.56
1437693_at	D1Pas1	DNA segment, Chr 1, Pasteur Institute 1	1.02	0.903	1.11	0.827	-1.17	0.82	2.35	0.024	0.83
1435601_at	AI481772	expressed sequence AI481772	1.03	0.667	1.11	0.766	-1.19	0.558	1.57	0.363	0.63
1454084_a_at	Senp8	SUMO/sentrin specific peptidase 8	-1.11	0.448	1.08	0.378	1.01	0.916	1.01	0.936	0.5
1458158_at	Wdr67	WD repeat domain 67	-1.09	0.761	1.03	0.929	1.04	0.899	1.76	0.115	0.68
1420244_at	---	---	-1.83	0.567	1.42	0.531	1.02	0.929	1.68	0.38	0.57
1426349_s_at	Tmpo	thymopoietin	1	0.995	1.02	0.813	-1.04	0.693	1.91	0.149	0.72
1455478_at	Ppfia1	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	1.09	0.497	-1.12	0.034	1.01	0.906	1.05	0.823	0.51
1435148_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	1.06	0.547	-1.2	0.184	1.1	0.896	4.58	0.226	1.38
1416020_a_at	Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), i	1.01	0.963	-1.18	0.114	1.13	0.395	1.44	0.14	0.6
1457306_at	---	Transcribed locus	1.13	0.57	-1.17	0.408	1	0.978	5.75	0.218	1.68
1436388_a_at	3830406C13Rik	RIKEN cDNA 3830406C13 gene	1.06	0.818	1.08	0.193	-1.17	0.159	1.05	0.745	0.5
1422167_at	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmeml	1.14	0.713	1.05	0.827	-1.25	0.257	1.33	0.482	0.57
1430982_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	-1.16	0.475	1.08	0.578	1.05	0.802	1.26	0.025	0.56
1436451_a_at	Tmed2	transmembrane emp24 domain trafficking protein 2	1.06	0.587	1.15	0.023	-1.28	0.116	1.31	0.112	0.56
1456265_at	LOC624866	hypothetical protein LOC624866	1.03	0.878	-1.13	0.8	1.07	0.369	1.49	0.299	0.62

1418023_at	Narg1	NMDA receptor-regulated gene 1	1.13	0.539	-1.17	0.26	1	1	1.37	0.33	0.58
1440499_at	D9Ertd26e	DNA segment, Chr 9, ERATO Doi 26, expressed	1.24	0.45	1.25	0.693	-1.98	0.297	1.09	0.521	0.4
1459479_at	---	PREDICTED: Mus musculus similar to Uridine 5-monophosphate synthase (UMP	-1.51	0.711	1.19	0.756	1.14	0.714	1.68	0.414	0.62
1433644_at	Pomt2	protein-O-mannosyltransferase 2	-1.24	0.39	1.13	0.192	1.05	0.525	1.06	0.845	0.5
1438015_at	BC068171	cDNA sequence BC068171	1	0.995	-1.17	0.234	1.14	0.531	1.62	0.144	0.65
1439269_x_at	Mcm7 /// LOC4330	minichromosome maintenance deficient 7 (S. cerevisiae) /// similar to minichromo	-1.31	0.265	1.18	0.199	1.05	0.854	1.77	0.181	0.67
1421948_a_at	2610507L03Rik	RIKEN cDNA 2610507L03 gene	1.03	0.844	-1.21	0.423	1.14	0.451	1.24	0.602	0.55
1449915_at	Zfp202	zinc finger protein 202	-1.24	0.442	1.16	0.31	1.03	0.584	1.22	0.374	0.54
1417162_at	Tmbim1	transmembrane BAX inhibitor motif containing 1	1.07	0.519	1.04	0.615	-1.13	0.502	1.13	0.531	0.53
1456443_at	4930404N11Rik	RIKEN cDNA 4930404N11 gene	-1.35	0.476	1.02	0.979	1.23	0.295	3.38	0.021	1.07
1423621_a_at	Slc33a1	solute carrier family 33 (acetyl-CoA transporter), member 1	-1.17	0.278	1.03	0.771	1.1	0.345	1.06	0.779	0.51
1435241_at	D930036F22Rik	RIKEN cDNA D930036F22 gene	-1.24	0.239	1.11	0.349	1.07	0.469	1.38	0.261	0.58
1446731_at	A730016A17	hypothetical protein A730016A17	1.32	0.509	1.05	0.808	-1.63	0.083	1.04	0.84	0.45
1436620_at	Ccdc45	coiled-coil domain containing 45	1.02	0.968	-1.3	0.416	1.2	0.141	1.1	0.761	0.51
1450255_at	Cdgap	Cdc42 GTPase-activating protein	1.09	0.022	-1.13	0.759	1.01	0.952	1.49	0.342	0.62
1435346_at	Ccdc82	coiled-coil domain containing 82	1.06	0.371	1.14	0.364	-1.25	0.033	1.01	0.962	0.49
1455349_at	Rap1b	RAS related protein 1b	1.14	0.345	1.03	0.72	-1.23	0.094	1.05	0.778	0.5
1433680_x_at	Siva	Cd27 binding protein (Hindu God of destruction)	1.1	0.645	-1.15	0.531	1.02	0.896	1.25	0.594	0.56
1449485_at	Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1	1.01	0.85	1.14	0.194	-1.18	0.416	1.13	0.249	0.52
1456454_at	Cart1	cartilage homeo protein 1	-1.64	0.213	1.13	0.617	1.25	0.642	1.01	0.976	0.44
1441867_x_at	4930534B04Rik	RIKEN cDNA 4930534B04 gene	-1.49	0.008	1.06	0.862	1.27	0.216	2.2	0.265	0.76
1426757_at	Ampd2	adenosine monophosphate deaminase 2 (isoform L)	1.06	0.792	-1.31	0.001	1.16	0.415	1.25	0.012	0.54
1431421_x_at	2610524G07Rik	RIKEN cDNA 2610524G07 gene	-1.3	0.014	1.03	0.772	1.19	0.477	1.09	0.454	0.5
1454565_at	C030046M01Rik	RIKEN cDNA C030046M01 gene	1.02	0.92	1.08	0.914	-1.12	0.774	1.52	0.335	0.63
1416659_at	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)	1.01	0.966	1.07	0.231	-1.09	0.269	1.14	0.171	0.53
1428783_at	Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	1.02	0.799	1.09	0.131	-1.13	0.312	1.36	0.243	0.59
1448873_at	Ocln	occludin	1.12	0.233	-1.23	0.065	1.06	0.751	1.8	0.197	0.69
1416087_at	Ap1s1	adaptor protein complex AP-1, sigma 1	1.05	0.902	1.05	0.663	-1.12	0.522	1.06	0.821	0.51
1423736_a_at	Dym	dymeclin	1.06	0.815	-1.3	0.209	1.17	0.079	1.85	0.107	0.69
1429170_a_at	Mtf1	metal response element binding transcription factor 1	-1.09	0.668	1	0.976	1.07	0.64	1.11	0.806	0.52
1415862_at	Tyrp1	tyrosinase-related protein 1	1.25	0.723	-1.5	0.41	1.08	0.541	1.73	0.336	0.64
1445539_at	---	PREDICTED: Mus musculus similar to 60S ribosomal protein L12 (LOC382344),	1.01	0.919	1.04	0.705	-1.06	0.742	1.07	0.872	0.52
1453063_at	Cltb	clathrin, light polypeptide (Lcb)	1	0.985	1.01	0.952	-1.01	0.938	1.04	0.812	0.51
1450927_at	Lztr1	leucine-zipper-like transcriptional regulator, 1	-1.17	0.23	1.02	0.732	1.12	0.241	1.2	0.341	0.54
1446771_at	Tuba8	Tubulin, alpha 8	1.04	0.636	1.01	0.956	-1.05	0.592	1.94	0.268	0.73
1428181_at	Etfb	electron transferring flavoprotein, beta polypeptide	1	0.991	-1.22	0.064	1.18	0.328	1.11	0.484	0.52
1422883_at	Usp8	ubiquitin specific peptidase 8	-1.03	0.847	1.02	0.843	1.01	0.977	1.12	0.461	0.53
1440338_at	E430028B21Rik	RIKEN cDNA E430028B21 gene	1.04	0.62	1.22	0.431	-1.34	0.176	1.13	0.637	0.51
1456621_at	D430015B01Rik	RIKEN cDNA D430015B01 gene	1.03	0.862	-1.8	0.194	1.41	0.443	1.85	0.058	0.62
1450420_at	Stag1	stromal antigen 1	1.03	0.877	1.01	0.949	-1.04	0.616	1.29	0.211	0.57
1442737_at	4.93E+23	Hypothetical protein 4933423E17	-1.61	0.201	1.06	0.88	1.31	0.537	1.15	0.281	0.48
1447264_at	Rab11fip1	RAB11 family interacting protein 1 (class I)	1.05	0.953	-1.43	0.542	1.25	0.243	1.08	0.901	0.49
1423500_a_at	Sox5	SRY-box containing gene 5	1.14	0.083	-1.33	0.247	1.1	0.799	1.83	0.146	0.69
1421144_at	Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1	1.06	0.816	1.09	0.56	-1.18	0.338	1.33	0.433	0.57
1443869_at	E430028B21Rik	RIKEN cDNA E430028B21 gene	1.02	0.921	-1.35	0.321	1.24	0.406	1.23	0.597	0.53
1450023_at	Gtpbp1	GTP binding protein 1	1.01	0.937	-1.02	0.836	1	0.999	1.38	0.234	0.6
1460221_at	Ptges3	prostaglandin E synthase 3 (cytosolic)	1.04	0.743	-1.09	0.596	1.04	0.778	1.42	0.105	0.6
1454227_at	Htatip2	HIV-1 tat interactive protein 2, homolog (human)	-2.06	0.075	1.27	0.465	1.24	0.488	1.34	0.366	0.45
1455452_x_at	AI449310	expressed sequence AI449310	1.29	0.203	1.17	0.429	-1.85	0.055	1.86	0.235	0.62
1428675_at	1110049F12Rik	RIKEN cDNA 1110049F12 gene	1.13	0.73	-1.27	0.145	1.08	0.393	1.88	0.134	0.71
1453953_at	9130015A21Rik	RIKEN cDNA 9130015A21 gene	-1.83	0.068	1.11	0.661	1.34	0.36	1.36	0.158	0.5
1416060_at	Tbc1d15	TBC1 domain family, member 15	1.01	0.925	1.06	0.629	-1.08	0.504	1.05	0.552	0.51
1453767_a_at	Nt5m	5',3'-nucleotidase, mitochondrial	1.02	0.873	-1.16	0.037	1.12	0.409	1.02	0.776	0.5

1455604_at	Fzd5	frizzled homolog 5 (Drosophila)	-1.09	0.664	1.04	0.919	1.04	0.885	1.74	0.247	0.68
1428590_at	Mrpl41	mitochondrial ribosomal protein L41	1.03	0.919	1.42	0.054	-1.84	0.119	1.01	0.98	0.41
1460223_a_at	Epb4.9	erythrocyte protein band 4.9	1.06	0.785	-1.42	0.396	1.23	0.153	9.64	0.181	2.63
1450686_at	Pon2	paraoxonase 2	1.11	0.592	1.16	0.263	-1.37	0.018	1.2	0.088	0.52
1437802_x_at	Morf4l1 /// LOC433	mortality factor 4 like 1 /// similar to mortality factor 4 like 1 isoform b /// similar to	1.01	0.909	1.02	0.874	-1.03	0.785	1.18	0.271	0.54
1438256_at	Eif5a2	eukaryotic translation initiation factor 5A2	1.1	0.517	1.07	0.922	-1.22	0.476	1.82	0.271	0.7
1416667_at	Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	1	0.98	-1.02	0.88	1.01	0.947	1.23	0.318	0.56
1420729_at	Tcstv1	2-cell-stage, variable group, member 1	1.21	0.12	-2.08	0.326	1.31	0.544	1.47	0.615	0.48
1429437_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	1.25	0.721	1.14	0.355	-1.65	0.219	1.21	0.32	0.49
1424836_a_at	Clasp2	CLIP associating protein 2	1.11	0.372	1.01	0.943	-1.14	0.419	1.21	0.121	0.55
1417831_at	Smc1a	structural maintenance of chromosomes 1A	1.05	0.788	-1.11	0.572	1.05	0.815	1.37	0.315	0.59
1434425_at	Tchh	trichohyalin	-1.43	0.461	1.02	0.948	1.28	0.271	1.07	0.931	0.49
1447070_at	Wbscr1	Williams-Beuren syndrome chromosome region 1 homolog (human)	-1.22	0.485	1.13	0.819	1.05	0.809	1.17	0.41	0.53
1442807_at	---	---	-1.52	0.018	1.31	0.649	1.03	0.921	1.23	0.241	0.51
1442208_at	Scn8a	Sodium channel, voltage-gated, type VIII, alpha	1.08	0.524	1.37	0.241	-1.8	0.236	1.01	0.974	0.41
1423154_at	BC005537	cDNA sequence BC005537	1.1	0.147	-1.14	0.274	1.02	0.828	1.29	0.389	0.57
1440495_at	Dmt2	dorso-medial telencephalon gene 2	1.02	0.975	1.21	0.744	-1.3	0.494	2.08	0.043	0.75
1419645_at	Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	-1.09	0.088	1.02	0.698	1.06	0.644	1.06	0.565	0.51
1416954_at	Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member	1.01	0.915	1.01	0.976	-1.02	0.757	1.25	0.429	0.56
1433580_at	Nup54	nucleoporin 54	-1.18	0.055	1.06	0.509	1.09	0.509	1.21	0.401	0.55
1425333_at	1810048P08Rik	RIKEN cDNA 1810048P08 gene	1.13	0.384	-1.19	0.287	1.04	0.803	1.58	0.174	0.64
1456802_at	Rnf133	ring finger protein 133	1.07	0.927	-1.14	0.822	1.06	0.893	1.19	0.741	0.54
1423436_at	Gsta3	glutathione S-transferase, alpha 3	1.05	0.715	-1.16	0.545	1.09	0.683	1.15	0.562	0.53
1460327_at	Gpr88	G-protein coupled receptor 88	1.04	0.857	-1.52	0.486	1.3	0.499	2.17	0.101	0.75
1422549_at	Arl2	ADP-ribosylation factor-like 2	1.05	0.864	-1.27	0.126	1.17	0.302	1.23	0.317	0.54
1435236_at	A630018P17Rik	RIKEN cDNA A630018P17 gene	1.01	0.793	1.07	0.687	-1.08	0.442	1.09	0.733	0.52
1434371_x_at	Usp7	ubiquitin specific peptidase 7	-1.17	0.224	1.06	0.433	1.09	0.395	1.84	0.23	0.7
1451825_a_at	Copz1	coatomer protein complex, subunit zeta 1	-1.09	0.543	1.04	0.672	1.05	0.638	1.37	0.229	0.59
1429182_at	5430400D12Rik	RIKEN cDNA 5430400D12 gene	-1.48	0.47	1.04	0.856	1.29	0.231	1.15	0.751	0.5
1436150_at	1700066J24Rik	RIKEN cDNA 1700066J24 gene	-1.06	0.29	1.05	0.686	1.01	0.952	1.17	0.587	0.54
1429960_at	4930438A08Rik	RIKEN cDNA 4930438A08 gene	-1.08	0.908	1.04	0.923	1.04	0.953	1.87	0.452	0.72
1417397_at	Slc9a1	solute carrier family 9 (sodium/hydrogen exchanger), member 1	-1.16	0.449	1.08	0.704	1.06	0.56	1.13	0.604	0.53
1440887_at	C330005M16Rik	RIKEN cDNA C330005M16 gene	-3.17	0.254	1.07	0.896	1.62	0.283	1.09	0.854	0.15
1424234_s_at	Meox2	mesenchyme homeobox 2	1.16	0.834	1.11	0.854	-1.37	0.125	1.1	0.851	0.5
1418506_a_at	Prdx2	peroxiredoxin 2	-1.14	0.475	1.03	0.622	1.09	0.396	2.5	0.09	0.87
1428843_at	5-Mar	membrane-associated ring finger (C3HC4) 5	-1.04	0.729	1.02	0.86	1.02	0.694	1.96	0.154	0.74
1419987_at	---	---	1.11	0.747	1.14	0.785	-1.31	0.261	1.51	0.499	0.61
1426469_a_at	Tbp	TATA box binding protein	1.06	0.423	-1.16	0.516	1.08	0.427	1.1	0.665	0.52
1452362_at	Trim16	tripartite motif protein 16	-1.15	0.241	1.11	0.75	1.02	0.921	1.1	0.72	0.52
1423402_at	Creb1	cAMP responsive element binding protein 1	-1.03	0.9	1.03	0.93	1.01	0.975	1.1	0.113	0.53
1422663_at	Orc1l	origin recognition complex, subunit 1-like (S.cereviaiae)	-1.02	0.954	1	0.999	1.02	0.941	5.16	0.228	1.54
1433954_at	4632419I22Rik	RIKEN cDNA 4632419I22 gene	1.1	0.244	-1.17	0.154	1.06	0.678	1.6	0.095	0.64
1436205_at	---	Transcribed locus	-1.27	0.445	1.17	0.648	1.05	0.865	1.07	0.548	0.5
1451857_a_at	5730593N15Rik	RIKEN cDNA 5730593N15 gene	1	0.985	-1.5	0.07	1.34	0.147	1.45	0.565	0.57
1456561_s_at	Klf17	Kruppel-like factor 17	-1.07	0.769	1.06	0.731	1.01	0.985	1.18	0.665	0.54
1439490_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	-1.2	0.13	1.1	0.466	1.08	0.534	1.47	0.123	0.61
1459484_at	Tmem2	Transmembrane protein 2	1.03	0.969	-1.19	0.634	1.14	0.704	1.63	0.209	0.65
1443542_at	---	---	-2.27	0.152	1.16	0.614	1.41	0.161	1.3	0.359	0.4
1455634_at	---	---	1.01	0.956	1.05	0.517	-1.06	0.593	1.05	0.587	0.51
1432919_at	4921511E18Rik	RIKEN cDNA 4921511E18 gene	-3.09	0.387	1.31	0.735	1.38	0.33	1.32	0.528	0.23
1452365_at	4732435N03Rik	RIKEN cDNA 4732435N03 gene	-1.53	0.486	1.03	0.953	1.32	0.046	1.27	0.22	0.52
1416441_at	Pgcp	plasma glutamate carboxypeptidase	1.12	0.461	1.04	0.707	-1.18	0.127	1.27	0.586	0.56
1423138_at	Wdr4	WD repeat domain 4	1.05	0.531	-1.37	0.05	1.23	0.267	1.06	0.713	0.49

1429557_at	Mcm8	minichromosome maintenance deficient 8 (S. cerevisiae)	1.05	0.741	-1.39	0.22	1.24	0.036	1.49	0.332	0.6
1417156_at	Krt19	keratin 19	-1.26	0.591	1.02	0.947	1.2	0.381	1.89	0.033	0.71
1442483_at	Fut8	Fucosyltransferase 8	1.09	0.36	1.01	0.993	-1.09	0.701	1.18	0.365	0.54
1452769_at	3732413I11Rik	RIKEN cDNA 3732413I11 gene	1.03	0.608	1.08	0.52	-1.1	0.346	1.03	0.837	0.51
1444471_at	4432416J03Rik	RIKEN cDNA 4432416J03 gene	1.07	0.84	-1.77	0.011	1.38	0.31	4.36	0.205	1.26
1459653_at	---	---	1.07	0.913	-1.92	0.175	1.42	0.534	1.18	0.752	0.44
1441320_a_at	AI413194	expressed sequence AI413194	1.01	0.465	1.01	0.973	-1.01	0.972	1.17	0.636	0.54
1454892_at	Pitpnb	phosphatidylinositol transfer protein, beta	1.1	0.588	-1.12	0.276	1.02	0.824	1.06	0.346	0.51
1428522_at	Ttf2	transcription termination factor, RNA polymerase II	-1.05	0.553	1.01	0.941	1.04	0.528	1.22	0.153	0.56
1424160_at	Alg5	asparagine-linked glycosylation 5 homolog (yeast, dolichyl-phosphate beta-glucos	1	0.997	1.01	0.805	-1	0.976	1.22	0.36	0.56
1440916_at	2510049J12Rik	RIKEN cDNA 2510049J12 gene	1.42	0.057	1.21	0.105	-2.64	0.008	1.03	0.944	0.26
1433822_x_at	Anapc5	anaphase-promoting complex subunit 5	-1.03	0.701	1	0.952	1.04	0.761	1.25	0.077	0.56
1420825_at	Letm1	leucine zipper-EF-hand containing transmembrane protein 1	-1.15	0.642	1.08	0.839	1.06	0.801	1.05	0.851	0.51
1452185_at	Ipo8	importin 8	1.13	0.572	-1.16	0.793	1.02	0.938	1	0.987	0.5
1452686_s_at	D4Ertd196e	DNA segment, Chr 4, ERATO Doi 196, expressed	1.07	0.744	-1.09	0.565	1.03	0.729	1.05	0.224	0.51
1438446_x_at	RP23-136K12.4	putative phosphatase	1.19	0.58	-1.65	0.024	1.22	0.3	1.14	0.778	0.47
1416412_at	Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor	-1.26	0.425	1.09	0.616	1.12	0.128	1.06	0.752	0.5
1435473_at	Gm347	gene model 347, (NCBI)	1.25	0.2	-1.32	0.122	1	0.935	1.1	0.766	0.51
1450776_at	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransf	1.19	0.02	-1.35	0.314	1.08	0.499	1.1	0.615	0.51
1416628_at	0610006I08Rik	RIKEN cDNA 0610006I08 gene	1.02	0.836	-1.15	0.027	1.12	0.197	1.17	0.044	0.54
1441900_x_at	Hspbap1	Hspb associated protein 1	1.13	0.758	-1.14	0.747	1.01	0.979	1.06	0.863	0.51
1445731_at	Pik3cb	Phosphatidylinositol 3-kinase, catalytic, beta polypeptide	1.36	0.44	1.06	0.862	-1.69	0.527	1.14	0.551	0.47
1448120_at	Gdf9	growth differentiation factor 9	1.01	0.993	1.09	0.753	-1.09	0.746	1.23	0.566	0.56
1454824_s_at	Mtus1	mitochondrial tumor suppressor 1	-1.2	0.062	1.04	0.391	1.14	0.186	1.11	0.508	0.52
1449200_at	Nup155	nucleoporin 155	1.07	0.06	1.09	0.682	-1.17	0.195	1.76	0.055	0.69
1417810_a_at	Kcnb1 /// Pacsin2	potassium voltage gated channel, Shab-related subfamily, member 1 /// protein ki	1.07	0.103	-1.08	0.441	1.02	0.749	1.55	0.086	0.64
1434826_at	AI256775	expressed sequence AI256775	1.06	0.633	1.01	0.911	-1.05	0.768	2.06	0.262	0.77
1436394_at	Trim37	tripartite motif protein 37	1.13	0.262	1.05	0.783	-1.2	0.071	1.64	0.289	0.66
1416083_at	Zfand5	zinc finger, AN1-type domain 5	-1.1	0.294	1.03	0.548	1.08	0.153	1.06	0.71	0.52
1434272_at	Cpeb2	cytoplasmic polyadenylation element binding protein 2	-1.24	0.225	1.02	0.93	1.19	0.387	1.2	0.519	0.54
1434546_at	Smg5	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	1.13	0.426	1.01	0.945	-1.14	0.388	1.32	0.383	0.58
1454341_at	4933404I11Rik	RIKEN cDNA 4933404I11 gene	-2.62	0.02	1.25	0.446	1.38	0.273	1.24	0.008	0.31
1429659_at	Smc2	structural maintenance of chromosomes 2	-1.04	0.764	1.04	0.94	1.02	0.944	4.82	0.278	1.46
1435826_at	Rad18	RAD18 homolog (S. cerevisiae)	1.07	0.906	-1.26	0.544	1.15	0.478	1.08	0.41	0.51
1421099_at	Bhlhb3	basic helix-loop-helix domain containing, class B3	1.24	0.679	-1.65	0.371	1.17	0.268	1.75	0.182	0.63
1457375_at	---	PREDICTED: Mus musculus hypothetical protein LOC627707 (LOC627707), mR	-1.44	0.016	1.32	0.083	1	0.993	1.09	0.733	0.49
1416690_at	Gtpbp2	GTP binding protein 2	1.05	0.75	-1.03	0.547	1	0.994	1.79	0.215	0.7
1448090_at	---	Transcribed locus	1.06	0.933	1.52	0.599	-2.29	0.202	1.02	0.954	0.33
1426520_at	Btg4	B-cell translocation gene 4	1.22	0.461	-1.45	0.108	1.1	0.745	1.22	0.412	0.52
1417343_at	Fxyd6	FXYD domain-containing ion transport regulator 6	-1.22	0.195	1.07	0.902	1.13	0.441	1.07	0.868	0.51
1442957_at	G730013B05Rik	RIKEN cDNA G730013B05 gene	-1.88	0.268	1.36	0.265	1.12	0.783	1.5	0.135	0.53
1460169_a_at	Pctk1	PCTAIRE-motif protein kinase 1	1.05	0.885	-1.06	0.584	1.02	0.898	1.36	0.253	0.59
1457036_at	LOC639063	similar to upstream transcription factor 2	1.09	0.559	-1.32	0.547	1.17	0.684	1.1	0.648	0.51
1433224_at	5830442K09Rik	RIKEN cDNA 5830442K09 gene	1.27	0.485	1.01	0.982	-1.37	0.584	2.63	0.019	0.89
1436534_at	Trove2	TROVE domain family, member 2	1.03	0.837	1.28	0.113	-1.41	0.021	1.26	0.248	0.54
1427323_s_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	1.08	0.833	1.01	0.777	-1.08	0.861	1.18	0.36	0.55
1446900_at	D1Ertd218e	DNA segment, Chr 1, ERATO Doi 218, expressed	1.36	0.506	1.08	0.77	-1.73	0.32	1.67	0.409	0.6
1424760_a_at	Smyd2	SET and MYND domain containing 2	1.14	0.412	-1.29	0.304	1.1	0.566	1.11	0.683	0.52
1423917_a_at	Cttn	cortactin	-1.06	0.517	1.04	0.255	1.04	0.747	1.33	0.417	0.59
1452281_at	Sos2	Son of sevenless homolog 2 (Drosophila)	-1.06	0.654	1	0.994	1.07	0.418	1.06	0.28	0.52
1425645_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	1.09	0.924	-1.17	0.706	1.08	0.682	5.57	0.058	1.64
1436732_s_at	Fbxw8	F-box and WD-40 domain protein 8	1.02	0.939	1.02	0.897	-1.02	0.817	1.56	0.012	0.65
1428795_at	1110021L09Rik	RIKEN cDNA 1110021L09 gene	1.11	0.325	-1.12	0.088	1.02	0.82	1.06	0.799	0.52

1434060_at	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	-1.17	0.07	1.01	0.922	1.15	0.283	1.54	0.312	0.64
1445020_at	---	---	1.02	0.847	1.24	0.421	-1.32	0.269	1.15	0.69	0.52
1416698_a_at	Cks1b	CDC28 protein kinase 1b	1.01	0.978	-1.06	0.507	1.07	0.752	1.77	0.19	0.7
1423716_s_at	Atp5d	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	1	0.98	-1.12	0.338	1.12	0.27	1.07	0.635	0.52
1425517_s_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:p	-1.04	0.761	1.04	0.8	1.02	0.821	1.02	0.937	0.51
1421950_at	Pfdn2	prefoldin 2	1.24	0.347	-1.29	0.164	1.01	0.968	1.03	0.697	0.5
1430718_s_at	Zcsl3	zinc finger, CSL-type containing 3	-1.13	0.411	1.12	0.629	1.01	0.941	1.08	0.737	0.52
1424175_at	Tef	thyrotroph embryonic factor	1.01	0.982	-1.06	0.884	1.07	0.897	1.02	0.958	0.51
1417212_at	9530058B02Rik	RIKEN cDNA 9530058B02 gene	1.01	0.967	-1.13	0.618	1.13	0.257	1.58	0.143	0.65
1427456_at	Wdfy3	WD repeat and FYVE domain containing 3	1.3	0.505	1.01	0.942	-1.42	0.174	1.61	0.049	0.63
1452076_at	Spryd4	SPRY domain containing 4	-1.18	0.111	1.1	0.315	1.07	0.434	1.17	0.496	0.54
1450102_a_at	Amfr	autocrine motility factor receptor	-1.01	0.83	1	0.997	1.03	0.549	1.15	0.193	0.54
1418981_at	Casp12	caspase 12	1.02	0.772	1.15	0.329	-1.17	0.174	1.18	0.365	0.54
1429924_at	1700019O17Rik	RIKEN cDNA 1700019O17 gene	-1.28	0.747	1.02	0.963	1.22	0.734	1.05	0.926	0.5
1433113_at	4921504P20Rik	RIKEN cDNA 4921504P20 gene	1.09	0.46	-1.21	0.802	1.1	0.553	1.07	0.801	0.51
1454081_at	---	---	-1.13	0.877	1.09	0.862	1.05	0.941	2.23	0.132	0.81
1450434_s_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	1.12	0.527	-1.17	0.321	1.05	0.842	3.72	0.193	1.18
1425274_at	Asph	aspartate-beta-hydroxylase	1.37	0.393	1	0.995	-1.54	0.095	1.74	0.255	0.64
1443752_at	E230008N13Rik	RIKEN cDNA E230008N13 gene	-1.58	0.162	1.14	0.769	1.25	0.206	1.44	0.324	0.56
1428264_at	Wdr57	WD repeat domain 57 (U5 snRNP specific)	1.01	0.912	-1.06	0.708	1.07	0.69	1.19	0.4	0.55
1427910_at	Cst6	cystatin E/M	1.59	0.169	1.08	0.853	-2.82	0.007	2.42	0.339	0.57
1436517_at	H1fx	H1 histone family, member X	1.26	0.433	1.11	0.8	-1.54	0.221	1.54	0.494	0.59
1453035_at	Lnp	limb and neural patterns	1.05	0.454	-1.12	0.51	1.08	0.778	2.25	0.238	0.82
1451467_s_at	Gtpbp5	GTP binding protein 5	1.05	0.871	-1.12	0.63	1.07	0.628	1.08	0.631	0.52
1430230_at	Rcsd1	RCSD domain containing 1	-1.06	0.903	1.02	0.965	1.06	0.899	1.52	0.383	0.63
1421888_x_at	Aplp2	amyloid beta (A4) precursor-like protein 2	1.07	0.763	-1.19	0.288	1.11	0.285	1.42	0.239	0.6
1460558_at	Ccdc32	coiled-coil domain containing 32	1.02	0.748	1.08	0.553	-1.08	0.151	1.26	0.387	0.57
1416569_at	Actl6a	actin-like 6A	-1.09	0.545	1.09	0.616	1.01	0.934	1.18	0.497	0.55
1428652_at	0610010F05Rik	RIKEN cDNA 0610010F05 gene	1.16	0.611	1.03	0.779	-1.2	0.241	1.28	0.031	0.57
1431087_at	Spbc24	spindle pole body component 24 homolog (S. cerevisiae)	1.02	0.882	-1.14	0.763	1.12	0.634	3.45	0.19	1.11
1448344_at	Rps12 /// LOC4328	ribosomal protein S12 /// similar to ribosomal protein S12 /// similar to ribosomal p	1.01	0.881	1.01	0.935	1	0.993	-2.16	0.058	0.22
1455894_at	Ptrh2	peptidyl-tRNA hydrolase 2	1.14	0.322	-1.32	0.05	1.13	0.164	1.28	0.429	0.55
1418325_at	Sephs2	selenophosphate synthetase 2	1.12	0.289	-1.25	0.32	1.11	0.596	1.42	0.146	0.6
1425265_a_at	Prnpip1	prion protein interacting protein 1	1.13	0.538	1.01	0.949	-1.14	0.233	1.17	0.289	0.54
1435753_a_at	Nucks1	nuclear casein kinase and cyclin-dependent kinase substrate 1	1.06	0.129	-1.1	0.645	1.05	0.751	1.47	0.035	0.62
1455130_at	Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	-1.25	0.119	1.14	0.528	1.08	0.556	1.08	0.466	0.51
1435653_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730024P	1.16	0.214	1.08	0.692	-1.27	0.441	1.21	0.206	0.54
1434415_at	Dact3	dact 3	-1.18	0.42	1.02	0.852	1.16	0.277	1.25	0.029	0.56
1451889_at	Notch2	Notch gene homolog 2 (Drosophila)	-1.91	0.051	1.15	0.775	1.35	0.433	1.75	0.312	0.59
1452866_at	Nars	asparaginyl-tRNA synthetase	1.04	0.48	1.02	0.549	-1.04	0.717	1.37	0.102	0.6
1455389_s_at	2310051F07Rik	RIKEN cDNA 2310051F07 gene	-1.1	0.018	1.01	0.85	1.1	0.451	1.64	0.216	0.66
1415811_at	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	1.09	0.916	1.06	0.807	-1.13	0.831	4.37	0.242	1.35
1423545_a_at	Zfp207	zinc finger protein 207	1.07	0.812	1.01	0.968	-1.06	0.754	1	0.994	0.51
1420849_at	Crnkl1	Crn, crooked neck-like 1 (Drosophila)	-1.65	0.322	1.11	0.479	1.31	0.14	1.12	0.46	0.47
1455012_s_at	Trim37	tripartite motif protein 37	1.01	0.489	-1.07	0.606	1.08	0.66	1.92	0.184	0.73
1453882_at	1700034F02Rik	RIKEN cDNA 1700034F02 gene	1.21	0.736	1.06	0.909	-1.32	0.188	1.02	0.975	0.49
1449561_at	4921504I05Rik	RIKEN cDNA 4921504I05 gene	1.08	0.914	1.29	0.528	-1.53	0.197	1.01	0.983	0.46
1436106_x_at	2310015A05Rik	RIKEN cDNA 2310015A05 gene	1.05	0.944	1.09	0.752	-1.14	0.425	1.53	0.228	0.64
1444226_at	Foxo3a	forkhead box O3a	1.11	0.44	-1.26	0.458	1.12	0.503	2.77	0.301	0.94
1446687_at	Sf3a1	splicing factor 3a, subunit 1	-1.23	0.438	1.05	0.919	1.16	0.236	1.18	0.494	0.54
1434432_at	Rffl	ring finger and FYVE like domain containing protein	1.13	0.305	-1.19	0.15	1.06	0.586	1.78	0.191	0.69
1459381_at	Dach1	Dachshund 1 (Drosophila)	1.42	0.248	1.05	0.938	-1.82	0.137	2.35	0.248	0.75
1452890_at	Ttll5	tubulin tyrosine ligase like family 5	1.04	0.842	-1.06	0.846	1.05	0.654	1.28	0.171	0.57

1434403_at	Spred2	sprouty-related, EVH1 domain containing 2	1.02	0.471	-1.09	0.616	1.08	0.561	1.24	0.166	0.56
1428890_at	Fem1c	fem-1 homolog c (C.elegans)	1.08	0.343	1.12	0.499	-1.21	0.037	1.02	0.71	0.5
1434318_a_at	Tcfe3	transcription factor E3	-1.08	0.294	1.08	0.416	1.02	0.907	1.33	0.332	0.59
1415987_at	Hdlbp	high density lipoprotein (HDL) binding protein	1.02	0.876	1.07	0.568	-1.06	0.588	1.33	0.063	0.59
1456294_at	0610013E23Rik	RIKEN cDNA 0610013E23 gene	-1.33	0.448	1.11	0.62	1.16	0.307	1.27	0.285	0.55
1427852_x_at	Igh-VJ558	immunoglobulin heavy chain (J558 family)	-1.44	0.275	1.27	0.463	1.06	0.737	1.14	0.409	0.51
1436014_a_at	Rusc1	RUN and SH3 domain containing 1	-1.2	0.576	1.14	0.698	1.06	0.84	1.07	0.711	0.51
1452313_at	5930416I19Rik	RIKEN cDNA 5930416I19 gene	1.08	0.517	1.03	0.795	-1.1	0.382	1.23	0.199	0.56
1436055_at	Lrrc15	leucine rich repeat containing 15	1.04	0.77	-1.27	0.331	1.2	0.44	1.52	0.161	0.62
1447881_x_at	---	---	1.09	0.407	1.01	0.945	-1.09	0.698	1.62	0.38	0.66
1448684_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.09	0.348	-1.08	0.085	1.01	0.871	1.02	0.579	0.51
1440262_at	---	---	1.29	0.597	-1.66	0.385	1.14	0.793	1.84	0.246	0.65
1440750_at	---	Transcribed locus	1.09	0.686	-1.33	0.407	1.19	0.691	1.88	0.044	0.71
1428142_at	Etv5	ets variant gene 5	1.03	0.942	1.22	0.529	-1.29	0.341	1.15	0.552	0.53
1448229_s_at	Ccnd2	cyclin D2	1.22	0.566	1.08	0.781	-1.38	0.354	1.17	0.701	0.52
1460573_at	AI848100	expressed sequence AI848100	1	0.919	-1.09	0.618	1.1	0.665	1.39	0.115	0.6
1430798_x_at	Mrpl15	mitochondrial ribosomal protein L15	1.01	0.97	1.15	0.227	-1.15	0.566	1.16	0.492	0.54
1447807_s_at	Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	1.09	0.439	1.1	0.371	-1.2	0.18	1.02	0.957	0.5
1434614_at	---	---	1.21	0.76	-1.52	0.481	1.16	0.717	1.04	0.844	0.47
1454913_at	9930104L06Rik	RIKEN cDNA 9930104L06 gene	-1.1	0.342	1.02	0.959	1.1	0.478	1.1	0.695	0.53
1459657_s_at	Rpo1-3	RNA polymerase 1-3	-1.08	0.534	1.03	0.69	1.07	0.506	1	0.979	0.51
1433667_at	Lgi3	leucine-rich repeat LGI family, member 3	1.06	0.896	1.3	0.521	-1.49	0.031	1.22	0.597	0.52
1431931_a_at	Rabl2a	RAB, member of RAS oncogene family-like 2A	-1.11	0.409	1.03	0.834	1.1	0.623	1.02	0.953	0.51
1448843_at	LOC636537	similar to signal sequence receptor, alpha	1.05	0.388	1.02	0.943	-1.03	0.861	1.27	0.457	0.58
1454735_at	Odf2	outer dense fiber of sperm tails 2	1.08	0.488	-1.13	0.317	1.07	0.518	1.86	0.22	0.72
1426785_s_at	Mgll	monoglyceride lipase	1.28	0.189	-1.85	0.106	1.21	0.463	2.61	0.129	0.81
1442124_at	AI450326	expressed sequence AI450326	1.07	0.637	-1.05	0.518	1.01	0.974	1.17	0.107	0.55
1419501_at	Polk	polymerase (DNA directed), kappa	1.02	0.897	-1.26	0.543	1.22	0.273	1.33	0.18	0.58
1449839_at	---	---	-1.31	0.337	1.04	0.633	1.23	0.123	1.49	0.17	0.61
1424892_at	Zfp95	zinc finger protein 95	-1.15	0.439	1.11	0.008	1.05	0.678	1.08	0.792	0.52
1428666_at	Nars	asparaginyl-tRNA synthetase	-1.13	0.167	1.01	0.949	1.14	0.571	1.34	0.33	0.59
1449362_a_at	Mink1	misshapen-like kinase 1 (zebrafish)	-1.05	0.775	1.06	0.623	1.02	0.916	1.02	0.936	0.51
1441170_a_at	Dab2ip	disabled homolog 2 (Drosophila) interacting protein	-1.17	0.621	1.06	0.803	1.12	0.74	1.33	0.455	0.58
1460068_at	1110034C04Rik	RIKEN cDNA 1110034C04 gene	-1.43	0.625	1.21	0.416	1.12	0.764	1.03	0.95	0.48
1419753_at	Nfx1	nuclear transcription factor, X-box binding 1	1.07	0.189	-1.23	0.03	1.14	0.649	1.08	0.562	0.52
1454685_at	Gpr146	G protein-coupled receptor 146	1.09	0.51	-1.13	0.525	1.05	0.612	1.68	0.217	0.67
1444880_at	---	Transcribed locus	-1.86	0.494	1.24	0.345	1.25	0.551	1.03	0.642	0.42
1453570_x_at	Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like	1.03	0.681	1.2	0.255	-1.26	0.194	1.03	0.877	0.5
1435372_a_at	Pa2g4	proliferation-associated 2G4	1.02	0.942	-1.18	0.194	1.16	0.533	1.27	0.147	0.57
1459662_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933019	1.22	0.7	-1.64	0.226	1.2	0.67	1.24	0.647	0.51
1433141_at	4921504P05Rik	RIKEN cDNA 4921504P05 gene	1.29	0.721	-1.79	0.344	1.18	0.686	2.14	0.102	0.7
1432388_at	5430440P10Rik	RIKEN cDNA 5430440P10 gene	-1.3	0.491	1.13	0.835	1.14	0.724	1.12	0.351	0.52
1430141_at	1200015N20Rik	RIKEN cDNA 1200015N20 gene	1.2	0.106	1.02	0.974	-1.22	0.668	1.41	0.32	0.6
1441583_at	---	---	-1.45	0.443	1.04	0.889	1.31	0.67	1.16	0.06	0.51
1447591_x_at	A830082N09Rik	RIKEN cDNA A830082N09 gene	1.19	0.82	1.1	0.817	-1.35	0.601	1.43	0.582	0.59
1439735_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4933414F24 pr	-2.23	0.008	1.56	0.023	1.02	0.956	1.38	0.603	0.43
1452915_at	Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	1.16	0.131	1.11	0.128	-1.32	0.017	1.33	0.232	0.57
1452907_at	Galc	galactosylceramidase	1.02	0.743	1.13	0.217	-1.13	0.014	1.34	0.126	0.59
1426697_a_at	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	1.15	0.13	1.02	0.642	-1.16	0.413	1.09	0.485	0.52
1451700_a_at	1110007L15Rik	RIKEN cDNA 1110007L15 gene	1.04	0.796	-1.12	0.275	1.1	0.403	1.52	0.303	0.64
1442404_at	Ncl	nucleolin	1.1	0.895	1.14	0.702	-1.27	0.45	1.11	0.709	0.52
1427708_a_at	Nf2	neurofibromatosis 2	1.21	0.214	-1.46	0.118	1.13	0.717	1.3	0.433	0.55
1422767_at	Bysl	bystin-like	1.01	0.616	-1.26	0.198	1.23	0.465	1.74	0.188	0.68

1455857_a_at	Rab2b	RAB2B, member RAS oncogene family	1.09	0.818	-1.44	0.2	1.25	0.428	1.01	0.964	0.48
1444201_at	Cep135	centrosomal protein 135	-1.84	0.518	1.25	0.766	1.24	0.502	1.47	0.231	0.53
1422465_a_at	Nxn	nucleoredoxin	1.1	0.594	-1.27	0.102	1.14	0.412	1.03	0.798	0.5
1420835_at	Slc25a30	solute carrier family 25, member 30	1.3	0.495	-2.81	0.086	1.38	0.372	1.3	0.426	0.29
1415702_a_at	Ctbp1	C-terminal binding protein 1	-1.07	0.424	1.05	0.218	1.04	0.752	1.27	0.16	0.57
1451938_a_at	Sntb1	syntrophin, basic 1	1.06	0.829	-1.12	0.749	1.08	0.813	1.06	0.841	0.52
1433080_at	4933436P19Rik	RIKEN cDNA 4933436P19 gene	-1.46	0.071	1.13	0.637	1.22	0.205	1.21	0.29	0.53
1417324_at	Mast2	microtubule associated serine/threonine kinase 2	1.08	0.392	-1.35	0.079	1.22	0.169	1.93	0.125	0.72
1421848_at	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	1.08	0.799	-1.16	0.494	1.09	0.737	1.01	0.963	0.51
1453756_at	2900075N08Rik	RIKEN cDNA 2900075N08 gene	1.17	0.644	-1.2	0.681	1.03	0.935	1.8	0.331	0.7
1436289_x_at	1600014C10Rik	RIKEN cDNA 1600014C10 gene	-1.32	0.234	1.02	0.914	1.25	0.623	1.52	0.192	0.62
1432538_a_at	Rfc3	replication factor C (activator 1) 3	1.04	0.915	1	0.994	-1.01	0.974	1.47	0.504	0.63
1456830_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.16	0.647	-1.19	0.258	1.04	0.627	1.21	0.376	0.55
1419355_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.05	0.83	1.19	0.554	-1.26	0.355	1.21	0.381	0.55
1417515_at	Lsm10	U7 snRNP-specific Sm-like protein LSM10	-1.17	0.122	1.01	0.945	1.18	0.31	1.1	0.219	0.53
1451187_at	0610037P05Rik	RIKEN cDNA 0610037P05 gene	1.06	0.624	1.02	0.803	-1.04	0.711	1.17	0.416	0.55
1423933_a_at	1600029D21Rik	RIKEN cDNA 1600029D21 gene	1.02	0.778	-1.33	0.454	1.26	0.014	1.05	0.896	0.5
1435155_at	Cgn	cingulin	1.02	0.901	-1.01	0.96	1.02	0.856	1.58	0.467	0.65
1451943_a_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	1.08	0.524	1.01	0.938	-1.05	0.719	1.24	0.375	0.57
1416917_at	1700123O20Rik	RIKEN cDNA 1700123O20 gene	1.12	0.302	1.1	0.498	-1.23	0.033	1.09	0.581	0.52
1431687_at	Gmfb	glia maturation factor, beta	-1.31	0.331	1.11	0.816	1.16	0.792	1.3	0.12	0.56
1453592_at	Lrrc39	leucine rich repeat containing 39	-2.7	0.21	1.04	0.945	1.62	0.44	3.89	0.222	0.96
1433632_at	Irf2bp2 /// LOC6729	interferon regulatory factor 2 binding protein 2 /// similar to interferon regulatory fa	1.01	0.936	-1.15	0.571	1.15	0.477	1.01	0.968	0.51
1431779_at	---	---	-1.15	0.805	1.1	0.868	1.07	0.906	1.15	0.754	0.54
1431209_s_at	Tmem42	transmembrane protein 42	1	0.991	1.01	0.966	1.03	0.91	-1.52	0.141	0.38
1432135_s_at	Spdya /// LOC6384	speedy homolog A (Drosophila) /// similar to speedy homolog 1	1.16	0.751	-1.89	0.348	1.34	0.394	2.1	0.108	0.68
1421097_at	Endog	endonuclease G	1.15	0.393	-1.14	0.01	1.01	0.969	1.12	0.329	0.54
1437465_a_at	P4hb	prolyl 4-hydroxylase, beta polypeptide	-1.04	0.583	1.07	0.369	1	0.964	1.17	0.208	0.55
1428480_at	Cdca8	cell division cycle associated 8	1.04	0.955	-1.35	0.456	1.26	0.495	3.63	0.19	1.14
1425195_a_at	Acat2 /// Acat3	acetyl-Coenzyme A acetyltransferase 2 /// acetyl-Coenzyme A acetyltransferase 3	1.11	0.154	-1.13	0.213	1.04	0.851	1.3	0.294	0.58
1443498_at	Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	1.02	0.952	-1.02	0.903	1.04	0.947	1.42	0.504	0.61
1451229_at	Hdac11	histone deacetylase 11	1.11	0.726	-1.24	0.33	1.12	0.52	1.17	0.548	0.54
1452528_a_at	Nkx2-3	NK2 transcription factor related, locus 3 (Drosophila)	-1.85	0.378	1.46	0.361	1.04	0.919	1.24	0.592	0.47
1428788_at	1700012G19Rik	RIKEN cDNA 1700012G19 gene	1.01	0.863	1.05	0.416	-1.03	0.842	1.52	0.178	0.64
1423260_at	Id4	inhibitor of DNA binding 4	-1.01	0.972	1.02	0.953	1.03	0.874	1.24	0.343	0.57
1416975_at	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	1.04	0.608	-1.86	0.041	1.46	0.075	1.11	0.722	0.44
1437262_x_at	Bcas2	breast carcinoma amplified sequence 2	-1.44	0.471	1.2	0.584	1.15	0.533	1.27	0.466	0.54
1421245_at	Sost	sclerostin	1.18	0.665	-1.51	0.479	1.19	0.704	1.4	0.012	0.57
1451273_x_at	BC025546	cDNA sequence BC025546	1.14	0.219	1.1	0.807	-1.25	0.148	1.02	0.918	0.5
1426243_at	Cth	cystathionase (cystathionine gamma-lyase)	1.07	0.616	-1.06	0.722	1.02	0.846	2.26	0.111	0.82
1445137_at	Ptk2	PTK2 protein tyrosine kinase 2	1.07	0.758	1.47	0.19	-2	0.062	1	0.991	0.39
1446099_at	Mthfd1l	Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	-1.23	0.571	1.03	0.912	1.2	0.395	2.23	0.422	0.81
1439062_at	Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	1.12	0.663	1	0.998	-1.08	0.489	1.05	0.72	0.52
1443475_at	Hist1h3i	Histone 1, H3i	1.07	0.868	1.22	0.748	-1.34	0.411	2.52	0.386	0.87
1448636_at	Myoz1	myozenin 1	-2.26	0.384	1.25	0.522	1.35	0.292	1.89	0.287	0.56
1438741_at	BC019943	cDNA sequence BC019943	1.03	0.969	-1.04	0.92	1.05	0.556	1.01	0.961	0.51
1436021_at	A930031D07Rik	RIKEN cDNA A930031D07 gene	1.33	0.494	-1.9	0.401	1.18	0.617	1.51	0.284	0.53
1446825_at	---	---	1.06	0.743	-1.21	0.318	1.16	0.485	1.02	0.934	0.51
1442526_at	C77681	expressed sequence C77681	1.39	0.204	-1.89	0.458	1.12	0.853	1.28	0.375	0.48
1451714_a_at	Map2k3	mitogen activated protein kinase kinase 3	1.01	0.973	-1.09	0.514	1.12	0.423	3.25	0.177	1.07
1441595_at	Ercc6	Excision repair cross-complementing rodent repair deficiency, complementation g	-1.34	0.646	1.08	0.835	1.21	0.772	1.37	0.483	0.58
1417416_at	Kcna1	potassium voltage-gated channel, shaker-related subfamily, member 1	-1.96	0.327	1.47	0.312	1.06	0.876	1.42	0.496	0.5
1447549_x_at	Ninj1	ninjurin 1	1.09	0.525	-1.12	0.542	1.06	0.826	1.06	0.786	0.52

1422257_s_at	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	1.14	0.707	-1.11	0.806	1.01	0.971	5.17	0.004	1.55
1418620_at	Phox2a	paired-like homeobox 2a	1.03	0.933	1.14	0.736	-1.15	0.526	1.27	0.318	0.57
1459628_at	Zmat4	Zinc finger, matrin type 4	1.33	0.511	1.29	0.659	-2.39	0.209	1.01	0.943	0.31
1449089_at	Nrip1	nuclear receptor interacting protein 1	1.17	0.139	1.14	0.341	-1.36	0.018	1.16	0.295	0.53
1421572_at	Hif3a	hypoxia inducible factor 3, alpha subunit	1.19	0.502	1.1	0.514	-1.32	0.04	1.04	0.784	0.5
1421501_a_at	Erc1	ELKS/RAB6-interacting/CAST family member 1	1.06	0.811	-1.34	0.207	1.24	0.383	1.2	0.404	0.54
1423263_at	H3f3a	H3 histone, family 3A	-1.05	0.184	1.02	0.721	1.07	0.315	1.06	0.706	0.53
1455781_at	BC027231	cDNA sequence BC027231	-1.04	0.649	1.03	0.88	1.05	0.801	1.05	0.814	0.52
1456480_at	Fry	furry homolog (Drosophila)	1.07	0.734	-1.15	0.669	1.1	0.603	1.23	0.429	0.56
1439507_at	Trafd1	TRAF type zinc finger domain containing 1	1.24	0.768	1.48	0.345	-3.06	0.317	1.11	0.717	0.19
AFFX-r2-Ec-bioB-3_	---	---	1.25	0.149	1.13	0.273	-1.5	0.106	1.01	0.978	0.47
1417968_a_at	Mbd1	methyl-CpG binding domain protein 1	1.15	0.403	1.01	0.955	-1.13	0.285	1.05	0.716	0.52
1427332_at	Med19	mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)	1.09	0.71	-1.07	0.619	1.02	0.896	1.01	0.958	0.51
1444552_at	---	---	1.39	0.577	1.06	0.839	-1.69	0.022	1.13	0.777	0.47
1444888_at	AU022852	expressed sequence AU022852	1.08	0.608	-1.53	0.362	1.31	0.008	1.1	0.836	0.49
1445027_at	Cdr2l	cerebellar degeneration-related protein 2-like	1.04	0.725	-1.27	0.431	1.22	0.411	1.11	0.66	0.52
1429134_at	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	1.01	0.986	-1.04	0.884	1.07	0.692	1.23	0.131	0.57
1451668_at	C530043G21Rik	RIKEN cDNA C530043G21 gene	1.04	0.274	1.11	0.34	-1.12	0.36	1.03	0.769	0.52
1459992_x_at	Cln8	ceroid-lipofuscinosis, neuronal 8	1.08	0.746	1.06	0.653	-1.1	0.559	1.87	0.22	0.73
1450877_at	BC005537	cDNA sequence BC005537	-1.07	0.415	1.02	0.913	1.1	0.173	1.16	0.136	0.55
1417449_at	Acot8	acyl-CoA thioesterase 8	1.14	0.493	-1.28	0.038	1.12	0.322	1.4	0.145	0.6
1427083_a_at	Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	-1.62	0.269	1.34	0.141	1.09	0.712	2.48	0.215	0.82
1428641_at	Hsf2bp	heat shock transcription factor 2 binding protein	1.03	0.852	-1.31	0.661	1.25	0.413	1.1	0.873	0.52
1426791_at	Rusc2	RUN and SH3 domain containing 2	1.01	0.97	-1.24	0.635	1.22	0.367	1.68	0.453	0.67
1455050_at	E130203B14Rik	RIKEN cDNA E130203B14 gene	1.2	0.277	1.22	0.393	-1.59	0.092	1.06	0.825	0.47
1431128_at	D8Bwg1414e	DNA segment, Chr 8, Brigham & Women's Genetics 1414 expressed	-1.49	0.381	1.3	0.31	1.08	0.75	1.86	0.094	0.68
1452237_at	Hrb	HIV-1 Rev binding protein	1.02	0.948	1.17	0.208	-1.17	0.28	1.1	0.631	0.53
1448405_a_at	Cri1	CREBBP/EP300 inhibitory protein 1	1.02	0.716	1.35	0.049	-1.48	0.009	1.06	0.596	0.49
1442271_at	Ckap5	Cytoskeleton associated protein 5	1.48	0.27	1.07	0.892	-2.03	0.011	1.19	0.47	0.43
1443976_at	Cdk5rap2	CDK5 regulatory subunit associated protein 2	1.12	0.687	-1.37	0.499	1.2	0.473	1.44	0.494	0.6
1420430_a_at	2510048L02Rik	RIKEN cDNA 2510048L02 gene	1.23	0.781	1.04	0.828	-1.29	0.373	1.05	0.837	0.51
1428372_at	St5	suppression of tumorigenicity 5	1.04	0.36	1.16	0.218	-1.18	0.35	1.56	0.069	0.65
1450333_a_at	Gata2	GATA binding protein 2	-1.35	0.328	1.17	0.472	1.14	0.477	1.16	0.589	0.53
1433838_at	Dars2	aspartyl-tRNA synthetase 2 (mitochondrial)	1.04	0.804	-1.05	0.691	1.06	0.513	1.48	0.359	0.63
1420549_at	Gbp1	guanylate nucleotide binding protein 1	-1.02	0.978	1.04	0.713	1.03	0.9	2.26	0.032	0.83
1451929_a_at	Vrk2	vaccinia related kinase 2	1.04	0.706	-1.11	0.66	1.12	0.402	1.2	0.001	0.56
1438170_x_at	Adrm1	adhesion regulating molecule 1	1.06	0.776	-1.13	0.557	1.1	0.604	1.06	0.756	0.52
1439031_at	Jph4	junctophilin 4	1.01	0.99	-1.37	0.449	1.31	0.249	1.19	0.695	0.53
1416900_s_at	Gdf1 /// Lass1	growth differentiation factor 1 /// longevity assurance homolog 1 (S. cerevisiae)	1.25	0.201	-1.49	0.379	1.13	0.645	1.88	0.352	0.69
1450452_a_at	Narfl	nuclear prelamin A recognition factor-like	1	0.998	-1.1	0.219	1.14	0.425	1.08	0.47	0.53
1434256_s_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	1.01	0.958	1.2	0.119	-1.19	0.398	1.15	0.394	0.54
1452902_at	Dhrs13	dehydrogenase/reductase (SDR family) member 13	-1.02	0.819	1.02	0.868	1.05	0.75	2.32	0.27	0.84
1419079_at	Scnn1g	sodium channel, nonvoltage-gated 1 gamma	-1.7	0.037	1.45	0.245	1.01	0.958	1.05	0.878	0.45
1435600_s_at	BC020535	cDNA sequence BC020535	1.28	0.563	-1.82	0.191	1.22	0.5	1.05	0.823	0.43
1459148_at	Pax3	Paired box gene 3	-2.16	0.338	1.29	0.649	1.3	0.491	1.21	0.587	0.41
1442791_x_at	6720407P12Rik	RIKEN cDNA 6720407P12 gene	-1.41	0.631	1.31	0.672	1.03	0.951	1.98	0.137	0.73
1438758_at	---	---	1.02	0.935	-1.1	0.588	1.12	0.133	1.14	0.392	0.55
1417891_at	Spsb3	splA/ryanodine receptor domain and SOCS box containing 3	1.08	0.705	-1.1	0.291	1.06	0.72	1.57	0.203	0.65
1437244_at	Gas2l3	growth arrest-specific 2 like 3	-1.19	0.807	1.18	0.63	1.03	0.905	2.39	0.222	0.85
1448824_at	Ube2j1	ubiquitin-conjugating enzyme E2, J1	1.06	0.421	-1.2	0.207	1.16	0.278	1.33	0.097	0.59
1455880_s_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	1.04	0.569	1.06	0.452	-1.06	0.612	1.18	0.318	0.56
1423185_a_at	Ubap1	ubiquitin-associated protein 1	-1.2	0.318	1.04	0.522	1.18	0.195	1.28	0.253	0.57
1423799_at	Eif1	eukaryotic translation initiation factor 1	1.18	0.174	-1.15	0.405	1	1	1.33	0.012	0.59

1454187_at	Pkd1l2	polycystic kidney disease 1 like 2	1.07	0.621	-1.62	0.063	1.36	0.421	1.52	0.236	0.58
1429357_at	4921533L14Rik	RIKEN cDNA 4921533L14 gene	-1.54	0.068	1.09	0.882	1.31	0.655	1.08	0.852	0.49
1426095_a_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	-1.45	0.092	1.21	0.56	1.15	0.269	1.17	0.594	0.52
1450919_at	Mpp1	membrane protein, palmitoylated	-1.3	0.123	1.01	0.923	1.28	0.016	2.23	0.189	0.8
1459814_at	Tmem109	transmembrane protein 109	-2.19	0.04	1.14	0.862	1.46	0.387	1.01	0.959	0.35
1427497_at	2610015P09Rik	RIKEN cDNA 2610015P09 gene	1.04	0.5	-1.01	0.982	1.02	0.97	1.05	0.902	0.52
1433899_x_at	Tsc22d1	TSC22 domain family, member 1	1.08	0.85	1.07	0.695	-1.11	0.428	1.51	0.272	0.64
1433918_at	Atg4d	autophagy-related 4D (yeast)	1.16	0.308	-1.22	0.391	1.07	0.79	3.48	0.142	1.12
1425384_a_at	Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	1.02	0.868	-1.14	0.338	1.15	0.373	1.08	0.767	0.53
1457969_at	Rabif	RAB interacting factor	1.09	0.783	-1.19	0.1	1.12	0.535	1.15	0.414	0.54
1444572_at	Mmd2	monocyte to macrophage differentiation-associated 2	-1.47	0.046	1.12	0.833	1.26	0.494	1.06	0.859	0.49
1450130_at	Xpr1	xenotropic and polytropic retrovirus receptor 1	1.04	0.698	-1.13	0.31	1.13	0.379	1.03	0.902	0.52
1460592_at	Epb4.1l1	erythrocyte protein band 4.1-like 1	-1.26	0.209	1.21	0.411	1.05	0.759	1.18	0.27	0.54
1448625_at	Golga2	golgi autoantigen, golgin subfamily a, 2	1.05	0.549	1.03	0.756	-1.03	0.802	1.03	0.86	0.52
1426788_a_at	Ssrp1	structure specific recognition protein 1	-1.18	0.153	1.18	0.063	1.03	0.772	1.13	0.485	0.54
1415974_at	Map2k2	mitogen activated protein kinase kinase 2	1.03	0.821	-1.36	0.211	1.29	0.275	1.38	0.081	0.59
1452626_a_at	1810014F10Rik	RIKEN cDNA 1810014F10 gene	-1.06	0.568	1.02	0.806	1.09	0.277	1.17	0.563	0.55
1453686_x_at	Nphp1	nephronophthisis 1 (juvenile) homolog (human)	-1.57	0.011	1.3	0.374	1.12	0.723	1.28	0.469	0.53
1452979_at	2610110G12Rik	RIKEN cDNA 2610110G12 gene	-1.12	0.814	1.04	0.796	1.12	0.625	1.06	0.867	0.53
1435742_at	1110034C04Rik	RIKEN cDNA 1110034C04 gene	1.04	0.836	1.06	0.535	-1.05	0.855	1.33	0.192	0.6
1422460_at	Mad2l1	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	1.1	0.351	-1.2	0.381	1.12	0.61	2.81	0.192	0.96
1418463_at	Pik3r2	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	1.11	0.229	-1.08	0.345	1.01	0.843	1.46	0.178	0.63
1452119_at	2600005C20Rik	RIKEN cDNA 2600005C20 gene	-1.03	0.863	1.01	0.967	1.08	0.649	1.07	0.705	0.53
1416448_at	Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	1.11	0.548	-1.07	0.504	1.01	0.935	1.37	0.241	0.61
1432185_a_at	Spdyb	speedy homolog B (Drosophila)	1.27	0.329	-1.93	0.265	1.27	0.342	1.32	0.585	0.48
1419923_at	LOC626391	Similar to Zinc finger protein 124 (HZF-16)	-1.29	0.73	1.01	0.964	1.28	0.596	1.17	0.452	0.54
1454399_at	2010003H20Rik	RIKEN cDNA 2010003H20 gene	-1.66	0.143	1.13	0.746	1.32	0.57	1.3	0.496	0.52
1424715_at	Retsat	retinol saturase (all trans retinol 13,14 reductase)	1.25	0.268	-2.32	0.083	1.38	0.096	1.42	0.02	0.43
1452906_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	1.11	0.818	1.22	0.538	-1.39	0.104	1.73	0.33	0.67
1434569_at	AA474455	expressed sequence AA474455	-1.09	0.088	1.04	0.719	1.09	0.323	1.12	0.134	0.54
1424692_at	2810055F11Rik	RIKEN cDNA 2810055F11 gene	-1.1	0.403	1.01	0.948	1.14	0.624	1	1	0.51
1419687_at	D930010J01Rik	RIKEN cDNA D930010J01 gene	1.11	0.142	-1.11	0.707	1.05	0.766	1.04	0.457	0.52
1451366_at	Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (Arabidopsis thaliana)	1.09	0.595	-1.03	0.608	1	0.986	1.06	0.799	0.53
1437452_x_at	Vdac1	voltage-dependent anion channel 1	1	0.995	1.25	0.125	-1.24	0.4	1.11	0.198	0.53
1425767_a_at	Six4	sine oculis-related homeobox 4 homolog (Drosophila)	1.02	0.813	-1.12	0.704	1.14	0.569	1	0.998	0.51
1437298_at	5730509C05Rik	RIKEN cDNA 5730509C05 gene	1.1	0.52	-1.25	0.277	1.16	0.316	1.23	0.035	0.56
1417477_at	Gtlf3b	gene trap locus F3b	-1.03	0.515	1.07	0.347	1.02	0.933	2.19	0.152	0.81
1449954_at	Hyal1 /// Nat6	hyaluronoglucosaminidase 1 /// N-acetyltransferase 6	1.11	0.374	-1.17	0.16	1.09	0.625	1.57	0.236	0.65
1418530_at	Nup160	nucleoporin 160	-1.11	0.625	1.01	0.959	1.15	0.395	1.24	0.348	0.57
1451369_at	Commd5	COMM domain containing 5	-1.08	0.017	1.04	0.674	1.09	0.49	1.17	0.187	0.56
1455081_at	Txnl4b	thioredoxin-like 4B	1.09	0.463	1.01	0.968	-1.04	0.813	1.05	0.59	0.53
1431017_at	Rcbtb2	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	-2.1	0.115	1.4	0.483	1.18	0.097	1.24	0.682	0.43
1453744_a_at	Ankrd40	ankyrin repeat domain 40	1.06	0.706	-1.02	0.793	1.02	0.921	1.05	0.827	0.53
1423296_at	Psmd8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	1.09	0.728	-1.07	0.498	1.04	0.867	1.1	0.662	0.54
1452058_a_at	Rnf11	ring finger protein 11	1.13	0.613	1.08	0.501	-1.17	0.543	2.5	0.236	0.88
1454619_at	Tmem153	transmembrane protein 153	1.01	0.957	-1.08	0.434	1.12	0.492	1.32	0.086	0.59
1448019_at	2900006A08Rik	RIKEN cDNA 2900006A08 gene	1.11	0.688	1.03	0.806	-1.09	0.466	1.39	0.118	0.61
1430508_at	1700084F23Rik	RIKEN cDNA 1700084F23 gene	1.05	0.861	1.3	0.159	-1.41	0.187	1.01	0.963	0.49
1446131_at	---	---	1.21	0.563	-1.27	0.529	1.06	0.819	2.21	0.261	0.8
1436579_s_at	AI839402	expressed sequence AI839402	1.21	0.824	1.12	0.846	-1.36	0.478	2.34	0.006	0.83
1452877_at	2700029M09Rik	RIKEN cDNA 2700029M09 gene	1.06	0.641	1.17	0.36	-1.21	0.099	1.67	0.258	0.67
1416198_at	Th1l	TH1-like homolog (Drosophila)	1.15	0.059	-1.29	0	1.14	0.25	1.49	0.328	0.62
1432830_at	6230424H07Rik	RIKEN cDNA 6230424H07 gene	1.02	0.944	1.3	0.618	-1.34	0.233	1.2	0.702	0.54

1452725_a_at	Rnaseh2a	ribonuclease H2, large subunit	1.01	0.955	-1.19	0.212	1.2	0.264	1.42	0.255	0.61
1459560_at	4921517N04Rik	RIKEN cDNA 4921517N04 gene	1.31	0.007	1.12	0.092	-1.58	0.038	1.02	0.867	0.47
1459566_at	Rgs12	Regulator of G-protein signaling 12	-1.16	0.846	1.09	0.845	1.11	0.659	2.09	0.09	0.78
1443133_at	A230070E04Rik	RIKEN cDNA A230070E04 gene	-1.06	0.703	1.11	0.757	1.01	0.947	1.22	0.603	0.57
1455752_a_at	Tmem134	transmembrane protein 134	1.01	0.971	-1.1	0.632	1.14	0.528	1.04	0.791	0.52
1455960_at	Megf9	multiple EGF-like-domains 9	-1.18	0.346	1.03	0.925	1.18	0.156	2.56	0.329	0.9
1426875_s_at	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	-1.01	0.864	1.02	0.781	1.05	0.574	1.71	0.241	0.69
1423023_at	Sfrp5	secreted frizzled-related sequence protein 5	1.22	0.269	1.17	0.782	-1.48	0.307	1.11	0.863	0.5
1434961_at	Asb1	ankyrin repeat and SOCS box-containing protein 1	1.02	0.589	-1.19	0.471	1.2	0.16	4.67	0.192	1.43
1416995_at	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	-1.08	0.745	1.01	0.953	1.13	0.517	1.24	0.501	0.57
1418455_at	Copz2	coatomer protein complex, subunit zeta 2	1.07	0.703	1.17	0.372	-1.22	0.218	1.24	0.193	0.57
1429535_at	Armc8	armadillo repeat containing 8	-1.2	0.134	1.06	0.544	1.16	0.357	1.17	0.014	0.55
1445721_at	A830021M18	hypothetical protein A830021M18	-1.4	0.709	1.15	0.547	1.2	0.795	1.14	0.739	0.52
1419066_at	Ier5l	immediate early response 5-like	1.27	0.401	1.03	0.945	-1.3	0.188	1.08	0.718	0.52
1436026_at	Zfp703	zinc finger protein 703	-1.01	0.893	1.02	0.925	1.06	0.791	1.5	0.257	0.64
1442884_at	Hgf	hepatocyte growth factor	1.18	0.595	1.14	0.587	-1.34	0.283	2.03	0.18	0.75
1453274_at	Ccdc103	coiled-coil domain containing 103	1.01	0.95	-1.16	0.671	1.19	0.645	1.13	0.791	0.54
1442462_at	C87042	expressed sequence C87042	1.01	0.928	-1.07	0.832	1.12	0.503	1.39	0.001	0.61
1453947_at	Kif24	kinesin family member 24	1.05	0.935	-1.64	0.031	1.4	0.242	1.07	0.892	0.47
1428368_at	Arhgap21	Rho GTPase activating protein 21	-1.06	0.294	1.02	0.902	1.1	0.731	2.13	0.274	0.8
1441235_at	Nup133	nucleoporin 133	1.61	0.013	-2.29	0.2	1.02	0.943	1.04	0.813	0.34
1428605_at	LOC669879	similar to Y73E7A.1	1.05	0.616	-1.01	0.855	1.02	0.878	1.08	0.697	0.54
1418540_a_at	Ptpre	protein tyrosine phosphatase, receptor type, E	1.15	0.42	1.24	0.481	-1.47	0.151	1.12	0.482	0.51
1425054_a_at	2510006D16Rik	RIKEN cDNA 2510006D16 gene	1.07	0.749	-1.06	0.563	1.05	0.758	1.24	0.256	0.58
1418341_at	Rab4a	RAB4A, member RAS oncogene family	-1.28	0.121	1.23	0.112	1.05	0.648	1.55	0.296	0.64
1440823_x_at	D130058I21Rik	RIKEN cDNA D130058I21 gene	-2.17	0.109	1.3	0.516	1.3	0.107	1.1	0.632	0.38
1430604_a_at	Dab2	disabled homolog 2 (Drosophila)	-1.07	0.867	1.05	0.905	1.08	0.778	1.18	0.48	0.56
1434304_s_at	D10Ertd438e	DNA segment, Chr 10, ERATO Doi 438, expressed	-1.04	0.854	1.07	0.609	1.03	0.773	1	0.996	0.52
1449643_s_at	Btf3	basic transcription factor 3	1.04	0.735	1.01	0.929	1.02	0.799	-1.34	0.087	0.43
1448705_at	Zbtb22	zinc finger and BTB domain containing 22	1.07	0.686	-1.01	0.883	1	0.991	1.02	0.877	0.52
1450864_at	Calm3	calmodulin 3	1.05	0.568	-1.03	0.821	1.04	0.882	1.15	0.64	0.55
1439530_a_at	LOC669005	similar to NFkB interacting protein 1	-1.41	0.287	1.15	0.451	1.21	0.169	1.02	0.952	0.49
1416113_at	Fkbp8	FK506 binding protein 8	1.06	0.847	1.17	0.292	-1.2	0.079	1.23	0.407	0.57
1449930_a_at	Ssr2	signal sequence receptor, beta	1.14	0.392	1.07	0.666	-1.17	0.163	1.03	0.908	0.52
1426560_a_at	Npnt	nephronectin	1.18	0.546	1.36	0.383	-1.88	0.07	1.36	0.111	0.5
1427828_at	---	Murine retrovirus readthrough RNA sequence	1.14	0.645	-1.84	0.099	1.38	0.463	3.81	0.256	1.12
1457416_at	Metap2	Methionine aminopeptidase 2	1.02	0.937	-1.06	0.836	1.1	0.789	1.84	0.13	0.73
1451449_at	4933407N01Rik	RIKEN cDNA 4933407N01 gene	-1.05	0.5	1.04	0.776	1.08	0.269	1.04	0.769	0.53
1443872_at	2-Mar	Membrane-associated ring finger (C3HC4) 2	1.13	0.765	1	1	-1.07	0.787	4.19	0.188	1.31
1418813_at	Serpina5	serine (or cysteine) peptidase inhibitor, clade A, member 5	1.3	0.123	1	0.993	-1.31	0.258	1.06	0.694	0.51
1428197_at	Tspan9	tetraspanin 9	-1.08	0.45	1.11	0.419	1.03	0.831	1.16	0.3	0.55
1417220_at	Fah	fumarylacetoacetate hydrolase	1.07	0.109	-1.22	0.325	1.18	0.017	2.96	0.018	1
1460284_at	Letm1	leucine zipper-EF-hand containing transmembrane protein 1	-1.1	0.688	1.04	0.91	1.12	0.542	1.74	0.128	0.7
1451422_at	Myo18a	myosin XVIIIa	-1.07	0.715	1.02	0.799	1.11	0.49	1.11	0.491	0.54
1422684_a_at	Exoc4	exocyst complex component 4	1.02	0.914	1.09	0.377	-1.05	0.688	1.13	0.197	0.55
1421725_at	Slc26a5	solute carrier family 26, member 5	1.19	0.762	-1.3	0.728	1.11	0.793	1.13	0.862	0.53
1424120_at	Rnf8	ring finger protein 8	1.15	0.078	1.03	0.758	-1.13	0.055	1.28	0.205	0.58
1426681_at	Zc3h5	zinc finger CCCH type containing 5	-1.12	0.389	1.09	0.574	1.08	0.72	1.01	0.971	0.52
1432159_a_at	Tex13	testis expressed gene 13	1.25	0.81	1.06	0.073	-1.31	0.501	1.16	0.419	0.54
1439613_at	Sacy	soluble adenylyl cyclase	1.32	0.569	1.23	0.644	-1.92	0.124	1.37	0.455	0.5
1435542_s_at	Cttnbp2nl	CTTNBP2 N-terminal like	1	0.985	1.1	0.333	-1.04	0.834	1.06	0.793	0.53
1445218_at	Vax2	Ventral anterior homeobox containing gene 2	1.19	0.744	1.07	0.893	-1.24	0.558	1.85	0.247	0.72
1425966_x_at	Ubc	ubiquitin C	-1.26	0.203	1.14	0.672	1.14	0.53	1.34	0.218	0.59

1450353_at	Slc25a17	solute carrier family 25 (mitochondrial carrier, peroxisomal membrane protein), m	1.03	0.978	1.37	0.474	-1.5	0.236	1.38	0.354	0.57
1458024_at	B930018B01	hypothetical protein B930018B01	1.12	0.686	1.18	0.776	-1.32	0.085	1.02	0.963	0.5
1435356_at	Fbxo42	F-box protein 42	-1.05	0.804	1.1	0.808	1.01	0.971	1.48	0.173	0.64
1422045_a_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	1.02	0.944	1.1	0.454	-1.04	0.642	1.18	0.212	0.56
1432245_s_at	Ttc9c	tetratricopeptide repeat domain 9C	-1.08	0.771	1.11	0.521	1.03	0.79	1.47	0.282	0.63
1422778_at	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	-1.14	0.423	1.09	0.639	1.1	0.512	1.11	0.685	0.54
1417166_at	Psip1	PC4 and SFRS1 interacting protein 1	1.2	0.089	1.04	0.535	-1.2	0.042	1.31	0.244	0.59
1439499_at	AA415398	expressed sequence AA415398	1.21	0.028	-1.24	0.333	1.05	0.595	1.68	0.165	0.68
1429620_at	8430406I07Rik	RIKEN cDNA 8430406I07 gene	1	0.994	1.16	0.763	-1.11	0.63	1.54	0.448	0.65
1448336_at	Drg1	developmentally regulated GTP binding protein 1	1.03	0.12	-1.02	0.796	1.06	0.646	1.25	0.288	0.58
1433533_x_at	Prkag1	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	1.14	0.599	1.05	0.882	-1.15	0.543	1.89	0.286	0.73
1448787_at	Moap1	modulator of apoptosis 1	1.08	0.369	-1.21	0.054	1.16	0.269	1.52	0.305	0.64
1451695_a_at	Gpx4	glutathione peroxidase 4	1.1	0.64	1.1	0.089	-1.15	0.078	1.54	0.218	0.65
1424239_at	2310066E14Rik	RIKEN cDNA 2310066E14 gene	1.09	0.524	-1.23	0.085	1.17	0.563	1.16	0.235	0.55
1419766_at	Snf1lk	SNF1-like kinase	1.08	0.792	-1.06	0.84	1.04	0.843	1.37	0.279	0.61
1418965_at	Nosip	nitric oxide synthase interacting protein	1.02	0.924	1.04	0.747	1.01	0.912	-1.05	0.692	0.51
1433689_s_at	Rps9	ribosomal protein S9	1.02	0.476	1.01	0.918	1.05	0.619	-1.37	0.026	0.42
1424232_a_at	BC025546	cDNA sequence BC025546	1.06	0.748	-1.28	0.352	1.23	0.415	1.01	0.933	0.5
1456240_x_at	Cdca4	cell division cycle associated 4	-1.61	0.004	1.25	0.236	1.2	0.267	1.59	0.326	0.61
1428334_at	Ostm1	osteopetrosis associated transmembrane protein 1	1.11	0.08	1.01	0.935	-1.05	0.572	1	0.978	0.52
1421968_a_at	Nipa2	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	1.03	0.476	-1.02	0.878	1.06	0.687	1.42	0.231	0.62
1430327_at	Scamp4	secretory carrier membrane protein 4	-1.05	0.796	1.05	0.751	1.07	0.811	1.3	0.243	0.59
1423558_at	Ifngr2	interferon gamma receptor 2	-1.33	0	1.15	0.202	1.17	0.481	1.08	0.703	0.52
1443948_at	Ttc9c	tetratricopeptide repeat domain 9C	1.02	0.965	-1.06	0.582	1.11	0.681	1.04	0.901	0.53
1422551_at	Zfp306	zinc finger protein 306	-1	0.987	1.03	0.369	1.04	0.744	1.01	0.955	0.52
1440445_at	Pax6os1	Pax6 opposite strand transcript 1	-1.24	0.392	1.15	0.854	1.12	0.721	1.46	0.511	0.62
1441931_x_at	Gss	glutathione synthetase	1.04	0.859	1.26	0.132	-1.3	0.092	1.13	0.54	0.53
1417702_a_at	Hnmt	histamine N-methyltransferase	-1.12	0.207	1.15	0.267	1.04	0.855	1.27	0.314	0.58
1455985_x_at	Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)	1.01	0.893	-1.1	0.615	1.15	0.604	1.19	0.081	0.56
1452744_at	2210016F16Rik	RIKEN cDNA 2210016F16 gene	-1.07	0.497	1.08	0.659	1.05	0.758	1.04	0.602	0.53
1417459_at	Dcpp	demilune cell and parotid protein	-1.32	0.584	1.03	0.925	1.28	0.642	2.14	0.313	0.78
1423680_at	Fads1	fatty acid desaturase 1	-1.15	0.372	1.08	0.655	1.12	0.277	1.87	0.109	0.73
1438600_at	LOC624855	similar to Cyclin-dependent kinases regulatory subunit 1 (CKS-1) (Sid 1334)	1.08	0.791	1.3	0.599	-1.45	0.359	1.12	0.765	0.51
1443515_at	1110032F04Rik	RIKEN cDNA 1110032F04 gene	-3.05	0.173	1.28	0.613	1.46	0.436	1.12	0.41	0.2
1429360_at	Klf3	Kruppel-like factor 3 (basic)	1.07	0.805	-1.1	0.435	1.09	0.228	1.25	0.372	0.58
1430325_at	---	---	-1.66	0.5	1.43	0.282	1.05	0.932	1.64	0.283	0.61
AFFX-TrpnX-5_at	---	---	-1.29	0.593	1.19	0.687	1.1	0.315	1.27	0.412	0.57
1452840_at	1500009L16Rik	RIKEN cDNA 1500009L16 gene	1.11	0.725	1.21	0.657	-1.33	0.039	1.1	0.899	0.52
1459235_at	---	---	1.16	0.809	1.52	0.483	-2.53	0.038	1.22	0.768	0.34
1425520_a_at	Dhdds	dehydrodolichyl diphosphate synthase	1.06	0.836	-1.19	0.554	1.18	0.505	1.1	0.584	0.54
1448635_at	Smc2	structural maintenance of chromosomes 2	1.09	0.523	-1.12	0.329	1.09	0.207	3.3	0.148	1.09
1433356_at	2610021J01Rik	RIKEN cDNA 2610021J01 gene	1.04	0.843	1.2	0.698	-1.19	0.65	1.27	0.586	0.58
1444389_at	D14Ertd426e	DNA segment, Chr 14, ERATO Doi 426, expressed	-2.5	0.289	1.57	0.11	1.1	0.839	1.14	0.835	0.33
1421974_at	Lrrc50	leucine rich repeat containing 50	1.15	0.765	-1.56	0.475	1.28	0.575	1.12	0.874	0.5
1451826_at	Cabp5	calcium binding protein 5	1.23	0.555	-2.08	0.119	1.37	0.553	1.25	0.568	0.44
1460320_at	Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	1.1	0.047	-1.12	0.313	1.08	0.686	1.34	0.1	0.6
1454963_at	E430028B21Rik	RIKEN cDNA E430028B21 gene	-1.14	0.202	1.01	0.95	1.18	0.31	1.14	0.603	0.55
1448410_at	Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	-1.08	0.246	1.12	0.391	1.03	0.654	1.12	0.191	0.55
1419213_at	Nat6	N-acetyltransferase 6	1.12	0.551	-1.09	0.525	1.03	0.64	1.67	0.114	0.68
1423927_at	Slc35b2	solute carrier family 35, member B2	-1.19	0.333	1.07	0.579	1.17	0.468	1.01	0.9	0.51
1422093_at	Wnt3a	wingless-related MMTV integration site 3A	-1.4	0.655	1.1	0.82	1.26	0.396	1.06	0.939	0.5
1442270_at	Pbx3	Pre B-cell leukemia transcription factor 3	1.54	0.16	1.04	0.577	-2.01	0.036	2.11	0.194	0.67
1442524_at	---	Transcribed locus	1.08	0.842	-1.02	0.957	1.02	0.925	1.04	0.798	0.53

1424474_a_at	Camkk2	calcium/calmodulin-dependent protein kinase kinase 2, beta	-1.15	0.181	1.08	0.671	1.12	0.309	1.05	0.792	0.53
1453740_a_at	Ccnl2	cyclin L2	1.02	0.96	1.02	0.921	1.03	0.884	-1.02	0.954	0.51
1451450_at	2010011I20Rik	RIKEN cDNA 2010011I20 gene	1.06	0.642	-1.12	0.288	1.12	0.666	4.71	0.222	1.44
1434433_x_at	Wdr61	WD repeat domain 61	1.17	0.702	-1.42	0.296	1.2	0.477	1.54	0.309	0.62
1430182_a_at	1700006J14Rik	RIKEN cDNA 1700006J14 gene	-2.75	0.275	1.06	0.888	1.65	0.104	2.21	0.31	0.54
1417109_at	Tinagl	tubulointerstitial nephritis antigen-like	1.12	0.529	1.04	0.904	-1.09	0.659	1.94	0.247	0.75
1454909_at	Tacc1	transforming, acidic coiled-coil containing protein 1	1.07	0.687	1.03	0.823	-1.02	0.881	1.14	0.405	0.55
1420082_at	D2Ertd750e	DNA segment, Chr 2, ERATO Doi 750, expressed	1.02	0.975	1.07	0.853	-1.02	0.937	1.5	0.194	0.64
1429394_at	A130010J15Rik	RIKEN cDNA A130010J15 gene	1.08	0.618	-1.26	0.093	1.19	0.35	1.1	0.529	0.53
1426876_at	4732466D17Rik	RIKEN cDNA 4732466D17 gene	1.05	0.747	-1.02	0.823	1.04	0.804	1.45	0.232	0.63
1435841_s_at	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	-1.23	0.136	1.08	0.389	1.18	0.241	1.12	0.197	0.54
1438734_at	A530016L24Rik	RIKEN cDNA A530016L24 gene	-1.18	0.383	1.13	0.68	1.1	0.853	1.12	0.485	0.54
1439259_x_at	Abhd4	abhydrolase domain containing 4	1.07	0.181	-1	0.949	1.01	0.933	1.45	0.19	0.63
1418518_at	Furin	furin (paired basic amino acid cleaving enzyme)	1.12	0.426	-1.19	0.195	1.11	0.456	1.33	0.257	0.59
1433569_x_at	Ran /// LOC625094	RAN, member RAS oncogene family /// similar to RAN, member RAS oncogene f	-1.02	0.53	1.04	0.745	1.05	0.495	1.12	0.471	0.55
1428701_at	Pvrl4	poliovirus receptor-related 4	-1.19	0.308	1.03	0.939	1.2	0.449	1.14	0.712	0.55
1446179_at	C030014K22Rik	RIKEN cDNA C030014K22 gene	-1.28	0.017	1.01	0.976	1.29	0.057	1.13	0.345	0.54
1430968_at	4930517O19Rik	RIKEN cDNA 4930517O19 gene	1.41	0.488	-2.24	0.222	1.22	0.382	1.48	0.403	0.47
1449006_at	Gla	galactosidase, alpha	-1.25	0.765	1.23	0.548	1.05	0.878	1.84	0.333	0.72
1432225_at	---	---	-1.89	0.252	1.3	0.702	1.25	0.647	1.2	0.373	0.46
1420655_at	Pnpla3	patatin-like phospholipase domain containing 3	-1.24	0.028	1.03	0.857	1.24	0.101	1.4	0.172	0.61
1460348_at	Mad2l2	MAD2 mitotic arrest deficient-like 2 (yeast)	1.05	0.286	1.04	0.831	-1.02	0.898	1.2	0.359	0.57
1451400_at	BC023488	cDNA sequence BC023488	-1.58	0.003	1.26	0.491	1.18	0.036	1.26	0.395	0.53
1416534_at	Dpf2	D4, zinc and double PHD fingers family 2	1.05	0.376	-1.11	0.32	1.13	0.272	1.12	0.588	0.55
1453674_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	-1.25	0.008	1.2	0.765	1.08	0.883	2.1	0.2	0.78
1423330_at	Ensa	endosulfine alpha	1.12	0.658	1.04	0.804	-1.09	0.614	1.1	0.596	0.54
1438656_x_at	Timm17b	translocase of inner mitochondrial membrane 17b	1.02	0.898	-1.05	0.357	1.1	0.7	1.16	0.516	0.56
1459765_s_at	Sf1	Splicing factor 1	1.09	0.552	-1.02	0.744	1	0.942	1.03	0.751	0.53
1434153_at	Shb	src homology 2 domain-containing transforming protein B	-1.09	0.527	1.07	0.683	1.1	0.685	1.09	0.459	0.54
1431573_at	Satl1	spermidine/spermine N1-acetyl transferase-like 1	-1.92	0.137	1.29	0.175	1.26	0.419	1.47	0.622	0.53
1423912_at	Aspscr1	alveolar soft part sarcoma chromosome region, candidate 1 (human)	1.03	0.885	1.01	0.967	1.04	0.799	-1.13	0.492	0.49
1416374_at	Ap3m1 /// LOC671	adaptor-related protein complex 3, mu 1 subunit /// similar to AP-3 complex subur	1.07	0.317	-1.16	0.446	1.14	0.659	1.06	0.845	0.53
1436019_a_at	Trappc1	trafficking protein particle complex 1	-1.06	0.689	1.05	0.424	1.08	0.611	1.13	0.315	0.55
1436552_at	Jakmip2	janus kinase and microtubule interacting protein 2	1.02	0.937	-1	0.994	1.07	0.76	1.36	0.364	0.61
1426205_at	Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	-1.09	0.255	1.11	0.458	1.04	0.742	1.37	0.25	0.61
1453738_at	C330018D20Rik	RIKEN cDNA C330018D20 gene	-1.1	0.581	1.08	0.473	1.09	0.68	1.17	0.442	0.56
1434094_at	6330530A05Rik	RIKEN cDNA 6330530A05 gene	1.04	0.793	-1.09	0.632	1.13	0.67	1.21	0.469	0.57
1422709_a_at	Wdr46	WD repeat domain 46	-1	0.988	1.02	0.923	1.06	0.607	1.05	0.81	0.53
1426355_a_at	6330578E17Rik	RIKEN cDNA 6330578E17 gene	-1.02	0.869	1.02	0.774	1.08	0.446	1.22	0.168	0.57
1426987_at	5430417L22Rik	RIKEN cDNA 5430417L22 gene	1.05	0.73	-1.14	0.427	1.16	0.528	1.46	0.415	0.63
1434719_at	A2m /// LOC67736	alpha-2-macroglobulin /// hypothetical protein LOC677369	1.28	0.21	1.06	0.858	-1.34	0.507	1.63	0.089	0.65
1451979_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	-1.04	0.757	1.08	0.598	1.04	0.615	1.07	0.587	0.54
1433686_at	Cabin1	calcineurin binding protein 1	-1.37	0.156	1.04	0.674	1.31	0.004	1.2	0.542	0.55
1451480_at	E2f4	E2F transcription factor 4	-1.24	0.321	1.01	0.967	1.27	0.294	2	0.124	0.76
1442379_at	MGC99845	hypothetical protein LOC574403	1.1	0.798	1.03	0.951	-1.06	0.871	1.08	0.686	0.54
1418592_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	1	0.969	-1.19	0.658	1.24	0.644	4.38	0.235	1.36
1434578_x_at	Ran /// LOC625094	RAN, member RAS oncogene family /// similar to RAN, member RAS oncogene f	-1.12	0.124	1.08	0.532	1.11	0.438	1.16	0.399	0.56
1434758_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	1.24	0.217	1.14	0.788	-1.43	0.05	1.12	0.605	0.52
1455259_a_at	D530033C11Rik	RIKEN cDNA D530033C11 gene	1.03	0.673	-1.67	0.084	1.46	0.345	1.08	0.818	0.47
1433664_at	Ube2q2	ubiquitin-conjugating enzyme E2Q (putative) 2	1.26	0.061	1.02	0.873	-1.25	0.124	1.27	0.078	0.58
1453842_at	4930448K12Rik	RIKEN cDNA 4930448K12 gene	1.06	0.877	-1.66	0.32	1.42	0.216	1.63	0.013	0.61
1426474_at	Atpaf2	ATP synthase mitochondrial F1 complex assembly factor 2	1	0.991	-1.16	0.228	1.22	0.082	1.58	0.298	0.66
1423241_a_at	Tfdp1 /// LOC6648	transcription factor Dp 1 /// similar to Transcription factor Dp-1 (E2F dimerization	-1.12	0.182	1.02	0.815	1.16	0.309	2.04	0.242	0.78

1457240_at	Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	1.17	0.43	1.03	0.896	-1.14	0.622	1.02	0.821	0.52
1447840_x_at	E2f1	E2F transcription factor 1	1.15	0.561	-1.22	0.116	1.11	0.665	3.05	0.277	1.02
1447151_at	4930519N13Rik	RIKEN cDNA 4930519N13 gene	1.72	0.429	-2.91	0.03	1.02	0.969	2.38	0.29	0.55
1432796_at	3110067C02Rik	RIKEN cDNA 3110067C02 gene	1.31	0.613	-1.3	0.684	1.01	0.986	1.37	0.485	0.59
1426705_s_at	Iars	isoleucine-tRNA synthetase	1.04	0.777	-1.02	0.563	1.06	0.588	1.23	0.286	0.58
1443525_at	Dbx2	Developing brain homeobox 2	1.17	0.089	1.21	0.695	-1.43	0.615	1.07	0.888	0.5
1441538_at	Dpp6	Dipeptidylpeptidase 6	1.05	0.717	1.13	0.461	-1.12	0.499	1.34	0.276	0.6
1416937_at	Gabarap	gamma-aminobutyric acid receptor associated protein	1.05	0.849	1.09	0.466	-1.07	0.634	1.06	0.68	0.53
1439432_x_at	Morf4l2 /// LOC433	mortality factor 4 like 2 /// similar to Mortality factor 4-like protein 2 (MORF-relatec	1.11	0.598	1.2	0.327	-1.29	0.034	1.09	0.199	0.53
1428774_at	Gpc6	glypican 6	1.09	0.304	1.33	0.092	-1.51	0.032	1.09	0.277	0.5
1426797_at	2700094F01Rik	RIKEN cDNA 2700094F01 gene	-1.13	0.267	1.03	0.846	1.17	0.27	1.14	0.561	0.55
1432223_at	4930552N02Rik	RIKEN cDNA 4930552N02 gene	1.41	0.185	1.21	0.737	-2.13	0.265	1.05	0.932	0.38
1419257_at	Tcea1	transcription elongation factor A (SII) 1	1.08	0.837	-1.25	0.543	1.21	0.591	1.32	0.571	0.59
1455212_at	Wdr24	WD repeat domain 24	1.02	0.938	1.05	0.688	1.01	0.938	-1.01	0.896	0.52
1448339_at	Tmem30a	transmembrane protein 30A	1.13	0.443	-1.12	0.456	1.07	0.777	1.01	0.934	0.52
1426703_at	Gak	cyclin G associated kinase	1.05	0.439	-1.08	0.491	1.11	0.51	1.12	0.375	0.55
1460644_at	Bckdk	branched chain ketoacid dehydrogenase kinase	1.02	0.854	-1.01	0.938	1.07	0.531	1.1	0.452	0.55
1455674_at	Wdr76	WD repeat domain 76	1.07	0.719	-1.01	0.954	1.03	0.885	1.71	0.243	0.7
1444305_at	LOC668940 /// LOC	hypothetical protein LOC668940 /// hypothetical protein LOC669705 /// hypothetic	1.09	0.895	1.13	0.703	-1.16	0.707	1.44	0.455	0.63
AFFX-BioB-3_at	---	---	1.41	0.047	1.08	0.529	-1.69	0.1	1.04	0.899	0.46
1437309_a_at	Rpa1	replication protein A1	1.07	0.466	-1.13	0.123	1.13	0.23	1.06	0.681	0.53
1441288_at	---	---	-2.28	0.131	1.28	0.655	1.36	0.51	1.27	0.6	0.41
1431990_at	4930429D17Rik	RIKEN cDNA 4930429D17 gene	1.07	0.898	-1.13	0.789	1.14	0.547	1.02	0.963	0.52
1460570_at	Pgbd5	piggyBac transposable element derived 5	1.28	0.57	1.07	0.75	-1.36	0.278	2.09	0.171	0.77
1452235_at	Man1b1	mannosidase, alpha, class 1B, member 1	1.3	0.478	1.05	0.452	-1.36	0.16	1.31	0.088	0.57
1428930_at	Tmem29	transmembrane protein 29	1.06	0.739	1.07	0.453	-1.05	0.729	1.34	0.289	0.6
1454902_at	Prkcz	protein kinase C, zeta	-1.07	0.579	1.09	0.788	1.06	0.547	1.25	0.617	0.58
1445825_at	---	---	1.19	0.55	1.11	0.737	-1.28	0.608	3.02	0.004	1.01
1441876_x_at	Zfp93	Zinc finger protein 93	1.32	0.262	-1.7	0.435	1.18	0.661	1.21	0.69	0.5
1423700_at	Rfc3	replication factor C (activator 1) 3	1.07	0.768	-1.22	0.465	1.19	0.546	1.66	0.346	0.68
1417566_at	Abhd5	abhydrolase domain containing 5	1.07	0.452	-1.08	0.692	1.08	0.773	2.71	0.232	0.95
1418527_a_at	Fusip1	FUS interacting protein (serine-arginine rich) 1	1.04	0.811	-1.13	0.108	1.16	0.519	1.43	0.429	0.63
1460094_at	---	---	1.28	0.733	1.18	0.765	-1.62	0.416	1.77	0.357	0.65
1433906_at	4933402J24Rik	RIKEN cDNA 4933402J24 gene	1.07	0.875	1.27	0.137	-1.35	0.305	1.71	0.175	0.68
1451697_a_at	Evc	Ellis van Creveld gene homolog (human)	1.09	0.89	1.5	0.566	-2	0.123	1.05	0.91	0.41
1421611_at	AB041806	hypothetical protein, MNCb-2457	1.21	0.417	1.16	0.573	-1.4	0.143	1.89	0.029	0.71
1440156_s_at	AI851523	expressed sequence AI851523	-1.52	0.32	1.11	0.637	1.32	0.32	1.18	0.698	0.52
1429618_at	Cyld	cylindromatosis (turban tumor syndrome)	1.03	0.886	1.01	0.947	1.05	0.594	-1.18	0.55	0.48
1452173_at	Hadha	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl	1.05	0.74	-1.16	0.181	1.17	0.156	1.25	0.097	0.58
1458387_at	Ptdss2	phosphatidylserine synthase 2	1.45	0.288	1.03	0.953	-1.66	0.285	2.88	0.274	0.93
1431358_at	4930547N16Rik	RIKEN cDNA 4930547N16 gene	-1.09	0.748	1.07	0.871	1.1	0.599	2.84	0.263	0.98
1416162_at	Rad21	RAD21 homolog (S. pombe)	1.1	0.611	-1.18	0.193	1.15	0.65	2.05	0.262	0.78
1460539_at	4933404K13Rik	RIKEN cDNA 4933404K13 gene	-1.87	0.002	1.28	0.131	1.27	0.321	1.55	0.503	0.56
1452969_at	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	1.1	0.556	1.29	0.425	-1.44	0.347	1.05	0.877	0.5
1452218_at	Ccdc117	coiled-coil domain containing 117	1.07	0.364	-1.17	0.473	1.16	0.626	1.24	0.547	0.57
1434045_at	Cdkn1b	cyclin-dependent kinase inhibitor 1B	1.02	0.061	-1.15	0.564	1.19	0.366	1.35	0.231	0.6
1419578_at	Mbl1	mannose binding lectin (A)	1.22	0.495	1.04	0.82	-1.21	0.231	1.11	0.725	0.54
1428976_at	Tmpo	thymopoietin	1.01	0.882	1.18	0.178	-1.12	0.36	2.34	0.068	0.85
1425979_a_at	Fbf1	Fas (TNFRSF6) binding factor 1	1.06	0.299	1.18	0.588	-1.18	0.418	1.33	0.173	0.6
1437193_s_at	Snrpb	small nuclear ribonucleoprotein B	-1.01	0.969	1.05	0.437	1.04	0.817	1.14	0.342	0.56
1444852_at	Fmo4	Flavin containing monooxygenase 4	-4.09	0.004	1.18	0.796	1.66	0.28	2.1	0.039	0.21
1456786_at	Ldb2	LIM domain binding 2	1.11	0.653	1.14	0.815	-1.19	0.455	1.03	0.951	0.52
1434342_at	S100b	S100 protein, beta polypeptide, neural	-1.29	0.67	1.18	0.712	1.14	0.689	1.15	0.686	0.54

1426015_s_at	Asph	aspartate-beta-hydroxylase	1.06	0.487	1.07	0.592	-1.04	0.679	1.56	0.132	0.66
1438274_at	Zfpn1a4	zinc finger protein, subfamily 1A, 4 (Eos)	1.19	0.536	-1.46	0.221	1.21	0.572	1.18	0.349	0.53
1435824_at	Yy1	YY1 transcription factor	1.05	0.474	-1.13	0.367	1.16	0.133	1.07	0.598	0.54
1417666_at	Dnttip1	deoxynucleotidyltransferase, terminal, interacting protein 1	-1.04	0.626	1.07	0.544	1.06	0.486	1.21	0.414	0.57
1455482_at	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	1.19	0.504	1.06	0.558	-1.2	0.596	2.58	0.139	0.91
1432663_at	1500005C15Rik	RIKEN cDNA 1500005C15 gene	1.49	0.334	-1.92	0.264	1.08	0.851	1.26	0.649	0.48
1455321_at	Ddhd1	DDHD domain containing 1	1.06	0.856	1.23	0.316	-1.25	0.18	1.06	0.819	0.52
1456170_x_at	Calr	calreticulin	1.08	0.549	1.11	0.404	-1.11	0.161	1.21	0.28	0.57
1421407_at	F2rl2	coagulation factor II (thrombin) receptor-like 2	-1.45	0.432	1.06	0.617	1.34	0.32	2.47	0.326	0.85
1426854_a_at	Set	SET translocation	1.11	0.582	1.05	0.667	-1.07	0.691	1.05	0.352	0.53
1458781_at	Kcnk13	Potassium channel, subfamily K, member 13	1.06	0.878	1.54	0.459	-2.05	0.061	1.02	0.935	0.39
1448903_at	15-Sep	selenoprotein	1.03	0.22	1.15	0.383	-1.09	0.248	1.17	0.05	0.56
1443454_at	Sctr	secretin receptor	-1.63	0.18	1.2	0.676	1.28	0.49	1.19	0.492	0.51
1431921_a_at	Stag1	stromal antigen 1	1.05	0.218	1.11	0.538	-1.08	0.4	1.15	0.312	0.56
1418844_at	Alg9	asparagine-linked glycosylation 9 homolog (yeast, alpha 1,2 mannosyltransferase	1.07	0.076	1.05	0.49	-1.04	0.67	1.7	0.075	0.7
1432069_at	1700023G09Rik	RIKEN cDNA 1700023G09 gene	-1.44	0.163	1.23	0.528	1.16	0.533	1.61	0.266	0.64
1427247_at	D3Bwg0562e	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	1.33	0.171	-1.36	0.502	1.02	0.915	1.75	0.253	0.69
1453970_at	4833417A11Rik	RIKEN cDNA 4833417A11 gene	-1.36	0.264	1.33	0.465	1.02	0.932	1	0.99	0.5
1454065_at	4930562D21Rik	RIKEN cDNA 4930562D21 gene	-2.01	0.343	1.47	0.389	1.13	0.79	1.22	0.684	0.45
1425390_at	Adat1	adenosine deaminase, tRNA-specific 1	1.15	0.353	-1.19	0.6	1.1	0.777	1.01	0.964	0.52
1458929_at	Abca9	ATP-binding cassette transporter sub-family A member 9	1.44	0.654	-2.21	0.057	1.2	0.64	1.2	0.732	0.41
1455952_at	Adprhl1	ADP-ribosylhydrolase like 1	-1.66	0.304	1.23	0.625	1.25	0.54	1.23	0.696	0.51
1426831_at	Ahcyl1	S-adenosylhomocysteine hydrolase-like 1	1.09	0.689	-1.04	0.843	1.04	0.877	1.04	0.889	0.53
1429189_at	1110007C02Rik	RIKEN cDNA 1110007C02 gene	-1.08	0.552	1.09	0.141	1.08	0.762	1.16	0.697	0.56
1416004_at	Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta p	-1.08	0.258	1.03	0.631	1.13	0.231	1.43	0.081	0.63
1447980_s_at	Rutbc2	RUN and TBC1 domain containing 2	-1.19	0.368	1.16	0.677	1.09	0.735	1.95	0.315	0.75
1418329_at	Pgpep1	pyroglutamyl-peptidase I	-1.14	0.604	1.19	0.216	1.03	0.838	1.08	0.693	0.54
1437678_at	Gm1564	gene model 1564, (NCBI)	1.31	0.244	1.09	0.87	-1.44	0.443	1.39	0.609	0.59
1420917_at	Prpf40a	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	1.01	0.983	-1.22	0.648	1.26	0.584	1.2	0.796	0.56
1431123_s_at	Dnajc8 /// LOC6692	DnaJ (Hsp40) homolog, subfamily C, member 8 /// similar to DnaJ (Hsp40) homol	1.04	0.852	1.05	0.477	-1	0.982	1.09	0.588	0.55
1446108_at	Ank2	Ankyrin 2, brain	-1.16	0.656	1.17	0.803	1.06	0.874	1.31	0.648	0.59
1425585_at	Med12	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)	1.12	0.612	-1.29	0.004	1.2	0.206	1.34	0.093	0.59
1434196_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	-1.03	0.848	1.04	0.814	1.08	0.655	3.26	0.196	1.09
1433601_at	Adra2a	adrenergic receptor, alpha 2a	1.39	0.727	-1.63	0.345	1.08	0.236	1.07	0.732	0.48
1453607_at	Mfap3l	microfibrillar-associated protein 3-like	-1.35	0.634	1.22	0.775	1.13	0.491	2.49	0.058	0.87
1428262_s_at	Hnrpa3 /// LOC545	heterogeneous nuclear ribonucleoprotein A3 /// similar to heterogeneous nuclear	1.05	0.406	1.19	0.139	-1.18	0.058	1.02	0.759	0.52
1422887_a_at	Ctbp2	C-terminal binding protein 2	1.06	0.198	1.22	0.112	-1.23	0.046	1.01	0.941	0.51
1453884_at	4930402K13Rik	RIKEN cDNA 4930402K13 gene	1.59	0.578	1.08	0.909	-2.35	0.151	1.58	0.539	0.47
1423732_at	Tram1	translocating chain-associating membrane protein 1	1.04	0.242	1.2	0.222	-1.17	0.065	1.2	0.002	0.57
1435678_at	2610017I09Rik	RIKEN cDNA 2610017I09 gene	1.09	0.544	-1.24	0.744	1.2	0.683	1.22	0.718	0.57
1450908_at	Eif4e /// LOC63052	eukaryotic translation initiation factor 4E /// hypothetical LOC630527	-1.05	0.752	1.1	0.526	1.04	0.708	1.45	0.275	0.64
1452338_s_at	Itsn1	intersectin 1 (SH3 domain protein 1A)	-1.21	0.32	1.2	0.168	1.07	0.797	2.88	0.185	0.98
1418459_at	Ccdc91	coiled-coil domain containing 91	1.06	0.648	1.02	0.909	1.01	0.978	-2.12	0.027	0.24
1431095_a_at	Herc5	hect domain and RLD 5	-1.26	0.597	1.15	0.648	1.15	0.347	1.25	0.372	0.57
1434001_at	Ttc9c	tetratricopeptide repeat domain 9C	-1.07	0.619	1.14	0.069	1.02	0.893	1.21	0.108	0.58
1420898_at	Snap23	synaptosomal-associated protein 23	1.01	0.953	1.07	0.574	1.02	0.893	-1.03	0.82	0.52
1418866_at	Cyp24a1	cytochrome P450, family 24, subfamily a, polypeptide 1	1.2	0.731	-3.32	0.101	1.59	0.064	1.05	0.91	0.13
1436208_at	Asb1	ankyrin repeat and SOCS box-containing protein 1	1.14	0.657	-1.25	0.413	1.16	0.339	4.87	0.212	1.48
1459441_at	Odz3	Odd Oz/ten-m homolog 3 (Drosophila)	-1.73	0.065	1.27	0.52	1.25	0.544	1.07	0.914	0.46
1426612_at	Tipin	timeless interacting protein	1.15	0.613	-1.09	0.713	1.02	0.857	2.78	0.2	0.97
1435051_at	Wdr44	WD repeat domain 44	-1.07	0.622	1.09	0.703	1.06	0.82	1.05	0.824	0.54
1447683_x_at	Mettl1	methyltransferase-like 1	-1.17	0.364	1.18	0.409	1.07	0.884	1.15	0.471	0.56
1423165_a_at	Mta2	metastasis-associated gene family, member 2	1.01	0.91	-1.2	0.32	1.25	0.084	1.1	0.323	0.54

1451018_at	Leprotl1	leptin receptor overlapping transcript-like 1	1.01	0.283	1.06	0.788	1.02	0.901	-1.62	0.142	0.37
1454075_s_at	Nudt13	nudix (nucleoside diphosphate linked moiety X)-type motif 13	1.01	0.939	1.04	0.872	1.05	0.862	-1.13	0.553	0.49
1416049_at	Gldc	glycine decarboxylase	-1.16	0.716	1.05	0.472	1.18	0.781	1.12	0.861	0.55
1431402_at	Kirrel3	kin of IRRE like 3 (Drosophila)	1.42	0.618	1.05	0.879	-1.61	0.258	1.04	0.887	0.48
1448880_at	Ube2l3	ubiquitin-conjugating enzyme E2L 3	-1.17	0.452	1.01	0.913	1.23	0.301	1.43	0.163	0.63
1443647_at	Rora	RAR-related orphan receptor alpha	1.32	0.559	-1.29	0.702	1	0.997	1.08	0.877	0.53
1437119_at	Ern1	Endoplasmic reticulum (ER) to nucleus signalling 1	1.09	0.537	1.02	0.879	-1.02	0.842	1.1	0.487	0.55
1422522_at	Fxr2h	fragile X mental retardation gene 2, autosomal homolog	1.1	0.368	-1.3	0.074	1.23	0.283	1.13	0.748	0.54
1417471_s_at	D1Ertd622e	DNA segment, Chr 1, ERATO Doi 622, expressed	1.12	0.722	-1.15	0.435	1.11	0.608	1.37	0.446	0.61
1421095_a_at	Trpc1	transient receptor potential cation channel, subfamily C, member 1	1.28	0.116	-1.57	0.34	1.17	0.559	2.02	0.144	0.73
1434117_at	Tceb3	transcription elongation factor B (SIII), polypeptide 3	-1.02	0.859	1.01	0.922	1.11	0.629	1.65	0.238	0.69
1438001_x_at	Reep5	receptor accessory protein 5	1.1	0.516	1.08	0.538	-1.1	0.505	1.27	0.146	0.59
1418234_s_at	Bcas2	breast carcinoma amplified sequence 2	1.09	0.329	1.02	0.782	-1.01	0.895	1.39	0.275	0.62
1419546_at	Atp6v1c1	ATPase, H+ transporting, lysosomal V1 subunit C1	-1.13	0.051	1.08	0.519	1.13	0.131	1.01	0.865	0.52
1451990_at	Mapre2	microtubule-associated protein, RP/EB family, member 2	1.03	0.913	-1.02	0.965	1.09	0.823	1.03	0.898	0.53
1416906_at	Anapc5	anaphase-promoting complex subunit 5	1.09	0.052	-1.01	0.866	1.02	0.823	1.36	0.188	0.61
1451435_at	Cutl1	cut-like 1 (Drosophila)	1.08	0.647	-1.17	0.076	1.17	0.523	1.32	0.26	0.6
1424378_at	Ldlrap1	low density lipoprotein receptor adaptor protein 1	-1.14	0.437	1.05	0.545	1.17	0.06	1.39	0.286	0.62
1436343_at	Chd4	chromodomain helicase DNA binding protein 4	1.12	0.503	-1.28	0.325	1.2	0.504	1.05	0.828	0.52
1441937_s_at	Pink1	PTEN induced putative kinase 1	1.11	0.371	1.03	0.84	-1.05	0.573	1.15	0.242	0.56
1437973_at	Lrrn6c	leucine rich repeat neuronal 6C	1.1	0.816	1.06	0.795	-1.07	0.75	1.2	0.551	0.57
1438202_at	C920005C14Rik	RIKEN cDNA C920005C14 gene	1.04	0.947	1.37	0.678	-1.45	0.143	6.32	0.195	1.82
1433739_at	Nol10	nucleolar protein 10	1.06	0.636	-1.18	0.553	1.19	0.333	1.2	0.533	0.57
1449933_a_at	5730449L18Rik	RIKEN cDNA 5730449L18 gene	1.06	0.526	1.11	0.123	-1.08	0.449	1.38	0.297	0.62
1422480_at	Snx3	sorting nexin 3	1.05	0.222	-1.04	0.642	1.09	0.268	1.34	0.042	0.61
1456693_at	4933406F09Rik	RIKEN cDNA 4933406F09 gene	1.16	0.668	1.07	0.891	-1.16	0.674	1.58	0.297	0.66
1442604_at	Ercc6	excision repair cross-complementing rodent repair deficiency, complementation g	1.07	0.744	1.33	0.353	-1.44	0.231	1.21	0.551	0.54
1425917_at	H28	histocompatibility 28	1.16	0.712	-1.11	0.573	1.03	0.887	2.4	0.418	0.87
1459449_at	Cnot4	CCR4-NOT transcription complex, subunit 4	1.13	0.756	1.32	0.116	-1.55	0.014	1.17	0.561	0.52
1434309_at	Fntb	farnesyltransferase, CAAX box, beta	-1.11	0.758	1.14	0.755	1.05	0.817	2.39	0.205	0.87
1457757_at	LOC269389	similar to granulosa cell HMG-box protein-1	1.08	0.857	1.15	0.614	-1.15	0.728	1.59	0.565	0.67
1425497_a_at	Prpf4b	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1.08	0.163	-1.02	0.924	1.03	0.795	1.02	0.867	0.53
1443723_at	Trpm3	transient receptor potential cation channel, subfamily M, member 3	-1.98	0.165	1.11	0.885	1.49	0.418	1.64	0.256	0.56
1453333_at	1700012P22Rik	RIKEN cDNA 1700012P22 gene	1.09	0.865	-1.34	0.598	1.27	0.586	1.23	0.686	0.56
1435052_at	4930455F23Rik	RIKEN cDNA 4930455F23 gene	1.11	0.63	1.05	0.881	-1.07	0.678	1.05	0.799	0.54
1420556_at	Oxt	oxytocin	-1.11	0.353	1.17	0.44	1.03	0.887	1.02	0.954	0.53
1456767_at	Lrfn3	leucine rich repeat and fibronectin type III domain containing 3	-1.15	0.318	1.01	0.97	1.22	0.319	1.03	0.748	0.53
1416159_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	1.25	0.379	1.02	0.932	-1.19	0.204	1.05	0.847	0.53
1432999_at	Pde11a	phosphodiesterase 11A	1.05	0.882	-1.78	0.141	1.49	0.087	1.66	0.332	0.6
1417739_at	Med11	mediator of RNA polymerase II transcription, subunit 11 homolog (S. cerevisiae)	1	0.986	1.04	0.737	1.06	0.761	-1.51	0.135	0.4
1441476_at	Socs2	suppressor of cytokine signaling 2	1.41	0.573	1.01	0.963	-1.47	0.232	1.18	0.301	0.53
1426341_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	-1.64	0.146	1.27	0.636	1.22	0.62	2.25	0.068	0.78
1447324_at	---	---	1.23	0.465	-1.22	0.542	1.05	0.757	1.05	0.689	0.53
1415682_at	Xpo7	exportin 7	1.03	0.818	-1.12	0.548	1.18	0.449	4.46	0.174	1.39
1421871_at	Sh3bgrl	SH3-binding domain glutamic acid-rich protein like	1.08	0.396	-1.04	0.733	1.06	0.769	1.14	0.249	0.56
1437360_at	Pcdh19	protocadherin 19	1.24	0.588	1.09	0.859	-1.3	0.408	2.01	0.38	0.76
1434650_at	Pogz	pogo transposable element with ZNF domain	1	0.997	1.07	0.629	1.03	0.924	-1.04	0.79	0.52
1458798_at	---	Transcribed locus	1.2	0.578	1.24	0.238	-1.52	0.069	1.05	0.898	0.49
1445186_at	Stc2	stanniocalcin 2	1.2	0.176	-1.12	0.754	1.01	0.953	1.03	0.732	0.53
1423739_x_at	Aplp2	amyloid beta (A4) precursor-like protein 2	1	0.984	-1.01	0.858	1.11	0.547	1.58	0.029	0.67
1417947_at	Pcna	proliferating cell nuclear antigen	-1.06	0.427	1.11	0.259	1.05	0.43	1.51	0.197	0.65
1452556_at	---	Envelope protein, mRNA sequence	1.13	0.054	-1.23	0.561	1.15	0.499	1.74	0.348	0.7
1455711_at	Dtx4	deltex 4 homolog (Drosophila)	1	0.994	-1.14	0.456	1.22	0.312	1.02	0.913	0.52

1433844_a_at	Dusp9	dual specificity phosphatase 9	-1.35	0.131	1.15	0.87	1.22	0.713	1.53	0.442	0.63
1415698_at	Golph2	golgi phosphoprotein 2	1.34	0.2	1.06	0.375	-1.42	0.141	1.61	0.143	0.65
1427953_at	BC025462	cDNA sequence BC025462	1.22	0.336	1.15	0.707	-1.36	0.364	2.79	0.26	0.95
1448644_at	Pef1	penta-EF hand domain containing 1	1.11	0.67	1.03	0.849	-1.04	0.881	1.99	0.174	0.77
1417295_at	Mta1	metastasis associated 1	-1.04	0.705	1.08	0.44	1.06	0.561	1.28	0.136	0.6
1421077_at	Sertad3	SERTA domain containing 3	-1.21	0.105	1.11	0.33	1.17	0.337	2.11	0.176	0.79
1417272_at	9130005N14Rik	RIKEN cDNA 9130005N14 gene	1.15	0.046	1.3	0.063	-1.53	0.007	1.06	0.751	0.49
1433448_at	B430110G05Rik	RIKEN cDNA B430110G05 gene	-1.21	0.437	1.03	0.853	1.24	0.3	1.75	0.125	0.7
1425615_a_at	Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-1.09	0.758	1.08	0.782	1.11	0.478	1.92	0.139	0.75
1444577_x_at	Numa1	Nuclear mitotic apparatus protein 1	-3.15	0.06	1.77	0.173	1.01	0.912	1.16	0.282	0.2
1417296_at	Atf1	activating transcription factor 1	1.06	0.406	-1.05	0.008	1.08	0.549	1.57	0.175	0.67
1415771_at	Ncl	nucleolin	1.01	0.851	-1.04	0.454	1.14	0.383	1.04	0.607	0.54
1428827_at	Whsc1	Wolf-Hirschhorn syndrome candidate 1 (human)	1.27	0.077	-1.39	0.453	1.11	0.49	2.36	0.23	0.84
1455562_at	Sox12	SRY-box containing gene 12	1.17	0.774	-1.2	0.317	1.11	0.721	1.44	0.183	0.63
1422260_x_at	Ccr5	chemokine (C-C motif) receptor 5	1.05	0.913	1.5	0.524	-1.8	0.063	1.35	0.432	0.52
1437394_at	Centg2	centaurin, gamma 2	1.08	0.701	1.14	0.567	-1.14	0.585	1.1	0.724	0.55
1445205_at	Gtpbp3	GTP binding protein 3	1.19	0.709	1.18	0.791	-1.35	0.23	1.1	0.702	0.53
1420018_s_at	Tspan8	tetraspanin 8	1.19	0.599	1.24	0.646	-1.48	0.01	3.42	0.141	1.09
1443794_x_at	Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	1.1	0.258	-1.28	0.281	1.22	0.342	1.35	0.348	0.6
1456956_at	Zfpn1a2	zinc finger protein, subfamily 1A, 2 (Helios)	1.13	0.654	1.17	0.484	-1.24	0.378	1.03	0.944	0.52
1418003_at	1190002H23Rik	RIKEN cDNA 1190002H23 gene	1.01	0.978	1.27	0.443	-1.22	0.586	3.98	0.209	1.26
1442106_at	Fancm	Fanconi anemia, complementation group M	-2.25	0.039	1.47	0.629	1.2	0.596	1.61	0.467	0.5
1429069_at	Stub1	STIP1 homology and U-Box containing protein 1	1.05	0.808	-1.01	0.954	1.07	0.818	1	0.995	0.53
1460704_at	Rfng	radical fringe gene homolog (Drosophila)	-1.05	0.672	1.08	0.313	1.07	0.529	1.18	0.204	0.57
1449774_at	---	---	-3.23	0.001	1.52	0.407	1.27	0.346	2.28	0.071	0.46
1444189_at	---	Transcribed locus	1.19	0.826	1.06	0.792	-1.17	0.206	1.09	0.782	0.54
1429600_at	C630010D07Rik ///	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofolate dehydro	-1.2	0.4	1.11	0.54	1.16	0.179	1.43	0.252	0.63
1438297_at	AA545190	EST AA545190	1.28	0.772	1.03	0.95	-1.26	0.448	1.44	0.639	0.62
1431007_at	9030025P20Rik	RIKEN cDNA 9030025P20 gene	1.28	0.588	-1.26	0.343	1.04	0.806	1.06	0.872	0.53
1417754_at	Topors	topoisomerase I binding, arginine/serine-rich	1.18	0.012	-1.1	0.584	1.01	0.835	1.36	0.204	0.61
1423794_at	D2Ertd391e	DNA segment, Chr 2, ERATO Doi 391, expressed	1.02	0.933	-1.19	0.523	1.24	0.282	1.06	0.731	0.53
1433854_at	Tmem164	transmembrane protein 164	-1.32	0.292	1.25	0.495	1.1	0.249	1.12	0.277	0.54
1429322_at	Exosc6	Exosome component 6	1.13	0.751	1.04	0.89	-1.07	0.788	1.09	0.814	0.55
1435702_s_at	Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsil	-1.18	0.244	1.05	0.697	1.21	0.113	1.01	0.935	0.52
1417050_at	C1qtnf4	C1q and tumor necrosis factor related protein 4	1.15	0.601	-1.42	0.635	1.25	0.308	2.51	0.017	0.87
1420511_at	Rds	retinal degeneration, slow (retinitis pigmentosa 7)	-1.02	0.938	1.12	0.741	1	0.966	1.19	0.49	0.57
1453386_at	Tusc1	tumor suppressor candidate 1	1.12	0.513	1.13	0.402	-1.16	0.499	2.32	0.129	0.85
1437539_at	Prkaa1	protein kinase, AMP-activated, alpha 1 catalytic subunit	-1.11	0.503	1.12	0.427	1.09	0.324	1.3	0.291	0.6
1429546_at	4930423K06Rik	RIKEN cDNA 4930423K06 gene	1.3	0.622	1.12	0.759	-1.46	0.114	1.72	0.379	0.67
1446898_at	Ubadc1	Ubiquitin associated domain containing 1	1.08	0.792	1.2	0.659	-1.21	0.686	5.18	0.128	1.56
1417849_at	Zfp704	zinc finger protein 704	1.09	0.634	-1	0.998	1.01	0.919	1.2	0.613	0.58
1427235_at	Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1.06	0.762	1.1	0.445	-1.05	0.763	1.29	0.338	0.6
1433095_at	---	---	-1.24	0.317	1.11	0.81	1.19	0.667	1.23	0.677	0.57
1434864_at	Nipa1	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	1.15	0.377	1.21	0.289	-1.33	0.152	6.27	0.19	1.82
1428391_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	1.12	0.514	1.07	0.725	-1.1	0.685	3.5	0.161	1.15
1428295_at	Synpo2l	synaptopodin 2-like	1.07	0.906	-1.73	0.297	1.46	0.387	1.3	0.67	0.52
1421972_s_at	Hcfc1	host cell factor C1	-1.03	0.946	1.02	0.97	1.12	0.712	1.91	0.177	0.75
1453375_at	4930422N03Rik	RIKEN cDNA 4930422N03 gene	1.07	0.83	1.06	0.922	-1.02	0.911	1.22	0.196	0.58
1431253_s_at	Tbc1d9	TBC1 domain family, member 9	1.05	0.904	-1.19	0.815	1.22	0.462	1.02	0.796	0.53
1421491_a_at	Tmem49	transmembrane protein 49	1.07	0.82	-1.04	0.887	1.08	0.827	1.82	0.223	0.73
1455335_at	Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2	1.02	0.939	1.09	0.734	-1	0.991	1.49	0.014	0.65
1420934_a_at	Srrm1	serine/arginine repetitive matrix 1	1.09	0.71	-1.06	0.783	1.08	0.804	1.34	0.063	0.61
1428310_at	Larp7	La ribonucleoprotein domain family, member 7	1.02	0.937	1.21	0.024	-1.14	0.104	1.35	0.333	0.61

1433916_at	Vamp3	vesicle-associated membrane protein 3	1.04	0.792	1.15	0.272	-1.09	0.211	1.64	0.132	0.68
1455573_at	Krt14	keratin 14	1.37	0.495	1.09	0.737	-1.55	0.186	1.07	0.703	0.5
1421015_s_at	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	1.04	0.708	-1.06	0.57	1.13	0.699	3.05	0.226	1.04
1426381_at	Pprc1	peroxisome proliferative activated receptor, gamma, coactivator-related 1	-1.11	0.508	1.04	0.784	1.17	0.592	1.15	0.501	0.56
1436348_at	---	Transcribed locus	-1.02	0.837	1.12	0.137	1.02	0.884	1.21	0.262	0.58
1426782_at	Gpr125	G protein-coupled receptor 125	1.13	0.304	-1.09	0.61	1.06	0.83	1.19	0.411	0.57
1417828_at	Aqp8	aquaporin 8	-1.18	0.742	1.04	0.895	1.23	0.415	1.06	0.703	0.54
1436078_at	Fcho1	FCH domain only 1	1.41	0.335	-1.52	0.648	1.05	0.911	1.15	0.679	0.52
1424449_at	Frs3	fibroblast growth factor receptor substrate 3	1.04	0.818	-1.07	0.9	1.13	0.532	1.67	0.378	0.69
1419874_x_at	Zbtb16	zinc finger and BTB domain containing 16	1.03	0.979	1.03	0.952	1.05	0.933	-1.77	0.203	0.33
1436630_at	Aqp11	Aquaporin 11	1.04	0.709	1.08	0.547	-1.01	0.953	1.15	0.569	0.57
1423119_at	Rshl2a	radial spokehead-like 2A	1.06	0.483	-1.13	0.105	1.17	0.156	1.19	0.182	0.57
1428531_at	Ints7	integrator complex subunit 7	1.02	0.837	1.1	0.504	-1.01	0.96	1.04	0.752	0.54
1419934_at	---	---	1.33	0.539	1.38	0.316	-2.49	0.137	1.52	0.483	0.44
1436416_x_at	Fxc1	fractured callus expressed transcript 1	-1.1	0.64	1.1	0.264	1.11	0.605	1.03	0.879	0.53
1425496_at	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3	-1.12	0.567	1.17	0.394	1.05	0.8	1.16	0.525	0.57
1450746_at	Keap1	kelch-like ECH-associated protein 1	-1.11	0.266	1.1	0.105	1.11	0.401	1.04	0.834	0.54
1428897_at	2610029I01Rik	RIKEN cDNA 2610029I01 gene	-1.31	0.236	1.1	0.211	1.25	0.011	1.26	0.343	0.58
1456613_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	1.2	0.793	-1.25	0.636	1.11	0.763	2.15	0.33	0.8
1423315_at	Bbc3	Bcl-2 binding component 3	-1.36	0.318	1.19	0.605	1.18	0.017	1	0.997	0.51
1442030_at	---	---	1.06	0.64	1.32	0.507	-1.35	0.153	1.37	0.51	0.6
1417118_a_at	Ard1	N-acetyltransferase ARD1 homolog (S. cerevisiae)	1.06	0.625	-1.09	0.196	1.14	0.173	1.03	0.91	0.53
1425191_at	9430098E02Rik	RIKEN cDNA 9430098E02 gene	1.07	0.745	-1.07	0.773	1.11	0.505	1.12	0.323	0.56
1441971_at	---	Transcribed locus	1.34	0.159	-1.31	0.48	1.02	0.896	1.02	0.917	0.52
1423293_at	Rpa1	replication protein A1	1	0.92	-1.06	0.647	1.17	0.411	1.33	0.27	0.61
1455414_at	Ttc16	tetratricopeptide repeat domain 16	-1.38	0.175	1.06	0.894	1.33	0.123	1.07	0.906	0.52
1458856_at	---	---	1.15	0.686	-1.06	0.766	1.02	0.93	1.07	0.894	0.54
1442537_at	---	---	1.17	0.087	-2.87	0.008	1.59	0.158	1.69	0.206	0.4
1428857_at	Sap130	Sin3A associated protein, 130kDa	1.09	0.722	-1.02	0.94	1.04	0.756	1.23	0.059	0.59
1426904_s_at	Dnajc10	DnaJ (Hsp40) homolog, subfamily C, member 10	1.03	0.044	1.18	0.484	-1.11	0.095	1.14	0.304	0.56
1415802_at	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	-1.25	0.641	1.17	0.574	1.15	0.705	2.29	0.157	0.84
1416043_at	Nasp	nuclear autoantigenic sperm protein (histone-binding)	-1.03	0.925	1.03	0.904	1.12	0.637	2.07	0.126	0.8
1418857_at	Slc13a2	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	1.11	0.771	-1.32	0.317	1.25	0.322	1.16	0.848	0.55
1435256_at	1500005P14Rik	RIKEN cDNA 1500005P14 gene	1.27	0.045	-1.31	0.507	1.08	0.701	1.36	0.242	0.6
1459496_at	C77267	expressed sequence C77267	-1.77	0.108	1.53	0.38	1.02	0.955	1.24	0.61	0.51
1438606_a_at	Clic4	chloride intracellular channel 4 (mitochondrial)	1.07	0.514	1.08	0.582	-1.03	0.692	1.35	0.147	0.62
1430059_at	Wdr40a	WD repeat domain 40A	-1.43	0.134	1.27	0.489	1.15	0.608	1.35	0.191	0.59
1439746_at	Dusp27	dual specificity phosphatase 27 (putative)	1.47	0.455	-2.19	0.035	1.19	0.638	1.51	0.6	0.5
1416931_at	Nif3l1	Ngg1 interacting factor 3-like 1 (S. pombe)	-1.08	0.383	1.08	0.658	1.1	0.467	1.05	0.781	0.54
1426784_at	Trim47	tripartite motif protein 47	-1.09	0.75	1.16	0.52	1.04	0.846	1.03	0.878	0.54
1433946_at	Zik1	zinc finger protein interacting with K protein 1	-1.21	0.544	1.25	0.352	1.03	0.891	1.06	0.889	0.53
1450077_at	Chd1	chromodomain helicase DNA binding protein 1	-1.49	0.422	1.17	0.347	1.28	0.168	1.25	0.062	0.55
1455099_at	Mogat2	monoacylglycerol O-acyltransferase 2	-1.49	0.203	1.28	0.593	1.16	0.767	2.18	0.322	0.78
1439675_at	4933429D07Rik	RIKEN cDNA 4933429D07 gene	1.19	0.495	-1.26	0.444	1.14	0.235	1.08	0.758	0.54
1418112_at	Mrpl10	mitochondrial ribosomal protein L10	1.02	0.879	-1.06	0.269	1.16	0.047	1.04	0.71	0.54
1450552_at	Atp6v1e2	ATPase, H+ transporting, lysosomal V1 subunit E2	-2.44	0.342	1.32	0.418	1.38	0.335	1.04	0.872	0.33
1417610_at	Apoa5	apolipoprotein A-V	1.33	0.449	-1.36	0.396	1.06	0.893	1.33	0.58	0.59
1454485_at	4930456G14Rik	RIKEN cDNA 4930456G14 gene	-1.16	0.678	1	0.998	1.25	0.658	1.11	0.684	0.55
1430189_at	Nol4	nucleolar protein 4	1.03	0.911	1.37	0.418	-1.39	0.006	1.11	0.745	0.53
1441494_at	Rb1	Retinoblastoma 1	1.28	0.445	-1.29	0.726	1.07	0.889	1.78	0.21	0.71
1417352_s_at	Snrpa1	small nuclear ribonucleoprotein polypeptide A'	1.09	0.582	-1.01	0.899	1.04	0.818	1.05	0.765	0.54
1423918_at	Rhbdd1	rhomboid domain containing 1	1.09	0.008	-1.16	0.055	1.16	0.306	1.08	0.488	0.54
1425755_at	Mtcp1	mature T-cell proliferation 1	1.05	0.869	1.15	0.436	-1.09	0.506	1.78	0.161	0.72

1439625_at	Krtap5-5	Keratin associated protein 5-5	-1.44	0.253	1.08	0.867	1.35	0.369	2.01	0.433	0.75
1426553_at	Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	1.02	0.764	-1.07	0.504	1.16	0.268	1.05	0.741	0.54
1455586_at	Rnf168	ring fnger protein 168	-1.18	0.739	1.26	0.378	1.01	0.97	1.55	0.186	0.66
1448406_at	Cri1	CREBBP/EP300 inhibitory protein 1	1.24	0.31	1.16	0.426	-1.39	0.044	1.25	0.425	0.56
1456449_at	Supt16h	Suppressor of Ty 16 homolog (S. cerevisiae)	1.35	0.557	1.09	0.877	-1.46	0.338	1.15	0.662	0.53
1427048_at	Smo	smoothened homolog (Drosophila)	-1.06	0.861	1.13	0.701	1.05	0.897	1.05	0.861	0.54
1452368_at	Bcr	breakpoint cluster region homolog	1.06	0.545	1.22	0.034	-1.2	0.422	1.03	0.833	0.53
1429078_a_at	Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana	1.02	0.927	1.09	0.641	1	0.989	-1.21	0.514	0.48
1441313_x_at	Lhx9	LIM homeobox protein 9	1.06	0.939	1.22	0.756	-1.19	0.76	1.25	0.628	0.58
1427313_at	Ptgir	prostaglandin I receptor (IP)	1.08	0.477	-1.86	0.258	1.5	0.274	1.07	0.77	0.45
1445935_at	---	---	-1.68	0.062	1.08	0.676	1.45	0.054	1.17	0.578	0.5
1446405_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	-1.4	0.024	1.32	0.625	1.08	0.859	1.01	0.976	0.5
1460422_at	D0Kist5	DNA segment, KIST 5	1.13	0.613	1.35	0.533	-1.57	0.376	1.75	0.118	0.67
1445268_at	---	Transcribed locus, weakly similar to NP_059506.1 coatomer protein complex, sut	1.13	0.721	-1.8	0.205	1.44	0.448	1.25	0.572	0.5
1460649_at	Irak1	interleukin-1 receptor-associated kinase 1	1.14	0.392	1.04	0.536	-1.06	0.687	1.07	0.81	0.55
1418911_s_at	Acsl4	acyl-CoA synthetase long-chain family member 4	1.15	0.017	-1.11	0.657	1.07	0.696	1.52	0.102	0.66
1458151_at	4833444G19Rik	RIKEN cDNA 4833444G19 gene	1.16	0.704	1.1	0.787	-1.16	0.806	1.07	0.879	0.54
1455895_x_at	1110012M11Rik	RIKEN cDNA 1110012M11 gene	1.03	0.811	1.01	0.922	1.08	0.44	-1.11	0.548	0.5
1417762_a_at	Rpl8	ribosomal protein L8	1.03	0.802	1.02	0.751	1.07	0.287	-1.19	0.016	0.48
1423992_at	Gatad2a	GATA zinc finger domain containing 2A	1.01	0.973	-1.15	0.151	1.25	0.146	1.2	0.27	0.58
1435371_x_at	Ces3	carboxylesterase 3	-1.95	0.327	1.15	0.819	1.45	0.187	2.07	0.044	0.68
1418284_at	Vps72	vacuolar protein sorting 72 (yeast)	1.08	0.803	-1.08	0.632	1.12	0.521	1.21	0.498	0.58
1435884_at	Itsn1	intersectin 1 (SH3 domain protein 1A)	-1.24	0.271	1.32	0.309	1	0.995	2.11	0.193	0.8
1417902_at	Slc19a2	solute carrier family 19 (thiamine transporter), member 2	1.09	0.611	-1.08	0.046	1.11	0.469	1.91	0.297	0.76
1428237_at	2700059D21Rik	RIKEN cDNA 2700059D21 gene	1.1	0.317	-1.12	0.086	1.14	0.321	1.21	0.28	0.58
1419742_at	1700037H04Rik	RIKEN cDNA 1700037H04 gene	1.05	0.807	-1.18	0.649	1.23	0.357	3.02	0.227	1.03
1456500_at	Aph1b	anterior pharynx defective 1b homolog (C. elegans)	1.11	0.073	1.11	0.534	-1.12	0.47	1.24	0.069	0.59
1424131_at	Col6a3 /// LOC674	procollagen, type VI, alpha 3 /// similar to alpha 3 type VI collagen isoform 1 precu	1.07	0.528	1.37	0.132	-1.46	0.323	1.22	0.243	0.55
1453681_at	Atpif1	ATPase inhibitory factor 1	-1.03	0.919	1.05	0.755	1.1	0.618	2.55	0.195	0.92
1451063_at	Stxbp4	syntaxin binding protein 4	-1.07	0.193	1.12	0.466	1.07	0.693	2.37	0.252	0.87
1420615_at	Ash2l	ash2 (absent, small, or homeotic)-like (Drosophila)	1.22	0.52	-1.53	0.179	1.25	0.532	1.79	0.412	0.68
1423896_a_at	Rnf187	ring finger protein 187	-1.04	0.685	1.1	0.027	1.07	0.407	1.14	0.207	0.57
1422752_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	-1.05	0.794	1.12	0.433	1.05	0.807	1.03	0.845	0.54
1427650_a_at	Runx1	runt related transcription factor 1	1.53	0.008	-3.29	0.11	1.29	0.355	1.54	0.046	0.27
1421763_at	Bmp10	bone morphogenetic protein 10	-1.76	0.304	1.02	0.952	1.54	0.406	2	0	0.7
1455385_at	Exoc6	exocyst complex component 6	1.08	0.565	1.18	0.301	-1.16	0.346	1.4	0.07	0.62
1453429_at	9530057J20Rik /// I	RIKEN cDNA 9530057J20 gene /// hypothetical protein LOC665756 /// hypothetic	1.25	0.026	1.02	0.89	-1.17	0.33	1.14	0.651	0.56
1432462_a_at	Crsp8	cofactor required for Sp1 transcriptional activation, subunit 8	1.06	0.817	-1.23	0.498	1.25	0.215	1.18	0.588	0.57
1436644_x_at	Tmem25	transmembrane protein 25	1.07	0.554	-1.33	0.371	1.3	0.521	1.32	0.639	0.59
1443749_x_at	Slc1a3	solute carrier family 1 (glial high affinity glutamate transporter), member 3	1.03	0.76	1.33	0.526	-1.31	0.117	1.29	0.579	0.59
1444521_at	---	Transcribed locus	1.24	0.204	-1.2	0.295	1.05	0.304	1.19	0.183	0.57
1427079_at	Mapre3	microtubule-associated protein, RP/EB family, member 3	1.12	0.706	-1.05	0.804	1.06	0.831	1.04	0.945	0.54
1453007_at	3110082I17Rik	RIKEN cDNA 3110082I17 gene	1.25	0.715	-1.2	0.587	1.04	0.836	2.02	0.09	0.78
1455841_s_at	Grwd1	glutamate-rich WD repeat containing 1	1.01	0.95	1.06	0.71	1.06	0.88	-1.08	0.818	0.51
1429901_at	Tcba1	T-cell lymphoma breakpoint associated target 1	1.43	0.235	1.09	0.884	-1.67	0.312	1.08	0.862	0.48
1426404_a_at	Rnf11	ring finger protein 11	-1.1	0.277	1.03	0.695	1.18	0.005	2.17	0.241	0.82
1436509_at	2410014A08Rik	RIKEN cDNA 2410014A08 gene	1	0.681	1.13	0.275	-1.01	0.953	1.12	0.306	0.56
1452392_a_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	1.28	0.26	-1.2	0.764	1.02	0.947	2.44	0.12	0.88
1450376_at	Mxi1	Max interacting protein 1	1.06	0.01	-1.11	0.476	1.17	0.144	2.84	0.173	0.99
1423507_a_at	Sirt2	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	1.06	0.803	1.05	0.79	1.01	0.932	-1.14	0.498	0.5
1431827_a_at	Tlk2	tousled-like kinase 2 (Arabidopsis)	1.08	0.392	-1.07	0.711	1.11	0.104	1.13	0.675	0.56
1419939_at	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17	-1.28	0.699	1.1	0.775	1.25	0.295	1.04	0.904	0.53
1439270_x_at	Ran /// LOC671251	RAN, member RAS oncogene family /// similar to RAN, member RAS oncogene f	-1.14	0.081	1.03	0.834	1.22	0.263	1.11	0.451	0.55

1436897_at	Mfhas1	malignant fibrous histiocytoma amplified sequence 1	1	0.988	-1.14	0.038	1.25	0.132	1.2	0.451	0.58
1450455_s_at	Akr1c12	aldo-keto reductase family 1, member C12	1.05	0.733	-1.33	0.039	1.33	0.173	1.13	0.683	0.54
1449223_at	Dnajb8	DnaJ (Hsp40) homolog, subfamily B, member 8	-1.6	0.044	1.18	0.607	1.31	0.296	1.15	0.705	0.51
1420383_a_at	Col4a3bp	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	-1.06	0.735	1.11	0.697	1.07	0.713	1.27	0.501	0.6
1425230_at	Nags	N-acetylglutamate synthase	1.12	0.685	-1.02	0.76	1.03	0.934	2.28	0.11	0.85
1457255_x_at	Kif5c	Kinesin family member 5C	1.2	0.72	1.24	0.776	-1.46	0.545	1.73	0.559	0.68
1430236_s_at	Gsdm2	gasdermin 2	1.33	0.446	-1.43	0.115	1.1	0.5	1.4	0.013	0.6
1435745_at	5031439G07Rik	RIKEN cDNA 5031439G07 gene	1.07	0.503	1	0.986	1.06	0.607	-1.67	0.196	0.36
1416018_at	Dr1	down-regulator of transcription 1	1.1	0.68	1.12	0.33	-1.1	0.404	1.17	0.174	0.57
1423469_at	1700129C05Rik	RIKEN cDNA 1700129C05 gene	1.48	0.374	1.08	0.886	-1.76	0.297	1.86	0.165	0.66
1438095_x_at	Noc4l	Nucleolar complex associated 4 homolog (S. cerevisiae)	1.04	0.612	-1.11	0.56	1.18	0.479	1.3	0.48	0.6
1444782_at	4930417H01Rik	RIKEN cDNA 4930417H01 gene	-1.29	0.473	1.17	0.556	1.19	0.308	1.23	0.258	0.57
1430932_at	Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	1.3	0.262	1.05	0.9	-1.29	0.103	1.1	0.283	0.54
1445348_at	Cdc40	cell division cycle 40 homolog (yeast)	1.15	0.775	1.15	0.744	-1.21	0.071	1.06	0.759	0.54
1448464_at	Ykt6	YKT6 homolog (S. Cerevisiae)	-1.04	0.683	1.03	0.729	1.13	0.52	1.11	0.344	0.56
1449233_at	Bhlhb8	basic helix-loop-helix domain containing, class B, 8	-1.17	0.013	1.02	0.953	1.25	0.539	1.73	0.052	0.71
1452221_a_at	Cxxc1	CXXC finger 1 (PHD domain)	1.04	0.833	-1.02	0.826	1.11	0.468	1.02	0.873	0.54
1444534_at	LOC666801 /// LOC	similar to CG3950-PA /// similar to CG3950-PA	1.18	0.656	1.24	0.706	-1.41	0.39	1.52	0.231	0.63
1452231_x_at	Ifi203	interferon activated gene 203	1.01	0.965	1.02	0.827	1.1	0.727	-2.28	0.083	0.21
1449980_a_at	Gabrd	gamma-aminobutyric acid (GABA-A) receptor, subunit delta	1.1	0.866	-1.05	0.856	1.08	0.81	1.51	0.132	0.66
1457615_at	Cyfip1	Cytoplasmic FMR1 interacting protein 1	1.6	0.677	-2.21	0.08	1.08	0.783	3.45	0.003	0.98
1418064_at	Tfpt	TCF3 (E2A) fusion partner	1.09	0.567	1.16	0.739	-1.14	0.34	1.08	0.45	0.55
1452788_at	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	1.18	0.02	-1.26	0.207	1.16	0.665	1.43	0.39	0.63
1423963_at	Wdr26	WD repeat domain 26	1.02	0.443	-1.1	0.605	1.2	0.429	2.29	0.17	0.85
1456271_at	Gm944	gene model 944, (NCBI)	-1.27	0.728	1.21	0.505	1.13	0.622	2.24	0.237	0.83
1434299_x_at	Rabl4	RAB, member of RAS oncogene family-like 4	1.07	0.616	1.03	0.657	1.03	0.805	-1.25	0.399	0.47
1428325_at	2610019P18Rik	RIKEN cDNA 2610019P18 gene	1.18	0.227	1.28	0.143	-1.5	0.004	1.06	0.112	0.5
1425542_a_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	1.03	0.682	-1.03	0.81	1.12	0.571	1.01	0.937	0.54
1431450_at	4930444P10Rik ///	RIKEN cDNA 4930444P10 gene /// hypothetical protein LOC638108	1.12	0.909	-1.23	0.458	1.19	0.623	1.86	0.002	0.74
1443033_at	Rbm14	RNA binding motif protein 14	1.32	0.681	-1.6	0.366	1.18	0.539	2.05	0.278	0.74
1425491_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	1.27	0.048	1	0.991	-1.17	0.164	1.25	0.105	0.59
1455488_at	6230416J20Rik	RIKEN cDNA 6230416J20 gene	1.02	0.953	-1.16	0.279	1.25	0.138	1.47	0.292	0.64
1448634_at	Ralbp1	ralA binding protein 1	1.12	0.248	1.03	0.723	-1.02	0.826	1.15	0.235	0.57
1454219_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	-1.42	0.284	1.34	0.447	1.09	0.726	1.02	0.926	0.5
1449503_at	Kpna1	karyopherin (importin) alpha 1	-1	0.979	1	0.99	1.13	0.636	1.92	0.282	0.76
1423758_at	E430034L04Rik	RIKEN cDNA E430034L04 gene	1.02	0.86	1.09	0.446	1.02	0.635	-1.12	0.539	0.5
1423269_a_at	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	1.05	0.726	1.05	0.804	1.03	0.859	-1.5	0.118	0.41
1449314_at	Zfpm2	zinc finger protein, multitype 2	1.05	0.66	1.2	0.117	-1.14	0.68	1.12	0.349	0.56
1420057_at	Ptdsr	Phosphatidylserine receptor	1.28	0.442	1.05	0.705	-1.24	0.052	1.19	0.558	0.57
1426918_at	Itgb1	integrin beta 1 (fibronectin receptor beta)	1.15	0.121	1.1	0.202	-1.13	0.447	1.12	0.097	0.56
1455757_at	D3Ertd254e	DNA segment, Chr 3, ERATO Doi 254, expressed	1.18	0.52	1.21	0.053	-1.35	0.129	1.01	0.97	0.51
1458735_at	---	Transcribed locus	1.38	0.73	1.21	0.743	-1.83	0.201	1.21	0.432	0.49
1460146_at	---	---	1.18	0.828	-1.44	0.538	1.26	0.563	1.02	0.937	0.51
1444363_at	---	10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830040	-1.24	0.75	1.02	0.969	1.3	0.645	3.65	0.002	1.18
1458249_at	---	---	1.12	0.306	1.01	0.971	1	0.995	-1.85	0.057	0.32
1452754_at	Creld2	cysteine-rich with EGF-like domains 2	1.06	0.841	-1.14	0.715	1.19	0.157	1.69	0.274	0.7
1457880_at	---	Transcribed locus	-1.74	0.56	1.17	0.689	1.39	0.263	1.15	0.708	0.49
1426428_at	Thap7	THAP domain containing 7	1.03	0.662	1.01	0.958	1.09	0.63	-1.03	0.791	0.52
1439274_at	A230083H22Rik	RIKEN cDNA A230083H22 gene	-1.25	0.115	1.31	0.776	1.02	0.973	1.05	0.927	0.53
1423464_at	D2Ertd750e	DNA segment, Chr 2, ERATO Doi 750, expressed	-2.47	0.113	1.33	0.603	1.4	0.271	6.21	0.076	1.62
1434021_at	C230096C10Rik	RIKEN cDNA C230096C10 gene	1.1	0.049	1.01	0.898	1.02	0.839	-1.11	0.102	0.51
1424700_at	Tmem38b	transmembrane protein 38B	-1.16	0.204	1.07	0.508	1.19	0.294	1.21	0.572	0.58
1416406_at	Pea15	phosphoprotein enriched in astrocytes 15	1.18	0.124	1.26	0.148	-1.43	0.025	1.06	0.894	0.51

1430522_a_at	Vamp5	vesicle-associated membrane protein 5	1.1	0.593	1.26	0.158	-1.28	0.04	1.26	0.145	0.58
1458458_at	Slfn5	schlafen 5	-3.3	0.221	1.02	0.973	1.81	0.515	1.26	0.631	0.2
1423409_a_at	2500003M10Rik	RIKEN cDNA 2500003M10 gene	-1.05	0.19	1.03	0.737	1.15	0.114	1.07	0.48	0.55
1421273_at	Socs4	suppressor of cytokine signaling 4	1.06	0.774	-1.09	0.737	1.15	0.72	1.14	0.356	0.57
1424198_at	Dlg5	discs, large homolog 5 (Drosophila)	1.13	0.253	-1.09	0.63	1.09	0.525	1.16	0.495	0.57
1448432_at	Plcd1	phospholipase C, delta 1	-1.24	0.443	1.28	0.5	1.05	0.728	1.13	0.892	0.55
1420755_a_at	Park2	parkin	1.57	0.358	-1.92	0.403	1.04	0.947	1.86	0.062	0.64
1424380_at	Vps37b	vacuolar protein sorting 37B (yeast)	1	0.989	1.12	0.533	1.01	0.949	-1.27	0.22	0.47
1455294_at	1110029L17Rik	RIKEN cDNA 1110029L17 gene	-1.17	0.426	1.13	0.555	1.15	0.412	2.12	0.2	0.81
1427915_s_at	Tceb1	transcription elongation factor B (SIII), polypeptide 1	-1.04	0.755	1.11	0.544	1.07	0.817	1.23	0.622	0.59
1416660_at	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)	-1.07	0.416	1.05	0.815	1.15	0.225	1.18	0.298	0.58
1415882_at	Ghitm	growth hormone inducible transmembrane protein	1.01	0.901	-1.2	0.23	1.28	0.026	1.31	0.393	0.6
1424102_at	Atg4b	autophagy-related 4B (yeast)	1.08	0.279	-1.08	0.657	1.13	0.584	1.33	0.484	0.61
1434315_at	Npal3	NIPA-like domain containing 3	1.04	0.72	1.07	0.802	1.03	0.817	-1.13	0.314	0.5
1422261_a_at	Msh3	mutS homolog 3 (E. coli)	1.22	0.48	-1.37	0.482	1.18	0.358	1.14	0.78	0.54
1416781_at	Praf2	PRA1 domain family 2	-1.05	0.866	1.02	0.91	1.16	0.464	1.01	0.896	0.54
1451086_s_at	Rac1	RAS-related C3 botulinum substrate 1	1.06	0.717	-1.06	0.762	1.13	0.429	1.19	0.383	0.58
1448415_a_at	Sema3b	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	-1.22	0.191	1.03	0.96	1.28	0.355	1.3	0.533	0.6
1422837_at	Scel	sciellin	1.12	0.35	1.13	0.843	-1.14	0.455	1.39	0.515	0.63
1442621_at	C77798	expressed sequence C77798	1.22	0.748	1.18	0.772	-1.37	0.291	1.06	0.779	0.52
1432400_at	Epha1	Eph receptor A1	1.32	0.417	-1.4	0.375	1.1	0.475	1.46	0.221	0.62
1458861_at	---	---	1.6	0.43	1.03	0.945	-1.96	0.192	1.17	0.823	0.46
1417547_at	Sart3	squamous cell carcinoma antigen recognized by T-cells 3	-1.08	0.275	1.03	0.891	1.17	0.394	1.05	0.667	0.54
1451166_a_at	Ccdc101	coiled-coil domain containing 101	1.02	0.95	1.02	0.766	1.1	0.397	-1.2	0.194	0.48
1460189_at	Wdr23	WD repeat domain 23	1.03	0.767	1	0.963	1.1	0.555	-1.1	0.384	0.51
1429303_at	Klf17	Kruppel-like factor 17	-1.26	0.589	1.09	0.84	1.26	0.218	1.18	0.634	0.57
1454844_at	Mchr1	melanin-concentrating hormone receptor 1	-1.29	0.527	1.09	0.637	1.27	0.17	1.17	0.754	0.56
1444025_at	---	---	1.71	0.32	-2.68	0.168	1.05	0.875	1.03	0.905	0.28
1427927_at	AW049829	expressed sequence AW049829	-1.2	0.031	1	0.981	1.3	0.192	1.19	0.504	0.57
1455043_at	Tnpo1	transportin 1	-1.04	0.646	1.16	0.249	1.02	0.882	1.03	0.91	0.54
1423060_at	Pa2g4	proliferation-associated 2G4	1.02	0.895	-1.24	0.084	1.31	0.333	1.18	0.478	0.57
1420524_a_at	Masp2	mannan-binding lectin serine peptidase 2	1.08	0.498	1.11	0.573	-1.05	0.782	1.18	0.3	0.58
1444466_at	Ncald	Neurocalcin delta	1.61	0.01	1.06	0.856	-2.17	0	1.48	0.421	0.5
1428517_at	Wdfy3	WD repeat and FYVE domain containing 3	-1.21	0.195	1.07	0.562	1.24	0.1	1.27	0.28	0.59
1446367_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.01	0.978	1.08	0.89	1.05	0.908	-1.57	0.562	0.39
1459417_at	Zfp609	Zinc finger protein 609	1.7	0.269	1.03	0.938	-2.42	0.009	1.76	0.26	0.52
1417517_at	Plagl2	pleiomorphic adenoma gene-like 2	1	0.991	-1.07	0.788	1.2	0.336	1.57	0.195	0.68
1424073_at	5430437P03Rik	RIKEN cDNA 5430437P03 gene	1.03	0.726	-1.07	0.372	1.18	0.225	1.14	0.197	0.57
1453165_at	Mettl4	methyltransferase like 4	-1.12	0.265	1.04	0.818	1.2	0.45	1.52	0.147	0.66
1437148_at	Arpc2	actin related protein 2/3 complex, subunit 2	1.08	0.277	1.04	0.278	1.02	0.829	-1.25	0.191	0.47
1439334_at	---	Transcribed locus	-4.69	0.033	1.16	0.853	1.77	0.294	1.62	0.532	-0.04
1429717_at	Ipo11	importin 11	1.17	0.604	-1.99	0.01	1.47	0.328	1.9	0.324	0.64
1422570_at	---	---	1.27	0.163	-1.22	0.059	1.05	0.856	1.09	0.637	0.55
1433593_at	Ypel5	yippee-like 5 (Drosophila)	1.11	0.305	-1.08	0.221	1.1	0.605	1.93	0.247	0.77
1431545_at	4921532D01Rik	RIKEN cDNA 4921532D01 gene	1.05	0.772	1.43	0.645	-1.52	0.199	1.2	0.713	0.54
1417985_at	Nrarp	Notch-regulated ankyrin repeat protein	-1.28	0.213	1.35	0.395	1.02	0.926	1.63	0.013	0.68
1451225_at	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	1.11	0.263	-1.05	0.189	1.08	0.59	1.2	0.123	0.58
1451106_at	Rbm21	RNA binding motif protein 21	1.11	0.806	1.03	0.902	1.01	0.984	-1.76	0.142	0.34
1435117_a_at	C330021A05Rik	RIKEN cDNA C330021A05 gene	-1.36	0.037	1.36	0.574	1.04	0.785	1.17	0.48	0.55
1448815_at	Ogg1	8-oxoguanine DNA-glycosylase 1	-1.04	0.859	1.09	0.687	1.09	0.741	1.01	0.948	0.54
1451364_at	Polr3gl	polymerase (RNA) III (DNA directed) polypeptide G like	1.25	0.381	1.02	0.922	-1.15	0.252	1.02	0.919	0.54
1426312_at	Bre	brain and reproductive organ-expressed protein	1.07	0.673	-1.01	0.853	1.09	0.627	1.07	0.705	0.55
1419342_at	Tram2	translocating chain-associating membrane protein 2	1.4	0.169	-1.9	0.112	1.21	0.538	1.48	0.164	0.55

1449589_x_at	2610020O08Rik	RIKEN cDNA 2610020O08 gene	1.24	0.134	1.13	0.712	-1.29	0.331	1.07	0.781	0.54
1427261_at	Wwc1	WW, C2 and coiled-coil domain containing 1	1.22	0.343	-1.15	0.53	1.05	0.848	1.26	0.647	0.6
1424749_at	Wdfy1	WD repeat and FYVE domain containing 1	1.07	0.716	-1.01	0.956	1.08	0.769	1.11	0.49	0.56
1416358_at	0610009O03Rik	RIKEN cDNA 0610009O03 gene	-1.28	0.694	1.27	0.457	1.09	0.591	1.11	0.311	0.55
1448524_s_at	Ssr4	signal sequence receptor, delta	-1.03	0.568	1.03	0.771	1.14	0.399	1.17	0.45	0.58
1416517_at	Pnpla6	patatin-like phospholipase domain containing 6	1.02	0.566	-1.05	0.362	1.16	0.296	1.21	0.4	0.59
1455278_at	Wdr37	WD repeat domain 37	1.02	0.957	-1.04	0.85	1.16	0.385	1.15	0.392	0.57
1419356_at	Klf7	Kruppel-like factor 7 (ubiquitous)	1.42	0.383	1.03	0.87	-1.45	0.337	1.12	0.711	0.53
1438423_at	Ssbp2	single-stranded DNA binding protein 2	1.03	0.951	1.45	0.437	-1.51	0.155	1.46	0.136	0.61
1420977_at	Man1a2	mannosidase, alpha, class 1A, member 2	1.09	0.521	1.11	0.721	-1.07	0.524	1.07	0.594	0.55
1428443_a_at	Rap1gap	Rap1 GTPase-activating protein	1.11	0.806	1.09	0.848	-1.06	0.736	1.03	0.932	0.54
1442808_at	---	Transcribed locus, weakly similar to XP_342027.2 PREDICTED: similar to MS4A	1.16	0.721	1.45	0.607	-1.88	0.072	1.37	0.284	0.53
1458918_at	Slc12a8	solute carrier family 12 (potassium/chloride transporters), member 8	1.01	0.863	1.08	0.54	1.05	0.699	-1.04	0.81	0.53
1433928_a_at	Rpl13a	ribosomal protein L13a	1.04	0.384	1.05	0.791	1.05	0.841	-1.11	0.468	0.51
1460648_at	Nr2f6	nuclear receptor subfamily 2, group F, member 6	1.22	0.353	1	0.936	-1.09	0.744	1.01	0.964	0.54
1429705_at	Spaca4	sperm acrosome associated 4	1.27	0.697	-1.78	0.267	1.31	0.249	1.37	0.539	0.54
1432136_s_at	Zdhhc4	zinc finger, DHHC domain containing 4	1.01	0.86	-1.05	0.601	1.18	0.239	1.08	0.324	0.56
1417467_a_at	Tada3l	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	1.09	0.727	-1.08	0.327	1.13	0.328	1.12	0.238	0.56
1424539_at	Ubl4	ubiquitin-like 4	1.12	0.326	1.12	0.26	-1.1	0.447	1.01	0.728	0.53
1428759_s_at	Ccdc49	coiled-coil domain containing 49	1.07	0.797	1.09	0.655	-1.01	0.949	1.47	0.324	0.65
1444870_at	AU015438	expressed sequence AU015438	-1.41	0.678	1.16	0.674	1.27	0.594	1.24	0.529	0.57
1455407_at	Zfp236	zinc finger protein 236	1.04	0.847	1.08	0.599	1.03	0.805	-1.19	0.634	0.49
1425466_at	Senp2	SUMO/sentrin specific peptidase 2	1.2	0.198	-1.23	0.029	1.13	0.477	1.67	0.17	0.69
1417667_a_at	Pter	phosphotriesterase related	-1.13	0.107	1.23	0.428	1.03	0.88	1.52	0.042	0.66
1433544_at	Als2cr2	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2 (huma	-1.07	0.353	1.04	0.59	1.17	0.114	2.85	0.172	1
1422370_at	Olfr49	olfactory receptor 49	1.39	0.602	1.03	0.967	-1.37	0.409	1.44	0.443	0.62
1451365_at	Rbm19	RNA binding motif protein 19	-1.17	0.575	1.02	0.905	1.27	0.063	1.14	0.61	0.56
1441528_at	Ttc15	tetratricopeptide repeat domain 15	1.28	0.651	-1.64	0.015	1.25	0.384	1.03	0.889	0.48
1459299_at	Myo3b	myosin IIIB	1.17	0.334	-1.21	0.62	1.15	0.691	1.87	0.06	0.75
1435233_at	Ncoa2	nuclear receptor coactivator 2	1.04	0.767	1.04	0.746	1.07	0.556	-1.26	0.08	0.47
1423742_at	Rbm10	RNA binding motif protein 10	1.05	0.84	-1.19	0.539	1.26	0.437	1.04	0.924	0.54
1458624_at	LOC380843 /// LOC	similar to RNA binding motif protein 24 /// similar to RNA binding motif protein 24	1.39	0.592	-1.4	0.374	1.04	0.936	2.03	0	0.77
1442675_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	1.42	0.449	-1.58	0.571	1.1	0.861	1.26	0.718	0.55
1427590_at	Zfp39	zinc finger protein 39	1.44	0.085	1.05	0.757	-1.53	0.055	1.85	0.272	0.7
1429508_at	2310057M21Rik	RIKEN cDNA 2310057M21 gene	-1.09	0.313	1.13	0.585	1.1	0.087	1.05	0.804	0.55
1423827_s_at	Noc4l	nucleolar complex associated 4 homolog (S. cerevisiae)	-1.05	0.786	1.01	0.948	1.19	0.486	1.22	0.557	0.59
1434519_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	-1.51	0.201	1.05	0.827	1.43	0.282	2.11	0.204	0.77
1451053_a_at	Mdm1	transformed mouse 3T3 cell double minute 1	1.12	0.055	-1.34	0.548	1.28	0.245	1.38	0.497	0.61
1426376_at	Reep5	receptor accessory protein 5	1.13	0.204	1.05	0.773	-1.03	0.835	1.39	0.143	0.63
1428611_at	Atg7	autophagy-related 7 (yeast)	-1.32	0.005	1.12	0.794	1.27	0.45	1.04	0.945	0.53
1440801_s_at	Adrbk2	adrenergic receptor kinase, beta 2	1.07	0.767	1.24	0.389	-1.2	0.433	1.09	0.853	0.55
1455599_at	Gfod1	glucose-fructose oxidoreductase domain containing 1	1.04	0.952	1.02	0.924	1.08	0.808	-2.22	0.011	0.23
1432565_at	---	---	1.23	0.45	-1.12	0.479	1.02	0.944	1.34	0.341	0.62
1454265_a_at	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	-2.22	0.409	1.65	0.25	1.05	0.909	4.38	0.119	1.21
1436076_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	1.03	0.81	1.38	0.22	-1.36	0.389	1.06	0.541	0.53
1426624_a_at	Ypel3	yippee-like 3 (Drosophila)	1.12	0.28	-1.03	0.785	1.06	0.712	1.01	0.922	0.54
1454416_at	5730575I04Rik	RIKEN cDNA 5730575I04 gene	1.04	0.835	-1.07	0.668	1.17	0.647	1.26	0.482	0.6
1420644_a_at	Sec61a2	Sec61, alpha subunit 2 (S. cerevisiae)	-1.14	0.443	1.26	0.407	1.01	0.984	1.21	0.425	0.58
1428803_at	4632408A20Rik	RIKEN cDNA 4632408A20 gene	-1.47	0.039	1.13	0.611	1.33	0.039	1.42	0.262	0.6
1423398_at	Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.08	0.701	-1.05	0.694	1.11	0.608	1.21	0.492	0.59
1443147_at	Acot3	Acyl-CoA thioesterase 3	1	0.992	1.13	0.905	1.01	0.982	-1.3	0.77	0.46
1417035_at	Sac3d1	SAC3 domain containing 1	1.08	0.587	-1.03	0.66	1.1	0.104	1.16	0.529	0.58
1416618_at	Ppox	protoporphyrinogen oxidase	-1.01	0.928	1.08	0.558	1.08	0.264	3.47	0.23	1.15

1428596_at	Tbc1d9b	TBC1 domain family, member 9B	1.08	0.495	-1.04	0.824	1.1	0.321	1.16	0.584	0.58
1451782_a_at	Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	1.19	0.146	-1.07	0.642	1.03	0.915	2.06	0.083	0.8
1423056_at	Nsg1	neuron specific gene family member 1	1.51	0.61	-1.58	0.365	1	0.99	1.7	0.11	0.66
1425680_a_at	Btrc	beta-transducin repeat containing protein	1.2	0.03	-1.11	0.406	1.04	0.795	1.69	0.195	0.71
1442724_at	AW060763	expressed sequence AW060763	-2.05	0.167	1.11	0.67	1.55	0.03	1.08	0.804	0.42
1420014_at	Lss	Lanosterol synthase	-1.13	0.874	1.12	0.807	1.14	0.392	1.51	0.07	0.66
1433560_at	Slc45a4	solute carrier family 45, member 4	1.32	0.549	-1.32	0.533	1.07	0.773	1.33	0.399	0.6
1434586_a_at	Ptdss2	phosphatidylserine synthase 2	1.01	0.939	-1.17	0.293	1.29	0.009	3.73	0.129	1.21
1442236_at	Zfand6	zinc finger, AN1-type domain 6	1.17	0.789	1.02	0.974	-1.04	0.941	1.59	0.403	0.69
1458855_at	D11Ertd49e	DNA segment, Chr 11, ERATO Doi 49, expressed	1.27	0.582	-1.66	0.351	1.28	0.571	1.33	0.553	0.56
1429689_at	4932433N03Rik	RIKEN cDNA 4932433N03 gene	1.17	0.502	1.12	0.601	-1.17	0.333	1.34	0.439	0.62
1430402_at	Sucla2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	1.11	0.876	1.26	0.5	-1.29	0.457	1.44	0.4	0.63
1458480_at	Topbp1	topoisomerase (DNA) II beta binding protein	-1.15	0.833	1.2	0.777	1.07	0.878	1.74	0.14	0.72
1421468_at	Kcnj3	potassium inwardly-rectifying channel, subfamily J, member 3	-1.88	0.076	1.31	0.248	1.31	0.166	1.22	0.194	0.49
1416081_at	Smad1	MAD homolog 1 (Drosophila)	1.17	0.488	-1.1	0.456	1.07	0.728	1.07	0.706	0.55
1448184_at	Fkbp1a	FK506 binding protein 1a	1.01	0.963	1.12	0.201	1.02	0.789	-1.31	0.164	0.46
1428580_at	Blvra	biliverdin reductase A	1.04	0.599	1.19	0.001	-1.08	0.481	1.23	0.192	0.59
1419794_at	---	Transcribed locus	-1.05	0.957	1.11	0.641	1.09	0.778	1.23	0.68	0.59
1437836_x_at	0610011L14Rik	RIKEN cDNA 0610011L14 gene	-1.4	0.305	1.32	0.594	1.12	0.578	1.1	0.73	0.54
1417139_at	1700022L09Rik	RIKEN cDNA 1700022L09 gene	1.14	0.699	-1.15	0.69	1.14	0.648	1.48	0.425	0.65
1450137_at	Pofut1	protein O-fucosyltransferase 1	-1.43	0.078	1.1	0.655	1.35	0.27	1.07	0.809	0.52
1422521_at	Dctn1	dynactin 1	1.06	0.815	-1.04	0.799	1.14	0.106	1	0.989	0.54
1454198_a_at	Efcab1	EF hand calcium binding domain 1	1.26	0.536	-1.39	0.409	1.17	0.772	1.97	0.488	0.75
1419513_a_at	Ect2	ect2 oncogene	-1	0.997	1.14	0.596	1.02	0.942	4.05	0.169	1.3
1458410_at	Garnl1	GTPase activating RANGAP domain-like 1	-1.94	0.307	1.02	0.962	1.61	0.007	1.05	0.895	0.44
1418269_at	Loxl3	lysyl oxidase-like 3	1.13	0.584	1.07	0.853	-1.05	0.694	1.19	0.131	0.59
1438067_at	Nf1	neurofibromatosis 1	-1.03	0.886	1.09	0.564	1.1	0.696	1.17	0.418	0.58
1420915_at	Stat1	signal transducer and activator of transcription 1	1.01	0.596	1	0.928	1.14	0.467	-1.34	0.188	0.45
1421616_at	Grin2a	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	1.1	0.848	-1.4	0.63	1.34	0.471	1.18	0.796	0.55
1418867_at	Cyp24a1	cytochrome P450, family 24, subfamily a, polypeptide 1	1.14	0.848	-2.89	0.073	1.67	0.147	1.57	0.458	0.37
1420419_a_at	Otof	otoferlin	-1.39	0.52	1.04	0.896	1.4	0.466	1.25	0.056	0.57
1453787_at	Txndc13	thioredoxin domain containing 13	1.01	0.967	-1.33	0.478	1.39	0.544	2.19	0.16	0.81
1457380_at	C85504	expressed sequence C85504	1.11	0.814	-1.03	0.95	1.08	0.849	2.56	0.058	0.93
1448088_at	C78228	expressed sequence C78228	-1.85	0.073	1.45	0.302	1.17	0.543	1.04	0.862	0.45
1446978_at	---	---	1.12	0.791	1.08	0.824	-1.05	0.902	1.55	0.136	0.68
1452454_at	Sdad1	SDA1 domain containing 1	1.14	0.809	-1.18	0.344	1.17	0.669	1.13	0.483	0.56
1456646_at	Pex10	peroxisome biogenesis factor 10	1.07	0.356	1.03	0.83	1.06	0.635	-1.22	0.677	0.48
1448218_s_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	1.01	0.982	-1.04	0.417	1.19	0.005	1.12	0.609	0.57
1431635_at	4930412F09Rik	RIKEN cDNA 4930412F09 gene	1.07	0.935	1.36	0.312	-1.4	0.366	1.31	0.646	0.59
1445709_at	Mdm1	transformed mouse 3T3 cell double minute 1	-1.36	0.536	1.09	0.831	1.33	0.25	1.26	0.425	0.58
1429616_at	Zfp91	zinc finger protein 91	1.29	0.347	1.07	0.726	-1.26	0.203	1.9	0.215	0.75
1415671_at	Atp6v0d1	ATPase, H+ transporting, lysosomal V0 subunit D1	-1.11	0.261	1.06	0.549	1.19	0.058	1.14	0.044	0.57
1436601_at	Fbxo46	F-box protein 46	-1.08	0.817	1.01	0.972	1.22	0.555	1.26	0.22	0.6
1458513_at	Mapk10	mitogen activated protein kinase 10	1.41	0.394	-1.41	0.501	1.03	0.951	1.26	0.669	0.57
1427886_at	Pom121	nuclear pore membrane protein 121	1.01	0.948	-1.07	0.09	1.21	0.065	1.26	0.317	0.6
1442951_at	Drr1	Developmentally regulated repeat element-containing transcript 1	1.01	0.982	1.48	0.165	-1.5	0.163	1.39	0.282	0.6
1449788_at	---	---	-1.19	0.831	1.25	0.683	1.07	0.86	1.66	0.072	0.7
1418279_a_at	Akap1	A kinase (PRKA) anchor protein 1	1.14	0.419	-1	0.971	1.02	0.893	2.03	0.043	0.8
1459178_at	D8Ertd503e	DNA segment, Chr 8, ERATO Doi 503, expressed	1.43	0.19	-1.46	0.046	1.04	0.909	1.52	0.23	0.63
1448525_a_at	Bnip3l	BCL2/adenovirus E1B interacting protein 3-like	1.15	0.371	-1.07	0.351	1.07	0.717	1.61	0.302	0.69
1442043_at	Lhfpl4	lipoma HMGIC fusion partner-like protein 4	1.14	0.878	1.14	0.558	-1.14	0.278	1.52	0.083	0.66
1438435_at	Phca	phytoceramidase, alkaline	1.1	0.454	1.24	0.105	-1.23	0.011	1.21	0.441	0.58
1425494_s_at	Bmpr1a	bone morphogenetic protein receptor, type 1A	1.34	0.099	1.1	0.558	-1.4	0.232	1.1	0.351	0.54

1430252_at	3110027N22Rik	RIKEN cDNA 3110027N22 gene	1.24	0.762	-1.47	0.438	1.23	0.246	1.03	0.887	0.51
1423846_x_at	Tuba2	tubulin, alpha 2	1.03	0.895	1.24	0.067	-1.13	0.079	1.03	0.746	0.54
1454319_at	4930402H05Rik	RIKEN cDNA 4930402H05 gene	1.14	0.854	-1.02	0.972	1.04	0.891	1.02	0.924	0.54
1441862_at	Ppox	protoporphyrinogen oxidase	1.6	0.199	1.07	0.882	-2.04	0.005	1.45	0.27	0.52
1450860_at	Lap3	leucine aminopeptidase 3	1.09	0.403	-1.05	0.715	1.11	0.586	1.31	0.193	0.62
1437777_at	Atf2	activating transcription factor 2	1.32	0.247	1.18	0.55	-1.52	0.096	1.02	0.973	0.5
1422748_at	Zfhx1b	zinc finger homeobox 1b	1.23	0.611	1.22	0.274	-1.42	0.203	1.11	0.375	0.54
1434879_at	Cdc34	cell division cycle 34 homolog (S. cerevisiae)	1.01	0.795	-1.01	0.949	1.15	0.464	1.25	0.418	0.6
1417749_a_at	Tjp1	tight junction protein 1	1.03	0.708	1.21	0.091	-1.09	0.284	1.91	0.225	0.77
1420400_at	Sval1	seminal vesicle antigen-like 1	1.47	0.558	1.12	0.07	-1.79	0.343	1.15	0.276	0.49
1452294_at	Pcdh1	protocadherin 1	1.2	0.558	1.08	0.634	-1.13	0.556	1.01	0.983	0.54
1452241_at	Topbp1	topoisomerase (DNA) II beta binding protein	1.08	0.662	1.14	0.424	-1.06	0.807	1.34	0.35	0.62
1438384_at	1700047L15Rik	RIKEN cDNA 1700047L15 gene	1.07	0.922	-1.03	0.962	1.11	0.733	1.12	0.879	0.57
1450944_at	Cspg4	chondroitin sulfate proteoglycan 4	-1.23	0.369	1.05	0.922	1.29	0.196	1.29	0.443	0.6
1448679_at	Hyal2	hyaluronoglucosaminidase 2	1.17	0.647	1.06	0.633	-1.07	0.581	1.19	0.371	0.59
1425133_s_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	-1.21	0.153	1.29	0.359	1.04	0.861	3.67	0.194	1.2
1453753_at	Dtl	denticleless homolog (Drosophila)	1.28	0.084	1.08	0.711	-1.26	0.159	4.18	0.202	1.32
1452884_at	Sfrs2ip	splicing factor, arginine/serine-rich 2, interacting protein	1.11	0.592	1.01	0.877	1.04	0.806	-1.03	0.485	0.53
1419122_at	Mettl1	methyltransferase-like 1	-1.24	0.297	1.2	0.397	1.15	0.573	1.13	0.163	0.56
1419060_at	Gzmb	granzyme B	1.11	0.856	1.11	0.347	-1.06	0.893	2.77	0.265	0.98
1454594_at	2900078I11Rik	RIKEN cDNA 2900078I11 gene	-1.23	0.032	1.33	0.523	1.02	0.891	1.04	0.253	0.54
1442054_at	---	PREDICTED: Mus musculus similar to serine-threonine protein kinase pim-2 isof	1.17	0.563	1.31	0.37	-1.47	0.12	1.17	0.176	0.54
1425261_at	Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	1.1	0.725	1.21	0.566	-1.18	0.373	1.34	0.481	0.62
1448935_at	Cdyl	chromodomain protein, Y chromosome-like	1.25	0.286	-1.19	0.791	1.07	0.736	2.19	0.205	0.83
1432398_at	1700084J12Rik	RIKEN cDNA 1700084J12 gene	-1.91	0.175	1.53	0.576	1.1	0.83	1.36	0.158	0.52
1453735_at	5730455P16Rik	RIKEN cDNA 5730455P16 gene	-1.14	0.004	1.22	0.499	1.06	0.809	1.36	0.326	0.62
1435520_at	Msi2	Musashi homolog 2 (Drosophila)	1.06	0.806	1.18	0.383	-1.09	0.708	1.01	0.981	0.54
1452194_at	Tbcd	tubulin-specific chaperone d	-1.09	0.643	1.06	0.382	1.18	0.244	1.55	0.09	0.68
1440923_at	---	---	-1.19	0.356	1.08	0.82	1.24	0.319	1.67	0.441	0.7
1439439_x_at	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange pro	1.01	0.96	1.03	0.769	1.12	0.637	-1.02	0.928	0.54
1422948_s_at	Hist1h4h /// Hist2h4	histone 1, H4h /// histone 2, H4 /// histone 1, H4c /// histone 1, H4i /// histone 1, H4	-1.16	0.272	1.17	0.618	1.13	0.598	2.29	0.252	0.86
1419404_s_at	Siah1a /// Siah1b	seven in absentia 1A /// seven in absentia 1B	-1.12	0.183	1.15	0.716	1.12	0.29	1.73	0.332	0.72
1441689_at	Nup153	nucleoporin 153	1.1	0.586	1.41	0.336	-1.53	0.007	1.33	0.075	0.58
1423587_a_at	Exosc10	exosome component 10	1.03	0.816	1.07	0.383	1.06	0.586	-1.19	0.219	0.49
1430822_at	Smarce1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	-1.91	0.125	1.13	0.865	1.51	0.461	1.44	0.336	0.54
1444843_at	---	---	1.1	0.859	1.54	0.508	-1.92	0.265	1.95	0.421	0.67
1417604_at	Camk1	calcium/calmodulin-dependent protein kinase I	-1.14	0.168	1.13	0.033	1.15	0.267	1.1	0.625	0.56
1453412_a_at	Sec14l1	SEC14-like 1 (S. cerevisiae)	-1.02	0.81	1.06	0.586	1.12	0.544	1.43	0.036	0.65
1424766_at	Ercc6l	excision repair cross-complementing rodent repair deficiency complementation gr	-1.1	0.755	1.14	0.752	1.11	0.6	2.38	0.189	0.88
1450821_at	Pcaf	p300/CBP-associated factor	1.16	0.536	-1.49	0.268	1.33	0.443	1.83	0.431	0.71
1429520_a_at	Phca	phytoceramidase, alkaline	-1.14	0.348	1.28	0.18	1	0.974	1.43	0.302	0.64
1415748_a_at	Dctn5	dynactin 5	1.08	0.727	1.06	0.675	1.02	0.92	-1.11	0.457	0.51
1437909_at	D030022P06Rik	RIKEN cDNA D030022P06 gene	1.11	0.599	-1.07	0.738	1.11	0.211	1.07	0.768	0.56
1427441_a_at	Suclg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	-1.14	0.381	1.12	0.282	1.17	0.399	1.05	0.622	0.55
1440218_at	BC040758	cDNA sequence BC040758	1.29	0.009	-1.65	0.266	1.26	0.669	1.1	0.758	0.5
1441249_at	4930403D09Rik	RIKEN cDNA 4930403D09 gene	-1.65	0.268	1.05	0.875	1.51	0.331	1.34	0.662	0.56
1423776_s_at	Tbc1d22a	TBC1 domain family, member 22a	-1.38	0.192	1.17	0.45	1.27	0.133	1.05	0.732	0.53
1450853_at	Tle4	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	1.11	0.079	1.04	0.795	1.01	0.909	-1.18	0.223	0.49
1450120_at	Scn1a	sodium channel, voltage-gated, type I, alpha	1.04	0.936	1.46	0.379	-1.52	0.494	1.11	0.701	0.52
1425021_a_at	Pex16	peroxisome biogenesis factor 16	1.05	0.838	-1.08	0.522	1.19	0.277	1.02	0.892	0.54
1430880_at	Psd3	pleckstrin and Sec7 domain containing 3	1.08	0.906	1.18	0.625	-1.11	0.825	1.5	0.379	0.66
1417908_s_at	Ube2l3 /// Rps28	ubiquitin-conjugating enzyme E2L 3 /// ribosomal protein S28	-1.07	0.739	1.11	0.121	1.12	0.396	1.12	0.343	0.57
1451547_at	Iyd	iodotyrosine deiodinase	1.01	0.881	-1.03	0.293	1.18	0.649	2.64	0.02	0.95

1448913_at	Smarcd1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.15	0.587	-1.16	0.583	1.15	0.523	1.01	0.875	0.54
1429201_at	Cyld	cylindromatosis (turban tumor syndrome)	1.06	0.598	1.06	0.658	1.05	0.812	-1.31	0.321	0.46
1430735_at	4930424G05Rik	RIKEN cDNA 4930424G05 gene	-1.37	0.484	1.05	0.912	1.38	0.282	1.18	0.293	0.56
1424056_at	Usp48	ubiquitin specific peptidase 48	1.03	0.796	1.1	0.352	1.03	0.869	-1.07	0.763	0.52
1431615_at	4930558J22Rik	RIKEN cDNA 4930558J22 gene	1.08	0.907	1.04	0.933	1.05	0.917	-1.39	0.21	0.44
1425379_at	Hgf	hepatocyte growth factor	1.08	0.699	-1.09	0.817	1.17	0.638	2.32	0.173	0.87
1441226_at	Spon1	spondin 1, (f-spondin) extracellular matrix protein	1.33	0.606	-1.37	0.45	1.1	0.729	1.29	0.413	0.59
1436200_at	Lonrf3	LON peptidase N-terminal domain and ring finger 3	1.22	0.634	1.07	0.697	-1.15	0.245	1.33	0.422	0.62
1417969_at	Fbxo31	F-box only protein 31	1.03	0.763	-1.3	0.262	1.36	0.395	1.26	0.226	0.59
1438724_at	Osbpl3	oxysterol binding protein-like 3	-1.01	0.943	1.07	0.916	1.11	0.567	1.39	0.353	0.64
1443707_at	2900046B09Rik	RIKEN cDNA 2900046B09 gene	-1.17	0.294	1.22	0.708	1.1	0.739	2.34	0.121	0.87
1418275_a_at	Elf2	E74-like factor 2	1.07	0.707	-1.07	0.703	1.16	0.474	1.13	0.563	0.57
1440469_at	LOC629141	hypothetical protein LOC629141	1.13	0.036	1.6	0.208	-2.27	0.238	1.42	0.568	0.47
1458587_at	2310047D07Rik	RIKEN cDNA 2310047D07 gene	-1.31	0.431	1.27	0.347	1.13	0.522	1.42	0.194	0.63
1448737_at	Tspan7	tetraspanin 7	-1.17	0.08	1.21	0.211	1.1	0.329	1.49	0.214	0.66
1434445_at	D15Wsu169e	DNA segment, Chr 15, Wayne State University 169, expressed	-1.15	0.206	1.24	0.658	1.06	0.616	1.29	0.366	0.61
1425430_at	Krtap16-5	keratin associated protein 16-5	1.01	0.926	1.18	0.647	-1.03	0.843	1.17	0.394	0.58
1460234_at	Wdr81	WD repeat domain 81	-1.17	0.309	1.06	0.341	1.25	0.24	1.75	0.088	0.72
1435606_at	Gal3st4	galactose-3-O-sulfotransferase 4	1.38	0.648	-1.29	0.392	1.01	0.965	1.06	0.857	0.54
1460115_at	Slc26a11	Solute carrier family 26, member 11	1.32	0.045	1.02	0.972	-1.22	0.642	1.1	0.47	0.56
1429124_s_at	Rexo1	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	1.15	0.35	1.02	0.911	-1.01	0.956	1.02	0.926	0.55
1451446_at	Antxr1	anthrax toxin receptor 1	1.25	0.293	1.13	0.418	-1.28	0.508	1	0.997	0.53
1443782_x_at	Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	1.19	0.729	1.11	0.737	-1.16	0.423	1.54	0.35	0.67
1453994_at	C230094A16Rik	RIKEN cDNA C230094A16 gene	-1.32	0.342	1.39	0.067	1.02	0.942	1.44	0.217	0.63
1438476_a_at	Chd4	chromodomain helicase DNA binding protein 4	1.19	0.577	-1.61	0.309	1.36	0.48	1.32	0.487	0.56
1446724_at	Fcho2	FCH domain only 2	1.21	0.564	-1.2	0.424	1.12	0.752	1.83	0.267	0.74
1457317_at	---	---	1.26	0.261	1.24	0.704	-1.52	0.356	1.1	0.898	0.52
1421665_a_at	Gnrhr	gonadotropin releasing hormone receptor	-2.6	0.173	1.03	0.89	1.75	0.286	1.81	0.216	0.5
1429100_at	2010109K11Rik	RIKEN cDNA 2010109K11 gene	-1.14	0.414	1.01	0.964	1.28	0.03	1.38	0.406	0.63
1423962_at	Wdr26	WD repeat domain 26	-1.06	0.519	1.04	0.853	1.19	0.16	1.92	0.259	0.77
1457676_at	Tirap	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein	-1.11	0.174	1.19	0.422	1.08	0.477	1.09	0.549	0.56
1434416_a_at	Solh	Small optic lobes homolog (Drosophila)	-1.19	0.164	1.16	0.178	1.17	0.463	1.01	0.967	0.54
1419792_at	Mphosph1	M-phase phosphoprotein 1	-1.41	0.542	1.45	0.486	1.01	0.982	1.08	0.863	0.53
1453742_at	Vps33a	vacuolar protein sorting 33A (yeast)	1.03	0.871	-1.15	0.653	1.27	0.43	1.12	0.608	0.57
1434936_at	Hirip3	HIRA interacting protein 3	1.08	0.663	-1.38	0.036	1.36	0.172	2.26	0.238	0.83
1417655_a_at	Ars2	arsenate resistance protein 2	-1.15	0.031	1.1	0.241	1.19	0.207	1.04	0.832	0.55
1438753_at	Porcn	Porcupine homolog (Drosophila)	1.01	0.955	1.16	0.629	-1.01	0.974	1.55	0.355	0.68
1451549_at	BC016201	cDNA sequence BC016201	1.14	0.732	-1.02	0.955	1.05	0.8	1.26	0.647	0.61
1452513_a_at	Fanca	Fanconi anemia, complementation group A	1.1	0.72	-1.56	0.323	1.43	0.691	2.67	0.222	0.91
1455655_a_at	Tardbp	TAR DNA binding protein	1.02	0.87	-1.01	0.938	1.15	0.22	1.04	0.624	0.55
1450014_at	Cldn1	claudin 1	1.32	0.543	-1.19	0.766	1.01	0.985	1.25	0.633	0.6
1426590_at	Gfm2	G elongation factor, mitochondrial 2	1.03	0.564	-1.11	0.325	1.24	0.038	1.27	0.013	0.61
1426986_at	2810485I05Rik	RIKEN cDNA 2810485I05 gene	-1.16	0.019	1.16	0.511	1.14	0.162	1.5	0.084	0.66
1442160_at	7530404M11Rik	RIKEN cDNA 7530404M11 gene	1.31	0.501	1.02	0.939	-1.2	0.557	1.84	0.043	0.74
1424051_at	Col4a2	procollagen, type IV, alpha 2	1.06	0.842	1.02	0.764	1.09	0.647	-1.15	0.458	0.51
1434837_at	Mdc1	mediator of DNA damage checkpoint 1	-1.13	0.483	1.1	0.585	1.18	0.477	1.46	0.198	0.65
1422827_x_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	-1.04	0.909	1.06	0.716	1.14	0.276	1.39	0.319	0.64
1436333_a_at	Synj1	synaptojanin 1	-1.15	0.143	1.07	0.713	1.23	0.096	1.41	0.178	0.64
1451067_at	Sgta	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	1.03	0.918	1.05	0.787	1.08	0.468	-1	0.998	0.54
1439628_x_at	Rab38	Rab38, member of RAS oncogene family	1.25	0.067	1.14	0.606	-1.28	0.401	1.65	0.162	0.69
1427987_at	Safb2	scaffold attachment factor B2	1.03	0.824	1.1	0.299	1.04	0.802	-1.22	0.314	0.49
1459061_at	Trfr2	Transferrin receptor 2	1.26	0.781	1.21	0.243	-1.42	0.127	2.41	0.138	0.86
1422882_at	Sypl	synaptophysin-like protein	1.05	0.85	-1.16	0.576	1.25	0.511	1.01	0.972	0.54

1416511_a_at	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	-1	0.999	1.07	0.559	1.1	0.439	1.05	0.843	0.55
1460636_at	Map2k2	mitogen activated protein kinase kinase 2	1.19	0.71	-1.1	0.375	1.07	0.787	1.81	0.138	0.74
1448140_at	Ciapin1	cytokine induced apoptosis inhibitor 1	1.22	0.369	-1.16	0.099	1.09	0.427	1.25	0.484	0.6
1458758_at	Vav2	Vav2 oncogene	1.06	0.797	1.02	0.947	1.09	0.652	-1.46	0.205	0.43
1428058_at	Ahnak	AHNAK nucleoprotein (desmoyokin)	1.04	0.366	1.52	0.404	-1.63	0.022	1.18	0.702	0.53
1455544_at	Zranb3	zinc finger, RAN-binding domain containing 3	1.04	0.818	-1.1	0.788	1.22	0.415	1.43	0.303	0.65
1455135_at	2610014I16Rik	RIKEN cDNA 2610014I16 gene	-1.08	0.772	1.18	0.23	1.07	0.815	1.03	0.888	0.55
1451989_a_at	Mapre2	microtubule-associated protein, RP/EB family, member 2	1.15	0.712	1.11	0.785	-1.09	0.635	1.19	0.772	0.59
1452432_at	Tfpi	tissue factor pathway inhibitor	1.04	0.911	1.2	0.548	-1.07	0.791	1.02	0.919	0.55
1452883_a_at	2310002J21Rik	RIKEN cDNA 2310002J21 gene	1.03	0.72	1.29	0.051	-1.18	0.406	1.02	0.923	0.54
1440252_at	H2afj	H2A histone family, member J	1.17	0.34	1.2	0.649	-1.25	0.353	1.34	0.355	0.62
1452395_at	Med19	mediator of RNA polymerase II transcription, subunit 19 homolog (yeast)	1.2	0.015	-1.12	0.248	1.07	0.575	1.26	0.424	0.6
1443484_at	Rpap1	RNA polymerase II associated protein 1	1.14	0.218	1.09	0.761	-1.06	0.737	1.39	0.181	0.64
1426909_at	Uck2	uridine-cytidine kinase 2	1.15	0.709	-1.14	0.464	1.15	0.529	1.13	0.736	0.57
1431382_a_at	Rsnl2	restin-like 2	-1.48	0.715	1.07	0.906	1.43	0.558	2.22	0.118	0.81
1416408_at	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	1.01	0.972	-1.07	0.542	1.24	0.295	1.03	0.919	0.55
1456062_at	Nppa	natriuretic peptide precursor type A	-1.16	0.862	1.27	0.753	1.04	0.937	1.07	0.817	0.56
1423784_at	Gars	glycyl-tRNA synthetase	-1.1	0.066	1.17	0.138	1.1	0.074	1.44	0.081	0.65
1429110_a_at	Nsun4	NOL1/NOP2/Sun domain family, member 4	1.16	0.3	-1.05	0.796	1.06	0.754	1.11	0.638	0.57
1448621_a_at	Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	1.03	0.821	1.15	0.477	-1.01	0.908	1.1	0.604	0.57
1442686_at	Dpf3	D4, zinc and double PHD fingers, family 3	1.08	0.67	-1.07	0.89	1.16	0.798	2.06	0.237	0.81
1431076_at	Add2	adducin 2 (beta)	1.02	0.948	-1.21	0.421	1.33	0.248	8.71	0.216	2.46
1459527_at	---	---	1.23	0.589	1.21	0.752	-1.36	0.128	1.34	0.154	0.6
1443683_at	Ptprj	Protein tyrosine phosphatase, receptor type, J	1.03	0.94	1.07	0.897	1.07	0.719	-1.02	0.981	0.54
1415929_at	Map1lc3b	microtubule-associated protein 1 light chain 3 beta	-1.03	0.829	1.06	0.71	1.14	0.113	1.41	0.201	0.65
1434900_at	Mkl1	MKL (megakaryoblastic leukemia)/myocardin-like 1	1.05	0.744	1.08	0.579	1.04	0.77	-1.5	0.199	0.42
1453887_a_at	Tiam1	T-cell lymphoma invasion and metastasis 1	-1.46	0.5	1.46	0.445	1.03	0.958	1.48	0.076	0.63
1459655_at	---	---	1.04	0.932	1.34	0.179	-1.26	0.559	1.04	0.841	0.54
1448146_at	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	1.03	0.895	-1.37	0.142	1.41	0.108	1.05	0.671	0.53
1454112_a_at	Cep27	centrosomal protein 27	-1.11	0.69	1.07	0.454	1.2	0.484	1.73	0.049	0.72
1425242_at	1810006K21Rik	RIKEN cDNA 1810006K21 gene	1.06	0.722	1.1	0.596	1.01	0.923	-1.02	0.959	0.54
1416017_at	Copg	coatomer protein complex, subunit gamma	1.19	0.164	1.07	0.559	-1.09	0.456	1.04	0.685	0.55
1424321_at	Rfc4	replication factor C (activator 1) 4	-1.23	0.571	1.18	0.15	1.18	0.502	2.5	0.255	0.91
1448693_at	BC002216	cDNA sequence BC002216	1.29	0.062	-1.2	0.298	1.05	0.351	1.43	0.072	0.64
1451108_at	Rnf185	ring finger protein 185	1.03	0.742	1.09	0.405	1.05	0.65	-1.33	0.353	0.46
1436816_at	Nup133	Nucleoporin 133	1.22	0.602	1.03	0.93	-1.07	0.709	2.01	0.171	0.8
1441048_at	5930430L01Rik	RIKEN cDNA 5930430L01 gene	1.09	0.868	-1.13	0.842	1.2	0.69	2.2	0.279	0.84
1416080_at	Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)	1.45	0.292	-1.69	0.301	1.14	0.619	1.21	0.358	0.52
1452964_at	Ttll11	tubulin tyrosine ligase-like family, member 11	-2.16	0.226	1.06	0.918	1.65	0.113	1.7	0.506	0.56
1443987_at	Klhl18	kelch-like 18 (Drosophila)	-1.28	0.071	1.05	0.785	1.34	0.283	1.52	0.248	0.66
1440578_at	Kif13a	Kinesin family member 13A	1.35	0.259	1.34	0.153	-2.06	0.047	1.3	0.307	0.48
1434026_at	Atp8b2	Atpase, class I, type 8B, member 2	1.12	0.6	1.04	0.79	1.01	0.94	-1.48	0.322	0.42
1423022_at	Adra2a	adrenergic receptor, alpha 2a	-2.35	0.274	1.45	0.583	1.3	0.443	1.06	0.912	0.36
1425927_a_at	Atf5	activating transcription factor 5	1.06	0.843	-1.07	0.748	1.19	0.487	1.21	0.205	0.6
1424580_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), m	1.06	0.851	-1.38	0.351	1.4	0.48	1.18	0.679	0.56
1459018_at	D10Ertd447e	DNA segment, Chr 10, ERATO Doi 447, expressed	1.12	0.603	1.05	0.945	1.01	0.981	-1.52	0.691	0.41
1452509_at	Usp9y	ubiquitin specific peptidase 9, Y chromosome	-1.8	0.345	1.51	0.344	1.11	0.833	2.32	0.056	0.79
1431815_a_at	Mms19l	MMS19 (MET18 S. cerevisiae)-like	1.1	0.503	-1.25	0.459	1.28	0.268	1.13	0.522	0.56
1416401_at	Cd82	CD82 antigen	1.04	0.783	-1.11	0.561	1.24	0.255	1.5	0.128	0.67
1420498_a_at	Dab2	disabled homolog 2 (Drosophila)	-1.07	0.556	1.12	0.623	1.12	0.69	1.2	0.344	0.59
1448326_a_at	Crabp1	cellular retinoic acid binding protein I	1.27	0.778	1.14	0.712	-1.29	0.652	2.12	0.008	0.81
1447230_at	AI553587	Expressed sequence AI553587	1.21	0.747	-1.07	0.917	1.04	0.921	1.86	0.303	0.76
1446370_at	Rab11fip4	RAB11 family interacting protein 4 (class II)	1.08	0.808	1.42	0.682	-1.47	0.193	1.29	0.557	0.58

1455388_at	Pcmtd1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	1.17	0.273	-1.16	0.419	1.15	0.524	1.02	0.918	0.54
1450984_at	Tjp2	tight junction protein 2	1.05	0.72	1.08	0.662	1.05	0.645	-1.08	0.407	0.52
1434530_at	Odz4	odd Oz/ten-m homolog 4 (Drosophila)	1.13	0.239	-2.03	0.181	1.55	0.476	1.87	0.058	0.63
1446089_at	C86400	expressed sequence C86400	-1.04	0.865	1.17	0.836	1.05	0.806	1.22	0.383	0.6
1453552_at	2310014F07Rik	RIKEN cDNA 2310014F07 gene	-1.76	0.194	1.17	0.383	1.44	0.206	1.38	0.45	0.56
1427263_at	Xist	inactive X specific transcripts	1.36	0.432	-1.64	0.114	1.21	0.502	1.37	0.039	0.57
1443337_at	Grip1	Glutamate receptor interacting protein 1	1.16	0.676	1.34	0.385	-1.48	0.077	1.02	0.905	0.51
1420938_at	Hs6st2	heparan sulfate 6-O-sulfotransferase 2	1.19	0.73	-1.31	0.305	1.23	0.53	1.08	0.548	0.55
1455723_at	D1Ertd448e	DNA segment, Chr 1, ERATO Doi 448, expressed	-1.06	0.736	1.06	0.519	1.17	0.063	1.06	0.617	0.56
1430540_at	Chchd8	coiled-coil-helix-coiled-coil-helix domain containing 8	1.06	0.89	-1	0.998	1.12	0.352	1.04	0.89	0.55
1456032_x_at	H2afz /// LOC66663	H2A histone family, member Z /// similar to H2A histone family, member Z /// simil	-1.01	0.904	1.1	0.015	1.08	0.739	1.24	0.3	0.6
1450061_at	Enc1	ectodermal-neural cortex 1	-1.16	0.278	1.2	0.179	1.11	0.203	1.11	0.52	0.57
1424490_at	Zfp428	zinc finger protein 428	-1.48	0.259	1.45	0.524	1.05	0.916	1.2	0.618	0.56
1421697_at	Ush2a	Usher syndrome 2A (autosomal recessive, mild) homolog (human)	-2.96	0.257	1.21	0.103	1.63	0.183	2.8	0.311	0.67
1448202_x_at	2610524G07Rik	RIKEN cDNA 2610524G07 gene	1.11	0.262	1.04	0.589	1.03	0.716	-1.23	0.33	0.49
1427081_at	A630072M18Rik	RIKEN cDNA A630072M18 gene	1.25	0.041	-1.13	0.69	1.04	0.808	1.1	0.661	0.57
1433873_s_at	Pcnt	pericentrin (kendrin)	1.09	0.524	1.12	0.504	-1.03	0.83	1.14	0.243	0.58
1426214_at	Imp4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	1.25	0.141	-1.41	0.039	1.22	0.609	1.09	0.707	0.54
1448772_at	Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	1	0.977	-1.05	0.519	1.22	0.317	1.34	0.095	0.63
1424746_at	---	---	1.15	0.168	1	0.965	1.03	0.815	-1.23	0.459	0.49
1451029_at	Bcl2l2	Bcl2-like 2	1.25	0.826	1.58	0.477	-2.87	0.024	1.67	0.355	0.41
1444243_at	Wasf3	WAS protein family, member 3	1.56	0.131	-1.87	0.337	1.09	0.887	1.48	0.379	0.56
1437856_at	Ipmk	inositol polyphosphate multikinase	1.27	0.099	1.06	0.726	-1.17	0.403	1.47	0.181	0.66
1460681_at	Ceacam1	CEA-related cell adhesion molecule 1	1.33	0.065	-1.19	0.041	1.01	0.913	1.14	0.713	0.57
1459155_at	AU015696	expressed sequence AU015696	1.1	0.889	-1.31	0.614	1.32	0.159	1.34	0.315	0.61
1449450_at	Ptges	prostaglandin E synthase	1.02	0.758	1.05	0.916	1.12	0.546	-1.23	0.529	0.49
1434470_at	Syt13	synaptotagmin XIII	1.01	0.981	1.24	0.625	-1.07	0.868	1.75	0.03	0.73
1437302_at	Adrb2	adrenergic receptor, beta 2	-1.01	0.981	1.13	0.755	1.06	0.755	1.42	0.32	0.65
1441165_s_at	Clstn2	calsyntenin 2	1.08	0.779	1.47	0.553	-1.58	0.204	1.08	0.808	0.51
1450893_a_at	Ubap1	ubiquitin-associated protein 1	-1.02	0.877	1.11	0.314	1.09	0.466	1.4	0.298	0.64
1450294_a_at	Kcnj6	potassium inwardly-rectifying channel, subfamily J, member 6	1.04	0.9	1.02	0.94	1.12	0.227	-1.16	0.644	0.51
1429399_at	Rnf125	ring finger protein 125	1.15	0.197	1.06	0.852	-1.03	0.873	1.02	0.95	0.55
1451828_a_at	Acsl4	acyl-CoA synthetase long-chain family member 4	1.19	0.693	-1.3	0.342	1.23	0.487	1.4	0.192	0.63
1426475_at	Hmbs	hydroxymethylbilane synthase	-1.01	0.951	1.02	0.665	1.17	0.201	4.21	0.106	1.35
1431048_at	Styx	phosphoserine/threonine/tyrosine interaction protein	1.03	0.791	1.31	0.674	-1.18	0.533	1.05	0.88	0.55
1453401_at	4930428O21Rik	RIKEN cDNA 4930428O21 gene	-1.06	0.614	1.02	0.981	1.23	0.469	2.75	0.181	0.98
1418018_at	Cpd	carboxypeptidase D	1.39	0.42	1.01	0.971	-1.28	0.523	2.05	0.243	0.79
1436450_at	D11Bwg0517e	DNA segment, Chr 11, Brigham & Women's Genetics 0517 expressed	1.5	0.094	1.15	0.738	-1.85	0.148	1.11	0.769	0.47
1427271_at	Btbd15	BTB (POZ) domain containing 15	1.16	0.135	1.06	0.602	-1.03	0.867	1.39	0.375	0.64
1432241_at	9030205G03Rik	RIKEN cDNA 9030205G03 gene	1.77	0.305	-2.56	0.426	1.02	0.973	1.99	0.21	0.56
1446897_at	---	---	1.62	0.478	-1.88	0.298	1.03	0.92	1.64	0.075	0.6
1454996_at	Hsdl1	hydroxysteroid dehydrogenase like 1	1.01	0.893	1.09	0.634	1.08	0.554	-1.48	0.051	0.43
1425042_s_at	Pelp1	proline, glutamic acid and leucine rich protein 1	-1.21	0.497	1.02	0.92	1.34	0.05	1.23	0.23	0.6
1429409_at	Nalp14	NACHT, leucine rich repeat and PYD containing 14	1.08	0.803	-1.02	0.884	1.13	0.82	1.08	0.68	0.57
1416840_at	Mid1ip1	Mid1 interacting protein 1 (gastrulation specific G12-like (zebrafish))	-1.03	0.785	1.13	0.608	1.09	0.363	1.79	0.146	0.74
1454688_x_at	Tmed10 /// LOC634	transmembrane emp24-like trafficking protein 10 (yeast) /// similar to transmembr	-1.08	0.412	1.21	0.243	1.04	0.318	1.09	0.714	0.57
1452707_at	4631423F02Rik	RIKEN cDNA 4631423F02 gene	-1.06	0.918	1.02	0.982	1.22	0.685	1.14	0.516	0.58
1460067_at	Ccr2	chemokine (C-C motif) receptor 2	1.16	0.855	1.21	0.459	-1.22	0.689	1.11	0.762	0.57
1429971_at	Txnrd2	thioredoxin reductase 2	1.01	0.957	-1.41	0.291	1.47	0.396	2.96	0.271	1.01
1434206_s_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	1.21	0.123	1.02	0.812	-1.04	0.697	1.06	0.802	0.56
1457695_at	Ap1gbp1	AP1 gamma subunit binding protein 1	1.17	0.444	-1.04	0.91	1.06	0.864	1.1	0.204	0.57
1451291_at	Obfc2b	oligonucleotide/oligosaccharide-binding fold containing 2B	1.04	0.887	-1.04	0.854	1.18	0.349	1.05	0.79	0.56
1418041_at	4432406C05Rik	RIKEN cDNA 4432406C05 gene	1.32	0.368	-1.46	0.258	1.18	0.526	1.36	0.542	0.6

1450072_at	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	1.01	0.955	1.15	0.406	1.03	0.874	-1.69	0.116	0.37
1458164_at	LOC552913	hypothetical LOC552913	1.12	0.488	1.18	0.725	-1.12	0.655	1.17	0.367	0.59
1456950_at	Alms1	Alstrom syndrome 1 homolog (human)	-2.47	0.146	1.39	0.3	1.39	0.213	2.27	0.165	0.65
1427730_a_at	Zfp148	zinc finger protein 148	1.08	0.12	1.05	0.498	1.05	0.785	-1.1	0.164	0.52
1454373_x_at	Ubc	ubiquitin C	-1.09	0.833	1.02	0.803	1.25	0.478	1.13	0.633	0.58
1425539_a_at	Rtn3	reticulon 3	1.04	0.517	-1	0.996	1.14	0.565	1.4	0.252	0.65
1451317_at	Ythdf2	YTH domain family 2	1.02	0.847	1.08	0.675	1.08	0.7	-1.18	0.275	0.5
1442303_at	---	10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2	1.32	0.452	-1.33	0.521	1.11	0.543	1.98	0.07	0.77
1451176_at	D430028G21Rik	RIKEN cDNA D430028G21 gene	-1.06	0.726	1.03	0.663	1.21	0.262	1.03	0.723	0.55
1447512_at	Chl1	Cell adhesion molecule with homology to L1CAM	1.12	0.824	1.43	0.425	-1.59	0.353	1.19	0.767	0.54
1439972_at	Etnk1	ethanolamine kinase 1	1.05	0.822	1.12	0.628	1.02	0.906	-1.33	0.494	0.47
1424720_at	Mgat4b	mannoside acetylglucosaminyltransferase 4, isoenzyme B	-1.07	0.554	1.08	0.436	1.17	0.417	1.49	0.143	0.67
1429852_at	Ccdc57	coiled-coil domain containing 57	1.17	0.7	-1.04	0.895	1.05	0.831	2.72	0.315	0.98
1440293_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	-1.8	0.185	1.58	0.401	1.05	0.798	2.22	0.154	0.76
1452736_at	R3hcc1	R3H domain and coiled-coil containing 1	1.03	0.855	1.07	0.729	1.1	0.622	-1.07	0.687	0.53
1448481_at	Neu1	neuraminidase 1	1.33	0.583	-1.61	0.122	1.23	0.559	1.17	0.441	0.53
1454683_at	Sfrs8	splicing factor, arginine/serine-rich 8	1.22	0.557	-1.28	0.497	1.19	0.23	1.3	0.309	0.61
1417710_at	Mettl9	methyltransferase like 9	-1.11	0.068	1.09	0.289	1.19	0.412	1.01	0.942	0.55
1427346_at	Ott /// LOC434863	ovary testis transcribed /// similar to ovary testis transcribed /// similar to ovary tes	-1.15	0.816	1.29	0.534	1.02	0.902	1.12	0.848	0.57
1417503_at	Rfc2	replication factor C (activator 1) 2	-1.06	0.404	1.24	0.069	1.01	0.95	1.13	0.414	0.58
1438817_at	Dna2l	DNA2 DNA replication helicase 2-like (yeast)	1.07	0.881	1.12	0.348	-1.01	0.97	1.41	0.555	0.65
1442610_at	Plxdc1	Plexin domain containing 1	1.14	0.731	-1.03	0.931	1.08	0.834	1.05	0.689	0.56
1450544_at	AB041550	hypothetical protein, MNCb-4779	1.44	0.644	1.3	0.66	-2.22	0.12	1.18	0.492	0.42
1459225_at	---	---	1.1	0.819	1.52	0.298	-1.77	0.037	1.01	0.974	0.46
1453961_a_at	Mospd3	motile sperm domain containing 3	-1.04	0.93	1.05	0.893	1.18	0.326	1.12	0.733	0.58
1444331_at	Synpr	Synaptoporin	1.16	0.83	-1.32	0.532	1.27	0.623	1.7	0.237	0.7
1438625_s_at	Ndn /// Pctk1	necdin /// PCTAIRE-motif protein kinase 1	1.23	0.393	1.04	0.494	-1.08	0.388	1.36	0.134	0.63
1420436_x_at	Tex21	testis expressed gene 21	1.02	0.985	-2.21	0.256	1.72	0.214	1.21	0.462	0.43
1453920_a_at	Mospd2	motile sperm domain containing 2	1.03	0.919	-1.31	0.254	1.4	0.335	1.42	0.234	0.63
1453355_at	Wnk2	WNK lysine deficient protein kinase 2	1	0.955	-1.3	0.37	1.41	0.055	1.15	0.586	0.57
1442366_at	6820408C15Rik	RIKEN cDNA 6820408C15 gene	-1.12	0.278	1.14	0.8	1.16	0.614	1.38	0.045	0.64
1456366_at	1700015F17Rik	RIKEN cDNA 1700015F17 gene	-1.49	0.587	1.23	0.642	1.28	0.515	1.13	0.831	0.54
1440928_at	D630037F22Rik	RIKEN cDNA D630037F22 gene	-1.02	0.454	1.19	0.452	1.02	0.561	1.11	0.763	0.58
1416949_s_at	Slc39a7	solute carrier family 39 (zinc transporter), member 7	1	0.989	1.18	0.054	1.01	0.975	-1.08	0.76	0.53
1433952_at	Tufm	Tu translation elongation factor, mitochondrial	-1.19	0.392	1.27	0.371	1.08	0.833	1.19	0.65	0.59
1425544_at	Plekha5	pleckstrin homology domain containing, family A member 5	1.22	0.7	-1.81	0.144	1.41	0.641	1.12	0.836	0.49
1439753_x_at	Six4	sine oculis-related homeobox 4 homolog (Drosophila)	-1.47	0.384	1.35	0.683	1.16	0.414	2.59	0.109	0.91
1417493_at	Bmi1	B lymphoma Mo-MLV insertion region 1	1.01	0.736	1.11	0.487	1.06	0.614	-1.24	0.306	0.49
1452768_at	Tex261	testis expressed gene 261	1.09	0.755	1.13	0.563	-1.04	0.783	1.31	0.054	0.63
1436020_at	D8Ertd457e	DNA segment, Chr 8, ERATO Doi 457, expressed	-1.08	0.749	1.14	0.348	1.12	0.135	1.11	0.644	0.57
1457706_at	BC030336	cDNA sequence BC030336	1.47	0.337	1.01	0.966	-1.42	0.186	1.09	0.659	0.54
1445219_at	Olfr315	olfactory receptor 315	1.86	0.276	1.03	0.948	-3.32	0.071	1.25	0.241	0.2
1431363_at	4933425K02Rik	RIKEN cDNA 4933425K02 gene	1.36	0.291	-1.36	0.322	1.1	0.698	1.01	0.962	0.53
1418248_at	Gla	galactosidase, alpha	-1.23	0.517	1.08	0.401	1.3	0.072	1.55	0.016	0.68
1440589_at	Samd12	Sterile alpha motif domain containing 12	1.32	0.16	1.03	0.947	-1.19	0.267	1.34	0.088	0.62
1438965_x_at	A230056P14Rik	RIKEN cDNA A230056P14 gene	1.26	0.661	-1.74	0.109	1.36	0.34	1.21	0.451	0.52
1417542_at	Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	-1.14	0.176	1.07	0.675	1.24	0.288	1.06	0.765	0.56
1444074_at	Syne2 /// LOC6772	synaptic nuclear envelope 2 /// similar to Nesprin-2 (Nuclear envelope spectrin re	1.4	0.646	1.07	0.905	-1.38	0.591	1.29	0.498	0.59
1424727_at	Ccr5	chemokine (C-C motif) receptor 5	1.04	0.903	1.21	0.452	-1.07	0.764	1.51	0.428	0.67
1450573_at	Amh	anti-Mullerian hormone	1.06	0.843	-1.62	0.317	1.52	0.483	1.15	0.25	0.53
1453468_at	4930430F08Rik	RIKEN cDNA 4930430F08 gene	-1.19	0.18	1.09	0.76	1.26	0.317	1.84	0.185	0.75
1448539_a_at	Acy3	aspartoacylase (aminoacylase) 3	1.09	0.728	-1.21	0.335	1.27	0.011	1.52	0.153	0.67
1434554_at	Trim37	tripartite motif protein 37	-1.13	0.526	1.01	0.961	1.3	0.225	2.47	0.179	0.91

1452401_at	Wtap	Wilms' tumour 1-associating protein	1.11	0.037	1.25	0.19	-1.21	0.324	1.15	0.425	0.58
1450075_at	Polh	polymerase (DNA directed), eta (RAD 30 related)	1.36	0.285	-1.4	0.245	1.12	0.73	1.76	0.104	0.71
1438164_x_at	Flot2	flotillin 2	-1.1	0.265	1.1	0.241	1.18	0.022	1.3	0.029	0.62
1425599_a_at	Gatad1	GATA zinc finger domain containing 1	1.06	0.509	-1.02	0.781	1.15	0.405	1.27	0.356	0.62
1420887_a_at	Bcl2l1	Bcl2-like 1	1.14	0.835	-1.01	0.982	1.06	0.826	3.37	0.195	1.14
1430954_at	Ppil3	peptidylprolyl isomerase (cyclophilin)-like 3	-1.6	0.118	1.08	0.871	1.48	0.495	1.94	0.322	0.73
1452554_at	---	Strain DBA/2J thiopurine S-methyltransferase (Tpmt) pseudogene, mRNA sequer	1.11	0.631	1.23	0.515	-1.19	0.575	1.21	0.645	0.59
1440523_at	Rdhe2	retinal short chain dehydrogenase reductase 2	1.54	0.571	1.2	0.686	-2.24	0.262	1.3	0.485	0.45
1436623_at	Entpd7	ectonucleoside triphosphate diphosphohydrolase 7	1.01	0.987	1.29	0.56	-1.11	0.427	1.06	0.67	0.56
1449414_at	Zfp53	zinc finger protein 53	1.05	0.762	1.04	0.864	1.11	0.638	-3.11	0.015	0.02
1428129_at	Lman1	lectin, mannose-binding, 1	1.21	0.526	-1.03	0.953	1.01	0.98	1.68	0.028	0.72
1429626_at	Sftpa1	surfactant associated protein A1	1.27	0.252	1.16	0.814	-1.32	0.062	1.49	0.602	0.65
1435925_at	Git2	G protein-coupled receptor kinase-interactor 2	1.14	0.425	1.08	0.496	-1.03	0.855	1.12	0.498	0.58
1436132_at	9830001H06Rik	RIKEN cDNA 9830001H06 gene	-1.3	0.131	1.4	0.514	1.02	0.88	1.19	0.704	0.58
1426663_s_at	Slc45a3	solute carrier family 45, member 3	-1.15	0.481	1.2	0.415	1.12	0.61	1.18	0.647	0.59
1428284_at	8430427H17Rik	RIKEN cDNA 8430427H17 gene	-1.3	0.044	1.3	0.164	1.12	0.445	1.33	0.529	0.61
1417873_at	Pwp1	PWP1 homolog (S. cerevisiae)	1.03	0.852	1.03	0.752	1.14	0.523	-1.06	0.576	0.53
1430772_at	---	---	1.31	0.622	-1.2	0.489	1.05	0.873	1.16	0.559	0.58
1420376_a_at	H3f3b	H3 histone, family 3B	1.07	0.273	1.18	0.097	-1.05	0.498	1.2	0.322	0.6
1456267_at	AI451606	expressed sequence AI451606	1.01	0.968	1.04	0.806	1.15	0.559	-1.51	0.179	0.42
1441124_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130032O	-1.07	0.86	1.01	0.977	1.25	0.198	1.6	0.102	0.7
1445241_at	Rab11fip4	RAB11 family interacting protein 4 (class II)	-1.51	0.249	1.1	0.679	1.43	0.285	1.06	0.827	0.52
1438957_x_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	1	0.983	1.22	0.021	-1.03	0.585	1.01	0.919	0.55
1418755_at	Tbx15	T-box 15	1.55	0.569	1.09	0.902	-1.78	0.349	1.77	0.435	0.66
1424054_at	Btbd2	BTB (POZ) domain containing 2	1.07	0.534	-1.08	0.672	1.2	0.366	1.1	0.592	0.57
1454248_at	1700041E20Rik	RIKEN cDNA 1700041E20 gene	-1.11	0.905	1.2	0.19	1.09	0.726	1.13	0.518	0.58
1431712_a_at	2310022A10Rik	RIKEN cDNA 2310022A10 gene	-1.1	0.704	1.27	0.366	1.02	0.936	1.23	0.344	0.61
1440898_at	4632412N22Rik	RIKEN cDNA 4632412N22 gene	-1.24	0.434	1.32	0.662	1.08	0.519	1.34	0.397	0.62
1431509_at	4933404G15Rik	RIKEN cDNA 4933404G15 gene	1.1	0.736	-1.24	0.233	1.29	0.643	1.1	0.904	0.56
1416449_x_at	Stxbp2	syntaxin binding protein 2	1.11	0.519	1.03	0.831	1.05	0.683	-1.52	0.031	0.42
1423668_at	Zdhhc14	zinc finger, DHHC domain containing 14	1.09	0.678	1.36	0.366	-1.35	0.127	2.27	0.232	0.84
1417570_at	Anapc1	anaphase promoting complex subunit 1	-1.12	0.584	1.13	0.575	1.17	0.635	1.04	0.707	0.56
1415706_at	Copa	coatomer protein complex subunit alpha	1.03	0.911	1.04	0.602	1.13	0.283	-1.02	0.934	0.55
1452070_at	Dedd2	death effector domain-containing DNA binding protein 2	1.1	0.644	-1.12	0.503	1.2	0.131	1.3	0.498	0.62
1417087_at	Glg1	golgi apparatus protein 1	-1.05	0.691	1.21	0.268	1.04	0.703	1.08	0.511	0.57
1433480_at	2900010J23Rik	RIKEN cDNA 2900010J23 gene	1.05	0.29	1.08	0.213	1.07	0.621	-1.11	0.492	0.52
1459341_at	8030448K23Rik	RIKEN cDNA 8030448K23 gene	1.12	0.336	1.34	0.549	-1.35	0.05	1.03	0.615	0.53
1416767_a_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	1.07	0.436	1.1	0.256	1.03	0.835	-1.66	0.114	0.38
1456445_at	4930563D23Rik	RIKEN cDNA 4930563D23 gene	-2.38	0.063	1.08	0.856	1.7	0.265	2.17	0.197	0.64
1416898_a_at	Irf3	interferon regulatory factor 3	1.09	0.722	1.1	0.594	1.01	0.961	-1.33	0.479	0.47
1438710_at	Htr1a	5-hydroxytryptamine (serotonin) receptor 1A	1.22	0.736	1.06	0.807	-1.1	0.873	2.28	0.29	0.87
1430569_at	Ttc9c	tetratricopeptide repeat domain 9C	1.21	0.206	-1.54	0.084	1.34	0.065	1.36	0.415	0.59
1448847_at	Serinc3	serine incorporator 3	1.28	0.56	1.09	0.744	-1.21	0.399	1.02	0.929	0.54
1421149_a_at	Atn1	atrophin 1	-1.22	0.51	1.08	0.467	1.29	0.258	1.04	0.888	0.55
1456048_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	1.15	0.689	1.09	0.794	-1.04	0.808	3.31	0.119	1.13
1425330_a_at	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	1.05	0.408	-1.22	0.178	1.33	0.134	1.45	0.386	0.65
1428195_at	4631427C17Rik	RIKEN cDNA 4631427C17 gene	1.06	0.672	-1.14	0.752	1.26	0.471	1.02	0.942	0.55
1459647_at	Pold3	Polymerase (DNA-directed), delta 3, accessory subunit	1	0.995	-1.03	0.857	1.22	0.431	1.53	0.553	0.68
1455600_at	Rps3	ribosomal protein S3	1.18	0.034	1.19	0.215	-1.21	0.425	1.1	0.686	0.57
1423597_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	1.17	0.665	1.24	0.185	-1.28	0.27	1.68	0.091	0.7
1438925_x_at	Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	-1.15	0.324	1.16	0.215	1.17	0.193	1.34	0.014	0.63
1427378_at	Krt75	keratin 75	1.08	0.87	-1.24	0.493	1.31	0.525	2.55	0.001	0.93
1450830_a_at	Pde6c	phosphodiesterase 6C, cGMP specific, cone, alpha prime	1.57	0.561	-1.81	0.254	1.07	0.876	1.45	0.579	0.57

1457726_at	Rps15a	ribosomal protein S15a	-1.34	0.691	1.27	0.238	1.18	0.709	1.04	0.909	0.54
1427153_at	Bckdhb	branched chain ketoacid dehydrogenase E1, beta polypeptide	1.03	0.763	1.12	0.104	1.05	0.759	-1.11	0.722	0.52
1439370_x_at	Sf3b5	splicing factor 3b, subunit 5	1.18	0.74	1.17	0.612	-1.18	0.752	1.04	0.91	0.55
1455836_at	Papola	poly (A) polymerase alpha	1.34	0.259	-1.23	0.055	1.05	0.896	1.64	0.064	0.7
1451460_a_at	Slc22a7	solute carrier family 22 (organic anion transporter), member 7	1.04	0.793	1.03	0.938	1.13	0.799	-1.01	0.969	0.55
1438513_at	Tatdn1	TatD DNase domain containing 1	1.3	0.47	1.27	0.132	-1.57	0.078	1.25	0.382	0.56
1454144_a_at	Ccnc	cyclin C	1.12	0.405	-1.46	0.001	1.4	0.197	1.21	0.658	0.57
1430769_s_at	2900009I07Rik	RIKEN cDNA 2900009I07 gene	-1.01	0.801	1.03	0.611	1.18	0.165	1.45	0.211	0.66
1425312_s_at	D11Ertd636e	DNA segment, Chr 11, ERATO Doi 636, expressed	-1.32	0.009	1.03	0.833	1.42	0.122	1.78	0.201	0.72
1458454_at	---	Transcribed locus	-1.25	0.217	1.14	0.624	1.26	0.344	1.41	0.16	0.64
1444569_at	LOC666752 /// LOC	hypothetical protein LOC666752 /// hypothetical protein LOC669447 /// hypothetic	1.05	0.838	1.11	0.875	1.04	0.677	-1.87	0.065	0.33
1429786_a_at	Zwint	ZW10 interactor	1.14	0.43	-1.12	0.515	1.17	0.594	1.85	0.298	0.76
1425706_a_at	Ddb2	damage specific DNA binding protein 2	1.11	0.457	1.04	0.811	1.05	0.769	-1.97	0.038	0.31
1455371_at	Rfxank	regulatory factor X-associated ankyrin-containing protein	-1.18	0.479	1.17	0.645	1.19	0.201	1.5	0.241	0.67
1444038_at	AU015836	expressed sequence AU015836	-2.02	0.25	1.64	0.477	1.07	0.897	1.61	0.271	0.57
1440637_at	Itsn1	Intersectin 1 (SH3 domain protein 1A)	1.21	0.457	1.23	0.279	-1.31	0.169	3.71	0.191	1.21
1449339_at	D10Ertd641e	DNA segment, Chr 10, ERATO Doi 641, expressed	1.2	0.614	-1.03	0.853	1.03	0.714	1	0.995	0.55
1452924_at	2310007D09Rik	RIKEN cDNA 2310007D09 gene	-1.52	0.048	1.14	0.596	1.4	0.191	2.98	0.247	1
1452664_a_at	Tm7sf3	transmembrane 7 superfamily member 3	-1.09	0.502	1.2	0.057	1.09	0.682	1.68	0.227	0.72
1446842_at	D4Ertd571e	DNA segment, Chr 4, ERATO Doi 571, expressed	1.19	0.677	1.03	0.912	-1.02	0.96	1.45	0.395	0.66
1422718_at	Ap3s2	adaptor-related protein complex 3, sigma 2 subunit	-1.04	0.768	1.08	0.706	1.16	0.446	1.13	0.192	0.58
1417284_at	Mapkap1	mitogen-activated protein kinase associated protein 1	1.08	0.021	-1	0.961	1.13	0.392	1.01	0.97	0.55
1421041_s_at	Gsta1 /// Gsta2	glutathione S-transferase, alpha 1 (Ya) /// glutathione S-transferase, alpha 2 (Yc2	-1.25	0.094	1.31	0.712	1.09	0.711	1.24	0.544	0.6
1449340_at	Sostdc1	sclerostin domain containing 1	1.22	0.448	-2.79	0.052	1.63	0.379	1.1	0.848	0.29
1423785_at	Egln1	EGL nine homolog 1 (C. elegans)	1.03	0.796	1.1	0.356	1.07	0.711	-1.19	0.149	0.5
1450969_at	Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	1.02	0.892	-1.13	0.492	1.3	0.152	1.24	0.511	0.61
1433646_at	Mrps27	mitochondrial ribosomal protein S27	1.01	0.951	1.08	0.162	1.11	0.082	-1.2	0.462	0.5
1430653_at	A930026B05Rik	RIKEN cDNA A930026B05 gene	1.3	0.232	1.42	0.11	-2.1	0.019	1.13	0.295	0.44
1455725_a_at	H3f3b	H3 histone, family 3B	1.05	0.679	1.13	0.306	1.02	0.861	-1.02	0.821	0.55
1433102_at	3100002H20Rik	RIKEN cDNA 3100002H20 gene	1	0.997	1.44	0.186	-1.31	0.355	1.66	0.284	0.7
1455023_at	N28178	expressed sequence N28178	-1.04	0.933	1.14	0.756	1.1	0.6	1.26	0.576	0.62
1443501_at	---	Transcribed locus, moderately similar to XP_345375.2 PREDICTED: similar to H(	1.1	0.676	-1.5	0.001	1.44	0.421	1.81	0.153	0.71
1446858_at	AU022245	expressed sequence AU022245	1.08	0.288	-1.35	0.58	1.39	0.478	1.94	0.267	0.76
1444238_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	1.07	0.825	-1.02	0.97	1.16	0.595	1.17	0.667	0.59
1435414_s_at	Dctn1	dynactin 1	-1.08	0.652	1.04	0.262	1.24	0.009	1.05	0.643	0.56
1419829_a_at	Gab2	Growth factor receptor bound protein 2-associated protein 2	1.07	0.719	1.28	0.091	-1.17	0.377	1.2	0.321	0.6
1425708_at	Rnf17	ring finger protein 17	1.1	0.583	-2.03	0.313	1.61	0.168	1.35	0.392	0.51
1451021_a_at	Klf5	Kruppel-like factor 5	-1.18	0.136	1.2	0.688	1.15	0.273	3.91	0.281	1.27
1450894_a_at	Ap2m1	adaptor protein complex AP-2, mu1	1.13	0.4	1.12	0.364	-1.05	0.767	1.44	0.211	0.66
1436703_x_at	Snapc2	small nuclear RNA activating complex, polypeptide 2	1.12	0.574	-1.13	0.034	1.2	0.284	1.02	0.887	0.55
1435692_at	LOC622320	similar to retinoic acid, EGF, and NGF upregulated	1.11	0.337	1.02	0.891	1.07	0.22	-1.12	0.398	0.52
1441590_at	Kcnj5	potassium inwardly-rectifying channel, subfamily J, member 5	1.41	0.507	-1.64	0.44	1.19	0.804	1.42	0.537	0.59
1424535_at	4930521E07Rik	RIKEN cDNA 4930521E07 gene	-1.02	0.934	1.13	0.45	1.1	0.611	1.1	0.461	0.58
1448924_at	4432406C05Rik	RIKEN cDNA 4432406C05 gene	1.14	0.63	1.33	0.493	-1.37	0.464	1.2	0.193	0.58
1442523_at	LOC331392	similar to Nucleolar phosphoprotein p130 (Nucleolar 130 kDa protein) (140 kDa n	1.11	0.128	-1.11	0.791	1.2	0.524	1.47	0.289	0.67
1453081_at	2410022M11Rik	RIKEN cDNA 2410022M11 gene	1.18	0.165	-1.01	0.953	1.03	0.91	1.02	0.886	0.56
1429405_at	2010317E24Rik	RIKEN cDNA 2010317E24 gene	-1.71	0.355	1.44	0.183	1.18	0.469	2.02	0.027	0.73
1421500_at	Sts	steroid sulfatase	1.23	0.532	-1.11	0.687	1.07	0.541	1.54	0.413	0.68
1432951_at	4930448E22Rik	RIKEN cDNA 4930448E22 gene	-1.48	0.069	1.45	0.375	1.08	0.861	2.47	0.104	0.88
1451716_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	1.08	0.366	-1.48	0.209	1.45	0.091	1.17	0.689	0.55
1432753_at	9130214F15Rik	RIKEN cDNA 9130214F15 gene	-1.2	0.594	1.2	0.684	1.17	0.706	1.13	0.806	0.58
1418900_at	Ufm1	ubiquitin-fold modifier 1	1.32	0.458	-1.16	0.447	1.02	0.89	1.29	0.434	0.62
1456905_at	Ccdc24	coiled-coil domain containing 24	1.13	0.527	-1.04	0.898	1.11	0.524	1.17	0.716	0.59

1438980_x_at	4732466D17Rik	RIKEN cDNA 4732466D17 gene	1.17	0.387	1.17	0.054	-1.15	0.324	1.8	0.364	0.75
1417582_s_at	Dhodh	dihydroorotate dehydrogenase	1.06	0.691	1.01	0.956	1.13	0.224	-1.16	0.303	0.51
1450147_at	Nptxr	neuronal pentraxin receptor	-1.18	0.583	1.03	0.784	1.33	0.384	1.63	0.006	0.7
1425760_a_at	Pitpnm1	phosphatidylinositol membrane-associated 1	1.01	0.898	-1.14	0.604	1.31	0.056	1.01	0.968	0.55
1456618_at	Mark4	MAP/microtubule affinity-regulating kinase 4	1.07	0.818	1.08	0.804	1.06	0.794	-1.05	0.921	0.54
1454818_at	Gmeb2	glucocorticoid modulatory element binding protein 2	-1.11	0.527	1.03	0.793	1.28	0.101	1.26	0.257	0.61
1452394_at	Cars	cysteinyl-tRNA synthetase	1.1	0.078	-1.16	0.462	1.24	0.319	2.02	0.23	0.8
1450907_at	Spcs2	signal peptidase complex subunit 2 homolog (S. cerevisiae)	1.02	0.857	1.19	0.283	-1.01	0.96	1.08	0.572	0.57
1441230_at	Fndc3b	Fibronectin type III domain containing 3B	1.01	0.985	1.56	0.241	-1.55	0.103	1.24	0.182	0.56
1438494_at	Hrh1	histamine receptor H 1	1.33	0.47	-1.36	0.453	1.14	0.287	1.15	0.674	0.56
1431458_at	4921507L20Rik	RIKEN cDNA 4921507L20 gene	1.05	0.884	-1.4	0.651	1.44	0.497	1.41	0.403	0.63
1436311_at	Gemin5	gem (nuclear organelle) associated protein 5	-1.09	0.891	1.21	0.534	1.08	0.844	1.1	0.91	0.57
1422245_a_at	Mrvi1	MRV integration site 1	-1.3	0.432	1.3	0.581	1.14	0.561	1.56	0.417	0.68
1460673_at	Fpgs	folylpolyglutamyl synthetase	1.18	0.651	1.04	0.742	-1.01	0.939	1.59	0.251	0.7
1429039_s_at	1500034J01Rik	RIKEN cDNA 1500034J01 gene	1.14	0.47	-1.15	0.319	1.2	0.09	1.15	0.533	0.58
1450256_at	Cer1	cerberus 1 homolog (Xenopus laevis)	-1.13	0.794	1.09	0.882	1.24	0.722	1.72	0.549	0.73
1442945_at	2010109K09Rik	RIKEN cDNA 2010109K09 gene	1.01	0.961	1.07	0.707	1.13	0.688	-1.25	0.359	0.49
1428501_at	1110051M20Rik	RIKEN cDNA 1110051M20 gene	-1.05	0.632	1.17	0.442	1.08	0.512	1.09	0.562	0.57
1442851_at	C79818	expressed sequence C79818	-1.13	0.673	1.14	0.315	1.18	0.725	1.77	0.158	0.74
1425074_at	Wrn	Werner syndrome homolog (human)	1.06	0.727	1.27	0.047	-1.14	0.489	1.46	0.116	0.66
1427749_at	LOC620893	hypothetical protein LOC620893	1.13	0.242	1.34	0.709	-1.35	0.16	1.34	0.126	0.61
1452373_at	1700081L11Rik	RIKEN cDNA 1700081L11 gene	1.09	0.068	1.03	0.899	1.1	0.634	-1.07	0.756	0.54
1425932_a_at	Cugbp1	CUG triplet repeat, RNA binding protein 1	1.02	0.78	-1.38	0.241	1.47	0.296	1.71	0.435	0.7
1419713_at	Atp8b3	ATPase, Class I, type 8B, member 3	1.17	0.846	-1.93	0.247	1.52	0.279	1.21	0.272	0.49
1452265_at	Clasp1	CLIP associating protein 1	-1.01	0.952	1.1	0.196	1.12	0.413	1.04	0.683	0.56
1427665_a_at	Nfic	nuclear factor I/C	1.15	0.453	-1.43	0.301	1.37	0.456	1.4	0.587	0.62
1445228_at	Spred1	Sprouty protein with EVH-1 domain 1, related sequence	-2.45	0.401	1.41	0.349	1.39	0.064	1.17	0.669	0.38
1422763_at	Gipc1	GIPC PDZ domain containing family, member 1	1.21	0.489	-1.02	0.826	1.02	0.872	1.4	0.349	0.65
1423675_at	Usp1	ubiquitin specific peptdiase 1	-1.19	0.039	1.13	0.606	1.25	0.345	1.48	0.384	0.66
1430497_at	Rxra	retinoid X receptor alpha	1.1	0.299	1.02	0.929	1.09	0.793	-2.13	0.527	0.27
1454451_at	5330430B06Rik	RIKEN cDNA 5330430B06 gene	-1.05	0.572	1.23	0.7	1.03	0.865	2.09	0.141	0.82
1422035_at	Serpinb9c	serine (or cysteine) peptidase inhibitor, clade B, member 9c	1.17	0.589	1.07	0.926	-1.03	0.963	1.81	0.418	0.76
1431804_a_at	Sp3	trans-acting transcription factor 3	1.06	0.782	1.16	0.479	-1.01	0.963	1.57	0.251	0.69
1422346_at	Titf1	thyroid transcription factor 1	1.67	0.623	-2.59	0.112	1.15	0.624	1.24	0.735	0.37
1446719_at	D530031C13Rik	RIKEN cDNA D530031C13 gene	1.06	0.892	1.64	0.159	-1.95	0.036	1.19	0.581	0.49
1437968_at	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	-1.17	0.852	1.05	0.916	1.31	0.315	2.42	0.004	0.9
1421465_at	Wnt2b	wingless related MMTV integration site 2b	1.53	0.028	-1.48	0.446	1	0.998	2.12	0.204	0.79
1448390_a_at	Dhrs3	dehydrogenase/reductase (SDR family) member 3	-1.05	0.544	1.15	0.132	1.1	0.225	1.23	0.508	0.61
1431016_at	Cwf19l1	CWF19-like 1, cell cycle control (S. pombe)	1.14	0.777	1	0.996	1.07	0.766	-1.31	0.031	0.47
1434963_at	Supt3h	suppressor of Ty 3 homolog (S. cerevisiae)	1.07	0.74	1.02	0.941	1.12	0.371	-1.09	0.387	0.53
1439861_at	Zfp583	zinc finger protein 583	1.3	0.579	-1.2	0.444	1.08	0.812	1	0.991	0.55
1437434_a_at	Gpr177	G protein-coupled receptor 177	-1.22	0.194	1.34	0.155	1.05	0.662	1.05	0.811	0.55
1425815_a_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	-1.39	0.215	1.48	0.475	1.02	0.94	4.23	0.182	1.33
1452489_at	Vps11	vacuolar protein sorting 11 (yeast)	1.29	0.364	1.3	0.375	-1.59	0.325	1.17	0.745	0.54
1434812_s_at	Dok7	docking protein 7	1.35	0.213	-1.31	0.449	1.1	0.639	1.21	0.347	0.59
1421613_at	H2afy3	H2A histone family, member Y3	-1.69	0.56	1.23	0.271	1.39	0.143	1.17	0.778	0.52
1455732_at	1700025G04Rik	RIKEN cDNA 1700025G04 gene	1.35	0.032	1.15	0.504	-1.42	0.177	1.03	0.938	0.53
1441081_a_at	1110038B12Rik	RIKEN cDNA 1110038B12 gene	1.18	0.117	-1.08	0.597	1.11	0.798	1.36	0.393	0.64
1423243_at	Mpp1	membrane protein, palmitoylated	-1.27	0.342	1.02	0.98	1.41	0.429	1.58	0.376	0.68
1431549_at	---	---	-1.02	0.877	1.17	0.549	1.06	0.823	1.02	0.94	0.56
1432043_at	Smu1	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	1.63	0.138	1.06	0.901	-1.91	0.026	1.57	0.139	0.59
1429796_at	Kalrn	kalirin, RhoGEF kinase	1.08	0.444	-1.13	0.426	1.25	0.474	1.56	0.408	0.69
1432172_at	LOC670300	hypothetical protein LOC670300	-2.03	0.04	1.45	0.32	1.27	0.618	1.34	0.462	0.51

1428015_at	D12Wsu118e	DNA segment, Chr 12, Wayne State University 118, expressed	1.11	0.693	-1.07	0.835	1.16	0.554	1.01	0.971	0.56
1419719_at	Gabrb1 /// B230208	gamma-aminobutyric acid (GABA-A) receptor, subunit beta 1 /// RIKEN cDNA B2	1.01	0.968	-1.8	0.327	1.65	0.174	1.85	0.434	0.68
1450479_x_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	-1	0.991	1.16	0.489	1.06	0.693	1.41	0.023	0.66
1434138_at	Prune	prune homolog (Drosophila)	-1.33	0.023	1.19	0.042	1.27	0.085	1.27	0.415	0.6
1431265_at	Zfp28	zinc finger protein 28	1.09	0.528	1	0.996	1.12	0.779	-1.26	0.766	0.49
1450494_x_at	Ceacam1	CEA-related cell adhesion molecule 1	1.18	0.501	-1.13	0.617	1.15	0.693	1.17	0.722	0.59
1446627_at	Stk3	Serine/threonine kinase 3 (Ste20, yeast homolog)	1.08	0.666	-1.15	0.527	1.26	0.689	1.55	0.055	0.69
1445648_at	---	Transcribed locus	1.12	0.838	-1.62	0.41	1.48	0.384	1.33	0.535	0.58
1421351_at	Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	-1.14	0.336	1.13	0.735	1.2	0.511	1.31	0.072	0.63
1440805_at	---	---	1.8	0.433	1.06	0.881	-2.81	0.09	1.41	0.475	0.36
1452073_at	6720460F02Rik	RIKEN cDNA 6720460F02 gene	-1.21	0.723	1.28	0.627	1.11	0.719	1.16	0.388	0.58
1420336_at	Adamtsl5	ADAMTS-like 5	-1.69	0.226	1.24	0.739	1.38	0.263	3.12	0.098	1.01
1420733_at	Cab39l	calcium binding protein 39-like	-1.16	0.459	1.18	0.684	1.17	0.517	1.09	0.84	0.57
1450428_at	Lhx1	LIM homeobox protein 1	1.07	0.346	-1.25	0.394	1.35	0.144	1.21	0.176	0.59
1436501_at	Mtus1	mitochondrial tumor suppressor 1	-1.1	0.157	1.08	0.15	1.23	0.24	1.68	0.11	0.72
1416148_at	Laptm4b	lysosomal-associated protein transmembrane 4B	1.19	0.166	1.05	0.467	-1.03	0.824	1.16	0.564	0.6
1423067_at	Cdk5rap3	CDK5 regulatory subunit associated protein 3	1.09	0.633	1.04	0.449	1.08	0.373	-1.2	0.515	0.5
1423632_at	Gpr146	G protein-coupled receptor 146	-1.27	0.202	1.04	0.855	1.39	0.091	2.02	0.15	0.8
1420694_a_at	Dach1	dachshund 1 (Drosophila)	1.45	0.67	-3.63	0.204	1.49	0.206	1.13	0.812	0.11
1416435_at	Ltbr	lymphotoxin B receptor	-1.01	0.918	1.18	0.213	1.05	0.766	1.28	0.255	0.62
1440493_at	Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.29	0.528	-1.27	0.699	1.14	0.662	1.89	0.312	0.76
1422657_at	Prlpl	prolactin-like protein L	1.07	0.915	-1.04	0.921	1.19	0.509	1.21	0.764	0.61
1445809_at	Eya4	Eyes absent 4 homolog (Drosophila)	1.04	0.527	1.23	0.476	-1.05	0.356	1.74	0.308	0.74
1428246_at	Vps26b	vacuolar protein sorting 26 homolog B (yeast)	1.07	0.326	-1.01	0.943	1.15	0.501	1.06	0.594	0.57
1422664_at	Rab10	RAB10, member RAS oncogene family	1.01	0.89	-1.04	0.751	1.25	0.279	1.48	0.329	0.67
1431272_at	5430405H02Rik	RIKEN cDNA 5430405H02 gene	1.49	0.382	-1.85	0.175	1.19	0.799	1.78	0.458	0.65
1457816_at	Casp9	caspase 9	1.09	0.727	-1.24	0.026	1.32	0.504	1.35	0.434	0.63
1458001_at	---	---	-1.27	0.79	1.3	0.536	1.13	0.853	1.34	0.511	0.62
1459889_at	Clca3	chloride channel calcium activated 3	-1.5	0.204	1.08	0.821	1.47	0.131	1.15	0.253	0.55
1449096_at	0610011N22Rik	RIKEN cDNA 0610011N22 gene	1.28	0.318	-1.12	0.492	1.04	0.773	1.22	0.554	0.61
1425975_a_at	Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	-1	0.974	1.03	0.855	1.19	0.65	1.01	0.969	0.56
1448817_at	Otub1	OTU domain, ubiquitin aldehyde binding 1	1.04	0.869	-1.03	0.856	1.2	0.211	1.03	0.716	0.56
1438432_at	Lnpep	leucyl/cystinyl aminopeptidase	1.03	0.815	1.09	0.582	1.1	0.698	-1.03	0.859	0.55
1417014_at	Hspb8	heat shock protein 8	-1.06	0.748	1.11	0.672	1.17	0.559	1.06	0.753	0.57
1435968_at	Ptprn2	Protein tyrosine phosphatase, receptor type, N polypeptide 2	1.38	0.423	-1.58	0.419	1.2	0.612	1.11	0.737	0.53
1418789_at	Sntg2	syntrophin, gamma 2	1.31	0.005	-1.75	0.003	1.33	0.231	1.09	0.67	0.5
1448144_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	-1.06	0.717	1.07	0.515	1.2	0.053	1.29	0.216	0.62
1452149_at	Ube3b	ubiquitin protein ligase E3B	-1.1	0.661	1.02	0.728	1.29	0.138	1.55	0.02	0.69
1416236_a_at	Eva1	epithelial V-like antigen 1	-1.19	0.526	1.04	0.831	1.35	0.133	1.2	0.417	0.6
1433541_a_at	Ubap2l	ubiquitin associated protein 2-like	-1.02	0.863	1.06	0.725	1.18	0.032	1.03	0.835	0.56
1459949_at	Atp5s	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	1.47	0.267	1.13	0.73	-1.6	0.076	1.88	0.052	0.72
1426115_a_at	Kcnj9	potassium inwardly-rectifying channel, subfamily J, member 9	1.16	0.75	1.4	0.293	-1.5	0.268	1.04	0.909	0.52
1445436_at	---	Transcribed locus	1.23	0.339	-1.18	0.576	1.15	0.725	1.33	0.276	0.63
1436379_at	Crtc3	CREB regulated transcription coactivator 3	1.01	0.929	1.05	0.759	1.17	0.131	-1.32	0.049	0.48
1429019_s_at	Pon2	paraoxonase 2	1.21	0.271	1.22	0.116	-1.26	0.01	1.35	0.025	0.63
1416750_at	Oprs1	opioid receptor, sigma 1	1.01	0.876	1.02	0.914	1.19	0.223	-1.11	0.536	0.53
1451853_at	Fcmd	Fukuyama type congenital muscular dystrophy homolog (human)	1.03	0.972	-1.18	0.514	1.34	0.277	1.09	0.721	0.57
1448668_a_at	Irak1	interleukin-1 receptor-associated kinase 1	1.07	0.639	1.08	0.233	1.07	0.761	-1.11	0.69	0.53
1421756_a_at	Gpr19	G protein-coupled receptor 19	1.11	0.631	1.16	0.517	-1.05	0.758	1.45	0.267	0.67
1454130_at	4930432J01Rik	RIKEN cDNA 4930432J01 gene	-2.85	0.065	1.7	0.129	1.16	0.622	1.84	0.156	0.47
1432279_at	4930452L02Rik	RIKEN cDNA 4930452L02 gene	-1.36	0.359	1.16	0.538	1.32	0.265	1.32	0.244	0.61
1444282_at	Samd10	Sterile alpha motif domain containing 10	1.1	0.899	1.39	0.488	-1.36	0.394	1.19	0.585	0.58
1425268_a_at	3110045G13Rik	RIKEN cDNA 3110045G13 gene	1.07	0.83	1.14	0.644	1.01	0.972	-1.21	0.284	0.5

1437950_at	BC035537	cDNA sequence BC035537	-1.26	0.161	1.04	0.854	1.39	0.054	1.1	0.844	0.57
1423669_at	Col1a1	procollagen, type I, alpha 1	1.36	0.058	1.23	0.58	-1.6	0.312	1.01	0.935	0.5
1416769_s_at	Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	1.09	0.432	1.07	0.336	1.06	0.794	-1.21	0.216	0.5
1428300_at	4932439K10Rik	RIKEN cDNA 4932439K10 gene	1.06	0.506	1.16	0.546	1	0.983	-1.19	0.409	0.51
1422143_at	Akap7	A kinase (PRKA) anchor protein 7	1.41	0.45	-1.5	0.271	1.15	0.662	1.2	0.778	0.56
1456785_at	Crsp2	cofactor required for Sp1 transcriptional activation, subunit 2	1.23	0.167	-1.7	0.052	1.41	0.106	1.15	0.104	0.52
1452727_at	R3hdm2	R3H domain containing 2	1.11	0.626	1.14	0.192	-1.02	0.9	1.03	0.823	0.56
1440763_at	---	Transcribed locus	-1.04	0.781	1.24	0.657	1.02	0.891	1.13	0.774	0.59
1418046_at	Nap1l2	nucleosome assembly protein 1-like 2	1.13	0.522	-1.01	0.982	1.1	0.576	1.53	0.237	0.69
1424595_at	F11r	F11 receptor	1.07	0.574	1.17	0.133	-1.02	0.778	1.05	0.799	0.57
1417293_at	Hs6st1	heparan sulfate 6-O-sulfotransferase 1	-1.07	0.722	1.01	0.971	1.28	0.112	2.06	0.207	0.82
1460665_a_at	Cnot7	CCR4-NOT transcription complex, subunit 7	-1.11	0.523	1.04	0.775	1.28	0.309	1.07	0.318	0.57
1437547_s_at	Dnajc14	DnaJ (Hsp40) homolog, subfamily C, member 14	1.09	0.404	1.11	0.454	1.03	0.693	-1.15	0.411	0.52
1452436_at	Loxl2	lysyl oxidase-like 2	1.4	0.669	1.06	0.875	-1.31	0.624	1.01	0.989	0.54
1452269_at	Spnb3	spectrin beta 3	1.11	0.714	-1.13	0.134	1.23	0.18	1.28	0.392	0.62
1430937_at	A930016O22Rik	RIKEN cDNA A930016O22 gene	-1.51	0.496	1.49	0.624	1.07	0.804	1.04	0.917	0.52
1448129_at	Arpc5	actin related protein 2/3 complex, subunit 5	1.04	0.703	1.08	0.263	1.11	0.493	-1.25	0.176	0.49
1446458_at	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	1.4	0.553	1.07	0.819	-1.33	0.606	1.2	0.564	0.59
1422421_at	Defcr-rs12	defensin related cryptdin, related sequence 12	1.24	0.056	1.06	0.744	-1.08	0.286	1.22	0.372	0.61
1452327_at	Iqsec1	IQ motif and Sec7 domain 1	-1.18	0.331	1.1	0.223	1.28	0.317	1.09	0.588	0.57
1423607_at	Lum	lumican	1.1	0.537	1.31	0.123	-1.22	0.505	2.01	0.081	0.8
1416740_at	Col5a1	procollagen, type V, alpha 1	1.14	0.594	1.34	0.143	-1.35	0.224	2.49	0.128	0.91
1435626_a_at	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like dor	1.01	0.976	-1.37	0.383	1.48	0.025	1.11	0.731	0.56
1456225_x_at	Trib3	tribbles homolog 3 (Drosophila)	1.12	0.518	-1.24	0.3	1.3	0.308	1.85	0.1	0.76
1445265_at	Uty	Ubiquitously transcribed tetratricopeptide repeat gene, Y chromosome	-1.14	0.814	1.08	0.878	1.27	0.338	1.11	0.696	0.58
1416261_at	Tmem19	transmembrane protein 19	1.01	0.918	1.05	0.68	1.17	0.062	-1.04	0.822	0.55
1448145_at	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	-1.07	0.607	1.18	0.131	1.11	0.537	1.04	0.86	0.56
1417141_at	Igtp	interferon gamma induced GTPase	1.03	0.805	-1.06	0.663	1.26	0.38	1.04	0.762	0.57
1432442_at	4930481F22Rik	RIKEN cDNA 4930481F22 gene	1.16	0.557	-1.23	0.281	1.24	0.308	2.04	0.072	0.81
1434469_at	Otud4	OTU domain containing 4	1.08	0.475	-1.11	0.512	1.25	0.392	1.16	0.454	0.59
1423865_at	Slc44a1	solute carrier family 44, member 1	-1.25	0.241	1.24	0.182	1.19	0.406	1.22	0.184	0.6
1440965_at	Pigl	Phosphatidylinositol glycan, class L	1.05	0.72	-1.28	0.081	1.39	0.11	1.06	0.724	0.56
1422452_at	Bag3	Bcl2-associated athanogene 3	-1.03	0.811	1.14	0.531	1.11	0.706	1.29	0.022	0.63
1454104_a_at	Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), member 9	1.19	0.598	1.21	0.142	-1.21	0.622	1	1	0.55
1455814_x_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-1.01	0.932	1.15	0.34	1.09	0.631	1.11	0.713	0.58
1453493_at	4921528O07Rik ///	RIKEN cDNA 4921528O07 gene /// similar to RIKEN cDNA 4921528O07 gene ///	1.23	0.648	1.15	0.801	-1.19	0.786	1.94	0.311	0.78
1449013_at	Eef2k	eukaryotic elongation factor-2 kinase	1	0.998	-1.47	0.367	1.54	0.082	1.99	0.231	0.77
1428558_at	Osgepl1	O-sialoglycoprotein endopeptidase-like 1	1.14	0.404	-1.05	0.749	1.14	0.598	1.72	0.291	0.74
1453680_at	8030456M14Rik	RIKEN cDNA 8030456M14 gene	1.08	0.93	1.31	0.663	-1.2	0.758	1.38	0.568	0.64
1420305_at	---	Transcribed locus	-1.29	0.793	1.27	0.707	1.18	0.748	1.26	0.64	0.6
1417213_a_at	Rbm6	RNA binding motif protein 6	1.01	0.967	1	0.998	1.22	0.574	-1.02	0.93	0.55
1424971_at	Ccdc99	coiled-coil domain containing 99	1.36	0.692	-1.66	0.271	1.26	0.408	2.56	0.208	0.88
1431227_at	2310040A13Rik	RIKEN cDNA 2310040A13 gene	-1.11	0.86	1	0.998	1.33	0.53	1.52	0.253	0.68
1460310_a_at	Gh	growth hormone	1.42	0.654	-1.73	0.102	1.23	0.52	1.26	0.233	0.55
1447694_x_at	Neo1	neogenin	1.01	0.843	1.33	0.639	-1.12	0.595	1.4	0.243	0.65
1455951_at	Mars	methionine-tRNA synthetase	1.03	0.862	-1.08	0.105	1.27	0.102	1.3	0.297	0.63
1423839_a_at	Btf3	basic transcription factor 3	1.14	0.441	1.09	0.267	1	0.98	-1.19	0.373	0.51
1456224_x_at	Cage1	cancer antigen 1	1.33	0.193	1.08	0.855	-1.22	0.658	1.06	0.886	0.56
1458869_at	2900076A13Rik	RIKEN cDNA 2900076A13 gene	-1.5	0.135	1.5	0.457	1.07	0.874	1.34	0.453	0.6
1453745_at	2700038G22Rik	RIKEN cDNA 2700038G22 gene	1.06	0.903	-1.13	0.447	1.29	0.509	1.02	0.888	0.56
1452355_at	3322402L07Rik	RIKEN cDNA 3322402L07 gene	-4.51	0.04	2	0.327	1	0.987	1.15	0.825	-0.09
1444535_at	---	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:95300	1	0.998	1.11	0.718	1.12	0.431	-1.39	0.261	0.46
1431117_x_at	1810029B16Rik ///	RIKEN cDNA 1810029B16 gene /// hypothetical LOC383495 /// hypothetical prote	1.07	0.158	1.09	0.886	1.07	0.86	-2.26	0.128	0.24

1416614_at	Cri1	CREBBP/EP300 inhibitory protein 1	1.14	0.47	1.35	0.065	-1.34	0.117	1.12	0.592	0.57
1438978_x_at	Ndn	necdin	1.14	0.765	1.21	0.492	-1.15	0.729	1.6	0.299	0.7
1457335_at	---	Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library,	1.01	0.95	1.08	0.853	1.14	0.383	-1.13	0.396	0.52
1452389_at	Tnfrsf7	tumor necrosis factor receptor superfamily, member 7	1.03	0.969	1.09	0.86	1.11	0.359	-1.71	0.231	0.38
1455353_at	Tmcc1	transmembrane and coiled coil domains 1	-1.19	0.515	1	0.992	1.39	0.24	1.08	0.443	0.57
1449932_at	Csnk1d	casein kinase 1, delta	1.14	0.071	-1.09	0.391	1.17	0.471	1.03	0.594	0.56
1415739_at	3100004P22Rik	RIKEN cDNA 3100004P22 gene	1.01	0.939	1.02	0.852	1.21	0.091	-1.19	0.297	0.51
1452618_at	Cdk5rap2	CDK5 regulatory subunit associated protein 2	-1.1	0.24	1.3	0.64	1.03	0.857	1.25	0.466	0.62
1424907_a_at	Farsla	phenylalanine-tRNA synthetase-like, alpha subunit	1.1	0.828	-1.22	0.273	1.31	0.271	1.87	0.168	0.77
1446247_at	Adamts18	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.09	0.801	1.02	0.974	1.29	0.524	1.18	0.75	0.6
1417697_at	Soat1	sterol O-acyltransferase 1	-1.05	0.708	1.17	0.645	1.1	0.652	1.01	0.97	0.56
1427938_at	Mycbp	c-myc binding protein	1.23	0.384	-1.03	0.805	1.03	0.918	1.31	0.468	0.64
1418940_at	Sult1b1	sulfotransferase family 1B, member 1	1.05	0.453	-1.32	0.269	1.43	0.565	1.1	0.727	0.56
1448960_at	Cxxc5	CXXC finger 5	1.02	0.933	1.03	0.602	1.18	0.579	-1.71	0.117	0.38
1418085_at	Prkcz	protein kinase C, zeta	-1.08	0.47	1.08	0.409	1.22	0.032	1.34	0.298	0.64
1460428_at	Ankrd13a	ankyrin repeat domain 13a	-1.06	0.797	1.12	0.211	1.17	0.103	1.13	0.411	0.59
1429042_at	2010200O16Rik	RIKEN cDNA 2010200O16 gene	1.23	0.075	1.07	0.549	-1.07	0.414	1.04	0.701	0.57
1454213_at	Armc9	armadillo repeat containing 9	1.55	0.158	1.14	0.645	-1.85	0.107	2.11	0.236	0.74
1431188_a_at	Tom1 /// LOC54587	target of myb1 homolog (chicken) /// similar to TOM1	-1.12	0.596	1.03	0.819	1.31	0.195	1.19	0.253	0.6
1427168_a_at	Col14a1	procollagen, type XIV, alpha 1	1.12	0.541	1.28	0.008	-1.2	0.491	1.07	0.525	0.57
1434235_at	Slc20a2	solute carrier family 20, member 2	1.05	0.758	-1.11	0.422	1.28	0.308	1.02	0.932	0.56
1419299_at	2010012O05Rik	RIKEN cDNA 2010012O05 gene	-1	0.971	1.13	0.359	1.11	0.549	1.01	0.94	0.56
1424686_at	2700008B19Rik	RIKEN cDNA 2700008B19 gene	1.01	0.936	1.03	0.907	1.2	0.454	-1.18	0.335	0.51
1441755_at	Mapk15	mitogen-activated protein kinase 15	1.12	0.454	1.01	0.911	1.1	0.623	-1.87	0.095	0.34
1424985_a_at	Sox10	SRY-box containing gene 10	-1.07	0.871	1.27	0.215	1.03	0.912	1.36	0.483	0.65
1449467_at	Ssty1 /// LOC66527	spermiogenesis specific transcript on the Y 1 /// similar to Y-linked testis-specific	-1.03	0.833	1.05	0.882	1.21	0.669	2.03	0.084	0.82
1434662_at	Atg4a /// LOC66647	autophagy-related 4A (yeast) /// similar to Cysteine protease ATG4A (Autophagy-	1.1	0.238	1.15	0.271	-1.01	0.953	2.96	0.195	1.05
1460434_at	Fundc2	FUN14 domain containing 2	-1.23	0.065	1.3	0.327	1.12	0.664	1.6	0.023	0.7
1425676_a_at	Elovl1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.02	0.965	1.09	0.732	1.16	0.641	1.42	0.336	0.66
1448522_at	Sars2	seryl-aminoacyl-tRNA synthetase 2	-1.03	0.904	1.2	0.272	1.06	0.862	1.13	0.542	0.59
1453927_at	Mrpl47	mitochondrial ribosomal protein L47	1.03	0.896	1.35	0.103	-1.17	0.375	1.61	0.013	0.71
1426739_at	Donson	downstream neighbor of SON	-1.11	0.206	1.14	0.556	1.19	0.203	1.47	0.327	0.67
1460626_at	11-Sep	septin 11	-1.32	0.312	1.42	0.205	1.06	0.644	1.2	0.465	0.59
1417108_at	Klc4	kinesin light chain 4	1.03	0.772	1.1	0.428	1.11	0.209	-1.51	0.033	0.43
1424418_at	BC010801	cDNA sequence BC010801	1.05	0.829	-1.1	0.349	1.28	0.313	3.59	0.218	1.2
1433634_at	Irf2bp2 /// LOC6729	interferon regulatory factor 2 binding protein 2 /// similar to interferon regulatory fa	1.05	0.801	1.07	0.703	1.12	0.68	-1.29	0.512	0.49
1457094_at	She	src homology 2 domain-containing transforming protein E	1.09	0.571	1.13	0.437	1.02	0.851	-1.04	0.859	0.55
1433922_at	Rab35	RAB35, member RAS oncogene family	-1.04	0.458	1.02	0.349	1.25	0.102	1.15	0.548	0.6
1416773_at	Wee1	wee 1 homolog (S. pombe)	1.22	0.564	1.16	0.82	-1.17	0.238	2.72	0.059	0.98
1449780_at	---	---	1.56	0.624	1.17	0.838	-1.97	0.083	1.08	0.9	0.46
1423394_at	Pcyox1	prenylcysteine oxidase 1	-1.01	0.925	1.07	0.134	1.17	0.499	1.02	0.889	0.56
1437089_at	4833409A17Rik	RIKEN cDNA 4833409A17 gene	-1.14	0.159	1.18	0.457	1.18	0.558	1.35	0.091	0.64
1434678_at	Mbnl3	muscleblind-like 3 (Drosophila)	1.31	0.439	1.36	0.012	-1.76	0.001	1.74	0.222	0.66
1442582_at	Gcet2	germinal center expressed transcript 2	1.12	0.693	-1.55	0.573	1.47	0.435	1.26	0.553	0.58
1424424_at	Slc39a1	solute carrier family 39 (zinc transporter), member 1	1.12	0.207	1.22	0.082	-1.13	0.514	1.02	0.859	0.56
1429498_at	Sft2d3	SFT2 domain containing 3	1.74	0.439	-3.47	0.147	1.21	0.667	1.54	0.356	0.25
1428245_at	G6pc3	glucose 6 phosphatase, catalytic, 3	1.02	0.816	-1.13	0.277	1.33	0.044	1	0.992	0.56
1458840_at	---	Transcribed locus	1.04	0.937	1.25	0.543	-1.05	0.875	1.29	0.607	0.63
1416469_at	Luzp1	leucine zipper protein 1	1.01	0.859	1.38	0.034	-1.18	0.352	1.08	0.581	0.57
1435087_at	BC039093	cDNA sequence BC039093	1.05	0.538	-1.12	0.503	1.29	0.187	1.02	0.935	0.56
1460132_at	Ube2b	Ubiquitin-conjugating enzyme E2B, RAD6 homology (S. cerevisiae)	1.01	0.985	1.27	0.691	-1.05	0.886	1.59	0.536	0.71
1421784_a_at	Efna4	ephrin A4	-1.45	0.096	1.24	0.667	1.31	0.341	1.08	0.803	0.54
1424492_at	Trpc2	transient receptor potential cation channel, subfamily C, member 2	1.01	0.971	-1.12	0.347	1.33	0.027	1.09	0.727	0.58

1424227_at	Polr3h	polymerase (RNA) III (DNA directed) polypeptide H	-1.02	0.829	1.09	0.126	1.17	0.164	1.51	0.246	0.69
1453993_a_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	1.18	0.466	1.05	0.677	1.01	0.975	-1.09	0.644	0.54
1458466_at	Ppgb	protective protein for beta-galactosidase	1.2	0.541	-1.2	0.434	1.2	0.376	1.4	0.297	0.65
1427715_a_at	Nt5c1b	5'-nucleotidase, cytosolic IB	-2.05	0.249	1.75	0.493	1.01	0.984	3.18	0.101	0.97
1426955_at	Col18a1	procollagen, type XVIII, alpha 1	1.18	0.518	-1.05	0.3	1.1	0.552	1.21	0.504	0.61
1419398_a_at	Reep5	receptor accessory protein 5	1.2	0.054	1.13	0.586	-1.1	0.66	1.44	0.116	0.67
1424350_s_at	Lpgat1	lysophosphatidylglycerol acyltransferase 1	1.01	0.929	1.22	0.352	1.01	0.958	-1.47	0.452	0.44
1417081_a_at	Syngr2	synaptogyrin 2	1.07	0.58	1.11	0.026	1.06	0.636	-1.27	0.376	0.49
1426750_at	Flnb	filamin, beta	1.03	0.887	1.02	0.894	1.2	0.003	-1.26	0.437	0.49
1454928_at	Safb	scaffold attachment factor B	-1.09	0.416	1.11	0.481	1.22	0.363	1.21	0.382	0.61
1417833_at	Zc3h10	zinc finger CCCH type containing 10	1.1	0.775	1.05	0.705	1.09	0.583	-1.52	0.05	0.43
1431335_a_at	Wfdc1	WAP four-disulfide core domain 1	1.19	0.73	-1.31	0.022	1.29	0.494	1.05	0.884	0.55
1460344_at	2310033F14Rik	RIKEN cDNA 2310033F14 gene	1.01	0.936	1.13	0.358	1.1	0.456	-1.47	0.209	0.44
1424498_at	5730596K20Rik	RIKEN cDNA 5730596K20 gene	1.4	0.629	-1.5	0.25	1.17	0.308	1.32	0.371	0.6
1456195_x_at	Itgb5	integrin beta 5	1.16	0.068	1.21	0.052	-1.14	0.102	1.16	0.406	0.6
1421779_at	Rit2	Ras-like without CAAX 2	1.75	0.292	-2.96	0.02	1.15	0.756	1	0.999	0.24
1453564_a_at	Vps24	vacuolar protein sorting 24 (yeast)	1.07	0.002	1.26	0.098	-1.1	0.446	1.12	0.68	0.59
1439331_at	4932439E07Rik	RIKEN cDNA 4932439E07 gene	1.35	0.164	-1.35	0.03	1.15	0.63	1.05	0.766	0.55
1415886_at	Sh2d3c	SH2 domain containing 3C	1.03	0.9	1.08	0.608	1.13	0.334	-1.32	0.215	0.48
1435666_at	Mast3	microtubule associated serine/threonine kinase 3	1.01	0.95	1.02	0.942	1.21	0.088	-1.63	0.101	0.4
1429998_at	Trim23	tripartite motif protein 23	1.25	0.771	-2.13	0.22	1.52	0.251	1.03	0.967	0.42
1449373_at	Dnajc3	DnaJ (Hsp40) homolog, subfamily C, member 3	-1.24	0.514	1.11	0.639	1.32	0.301	1.26	0.276	0.62
1449207_a_at	Kif20a	kinesin family member 20A	1.42	0.588	1.09	0.774	-1.36	0.107	3.45	0.176	1.15
1418011_a_at	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	1.16	0.499	1.14	0.049	-1.07	0.444	1.65	0.027	0.72
1423569_at	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	-1.38	0.111	1.03	0.94	1.49	0.105	2.81	0.146	0.99
1454905_at	Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	-1.1	0.698	1.16	0.233	1.17	0.165	1.69	0.242	0.73
1434805_at	Mllt1	myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosoph	1.01	0.973	-1	0.995	1.23	0.37	1.13	0.491	0.59
1420592_a_at	Anp32e	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	-1.19	0.119	1.19	0.225	1.21	0.135	1.52	0.174	0.68
1449162_at	Pop7	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	1.02	0.856	1.18	0.431	1.05	0.769	-1.19	0.421	0.51
1417088_at	Zfp346	zinc finger protein 346	1.05	0.825	-1.17	0.043	1.34	0.353	1	0.984	0.56
1428477_at	Elac2	elaC homolog 2 (E. coli)	1.19	0.098	-1.26	0.007	1.26	0.136	1.07	0.683	0.56
1451118_a_at	2410018C17Rik	RIKEN cDNA 2410018C17 gene	1.07	0.803	1.06	0.529	1.11	0.183	-1.18	0.273	0.52
1418701_at	Comt	catechol-O-methyltransferase	1.29	0.552	1.17	0.233	-1.27	0.051	2.29	0.132	0.87
1436209_at	Dnajc16	DnaJ (Hsp40) homolog, subfamily C, member 16	1.23	0.313	-1.29	0.055	1.23	0.129	1.44	0.247	0.66
1435631_x_at	Exoc6	exocyst complex component 6	1.44	0.13	1.01	0.911	-1.27	0.156	1.76	0.058	0.74
1453101_at	Klhl25	Kelch-like 25 (Drosophila)	1.09	0.502	1.17	0.341	-1.02	0.86	1.92	0.177	0.79
1438012_at	Ppm1l	protein phosphatase 1 (formerly 2C)-like	-1.34	0.465	1.18	0.005	1.32	0.264	2.53	0.28	0.92
1453708_a_at	Gsto2	glutathione S-transferase omega 2	1.15	0.521	-1.27	0.649	1.31	0.274	1.66	0.368	0.71
1431575_at	Clec4g	C-type lectin domain family 4, member g	1.2	0.804	-2.32	0.088	1.61	0.067	1.15	0.762	0.41
1452046_a_at	Ppp1cc /// LOC434	protein phosphatase 1, catalytic subunit, gamma isoform /// similar to protein pho	-1.02	0.777	1.04	0.716	1.22	0.132	1.06	0.723	0.58
1459255_at	1700034P13Rik	RIKEN cDNA 1700034P13 gene	1.18	0.276	1.23	0.204	-1.2	0.727	1.46	0.493	0.67
1437108_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.05	0.326	1.18	0.426	1.02	0.67	-1.27	0.265	0.49
1425821_at	Clcn7	chloride channel 7	1.3	0.499	1.29	0.417	-1.53	0.056	1.45	0.226	0.63
1451377_a_at	Aaas	achalasia, adrenocortical insufficiency, alacrimia	1.03	0.881	-1.26	0.003	1.43	0.028	1.38	0.089	0.64
1459419_at	---	---	1.35	0.022	1.19	0.547	-1.42	0.136	1.21	0.752	0.58
1426245_s_at	Mapre2	microtubule-associated protein, RP/EB family, member 2	-1.11	0.074	1.26	0.022	1.08	0.131	1.12	0.545	0.59
1421966_at	Ncam1	neural cell adhesion molecule 1	1.08	0.649	1.18	0.553	-1.02	0.879	1.04	0.905	0.57
1449039_a_at	Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	1	0.998	1.19	0.004	1.05	0.71	-1.16	0.582	0.52
1422764_at	Mapre1	microtubule-associated protein, RP/EB family, member 1	-1	0.996	1.08	0.714	1.17	0.405	1.15	0.535	0.6
1418375_at	Mbd6	methyl-CpG binding domain protein 6	-1.09	0.731	1.03	0.809	1.3	0.207	1.22	0.144	0.61
1420239_x_at	2-Mar	membrane-associated ring finger (C3HC4) 2	1.31	0.619	1.4	0.505	-1.84	0.006	1.77	0.356	0.66
1440036_x_at	LOC230010	similar to poly(A) binding protein, cytoplasmic 4 isoform 1	-1.26	0.41	1.04	0.805	1.42	0.022	1.56	0.297	0.69
1443497_at	Abtb2	Ankyrin repeat and BTB (POZ) domain containing 2	-1.38	0.336	1.47	0.238	1.05	0.879	1.17	0.755	0.58

1417560_at	Sfxn1	sideroflexin 1	-1.07	0.625	1.1	0.56	1.22	0.159	1.33	0.112	0.64
1455673_at	Alkbh2	alkB, alkylation repair homolog 2 (E. coli)	-1.01	0.986	1.14	0.565	1.12	0.755	1.39	0.363	0.66
1452709_at	Poldip3	polymerase (DNA-directed), delta interacting protein 3	1.04	0.706	1.04	0.231	1.17	0.317	-1.02	0.766	0.56
1452589_at	Ptk7	PTK7 protein tyrosine kinase 7	-2.18	0.328	1.49	0.527	1.3	0.505	1.49	0.052	0.52
1429241_at	Npal3	NIPA-like domain containing 3	1.1	0.665	-1.39	0.152	1.42	0.283	1.07	0.551	0.55
1424343_a_at	Eif1a	eukaryotic translation initiation factor 1A	1	0.998	1.26	0.452	-1.01	0.943	1.13	0.285	0.59
1450280_a_at	Rrh	retinal pigment epithelium derived rhodopsin homolog	1.24	0.555	-1.27	0.403	1.22	0.706	1.41	0.16	0.65
1459375_at	Pappa	Pregnancy-associated plasma protein A	1.33	0.436	-2.77	0.083	1.56	0.446	1.07	0.921	0.3
1434130_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	-1.17	0.537	1.17	0.547	1.23	0.621	1.61	0.127	0.71
1430940_at	3110045A19Rik	RIKEN cDNA 3110045A19 gene	1.28	0.363	1.31	0.495	-1.53	0.005	1.04	0.827	0.53
1421442_at	Flt4	FMS-like tyrosine kinase 4	1.16	0.381	1.22	0.491	-1.15	0.268	1.59	0.116	0.71
1436306_at	Saps1	SAPS domain family, member 1	1.18	0.743	-1.14	0.671	1.19	0.403	1.06	0.842	0.57
1457624_at	Rab8a	RAB8A, member RAS oncogene family	1.31	0.748	-1.15	0.826	1.07	0.875	2.07	0.38	0.83
1456015_x_at	Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	1.2	0.059	-1.14	0.102	1.17	0.267	1.28	0.121	0.63
1428508_at	Tbc1d2b	TBC1 domain family, member 2B	1.39	0.08	-1.21	0.179	1.03	0.843	1.17	0.276	0.59
1431290_at	4930588J15Rik	RIKEN cDNA 4930588J15 gene	1.52	0.044	-1.47	0.452	1.04	0.906	1.13	0.702	0.56
1448441_at	Cks1b	CDC28 protein kinase 1b	1.12	0.194	-1.22	0.135	1.3	0.104	2.34	0.21	0.89
1457670_s_at	Lmna	lamin A	1.25	0.324	1.39	0.123	-1.64	0.044	2.46	0.181	0.87
1456151_at	Zfp358	zinc finger protein 358	1.56	0.475	-2.08	0.28	1.21	0.518	1.61	0.363	0.57
1445112_at	Adcy1	Adenylate cyclase 1	1.02	0.948	1.51	0.212	-1.39	0.105	1.31	0.393	0.61
1458045_at	Odz4	Odd Oz/ten-m homolog 4 (Drosophila)	1.31	0.709	1.12	0.73	-1.23	0.577	1.75	0.08	0.74
1415799_at	Wbp11	WW domain binding protein 11	-1.17	0.12	1.01	0.671	1.38	0.043	1.32	0.231	0.64
1458430_at	C87436	expressed sequence C87436	1.56	0.033	-1.7	0.085	1.1	0.854	1.09	0.703	0.51
1458331_x_at	Ces7	carboxylesterase 7	1.36	0.587	1.25	0.74	-1.58	0.357	1.04	0.896	0.52
1419235_s_at	Helb	helicase (DNA) B	1.01	0.961	-1.14	0.307	1.36	0.166	1.29	0.166	0.63
1420112_at	Pacs1	Phosphofurin acidic cluster sorting protein 1	1.26	0.077	1.32	0.647	-1.48	0.254	1.27	0.287	0.59
1458075_at	Dst	Dystonin	1.26	0.634	1.31	0.638	-1.46	0.247	1.04	0.838	0.54
1433066_at	6330510M09Rik	RIKEN cDNA 6330510M09 gene	-2.9	0.417	1.79	0.332	1.12	0.345	1.38	0.331	0.35
1418412_at	Tpd52l1	tumor protein D52-like 1	-1.21	0.197	1.01	0.958	1.41	0.169	5.73	0.268	1.74
1422268_a_at	Rps6kb2	ribosomal protein S6 kinase, polypeptide 2	1.03	0.912	-1.08	0.696	1.3	0.216	1.51	0.087	0.69
1449872_at	Hspb3	heat shock protein 3	1.36	0.604	-1.3	0.509	1.12	0.821	2.04	0.324	0.81
1443103_at	D830046C22Rik	RIKEN cDNA D830046C22 gene	1.13	0.664	-1.02	0.94	1.14	0.805	2.54	0.355	0.95
1455794_at	D130058I21Rik	RIKEN cDNA D130058I21 gene	-1.17	0.048	1.05	0.903	1.35	0.267	1.48	0.09	0.68
1430748_at	1810063B07Rik	RIKEN cDNA 1810063B07 gene	-1.39	0.354	1.2	0.17	1.34	0.575	1.66	0.308	0.7
1422034_a_at	Palm	paralemmin	1.21	0.659	1	0.999	1.04	0.892	-1.6	0.374	0.41
1422153_a_at	Asb11	ankyrin repeat and SOCS box-containing protein 11	1.35	0.148	-4.17	0.114	1.66	0.032	1.38	0.567	0.05
1431066_at	Fut11	fucosyltransferase 11	-1.06	0.862	1.02	0.968	1.3	0.354	1.34	0.234	0.65
1431369_at	Ddef2	development and differentiation enhancing factor 2	1.2	0.783	-1.38	0.564	1.33	0.144	1.2	0.637	0.59
1451436_at	Sbno1	sno, strawberry notch homolog 1 (Drosophila)	-1.14	0.314	1.08	0.542	1.29	0.028	1.17	0.099	0.6
1429863_at	Lonrf3	LON peptidase N-terminal domain and ring finger 3	1.22	0.503	-1.11	0.721	1.13	0.588	1.66	0.059	0.73
1436022_at	Endogl1	endonuclease G-like 1	1.12	0.399	-1.12	0.397	1.24	0.012	1.01	0.982	0.56
1429187_at	Tmed7	transmembrane emp24 protein transport domain containing 7	1.17	0.507	1.06	0.891	1.03	0.934	-1.14	0.701	0.53
1439389_s_at	Myadm	myeloid-associated differentiation marker	1.08	0.461	1.12	0.253	1.06	0.491	-1.11	0.758	0.54
1423964_at	Cpsf3l	cleavage and polyadenylation specific factor 3-like	1.16	0.393	-1.15	0.275	1.23	0.099	1.05	0.72	0.57
1428793_at	Slc36a1	solute carrier family 36 (proton/amino acid symporter), member 1	-1.17	0.278	1.27	0.137	1.13	0.58	1.13	0.608	0.59
1417850_at	Rb1	retinoblastoma 1	-1.1	0.412	1.16	0.139	1.19	0.118	1.92	0.181	0.79
1449795_at	D2Ertd63e	DNA segment, Chr 2, ERATO Doi 63, expressed	1.15	0.634	1.56	0.297	-1.82	0.212	2.12	0.256	0.75
1452927_x_at	Tpi1	triosephosphate isomerase 1	-1.04	0.644	1.2	0.108	1.09	0.177	1.32	0.155	0.64
1423960_at	Mboat5	membrane bound O-acyltransferase domain containing 5	1.03	0.919	-1.03	0.871	1.25	0.423	2.48	0.15	0.93
1426400_a_at	Capns1	calpain, small subunit 1	1.09	0.578	-1.01	0.91	1.18	0.098	1.11	0.174	0.59
1455499_at	Nrxn2	neurexin II	1.64	0.06	1.05	0.951	-1.77	0.247	1.16	0.67	0.52
1427929_a_at	Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	1	0.989	1.01	0.951	1.24	0.292	-1.26	0.436	0.5
1422147_a_at	Pla2g6	phospholipase A2, group VI	1.06	0.749	-1.21	0.296	1.37	0.111	1.14	0.369	0.59

1424899_at	Nmnat3	nicotinamide nucleotide adenylyltransferase 3	-1.02	0.438	1.15	0.546	1.13	0.285	3.53	0.171	1.2
1441215_at	Trabd	TraB domain containing	-1.73	0.276	1.44	0.551	1.24	0.124	1.1	0.871	0.51
1416830_at	0610031J06Rik	RIKEN cDNA 0610031J06 gene	1	0.985	1.15	0.337	1.1	0.281	-1.19	0.502	0.52
1442015_at	2500002B13Rik	RIKEN cDNA 2500002B13 gene	-1.2	0.69	1.23	0.241	1.19	0.399	2.97	0.272	1.05
1446399_at	Cdh10	cadherin 10	1.02	0.933	1.44	0.538	-1.25	0.253	1.16	0.487	0.59
1445860_at	Tspan11	tetraspanin 11	-1.13	0.743	1.16	0.658	1.21	0.691	1.03	0.958	0.57
1460424_at	Tmem160	transmembrane protein 160	1.11	0.328	1.09	0.337	1.06	0.517	-1.33	0.421	0.48
1421901_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	1.18	0.245	-1.21	0.093	1.25	0.119	3.32	0.14	1.14
1417811_at	Slc24a6	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	-1.03	0.916	1.04	0.81	1.24	0.044	1.02	0.936	0.57
1415765_at	Hnrpul2	heterogeneous nuclear ribonucleoprotein U-like 2	1.12	0.581	-1.15	0.232	1.27	0.088	1.05	0.704	0.57
1420677_x_at	Sprrl3	small proline rich-like 3	-1.22	0.603	1.36	0.512	1.08	0.772	1.44	0.04	0.66
1440228_at	Ranbp6	RAN binding protein 6	1.12	0.616	-1.03	0.935	1.16	0.639	1.09	0.769	0.59
1452080_a_at	Dcun1d1	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerev	1.16	0.277	-1.14	0.554	1.22	0.477	1.95	0.322	0.8
1439577_at	---	---	1.04	0.96	1.06	0.907	1.16	0.738	-1.15	0.637	0.53
1451315_at	Tmem101	transmembrane protein 101	-1.18	0.416	1.03	0.837	1.37	0.009	1.13	0.308	0.59
1416443_a_at	Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A	-1.12	0.344	1.07	0.403	1.3	0.028	1.18	0.186	0.61
1416888_at	Fadd	Fas (TNFRSF6)-associated via death domain	1.09	0.726	1.15	0.037	1.02	0.873	-1.11	0.379	0.54
1450493_at	Kiss1r	KISS1 receptor	-1.07	0.876	1.02	0.961	1.3	0.083	1.19	0.676	0.61
1452289_a_at	Rnf135	ring finger protein 135	1.01	0.966	1.11	0.416	1.14	0.122	-1.2	0.518	0.51
1458125_at	C80913	Expressed sequence C80913	1.29	0.584	1.52	0.426	-2.22	0.251	1.61	0.519	0.55
1433078_at	5830435N06Rik	RIKEN cDNA 5830435N06 gene	-1.35	0.413	1.5	0.443	1.02	0.884	1.33	0.326	0.62
1420866_at	Zfp161	zinc finger protein 161	1	0.982	-1.05	0.668	1.31	0.196	1.71	0.168	0.74
1457694_at	6430537H07Rik	RIKEN cDNA 6430537H07 gene	1.26	0.634	-1.34	0.283	1.25	0.073	2.31	0.151	0.87
1451252_at	Irf2bp1	interferon regulatory factor 2 binding protein 1	1.16	0.375	-1.12	0.564	1.2	0.245	1.14	0.356	0.6
1452760_at	2510012J08Rik	RIKEN cDNA 2510012J08 gene	1.04	0.431	-1.08	0.426	1.3	0.071	1.18	0.323	0.61
1418121_at	Vrk3	vaccinia related kinase 3	1.03	0.767	1.09	0.495	1.13	0.416	-1.13	0.57	0.53
1416030_a_at	Mcm7	minichromosome maintenance deficient 7 (S. cerevisiae)	1.13	0.323	-1.1	0.525	1.22	0.132	2.55	0.188	0.95
1426142_a_at	Trdn	triadin	1.05	0.591	-1.03	0.942	1.24	0.652	1.31	0.557	0.64
1451386_at	Blvrb	biliverdin reductase B (flavin reductase (NADPH))	1.05	0.726	-1.03	0.784	1.24	0.459	2.64	0.119	0.98
1422854_at	Shc1	src homology 2 domain-containing transforming protein C1	1.12	0.534	-1.04	0.637	1.18	0.118	1.31	0.116	0.64
1455858_x_at	Pomc1	pro-opiomelanocortin-alpha	1.02	0.928	1.03	0.871	1.21	0.771	-1.8	0.478	0.37
1424201_a_at	Seh1l	SEH1-like (S. cerevisiae	-1.01	0.965	1.09	0.693	1.18	0.473	1.54	0.351	0.7
1448868_at	Scand1	SCAN domain-containing 1	1.04	0.921	1.14	0.056	1.08	0.764	-1.2	0.501	0.51
1456425_at	9230115E21Rik	RIKEN cDNA 9230115E21 gene	-1.57	0.077	1.43	0.515	1.19	0.709	2.24	0.119	0.82
1451057_x_at	Dnm2	dynamin 2	1.07	0.803	-1.07	0.69	1.26	0.265	1.11	0.697	0.59
1430197_a_at	Pitpnm2	phosphatidylinositol transfer protein, membrane-associated 2	1.07	0.724	1.36	0.047	-1.2	0.61	1.21	0.305	0.61
1439585_at	Mdn1	midasin homolog (yeast)	1.35	0.595	1.05	0.929	-1.16	0.77	1.04	0.927	0.57
1455991_at	Ccbl2	cysteine conjugate-beta lyase 2	1.11	0.1	1.03	0.805	1.13	0.528	-1.35	0.235	0.48
1421887_a_at	Aplp2	amyloid beta (A4) precursor-like protein 2	-1.01	0.904	1.08	0.316	1.19	0.498	1.48	0.113	0.68
1424140_at	Gale	galactose-4-epimerase, UDP	-1.2	0.544	1.36	0.218	1.07	0.644	1.16	0.637	0.6
1450229_at	Crsp2	cofactor required for Sp1 transcriptional activation, subunit 2	1.23	0.442	-1.3	0.307	1.26	0.146	1.17	0.406	0.59
1438324_at	9330182L06Rik	RIKEN cDNA 9330182L06 gene	1.24	0.372	1	0.998	1.02	0.945	-1.68	0.365	0.39
1429826_at	Prlpn	prolactin-like protein N	-1.09	0.699	1.32	0.464	1.02	0.934	2.61	0.094	0.97
1419686_at	Tsga14	testis specific gene A14	-1.18	0.784	1.06	0.841	1.35	0.132	1.49	0.166	0.68
1420588_at	Spinlw1	serine protease inhibitor-like, with Kunitz and WAP domains 1 (eppin)	1.42	0.55	1.2	0.659	-1.54	0.229	1.02	0.966	0.52
1421221_at	Bcdo2	beta-carotene 9', 10'-dioxygenase 2	-1.21	0.286	1	0.979	1.43	0.017	1.1	0.837	0.58
1454037_a_at	Flt1	FMS-like tyrosine kinase 1	1.12	0.469	-1.15	0.767	1.27	0.496	1.15	0.439	0.6
1423140_at	Lip1	lysosomal acid lipase 1	1.17	0.716	-1.04	0.768	1.12	0.47	1.28	0.333	0.64
1439539_at	Tram2	translocating chain-associating membrane protein 2	1.12	0.539	-1.16	0.189	1.28	0.278	1.53	0.388	0.69
1456865_x_at	Rrs1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	-1.07	0.489	1.08	0.617	1.25	0.151	1.13	0.316	0.6
1448346_at	Cfl1	cofilin 1, non-muscle	1.05	0.834	1.12	0.44	1.09	0.69	-1.03	0.787	0.56
1435599_at	BC020535	cDNA sequence BC020535	1.47	0.614	1.15	0.718	-1.56	0.404	1.92	0.427	0.75
1451678_at	Narf	nuclear prelamin A recognition factor	1.1	0.508	-1.11	0.573	1.26	0.282	2.21	0.221	0.87

1453260_a_at	Ppp2r2a	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	1.12	0.181	1.04	0.626	1.1	0.409	-1.26	0.105	0.5
1451646_at	Pdik1l	PDLIM1 interacting kinase 1 like	1.05	0.9	-1.28	0.522	1.43	0.294	1.42	0.468	0.66
1451083_s_at	Aars	alanyl-tRNA synthetase	-1.01	0.927	1.06	0.482	1.22	0.07	1.68	0.062	0.74
1444480_at	---	---	1.14	0.786	1.14	0.726	-1.02	0.929	1.49	0.634	0.69
1453393_a_at	Chst4	carbohydrate (chondroitin 6/keratan) sulfotransferase 4	-1.5	0.47	1.2	0.335	1.4	0.634	1.1	0.619	0.55
1423103_at	Rfx5	regulatory factor X, 5 (influences HLA class II expression)	1.17	0.255	1.08	0.644	1.01	0.858	-1.75	0.122	0.38
1420011_s_at	Xbp1	X-box binding protein 1	1.05	0.667	1.23	0.303	-1.02	0.854	1.22	0.445	0.62
1440696_at	2300002D11Rik	RIKEN cDNA 2300002D11 gene	-1.42	0.509	1.07	0.844	1.49	0.058	1.18	0.707	0.58
1422092_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	1.28	0.742	1.04	0.871	-1.05	0.808	1.18	0.61	0.61
1419668_at	Sgcb	sarcoglycan, beta (dystrophin-associated glycoprotein)	1.03	0.808	1.04	0.833	1.2	0.287	-1.43	0.101	0.46
1433528_at	Gtf2a2	general transcription factor II A, 2	-1.05	0.191	1.23	0.151	1.08	0.423	1.24	0.37	0.63
1457384_at	---	0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833438M18	1.08	0.308	-1.17	0.176	1.33	0.043	1.2	0.465	0.61
1418877_at	Foxd1	Forkhead box D1	1.18	0.689	1.06	0.948	1.03	0.97	-2	0.312	0.32
1416338_at	Sh3gl1	SH3-domain GRB2-like 1	1.08	0.807	1.1	0.59	1.09	0.139	-1.14	0.41	0.53
1418879_at	9030611O19Rik	RIKEN cDNA 9030611O19 gene	-1.09	0.593	1.05	0.742	1.29	0.05	1.8	0.014	0.76
1440305_at	---	---	1.37	0.514	1.17	0.524	-1.38	0.105	1.41	0.45	0.64
1417082_at	Anp32b	acidic nuclear phosphoprotein 32 family, member B	-1.05	0.778	1.06	0.486	1.25	0.292	1.74	0.169	0.75
1438669_at	Wdr40a	WD repeat domain 40A	-1.15	0.329	1.02	0.896	1.38	0.446	1.98	0.246	0.81
1415746_at	Cic	capicua homolog (Drosophila)	-1.29	0.239	1.33	0.012	1.16	0.552	1.05	0.775	0.56
1460276_a_at	Gpr175	G protein-coupled receptor 175	-1.02	0.943	1.01	0.908	1.28	0.067	1.43	0.2	0.67
1451872_a_at	Neurl	neuralized-like homolog (Drosophila)	-1.14	0.796	1.13	0.765	1.26	0.591	1.17	0.123	0.6
1456173_at	Il10ra	Interleukin 10 receptor, alpha	1.02	0.666	1.23	0.218	1.02	0.84	-1.27	0.57	0.5
1443769_at	---	Transcribed locus	-1.96	0.18	1.73	0.462	1.03	0.946	1.67	0.384	0.62
1415717_at	4931406I20Rik	RIKEN cDNA 4931406I20 gene	1	0.999	1.2	0.25	1.07	0.463	-1.01	0.799	0.56
1450053_at	Kif2a	Kinesin family member 2A	-1.02	0.904	1.23	0.084	1.06	0.39	1.88	0.247	0.79
1421460_at	Dsc1	desmocollin 1	1.77	0.409	-2.15	0.046	1.03	0.963	2.1	0.132	0.69
1442543_at	Tex264	Testis expressed gene 264	1.39	0.457	1.22	0.22	-1.52	0.081	1.24	0.202	0.58
1431935_at	Lias	lipoic acid synthetase	1.4	0.53	1.02	0.957	-1.19	0.388	1.95	0.022	0.8
1439954_at	6430514M23Rik	RIKEN cDNA 6430514M23 gene	1.02	0.851	-1.61	0.497	1.63	0.463	1.84	0.346	0.72
1423216_a_at	2510049I19Rik	RIKEN cDNA 2510049I19 gene	1.08	0.179	1.04	0.647	1.15	0.473	-1.06	0.722	0.55
1424743_at	2610003J06Rik	RIKEN cDNA 2610003J06 gene	1.14	0.125	-1.02	0.721	1.15	0.334	1.18	0.324	0.61
1453836_a_at	Mgll	monoglyceride lipase	1.25	0.303	-1.82	0.005	1.47	0.118	2.9	0.198	0.95
1434591_at	4732460K03Rik	RIKEN cDNA 4732460K03 gene	1.48	0.096	-1.36	0.497	1.05	0.849	1.07	0.801	0.56
1457000_at	BC060267	cDNA sequence BC060267	1.31	0.65	-1.23	0.733	1.14	0.842	2.11	0.005	0.83
1441496_at	Tdrd3	tudor domain containing 3	-1.15	0.761	1.33	0.586	1.07	0.732	1.45	0.475	0.67
1459769_at	Zfpl1	Zinc finger like protein 1	1.33	0.661	-1.47	0.588	1.26	0.625	1.54	0.453	0.66
1418891_a_at	Rab3d	RAB3D, member RAS oncogene family	-1.16	0.341	1.08	0.545	1.32	0.1	1.22	0.439	0.62
1455487_at	2600014M03Rik	RIKEN cDNA 2600014M03 gene	-1.09	0.286	1.02	0.876	1.33	0	1.19	0.61	0.61
1451465_at	Ubl7	ubiquitin-like 7 (bone marrow stromal cell-derived)	1.17	0.575	-1.12	0.394	1.2	0.441	1.24	0.372	0.62
1430026_at	Stch	stress 70 protein chaperone, microsome-associated, human homolog	-1.15	0.101	1.16	0.734	1.24	0.426	1.35	0.526	0.65
1452748_at	Xrcc3	X-ray repair complementing defective repair in Chinese hamster cells 3	-1.27	0.005	1	0.995	1.47	0.202	1.77	0.053	0.75
1452272_a_at	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	1.06	0.399	1.01	0.893	1.19	0.589	-1.21	0.41	0.51
1439414_x_at	Sbno1	Sno, strawberry notch homolog 1 (Drosophila)	1.14	0.545	1.32	0.386	-1.25	0.229	1.38	0.203	0.65
1433126_at	5330422M15Rik	RIKEN cDNA 5330422M15 gene	-1.09	0.723	1.13	0.781	1.21	0.668	1.08	0.797	0.58
1455381_at	4921513D23Rik	RIKEN cDNA 4921513D23 gene	1.49	0.531	1.04	0.907	-1.36	0.481	1.02	0.979	0.55
1456651_a_at	Tpr	translocated promoter region	-1.1	0.705	1.1	0.711	1.26	0.453	1.08	0.834	0.58
1445741_at	Ppm1e	protein phosphatase 1E (PP2C domain containing)	1.24	0.855	1.31	0.547	-1.39	0.247	1.51	0.565	0.67
1438376_s_at	Trim27	tripartite motif protein 27	1.01	0.882	1.09	0.2	1.17	0.442	-1.04	0.779	0.56
1429569_a_at	Ccdc46	coiled-coil domain containing 46	1.5	0.403	1.16	0.859	-1.65	0.106	1.42	0.546	0.61
1448192_s_at	Prps1 /// AU021838	phosphoribosyl pyrophosphate synthetase 1 /// expressed sequence AU021838	1.01	0.949	-1.08	0.647	1.33	0.333	1.36	0.512	0.66
1434651_a_at	Cldn3	claudin 3	1.1	0.666	1.02	0.848	1.15	0.469	-1.29	0.444	0.5
1418922_at	Igsf4b	immunoglobulin superfamily, member 4B	1.61	0.023	-1.53	0.344	1.01	0.98	1.59	0.26	0.67
1419047_at	Pcnx	pecanex homolog (Drosophila)	1.11	0.025	1.02	0.874	1.14	0.334	-1.28	0.136	0.5

1416478_a_at	Mdh2	malate dehydrogenase 2, NAD (mitochondrial)	-1.18	0.065	1	0.986	1.42	0.021	1.02	0.771	0.56
1448805_at	Usf1	upstream transcription factor 1	1.17	0.727	1.25	0.435	-1.18	0.599	1.02	0.774	0.56
1422982_at	Ar	androgen receptor	-1.04	0.883	1.28	0.322	1.03	0.811	1.76	0.004	0.76
1450054_at	Add1	adducin 1 (alpha)	-1.05	0.77	1.08	0.345	1.24	0.018	1.47	0.202	0.69
1459563_x_at	---	Transcribed locus	1.07	0.877	1.06	0.813	1.14	0.601	-1.04	0.895	0.56
1441428_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730003N	1.12	0.344	-1.15	0.535	1.28	0.248	1.04	0.904	0.57
1456437_x_at	C1r /// LOC667277	complement component 1, r subcomponent /// similar to Complement C1r-B subc	1.12	0.775	1.15	0.522	1.01	0.978	-1.15	0.226	0.53
1416512_at	Nubp2	nucleotide binding protein 2	-1.01	0.935	1.05	0.481	1.23	0.284	1.4	0.22	0.67
1431502_a_at	Exosc3	exosome component 3	-1.03	0.606	1.06	0.392	1.24	0.064	1.05	0.847	0.58
1425073_at	Plekhg6	pleckstrin homology domain containing, family G (with RhoGef domain) member (	1.02	0.95	1.25	0.322	1.01	0.978	-1.1	0.64	0.54
1416741_at	Col5a1	Procollagen, type V, alpha 1	1.46	0.359	1.36	0.547	-2.21	0.164	4.9	0.265	1.38
1449257_at	D11Wsu99e	DNA segment, Chr 11, Wayne State University 99, expressed	1.1	0.573	1.22	0.146	-1.06	0.612	1.19	0.559	0.61
1416927_at	Trp53inp1	transformation related protein 53 inducible nuclear protein 1	1.21	0.823	-1.19	0.597	1.22	0.709	1.19	0.589	0.61
1446491_at	Gnal	Guanine nucleotide binding protein, alpha stimulating, olfactory type	1.26	0.769	1.12	0.839	-1.11	0.819	1.76	0.331	0.75
1433206_at	5033430J17Rik	RIKEN cDNA 5033430J17 gene	1.25	0.727	1.34	0.667	-1.47	0.48	1.49	0.06	0.65
1430696_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	1.25	0.115	1.38	0.511	-1.55	0.095	2.37	0.224	0.86
1446887_at	---	Transcribed locus	1	0.999	-1.08	0.869	1.35	0.445	1.28	0.622	0.64
1421940_at	Stag1	stromal antigen 1	1.1	0.551	-1	1	1.17	0.487	1.4	0.256	0.67
1434040_at	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1.32	0.059	-1.1	0.249	1.05	0.789	1.19	0.13	0.61
1434736_at	Hlf	hepatic leukemia factor	1.04	0.85	-1.39	0.318	1.51	0.59	1.67	0.312	0.71
1417544_a_at	Flot2	flotillin 2	-1.07	0.701	1.1	0.424	1.23	0.045	1.25	0.107	0.63
1424677_at	Cyp2j9	cytochrome P450, family 2, subfamily j, polypeptide 9	1.02	0.864	-1.02	0.942	1.27	0.223	1.12	0.81	0.6
1455556_at	Notch2	Notch gene homolog 2 (Drosophila)	1.15	0.177	1.11	0.521	1.01	0.954	-1.18	0.578	0.52
1442508_at	4933404M19Rik ///	RIKEN cDNA 4933404M19 gene /// similar to hypothetical protein MGC39650 ///	1.23	0.464	1.25	0.652	-1.26	0.434	1.24	0.717	0.61
1423808_at	Wdr79	WD repeat domain 79	-1.13	0.143	1.04	0.795	1.35	0.01	1.57	0.354	0.71
1419790_at	---	---	1.38	0.142	1.46	0.316	-2.33	0.235	1.28	0.683	0.45
1423871_at	Tmem63a	transmembrane protein 63a	-1.11	0.138	1.09	0.617	1.28	0.231	1.03	0.713	0.57
1428069_at	Cdca7	cell division cycle associated 7	1.21	0.838	-1.31	0.49	1.29	0.194	1.65	0.203	0.71
1433840_a_at	KIAA0415	KIAA0415 protein	-1.43	0.003	1.04	0.743	1.54	0	1.01	0.933	0.54
1459964_at	Jund1	Jun proto-oncogene related gene d1	-1.28	0.735	1.07	0.825	1.42	0.043	1.1	0.228	0.58
1453732_at	6230416A05Rik	RIKEN cDNA 6230416A05 gene	1.12	0.487	-1.04	0.901	1.2	0.178	1.12	0.412	0.6
1449575_a_at	Gstp1	glutathione S-transferase, pi 1	1.11	0.629	-1.02	0.851	1.19	0.065	1.14	0.22	0.6
1456354_at	Chrna4	cholinergic receptor, nicotinic, alpha polypeptide 4	-1.08	0.415	1.26	0.604	1.09	0.857	1.03	0.962	0.57
1431304_a_at	1300007B12Rik	RIKEN cDNA 1300007B12 gene	1.15	0.597	-1.16	0.606	1.27	0.557	1.59	0.439	0.71
1437349_at	Ckap5	cytoskeleton associated protein 5	-1.1	0.25	1.28	0.052	1.08	0.581	1.82	0.21	0.77
1441405_at	9630014M24Rik	RIKEN cDNA 9630014M24 gene	-1.39	0.592	1.32	0.575	1.23	0.47	1.58	0.319	0.69
1422489_at	Gcs1	glucosidase 1	1.02	0.946	-1.04	0.636	1.3	0.253	1.28	0.262	0.64
1435575_at	Kntc1	kinetochore associated 1	1.15	0.592	1.13	0.728	-1.01	0.969	3.88	0.239	1.29
1428003_s_at	Thtpa /// Zfhx2as	thiamine triphosphatase /// zinc finger homeobox 2, antisense	1.04	0.726	1.27	0.069	-1.04	0.572	1.4	0.065	0.67
1428354_at	Foxk2	forkhead box K2	1.01	0.959	-1.03	0.895	1.29	0.222	1.18	0.592	0.61
1435519_at	Rap1b	RAS related protein 1b	1.01	0.678	1.25	0.022	1.01	0.816	-1.07	0.412	0.55
1455479_a_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	1.09	0.568	-1.11	0.436	1.28	0.004	1.01	0.923	0.57
1448187_at	Pold1	polymerase (DNA directed), delta 1, catalytic subunit	1.06	0.829	-1.16	0.583	1.35	0.108	1.12	0.443	0.59
1416713_at	2700055K07Rik	RIKEN cDNA 2700055K07 gene	1.33	0.437	1.13	0.823	-1.23	0.04	1.87	0.023	0.77
1419552_at	Echdc1	enoyl Coenzyme A hydratase domain containing 1	-1.24	0.083	1.13	0.235	1.34	0.095	1.21	0.249	0.61
1436444_at	6030405A18Rik	RIKEN cDNA 6030405A18 gene	1.05	0.93	-1.05	0.887	1.28	0.513	1.52	0.267	0.7
1425929_a_at	Rnf14	ring finger protein 14	-1.03	0.934	1.02	0.948	1.28	0.423	1.42	0.369	0.67
1433433_at	Myst2	MYST histone acetyltransferase 2	-1.01	0.92	1.04	0.151	1.24	0.142	1.08	0.148	0.59
1419738_a_at	Tpm2	tropomyosin 2, beta	1.5	0.01	-1.45	0.459	1.08	0.451	1.1	0.252	0.56
1444132_at	2310003H01Rik	RIKEN cDNA 2310003H01 gene	-1.36	0.368	1.44	0.601	1.1	0.871	2.01	0.455	0.8
1433384_at	9330199C07Rik	RIKEN cDNA 9330199C07 gene	1.31	0.517	1.05	0.909	-1.1	0.768	1.14	0.783	0.6
1442354_at	B230325K18Rik	RIKEN cDNA B230325K18 gene	1.56	0.48	-1.63	0.045	1.1	0.863	2.66	0.058	0.92
1428856_at	H13	Histocompatibility 13	1.13	0.472	1.21	0.545	-1.07	0.717	1.83	0.079	0.78

1452353_at	Gpr155	G protein-coupled receptor 155	1.2	0.263	1.16	0.189	-1.09	0.631	1.83	0.078	0.78
1451813_at	Oprk1	opioid receptor, kappa 1	1.15	0.655	1.17	0.752	-1.04	0.89	1.05	0.818	0.58
1431743_a_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	1.07	0.513	-3.58	0.274	1.93	0.175	4.91	0.153	1.08
1441338_at	5930412G12Rik	RIKEN cDNA 5930412G12 gene	1.06	0.881	1.16	0.408	1.06	0.742	-1.13	0.368	0.54
1432211_a_at	Fbxo9	f-box only protein 9	1.08	0.588	-1.14	0.241	1.32	0.18	2.93	0.225	1.05
1456363_at	St7l	Suppression of tumorigenicity 7-like	-1.1	0.372	1.05	0.879	1.32	0.044	1.07	0.392	0.59
1458983_at	AU015559	expressed sequence AU015559	-1.15	0.826	1.38	0.298	1.03	0.951	1.77	0.326	0.76
1428475_at	1190005P17Rik	RIKEN cDNA 1190005P17 gene	1.03	0.869	1.03	0.601	1.21	0.403	-1.21	0.169	0.52
1445868_at	Cpeb3	cytoplasmic polyadenylation element binding protein 3	1.2	0.619	-1.24	0.579	1.27	0.509	2.27	0.179	0.88
1415693_at	Derl1	Der1-like domain family, member 1	-1.08	0.365	1.02	0.518	1.33	0.013	1.39	0.021	0.66
1438097_at	Rab20	RAB20, member RAS oncogene family	1.14	0.199	1.02	0.928	1.12	0.596	-1.35	0.224	0.48
1417026_at	Pfdn1	prefoldin 1	1.43	0.263	1.13	0.42	-1.38	0.046	1.07	0.828	0.56
1437221_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	1.29	0.354	1.03	0.953	-1.03	0.798	1.02	0.966	0.57
1442472_at	ttc21a	Tetratricopeptide repeat domain 21A	1.1	0.923	1.07	0.908	1.11	0.371	-1.01	0.98	0.57
1448950_at	Il1r1	interleukin 1 receptor, type I	1.13	0.783	1.28	0.652	-1.16	0.315	1.04	0.83	0.58
1453616_at	3830408C21Rik	RIKEN cDNA 3830408C21 gene	1.34	0.599	-1.75	0.248	1.37	0.421	1.16	0.672	0.53
1455886_at	Cbl	Casitas B-lineage lymphoma	1.05	0.68	1.17	0.306	1.07	0.72	-1.39	0.313	0.47
1420713_a_at	Mdfi	MyoD family inhibitor	-1.32	0.249	1.4	0.475	1.12	0.885	1.01	0.943	0.55
1450745_at	C1galt1	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransfe	-1.09	0.26	1.1	0.721	1.27	0.264	1.03	0.9	0.58
1424701_at	Pcdh20	protocadherin 20	1.17	0.86	1.47	0.588	-1.56	0.188	1.59	0.266	0.67
1437027_x_at	Rnps1	ribonucleic acid binding protein S1	1.01	0.46	-1.02	0.775	1.29	0.059	1.03	0.405	0.58
1420584_at	Pla2g2c	phospholipase A2, group IIC	-1.23	0.013	1.17	0.466	1.3	0.259	1.24	0.305	0.62
1451311_a_at	Adipor1	adiponectin receptor 1	-1.13	0.501	1.05	0.698	1.34	0.131	1.49	0.337	0.69
1452112_a_at	Rbm4b	RNA binding motif protein 4B	1.07	0.546	-1.02	0.855	1.23	0.134	1.1	0.363	0.6
1442581_at	Ksr1	kinase suppressor of ras 1	1.34	0.597	1.2	0.487	-1.34	0.331	1	0.981	0.55
1452220_at	Dock1	dedicator of cyto-kinesis 1	1.03	0.534	1.15	0.133	1.1	0.487	-1.21	0.424	0.52
1427067_at	4933439F18Rik	RIKEN cDNA 4933439F18 gene	1.31	0.39	-1.13	0.287	1.08	0.758	1.74	0.337	0.75
1426159_x_at	Tcrb-V13	T-cell receptor beta, variable 13	1.08	0.694	1.14	0.662	1.06	0.723	-2.58	0.079	0.17
1423203_a_at	Cetn1	centrin 1	-2.63	0.401	1.76	0.273	1.14	0.662	1.22	0.802	0.37
1425933_a_at	Nt5c2	5'-nucleotidase, cytosolic II	1.07	0.366	-1.01	0.942	1.22	0.44	1.68	0.271	0.74
1446852_at	Serpinb9b	Serine (or cysteine) peptidase inhibitor, clade B, member 9b	1.1	0.839	1.63	0.375	-1.8	0.153	3.41	0.289	1.08
1418256_at	Srf	serum response factor	-1.11	0.517	1.17	0.059	1.22	0.424	1.09	0.645	0.59
1441678_at	---	---	1.35	0.728	1.02	0.966	-1.1	0.721	1.39	0.652	0.67
1420261_at	Psen1	presenilin 1	-1.2	0.771	1.36	0.165	1.09	0.802	2.2	0.288	0.86
1433292_at	1500032O14Rik	RIKEN cDNA 1500032O14 gene	1.6	0.177	-1.7	0.566	1.09	0.864	1.1	0.691	0.52
1417882_at	Slc39a3	solute carrier family 39 (zinc transporter), member 3	-1.09	0.438	1.26	0.136	1.1	0.514	1.15	0.678	0.61
1449690_x_at	---	---	1.14	0.755	-2.06	0.241	1.66	0.188	1.31	0.725	0.51
1419390_at	Pde10a	phosphodiesterase 10A	1.22	0.816	1.02	0.955	1.04	0.855	-3.23	0.104	0.01
1429005_at	Mfhas1	malignant fibrous histiocytoma amplified sequence 1	1.22	0.149	-1.02	0.907	1.08	0.534	1.08	0.385	0.59
1449660_s_at	Coro1c	coronin, actin binding protein 1C	1.07	0.694	1.29	0.023	-1.08	0.692	1.2	0.06	0.62
1429586_at	4930558N01Rik	RIKEN cDNA 4930558N01 gene	1.04	0.835	-1.52	0.23	1.59	0.283	1.05	0.748	0.54
1453462_at	1110067M19Rik	RIKEN cDNA 1110067M19 gene	1.29	0.681	1.32	0.031	-1.5	0.279	1.69	0.26	0.7
1452766_at	2900041A09Rik	RIKEN cDNA 2900041A09 gene	1.04	0.865	1.29	0.475	-1.05	0.742	1.06	0.89	0.59
1432248_at	5430402P08Rik	RIKEN cDNA 5430402P08 gene	1.41	0.476	1.14	0.343	-1.37	0.378	1.64	0.04	0.71
1455873_a_at	Vps18	vacuolar protein sorting 18 (yeast)	-1.1	0.744	1.07	0.73	1.31	0.047	1.12	0.676	0.6
1424130_a_at	Ptrf	polymerase I and transcript release factor	-1.15	0.254	1.35	0.341	1.06	0.876	1.29	0.231	0.64
1454159_a_at	Igfbp2	insulin-like growth factor binding protein 2	1.15	0.306	-1.49	0.184	1.47	0.209	1.15	0.461	0.57
1456155_x_at	Fuca1	fucosidase, alpha-L- 1, tissue	1.06	0.755	1	0.996	1.22	0.34	-1.41	0.509	0.47
1434630_at	Ankrd28	ankyrin repeat domain 28	-1.09	0.449	1.06	0.552	1.31	0.331	1.26	0.446	0.63
1441681_at	Xpot	exportin, tRNA (nuclear export receptor for tRNAs)	-1.77	0.404	1.28	0.648	1.44	0.348	1.19	0.627	0.54
1447343_at	---	---	1.38	0.588	-1.65	0.409	1.3	0.359	1.29	0.764	0.58
1422308_a_at	Lgals7	lectin, galactose binding, soluble 7	1.35	0.523	-1.98	0.302	1.43	0.332	2.11	0.03	0.73
1421250_at	LOC674308	similar to solute carrier family 39 (zinc transporter), member 9	-1.38	0.534	1.01	0.976	1.55	0.406	1.26	0.651	0.61

1455210_at	Zhx2	zinc fingers and homeoboxes protein 2	1.02	0.884	1.13	0.253	1.13	0.437	-1.32	0.347	0.49
1450103_a_at	Pscd2	pleckstrin homology, Sec7 and coiled-coil domains 2	1.18	0.368	-1.17	0.317	1.25	0.037	1.01	0.976	0.57
1434652_at	Cdc42bpb	Cdc42 binding protein kinase beta	1.11	0.713	1.04	0.881	1.13	0.433	-1.21	0.598	0.52
1418644_a_at	Stk11	serine/threonine kinase 11	1.1	0.46	-1.04	0.636	1.22	0.116	1.92	0.234	0.8
1436488_at	---	---	1.18	0.631	1.08	0.468	1.03	0.942	-1.66	0.443	0.41
1437428_x_at	Eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta	-1.31	0.117	1.03	0.894	1.49	0.099	1.17	0.59	0.6
1435293_at	2900022I03Rik	RIKEN cDNA 2900022I03 gene	1.31	0.087	1.07	0.887	-1.1	0.6	1.09	0.823	0.59
1450868_at	D8Ertd354e	DNA segment, Chr 8, ERATO Doi 354, expressed	-1.01	0.798	1.19	0.058	1.11	0.39	1.13	0.666	0.6
1437645_at	Atf7	activating transcription factor 7	-1.09	0.906	1.28	0.398	1.09	0.743	1.18	0.432	0.62
1457838_at	Cdc45l	cell division cycle 45 homolog (S. cerevisiae)-like	1.03	0.955	1.35	0.509	-1.1	0.836	1.87	0.163	0.79
1425835_a_at	Bbx	bobby sox homolog (Drosophila)	1.12	0.522	1.08	0.748	1.09	0.726	-1.02	0.928	0.57
1439288_at	0710005I19Rik	RIKEN cDNA 0710005I19 gene	1.28	0.621	-1.88	0.364	1.48	0.117	1.03	0.941	0.48
1459895_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	-1.07	0.707	1.01	0.976	1.34	0.199	1.08	0.792	0.59
1449192_at	Atf7ip	activating transcription factor 7 interacting protein	-1.08	0.566	1.09	0.724	1.27	0.097	1.37	0.002	0.66
1430806_at	2810047F03Rik	RIKEN cDNA 2810047F03 gene	-1.3	0.338	1.38	0.179	1.14	0.622	1.96	0.108	0.8
1416621_at	Llgl1	lethal giant larvae homolog 1 (Drosophila)	-1.06	0.363	1.21	0.036	1.14	0.391	1.16	0.275	0.61
1436193_at	Man1c1	mannosidase, alpha, class 1C, member 1	1.11	0.757	1.25	0.249	-1.08	0.711	1.41	0.253	0.67
1449351_s_at	Pdgfc	platelet-derived growth factor, C polypeptide	1.03	0.594	1.41	0.216	-1.18	0.325	2.01	0.178	0.82
1443857_at	Hook3	hook homolog 3 (Drosophila)	1.03	0.867	-1.33	0.272	1.51	0.175	1.56	0.44	0.69
1428800_a_at	Pus7l	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	1.04	0.929	1.15	0.177	1.1	0.676	-1.02	0.88	0.57
1421076_at	Sertad3	SERTA domain containing 3	1.17	0.501	-1.13	0.388	1.23	0.516	1.75	0.281	0.76
1432143_a_at	Hbp1	high mobility group box transcription factor 1	1.15	0.613	-1.05	0.899	1.19	0.711	1.35	0.398	0.66
1429156_at	2610036L11Rik	RIKEN cDNA 2610036L11 gene	1.31	0.727	-1.44	0.031	1.28	0.362	2.51	0.271	0.92
1422788_at	Slc43a3	solute carrier family 43, member 3	1.2	0.596	1.15	0.316	-1.06	0.774	2.98	0.142	1.07
1438996_at	Gm118	gene model 118, (NCBI)	1.02	0.896	1.66	0.238	-1.65	0.109	1.09	0.82	0.53
1448657_a_at	Dnajb10	DnaJ (Hsp40) homolog, subfamily B, member 10	-1	0.989	1.09	0.53	1.2	0.14	3.52	0.189	1.2
1444322_at	Lcn11	lipocalin 11	1.5	0.464	1.07	0.867	-1.39	0.531	1.04	0.898	0.55
1431039_at	Otud4	OTU domain containing 4	1.41	0.586	-1.3	0.671	1.11	0.794	1.23	0.678	0.61
1449845_a_at	Ephb4	Eph receptor B4	1.13	0.477	1.09	0.81	1.07	0.667	-1.47	0.47	0.45
1434109_at	Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	1.06	0.784	-1.08	0.356	1.31	0.444	1.43	0.149	0.68
1435294_at	Mtmr11	myotubularin related protein 11	-1.72	0.58	1.34	0.544	1.36	0.519	1.55	0.456	0.63
1432422_at	1700063K16Rik	RIKEN cDNA 1700063K16 gene	-1.01	0.988	1.03	0.915	1.27	0.401	1.23	0.674	0.63
1432052_at	Exosc1	Exosome component 1	1.11	0.338	-1.11	0.822	1.27	0.067	1.2	0.563	0.62
1428101_at	Rnf38	ring finger protein 38	1	0.967	1.39	0.034	-1.11	0.465	1.25	0.279	0.63
1442982_at	Ccdc66	coiled-coil domain containing 66	1.03	0.419	1.23	0.215	1.04	0.691	-1.25	0.041	0.51
1450181_at	Cutl2	cut-like 2 (Drosophila)	-2.31	0.099	1.74	0.264	1.12	0.77	1.27	0.631	0.45
1426962_at	Phf20	PHD finger protein 20	1.15	0.08	1.13	0.316	1.01	0.925	-1.08	0.706	0.55
1432162_s_at	Ptar1	protein prenyltransferase alpha subunit repeat containing 1	1.22	0.474	-1.08	0.763	1.15	0.549	1.18	0.686	0.62
1427148_at	Pja2	praja 2, RING-H2 motif containing	1.31	0.175	-1.04	0.88	1.02	0.922	1.2	0.435	0.62
1424161_at	Ddx27	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	1.04	0.161	-1.13	0.132	1.36	0.044	1	0.985	0.57
1416189_a_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	1.02	0.435	1.14	0.119	1.13	0.192	-1.1	0.598	0.55
1454077_at	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	-1.49	0.285	1.61	0.325	1	0.981	1.63	0.067	0.69
1442690_at	Tmem143	Transmembrane protein 143	-1.5	0.086	1.22	0.593	1.41	0.313	1.44	0.39	0.64
1453808_at	2210416O15Rik	RIKEN cDNA 2210416O15 gene	1.46	0.496	-1.37	0.324	1.1	0.827	1.2	0.563	0.6
1424777_at	Wdr21	WD repeat domain 21	1.28	0.353	-1.05	0.861	1.06	0.73	1.08	0.656	0.59
1417163_at	Dusp10	dual specificity phosphatase 10	1.1	0.881	1.07	0.86	1.12	0.777	-1	0.994	0.57
1437254_at	Cep76	centrosomal protein 76	1.03	0.734	-1.01	0.972	1.27	0.641	4.7	0.228	1.5
1416831_at	Neu1	neuraminidase 1	1.06	0.716	1.1	0.315	1.13	0.244	-1.27	0.213	0.51
1436747_at	1110014K08Rik ///	RIKEN cDNA 1110014K08 gene /// hypothetical protein LOC664786 /// hypothetic	-1	0.986	1.16	0.123	1.13	0.559	1.51	0.179	0.7
1420784_at	Scn11a	sodium channel, voltage-gated, type XI, alpha	-1.22	0.498	1.42	0.49	1.05	0.92	1.72	0.238	0.74
1451075_s_at	Ctdsp2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phospha	1.16	0.352	1.1	0.28	1.04	0.635	-1.42	0.184	0.47
1422993_s_at	Thoc4 /// Refbp2	THO complex 4 /// RNA and export factor binding protein 2	1.28	0.37	1.06	0.834	-1.05	0.877	1.72	0.143	0.75
1416392_a_at	Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	-1.1	0.513	1.08	0.219	1.3	0.038	1.27	0.091	0.64

1450217_at	Ccl28	chemokine (C-C motif) ligand 28	-1.23	0.607	1.3	0.563	1.18	0.758	1.06	0.907	0.58
1431119_at	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	-1.32	0.506	1.33	0.174	1.21	0.538	1.51	0.019	0.68
1416768_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	1.02	0.287	1.07	0.332	1.2	0.101	-1.52	0.139	0.44
1426207_at	Ikbkb	inhibitor of kappaB kinase beta	1.12	0.185	1.07	0.127	1.1	0.5	-1.93	0.129	0.34
1443420_at	Usp8	Ubiquitin specific peptidase 8	1.07	0.783	1.26	0.671	-1.04	0.917	1.27	0.266	0.64
1423468_at	Steap3	STEAP family member 3	1.33	0.21	1.07	0.863	-1.11	0.794	2.6	0.105	0.97
1423271_at	Gjb2	gap junction membrane channel protein beta 2	-1.17	0.149	1.12	0.088	1.33	0.304	1.72	0.007	0.75
1456301_at	Hoxc5	homeo box C5	-1.02	0.974	1.28	0.692	1.03	0.911	1.8	0.355	0.77
1417008_at	Crat	carnitine acetyltransferase	1.13	0.315	-1.12	0.528	1.27	0.318	1.78	0.167	0.77
1449301_at	Slc7a13	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13	-1.5	0.511	1.36	0.555	1.27	0.683	3.19	0.369	1.08
1428071_at	1110038D17Rik	RIKEN cDNA 1110038D17 gene	1	0.977	-1.22	0.109	1.47	0.031	1.64	0.21	0.72
1421051_s_at	Vps25	vacuolar protein sorting 25 (yeast)	1.04	0.893	-1.12	0.475	1.36	0.351	1.06	0.841	0.59
1419685_at	Upf1	UPF1 regulator of nonsense transcripts homolog (yeast)	1.32	0.388	-1.17	0.227	1.12	0.65	1.22	0.044	0.62
1424710_a_at	Gorasp2	golgi reassembly stacking protein 2	1.14	0.237	1.05	0.706	1.11	0.19	-1.32	0.427	0.49
1444157_a_at	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	1.25	0.117	-1.06	0.753	1.1	0.489	1.23	0.144	0.63
1445491_at	C79685	expressed sequence C79685	-1.14	0.518	1.11	0.873	1.31	0.448	1.32	0.353	0.65
1457669_x_at	Rfc2	replication factor C (activator 1) 2	-1.07	0.163	1.19	0.541	1.17	0.193	1.29	0.341	0.65
1425944_a_at	Rad51l3	RAD51-like 3 (S. cerevisiae)	1.22	0.518	-1.39	0.068	1.36	0.352	1.18	0.327	0.59
1457246_at	Rai16	retinoic acid induced 16	1.07	0.477	1.11	0.636	1.12	0.5	-1.12	0.488	0.54
1431623_at	1700023H06Rik	RIKEN cDNA 1700023H06 gene	-1.34	0.606	1.44	0.442	1.11	0.706	1.22	0.48	0.61
1441841_at	Adamts16	a disintegrin-like and metallopetidase (reprolysin type) with thrombospondin type	-1.26	0.549	1.13	0.702	1.38	0.127	1.03	0.821	0.57
1449032_at	Prlpm	prolactin-like protein M	1.13	0.215	1.11	0.873	1.06	0.709	-1.14	0.227	0.54
1428801_at	Mgat3	mannoside acetylglucosaminyltransferase 3	1.01	0.908	1.09	0.729	1.19	0.489	-1.18	0.234	0.53
1423777_at	Usp20	ubiquitin specific peptidase 20	1.13	0.207	1.13	0.481	1.04	0.713	-1.1	0.445	0.55
1415982_at	Herpud2	HERPUD family member 2	-1.18	0.315	1.09	0.363	1.36	0.06	1.02	0.761	0.57
1437640_at	6430704M03Rik	RIKEN cDNA 6430704M03 gene	1.33	0.322	1.06	0.917	-1.11	0.832	1.73	0.106	0.75
1441129_at	11-Sep	Septin 11	1.08	0.594	1.41	0.411	-1.24	0.075	1.01	0.974	0.57
1428792_at	Bcas1	breast carcinoma amplified sequence 1	1.08	0.332	1.04	0.824	1.18	0.195	-1.32	0.368	0.49
1433434_at	AW551984	expressed sequence AW551984	-1.4	0.395	1.14	0.279	1.44	0.563	1.25	0.698	0.61
1455665_at	Lonrf1 /// LOC6316	LON peptidase N-terminal domain and ring finger 1 /// similar to CG32369-PB, isc	-1.06	0.908	1.14	0.629	1.22	0.237	1.64	0.143	0.73
1428436_at	Lsm14a	LSM14 homolog A (SCD6, S. cerevisiae)	-1.07	0.168	1.14	0.627	1.23	0.131	1.19	0.335	0.62
1435385_at	Tshz2	teashirt zinc finger family member 2	1.04	0.883	1.16	0.515	1.1	0.696	-1.16	0.564	0.53
1419277_at	Usp48	ubiquitin specific peptidase 48	1.05	0.242	-1.15	0.367	1.38	0.189	1.37	0.106	0.66
1437832_x_at	Wars	tryptophanyl-tRNA synthetase	-1.11	0.602	1.1	0.618	1.29	0.261	1.18	0.066	0.62
1429428_at	Tcf7l2	transcription factor 7-like 2, T-cell specific, HMG-box	1.15	0.578	1.23	0.121	-1.08	0.764	1.29	0.378	0.65
1429058_at	1110004B13Rik	RIKEN cDNA 1110004B13 gene	-1.13	0.545	1.06	0.744	1.35	0.204	3.69	0.202	1.24
1428986_at	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), m	1.01	0.988	1.14	0.723	1.16	0.621	-1.9	0.206	0.35
1428689_at	Tysnd1	trypsin domain containing 1	1.27	0.345	-1.15	0.215	1.16	0.351	1.07	0.698	0.59
1429667_at	Pou4f1	POU domain, class 4, transcription factor 1	1.47	0.121	1.05	0.874	-1.29	0.279	1.49	0.146	0.68
1460379_at	Hoxb4	homeo box B4	1.01	0.964	1.45	0.121	-1.19	0.594	1.03	0.911	0.57
1445100_at	---	---	1.26	0.306	1.22	0.373	-1.22	0.431	1.36	0.574	0.65
1435630_s_at	Acat2	acetyl-Coenzyme A acetyltransferase 2	1.01	0.862	1.44	0.008	-1.18	0.359	1.16	0.484	0.61
1424225_at	Asb8	ankyrin repeat and SOCS box-containing protein 8	1.05	0.852	-1.04	0.871	1.29	0.215	1.14	0.629	0.61
1424191_a_at	Tmem41a	transmembrane protein 41a	-1.05	0.697	1.32	0.252	1.03	0.804	1.57	0.325	0.72
1454665_at	Irf2bp2 /// LOC6729	interferon regulatory factor 2 binding protein 2 /// similar to interferon regulatory fa	1.13	0.682	-1.05	0.879	1.22	0.22	1.2	0.248	0.62
1453201_at	4632411J06Rik	RIKEN cDNA 4632411J06 gene	1.1	0.476	-1.03	0.933	1.23	0.263	1.32	0.438	0.66
1416646_at	Afp	alpha fetoprotein	1.04	0.927	-1.23	0.368	1.45	0.09	1.4	0.658	0.66
1444566_at	Dnajb13	DnaJ (Hsp40) related, subfamily B, member 13	1.32	0.303	-1.03	0.936	1.01	0.889	2.65	0.266	0.99
1447175_at	2610528M18Rik	RIKEN cDNA 2610528M18 gene	1.43	0.573	-1.34	0.625	1.13	0.753	2.01	0.02	0.81
1423875_at	AI450540	expressed sequence AI450540	1.27	0.48	-1.06	0.826	1.08	0.638	1.33	0.499	0.66
1430355_a_at	Steap3	STEAP family member 3	1.29	0.09	-1.47	0.457	1.34	0.363	2.97	0.245	1.03
1433885_at	Iqgap2	IQ motif containing GTPase activating protein 2	1.1	0.552	-1.09	0.328	1.28	0.439	2.05	0.188	0.83
1435750_at	Gchfr	GTP cyclohydrolase I feedback regulator	1.35	0.129	1.01	0.936	-1.06	0.812	1.77	0.418	0.77

1433625_at	5830434P21Rik	RIKEN cDNA 5830434P21 gene	1	0.987	-1	0.996	1.3	0.206	1.13	0.453	0.61
1437740_at	Plekhm2	pleckstrin homology domain containing, family M (with RUN domain) member 2	1.12	0.334	1.2	0.53	-1.02	0.846	1.2	0.457	0.62
1460596_at	Agtrap	angiotensin II, type I receptor-associated protein	-1.42	0.265	1.16	0.341	1.44	0.033	1.31	0.042	0.62
1421315_s_at	Cttn	cortactin	1.02	0.878	-1.01	0.941	1.29	0.454	1.39	0.465	0.67
1424119_at	Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-1.04	0.874	1.33	0.008	1.01	0.943	2.17	0.124	0.87
1449832_at	1700091H14Rik	RIKEN cDNA 1700091H14 gene	1.14	0.391	-1.13	0.817	1.28	0.683	1.95	0.217	0.81
1432794_at	2310058F05Rik	RIKEN cDNA 2310058F05 gene	1.09	0.897	1	0.999	1.21	0.634	-1.88	0.494	0.36
1451428_x_at	Egfl7	EGF-like domain 7	1.15	0.262	1.14	0.126	1.02	0.912	-1.1	0.411	0.55
1458835_at	---	---	1.5	0.589	-2.34	0.066	1.38	0.351	1.51	0.355	0.51
1450202_at	Grin1	glutamate receptor, ionotropic, NMDA1 (zeta 1)	1.19	0.84	-1	0.995	1.12	0.754	1.59	0.279	0.72
1433025_x_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	1.14	0.679	1.27	0.229	-1.12	0.602	1.18	0.582	0.62
1427178_at	Tmc4	transmembrane channel-like gene family 4	1.13	0.436	-1.45	0.184	1.48	0.012	1.2	0.415	0.59
1456133_x_at	Itgb5	integrin beta 5	1.09	0.452	1.2	0.101	1.01	0.928	-1.06	0.821	0.56
1430160_at	Ankib1	ankyrin repeat and IBR domain containing 1	-1.31	0.258	1.18	0.673	1.36	0.341	2.02	0.174	0.81
1429268_at	2610318N02Rik	RIKEN cDNA 2610318N02 gene	-1.66	0.388	1.41	0.375	1.3	0.485	2.07	0.165	0.78
1431417_at	Jam2	junction adhesion molecule 2	1.33	0.704	-1.59	0.311	1.34	0.443	1.65	0.483	0.68
1424359_at	Oplah	5-oxoprolinase (ATP-hydrolysing)	1.23	0.234	-1.03	0.837	1.11	0.656	1.27	0.569	0.64
1458943_at	---	---	1.49	0.373	1.03	0.922	-1.28	0.537	1.34	0.184	0.65
1443549_at	4930579E17Rik	RIKEN cDNA 4930579E17 gene	-1.19	0.442	1.35	0.566	1.12	0.562	2.61	0.054	0.97
1455689_at	Fzd10	frizzled homolog 10 (Drosophila)	1.26	0.734	1.34	0.622	-1.41	0.112	1.1	0.245	0.57
1416835_s_at	Amd1 /// Amd2	S-adenosylmethionine decarboxylase 1 /// S-adenosylmethionine decarboxylase	1.25	0.627	-1.12	0.784	1.16	0.701	2.14	0.347	0.86
1425996_a_at	Smarca3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.13	0.316	1.09	0.714	1.08	0.745	-1.6	0.093	0.43
1434976_x_at	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	1.2	0.251	1.11	0.232	-1	0.993	1.53	0.145	0.71
1445546_at	AI844685	expressed sequence AI844685	1.23	0.278	-1.15	0.814	1.21	0.542	2.53	0.132	0.95
1443461_at	C79130	expressed sequence C79130	1.15	0.278	1.14	0.721	1.02	0.977	-1.05	0.933	0.56
1434032_at	---	---	-1.25	0.756	1.36	0.719	1.14	0.378	1.88	0.021	0.78
1419236_at	Helb	helicase (DNA) B	1.44	0.414	1.04	0.935	-1.21	0.656	1.48	0.48	0.69
1449088_at	Fbp2	fructose bisphosphatase 2	1.21	0.141	1.24	0.754	-1.16	0.829	1.85	0.199	0.78
1417894_at	Gpr97	G protein-coupled receptor 97	-1.34	0.046	1.36	0.208	1.2	0.564	2.25	0.371	0.87
1448078_at	C76533	expressed sequence C76533	-1.07	0.848	1.19	0.5	1.19	0.517	1.09	0.786	0.6
1433892_at	Spag5	sperm associated antigen 5	1.67	0.21	-4.3	0.029	1.4	0.641	4.09	0.229	0.72
1444239_at	BC023488	CDNA sequence BC023488	-1.31	0.569	1.43	0.567	1.12	0.839	1.56	0.193	0.7
1450410_a_at	4930570C03Rik	RIKEN cDNA 4930570C03 gene	1.12	0.366	1.21	0.07	-1.03	0.844	2.21	0.122	0.88
1453832_at	5330430P22Rik	RIKEN cDNA 5330430P22 gene	1.38	0.343	-1.22	0.528	1.1	0.606	1.12	0.685	0.6
1452776_a_at	Nub1	negative regulator of ubiquitin-like proteins 1	1.05	0.901	1.17	0.161	1.09	0.541	-1.19	0.374	0.53
1424857_a_at	Trim34 /// LOC4342	tripartite motif protein 34 /// similar to Tripartite motif protein 34	1.15	0.327	1.03	0.81	1.13	0.69	-2.66	0.04	0.16
1420596_at	Cacng2	calcium channel, voltage-dependent, gamma subunit 2	-1.03	0.658	1.02	0.935	1.31	0.087	2.14	0.243	0.86
1460709_a_at	Bat5	HLA-B associated transcript 5	-1.03	0.836	1.08	0.027	1.26	0.178	1.47	0.174	0.69
1455249_at	---	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732480G1	1.2	0.035	1.12	0.477	-1.01	0.899	1.16	0.506	0.62
1416507_at	Tmem4	transmembrane protein 4	1.14	0.558	1.11	0.708	1.07	0.535	-1.41	0.281	0.48
1417060_at	Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	1.16	0.385	1.02	0.862	1.13	0.599	-1.33	0.47	0.5
1454837_at	Cln6	ceroid-lipofuscinosis, neuronal 6	-1.37	0.024	1.08	0.408	1.5	0.038	1.12	0.617	0.58
1427149_at	Plekha6	pleckstrin homology domain containing, family A member 6	-1.13	0.394	1.08	0.739	1.34	0.431	1.07	0.845	0.59
1434868_at	4933431E20Rik	RIKEN cDNA 4933431E20 gene	1.35	0.179	1.1	0.797	-1.16	0.703	1.05	0.908	0.58
1429995_at	1700036D21Rik	RIKEN cDNA 1700036D21 gene	-1.06	0.913	1.26	0.614	1.11	0.811	1.06	0.858	0.59
1460659_at	---	CDNA, clone:Y0G0114H22, strand:minus, reference:ENSEMBL:Mouse-Transcrip	1.11	0.801	1	0.992	1.2	0.703	-1.26	0.585	0.51
1436356_at	Lgals7	lectin, galactose binding, soluble 7	1.07	0.65	1.36	0.152	-1.14	0.558	1.08	0.712	0.59
1456107_x_at	Eftud2	elongation factor Tu GTP binding domain containing 2	1.1	0.742	-1.17	0.273	1.36	0.216	1.17	0.352	0.61
1423643_at	Ddx39	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	-1.05	0.684	1.13	0.434	1.24	0.352	1.18	0.502	0.62
1435406_at	Cchcr1	coiled-coil alpha-helical rod protein 1	-1.12	0.388	1.12	0.613	1.3	0.244	2.23	0.168	0.88
1449864_at	Il4	interleukin 4	1.33	0.792	1.39	0.596	-1.7	0.124	1.4	0.438	0.61
1424176_a_at	Anxa4	annexin A4	1.21	0.558	1.04	0.77	1.06	0.792	-1.01	0.968	0.58
1437701_at	Smcr8	Smith-Magenis syndrome chromosome region, candidate 8 homolog (human)	1.38	0.434	-2.38	0.028	1.51	0.388	1.5	0.567	0.5

1416961_at	Bub1b	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	-1.09	0.679	1.24	0.593	1.16	0.438	1.96	0.281	0.82
1456472_at	Armc4	armadillo repeat containing 4	-1.41	0.431	1.44	0.016	1.16	0.572	2.15	0.036	0.84
1438467_at	Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin 2	1.02	0.864	1.55	0.151	-1.36	0.222	1.25	0.557	0.62
1452476_at	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit	1.56	0.346	-1.64	0.459	1.15	0.853	1.84	0.021	0.73
1438801_at	Dnm3	dynamin 3	1.12	0.844	1.23	0.35	-1.05	0.858	1.42	0.316	0.68
1419570_at	Slc28a3	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	1.34	0.126	1.18	0.624	-1.27	0.593	1.25	0.75	0.63
1451709_at	Oprm1	opioid receptor, mu 1	1.64	0.614	-3.15	0.031	1.35	0.447	2.85	0.016	0.67
1444334_at	---	---	1.2	0.654	1.07	0.825	1.04	0.808	-1.02	0.978	0.57
1455041_at	Omt2b	oocyte maturation, beta	1.72	0.031	1.02	0.971	-1.74	0.482	1	0.996	0.5
1416706_at	Rpe	ribulose-5-phosphate-3-epimerase	1.03	0.857	-1.17	0.378	1.43	0.274	1.11	0.771	0.6
1416880_at	Mcl1	myeloid cell leukemia sequence 1	1.03	0.888	1.27	0.046	1.02	0.843	-1.33	0.234	0.5
1451107_at	Tbc1d22a	TBC1 domain family, member 22a	1.25	0.442	-1.16	0.582	1.2	0.46	1.51	0.404	0.7
1416497_at	Pdia4	protein disulfide isomerase associated 4	1.24	0.24	1.16	0.259	-1.1	0.809	1.58	0.352	0.72
1424483_at	---	---	1.08	0.726	1.17	0.456	1.06	0.712	-1.05	0.814	0.57
1447584_s_at	Myct1	myc target 1	1.39	0.007	1.19	0.585	-1.37	0.06	1.25	0.497	0.62
1460231_at	Irf5	interferon regulatory factor 5	1.17	0.618	1.01	0.932	1.14	0.311	-2.02	0.176	0.32
1456103_at	Pml	promyelocytic leukemia	1.02	0.868	1.11	0.6	1.19	0.609	-1.11	0.646	0.55
1454809_at	Ncoa7	nuclear receptor coactivator 7	-1.11	0.561	1.28	0.228	1.14	0.206	1.8	0.193	0.78
1449157_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	-1.02	0.924	1.3	0.24	1.04	0.887	1.03	0.861	0.59
1416758_at	Arhgap27	Rho GTPase activating protein 27	1.24	0.479	1.05	0.595	1.03	0.702	-1.54	0.095	0.44
1422202_at	Thrb	thyroid hormone receptor beta	-1.32	0.38	1.11	0.792	1.44	0.335	1.4	0.377	0.66
1455787_x_at	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	-1.22	0.356	1.1	0.659	1.39	0.138	2.9	0.097	1.04
1428623_at	Plxna1	plexin A1	-1.1	0.528	1.14	0.417	1.26	0.171	1.36	0.309	0.67
1444789_at	1700120C14Rik	RIKEN cDNA 1700120C14 gene	-1.55	0.005	1.54	0.328	1.13	0.047	1.06	0.771	0.55
1450233_a_at	Rshl1	radial spokehead-like 1	1.12	0.775	1.4	0.191	-1.25	0.624	1.57	0.457	0.71
1449405_at	Tns1	tensin 1	1.29	0.167	-1.01	0.977	1.03	0.753	1.52	0.11	0.71
1438705_at	AI465270	expressed sequence AI465270	1.29	0.367	-1.01	0.957	1.04	0.763	1.32	0.083	0.66
1459641_at	Psmb2	Proteasome (prosome, macropain) subunit, beta type 2	1.64	0.41	1.01	0.976	-1.5	0.077	1.47	0.207	0.66
1437218_at	Fn1	Fibronectin 1	1.03	0.92	1.46	0.156	-1.21	0.646	1.37	0.571	0.66
1438138_a_at	Pex6	peroxisomal biogenesis factor 6	1.23	0.37	-1.06	0.763	1.15	0.774	1.2	0.259	0.63
1418409_at	Jrk	jerky	1.17	0.282	1.12	0.773	1.02	0.786	-1.04	0.748	0.57
1448417_at	Ninj1	ninjurin 1	-1.02	0.934	1.2	0.289	1.14	0.384	1.04	0.888	0.59
1416036_at	Fkbp1a	FK506 binding protein 1a	1.03	0.94	1.1	0.661	1.19	0.501	-1.16	0.416	0.54
1432988_at	2610040L17Rik	RIKEN cDNA 2610040L17 gene	1.16	0.529	-1.31	0.498	1.39	0.513	1.51	0.171	0.69
1444692_at	AI316844	EST AI316844	1.33	0.531	1.07	0.873	-1.09	0.757	1.4	0.46	0.68
1450851_at	Wdr1	WD repeat domain 1	1.01	0.929	1.3	0.107	1.01	0.981	-1.24	0.48	0.52
1449464_at	Kcnq1	potassium voltage-gated channel, subfamily Q, member 1	1.18	0.039	1.12	0.533	1.02	0.872	-1.13	0.765	0.55
1458370_at	Bmp2k	BMP2 inducible kinase	-1.05	0.456	1.31	0.056	1.06	0.611	1.02	0.601	0.58
1451522_s_at	Lrch4	leucine-rich repeats and calponin homology (CH) domain containing 4	1.09	0.746	-1.13	0.528	1.34	0.226	1.22	0.53	0.63
1416424_at	M6prbp1	mannose-6-phosphate receptor binding protein 1	1.17	0.384	1.1	0.46	1.05	0.501	-1.02	0.761	0.57
1458250_at	1200015N20Rik	RIKEN cDNA 1200015N20 gene	1.38	0.497	-1.11	0.854	1.04	0.949	1.44	0.44	0.69
1432525_at	1700001C02Rik	RIKEN cDNA 1700001C02 gene	1.36	0.188	1.14	0.785	-1.23	0.504	1.36	0.265	0.66
1427504_s_at	Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	1.19	0.063	-1.09	0.654	1.21	0.032	1.61	0.036	0.73
1460186_at	Tm9sf3	transmembrane 9 superfamily member 3	1.12	0.367	1.11	0.472	1.1	0.57	-1.08	0.743	0.56
1446268_at	Pscd3	Pleckstrin homology, Sec7 and coiled-coil domains 3	1.07	0.781	1.28	0.089	-1.04	0.95	1.19	0.154	0.63
1424370_s_at	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	-1.02	0.902	1.07	0.146	1.27	0.211	1.98	0.203	0.82
1445475_at	Pak6	p21 (CDKN1A)-activated kinase 6	1.19	0.554	-1.68	0.076	1.54	0.053	1.21	0.587	0.56
1416384_a_at	Cope	coatomer protein complex, subunit epsilon	1.03	0.68	1.01	0.885	1.27	0.038	-1.02	0.895	0.58
1431034_at	Gpr125	G protein-coupled receptor 125	1.74	0.385	-1.95	0.241	1.07	0.904	1.08	0.894	0.49
1435244_at	Vav2	Vav2 oncogene	1.02	0.796	1.1	0.361	1.21	0.284	-1.48	0.225	0.46
1451591_a_at	Efnb1	ephrin B1	1.2	0.604	1.14	0.477	-1.02	0.934	1.3	0.02	0.65
1421793_at	Fgf11	fibroblast growth factor 11	1.02	0.951	-1.24	0.316	1.5	0.44	2.51	0.168	0.95
1460285_at	Itga9	integrin alpha 9	1.26	0.143	1.24	0.209	-1.21	0.311	1.14	0.306	0.61

1419194_s_at	Gmfg	glia maturation factor, gamma	1.04	0.784	1.28	0.073	1	0.99	-2.36	0.089	0.24
1427468_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	-1.06	0.395	1.15	0.272	1.22	0.32	1.02	0.929	0.59
1425572_a_at	Ddef1	development and differentiation enhancing	-1.18	0.032	1.05	0.671	1.42	0.046	1.86	0.11	0.79
1430947_at	4930549C15Rik	RIKEN cDNA 4930549C15 gene	-1.1	0.907	1.4	0.419	1.01	0.981	1.54	0.354	0.71
1456243_x_at	Mcl1	myeloid cell leukemia sequence 1	1.03	0.824	1.26	0.067	1.03	0.678	-1.44	0.091	0.47
1457076_at	Gm693 /// LOC670(	gene model 693, (NCBI) /// hypothetical protein LOC670665	1.23	0.727	-1.27	0.705	1.31	0.049	1.18	0.83	0.61
1416222_at	Nsdhl	NAD(P) dependent steroid dehydrogenase-like	-1.17	0.512	1.43	0.196	1.04	0.705	1.2	0.207	0.62
1453849_s_at	Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	1.05	0.501	-1	0.984	1.28	0.091	1.46	0.186	0.69
1442468_at	---	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430088L	-2.07	0.517	1.69	0.068	1.15	0.801	1.33	0.2	0.53
1415673_at	Psph	phosphoserine phosphatase	1.11	0.326	1.12	0.445	1.09	0.422	-1.28	0.004	0.51
1424145_at	Prr3	proline-rich polypeptide 3	1.06	0.677	1.08	0.526	1.18	0.29	-1.34	0.314	0.49
1422138_at	Plau	plasminogen activator, urokinase	1.33	0.405	1.09	0.787	-1.11	0.781	1.55	0.388	0.71
1437585_x_at	Zfp161	zinc finger protein 161	1.29	0.194	1.16	0.552	-1.14	0.518	1.14	0.38	0.61
1434820_s_at	Pkig	protein kinase inhibitor, gamma	1.02	0.811	1.03	0.711	1.28	0.352	-1.22	0.256	0.52
1436723_at	Cenpi	centromere protein I	1.02	0.959	-1.49	0.507	1.63	0.136	4.48	0.209	1.41
1421030_at	Zfp64	zinc finger protein 64	1.4	0.101	-1.17	0.022	1.06	0.415	1.04	0.715	0.58
1425154_a_at	Csf1	colony stimulating factor 1 (macrophage)	1.22	0.654	-1.47	0.354	1.42	0.074	1.25	0.153	0.6
1448325_at	Myd116	myeloid differentiation primary response gene 116	-1.05	0.551	1.36	0.277	1.01	0.927	3.98	0.136	1.32
1452783_at	Fndc3b	fibronectin type III domain containing 3B	1.08	0.177	1.46	0.328	-1.29	0.032	1.24	0.34	0.62
1431840_at	Dennd1c	DENN/MADD domain containing 1C	1.04	0.958	1.27	0.618	1.02	0.953	-1.29	0.512	0.51
1435949_at	Zc3h3	zinc finger CCCH type containing 3	-1.6	0.201	1.64	0.242	1.06	0.825	1.11	0.518	0.55
1433497_at	Aqr	aquarius	1.24	0.286	1.02	0.894	1.06	0.71	-1.01	0.809	0.58
1445508_at	---	---	-1.07	0.935	1.3	0.559	1.09	0.772	1.06	0.906	0.59
1415999_at	Hey1	hairy/enhancer-of-split related with YRPW motif 1	-1.66	0.44	1.68	0.168	1.04	0.874	1.09	0.836	0.54
1449669_at	Rabif	RAB interacting factor	-1.14	0.834	1.01	0.981	1.44	0.223	1.03	0.922	0.58
1449699_s_at	C330027C09Rik	RIKEN cDNA C330027C09 gene	1.15	0.84	-1.04	0.939	1.21	0.249	2.84	0.192	1.04
1456393_at	2310002J21Rik	RIKEN cDNA 2310002J21 gene	1.03	0.879	1.03	0.845	1.27	0.323	-1.84	0.042	0.37
1418808_at	Rdh5	retinol dehydrogenase 5	1.1	0.665	1.05	0.417	1.17	0.341	-1.85	0.012	0.37
1444844_at	Fabp3	fatty acid binding protein 3, muscle and heart	-1.19	0.406	1.23	0.258	1.25	0.417	1.61	0.17	0.73
1451418_a_at	Spsb4	splA/ryanodine receptor domain and SOCS box containing 4	-1.01	0.96	1.1	0.719	1.24	0.706	1.7	0.515	0.75
1440154_at	Pbx3	Pre B-cell leukemia transcription factor 3	-2.86	0.142	1.61	0.242	1.37	0.382	1.28	0.45	0.35
1431229_at	Ipw	imprinted gene in the Prader-Willi syndrome region	1.16	0.806	-1.14	0.409	1.29	0.576	1.7	0.499	0.75
1418478_at	Lmo1	LIM domain only 1	1.15	0.494	1.22	0.709	-1.04	0.921	1.04	0.903	0.59
1439324_at	D230004J03Rik ///	RIKEN cDNA D230004J03 gene /// RIKEN cDNA B430006D22 gene	1.11	0.547	1.04	0.902	1.17	0.774	-1.28	0.46	0.51
1453440_at	4921539E11Rik	RIKEN cDNA 4921539E11 gene	1.64	0.361	1.17	0.43	-1.93	0.434	1.96	0.087	0.71
1451350_a_at	Leprot	leptin receptor overlapping transcript	1.13	0.474	1.23	0.152	-1.04	0.791	1.26	0.018	0.65
1427423_at	2810410C14Rik	RIKEN cDNA 2810410C14 gene	1.07	0.793	1.07	0.774	1.19	0.381	-5.63	0.03	-0.58
1438112_at	9430021M05Rik	RIKEN cDNA 9430021M05 gene	-1.1	0.588	1.28	0.402	1.14	0.507	1.77	0.384	0.77
1454906_at	Rarb	retinoic acid receptor, beta	1.08	0.703	1.16	0.329	1.08	0.731	-1.01	0.984	0.58
1424845_a_at	Cep68	centrosomal protein 68	1.18	0.617	1.04	0.837	1.11	0.811	-1.76	0.275	0.39
1436839_at	---	---	1.04	0.906	1.34	0.027	-1.06	0.722	2.15	0.177	0.87
1448647_at	Man2a1	mannosidase 2, alpha 1	1.05	0.752	1.24	0.078	1.04	0.744	-1.19	0.59	0.53
1430914_at	5330426L24Rik	RIKEN cDNA 5330426L24 gene	1.01	0.984	1.15	0.671	1.16	0.64	-1.43	0.367	0.47
1438910_a_at	Stom	stomatin	1.18	0.208	-1.06	0.554	1.2	0.106	3.32	0.137	1.16
1448849_at	Mrpl40	mitochondrial ribosomal protein L40	1.26	0.431	1.07	0.547	-1.01	0.968	1.43	0.443	0.69
1452524_a_at	Elavl3	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	1.04	0.882	-1.03	0.925	1.32	0.116	2.12	0.026	0.86
1447849_s_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	1.05	0.72	1.2	0.125	1.08	0.784	-1.01	0.979	0.58
1421698_a_at	Col19a1	procollagen, type XIX, alpha 1	1.37	0.51	-1.16	0.789	1.1	0.784	1.6	0.213	0.73
1424788_at	BC021438	cDNA sequence BC021438	1.1	0.36	1.04	0.701	1.18	0.092	-1.36	0.046	0.49
1428610_at	Atg7	autophagy-related 7 (yeast)	1.25	0.611	1.06	0.889	1.02	0.916	-1.42	0.38	0.48
1422645_at	Hfe	hemochromatosis	1.07	0.595	1.18	0.017	1.08	0.366	-1.35	0.083	0.5
1435026_at	Spock2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	1.31	0.405	-1.07	0.911	1.08	0.796	1.04	0.956	0.59
1449022_at	Nes	nestin	1.45	0.273	1.07	0.808	-1.25	0.547	1.05	0.777	0.58

1430860_at	4833422M21Rik	RIKEN cDNA 4833422M21 gene	-1.95	0.503	1.53	0.428	1.29	0.671	1.96	0.122	0.71
1430925_at	4930556L07Rik	RIKEN cDNA 4930556L07 gene	-1.16	0.879	1.31	0.392	1.15	0.681	1.03	0.948	0.59
1428049_a_at	Nudt16l1	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	1.06	0.863	1.13	0.409	1.14	0.4	-1.36	0.458	0.49
1439256_x_at	Gpr137b /// LOC66	G protein-coupled receptor 137B /// similar to transmembrane 7 superfamily mem	1.04	0.884	1.14	0.739	1.15	0.414	-1.25	0.648	0.52
1452154_at	Iars	isoleucine-tRNA synthetase	-1.63	0.046	1.17	0.27	1.54	0.09	1.3	0.386	0.6
1449600_at	Gm1683	gene model 1683, (NCBI)	1.12	0.84	-1.32	0.599	1.45	0.518	1.67	0.235	0.73
1444977_at	---	---	-1.28	0.802	1.26	0.67	1.29	0.408	2.53	0.004	0.95
1421679_a_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	-1.05	0.933	1.16	0.699	1.21	0.653	1.17	0.689	0.63
1428370_at	1500011B03Rik	RIKEN cDNA 1500011B03 gene	-1.33	0.411	1.43	0.134	1.15	0.215	1.05	0.731	0.57
1453977_at	Exoc4	exocyst complex component 4	1.2	0.472	1	1	1.13	0.638	-1.05	0.909	0.57
1429862_at	Pla2g4e	phospholipase A2, group IVE	-1.24	0.61	1.48	0.279	1.04	0.891	1.42	0.405	0.68
1439129_at	1110060D06Rik ///	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	1.15	0.664	-1.3	0.505	1.41	0.404	1.56	0.325	0.71
1443493_at	Dhx37	DEAH (Asp-Glu-Ala-His) box polypeptide 37	1.22	0.239	1.15	0.682	-1.04	0.861	1.26	0.093	0.65
1443280_at	---	---	-1.24	0.792	1.08	0.9	1.45	0.557	3.05	0.037	1.08
1445413_at	Bmpr1a	Bone morphogenetic protein receptor, type 1A	1.09	0.934	1.65	0.317	-1.7	0.117	1.48	0.295	0.63
1421683_at	Tcte3	t-complex-associated testis expressed 3	-1.02	0.948	1.08	0.782	1.27	0.714	2.69	0.128	1.01
1447610_at	Tmem34	transmembrane protein 34	1.13	0.814	-1.38	0.103	1.48	0.219	1.3	0.403	0.63
1433965_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	1.28	0.33	1.39	0.175	-1.53	0.028	1.2	0.553	0.59
1453041_at	Trp53i5	Trp53 inducible protein 5	1.09	0.722	1.31	0.568	-1.07	0.899	3.22	0.002	1.14
1429192_at	Ski	Sloan-Kettering viral oncogene homolog	1.08	0.338	1.07	0.414	1.18	0.383	-1.12	0.511	0.55
1447935_at	Fancm	Fanconi anemia, complementation group M	1.24	0.184	1.07	0.791	1.03	0.917	-1.04	0.925	0.57
1419711_at	Cd7	CD7 antigen	1.2	0.162	1.12	0.829	1.01	0.954	-1.47	0.214	0.46
1444141_at	Snx13	sorting nexin 13	1.22	0.625	1.09	0.8	1.02	0.95	-1.17	0.554	0.54
1438835_a_at	Eftud2	elongation factor Tu GTP binding domain containing 2	-1.12	0.181	1.07	0.672	1.37	0.269	1.25	0.32	0.64
1450161_at	Ikbkg	inhibitor of kappaB kinase gamma	1.09	0.79	1.01	0.972	1.23	0.653	-1.07	0.808	0.57
1442889_at	---	Transcribed locus	1.07	0.924	1.54	0.573	-1.39	0.546	1.5	0.438	0.68
1440833_at	Cdc2l5	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	1.2	0.793	1.11	0.809	1.02	0.906	-1.78	0.181	0.39
1453893_at	4933412O06Rik	RIKEN cDNA 4933412O06 gene	1.07	0.729	-1.14	0.836	1.38	0.271	2.72	0.018	1.01
1441546_at	LOC624524	hypothetical LOC624524	1.29	0.455	-1.17	0.38	1.19	0.463	1.18	0.579	0.62
1459603_at	C330008K14Rik	RIKEN cDNA C330008K14 gene	1.5	0.065	1.12	0.887	-1.41	0.117	1	0.998	0.55
1455404_at	Jph2	junctophilin 2	-1.63	0.015	1.13	0.84	1.58	0.373	2.47	0.014	0.89
1445911_at	Chic2	Cysteine-rich hydrophobic domain 2	-1.01	0.889	1.03	0.909	1.31	0.154	1.05	0.879	0.6
1415869_a_at	Trim28	tripartite motif protein 28	1	0.963	-1.08	0.439	1.4	0.096	1.16	0.146	0.62
1432205_a_at	C130038G02Rik	RIKEN cDNA C130038G02 gene	-2.03	0.16	1.38	0.568	1.46	0.017	1.3	0.366	0.53
1421828_at	Kpna3	karyopherin (importin) alpha 3	1.14	0.556	-1.02	0.923	1.22	0.071	1.4	0.442	0.68
1423721_at	Tpm1	tropomyosin 1, alpha	1.29	0.073	1.2	0.312	-1.19	0.287	1.09	0.644	0.6
1430067_at	5430401F13Rik /// I	RIKEN cDNA 5430401F13 gene /// hypothetical LOC625758	1.05	0.939	1.68	0.404	-1.65	0.295	1.19	0.614	0.57
1438561_x_at	4930538D17Rik	RIKEN cDNA 4930538D17 gene	-1.14	0.157	1.21	0.063	1.24	0.153	1.64	0.306	0.74
1440206_at	A930024E05Rik	RIKEN cDNA A930024E05 gene	1.21	0.818	1.08	0.893	1.05	0.869	-2.36	0.085	0.24
1446086_s_at	Gli2	GLI-Kruppel family member GLI2	1.14	0.569	1.08	0.779	1.12	0.617	-1.59	0.257	0.44
1448648_at	9130005N14Rik	RIKEN cDNA 9130005N14 gene	1.19	0.406	1.29	0.209	-1.17	0.526	1.12	0.133	0.61
1427768_s_at	Myl3	myosin, light polypeptide 3	-1.01	0.982	1.13	0.79	1.22	0.754	1.03	0.882	0.59
1451756_at	Flt1	FMS-like tyrosine kinase 1	1.23	0.402	1.37	0.357	-1.37	0.032	1.02	0.924	0.56
1431837_at	1200007C13Rik	RIKEN cDNA 1200007C13 gene	1.15	0.112	1.31	0.3	-1.14	0.673	1.08	0.784	0.6
1425974_a_at	Trim25	tripartite motif protein 25	1.25	0.248	1.05	0.587	1.03	0.61	-1.25	0.376	0.52
1452063_at	2410081M15Rik	RIKEN cDNA 2410081M15 gene	1.21	0.596	1.35	0.078	-1.3	0.092	1.44	0.054	0.68
1429207_at	5730408K05Rik	RIKEN cDNA 5730408K05 gene	1.25	0.636	1.18	0.821	-1.1	0.772	1.06	0.775	0.6
1453055_at	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	1.22	0.268	1.23	0.162	-1.14	0.601	1.14	0.779	0.62
1417432_a_at	Gnb1	guanine nucleotide binding protein, beta 1	1.1	0.417	1.09	0.096	1.15	0.205	-1.12	0.188	0.55
1427166_a_at	Ryk /// Spg7	receptor-like tyrosine kinase /// spastic paraplegia 7 homolog (human)	1.08	0.453	-1.03	0.879	1.29	0.147	1.14	0.539	0.62
1417790_at	Dok1	docking protein 1	1.18	0.591	-1.02	0.942	1.18	0.416	1.11	0.598	0.61
1448272_at	Btg2	B-cell translocation gene 2, anti-proliferative	-1.43	0.18	1.63	0.283	1.01	0.973	1.02	0.845	0.56
1448169_at	Krt18	keratin 18	1.04	0.859	1.45	0.207	-1.18	0.028	2.65	0.111	0.99

1425412_at	Cias1	cold autoinflammatory syndrome 1 homolog (human)	-1.11	0.794	1.4	0.285	1.03	0.918	1.05	0.884	0.59
1422768_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	-1.07	0.762	1.16	0.353	1.25	0.2	1.15	0.628	0.62
1460313_at	Olfr2	olfactory receptor 2	-1.49	0.309	1.07	0.838	1.59	0.155	1.36	0.694	0.63
1436930_x_at	Hmbs /// LOC62381	hydroxymethylbilane synthase /// similar to hydroxymethylbilane synthase /// simil	-1.33	0.49	1.12	0.199	1.47	0.269	5.54	0.138	1.7
1435334_at	Ttc7	tetratricopeptide repeat domain 7	1.08	0.728	1.06	0.597	1.2	0.007	-1.22	0.13	0.53
1456967_at	Trim66	tripartite motif-containing 66	-1.61	0.321	1	0.995	1.71	0.29	1.37	0.374	0.62
1420356_at	Ninj2	ninjurin 2	-2.18	0.151	1.79	0.018	1.08	0.827	1.48	0.645	0.55
1435621_at	Mlstd1	male sterility domain containing 1	1.27	0.397	1.27	0.595	-1.25	0.483	1.89	0.274	0.79
1426422_at	Cc2d1a	coiled-coil and C2 domain containing 1A	1.06	0.298	1.06	0.374	1.22	0.407	-1.35	0.336	0.5
1459908_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.02	0.976	1.36	0.345	-1.04	0.744	2.19	0.157	0.88
1457058_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.4	0.213	1.23	0.515	-1.42	0.143	1.21	0.391	0.61
1443980_at	Agrin	agrin	1.33	0.618	1.22	0.717	-1.27	0.502	1.16	0.766	0.61
1417252_at	Nt5c	5',3'-nucleotidase, cytosolic	1.15	0.25	1.18	0.082	1.01	0.96	-1.45	0.223	0.47
1448060_at	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.1	0.825	1.3	0.261	1.13	0.666	1.09	0.697	0.6
1421795_s_at	Klrc2 /// Klrc3	killer cell lectin-like receptor subfamily C, member 2 /// killer cell lectin-like recepto	1.19	0.543	-1.07	0.905	1.21	0.291	1.1	0.682	0.61
1424351_at	Wfdc2	WAP four-disulfide core domain 2	1.34	0.092	1.26	0.439	-1.35	0.005	1.4	0.486	0.66
1450768_at	Dlgh1	discs, large homolog 1 (Drosophila)	-1.02	0.9	1.05	0.734	1.32	0.261	1.08	0.31	0.6
1421068_at	Phf2	PHD finger protein 2	-1.47	0.514	1.31	0.645	1.34	0.591	2.07	0.107	0.81
1420828_s_at	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	1.03	0.812	1.05	0.772	1.25	0.331	-1.12	0.62	0.56
1420563_at	Gria3	glutamate receptor, ionotropic, AMPA3 (alpha 3)	1.07	0.468	-1.28	0.744	1.5	0.108	1	0.999	0.57
1425012_at	Gng5 /// LOC66889	guanine nucleotide binding protein (G protein), gamma 5 subunit /// hypothetical p	1.51	0.001	-1.37	0.371	1.1	0.762	1.48	0.179	0.68
1457326_at	LOC545191 /// LOC	similar to zinc finger protein 616 /// similar to zinc finger protein 420	1.6	0.467	-1.41	0.486	1.03	0.907	1.06	0.902	0.57
1416779_at	Sdpr	serum deprivation response	1.31	0.345	1.32	0.234	-1.41	0.013	1.2	0.641	0.61
1440280_at	Ccdc45	coiled-coil domain containing 45	1.03	0.803	1.32	0.488	-1.01	0.963	1.2	0.39	0.64
1421846_at	Wsb2	WD repeat and SOCS box-containing 2	1.12	0.053	1.04	0.546	1.18	0.272	-1.02	0.912	0.58
1417168_a_at	Usp2	ubiquitin specific peptidase 2	1.12	0.825	-1.48	0.656	1.55	0.161	1.33	0.342	0.63
1443835_x_at	1110014K08Rik ///	RIKEN cDNA 1110014K08 gene /// hypothetical protein LOC664786 /// hypothetic	-1.17	0.124	1.24	0.233	1.25	0.423	1.23	0.295	0.64
1427039_at	Epn1	epsin 1	-1.01	0.98	1.09	0.138	1.25	0.352	1.46	0.157	0.7
1457475_at	C80993	expressed sequence C80993	1	0.997	1.35	0.571	-1.01	0.973	1.02	0.962	0.59
1429287_a_at	Prl	prolactin	1.17	0.769	1.38	0.44	-1.27	0.607	1.13	0.776	0.6
1451936_a_at	Txnrd2	thioredoxin reductase 2	1.03	0.875	-1.11	0.582	1.41	0.129	2.85	0.233	1.05
1442883_s_at	D10Bwg1364e	DNA segment, Chr 10, Brigham & Women's Genetics 1364 expressed	1.17	0.558	1.11	0.216	1.06	0.656	-1.44	0.151	0.48
1453183_at	1110034A24Rik	RIKEN cDNA 1110034A24 gene	-1.32	0.129	1	0.986	1.58	0.043	1.85	0.275	0.78
1451341_s_at	1700003N22Rik ///	RIKEN cDNA 1700003N22 gene /// expressed sequence AI840826	1.12	0.504	1.18	0.523	1.04	0.701	-1.17	0.253	0.54
1460097_at	Gria4	Glutamate receptor, ionotropic, AMPA4 (alpha 4)	1.13	0.421	1.74	0.41	-2.1	0.154	2.07	0.008	0.71
1430212_at	Zfp712	zinc finger protein 712	1.04	0.904	1.12	0.752	1.18	0.322	-1.75	0.036	0.4
1427027_a_at	Gtf3a	general transcription factor III A	1.17	0.466	-1.04	0.754	1.21	0.239	1	0.964	0.59
1419372_at	Gosr2	golgi SNAP receptor complex member 2	1.16	0.092	-1.1	0.723	1.27	0.604	1.02	0.975	0.59
1437834_s_at	Pacsin3	protein kinase C and casein kinase substrate in neurons 3	-1.05	0.706	1.36	0.114	1.03	0.884	1.41	0.234	0.69
1420073_s_at	---	---	1.35	0.472	1.13	0.635	-1.16	0.591	1.45	0.275	0.69
1446004_at	Atp7b	ATPase, Cu++ transporting, beta polypeptide	-1.14	0.615	1.35	0.095	1.11	0.443	1.78	0.325	0.78
1460053_at	Smyd4	SET and MYND domain containing 4	1.05	0.578	1.02	0.936	1.28	0.401	-1.14	0.529	0.55
1419782_at	AA517864	expressed sequence AA517864	1.05	0.879	1.03	0.786	1.27	0.425	-1.03	0.903	0.58
1434129_s_at	Lhfpl2	lipoma HMGIC fusion partner-like 2	-1.33	0.371	1.42	0.187	1.17	0.534	1.91	0.237	0.79
1453350_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	1.03	0.794	1.14	0.758	1.18	0.268	-1.43	0.194	0.48
1451670_at	1810048P08Rik	RIKEN cDNA 1810048P08 gene	1.41	0.466	-1.19	0.759	1.09	0.631	1.35	0.368	0.67
1439074_a_at	Son	Son cell proliferation protein	1.35	0.096	1.02	0.94	-1.03	0.881	1.24	0.199	0.65
1416563_at	Ctps	cytidine 5'-triphosphate synthase	1.41	0.16	-1.29	0.238	1.16	0.274	1.12	0.737	0.6
1425288_at	Samd11	sterile alpha motif domain containing 11	-1.6	0.257	1.48	0.615	1.25	0.654	6.69	0.218	1.95
1431755_a_at	Ccdc49	coiled-coil domain containing 49	-1.14	0.692	1.46	0.425	1.01	0.964	1.46	0.364	0.7
1452510_at	Pax7	paired box gene 7	1.41	0.243	-4.19	0.035	1.7	0.121	1.62	0.261	0.13
1436849_x_at	Gaa	glucosidase, alpha, acid	1.02	0.727	1	0.991	1.32	0.046	-1.1	0.639	0.56
1436433_at	BC049762	cDNA sequence BC049762	1.16	0.304	1.33	0.332	-1.16	0.778	1.43	0.446	0.69

1416757_at	Zwilch	Zwilch, kinetochore associated, homolog (Drosophila)	-1.03	0.768	1.08	0.758	1.29	0.198	3.89	0.182	1.31
1440591_at	---	---	1.23	0.794	1.07	0.727	1.05	0.81	-1.95	0.431	0.35
1448790_at	Sema6b	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-2.86	0.389	1.14	0.78	1.86	0.194	1.91	0.412	0.51
1429233_at	11-Sep	septin 11	-1.1	0.362	1.24	0.182	1.2	0.033	1.06	0.735	0.6
1424110_a_at	Nme1	expressed in non-metastatic cells 1, protein	-1.07	0.324	1.15	0.175	1.27	0.27	1.01	0.929	0.59
1455355_at	6030408C04Rik	RIKEN cDNA 6030408C04 gene	1.43	0.442	1.15	0.738	-1.3	0.306	2.4	0.174	0.92
1418542_s_at	Cenpo	centromere protein O	1.25	0.075	1.22	0.462	-1.14	0.255	1.27	0.192	0.65
1428660_s_at	Tor3a	torsin family 3, member A	1.17	0.332	1.08	0.545	1.09	0.586	-1.8	0.09	0.39
1435732_x_at	Atp6v0c	ATPase, H+ transporting, lysosomal V0 subunit C	-1.27	0.43	1.18	0.101	1.39	0.024	1.4	0.032	0.67
1436548_at	1810012P15Rik	RIKEN cDNA 1810012P15 gene	1.29	0.139	1.09	0.632	-1.03	0.867	1.04	0.703	0.6
1455496_at	Pfas	phosphoribosylformylglycinamidine synthase (FGAR amidotransferase)	-1.09	0.423	1	0.985	1.43	0.137	1.78	0.191	0.78
1437728_at	Alkbh5	alkB, alkylation repair homolog 5 (E. coli)	1.15	0.347	-1.02	0.813	1.22	0.395	1.38	0.2	0.68
1434755_at	Coro2b	coronin, actin binding protein, 2B	-1.56	0.145	1.61	0.024	1.1	0.682	1.74	0.454	0.72
1429199_s_at	Saal1	serum amyloid A-like 1	-1.03	0.753	1.13	0.291	1.25	0.057	1.13	0.58	0.62
1451024_at	Edg6	endothelial differentiation, G-protein-coupled receptor 6	1.16	0.634	1.09	0.654	1.1	0.66	-2.1	0.07	0.31
1418822_a_at	Arf6	ADP-ribosylation factor 6	1.02	0.781	1.16	0.359	1.17	0.312	-1.19	0.091	0.54
1415849_s_at	Stmn1	stathmin 1	1.13	0.386	1.42	0.163	-1.25	0.019	2	0.11	0.82
1457697_at	A330021E22Rik	RIKEN cDNA A330021E22 gene	1.08	0.846	-1.2	0.454	1.44	0.514	1.35	0.582	0.67
1420919_at	Sgk3	serum/glucocorticoid regulated kinase 3	-1.22	0.305	1.12	0.298	1.41	0.316	1.09	0.707	0.6
1460698_a_at	Sec11l3	Sec11-like 3 (S. cerevisiae)	1.1	0.331	1.11	0.445	1.15	0.484	-1	0.995	0.59
1449415_at	Chd1l	chromodomain helicase DNA binding protein 1-like	1.02	0.918	1.12	0.193	1.21	0.115	-1.06	0.505	0.57
1417819_at	Tor1b	torsin family 1, member B	1.29	0.192	-1.08	0.573	1.14	0.448	1.08	0.756	0.61
1430816_at	3110003A22Rik	RIKEN cDNA 3110003A22 gene	-1.11	0.288	1.43	0.064	1.02	0.867	1.51	0.294	0.71
1423694_at	Kctd10	potassium channel tetramerisation domain containing 10	1.12	0.182	1.06	0.605	1.16	0.342	-1.37	0.062	0.5
1449742_at	AA522020	expressed sequence AA522020	-2.13	0.428	1.02	0.985	1.86	0.4	1.23	0.486	0.5
1460642_at	Traf4	Tnf receptor associated factor 4	1.21	0.25	-1.17	0.694	1.29	0.457	1.47	0.494	0.7
1435910_at	Fads3	fatty acid desaturase 3	1.16	0.441	1.37	0.244	-1.22	0.22	1.97	0.108	0.82
1440581_at	A530088H08Rik	RIKEN cDNA A530088H08 gene	1.09	0.721	-2.23	0.323	1.81	0.192	1.92	0.126	0.65
1425803_a_at	Mbd2	methyl-CpG binding domain protein 2	1.03	0.826	-1.11	0.444	1.42	0.299	1.34	0.475	0.67
1450098_at	0610010D20Rik	RIKEN cDNA 0610010D20 gene	1.07	0.641	1.04	0.707	1.24	0.232	-1.14	0.729	0.55
1417646_a_at	Snx5	sorting nexin 5	1.01	0.949	1.17	0.072	1.17	0.423	-1.9	0.061	0.36
1442142_at	2700050L05Rik	RIKEN cDNA 2700050L05 gene	1.05	0.732	-1.15	0.776	1.43	0.246	1.36	0.423	0.67
1432907_at	1700126A01Rik	RIKEN cDNA 1700126A01 gene	1.17	0.778	-1.05	0.66	1.23	0.034	1.07	0.885	0.6
1438188_x_at	Slc25a29	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), mem	1.01	0.944	1.22	0.082	1.12	0.396	-1.2	0.018	0.54
1424345_s_at	Ube2m	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast)	1.23	0.518	-1.01	0.939	1.13	0.549	1.53	0.115	0.72
1423088_at	Tmod3	tropomodulin 3	1.18	0.412	1.18	0.18	1	0.995	-1.51	0.182	0.46
1444831_at	Sdccag8	Serologically defined colon cancer antigen 8	-2.22	0.053	1.84	0.52	1.06	0.919	2.52	0.08	0.8
1424905_a_at	Slc39a11	solute carrier family 39 (metal ion transporter), member 11	-1	0.967	1	0.999	1.36	0.021	1.22	0.087	0.64
1423391_at	Git2	G protein-coupled receptor kinase-interactor 2	1.02	0.919	1.12	0.192	1.21	0.108	-1.52	0.064	0.46
1454099_at	4930593A02Rik	RIKEN cDNA 4930593A02 gene	1.12	0.674	1.18	0.451	1.05	0.864	-1.8	0.549	0.39
1454757_s_at	D12Ertd647e	DNA segment, Chr 12, ERATO Doi 647, expressed	1.1	0.239	1.2	0.019	1.05	0.813	-1.07	0.762	0.57
1448277_at	Pold2	polymerase (DNA directed), delta 2, regulatory subunit	1.03	0.822	-1.08	0.629	1.4	0.085	1.4	0.126	0.69
1454034_a_at	Usp21	ubiquitin specific peptidase 21	1.08	0.324	-1.01	0.945	1.28	0.16	1.23	0.275	0.64
1440288_at	Ptchd2	patched domain containing 2	1.49	0.398	-1.19	0.776	1.03	0.975	1.01	0.989	0.58
1446136_at	---	---	1.07	0.922	1.37	0.612	-1.1	0.736	1.08	0.78	0.61
1448973_at	Sult1d1	sulfotransferase family 1D, member 1	1.1	0.447	-1.18	0.055	1.41	0.507	1.32	0.703	0.66
1432498_at	1700020C07Rik	RIKEN cDNA 1700020C07 gene	1.25	0.432	1.08	0.876	1.02	0.925	-2.46	0.112	0.22
1420157_s_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	1.07	0.442	-1.03	0.595	1.32	0.064	1.11	0.438	0.61
1458684_at	Ss18	synovial sarcoma translocation, Chromosome 18	1.24	0.459	1.33	0.125	-1.27	0.331	1.01	0.976	0.58
1418962_at	Necap2	NECAP endocytosis associated 2	-1.06	0.765	1.33	0.125	1.08	0.625	1.51	0.117	0.72
1442177_at	Slc6a5 /// LOC6773	solute carrier family 6 (neurotransmitter transporter, glycine), member 5 /// similar	-1.17	0.694	1.42	0.487	1.08	0.86	1.01	0.989	0.58
1447521_x_at	D15Wsu169e	DNA segment, Chr 15, Wayne State University 169, expressed	-1.12	0.662	1.19	0.418	1.27	0.369	1.24	0.58	0.65
1420219_at	4930461P20Rik	RIKEN cDNA 4930461P20 gene	1.23	0.751	1.01	0.979	1.11	0.67	-1.95	0.369	0.35

1429173_at	Dnase1l1	deoxyribonuclease 1-like 1	1.04	0.697	1.42	0.291	-1.12	0.268	1.3	0.425	0.66
1417796_at	Gps2	G protein pathway suppressor 2	1.14	0.523	-1.06	0.707	1.27	0.123	1.2	0.608	0.64
1446233_at	Adarb2	Adenosine deaminase, RNA-specific, B2	1.32	0.542	1.06	0.928	-1.03	0.962	1.19	0.531	0.64
1452921_at	B130050I23Rik	RIKEN cDNA B130050I23 gene	1.09	0.733	1.15	0.132	1.12	0.385	-1.11	0.266	0.56
1430278_a_at	Dqx1	DEAQ RNA-dependent ATPase	1.3	0.746	1.01	0.982	1.05	0.881	-1.07	0.898	0.57
1425786_a_at	Hsf4	heat shock transcription factor 4	-1.99	0.096	1.73	0.246	1.12	0.271	1.58	0.381	0.61
1423303_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	1.09	0.293	-1.2	0.03	1.44	0.011	2.01	0.197	0.83
1448728_a_at	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	-1.08	0.203	1.42	0.244	1	0.984	1.1	0.584	0.61
1451344_at	Tmem119	transmembrane protein 119	1.1	0.154	1.15	0.786	1.1	0.744	-1.29	0.643	0.52
1420708_at	Traip	TRAF-interacting protein	1.25	0.328	1.67	0.416	-2.31	0.22	2.89	0.245	0.88
1421039_at	Mip	major intrinsic protein of eye lens fiber	-1.08	0.449	1.23	0.353	1.19	0.544	1.25	0.125	0.65
1448048_at	BC016495	cDNA sequence BC016495	1.26	0.088	1.36	0.42	-1.36	0.208	1	0.996	0.57
1443179_at	Csmd1	CUB and Sushi multiple domains 1	1.33	0.292	1.01	0.985	1.01	0.966	-1.85	0.173	0.38
1460252_s_at	Zfp105	zinc finger protein 105	1.08	0.533	1.09	0.822	1.19	0.194	-1.13	0.009	0.56
1450038_s_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	1.35	0.238	-1.17	0.585	1.15	0.706	1.65	0.077	0.75
1418169_at	Zcchc14	zinc finger, CCHC domain containing 14	1.15	0.542	-1.14	0.475	1.32	0.415	1.14	0.55	0.62
1451821_a_at	Sp100	nuclear antigen Sp100	1.19	0.32	1.08	0.725	1.09	0.715	-1.92	0.065	0.36
1426421_s_at	Rbm26	RNA binding motif protein 26	1.1	0.486	1.08	0.652	1.17	0.453	-1.35	0.091	0.5
1455890_x_at	Snrpn /// LOC5450(	small nuclear ribonucleoprotein N /// similar to small nuclear ribonucleoparticle-as	1.15	0.797	1.25	0.614	-1.05	0.874	1.28	0.381	0.66
1452839_at	Dph5	DPH5 homolog (S. cerevisiae)	1.19	0.418	1.14	0.226	1.04	0.797	-2	0.023	0.34
1456108_x_at	Zfp179	zinc finger protein 179	1.12	0.264	1.24	0.249	-1	0.961	1.45	0.04	0.7
1448766_at	Gjb1	gap junction membrane channel protein beta 1	1.16	0.766	-1.27	0.542	1.42	0.527	1.43	0.244	0.68
1421534_at	Dfna5h	deafness, autosomal dominant 5 homolog (human)	1.01	0.981	-1.28	0.321	1.57	0.345	1.21	0.497	0.63
1422133_at	Spn	sialophorin	-1.42	0.452	1.07	0.88	1.58	0.015	1.11	0.522	0.59
1453066_at	2510022D24Rik	RIKEN cDNA 2510022D24 gene	1.01	0.955	1.08	0.798	1.27	0.641	-1.06	0.87	0.58
1451609_at	Tspan33	tetraspanin 33	1.09	0.298	-2.61	0.165	1.89	0.318	5.35	0.177	1.43
1430739_at	4930471M09Rik	RIKEN cDNA 4930471M09 gene	-1.92	0.42	1.16	0.743	1.68	0.377	1.37	0.637	0.57
1453498_x_at	Steap3	STEAP family member 3	1.66	0.435	-1.57	0.443	1.06	0.855	3.58	0.086	1.18
1451112_s_at	Dap	death-associated protein	-1.02	0.87	1.17	0.288	1.21	0.085	1.27	0.039	0.66
1446625_at	Tmem100	transmembrane protein 100	1.08	0.897	1.65	0.215	-1.58	0.1	1	0.995	0.54
1435263_at	Tmem106a	transmembrane protein 106A	-1.12	0.146	1.1	0.45	1.36	0.136	1.39	0.265	0.68
1425690_at	B3gat1	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P)	1.78	0.562	-2.23	0.021	1.13	0.785	1.43	0.433	0.53
1431014_at	Cecr2	cat eye syndrome chromosome region, candidate 2 homolog (human)	1.52	0.2	-1.36	0.218	1.1	0.764	1.19	0.522	0.61
1422744_at	Phka1	phosphorylase kinase alpha 1	1.13	0.345	1.23	0.423	1	0.974	-1.13	0.596	0.56
1417677_at	Opn3	opsin (encephalopsin)	1	0.993	1.34	0.304	1.01	0.969	-1.61	0.141	0.44
1419942_at	Srxn1	Sulfiredoxin 1 homolog (S. cerevisiae)	1.18	0.692	1.25	0.291	-1.07	0.907	1.58	0.251	0.73
1444404_at	D330010C22Rik	RIKEN cDNA 330010C22 gene	-1.7	0.347	1.14	0.554	1.63	0.074	1.2	0.54	0.57
1425726_x_at	Ppp2r5c	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	1.09	0.69	-1.11	0.76	1.37	0.317	1.22	0.548	0.64
1455643_s_at	Tsr1	TSR1, 20S rRNA accumulation, homolog (yeast)	1.15	0.357	1.04	0.723	1.17	0.65	-1.27	0.02	0.52
1454797_at	Tmem55b	transmembrane protein 55b	1.04	0.728	1.16	0.04	1.16	0.194	-1.21	0.216	0.54
1417428_at	Gng3	guanine nucleotide binding protein (G protein), gamma 3 subunit	1.12	0.7	-1	0.996	1.25	0.123	2.48	0.047	0.96
1451136_a_at	Eif2b2	eukaryotic translation initiation factor 2B, subunit 2 beta	-1.17	0.6	1.02	0.928	1.48	0.258	1.18	0.599	0.63
1440351_at	Birc4	Baculoviral IAP repeat-containing 4	1.63	0.165	1.15	0.435	-1.74	0.047	1.32	0.476	0.59
1455548_at	Dlgap4	discs, large homolog-associated protein 4 (Drosophila)	1.16	0.574	1.11	0.287	1.09	0.524	-1.24	0.303	0.53
1438642_at	---	---	1.11	0.874	1.45	0.127	-1.25	0.533	1.13	0.823	0.61
1416882_at	Rgs10	regulator of G-protein signalling 10	1.09	0.703	1.26	0.233	1.01	0.946	-1.18	0.25	0.55
1428821_at	Agpat2	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransf(	-1.11	0.659	1.15	0.372	1.31	0.453	1.09	0.598	0.61
1454637_at	Klhl8	kelch-like 8 (Drosophila)	1	0.963	1.19	0.81	1.17	0.603	-1.26	0.281	0.53
1435902_at	Nudt18	nudix (nucleoside diphosphate linked moiety X)-type motif 18	1.01	0.946	1.22	0.542	1.14	0.223	-1.31	0.368	0.51
1417572_at	Mpg	N-methylpurine-DNA glycosylase	1.3	0.036	1.09	0.521	-1.04	0.878	1.22	0.339	0.65
1419072_at	Gstm7	glutathione S-transferase, mu 7	1.28	0.326	1.01	0.959	1.08	0.662	-1.7	0.077	0.41
1424101_at	Hnrpl	heterogeneous nuclear ribonucleoprotein L	1.37	0.594	1.1	0.742	-1.13	0.754	1.66	0.108	0.75
1422975_at	Mme	membrane metallo endopeptidase	1.5	0.033	-2.42	0.045	1.46	0.419	1.06	0.848	0.4

1426065_a_at	Trib3	tribbles homolog 3 (Drosophila)	1.55	0.112	-1.45	0.326	1.12	0.603	1.7	0.3	0.73
1435602_at	---	Transcribed locus	1.09	0.773	-1.13	0.519	1.39	0.218	1.2	0.501	0.64
1424334_at	Tspan17	tetraspanin 17	1.08	0.523	1.1	0.68	1.18	0.33	-1.14	0.345	0.56
1434619_at	---	---	-1.01	0.961	1.04	0.608	1.33	0.053	1.2	0.12	0.64
1428743_at	Bri3bp	Bri3 binding protein	1.06	0.719	-1.3	0.079	1.54	0.205	1.11	0.688	0.6
1424015_at	Rab6ip1	Rab6 interacting protein 1	1.04	0.602	1.25	0.037	1.07	0.496	-1.05	0.8	0.58
1441746_at	---	---	1.07	0.938	1.73	0.336	-1.76	0.163	1.29	0.533	0.58
1423124_x_at	Rad54l	RAD54 like (S. cerevisiae)	1.24	0.421	1.13	0.555	-1.01	0.977	3.07	0.171	1.11
1435306_a_at	Kif11	kinesin family member 11	1.19	0.121	-1.18	0.637	1.33	0.199	4.04	0.209	1.34
1444523_s_at	Ube2v1 /// LOC545	ubiquitin-conjugating enzyme E2 variant 1 /// similar to ubiquitin-conjugating enzy	-1.02	0.856	1.07	0.233	1.32	0.04	1.4	0.331	0.69
1453255_at	Slc43a1	solute carrier family 43, member 1	-1.11	0.761	1.14	0.743	1.33	0.243	5.99	0.167	1.84
1423816_at	Cxx1b	CAAX box 1 homolog B (human)	-1.07	0.756	1.23	0.207	1.19	0.063	1.09	0.7	0.61
1431070_a_at	9130404D08Rik	RIKEN cDNA 9130404D08 gene	-1.43	0.298	1.54	0.481	1.13	0.784	1.3	0.22	0.63
1427382_a_at	Suv39h1	suppressor of variegation 3-9 homolog 1 (Drosophila)	1.3	0.235	-1.32	0.065	1.31	0.025	1.93	0.241	0.8
1422863_s_at	LOC669660	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ an	1.03	0.872	-1.05	0.82	1.39	0.457	1.2	0.613	0.64
1458358_at	Pank2	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	-1.12	0.535	1.23	0.315	1.25	0.145	1.08	0.707	0.61
1443499_at	A430075N02	hypothetical protein A430075N02	1.13	0.552	1.04	0.871	1.2	0.744	-2.71	0.115	0.16
1424793_a_at	Pbp2	phosphatidylethanolamine binding protein 2	1.09	0.752	-1.02	0.926	1.3	0.535	2.57	0.296	0.98
1435268_at	Gnaz	guanine nucleotide binding protein, alpha z subunit	1.11	0.86	1.32	0.602	-1.07	0.795	1.68	0.298	0.76
1439383_x_at	Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	1.51	0.334	-1.26	0.673	1.07	0.829	1.04	0.477	0.59
1435529_at	LOC667373 /// LOC	similar to interferon-induced protein with tetratricopeptide repeats 1 /// similar to ir	1.1	0.575	1.13	0.607	1.14	0.638	-1.27	0.663	0.52
1425408_a_at	2610034M16Rik	RIKEN cDNA 2610034M16 gene	1.75	0.241	-2.04	0.254	1.13	0.755	2.05	0.323	0.72
1457229_at	Gpr173	G-protein coupled receptor 173	1.16	0.873	1.19	0.786	1.02	0.929	-1.01	0.922	0.59
1422877_at	Pcdhb12	protocadherin beta 12	-1.46	0.658	1.26	0.44	1.42	0.216	1.44	0.23	0.66
1422127_at	Dhh	desert hedgehog	1.16	0.402	1.05	0.848	1.16	0.62	-1.07	0.665	0.57
1425844_a_at	Rngtt	RNA guanylyltransferase and 5'-phosphatase	-1.07	0.836	1.12	0.694	1.32	0.196	1.1	0.71	0.62
1426886_at	Cln5	ceroid-lipofuscinosis, neuronal 5	1.04	0.656	1.25	0.182	1.07	0.25	-1.08	0.015	0.57
1423628_s_at	Pcdhgb1 /// Pcdhgb	protocadherin gamma subfamily B, 1 /// protocadherin gamma subfamily B, 2 /// p	1.03	0.822	1.03	0.801	1.31	0.194	-1.01	0.931	0.59
1425129_a_at	Taldo1	transaldolase 1	-1.09	0.659	1.05	0.524	1.41	0.163	1.11	0.457	0.62
1416557_a_at	Eftud2	elongation factor Tu GTP binding domain containing 2	-1.07	0.285	1.06	0.648	1.38	0.086	1.24	0.197	0.65
1428271_at	Acbd4	acyl-Coenzyme A binding domain containing 4	1.01	0.954	-1.05	0.626	1.4	0.005	1.15	0.267	0.63
1430745_at	5930409G06Rik	RIKEN cDNA 5930409G06 gene	1.24	0.398	1.45	0.054	-1.48	0.43	1.34	0.426	0.64
1442549_at	Mbnl3	muscleblind-like 3 (Drosophila)	1.35	0.578	1.19	0.453	-1.2	0.186	1.86	0.315	0.8
1422477_at	Cables1 /// LOC635	Cdk5 and Abl enzyme substrate 1 /// similar to Cdk5 and Abl enzyme substrate 1	1.08	0.763	1.15	0.121	1.14	0.649	-1.05	0.464	0.58
1438709_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	1.47	0.261	1.27	0.182	-1.59	0.077	1.61	0.198	0.69
1430057_s_at	Lrrc57	leucine rich repeat containing 57	1.21	0.828	-1.11	0.681	1.26	0.245	1.72	0.169	0.77
1423283_at	Pitpna	phosphatidylinositol transfer protein, alpha	1.01	0.646	1.18	0.043	1.18	0.225	-1.32	0.357	0.51
1454421_at	4930423D22Rik	RIKEN cDNA 4930423D22 gene	1.05	0.833	1.78	0.461	-1.84	0.051	1.6	0.41	0.65
1452991_at	2810013C04Rik	RIKEN cDNA 2810013C04 gene	1.13	0.458	1.08	0.722	1.16	0.649	-1.59	0.007	0.45
1427117_at	Mtmr3	myotubularin related protein 3	1.11	0.2	-1.13	0.536	1.38	0.377	2.32	0.224	0.92
1426083_a_at	Btg1	B-cell translocation gene 1, anti-proliferative	1.09	0.192	1.02	0.793	1.27	0.368	-1.74	0.067	0.41
1459261_at	Sox5	SRY-box containing gene 5	1.15	0.844	1.08	0.902	1.14	0.485	-2.13	0.209	0.31
1437483_at	Zfp513	zinc finger protein 513	1.11	0.703	1.12	0.387	1.15	0.58	-1.54	0.098	0.46
1430378_at	2900011G08Rik	RIKEN cDNA 2900011G08 gene	1.43	0.536	-1.78	0.139	1.38	0.338	1.26	0.501	0.57
1417989_at	Tssk1	testis-specific serine kinase 1	1.53	0.523	-1.48	0.411	1.17	0.244	1.07	0.768	0.57
1416116_at	Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	1.12	0.483	1.24	0.204	1.01	0.966	-1.03	0.582	0.59
1456092_at	Kctd7	potassium channel tetramerisation domain containing 7	1.29	0.524	1.13	0.622	-1.04	0.81	2.9	0.195	1.07
1452180_at	Phf17	PHD finger protein 17	1.22	0.372	-1.06	0.757	1.22	0.649	1.25	0.671	0.66
1450022_at	Gtpbp1	GTP binding protein 1	1.39	0.631	-1.54	0.304	1.33	0.501	1.53	0.471	0.68
1424608_a_at	Bzw2	basic leucine zipper and W2 domains 2	1.22	0.324	-1.36	0.005	1.42	0.394	1.56	0.023	0.71
1436963_x_at	1810059G22Rik	RIKEN cDNA 1810059G22 gene	-1	0.989	1.01	0.91	1.36	0.283	1.07	0.748	0.61
1423722_at	Tmem49	transmembrane protein 49	-1.03	0.878	1.23	0.383	1.17	0.287	1.41	0.192	0.69
1419823_s_at	Ksr1	kinase suppressor of ras 1	-1.09	0.212	1.37	0.496	1.09	0.658	1.08	0.411	0.61

1419536_a_at	Rela	v-rel reticuloendotheliosis viral oncogene homolog A (avian)	1.07	0.516	1.08	0.244	1.23	0.197	-1.06	0.754	0.58
1452082_at	6430548M08Rik	RIKEN cDNA 6430548M08 gene	-1.28	0.09	1.37	0.607	1.22	0.569	1.1	0.693	0.6
1426030_a_at	Apeh	acylpeptide hydrolase	-1.03	0.849	1.04	0.641	1.36	0.09	1.92	0.201	0.82
1428695_at	2310014G06Rik	RIKEN cDNA 2310014G06 gene	1.06	0.746	1.2	0.192	1.11	0.576	-1.75	0.183	0.41
1441106_at	Zfand5	zinc finger, AN1-type domain 5	-3.84	0.044	1.01	0.968	2.1	0.018	1.09	0.504	0.09
1417278_a_at	Nkd1 /// LOC63437	naked cuticle 1 homolog (Drosophila) /// similar to naked cuticle 1 homolog /// sim	1.32	0.569	1.11	0.48	-1.06	0.639	1.33	0.173	0.68
1452067_at	Asahl	N-acylsphingosine amidohydrolase (acid ceramidase)-like	1.13	0.369	1.13	0.292	1.12	0.19	-1.17	0.538	0.55
1457518_at	C630004H02Rik	RIKEN cDNA C630004H02 gene	1.15	0.794	1.26	0.283	-1.04	0.848	1.1	0.763	0.62
1426756_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.25	0.507	-1.06	0.623	1.18	0.535	1.33	0.016	0.68
1432607_at	2610012C04Rik	RIKEN cDNA 2610012C04 gene	1.51	0.442	-1.48	0.305	1.19	0.664	1.89	0.019	0.78
1426941_at	---	---	1.36	0.556	-1.31	0.522	1.25	0.619	1	0.996	0.58
1438473_at	Arl15	ADP-ribosylation factor-like 15	-1.02	0.928	1.07	0.858	1.32	0.366	1.1	0.567	0.62
1444632_at	BC064078	cDNA sequence BC064078	-1.73	0.048	1.19	0.648	1.61	0.137	1.13	0.655	0.55
1434713_at	Smcr7l	Smith-Magenis syndrome chromosome region, candidate 7-like (human)	1.04	0.685	-1.06	0.399	1.4	0.049	1.39	0.167	0.69
1426288_at	Lrp4	low density lipoprotein receptor-related protein 4	1.48	0.097	1.09	0.757	-1.25	0.486	1.36	0.375	0.67
1431835_at	Tcerg1l	transcription elongation regulator 1-like	-2.29	0.141	1.54	0.295	1.4	0.212	1.12	0.75	0.44
1416842_at	Gstm5	glutathione S-transferase, mu 5	1.34	0.241	1.2	0.011	-1.19	0.153	4.27	0.188	1.4
1439604_at	Adamts16	a disintegrin-like and metallopetidase (reprolysin type) with thrombospondin type	1.04	0.906	1.43	0.425	-1.09	0.894	1.38	0.403	0.69
1423834_s_at	Gga1	golgi associated, gamma adaptin ear containing, ARF binding protein 1	1.38	0.248	-1.13	0.65	1.12	0.401	1.09	0.742	0.61
1418057_at	Tiam1	T-cell lymphoma invasion and metastasis 1	-1.63	0.144	1.24	0.75	1.53	0.102	1.57	0.038	0.68
1422276_at	P2ry4	pyrimidinergic receptor P2Y, G-protein coupled, 4	1.1	0.704	-1.27	0.662	1.49	0.155	1.67	0.254	0.75
1450951_at	Smc3	structural maintenace of chromosomes 3	1.06	0.848	1.48	0.391	-1.19	0.401	1.09	0.606	0.61
1418939_at	Hlx1	H2.0-like homeo box 1 (Drosophila)	1.14	0.587	1.1	0.744	1.13	0.593	-1.19	0.52	0.55
1417534_at	Itgb5	integrin beta 5	1.1	0.58	1.31	0.018	-1.04	0.722	1.23	0.273	0.65
1449943_at	Lfng	lunatic fringe gene homolog (Drosophila)	1.02	0.856	1.01	0.987	1.35	0.736	-1.29	0.81	0.52
1431620_at	4930442J19Rik	RIKEN cDNA 4930442J19 gene	1.36	0.568	1.21	0.667	-1.24	0.602	1.22	0.73	0.64
1419695_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	1.32	0.019	1.04	0.86	1.02	0.963	-4.2	0.052	-0.21
1420806_at	Fgf16	fibroblast growth factor 16	1.01	0.954	-1	0.991	1.38	0.459	1.43	0.536	0.7
1422539_at	Extl2	exotoses (multiple)-like 2	-1	0.983	1.1	0.466	1.29	0.408	1.18	0.496	0.64
1448456_at	Cln8	ceroid-lipofuscinosis, neuronal 8	1.29	0.415	-1.29	0.443	1.31	0.155	3.49	0.206	1.2
1424174_at	Shkbp1	Sh3kbp1 binding protein 1	1.2	0.324	1.07	0.585	1.1	0.51	-1.15	0.322	0.56
1417009_at	C1r	complement component 1, r subcomponent	1.22	0.125	1.03	0.804	1.13	0.736	-1.18	0.411	0.55
1419130_at	Deadc1	deaminase domain containing 1	1.08	0.44	-1.07	0.701	1.36	0.175	1.2	0.561	0.64
1422560_at	Ddi2 /// Rsc1a1	DNA-damage inducible protein 2 /// regulatory solute carrier protein, family 1, mer	1.09	0.486	-1.13	0.307	1.41	0.006	1.32	0.367	0.67
1437130_at	LOC432879	similar to Kelch repeat and BTB (POZ) domain containing 7 (predicted)	1.51	0.087	1.41	0.269	-2.14	0.012	3.95	0.217	1.18
1457258_at	---	PREDICTED: Mus musculus hypothetical LOC381645 (LOC381645), mRNA	1.43	0.514	-1.62	0.396	1.34	0.427	1.77	0.186	0.73
1424320_a_at	Traf7	Tnf receptor-associated factor 7	1.09	0.562	1.3	0.075	-1.02	0.93	1.02	0.904	0.6
1424975_at	Siglecf	sialic acid binding Ig-like lectin F	1.14	0.896	1.43	0.222	-1.25	0.415	1.61	0.159	0.73
1456964_at	Rbm12	RNA binding motif protein 12	1.12	0.888	1.29	0.604	-1.03	0.887	1.26	0.525	0.66
1431116_at	C030003D03Rik	RIKEN cDNA C030003D03 gene	1.04	0.95	1.03	0.77	1.3	0.606	-1.48	0.517	0.47
1455719_at	Tubb5	tubulin, beta 5	1.28	0.065	1.23	0.286	-1.15	0.689	1.2	0.7	0.64
1445015_at	---	---	-1.05	0.835	1.08	0.829	1.34	0.312	1.17	0.721	0.64
1417269_at	Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	1.17	0.241	1.01	0.888	1.2	0.366	-1.11	0.604	0.57
1422453_at	Prpf8	pre-mRNA processing factor 8	1.06	0.666	-1.09	0.361	1.4	0.089	1.03	0.756	0.6
1427769_x_at	Myl3	myosin, light polypeptide 3	1.39	0.575	-1.04	0.944	1.03	0.943	1.29	0.187	0.67
1460377_a_at	Tmem8	transmembrane protein 8 (five membrane-spanning domains)	-1.08	0.697	1.32	0.181	1.14	0.485	1.46	0.175	0.71
1439006_x_at	6430550H21Rik	RIKEN cDNA 6430550H21 gene	1.31	0.75	1.04	0.873	1.04	0.86	-1.64	0.063	0.43
1448632_at	Psmb10	proteasome (prosome, macropain) subunit, beta type 10	1.17	0.381	1.03	0.723	1.17	0.182	-1.56	0.148	0.46
1426373_at	Ski	Sloan-Kettering viral oncogene homolog	1.03	0.882	1.19	0.204	1.16	0.654	-1.24	0.448	0.54
1436258_at	Arhgef9	Cdc42 guanine nucleotide exchange factor (GEF) 9	-1.18	0.84	1.42	0.575	1.12	0.859	1.83	0.309	0.8
1455112_at	Amid	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death	1.07	0.145	-1.32	0.282	1.55	0.186	1.33	0.178	0.66
1446961_at	---	---	1.18	0.812	1.39	0.442	-1.23	0.606	1.52	0.562	0.72
1443269_at	D130009B15Rik	RIKEN cDNA D130009B15 gene	1.36	0.422	1.23	0.608	-1.25	0.154	1.45	0.559	0.7

1415866_at	Unc45a	unc-45 homolog A (C. elegans)	1.16	0.249	1.08	0.649	1.13	0.194	-1.11	0.392	0.57
1454168_a_at	Clpb	ClpB caseinolytic peptidase B homolog (E. coli)	-1.17	0.697	1.02	0.954	1.51	0.196	1.15	0.688	0.63
1415948_at	Creg1	cellular repressor of E1A-stimulated genes 1	1.12	0.287	-1.07	0.418	1.32	0.068	2.02	0.12	0.85
1433525_at	Ednra	endothelin receptor type A	1.14	0.67	1.44	0.102	-1.24	0.331	1.33	0.323	0.67
1421533_at	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	-1.31	0.639	1.17	0.717	1.45	0.511	1.59	0.52	0.73
1439377_x_at	Cdc20	cell division cycle 20 homolog (S. cerevisiae)	-1.19	0.358	1.26	0.48	1.29	0.336	3.04	0.152	1.1
1430490_at	---	---	1.18	0.276	1.28	0.717	-1.08	0.862	1.17	0.562	0.64
1432321_at	Cnbp2	cellular nucleic acid binding protein 2	1.05	0.795	-1.07	0.888	1.41	0.338	1.1	0.598	0.62
1434345_at	Tmem12	transmembrane protein 12	1	0.971	-1.45	0.565	1.69	0.138	2.21	0.27	0.86
1450087_a_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	1.2	0.301	-1.04	0.896	1.23	0.241	1.06	0.834	0.61
1443718_at	---	Transcribed locus	1.06	0.925	-1.01	0.957	1.33	0.507	1.16	0.59	0.64
1417235_at	Ehd3	EH-domain containing 3	-1.05	0.849	1.01	0.96	1.43	0.258	1.23	0.364	0.65
1422786_at	Slc30a1	solute carrier family 30 (zinc transporter), member 1	-1.43	0.115	1.16	0.648	1.52	0.468	1.6	0.443	0.71
1452328_s_at	Pja2	praja 2, RING-H2 motif containing	1.16	0.354	1.22	0.301	-1	0.996	1.17	0.18	0.64
1454250_at	Sec15l2	SEC15-like 2 (S. cerevisiae)	1.4	0.566	-1.4	0.292	1.27	0.407	1.18	0.38	0.61
1420424_at	1700054O13Rik	RIKEN cDNA 1700054O13 gene	1.08	0.909	1.34	0.654	-1.04	0.896	1.5	0.5	0.72
1460205_at	Dcakd	dephospho-CoA kinase domain containing	1.27	0.391	-1.16	0.057	1.26	0.174	1.32	0.17	0.67
1438636_s_at	Susd5	sushi domain containing 5	-1.21	0.437	1.29	0.401	1.27	0.374	1.21	0.686	0.64
1416230_at	Rfk	riboflavin kinase	1.14	0.365	-1.03	0.761	1.27	0.285	1.27	0.387	0.67
1427693_at	Itpr2	inositol 1,4,5-triphosphate receptor 2	-1.32	0.368	1.61	0.119	1.02	0.971	1.1	0.635	0.6
1423153_x_at	Cfh	complement component factor h	1.04	0.462	1.53	0.226	-1.21	0.313	1.34	0.068	0.67
1460602_at	Dlc1	deleted in liver cancer 1	1.08	0.675	1.22	0.495	1.08	0.773	-1.28	0.567	0.53
1420808_at	Ncoa4 /// LOC6275	nuclear receptor coactivator 4 /// similar to nuclear receptor coactivator 4	-1.04	0.916	1.05	0.562	1.37	0.162	1.56	0.315	0.74
1439974_at	C430014M02Rik	RIKEN cDNA C430014M02 gene	1.13	0.741	1.09	0.859	1.17	0.737	-1.65	0.378	0.44
1448726_at	Snapc2	small nuclear RNA activating complex, polypeptide 2	1.15	0.102	-1.01	0.901	1.25	0.004	1.14	0.59	0.63
1421379_at	Zfp354b	zinc finger protein 354B	1.33	0.347	-1.01	0.978	1.07	0.733	1.13	0.761	0.63
1459870_x_at	Il2rb	Interleukin 2 receptor, beta chain	-1.41	0.609	1.09	0.899	1.58	0.211	1.14	0.036	0.6
1448919_at	Cd302	CD302 antigen	1.26	0.042	1.17	0.347	-1.04	0.806	1.25	0.256	0.66
1433713_at	Gcn1l1	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	1.35	0.076	-1.26	0.215	1.24	0.382	1.1	0.648	0.61
1447055_at	Dnajc11	DnaJ (Hsp40) homolog, subfamily C, member 11	1.17	0.719	-1.04	0.855	1.25	0.174	1.21	0.61	0.65
1454973_at	Atf7ip	activating transcription factor 7 interacting protein	1.1	0.394	1.21	0.053	1.08	0.49	-1.16	0.229	0.56
1422179_at	Gjb4	gap junction membrane channel protein beta 4	1.32	0.7	1.17	0.401	-1.11	0.643	1.72	0.243	0.77
1419450_at	Ormdl3	ORM1-like 3 (S. cerevisiae)	1.17	0.085	-1.06	0.288	1.27	0.333	2.33	0.146	0.93
1428455_at	Col14a1	procollagen, type XIV, alpha 1	1.36	0.012	1.18	0.35	-1.18	0.564	1.28	0.191	0.66
1450107_a_at	Renbp	renin binding protein	-1.31	0.078	1.41	0.02	1.22	0.158	1.18	0.644	0.62
1454673_at	---	---	1.01	0.258	1.17	0.165	1.2	0.185	-1.2	0.125	0.55
1452105_a_at	Tsc2	tuberous sclerosis 2	1.02	0.871	-1.11	0.217	1.46	0.018	1.16	0.168	0.63
1445953_at	D17Ertd191e	DNA segment, Chr 17, ERATO Doi 191, expressed	1.12	0.882	-1.08	0.878	1.34	0.521	1.33	0.646	0.68
1418696_at	BC021608	cDNA sequence BC021608	1.11	0.475	-1.07	0.598	1.34	0.509	1.6	0.426	0.75
1443951_at	C230076A16Rik	RIKEN cDNA C230076A16 gene	1.25	0.174	-1.65	0.118	1.54	0.176	1.13	0.616	0.57
1435037_at	Perld1	per1-like domain containing 1	1.09	0.874	-1.22	0.729	1.48	0.333	1.42	0.133	0.69
1425483_at	Tox	thymocyte selection-associated HMG box gene	1.14	0.436	-1.05	0.829	1.3	0.108	1.07	0.82	0.61
1440024_at	Itpkc	inositol 1,4,5-trisphosphate 3-kinase C	1.32	0.014	-1.25	0.567	1.27	0.347	1.05	0.888	0.6
1419089_at	Timp3	tissue inhibitor of metalloproteinase 3	-1.16	0.069	1.38	0.337	1.15	0.591	1.22	0.414	0.65
1428626_at	Lysmd2	LysM, putative peptidoglycan-binding, domain containing 2	1.55	0.374	-1.21	0.434	1.01	0.865	1.19	0.449	0.64
1432202_a_at	Wdr51a	WD repeat domain 51A	1.17	0.626	-1.01	0.984	1.23	0.32	2.76	0.247	1.04
1449335_at	Timp3	tissue inhibitor of metalloproteinase 3	-1.11	0.51	1.43	0.188	1.06	0.788	1.1	0.736	0.62
1433621_at	Wdr41	WD repeat domain 41	1.04	0.887	1.2	0.32	1.15	0.573	-1.09	0.481	0.57
1418615_at	Astn1	astrotactin 1	1.16	0.773	1.25	0.666	-1.03	0.937	2.76	0.027	1.04
1416262_at	Tmem19	transmembrane protein 19	1.12	0.582	1.05	0.815	1.22	0.257	-1.25	0.186	0.53
1422036_at	Strn	striatin, calmodulin binding protein	1.34	0.124	-1.28	0.658	1.27	0.136	1.16	0.536	0.62
1421676_at	4930542N07Rik	RIKEN cDNA 4930542N07 gene	1.47	0.514	-1.19	0.724	1.09	0.811	1.6	0.326	0.74
1424426_at	Mtap	methylthioadenosine phosphorylase	1.13	0.57	1.01	0.935	1.25	0.065	-1.3	0.088	0.52

1444987_at	Ctsb	Cathepsin B	1.19	0.326	1.47	0.092	-1.37	0.317	1.67	0.176	0.74
1455085_at	1700086L19Rik	RIKEN cDNA 1700086L19 gene	1.82	0.377	-2.02	0.316	1.07	0.917	1.13	0.693	0.5
1452908_at	Dip2a	DIP2 disco-interacting protein 2 homolog A (Drosophila)	1.04	0.45	1.27	0.058	1.08	0.518	-1.16	0.233	0.56
1433253_at	5033423K11Rik	RIKEN cDNA 5033423K11 gene	-1.04	0.951	1.11	0.802	1.32	0.644	1.48	0.257	0.72
1435432_at	Centg2	centaurin, gamma 2	-1.11	0.22	1.18	0.488	1.31	0.133	1.52	0.259	0.72
1431037_a_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.15	0.265	-1.09	0.637	1.32	0.116	1.33	0.346	0.68
1444633_at	---	---	1.34	0.055	-1.1	0.676	1.14	0.595	1.07	0.838	0.61
1429766_at	2810013P06Rik	RIKEN cDNA 2810013P06 gene	1.5	0.228	-1.24	0.197	1.08	0.556	1.03	0.701	0.59
1449651_x_at	---	---	-1.07	0.913	1.31	0.48	1.14	0.603	1.39	0.64	0.69
1451625_a_at	C8g	complement component 8, gamma subunit	1.07	0.712	-1.12	0.348	1.43	0.46	1.12	0.769	0.63
1428833_at	4930406D14Rik	RIKEN cDNA 4930406D14 gene	-1.18	0.584	1.52	0.196	1.02	0.944	1.05	0.787	0.6
1439353_x_at	Tmem56	transmembrane protein 56	1.3	0.497	-1.3	0.057	1.32	0.517	3.35	0.321	1.17
1450089_a_at	Srprb	signal recognition particle receptor, B subunit	1.11	0.67	-1.16	0.678	1.42	0.46	1.31	0.517	0.67
1446224_at	Hectd2	HECT domain containing 2	1.54	0.21	1.06	0.752	-1.26	0.352	1.1	0.36	0.61
1419250_a_at	Pftk1	PFTAIRE protein kinase 1	1.33	0.029	-1.88	0.122	1.53	0.546	1.75	0.118	0.68
1436477_x_at	Rab2	RAB2, member RAS oncogene family	1.47	0.517	-1.34	0.404	1.18	0.446	1.26	0.421	0.64
1439185_x_at	D430028G21Rik	RIKEN cDNA D430028G21 gene	1.18	0.363	1.02	0.836	1.2	0.331	-1.17	0.665	0.56
1430543_at	1500005P14Rik	RIKEN cDNA 1500005P14 gene	1.06	0.887	1.3	0.639	1.04	0.864	-1.07	0.754	0.58
1419326_at	1700028P14Rik	RIKEN cDNA 1700028P14 gene	1.09	0.713	1.01	0.98	1.3	0.492	-1.69	0.548	0.43
1450876_at	Cfh	complement component factor h	1.1	0.529	1.56	0.222	-1.35	0.063	1.29	0.122	0.65
1440932_at	---	---	1.38	0.412	-1.06	0.792	1.07	0.67	1.39	0.579	0.7
1445877_at	AI256775	expressed sequence AI256775	1.14	0.713	-1.16	0.682	1.39	0.473	1.92	0.097	0.82
1438662_at	LOC433810	similar to transmembrane protein SHREW1	-1.48	0.449	1.12	0.755	1.6	0.158	1.34	0.239	0.64
1445836_at	Zfp516	Zinc finger protein 516	1.06	0.906	1.69	0.18	-1.55	0.096	1.39	0.115	0.65
1452307_at	Cables2	Cdk5 and Abl enzyme substrate 2	1.08	0.589	1.02	0.797	1.3	0.221	-1.4	0.1	0.5
1447958_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13008	1.5	0.237	1.01	0.983	-1.13	0.535	1.16	0.391	0.64
1424734_at	Rasgrf1	RAS protein-specific guanine nucleotide-releasing factor 1	1.56	0.628	-1.48	0.564	1.16	0.704	1.17	0.512	0.6
1417664_a_at	Ndrg3	N-myc downstream regulated gene 3	1.02	0.948	1.03	0.929	1.34	0.492	-1.1	0.801	0.57
1420387_at	Mpv17	Mpv17 transgene, kidney disease mutant	1.18	0.499	1.19	0.256	1.03	0.809	-1.04	0.833	0.59
1420625_at	2410016F19Rik	RIKEN cDNA 2410016F19 gene	1.12	0.747	1.26	0.477	1.02	0.931	-1.39	0.484	0.5
1431197_at	Arl6ip2	ADP-ribosylation factor-like 6 interacting protein 2	-1.07	0.863	1.01	0.987	1.45	0.414	1.73	0.442	0.78
1422803_at	Fstl3	follistatin-like 3	1.34	0.421	-1.01	0.972	1.06	0.6	1	0.996	0.6
1444972_at	C77626	expressed sequence C77626	1.48	0.372	-1.23	0.718	1.11	0.726	1.04	0.816	0.6
1428545_at	0610007L01Rik	RIKEN cDNA 0610007L01 gene	1.15	0.671	-1.06	0.811	1.3	0.136	1.45	0.236	0.71
1444161_at	A530020G20Rik	RIKEN cDNA A530020G20 gene	-1.3	0.255	1.54	0.135	1.09	0.624	1.11	0.309	0.61
1415852_at	Impdh2	inosine 5'-phosphate dehydrogenase 2	-1.08	0.38	1.06	0.541	1.41	0.004	1.05	0.798	0.61
1434634_at	Gm166	gene model 166, (NCBI)	-1.29	0.16	1.32	0.655	1.3	0.258	4.33	0.18	1.41
1441101_at	Hecw1	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 1	-1.23	0.141	1.45	0.382	1.13	0.534	1.22	0.358	0.64
1423084_at	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	-1.95	0.39	1.36	0.562	1.52	0.373	1.5	0.354	0.61
1455193_at	Zbtb8	zinc finger and BTB domain containing 8	-1.18	0.286	1.52	0.43	1.04	0.938	1.12	0.8	0.62
1450397_at	Mtap1b	microtubule-associated protein 1 B	1.46	0.494	-1.31	0.495	1.17	0.466	1.23	0.69	0.64
1423920_at	Brrn1	barren homolog (Drosophila)	-1.22	0.494	1.28	0.405	1.29	0.149	2.76	0.178	1.03
1421666_a_at	Aanat	arylalkylamine N-acetyltransferase	1.69	0.34	-1.69	0.079	1.12	0.809	2.22	0.391	0.83
1454382_at	Samd4	sterile alpha motif domain containing 4	-1.27	0.691	1.42	0.652	1.19	0.852	2.02	0.289	0.84
1448755_at	Col15a1	procollagen, type XV	-1.07	0.591	1.43	0.336	1.04	0.918	1.21	0.068	0.65
1422648_at	Slc7a2	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	-1.28	0.383	1.01	0.933	1.61	0.092	1.05	0.752	0.6
1447211_at	Nrip1	nuclear receptor interacting protein 1	1.49	0.176	-1.2	0.285	1.08	0.875	1.89	0.126	0.81
1423942_a_at	Camk2g	calcium/calmodulin-dependent protein kinase II gamma	1.15	0.667	1.15	0.363	1.09	0.57	-1.28	0.109	0.53
1434542_at	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	1.42	0.407	-1.11	0.63	1.09	0.883	1.43	0.425	0.7
1434547_at	Cpd	carboxypeptidase D	1.03	0.72	1.45	0.026	-1.09	0.42	2.28	0.242	0.92
1430117_a_at	Zfp64	zinc finger protein 64	1.08	0.861	1.08	0.854	1.24	0.539	-1.4	0.375	0.5
1447832_x_at	Ankrd10	Ankyrin repeat domain 10	1.1	0.854	1.35	0.635	-1.05	0.919	1.37	0.563	0.69
1451686_x_at	Amelx	amelogenin X chromosome	1.53	0.076	1.37	0.576	-2.01	0.068	1.09	0.643	0.5

1457962_at	---	---	-2.17	0.185	1.15	0.775	1.79	0.204	1.59	0.291	0.59
1457132_at	---	Transcribed locus	-1.42	0.651	1.11	0.376	1.59	0.173	1	0.973	0.57
1453908_at	Ptprb	protein tyrosine phosphatase, receptor type, B	1.34	0.623	1.23	0.66	-1.2	0.696	1.12	0.883	0.62
1433780_at	Ubn1	ubinuclein 1	-1.07	0.726	1.21	0.394	1.26	0.221	1.07	0.531	0.62
1423967_at	Palm	paralemmin	1.01	0.952	1.24	0.671	1.15	0.07	-1.13	0.671	0.57
1418305_s_at	Nola1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	-1.01	0.933	1.08	0.589	1.33	0.25	1.06	0.742	0.62
1453374_at	Zfand5	zinc finger, AN1-type domain 5	-1.07	0.79	1.17	0.605	1.3	0.013	1.19	0.699	0.65
1454425_at	5830495A06Rik	RIKEN cDNA 5830495A06 gene	1.31	0.451	1.13	0.396	-1.04	0.883	1.61	0.433	0.75
1455463_at	Phyhip	phytanoyl-CoA hydroxylase interacting protein	1.01	0.995	1.48	0.534	-1.1	0.557	5.69	0.154	1.77
1417727_at	Sfrs9	splicing factor, arginine/serine rich 9	1.11	0.291	-1.02	0.88	1.32	0.15	1.39	0.07	0.7
1418337_at	Rpia	ribose 5-phosphate isomerase A	-1.07	0.578	1.3	0.145	1.17	0.457	1.53	0.043	0.73
1426893_at	C230093N12Rik	RIKEN cDNA C230093N12 gene	1.05	0.905	1.02	0.952	1.33	0.237	-1.97	0.109	0.36
1452372_at	Bsdc1	BSD domain containing 1	1.17	0.312	-1.06	0.476	1.29	0.312	3.23	0.204	1.16
1427824_at	---	---	1.34	0.317	1.31	0.4	-1.32	0.627	1.16	0.535	0.62
1443431_at	---	---	-1.45	0.517	1.34	0.2	1.37	0.23	1.24	0.375	0.63
1460343_at	Neurl	neuralized-like homolog (Drosophila)	-1.7	0.161	1.17	0.389	1.65	0	1.51	0.425	0.66
1453283_at	Pgm1	phosphoglucomutase 1	-1.06	0.666	1.25	0.474	1.22	0.15	1.31	0.408	0.68
1422513_at	Ccnf	cyclin F	1.09	0.908	-1.07	0.805	1.38	0.229	4.28	0.175	1.42
1453051_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1.46	0.182	-1.1	0.863	1.04	0.953	1.53	0.502	0.73
1446591_at	Gm1574	gene model 1574, (NCBI)	-1.1	0.792	1.44	0.046	1.05	0.85	2.01	0.019	0.85
1449466_at	Clec3b	C-type lectin domain family 3, member b	1.58	0.564	1.21	0.484	-1.64	0.27	1.07	0.922	0.56
1421939_a_at	Stag1	stromal antigen 1	1.24	0.391	-1.1	0.491	1.26	0.075	1.38	0.43	0.69
1430787_at	2310050B05Rik	RIKEN cDNA 2310050B05 gene	-1.37	0.64	1.15	0.722	1.52	0.05	1.11	0.791	0.6
1454702_at	4930503L19Rik	RIKEN cDNA 4930503L19 gene	1.05	0.911	1.57	0.144	-1.27	0.209	1.68	0.305	0.76
1444163_at	Nek5	NIMA (never in mitosis gene a)-related expressed kinase 5	1.25	0.489	1.16	0.537	-1	0.997	1.1	0.904	0.63
1417961_a_at	Trim30	tripartite motif protein 30	1.06	0.643	1.26	0.081	1.09	0.595	-1.98	0.099	0.36
1432742_at	---	---	1.41	0.645	1.04	0.892	-1.05	0.939	1.32	0.565	0.68
1451784_x_at	H2-D1 /// H2-L /// L(	histocompatibility 2, D region locus 1 /// histocompatibility 2, D region /// similar to	1.25	0.282	1.04	0.729	1.11	0.09	-1.25	0.133	0.54
1423620_at	Cenpq	centromere protein Q	-1.04	0.82	1.42	0.116	1.02	0.923	1.46	0.32	0.72
1441540_at	Ncoa7	Nuclear receptor coactivator 7	1.36	0.494	1.13	0.715	-1.09	0.656	2.81	0.226	1.05
1425784_a_at	Olfm1	olfactomedin 1	1.04	0.837	1.14	0.8	1.23	0.291	-1.04	0.825	0.59
1453062_at	A930026I22Rik	RIKEN cDNA A930026I22 gene	-1.12	0.278	1.29	0.574	1.22	0.247	1.95	0.263	0.84
1445521_at	Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.55	0.451	-1.43	0.008	1.16	0.651	2.45	0.113	0.93
1427447_a_at	Triobp	TRIO and F-actin binding protein	1.1	0.512	-1.24	0.267	1.5	0.125	1.37	0.223	0.68
1459474_at	D1Ertd86e	DNA segment, Chr 1, ERATO Doi 86, expressed	1.1	0.911	-1.01	0.952	1.31	0.439	1.53	0.485	0.73
1457638_x_at	Rfc2	replication factor C (activator 1) 2	1.06	0.852	-1.17	0.397	1.49	0.133	1.1	0.79	0.62
1424411_at	AI840826	expressed sequence AI840826	1.14	0.536	1.1	0.706	1.17	0.42	-1.06	0.584	0.59
1423795_at	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associat	-1.05	0.782	1.04	0.757	1.41	0.193	1.34	0.108	0.69
1428045_a_at	Elf2	E74-like factor 2	1.58	0.23	-1.25	0.484	1.03	0.952	1.58	0.254	0.73
1444244_at	---	Transcribed locus	-1.11	0.574	1.33	0.303	1.18	0.483	2	0.231	0.85
1435402_at	Gramd1b	GRAM domain containing 1B	1.12	0.597	1.08	0.766	1.21	0.226	-1.3	0.305	0.53
1435076_at	2310047D13Rik	RIKEN cDNA 2310047D13 gene	1.39	0.623	-1.04	0.873	1.06	0.841	1.11	0.639	0.63
1419752_at	Nfx1	nuclear transcription factor, X-box binding 1	-1.04	0.811	1.17	0.545	1.28	0.048	1.01	0.909	0.61
1451579_at	BC024139	cDNA sequence BC024139	1.18	0.549	1.47	0.332	-1.33	0.226	1.07	0.38	0.6
1437429_at	5930437A14Rik	RIKEN cDNA 5930437A14 gene	-1.05	0.921	1.18	0.83	1.28	0.266	1.06	0.928	0.62
1451210_at	Ppap2c	phosphatidic acid phosphatase type 2c	1.04	0.722	1.21	0.202	1.16	0.232	-1.27	0.27	0.53
1434557_at	Hip1	huntingtin interacting protein 1	1.02	0.911	1.4	0.07	-1	0.987	1.02	0.967	0.61
1437929_at	Dact2	dapper homolog 2, antagonist of beta-catenin (xenopus)	1.22	0.632	1.53	0.285	-1.5	0.441	1.18	0.794	0.61
1434653_at	Ptk2b	PTK2 protein tyrosine kinase 2 beta	1.07	0.825	1.01	0.939	1.33	0.05	-1.45	0.248	0.49
1441957_x_at	2410076I21Rik	RIKEN cDNA 2410076I21 gene	-1.22	0.346	1.53	0.214	1.06	0.846	3.11	0.248	1.12
1426118_a_at	Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	1.12	0.673	-1	0.979	1.29	0.134	1.38	0.369	0.7
1433932_x_at	C030046I01Rik	RIKEN cDNA C030046I01 gene	1.18	0.389	-1.02	0.878	1.25	0.388	1.33	0.186	0.68
1429972_s_at	Txnrd2	thioredoxin reductase 2	1	0.998	-1.2	0.522	1.58	0.099	3.45	0.276	1.21

1455498_at	Gpr50	G-protein-coupled receptor 50	1.58	0.449	-1.47	0.666	1.15	0.637	2.66	0.01	0.98
1441813_at	LOC670358	hypothetical protein LOC670358	1.66	0.036	-2.38	0.03	1.33	0.342	1.1	0.817	0.43
1459897_a_at	Sbsn	suprabasin	-1.16	0.524	1.24	0.677	1.31	0.567	1.24	0.14	0.66
1450213_at	Pde7b	phosphodiesterase 7B	-1.21	0.735	1.08	0.785	1.51	0.236	1.16	0.48	0.63
1455639_at	---	Transcribed locus	1.27	0.599	-1	0.999	1.14	0.702	2.21	0.262	0.9
1435335_a_at	Gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	1.11	0.181	1.16	0.099	1.14	0.18	-1.14	0.509	0.57
1423174_a_at	Pard6b	par-6 (partitioning defective 6) homolog beta (C. elegans)	1.04	0.762	1.28	0.451	1.09	0.823	-1.42	0.252	0.5
1421276_a_at	Dst	dystonin	1.08	0.544	1.02	0.927	1.31	0.4	-1.25	0.499	0.54
1432848_a_at	1200004M23Rik	RIKEN cDNA 1200004M23 gene	1.04	0.78	1.13	0.278	1.24	0.123	-1.35	0.202	0.52
1426963_at	Pacs2	phosphofurin acidic cluster sorting protein 2	-1.17	0.401	1.16	0.456	1.4	0.336	1.28	0.634	0.67
1423831_at	Prkag2	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.09	0.483	1.1	0.69	1.22	0.236	-1.2	0.432	0.55
1433548_at	Mare	alpha globin regulatory element containing gene	1.11	0.139	-1.19	0.078	1.46	0.027	1.63	0.098	0.75
1446072_at	---	---	1.04	0.929	-1.11	0.673	1.48	0.274	1.14	0.663	0.63
1417779_at	2310079N02Rik	RIKEN cDNA 2310079N02 gene	1.06	0.366	1.18	0.216	1.18	0.169	-1.08	0.728	0.58
1451567_a_at	Ifi203	interferon activated gene 203	1.24	0.005	1.14	0.666	1.03	0.896	-2.51	0.046	0.23
1429934_at	4930502E18Rik	RIKEN cDNA 4930502E18 gene	1.36	0.541	-1.49	0.116	1.39	0.367	4.7	0.191	1.49
1424354_at	1110007F12Rik	RIKEN cDNA 1110007F12 gene	1.44	0.011	1.12	0.266	-1.18	0.128	1.22	0.197	0.65
1420392_at	Ubl4b	ubiquitin-like 4B	1.25	0.394	1.46	0.229	-1.42	0.474	1.33	0.587	0.66
1428859_at	Paox	polyamine oxidase (exo-N4-amino)	1.01	0.929	1.36	0.128	1.05	0.577	-1.25	0.264	0.54
1459447_at	---	Transcribed locus	-1.05	0.857	1.18	0.585	1.29	0.421	1	0.999	0.6
1445362_at	AW456874	expressed sequence AW456874	1.18	0.56	-1.5	0.3	1.57	0.307	1.06	0.875	0.58
1416992_at	Mfng	manic fringe homolog (Drosophila)	1.01	0.959	1.4	0.182	1.01	0.958	-1.7	0.131	0.43
1432059_x_at	5031425E22Rik	RIKEN cDNA 5031425E22 gene	1.28	0.303	-1.01	0.976	1.15	0.652	1.03	0.883	0.61
1431805_a_at	Rhpn2	rhophilin, Rho GTPase binding protein 2	1	0.977	-1.15	0.074	1.54	0.119	1.06	0.649	0.62
1427604_a_at	Atp9a	ATPase, class II, type 9A	1.16	0.544	1.1	0.36	1.15	0.45	-1.29	0.383	0.53
1436664_a_at	Slc35a2	solute carrier family 35 (UDP-galactose transporter), member 2	-1.12	0.319	1.1	0.379	1.43	0.147	1	0.985	0.6
1445962_at	Gria2	Glutamate receptor, ionotropic, AMPA2 (alpha 2)	1.05	0.692	2.04	0.368	-3.04	0.014	1.56	0.438	0.4
1433079_at	4933436P19Rik	RIKEN cDNA 4933436P19 gene	-1.04	0.457	1.21	0.482	1.24	0.18	1.05	0.602	0.62
1435989_x_at	LOC434261 /// LOC	similar to Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin endo A) /// sir	1.09	0.581	1.34	0.104	-1.02	0.904	2.16	0.475	0.89
1449507_a_at	Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.19	0.177	-1.01	0.933	1.23	0.005	1.55	0.179	0.74
1452980_at	2810468N07Rik	RIKEN cDNA 2810468N07 gene	1.03	0.933	-2.74	0.07	2.02	0.075	1.04	0.924	0.34
1436544_at	Atp10d	ATPase, Class V, type 10D	1.04	0.89	1.31	0.165	1.07	0.591	-1.57	0.384	0.46
1450052_at	Kif2a	kinesin family member 2A	1.28	0.308	-1.07	0.588	1.2	0.215	2.49	0.226	0.97
1421633_a_at	Hapln1	hyaluronan and proteoglycan link protein 1	1.03	0.965	-2.31	0.118	1.96	0.084	1.04	0.928	0.43
1420833_at	Vamp2	vesicle-associated membrane protein 2	1.04	0.802	-1.28	0.637	1.59	0.084	1.52	0.045	0.72
1444550_at	1110021J02Rik	RIKEN cDNA 1110021J02 gene	1.19	0.686	1.36	0.053	-1.15	0.229	1.22	0.072	0.65
1455239_at	6330512M04Rik	RIKEN cDNA 6330512M04 gene	1.48	0.593	-1.62	0.463	1.32	0.443	1.59	0.458	0.69
1435597_at	C130052G03Rik	RIKEN cDNA C130052G03 gene	-1.08	0.829	1.13	0.481	1.37	0.131	3.35	0.178	1.19
1452568_at	Gcap8	granule cell antiserum positive 8	-2.4	0.399	1.18	0.672	1.82	0.291	1.77	0.101	0.59
1431799_at	Mllt4	myeloid/lymphoid or mixed lineage-leukemia translocation to 4 homolog (Drosoph	1.48	0.139	-1.16	0.729	1.08	0.541	1.13	0.537	0.63
1416317_a_at	Stambp	Stam binding protein	1.03	0.947	-1.06	0.772	1.44	0.442	1.18	0.619	0.65
1425118_at	Spire2	spire homolog 2 (Drosophila)	-1.06	0.79	1.35	0.659	1.12	0.554	1.45	0.373	0.72
1453797_at	Phospho2	phosphatase, orphan 2	1.19	0.696	1.42	0.396	-1.24	0.44	1.92	0.4	0.82
1439518_at	Mmrn2	multimerin 2	1.37	0.162	1.04	0.901	1.01	0.93	-1.2	0.28	0.55
1428316_a_at	Fundc2	FUN14 domain containing 2	-1.09	0.431	1.47	0.003	1.03	0.622	1.31	0.202	0.68
1417019_a_at	Cdc6	cell division cycle 6 homolog (S. cerevisiae)	1.31	0.644	-1.09	0.875	1.19	0.415	5.23	0.171	1.66
1460742_at	Alg3	asparagine-linked glycosylation 3 homolog (yeast, alpha-1,3-mannosyltransferase	1.17	0.454	-1.08	0.587	1.32	0.09	1.24	0.225	0.66
1416204_at	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	1.24	0.672	-1.28	0.425	1.4	0.389	1.89	0.112	0.81
1454553_at	4930509E22Rik	RIKEN cDNA 4930509E22 gene	1.48	0.538	1.07	0.85	-1.14	0.6	1.36	0.481	0.69
1438329_at	Tlr12	toll-like receptor 12	1.29	0.448	1.08	0.894	1.05	0.6	-1.86	0.131	0.39
1423774_a_at	Prc1	protein regulator of cytokinesis 1	-1.08	0.707	1.35	0.338	1.14	0.373	6.05	0.192	1.87
1433449_at	B930037P14Rik	RIKEN cDNA B930037P14 gene	1.03	0.94	-1.02	0.966	1.41	0.061	1.1	0.707	0.63
1433361_at	4930527F18Rik	RIKEN cDNA 4930527F18 gene	1.42	0.629	-1.02	0.973	1.02	0.972	1.76	0.217	0.79

1450957_a_at	Sqstm1	sequestosome 1	1.03	0.734	1.01	0.918	1.38	0.101	-1.05	0.784	0.59
1442207_at	Atg16l2	Autophagy related 16 like 2 (S. cerevisiae)	1.15	0.624	1.16	0.465	1.12	0.388	-1.74	0.023	0.42
1417630_at	Mknk1	MAP kinase-interacting serine/threonine kinase 1	1.17	0.325	-1	0.988	1.25	0.104	1.13	0.537	0.64
1460360_at	Asrgl1	asparaginase like 1	-1.11	0.652	1.2	0.186	1.32	0.239	1.08	0.727	0.62
1453589_a_at	2610005L07Rik	RIKEN cDNA 2610005L07 gene	1.05	0.856	1.24	0.528	1.14	0.742	-1.22	0.613	0.55
1426036_a_at	Pde1c	phosphodiesterase 1C	-1.31	0.632	1.07	0.9	1.58	0.179	1.62	0.569	0.74
1429364_at	4930579G24Rik	RIKEN cDNA 4930579G24 gene	1.56	0.375	-1.23	0.379	1.04	0.591	2.84	0.182	1.05
1434909_at	Rragd	Ras-related GTP binding D	-1.05	0.407	1.09	0.692	1.38	0.013	1.65	0.258	0.77
1453978_at	4921522H14Rik	RIKEN cDNA 4921522H14 gene	-2.21	0.467	1.31	0.553	1.66	0.196	1.29	0.577	0.51
1454329_at	4933415J04Rik	RIKEN cDNA 4933415J04 gene	1.28	0.698	-1.36	0.633	1.4	0.426	1.02	0.977	0.59
1454799_at	A230097K15Rik	RIKEN cDNA A230097K15 gene	1.05	0.742	1.15	0.546	1.22	0.413	-1.38	0.186	0.51
1441907_s_at	Cd93	CD93 antigen	1.06	0.819	-1.18	0.737	1.51	0.402	1.09	0.803	0.62
1441290_at	4930506M07Rik	RIKEN cDNA 4930506M07 gene	1.16	0.832	1.7	0.358	-1.77	0.074	1.06	0.89	0.54
1436979_x_at	Rbm14	RNA binding motif protein 14	1.14	0.366	-1.15	0.393	1.41	0.158	1.05	0.832	0.61
1447629_at	1810020G14Rik	RIKEN cDNA 1810020G14 gene	-1.08	0.858	1.44	0.511	1.06	0.75	1.04	0.86	0.61
1449174_at	Art4	ADP-ribosyltransferase 4	1.72	0.151	1.13	0.779	-1.74	0.025	4.27	0.242	1.34
1429172_a_at	5730507H05Rik	RIKEN cDNA 5730507H05 gene	-3.15	0.003	1.46	0.339	1.64	0.604	3.92	0.208	0.97
1429591_at	Tacc1	transforming, acidic coiled-coil containing protein 1	1.63	0.482	-1.74	0.42	1.22	0.705	1.76	0.468	0.72
1424784_at	1700029I01Rik /// L	RIKEN cDNA 1700029I01 gene /// similar to zinc finger protein 665 /// similar to zi	-1.2	0.641	1.04	0.773	1.55	0.033	1.02	0.894	0.6
1430614_at	4632415K11Rik	RIKEN cDNA 4632415K11 gene	1.01	0.799	-1.03	0.853	1.44	0.214	1.11	0.833	0.63
1459672_at	Top1	Topoisomerase (DNA) I	1.22	0.676	1.47	0.534	-1.37	0.23	1.46	0.547	0.7
1456069_at	Dtna	dystrobrevin alpha	1.62	0.037	1.13	0.85	-1.48	0.254	1.11	0.895	0.59
1419147_at	Rec8L1	REC8-like 1 (yeast)	-1.18	0.37	1.25	0.661	1.32	0.263	2.78	0.162	1.04
1452666_a_at	Tmcc2	transmembrane and coiled-coil domains 2	1.24	0.42	1.19	0.485	-1.01	0.959	4.22	0.119	1.41
1439876_at	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	1.15	0.756	1.24	0.546	1.03	0.912	-1.16	0.472	0.56
1443893_at	Ywhaz	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	1.68	0.341	1.11	0.801	-1.57	0.33	1.53	0.313	0.69
1433559_at	Slc45a4	solute carrier family 45, member 4	-1.14	0.122	1.08	0.07	1.46	0.005	1.43	0.09	0.71
1428144_at	1200011O22Rik	RIKEN cDNA 1200011O22 gene	-1.07	0.47	1	0.981	1.49	0.017	1.35	0.372	0.69
1422847_a_at	Prkcd	protein kinase C, delta	1.01	0.884	1.21	0.107	1.2	0.101	-1.5	0.195	0.48
1418026_at	Exo1	exonuclease 1	1.36	0.05	-1.21	0.713	1.23	0.529	3.1	0.181	1.12
1418883_a_at	Pabpc1	poly A binding protein, cytoplasmic 1	1.09	0.561	1.09	0.577	1.24	0.272	-1.03	0.763	0.6
1416360_at	Snag1	sorting nexin associated golgi protein 1	1.24	0.26	1.08	0.644	1.1	0.78	-1.05	0.747	0.59
1430231_a_at	Cep70	centrosomal protein 70	1.68	0.618	-1.92	0.208	1.23	0.554	3.36	0.25	1.08
1421667_at	Nmur1	neuromedin U receptor 1	-1.66	0.108	1.43	0.01	1.39	0.204	1.21	0.77	0.59
1417409_at	Jun	Jun oncogene	-1.12	0.656	1.18	0.572	1.35	0.229	1.33	0.151	0.69
1428222_at	Dcamkl2	doublecortin and CaM kinase-like 2	1.34	0.173	-1.21	0.738	1.25	0.531	1.54	0.486	0.73
1443333_at	---	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330092A	1.46	0.57	-1.36	0.587	1.22	0.686	1.75	0.284	0.77
1446499_at	Fadd	Fas (TNFRSF6)-associated via death domain	1.26	0.533	-1.09	0.824	1.25	0.325	1.31	0.159	0.68
1437870_at	Slco4c1	solute carrier organic anion transporter family, member 4C1	1.23	0.586	1.47	0.404	-1.39	0.011	2.69	0.238	1
1424156_at	Rbl1	retinoblastoma-like 1 (p107)	-1.12	0.053	1.49	0.144	1.04	0.781	1.75	0.114	0.79
1439017_x_at	Adipor1	adiponectin receptor 1	-1.02	0.188	1.07	0.31	1.37	0.137	1.57	0.332	0.75
1438347_at	Ush3a	Usher syndrome 3A homolog (human)	-2.33	0.263	1.61	0.455	1.38	0.522	1.03	0.95	0.42
1427548_a_at	Clns1a	chloride channel, nucleotide-sensitive, 1A	1.11	0.556	-1.03	0.913	1.35	0.299	1.03	0.916	0.61
1452675_at	Rbm22	RNA binding motif protein 22	1.1	0.346	1	0.997	1.33	0.017	-1.11	0.024	0.58
1440914_s_at	Aftph	aftiphilin	1.09	0.521	1.18	0.445	1.16	0.627	-1.37	0.026	0.51
1450385_at	Kpna3	karyopherin (importin) alpha 3	1.3	0.565	-1.23	0.465	1.32	0.438	1.6	0.383	0.74
1448814_at	Gab1	growth factor receptor bound protein 2-associated protein 1	1.01	0.96	1.45	0.321	-1.04	0.941	1.26	0.668	0.67
1433703_s_at	Bahd1	bromo adjacent homology domain containing 1	1.06	0.151	1.11	0.204	1.26	0.288	-1.01	0.946	0.61
1454447_at	5830434F19Rik	RIKEN cDNA 5830434F19 gene	1.33	0.409	1.49	0.288	-1.65	0.032	1.08	0.83	0.56
1458329_x_at	1110051B16Rik	RIKEN cDNA 1110051B16 gene	1.99	0.011	1.01	0.947	-2.38	0.374	1.93	0.334	0.64
1428644_at	Mgat5	mannoside acetylglucosaminyltransferase 5	-1.02	0.766	1.16	0.506	1.28	0.282	1.14	0.241	0.64
1454169_a_at	Epsti1	epithelial stromal interaction 1 (breast)	1.02	0.947	1.06	0.858	1.34	0.142	-1.91	0.152	0.38
1425950_at	BC019537	cDNA sequence BC019537	1.01	0.953	1.26	0.364	1.15	0.354	-1.49	0.134	0.49

1460535_at	Golgb1	golgi autoantigen, golgin subfamily b, macrogolgin 1	1.47	0.308	1.07	0.916	-1.12	0.794	1.02	0.925	0.61
1425440_x_at	Slc41a3	solute carrier family 41, member 3	1.55	0.574	-1.4	0.366	1.17	0.523	1.46	0.042	0.69
1448851_a_at	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	1.11	0.717	-1.17	0.588	1.47	0.07	1.07	0.757	0.62
1455966_s_at	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	1.7	0.486	1.25	0.522	-2.09	0.049	1.18	0.759	0.51
1436802_at	Ilf3	interleukin enhancer binding factor 3	1.03	0.854	1.4	0.042	-1.01	0.961	1.2	0.006	0.66
1453163_at	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A	1.48	0.491	1.12	0.805	-1.21	0.596	1.42	0.426	0.7
1416894_at	1500019G21Rik	RIKEN cDNA 1500019G21 gene	1.08	0.743	-1.06	0.699	1.41	0.121	1.16	0.635	0.65
1431452_at	Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	1.21	0.467	-1.21	0.696	1.4	0.535	1.85	0.441	0.81
1455365_at	Cdh8	cadherin 8	1.47	0.312	-1.23	0.693	1.15	0.674	1.23	0.677	0.65
1453737_at	5730509C05Rik	RIKEN cDNA 5730509C05 gene	1.45	0.308	-1.05	0.853	1.03	0.894	1.23	0.574	0.66
1456098_a_at	Elmo2	engulfment and cell motility 2, ced-12 homolog (C. elegans)	1.03	0.849	1.22	0.142	1.18	0.432	-1.23	0.138	0.55
1424369_at	Psmf1	proteasome (prosome, macropain) inhibitor subunit 1	1.03	0.822	-1.16	0.025	1.54	0.047	2.41	0.181	0.95
1449389_at	Tal1	T-cell acute lymphocytic leukemia 1	-1.3	0.223	1.56	0.208	1.1	0.613	6.02	0.175	1.85
1444329_at	Gfpt1	glutamine fructose-6-phosphate transaminase 1	1.35	0.623	1.08	0.904	1	0.991	-1.27	0.181	0.54
1419071_at	Cys1	cystin 1	1.22	0.564	-1.04	0.901	1.25	0.689	1.24	0.65	0.67
1448028_at	Tbc1d24	TBC1 domain family, member 24	1.11	0.599	1.39	0.062	-1.07	0.732	1.92	0.195	0.84
1448744_at	Galns	galactosamine (N-acetyl)-6-sulfate sulfatase	1.01	0.935	-1.13	0.346	1.53	0.101	1.03	0.883	0.61
1460717_at	Tspyl1	testis-specific protein, Y-encoded-like 1	1.49	0.306	-1.33	0.369	1.2	0.595	1.64	0.289	0.75
1441295_at	Lman2l	lectin, mannose-binding 2-like	-1.18	0.638	1.44	0.34	1.15	0.719	1.68	0.263	0.77
1433455_at	Sh2b3	SH2B adaptor protein 3	1.02	0.891	1.1	0.6	1.31	0.059	-1.82	0.105	0.4
1443296_at	Pctk1	PCTAIRE-motif protein kinase 1	1.53	0.475	1.13	0.722	-1.28	0.26	1.24	0.223	0.65
1426591_at	Gfm2	G elongation factor, mitochondrial 2	-1.64	0.181	1.02	0.907	1.8	0.01	1.32	0.112	0.62
1455325_at	A230057G18Rik	RIKEN cDNA A230057G18 gene	1.08	0.914	1.66	0.196	-1.45	0.213	1.16	0.52	0.61
1439542_at	Zfp651	zinc finger protein 651	1.76	0.577	-2.22	0.104	1.22	0.705	1.18	0.293	0.48
1431561_a_at	Dhx34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-1	0.999	1.18	0.246	1.25	0.073	1.1	0.565	0.63
1454748_at	Naprt1	nicotinate phosphoribosyltransferase domain containing 1	1.17	0.654	-1.02	0.797	1.28	0.077	3.2	0.176	1.16
1444277_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730026F	1.02	0.965	1.39	0.399	1.02	0.949	-1.07	0.887	0.59
1423678_at	BC017643	cDNA sequence BC017643	1.14	0.069	1.05	0.656	1.24	0.249	-1.64	0.122	0.45
1438955_x_at	Ppif	peptidylprolyl isomerase F (cyclophilin F)	-1.31	0.569	1.3	0.249	1.37	0.183	1.16	0.34	0.63
1428767_at	Gsdmdc1	gasdermin domain containing 1	1.36	0.238	1.01	0.919	1.06	0.445	-1.61	0.044	0.46
1460100_at	Lbxcor1	Ladybird homeobox 1 homolog (Drosophila) corepressor 1	1.3	0.634	-1.13	0.514	1.25	0.582	1.97	0.449	0.85
1418913_at	Bhmt2	betaine-homocysteine methyltransferase 2	1.08	0.697	1.27	0.035	1.08	0.837	-1.03	0.96	0.6
1453482_at	2310024N18Rik	RIKEN cDNA 2310024N18 gene	1.3	0.497	1.11	0.669	1.02	0.968	-1.12	0.704	0.58
1457718_at	D030022P06Rik	RIKEN cDNA D030022P06 gene	1.42	0.219	1.07	0.922	-1.05	0.905	1.06	0.854	0.62
1440204_at	3110039M20Rik	RIKEN cDNA 3110039M20 gene	1.21	0.589	-1.08	0.91	1.3	0.566	1.52	0.263	0.74
1432176_a_at	---	---	1.3	0.2	1.06	0.704	1.08	0.578	-1.33	0.197	0.53
1421253_at	Nrap	nebulin-related anchoring protein	1.25	0.133	-1.7	0.366	1.59	0.283	1.09	0.701	0.56
1424288_at	Bcdin3	bin3, bicoid-interacting 3, homolog (Drosophila)	1.16	0.284	1.02	0.879	1.25	0.09	-1.08	0.464	0.59
1416855_at	Gas1	growth arrest specific 1	1.16	0.293	-1.56	0.293	1.63	0.47	1.05	0.797	0.57
1435007_s_at	AI132487	expressed sequence AI132487	1.27	0.321	-1.01	0.974	1.17	0.118	1.24	0.269	0.67
1425352_at	Rcor3	REST corepressor 3	1.42	0.268	-1.05	0.848	1.06	0.776	1.4	0.303	0.71
1459703_at	D7Ertd443e	DNA segment, Chr 7, ERATO Doi 443, expressed	-1.05	0.895	1.3	0.314	1.19	0.698	1.59	0.26	0.75
1423092_at	Incenp	inner centromere protein	1.19	0.734	-1.1	0.503	1.34	0.259	3.73	0.187	1.29
1437242_at	Ttll12	tubulin tyrosine ligase-like family, member 12	-1.03	0.712	1.34	0.075	1.13	0.365	2.43	0.156	0.97
1454711_at	Trio	triple functional domain (PTPRF interacting)	1.07	0.363	1.09	0.394	1.27	0.283	-1.27	0.111	0.54
1447928_at	Car5b	carbonic anhydrase 5b, mitochondrial	-1.02	0.873	1.29	0.289	1.17	0.716	1.34	0.487	0.69
1457542_at	Nup133	nucleoporin 133	1.11	0.123	1.52	0.108	-1.24	0.229	1.69	0.403	0.77
1434004_at	Dhps	deoxyhypusine synthase	1.14	0.548	1	0.989	1.29	0.03	-1.3	0.015	0.53
1421900_at	Eif2ak1	eukaryotic translation initiation factor 2 alpha kinase 1	1.13	0.706	-1.11	0.65	1.4	0.258	3.66	0.159	1.27
1451871_a_at	Ghr	growth hormone receptor	1.57	0.12	-1.39	0.41	1.15	0.68	1.66	0.29	0.75
1428780_at	Tha1	threonine aldolase 1	-1.13	0.721	1.45	0.208	1.1	0.453	1.07	0.752	0.62
1420482_at	Cnnm3	cyclin M3	1.07	0.645	-1.05	0.818	1.42	0.109	1.21	0.058	0.66
1421103_at	Bmp2k	BMP2 inducible kinase	-1.14	0.503	1.05	0.843	1.51	0.256	1.17	0.747	0.65

1431471_at	4833428M15Rik	RIKEN cDNA 4833428M15 gene	1.21	0.773	1.57	0.33	-1.54	0.374	1.01	0.988	0.56
1431461_at	4933417E11Rik	RIKEN cDNA 4933417E11 gene	1.56	0.528	-1.72	0.559	1.3	0.588	2.85	0.226	1
1419827_s_at	Kif17	kinesin family member 17	1.3	0.815	1.06	0.822	1.08	0.788	-1.12	0.502	0.58
1421139_a_at	Zfp386	zinc finger protein 386 (Kruppel-like)	1.16	0.248	1.04	0.872	1.24	0.594	-1.63	0.004	0.45
1416540_at	Hgs	HGF-regulated tyrosine kinase substrate	1	0.984	-1.01	0.892	1.45	0.041	1.19	0.4	0.66
1424466_at	Ipo9	importin 9	-1.01	0.786	1.12	0.446	1.33	0.122	1.21	0.163	0.66
1436553_at	Lhfpl4	lipoma HMGIC fusion partner-like protein 4	1.65	0.31	-2.65	0.289	1.41	0.345	1.43	0.596	0.46
1418070_at	Cdyl	chromodomain protein, Y chromosome-like	1.08	0.648	-1.09	0.764	1.44	0.051	1.62	0.335	0.76
1450729_at	Hs2st1	heparan sulfate 2-O-sulfotransferase 1	1.19	0.253	1.32	0.125	-1.07	0.717	1.04	0.806	0.62
1458762_at	AU015230	expressed sequence AU015230	1.37	0.234	1.25	0.393	-1.23	0.324	1.11	0.556	0.63
1443434_s_at	Plxnc1	plexin C1	1.29	0.767	1.31	0.64	-1.2	0.562	1.16	0.823	0.64
1448490_at	Adck4	aarF domain containing kinase 4	1.09	0.78	1.05	0.845	1.31	0.192	-1.09	0.56	0.59
1437955_at	4922504M18Rik	RIKEN cDNA 4922504M18 gene	1.36	0.517	1.17	0.703	-1.1	0.842	2.37	0.33	0.95
1437851_x_at	Rnps1	ribonucleic acid binding protein S1	1.05	0.653	-1.11	0.283	1.48	0.01	1.21	0.065	0.66
1421528_a_at	Surf5	surfeit gene 5	1.27	0.117	1.23	0.373	-1.06	0.761	1.3	0.23	0.68
1425464_at	Gata6	GATA binding protein 6	1.1	0.564	1.28	0.313	1.06	0.698	-1.08	0.669	0.59
1447434_at	Ccnd3	Cyclin D3	-1.26	0.416	1.16	0.77	1.49	0.408	1.01	0.981	0.6
1418639_at	Sftpc	surfactant associated protein C	1.57	0.367	1.05	0.895	-1.23	0.046	1.38	0.098	0.69
1431054_at	Lsm6	LSM6 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.42	0.147	1.1	0.353	-1.09	0.648	1.14	0.428	0.64
1434640_at	Nrsn2	neurensin 2	1.49	0.227	-1.13	0.798	1.07	0.883	2.54	0.071	0.99
1446713_at	Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	1.32	0.774	1.44	0.614	-1.47	0.414	2.01	0.14	0.82
1433587_at	Rgmb	RGM domain family, member B	1.22	0.385	1.16	0.508	1.07	0.768	-1.48	0.181	0.49
1448431_at	Asb6	ankyrin repeat and SOCS box-containing protein 6	-1.1	0.728	1.3	0.012	1.24	0.266	1.34	0.252	0.69
1435203_at	Man2a2	mannosidase 2, alpha 2	1.17	0.457	1.14	0.488	1.13	0.623	-1.03	0.932	0.6
1424281_at	Ubap2	ubiquitin-associated protein 2	-1.01	0.849	1.01	0.943	1.45	0.226	1.45	0.205	0.72
1452192_at	BC053440	cDNA sequence BC053440	-1.04	0.669	1.06	0.492	1.42	0.011	1.32	0.153	0.69
1438572_at	Csmd3	CUB and Sushi multiple domains 3	-1.1	0.803	1.52	0.238	1.01	0.953	1.03	0.873	0.62
1459372_at	Npas4	neuronal PAS domain protein 4	1.51	0.302	-1.09	0.874	1.01	0.981	1.03	0.953	0.62
1456088_at	Birc4	baculoviral IAP repeat-containing 4	1.35	0.301	-1.07	0.838	1.15	0.752	1.03	0.935	0.62
1443753_at	Galns	Galactosamine (N-acetyl)-6-sulfate sulfatase	-1.1	0.648	1.1	0.126	1.43	0.615	1.36	0.713	0.7
1457984_at	Crh	corticotropin releasing hormone	1.42	0.604	1.16	0.648	-1.16	0.782	1.25	0.76	0.67
1451072_a_at	Rnf4	ring finger protein 4	1.18	0.684	-1.05	0.871	1.31	0.507	1.26	0.59	0.68
1427501_at	BC007180	cDNA sequence BC007180	-1.14	0.793	1.1	0.911	1.46	0.042	1.31	0.591	0.69
1435627_x_at	Marcksl1 /// LOC67	MARCKS-like 1 /// similar to MARCKS-related protein (MARCKS-like protein 1) (M	1	0.987	1.36	0.415	1.08	0.801	-1.7	0.129	0.43
1457083_at	Prpf31	PRP31 pre-mRNA processing factor 31 homolog (yeast)	1.53	0.329	1.08	0.616	-1.2	0.317	1.02	0.962	0.61
1420817_at	Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polyp	-1.09	0.68	1.02	0.824	1.51	0.03	1.34	0.203	0.69
1428566_at	Hspbap1	Hspb associated protein 1	-1.16	0.645	1.52	0.372	1.06	0.754	1.83	0.319	0.81
1445631_at	---	---	-1.18	0.63	1.38	0.476	1.21	0.49	1.11	0.561	0.63
1432332_a_at	Nudt19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	1.17	0.625	-1.08	0.69	1.35	0.081	1.56	0.289	0.75
1433890_a_at	Bat3	HLA-B-associated transcript 3	1.04	0.755	-1.03	0.714	1.43	0.027	1.09	0.41	0.63
1457540_at	Slc25a26	Solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 26	1.32	0.412	1.11	0.798	1.02	0.958	-1.04	0.876	0.6
1417146_at	2410018C20Rik	RIKEN cDNA 2410018C20 gene	1.02	0.92	1.08	0.367	1.34	0.23	-1	1	0.61
1447784_x_at	9130023D20Rik	RIKEN cDNA 9130023D20 gene	1.46	0.07	1.12	0.479	-1.16	0.591	1.16	0.549	0.65
1416657_at	Akt1	thymoma viral proto-oncogene 1	1.09	0.698	1.3	0.082	1.05	0.227	-1.19	0.23	0.56
1446680_at	---	---	1.31	0.5	1.35	0.324	-1.28	0.189	1.28	0.443	0.67
1418896_a_at	Rpn2	ribophorin II	-1.03	0.691	1.11	0.363	1.36	0.018	1.09	0.19	0.63
1423929_at	Phgdhl1	phosphoglycerate dehydrogenase like 1	1.2	0.558	-1.02	0.919	1.27	0.201	1.04	0.852	0.62
1456760_at	---	CDNA clone IMAGE:6813709	-1.34	0.092	1.19	0.808	1.51	0.517	1.78	0.014	0.78
1424400_a_at	Aldh1l1	aldehyde dehydrogenase 1 family, member L1	1.01	0.823	-1.01	0.971	1.44	0.126	1.42	0.043	0.72
1424163_at	Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	1.12	0.531	1.23	0.067	1.09	0.507	-1.28	0.222	0.54
1419537_at	Tcfec	transcription factor EC	-1.24	0.519	1.33	0.091	1.31	0.039	1.45	0.223	0.71
1436797_a_at	Surf4	surfeit gene 4	1.04	0.831	1.14	0.4	1.27	0.239	-1.07	0.79	0.59
1459542_at	---	---	1.01	0.943	-1	0.999	1.44	0.089	1.21	0.777	0.66

1424044_at	Jmjd2b	jumonji domain containing 2B	1.12	0.063	1.12	0.769	1.21	0.119	-1.07	0.651	0.59
1454582_at	D530037P16Rik	RIKEN cDNA D530037P16 gene	-1.31	0.284	1.05	0.929	1.63	0.275	1.26	0.612	0.66
1438126_at	Exoc5	exocyst complex component 5	1.06	0.86	1.16	0.769	1.23	0.647	-1.55	0.536	0.47
1440720_s_at	Gle1l	GLE1 RNA export mediator-like (yeast	1.23	0.203	1.12	0.772	1.1	0.764	-1.23	0.289	0.55
1446837_at	Mett5d1	Methyltransferase 5 domain containing 1	1.3	0.767	1.1	0.717	1.05	0.902	-1.35	0.277	0.52
1449753_at	Myo1e	myosin IE	1.66	0.389	1.29	0.441	-1.99	0.125	1.03	0.908	0.5
1424125_at	Kcnk13	potassium channel, subfamily K, member 13	-1.58	0.406	1.72	0.093	1.09	0.784	1.21	0.229	0.61
1424797_a_at	Pitx2	paired-like homeodomain transcription factor 2	-1.26	0.19	1.55	0.138	1.1	0.71	1.96	0.053	0.84
1421768_a_at	Homer1	homer homolog 1 (Drosophila)	1.36	0.131	-1	0.994	1.09	0.786	1.17	0.652	0.66
1417658_at	Tbrg4	transforming growth factor beta regulated gene 4	-1	0.982	1.08	0.186	1.37	0.232	1.19	0.218	0.66
1423699_at	D15Ertd785e	DNA segment, Chr 15, ERATO Doi 785, expressed	-1.05	0.014	1.28	0.514	1.22	0.262	1.33	0.52	0.69
1438565_at	A830010M20Rik	RIKEN cDNA A830010M20 gene	1.17	0.242	1.12	0.834	1.16	0.28	-3	0.097	0.11
1444131_at	2610101N10Rik	RIKEN cDNA 2610101N10 gene	1.97	0.197	-2.32	0.251	1.05	0.891	1.13	0.719	0.46
1434333_a_at	Prkd2	protein kinase D2	1.15	0.301	1.28	0.211	1.02	0.925	-2.63	0.032	0.21
1421640_a_at	Tank	TRAF family member-associated Nf-kappa B activator	-1.02	0.942	1.15	0.569	1.32	0.379	1.06	0.613	0.63
1443421_s_at	Pcdhb15	protocadherin beta 15	-1.22	0.459	1.08	0.765	1.55	0.252	1.11	0.526	0.63
1456333_a_at	Arhgap6	Rho GTPase activating protein 6	1.22	0.528	-1.05	0.694	1.28	0.389	1.27	0.663	0.68
1449057_at	Kel	Kell blood group	-1.11	0.665	1.38	0.646	1.18	0.671	9.1	0.163	2.64
1430862_at	2310057M21Rik	RIKEN cDNA 2310057M21 gene	1.27	0.497	-1.06	0.889	1.24	0.323	1.24	0.373	0.67
1432989_at	2900011F02Rik	RIKEN cDNA 2900011F02 gene	-1.35	0.521	1.25	0.761	1.45	0.221	1.25	0.752	0.65
1425670_at	Rfxank	regulatory factor X-associated ankyrin-containing protein	1.08	0.751	1.72	0.03	-1.53	0.088	1.04	0.83	0.58
1416536_at	Mum1	melanoma associated antigen (mutated) 1	1.31	0.042	1.06	0.661	1.08	0.537	-1.26	0.094	0.55
1427615_at	Itga4	integrin alpha 4	-1.1	0.855	1.14	0.734	1.4	0.168	1.48	0.06	0.73
1460187_at	Sfrp1	secreted frizzled-related sequence protein 1	1.62	0.323	-1.85	0.356	1.29	0.438	3.86	0.111	1.23
1426022_a_at	Vill	villin-like	1.02	0.588	-1.03	0.799	1.47	0.163	1.2	0.361	0.66
1429290_at	Cbx6	chromobox homolog 6	-1.13	0.395	1.28	0.266	1.28	0.033	1.18	0.019	0.66
1450382_at	Nf2	neurofibromatosis 2	1.13	0.787	-1.11	0.521	1.42	0.206	1.43	0.426	0.72
1459207_at	---	Transcribed locus	1.35	0.664	-1.05	0.885	1.16	0.556	2.65	0.308	1.02
1459658_at	---	---	1.18	0.798	1.77	0.311	-1.99	0.026	2.74	0.229	0.93
1444989_at	LOC665914 /// LOC	hypothetical protein LOC665914 /// hypothetical protein LOC671445 /// hypothetic	1.03	0.943	1.22	0.694	1.2	0.147	-1.14	0.85	0.58
1425877_at	Hyal3	hyaluronoglucosaminidase 3	1.47	0.39	1.01	0.986	-1.02	0.938	3.34	0.243	1.2
1452319_at	Zfp82	zinc finger protein 82	1.15	0.646	1.16	0.558	1.14	0.274	-1.4	0.042	0.51
1417491_at	Ctsb	cathepsin B	-1.01	0.92	1.4	0.005	1.06	0.548	1.15	0.376	0.65
1446547_at	9330175E14Rik	RIKEN cDNA 9330175E14 gene	1.23	0.747	-1.26	0.474	1.43	0.167	1.19	0.304	0.65
1439776_at	Ogfod1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	1.01	0.98	-1.54	0.336	1.79	0.509	1.32	0.258	0.65
1416357_a_at	Mcam	melanoma cell adhesion molecule	1.15	0.298	1.32	0.383	-1.02	0.942	1.12	0.733	0.64
1443429_at	E130310K16Rik	RIKEN cDNA E130310K16 gene	1.48	0.372	-1.24	0.024	1.17	0.146	1.11	0.459	0.63
1447568_at	2010003O18Rik	RIKEN cDNA 2010003O18 gene	1.7	0.199	-1.37	0.51	1.02	0.868	1.01	0.957	0.59
1429857_at	2900092D14Rik	RIKEN cDNA 2900092D14 gene	1.35	0.345	1.09	0.882	1.02	0.975	-1.28	0.49	0.54
1426348_at	Col4a1	procollagen, type IV, alpha 1	-1.04	0.9	1.04	0.803	1.46	0.158	1.33	0.005	0.7
1416896_at	Rps6ka1	ribosomal protein S6 kinase polypeptide 1	-1.15	0.142	1.23	0.481	1.36	0.006	1.2	0.298	0.66
1440819_s_at	BC059842	cDNA sequence BC059842	1.05	0.742	1.28	0.057	1.12	0.598	-1.37	0.011	0.52
1459609_at	Arhgap10	Rho GTPase activating protein 10	1.21	0.803	1.76	0.236	-2.04	0.164	1.1	0.85	0.51
1454830_at	Fbn2	fibrillin 2	1.47	0.041	-1.04	0.922	1.02	0.913	1.38	0.397	0.71
1417056_at	Psme1	proteasome (prosome, macropain) 28 subunit, alpha	1	0.972	1.2	0.025	1.25	0.158	-1.18	0.405	0.57
1434250_at	Pak2	p21 (CDKN1A)-activated kinase 2	1.02	0.927	1.17	0.135	1.26	0.143	-1.18	0.483	0.57
1433609_s_at	Surf2	surfeit gene 2	1.06	0.519	1.3	0.146	1.09	0.511	-1.28	0.307	0.54
1429326_at	Cenpl	centromere protein L	1.59	0.086	-1.23	0.425	1.06	0.855	2.77	0.203	1.05
1420499_at	Gch1	GTP cyclohydrolase 1	1.47	0.443	-1.24	0.115	1.18	0.548	4.72	0.145	1.53
1460442_at	Rps19	ribosomal protein S19	1.35	0.661	1.08	0.901	1.03	0.952	-1.54	0.264	0.48
1442302_at	Mpg	N-methylpurine-DNA glycosylase	-1.1	0.762	1.41	0.225	1.13	0.398	1.33	0.485	0.7
1427006_at	Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1	1.05	0.737	1.05	0.717	1.36	0.365	-1.32	0.351	0.53
1429174_at	Wdr34	WD repeat domain 34	1.11	0.452	-1.32	0.411	1.59	0.138	1.6	0.192	0.75

1460331_at	Tm9sf2	transmembrane 9 superfamily member 2	1.12	0.289	1.05	0.643	1.28	0.136	-1.05	0.609	0.6
1431090_at	Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	-1.14	0.076	1.46	0.478	1.13	0.6	1.45	0.147	0.72
1447579_at	Rtn4ip1	Reticulon 4 interacting protein 1	1.59	0.647	-1.73	0.22	1.29	0.439	1.36	0.58	0.63
1459050_at	Gm996	gene model 996, (NCBI)	1.45	0.651	1.15	0.669	-1.17	0.796	1.8	0.213	0.81
1455157_a_at	BC039210	cDNA sequence BC039210	1.18	0.239	1.29	0.015	-1.01	0.948	1.01	0.95	0.62
1440569_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	-1.06	0.784	1.41	0.033	1.1	0.832	2.45	0.132	0.98
1419421_at	Ank1	ankyrin 1, erythroid	-1.38	0.466	1.07	0.884	1.67	0.048	13.62	0.195	3.74
1424864_at	Hipk2	homeodomain interacting protein kinase 2	1.15	0.797	-1.06	0.924	1.37	0.318	1.67	0.446	0.78
1456316_a_at	Acbd3	acyl-Coenzyme A binding domain containing 3	1.44	0.304	1.15	0.737	-1.15	0.764	1.29	0.591	0.68
1435183_at	Tbkbp1	TBK1 binding protein 1	1.08	0.587	1.51	0.011	-1.15	0.241	1.19	0.356	0.66
1449725_at	Gfpt1	Glutamine fructose-6-phosphate transaminase 1	1.56	0.613	1.12	0.82	-1.27	0.588	1.31	0.306	0.68
1420156_at	AA408954	expressed sequence AA408954	1.25	0.809	-1.31	0.532	1.45	0.547	1.3	0.362	0.67
1424830_at	Ccnk	cyclin K	1.08	0.854	1.03	0.741	1.35	0.116	-1.04	0.896	0.61
1448414_at	Rad1	RAD1 homolog (S. pombe)	1.28	0.41	-1.06	0.37	1.24	0.362	1.55	0.246	0.75
1420171_s_at	Myh9	myosin, heavy polypeptide 9, non-muscle	1.06	0.317	1.34	0.043	1.06	0.361	-1.22	0.469	0.56
1440443_at	E030016H06Rik	RIKEN cDNA E030016H06 gene	1.16	0.775	-1.03	0.884	1.33	0.504	1.29	0.341	0.69
1416827_at	Tbxas1	thromboxane A synthase 1, platelet	-1.01	0.942	1.24	0.342	1.23	0.094	1.79	0.024	0.81
1450658_at	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.19	0.284	1.26	0.454	1.02	0.89	-1.12	0.278	0.59
1418372_at	Adsl	adenylosuccinate lyase	1.21	0.454	-1.12	0.303	1.36	0.177	1.33	0.285	0.69
1446283_at	Dock4	Dedicator of cytokinesis 4	1	0.95	1.2	0.449	1.26	0.305	-1.08	0.761	0.6
1439421_x_at	Cbx3 /// LOC63301	chromobox homolog 3 (Drosophila HP1 gamma) /// similar to chromobox homolog	1.41	0.023	1.23	0.112	-1.22	0.324	2.03	0.01	0.86
1430283_s_at	4930418G15Rik	RIKEN cDNA 4930418G15 gene	1.04	0.947	1.2	0.79	1.23	0.618	-1.32	0.387	0.54
1429460_at	Gpr115	G protein-coupled receptor 115	1.38	0.262	-1.27	0.673	1.29	0.519	1.11	0.859	0.63
1423978_at	Sbk1	SH3-binding kinase 1	1.09	0.742	1.16	0.48	1.21	0.334	-2.86	0.101	0.15
1420647_a_at	Krt8 /// LOC434261	keratin 8 /// similar to Keratin, type II cytoskeletal 8 (Cytokeratin 8) (Cytokeratin en	-1.05	0.585	1.42	0.076	1.09	0.68	5.38	0.092	1.71
1423471_at	Ptbp2	polypyrimidine tract binding protein 2	1.39	0.448	-1.71	0.23	1.49	0.355	2.18	0.108	0.84
1415753_at	D10Bwg1364e	DNA segment, Chr 10, Brigham & Women's Genetics 1364 expressed	1.23	0.389	1.07	0.477	1.16	0.273	-1.47	0.139	0.5
1439084_at	Cxcl12	chemokine (C-X-C motif) ligand 12	-5.24	0.072	1.48	0.488	1.8	0.344	1.61	0.605	-0.09
1438059_at	LOC629147	similar to Cortexin-1	1.64	0.208	-3.44	0.172	1.54	0.293	1.78	0.325	0.38
1451544_at	Tapbpl	TAP binding protein-like	1.02	0.932	1.15	0.096	1.3	0.022	-1.24	0.612	0.56
1447920_at	Atxn10	Ataxin 10	1.37	0.569	1.36	0.551	-1.36	0.472	2.05	0.323	0.85
1419603_at	LOC672547	similar to Interferon-activatable protein 204 (Ifi-204) (Interferon-inducible protein p	1.05	0.93	1.18	0.257	1.24	0.428	-1.24	0.543	0.56
1432858_at	D730048M19Rik	RIKEN cDNA D730048M19 gene	1.36	0.609	-1.22	0.775	1.29	0.542	1.57	0.101	0.75
1457736_at	Vps37d	vacuolar protein sorting 37D (yeast)	-1.19	0.397	1.61	0.286	1.01	0.928	1.09	0.511	0.63
1443324_at	---	Transcribed locus, moderately similar to XP_515274.1 PREDICTED: similar to Fl	-1.43	0.356	1.52	0.417	1.25	0.338	1.15	0.718	0.62
1455410_at	Faim2	Fas apoptotic inhibitory molecule 2	1.1	0.848	1.07	0.793	1.3	0.219	-1.86	0.314	0.4
1438351_at	Msx2	homeo box, msh-like 2	1.13	0.461	1.37	0.373	-1.03	0.915	1.02	0.983	0.62
1422317_a_at	Il1rl1	interleukin 1 receptor-like 1	1.67	0.55	1.17	0.786	-1.59	0.484	3	0.163	1.06
1451026_at	Ftsj3	FtsJ homolog 3 (E. coli)	1.05	0.666	1.08	0.749	1.34	0.166	-1.07	0.671	0.6
1424064_at	Rab1b	RAB1B, member RAS oncogene family	1.1	0.688	-1	0.957	1.38	0.088	1.3	0.024	0.69
1456857_at	1500011B03Rik	RIKEN cDNA 1500011B03 gene	1.17	0.194	1.45	0.433	-1.17	0.547	1.2	0.631	0.66
1438731_at	---	---	1.11	0.569	1.05	0.704	1.31	0.252	-1.18	0.707	0.57
1454358_at	2900060N12Rik	RIKEN cDNA 2900060N12 gene	1.34	0.245	-1.21	0.692	1.3	0.36	1.94	0.164	0.84
1439594_at	D130062J10Rik	RIKEN cDNA D130062J10 gene	1.31	0.124	1.33	0.011	-1.21	0.472	1.05	0.819	0.62
1430186_at	Odam	odontogenic, ameloblast asssociated	1.29	0.682	-1.26	0.698	1.38	0.431	1.44	0.596	0.71
1449901_a_at	Map3k6	mitogen-activated protein kinase kinase kinase 6	1.15	0.867	1.1	0.851	1.22	0.624	-1.19	0.328	0.57
1441542_at	Drp2	dystrophin related protein 2	-1.38	0.679	1.29	0.288	1.46	0.386	1.23	0.662	0.65
1449427_at	1700016G05Rik	RIKEN cDNA 1700016G05 gene	1.34	0.296	1.13	0.651	1.01	0.965	-1.5	0.026	0.49
1421283_at	Bmp5	bone morphogenetic protein 5	1.12	0.864	1.48	0.088	-1.14	0.505	1.34	0.689	0.7
1418078_at	Psme3	proteaseome (prosome, macropain) 28 subunit, 3	1.22	0.406	-1.06	0.718	1.31	0.264	2.44	0.223	0.98
1443413_s_at	Trpm5	transient receptor potential cation channel, subfamily M, member 5	1.04	0.843	1.13	0.679	1.3	0.394	-1.26	0.095	0.55
1422988_at	Sgsh	N-sulfoglucosamine sulfohydrolase (sulfamidase)	1.26	0.818	1.14	0.683	1.08	0.843	-1.66	0.248	0.45
1418949_at	Gdf15	growth differentiation factor 15	1.18	0.16	-1.12	0.336	1.4	0.133	1.03	0.933	0.62

1453623_a_at	Rad23a	RAD23a homolog (S. cerevisiae)	1.09	0.814	-1.44	0.247	1.69	0.287	1.7	0.326	0.76
1427296_at	BC010304	cDNA sequence BC010304	1.05	0.38	-1.04	0.584	1.46	0.039	1.21	0.266	0.67
1446505_at	Cd84	CD84 antigen	1.27	0.494	1.02	0.961	1.18	0.606	-1.12	0.76	0.59
1453320_at	1700027A23Rik	RIKEN cDNA 1700027A23 gene	1.2	0.772	1.25	0.674	1.02	0.944	-4.09	0.174	-0.15
1445986_at	C86195	expressed sequence C86195	1.06	0.93	1.1	0.789	1.31	0.354	-1.29	0.637	0.55
1457201_at	As3mt	Arsenic (+3 oxidation state) methyltransferase	1.33	0.504	1.26	0.564	-1.13	0.764	1.13	0.549	0.65
1435913_at	B4galnt4	beta-1,4-N-acetyl-galactosaminyl transferase 4	-1.12	0.757	1.25	0.587	1.33	0.052	1.2	0.328	0.66
1420965_a_at	Enc1	ectodermal-neural cortex 1	1.01	0.978	1.19	0.584	1.28	0.049	-1.24	0.306	0.56
1435068_at	Pip5k2b	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	1.09	0.778	1.26	0.107	1.12	0.707	-1.63	0.245	0.46
1421266_s_at	Nfkbib	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	1.02	0.925	1.12	0.406	1.33	0.023	-1.22	0.26	0.56
1460290_at	Lpin2	lipin 2	1.34	0.679	-1.34	0.452	1.38	0.324	2.79	0.249	1.05
1458353_at	A230063L24Rik	RIKEN cDNA A230063L24 gene	-1.25	0.657	1.64	0.059	1.03	0.94	1.1	0.663	0.63
1415926_at	Nup62	nucleoporin 62	1.23	0.404	-1.02	0.863	1.26	0.104	1.3	0.425	0.69
1443784_at	A230046K03Rik	RIKEN cDNA A230046K03 gene	1.28	0.67	1.1	0.794	1.09	0.892	-1.05	0.883	0.61
1455029_at	Kif21a	kinesin family member 21A	1.09	0.732	1.12	0.238	1.27	0.263	-1.43	0.133	0.51
1460277_at	Dmbx1	diencephalon/mesencephalon homeobox 1	-1.61	0.044	1.42	0.53	1.43	0.21	1.3	0.596	0.64
1427506_at	Ppil5	peptidylprolyl isomerase (cyclophilin) like 5	1.24	0.527	-4.44	0.129	2.01	0.028	2.51	0.281	0.33
1434695_at	Dtl	denticleless homolog (Drosophila)	-1.03	0.97	1.06	0.881	1.44	0.337	3	0.205	1.12
1431237_at	Nr2f2	nuclear receptor subfamily 2, group F, member 2	-1.26	0.592	1.42	0.32	1.26	0.748	1.59	0.482	0.75
1443978_at	Ankrd41	ankyrin repeat domain 41	-1.62	0.043	1.4	0.483	1.45	0.232	2.68	0.19	0.98
1447304_at	---	Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library,	1.09	0.804	1.3	0.477	1.09	0.683	-1.21	0.119	0.57
1435928_at	---	---	1.01	0.96	1.36	0.063	1.11	0.584	-1.13	0.551	0.59
1426793_a_at	Rpl14	ribosomal protein L14	1.18	0.243	1.19	0.127	1.11	0.311	-1.25	0.051	0.56
1438981_at	Prkcb1	Protein kinase C, beta 1	1.16	0.86	1.12	0.568	1.2	0.733	-1.66	0.158	0.45
1447169_at	---	---	1.36	0.725	-1.04	0.951	1.15	0.795	3	0.03	1.12
1435005_at	Cenpe	centromere protein E	1.37	0.56	-1.06	0.812	1.16	0.647	3.78	0.218	1.31
1424027_at	Pxn	paxillin	1.05	0.745	1.14	0.216	1.28	0.016	-1.08	0.657	0.6
1428351_at	Ppm1m	protein phosphatase 1M	1.09	0.619	1.05	0.696	1.33	0.03	-1.61	0.201	0.47
1438140_a_at	Zfp64	zinc finger protein 64	1.26	0.548	-1.04	0.766	1.25	0.252	1.23	0.101	0.68
1449592_at	Tcf15	transcription factor 15	1.09	0.832	1.28	0.553	1.11	0.725	-1.25	0.327	0.56
1460431_at	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	-1	1	1.01	0.988	1.47	0.178	1.71	0.229	0.8
1448011_at	---	---	1.57	0.439	1.31	0.673	-1.68	0.372	1.38	0.447	0.64
1427684_at	Zfp264	zinc finger protein 264	-1.16	0.847	1.17	0.786	1.44	0.425	2.08	0.046	0.88
1420479_a_at	Nap1l1	nucleosome assembly protein 1-like 1	1.14	0.009	-1	0.992	1.34	0.453	1.09	0.631	0.64
1450602_at	V1rc7	vomeronasal 1 receptor, C7	-1.4	0.521	1.31	0.608	1.45	0.233	2.48	0.002	0.96
1457772_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	1.14	0.723	1.11	0.808	1.22	0.774	-1.01	0.965	0.62
1446384_at	B230339M05Rik	RIKEN cDNA B230339M05 gene	1.56	0.163	1.24	0.705	-1.47	0.293	1.02	0.927	0.59
1449837_at	Spesp1	sperm equatorial segment protein 1	1.25	0.747	1.52	0.442	-1.42	0.482	1.3	0.354	0.66
1429700_at	3110040M04Rik ///	RIKEN cDNA 3110040M04 gene /// similar to U2-associated SR140 protein /// hy	-1.99	0.23	1.15	0.737	1.82	0.288	4.02	0.234	1.25
1420173_at	D11Ertd326e	DNA segment, Chr 11, ERATO Doi 326, expressed	1.47	0.292	-1.14	0.87	1.13	0.797	1.62	0.306	0.77
1418467_at	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.11	0.11	1.11	0.779	1.25	0.207	-1.08	0.707	0.6
1416365_at	Hsp90ab1	heat shock protein 90kDa alpha (cytosolic), class B member 1	1.11	0.483	1.02	0.869	1.34	0.272	-1.01	0.97	0.62
1445994_at	---	---	-2.93	0.42	2.13	0.425	1.01	0.982	1	0.999	0.3
1453675_at	Slc16a10	solute carrier family 16 (monocarboxylic acid transporters), member 10	1.36	0.373	-1.32	0.389	1.37	0.412	6.11	0.162	1.88
1415670_at	Copg	coatomer protein complex, subunit gamma	1.2	0.105	1.12	0.18	1.16	0.296	-1.02	0.857	0.61
1441962_at	Alox5	arachidonate 5-lipoxygenase	1.17	0.724	-1.06	0.891	1.36	0.211	2.11	0.225	0.9
1422278_at	Drd3	dopamine receptor 3	1.43	0.533	1.14	0.712	-1.11	0.867	1.27	0.388	0.68
1450034_at	Stat1	signal transducer and activator of transcription 1	1.13	0.275	1.02	0.711	1.33	0.101	-1.41	0.128	0.52
1416124_at	Ccnd2	cyclin D2	-1.65	0.247	1.57	0.513	1.31	0.567	1.12	0.849	0.59
1435954_at	Zfp710	zinc finger protein 710	1.4	0.73	-1.76	0.212	1.51	0.311	2.45	0.014	0.9
1448810_at	Gne	glucosamine	-1.12	0.24	1.06	0.651	1.52	0.021	1.13	0.175	0.65
1451671_at	Gorasp1	golgi reassembly stacking protein 1	-1.12	0.58	1.05	0.805	1.53	0.178	1.22	0.02	0.67
1433278_at	5830440H09Rik	RIKEN cDNA 5830440H09 gene	1.48	0.585	-1.59	0.086	1.37	0.571	1.3	0.35	0.64

1459302_at	A030007N12Rik	RIKEN cDNA A030007N12 gene	1.3	0.63	1.51	0.326	-1.5	0.062	1.06	0.906	0.59
1456639_at	Zfp398	zinc finger protein 398	1.2	0.559	1.44	0.44	-1.19	0.529	1.13	0.746	0.64
1455271_at	LOC620695	hypothetical protein LOC620695	1.19	0.74	1.37	0.428	-1.09	0.749	1.35	0.552	0.71
1452581_at	2610304G08Rik	RIKEN cDNA 2610304G08 gene	1.2	0.408	-1.18	0.502	1.43	0.139	1.74	0.245	0.8
1446488_at	Pvrl1	Poliovirus receptor-related 1	1.42	0.575	-1.34	0.336	1.31	0.319	1.3	0.602	0.67
1416739_a_at	Brap	BRCA1 associated protein	1.39	0.601	-1.34	0.312	1.34	0.539	1.99	0.168	0.85
1459273_at	---	---	1.4	0.395	1.29	0.426	-1.26	0.432	1.92	0.049	0.84
1418626_a_at	Clu	clusterin	1.16	0.277	1.01	0.891	1.31	0.081	-1.85	0.175	0.41
1438465_at	5830428H23Rik	RIKEN cDNA 5830428H23 gene	1.22	0.58	-1.06	0.91	1.32	0.357	1.46	0.369	0.73
1449920_at	Cyp19a1	cytochrome P450, family 19, subfamily a, polypeptide 1	1.75	0.285	1.08	0.909	-1.54	0.403	1.57	0.432	0.72
1456616_a_at	Bsg	basigin	1.05	0.558	1.45	0.163	-1.02	0.887	2.45	0.133	0.98
1427511_at	B2m	Beta-2 microglobulin	1.13	0.532	1.22	0.131	1.14	0.722	-1.64	0.339	0.46
1428870_at	Nolc1	nucleolar and coiled-body phosphoprotein 1	1.32	0	-1.01	0.904	1.17	0.539	1.34	0.488	0.71
1429643_a_at	Pde1c	phosphodiesterase 1C	1.27	0.739	1.6	0.386	-1.64	0.523	1.9	0.155	0.78
1436059_at	Rfx1	regulatory factor X, 1 (influences HLA class II expression)	1.02	0.856	1.1	0.512	1.36	0.09	-1.24	0.247	0.56
1436507_at	Irak2	interleukin-1 receptor-associated kinase 2	1.24	0.65	-1.08	0.344	1.32	0.223	1.46	0.236	0.73
1435129_at	Ptp4a2	Protein tyrosine phosphatase 4a2	1.33	0.637	1.01	0.979	1.14	0.714	-1.11	0.819	0.59
1455316_x_at	Slc15a2 /// Kcnh6	Solute carrier family 15 (H+/peptide transporter), member 2 /// Potassium voltage	1.1	0.765	1.4	0.216	-1.02	0.929	1.06	0.607	0.64
1436886_x_at	Xab2	XPA binding protein 2	1.29	0.39	1.07	0.159	1.12	0.382	-1.15	0.347	0.58
1422360_at	Olfr672	olfactory receptor 672	-1.41	0.021	1.54	0.453	1.23	0.29	2.42	0.22	0.95
1450327_at	P2rxl1	purinergic receptor P2X-like 1, orphan receptor	1.25	0.557	1.16	0.722	1.07	0.722	-2.89	0.088	0.15
1421923_at	Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	1.01	0.943	1.16	0.177	1.31	0.472	-1.76	0.115	0.43
1437098_x_at	---	Transcribed locus	-1.45	0.353	1.36	0.534	1.44	0.555	1.01	0.976	0.59
1454580_at	5430427N15Rik	RIKEN cDNA 5430427N15 gene	1.34	0.57	-1.03	0.922	1.17	0.454	1.4	0.514	0.72
1445779_at	Grid1	Glutamate receptor, ionotropic, delta 1	-1.52	0.371	1.67	0.176	1.16	0.81	1.29	0.352	0.65
1457444_at	---	Adult male aorta and vein cDNA, RIKEN full-length enriched library, clone:A5300	1.04	0.913	1.34	0.68	1.1	0.279	-1.06	0.942	0.61
1428549_at	Ccdc3	coiled-coil domain containing 3	1.02	0.833	1.53	0.013	-1.07	0.849	1.13	0.656	0.65
1447300_at	AW551984	expressed sequence AW551984	1.17	0.163	1.07	0.903	1.25	0.641	-1.21	0.506	0.57
1430679_at	4933404O12Rik	RIKEN cDNA 4933404O12 gene	1.06	0.846	1.24	0.667	1.19	0.685	-1.07	0.897	0.6
1452408_at	Gpr31c	G protein-coupled receptor 31, D17Leh66c region	1.8	0.302	-2.25	0.077	1.24	0.343	1.16	0.791	0.49
1432558_a_at	Mal	myelin and lymphocyte protein, T-cell differentiation protein	1.02	0.918	1.21	0.588	1.26	0.544	-1.08	0.758	0.6
1421033_a_at	Tcerg1	transcription elongation regulator 1 (CA150)	-1.04	0.786	1.23	0.416	1.29	0.163	1.14	0.652	0.66
1444187_at	LOC544917 /// LOC	similar to spermatogenesis associated glutamate (E)-rich protein 4d /// similar to	1.58	0.558	1.47	0.345	-2.3	0.06	1.39	0.376	0.54
1454433_at	6330526H18Rik	RIKEN cDNA 6330526H18 gene	1.14	0.216	1.02	0.968	1.33	0.394	-1.85	0.023	0.41
1451569_at	Nr2c2	nuclear receptor subfamily 2, group C, member 2	1.45	0.545	-1.02	0.969	1.05	0.888	1.16	0.679	0.66
1420789_at	Klra5	killer cell lectin-like receptor, subfamily A, member 5	1.4	0.49	1.06	0.929	1.03	0.868	-1.4	0.556	0.52
1421043_s_at	Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	-1.2	0.478	1.65	0.069	1	0.977	1.06	0.843	0.63
1435527_at	Nfic	nuclear factor I/C	1.16	0.427	1.05	0.695	1.28	0.155	-1.17	0.733	0.58
1416437_a_at	Mapk8ip3	mitogen-activated protein kinase 8 interacting protein 3	1.22	0.724	-1.26	0.736	1.47	0.445	1.22	0.704	0.66
1447412_at	Gm996	gene model 996, (NCBI)	-1.46	0.366	1.72	0.237	1.09	0.866	2.41	0.058	0.94
1425535_at	Repin1	replication initiator 1	1.35	0.478	1.18	0.775	-1.05	0.797	1.24	0.759	0.68
1438461_at	---	---	-1.05	0.836	1.4	0.404	1.13	0.801	2.12	0.263	0.9
1460347_at	Krt14	keratin 14	1.36	0.361	1.03	0.903	1.1	0.572	-1.87	0.214	0.4
1439375_x_at	Aldoa /// LOC6674	aldolase 1, A isoform /// similar to Fructose-bisphosphate aldolase A (Muscle-type	1.09	0.135	1.1	0.112	1.3	0.192	-1.14	0.416	0.59
1448695_at	Prkci	protein kinase C, iota	-1.21	0.436	1.34	0.57	1.31	0.563	1.14	0.856	0.65
1451169_at	Nomo1	nodal modulator 1	1.06	0.741	-1.06	0.707	1.49	0.026	1.39	0.218	0.72
1431144_at	2810002G02Rik ///	RIKEN cDNA 2810002G02 gene /// region containing RIKEN cDNA 2810002G02	1.37	0.411	-1	0.996	1.12	0.678	1.22	0.256	0.68
1446568_at	Scap	SREBP cleavage activating protein	1.22	0.753	-1.09	0.863	1.35	0.438	1.03	0.94	0.63
1442261_at	Gpr150	G protein-coupled receptor 150	-1.25	0.603	1.4	0.607	1.29	0.738	1.55	0.571	0.75
1425860_x_at	Cklf	chemokine-like factor	1.16	0.431	1.21	0.129	1.11	0.587	-1.35	0.396	0.53
1429739_a_at	Zfp278	zinc finger protein 278	-1.1	0.233	1.21	0.221	1.37	0.033	1.15	0.398	0.66
1435958_at	Pigb	phosphatidylinositol glycan anchor biosynthesis, class B	1	0.989	1.16	0.343	1.33	0.022	-1.19	0.199	0.57
1432499_a_at	Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	-1.15	0.141	1.18	0.148	1.44	0.115	1.03	0.858	0.62

1452370_s_at	B230208H17Rik	RIKEN cDNA B230208H17 gene	1.37	0.415	1.17	0.744	-1.05	0.889	1.18	0.579	0.67
1430568_at	Zc3h13	zinc finger CCCH type containing 13	1.1	0.765	1.08	0.69	1.3	0.014	-1.03	0.896	0.62
1420873_at	Ptk9	protein tyrosine kinase 9	1.38	0.008	-1.09	0.811	1.19	0.665	1.05	0.794	0.63
1452458_s_at	Ppil5	peptidylprolyl isomerase (cyclophilin) like 5	-1.39	0.451	1.05	0.95	1.72	0.073	3.87	0.236	1.31
1421657_a_at	Sox17	SRY-box containing gene 17	1.18	0.406	-1.08	0.677	1.38	0.088	1.02	0.926	0.63
1421254_a_at	Sgcg	sarcoglycan, gamma (dystrophin-associated glycoprotein)	1.39	0.499	1.16	0.759	-1.06	0.887	1.64	0.406	0.78
1424153_s_at	Sall4	sal-like 4 (Drosophila)	-1.75	0.115	1.88	0.482	1.03	0.929	1.11	0.79	0.57
1429407_at	Pex11c	peroxisomal biogenesis factor 11c	1.17	0.045	1.19	0.46	1.13	0.377	-1.28	0.644	0.55
1430922_at	5530401A14Rik	RIKEN cDNA 5530401A14 gene	1.96	0.094	-3.47	0.17	1.24	0.793	2.71	0.279	0.61
1415890_at	Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	1.07	0.08	1.31	0.051	1.11	0.271	-1.17	0.392	0.58
1448396_at	Tmem131	transmembrane protein 131	-1.15	0.293	1.01	0.846	1.61	0.003	1.31	0.068	0.7
1448467_a_at	G430002G23Rik	RIKEN cDNA G430002G23 gene	1.11	0.368	1.52	0.2	-1.16	0.205	2.27	0.229	0.93
1422957_at	Ccr3	chemokine (C-C motif) receptor 3	1.01	0.985	1.59	0.501	-1.12	0.677	1.63	0.343	0.78
1450250_at	Otud7a	OTU domain containing 7A	-1.34	0.62	1.11	0.861	1.64	0.164	1.24	0.715	0.66
1417422_at	Gnmt	glycine N-methyltransferase	1.58	0.108	-1.11	0.701	1.01	0.979	8.34	0.285	2.46
1429533_at	Immt	inner membrane protein, mitochondrial	1.08	0.876	-1.55	0.348	1.77	0.451	1.23	0.711	0.63
1422865_at	Runx1	runt related transcription factor 1	-1.03	0.638	1.32	0.252	1.2	0.565	1.08	0.789	0.64
1423323_at	Tacstd2	tumor-associated calcium signal transducer 2	1.08	0.677	1.03	0.968	1.37	0.099	-2.6	0.024	0.22
1432884_at	2010003H20Rik	RIKEN cDNA 2010003H20 gene	1.21	0.806	-1	0.996	1.29	0.343	1.16	0.461	0.66
1422200_at	Omp	olfactory marker protein	-4.6	0.348	1.62	0.113	1.66	0.442	1.81	0.26	0.12
1415878_at	Rrm1	ribonucleotide reductase M1	-1.08	0.44	1.46	0.128	1.11	0.378	3.1	0.174	1.15
1424579_at	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), m	1.04	0.413	-1.18	0.515	1.6	0.075	1.31	0.408	0.69
1452670_at	Myl9	myosin, light polypeptide 9, regulatory	1.22	0.192	1.15	0.519	1.12	0.62	-1.14	0.211	0.59
1423417_at	Smarcc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.13	0.447	-1.27	0.14	1.58	0.17	1.35	0.12	0.7
1457980_x_at	Uck2	uridine-cytidine kinase 2	-1.05	0.702	1.1	0.733	1.45	0	1.28	0.527	0.69
1429778_at	Optn	optineurin	1.01	0.94	-1.06	0.367	1.54	0.002	2.65	0.244	1.03
1425484_at	Tox	thymocyte selection-associated HMG box gene	1.11	0.842	-1.06	0.854	1.44	0.07	1.04	0.927	0.63
1423734_at	Rac1	RAS-related C3 botulinum substrate 1	1.08	0.767	-1.09	0.28	1.5	0.078	1.08	0.352	0.64
1441850_x_at	Tcn2	transcobalamin 2	-1.16	0.113	1.15	0.109	1.48	0.222	1.12	0.334	0.65
1435062_at	1500001A10Rik	RIKEN cDNA 1500001A10 gene	-1	0.999	1.03	0.957	1.47	0.447	5.24	0.057	1.68
1420276_x_at	---	---	-1.25	0.35	1.02	0.88	1.68	0.055	1.06	0.511	0.63
1421288_at	F2rl3	coagulation factor II (thrombin) receptor-like 3	1.62	0.645	-2.08	0.398	1.4	0.492	1.42	0.518	0.59
1442187_at	Bdkrb2	bradykinin receptor, beta 2	1.27	0.549	1.27	0.708	-1.05	0.845	1.2	0.792	0.67
1425516_at	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:p	1	0.998	1.41	0.2	1.09	0.255	-1.1	0.536	0.6
1417169_at	Usp2	ubiquitin specific peptidase 2	1.13	0.819	-1.16	0.819	1.51	0.061	1.03	0.936	0.63
1442395_at	Dst	Dystonin	1.77	0.617	1.31	0.245	-2.39	0.034	1.81	0.242	0.62
1436170_a_at	Csn1s2a	casein alpha s2-like A	1.42	0.176	1.4	0.515	-1.48	0.244	1.09	0.684	0.61
1420845_at	Mrps2	mitochondrial ribosomal protein S2	-1.29	0.316	1.05	0.843	1.67	0.011	1.24	0.315	0.67
1457693_a_at	6430537H07Rik	RIKEN cDNA 6430537H07 gene	-3.09	0.104	1.64	0.319	1.53	0.033	1.3	0.314	0.35
1428764_at	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	1.43	0.343	-1.01	0.964	1.08	0.688	1.08	0.845	0.65
1452145_at	H6pd	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	1.16	0.198	1.29	0.182	1.05	0.822	-1.2	0.443	0.57
1455983_at	Cdca2	cell division cycle associated 2	-1.18	0.814	1.16	0.748	1.49	0.178	3.16	0.184	1.16
1437750_at	---	Transcribed locus	1.19	0.845	1.04	0.944	1.27	0.599	-1.31	0.543	0.55
1450413_at	Pdgfb	platelet derived growth factor, B polypeptide	-1.03	0.941	1.4	0.08	1.13	0.208	1.19	0.114	0.67
1431018_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	1.17	0.713	-1.05	0.51	1.37	0.349	1.41	0.364	0.73
1441967_at	Pddc1	Parkinson disease 7 domain containing 1	1.05	0.794	1.02	0.915	1.43	0.076	-1.22	0.088	0.57
1456254_at	Inpp4b	Inositol polyphosphate-4-phosphatase, type II	1.57	0.504	-2.41	0.235	1.51	0.2	1.29	0.488	0.49
1442665_at	C77874	expressed sequence C77874	-2.63	0.011	1.92	0.372	1.2	0.749	1.2	0.7	0.42
1437123_at	Mmrn2	multimerin 2	1.21	0.12	1.1	0.736	1.19	0.433	-1.68	0.06	0.46
1431166_at	---	---	-1.21	0.45	1.09	0.055	1.58	0.247	1.23	0.408	0.67
1445238_at	Ccl21b	chemokine (C-C motif) ligand 21b	1.14	0.664	1.77	0.176	-1.7	0.107	1.45	0.134	0.67
1433398_at	Fgd3	FYVE, RhoGEF and PH domain containing 3	1.25	0.147	1.12	0.808	1.13	0.605	-2.28	0.063	0.31
1429872_at	1700007N14Rik	RIKEN cDNA 1700007N14 gene	-1.51	0.487	1.37	0.545	1.47	0.441	1.05	0.879	0.59

1432517_a_at	Nnmt	nicotinamide N-methyltransferase	1.25	0.734	1.44	0.158	-1.24	0.534	1.79	0.02	0.81
1429177_x_at	Sox17	SRY-box containing gene 17	1.07	0.551	1.17	0.518	1.26	0.339	-1.68	0.28	0.46
1457819_at	Scn9a /// LOC6718	sodium channel, voltage-gated, type IX, alpha /// similar to sodium channel 25	1.02	0.977	-1.06	0.885	1.54	0.08	1.19	0.754	0.67
1419272_at	Myd88	myeloid differentiation primary response gene 88	1.13	0.448	1.15	0.292	1.21	0.193	-1.1	0.517	0.6
1442088_at	9230111E07Rik	RIKEN cDNA 9230111E07 gene	1.04	0.931	1.06	0.909	1.4	0.314	-1.02	0.964	0.62
1448498_at	Rps6ka4	ribosomal protein S6 kinase, polypeptide 4	1.16	0.585	1.08	0.676	1.26	0.017	-1.09	0.765	0.6
1451046_at	Zfpm1	zinc finger protein, multitype 1	1.06	0.834	-1.16	0.185	1.58	0.074	4.78	0.166	1.57
1450121_at	Scn1a	sodium channel, voltage-gated, type I, alpha	1.08	0.899	-2.32	0.005	1.99	0.212	1.57	0.225	0.58
1438804_at	10-Sep	septin 10	-1.05	0.832	1.41	0.283	1.14	0.673	1.51	0.4	0.75
1449252_at	9030611O19Rik	RIKEN cDNA 9030611O19 gene	-1.05	0.71	1.05	0.86	1.5	0.002	1.38	0.581	0.72
1440408_at	B830008J18Rik	RIKEN cDNA B830008J18 gene	1.02	0.956	1.52	0.055	-1.04	0.856	1.03	0.905	0.63
1430574_at	Cdkn3	cyclin-dependent kinase inhibitor 3	-1.08	0.78	1.47	0.277	1.1	0.663	4.6	0.208	1.53
1448962_at	Myh11	myosin, heavy polypeptide 11, smooth muscle	1.28	0.043	1	0.998	1.22	0.422	-1.48	0.349	0.51
1454333_at	Cryga	crystallin, gamma A	1.21	0.444	-1.1	0.597	1.39	0.141	1.05	0.866	0.64
1420998_at	Etv5	ets variant gene 5	1.25	0.545	-1.21	0.424	1.42	0.045	1.21	0.429	0.67
1440572_at	Dusp19	dual specificity phosphatase 19	1.28	0.705	1.11	0.864	1.11	0.803	-1.35	0.13	0.54
1438635_x_at	B930041F14Rik	RIKEN cDNA B930041F14 gene	1.13	0.413	1.2	0.302	1.18	0.503	-1.39	0.255	0.53
1456172_at	Txndc5	Thioredoxin domain containing 5	1.51	0.208	-1.05	0.653	1.04	0.933	1.45	0.316	0.74
1430289_a_at	Wdr77	WD repeat domain 77	-1.43	0.345	1.12	0.817	1.69	0.049	1.42	0.45	0.7
1427309_at	Pars2	prolyl-tRNA synthetase (mitochondrial)(putative)	1.03	0.83	1.05	0.753	1.43	0.014	-1.08	0.625	0.61
1418082_at	Nmt1	N-myristoyltransferase 1	1.31	0.51	-1.4	0.298	1.47	0.449	1.11	0.79	0.62
1415976_a_at	Carhsp1	calcium regulated heat stable protein 1	1.21	0.404	-1.17	0.477	1.44	0.458	4.89	0.234	1.59
1417236_at	Ehd3	EH-domain containing 3	1.12	0.58	-1.04	0.874	1.43	0.18	1.24	0.557	0.69
1418627_at	Gclm	glutamate-cysteine ligase , modifier subunit	1.25	0.23	-1.07	0.443	1.32	0.374	5.48	0.156	1.75
1460036_at	Ap1s2	adaptor-related protein complex 1, sigma 2 subunit	1.1	0.543	1.58	0.017	-1.21	0.195	1.03	0.891	0.63
1452801_at	Pigk	phosphatidylinositol glycan anchor biosynthesis, class K	1.57	0.184	-1.07	0.659	1	0.99	1.13	0.638	0.66
1425401_at	D11Ertd636e	DNA segment, Chr 11, ERATO Doi 636, expressed	1.02	0.97	1.46	0.452	1.03	0.944	-2.11	0.358	0.35
1454848_at	Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C	1.05	0.693	1.39	0.017	1.06	0.79	-1.1	0.631	0.6
1422944_a_at	Diap3	diaphanous homolog 3 (Drosophila)	1.24	0.14	-1.02	0.933	1.29	0.35	4.01	0.203	1.38
1437303_at	Il6st	interleukin 6 signal transducer	1.11	0.704	1.28	0.314	1.11	0.724	-1.53	0.359	0.49
1453266_at	---	---	1.18	0.352	1.31	0.047	1.01	0.922	-1.58	0.217	0.48
1418434_at	Mkrn1	makorin, ring finger protein, 1	-1.12	0.026	1.09	0.546	1.52	0.052	2.35	0.198	0.96
1450722_at	Nup50	nucleoporin 50	1.16	0.327	-1.16	0.283	1.49	0.099	1.69	0.279	0.79
1456652_at	Dtl	denticleless homolog (Drosophila)	1.27	0.065	1.35	0.576	-1.13	0.488	3.92	0.197	1.35
1440970_at	---	Transcribed locus	1.06	0.882	1.62	0.337	-1.21	0.715	1.04	0.937	0.63
1455065_x_at	Gnpda1 /// LOC231	glucosamine-6-phosphate deaminase 1 /// similar to Glucosamine-6-phosphate is	-1.05	0.752	1.03	0.916	1.53	0.085	1.23	0.317	0.68
1420632_a_at	Bscl2	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	-1.01	0.949	1.01	0.942	1.51	0.024	1.11	0.452	0.65
1432764_at	4933404I11Rik	RIKEN cDNA 4933404I11 gene	-1.59	0.365	1.63	0.09	1.25	0.289	1.02	0.915	0.58
1442099_at	Usp31	ubiquitin specific peptidase 31	1.61	0.319	-1.38	0.606	1.17	0.548	1.19	0.63	0.65
1418795_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	-1.16	0.31	1.37	0.47	1.28	0.569	1.2	0.382	0.67
1420847_a_at	Fgfr2	fibroblast growth factor receptor 2	1.13	0.593	1.13	0.704	1.25	0.579	-1.96	0.077	0.39
1425125_at	Oit3	oncoprotein induced transcript 3	1.48	0.517	1.12	0.54	-1.1	0.879	1.44	0.164	0.74
1440379_at	Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	1.95	0.098	-1.83	0.334	1.02	0.933	1.72	0.224	0.71
1444138_at	Cyp2r1	cytochrome P450, family 2, subfamily r, polypeptide 1	1.12	0.435	1.23	0.064	1.16	0.492	-1.02	0.943	0.62
1435142_at	Sft2d2	SFT2 domain containing 2	1.19	0.273	1.01	0.957	1.31	0.146	-1.22	0.14	0.57
1432280_at	2310007L24Rik	RIKEN cDNA 2310007L24 gene	1.12	0.83	-1.23	0.421	1.58	0.158	1.78	0.34	0.81
1440410_at	A930011G23Rik	RIKEN cDNA A930011G23 gene	1.67	0.465	1.08	0.891	-1.3	0.575	2.05	0.027	0.87
1416675_s_at	Plcd1	phospholipase C, delta 1	1.3	0.283	1.15	0.732	1.06	0.733	-1.32	0.663	0.55
1453226_at	3000004C01Rik	RIKEN cDNA 3000004C01 gene	-1.05	0.812	1.49	0.083	1.07	0.806	4.51	0.18	1.51
1422185_a_at	Cyb5r3	cytochrome b5 reductase 3	1.4	0.228	-1.07	0.76	1.18	0.322	1.66	0.008	0.79
1431871_at	Txndc3	thioredoxin domain containing 3 (spermatozoa)	1.22	0.758	-1	0.994	1.3	0.516	1.39	0.714	0.73
1451895_a_at	Dhcr24	24-dehydrocholesterol reductase	-1.12	0.491	1.48	0.012	1.14	0.367	1.36	0.472	0.71
1455064_at	Rab36	RAB36, member RAS oncogene family	-1.22	0.013	1.04	0.895	1.66	0.094	1.1	0.79	0.64

1447497_at	Rab21	RAB21, member RAS oncogene family	1.47	0.559	-1.12	0.813	1.15	0.765	1.25	0.622	0.69
1453159_at	Efhc1	EF-hand domain (C-terminal) containing 1	-1.06	0.841	1.35	0.128	1.22	0.397	1.01	0.951	0.63
1432138_at	1700080N15Rik	RIKEN cDNA 1700080N15 gene	1.4	0.129	-1.36	0.546	1.37	0.662	2.11	0.174	0.88
1418892_at	Rhoj	ras homolog gene family, member J	1.49	0.203	1.2	0.289	-1.22	0.274	1.33	0.324	0.7
1436618_at	Sfxn5	sideroflexin 5	1.12	0.694	-1.06	0.762	1.46	0.045	1.2	0.342	0.68
1441812_at	Cyp2u1	cytochrome P450, family 2, subfamily u, polypeptide 1	1.31	0.599	-1.7	0.11	1.62	0.146	1.24	0.43	0.62
1460439_at	BC033915	cDNA sequence BC033915	1.34	0.345	1.1	0.625	1.07	0.741	-1.18	0.493	0.58
1416629_at	Slc1a5	solute carrier family 1 (neutral amino acid transporter), member 5	-1.18	0.459	1.32	0.054	1.34	0.223	1.28	0.387	0.69
1437125_at	Camk2a	calcium/calmodulin-dependent protein kinase II alpha	1.71	0.321	1.13	0.434	-1.48	0.317	2.09	0.012	0.86
1432197_at	4933417D19Rik	RIKEN cDNA 4933417D19 gene	1.09	0.889	1.29	0.583	1.14	0.73	-1.83	0.133	0.42
1424528_at	Cgref1	cell growth regulator with EF hand domain 1	1.04	0.208	1.57	0.294	-1.1	0.834	2.08	0.157	0.89
1435024_at	4931428F04Rik	RIKEN cDNA 4931428F04 gene	1.76	0.217	-1.52	0.392	1.09	0.828	1.1	0.598	0.61
1439040_at	Cenpe	centromere protein E	-1.81	0.372	1.2	0.684	1.76	0.166	4.15	0.177	1.32
1443155_at	---	---	1.76	0.265	1.19	0.804	-1.76	0.136	1.15	0.409	0.58
1420983_at	Pctp	phosphatidylcholine transfer protein	1.21	0.569	-1.42	0.18	1.6	0.307	1.2	0.667	0.65
1431749_a_at	Rasgrp1	RAS guanyl releasing protein 1	1.28	0.364	1.02	0.972	1.22	0.456	-1.51	0.396	0.5
1439618_at	Pde10a	phosphodiesterase 10A	1.55	0.29	-1.04	0.899	1	0.991	1.14	0.458	0.66
1440355_at	Kctd12b	potassium channel tetramerisation domain containing 12b	1.1	0.458	1.67	0.059	-1.35	0.113	1.07	0.832	0.62
1432859_at	D730048M19Rik	RIKEN cDNA D730048M19 gene	1.35	0.464	1.59	0.449	-1.75	0.419	1.6	0.242	0.7
1439794_at	---	---	1.16	0.151	1.57	0.011	-1.27	0.085	1.64	0.228	0.77
1442149_at	Tbc1d16	TBC1 domain family, member 16	1.42	0.525	1.29	0.487	-1.25	0.666	1.54	0.241	0.75
1436773_x_at	Marveld1	MARVEL (membrane-associating) domain containing 1	1.04	0.909	-1.97	0.016	1.97	0.22	1.98	0.462	0.75
1425764_a_at	Bcat2	branched chain aminotransferase 2, mitochondrial	1.25	0.516	1.03	0.836	1.24	0.542	-1.05	0.824	0.62
1434285_at	Frmd4a	FERM domain containing 4A	1.15	0.066	1.48	0.033	-1.13	0.682	2.95	0.18	1.11
1424287_at	Prkx	protein kinase, X-linked	1.22	0.664	-1.18	0.487	1.45	0.399	1.18	0.465	0.67
1418889_a_at	Csnk1d	casein kinase 1, delta	1.17	0.268	-1.15	0.602	1.48	0.243	1.09	0.69	0.65
1457431_at	---	Transcribed locus	-1.54	0.141	1.63	0.275	1.24	0.745	1.15	0.181	0.62
1453891_at	Ptrf	polymerase I and transcript release factor	1.4	0.746	1.07	0.898	1.05	0.895	-1.4	0.592	0.53
1457700_at	4732474A20Rik	RIKEN cDNA 4732474A20 gene	1.08	0.788	1.29	0.399	1.14	0.301	-1.15	0.786	0.59
1418019_at	Cpd	carboxypeptidase D	1.08	0.801	-1.01	0.974	1.44	0.553	1.47	0.475	0.75
1460384_a_at	Arid4b	AT rich interactive domain 4B (Rbp1 like)	1.01	0.971	1.24	0.406	1.27	0.332	-1.03	0.877	0.62
1419008_at	Npy5r	neuropeptide Y receptor Y5	1.57	0.417	1.06	0.754	-1.13	0.772	1.61	0.539	0.78
1434185_at	LOC672245	similar to acetyl-coenzyme A carboxylase alpha	-1.15	0.662	1.16	0.313	1.48	0.513	1.05	0.518	0.64
1418358_at	Smcp	sperm mitochondria-associated cysteine-rich protein	1.76	0.005	1.1	0.848	-1.52	0.277	1	0.998	0.58
1427216_at	Ifnz	interferon zeta	1.63	0.102	-1.26	0.732	1.1	0.651	1.11	0.632	0.64
1441447_at	Nol4	nucleolar protein 4	1.54	0.483	-1.47	0.131	1.3	0.178	1.02	0.972	0.6
1440366_at	Slc24a2	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	1.9	0.467	1.06	0.873	-1.78	0.257	1.92	0.244	0.77
1439474_x_at	Nell1	RIKEN cDNA B230343H07 gene	1.64	0.369	1.21	0.75	-1.5	0.133	1.12	0.856	0.62
1419415_a_at	Rarg	retinoic acid receptor, gamma	1.15	0.121	1.14	0.138	1.22	0.438	-1.24	0.183	0.57
1450643_s_at	Acsl1	acyl-CoA synthetase long-chain family member 1	1.06	0.84	-2.06	0.034	1.97	0.125	3.33	0.171	1.08
1447944_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1.42	0.471	-1.11	0.833	1.19	0.547	1.95	0.274	0.87
1427128_at	Ptpn23	protein tyrosine phosphatase, non-receptor type 23	1.03	0.776	1.07	0.778	1.42	0.013	-1.11	0.665	0.6
1450575_at	Chrm4	cholinergic receptor, muscarinic 4	1.26	0.191	1.19	0.506	1.08	0.742	-1.65	0.404	0.47
1448779_at	Ciz1	CDKN1A interacting zinc finger protein 1	1.21	0.007	1.03	0.908	1.28	0.151	-1.11	0.349	0.6
1460600_at	LOC245350	similar to ubiquitin-conjugating enzyme E2Q (putative) 2	1.21	0.497	1.18	0.698	1.13	0.576	-2.17	0.108	0.34
1447316_at	---	Transcribed locus	-2.17	0.456	1.57	0.326	1.49	0.275	1.33	0.532	0.56
1439960_at	Rpusd2	RNA pseudouridylate synthase domain containing 2	1.24	0.462	-1.07	0.776	1.35	0.21	1.42	0.288	0.73
1438937_x_at	Ang1	angiogenin, ribonuclease A family, member 1	1.65	0.492	1.23	0.058	-1.55	0.125	1.35	0.433	0.67
1427954_at	BC048403	cDNA sequence BC048403	1.19	0.025	1.24	0.425	1.1	0.711	-1.02	0.893	0.62
1459426_at	Scel	Sciellin	-2.69	0.364	1.08	0.925	2.07	0.114	1.73	0.196	0.55
1459185_at	Npat	Nuclear protein in the AT region	1.56	0.136	1.23	0.061	-1.36	0.277	1.21	0.453	0.66
1445188_at	Gphn	Gephyrin	1.64	0.478	1.31	0.578	-1.75	0.21	1.24	0.645	0.61
1418858_at	Aox3	aldehyde oxidase 3	1.61	0.619	-1.12	0.117	1.01	0.943	1.01	0.966	0.63

1457001_at	Cenpk	centromere protein K	-1.6	0.111	1.24	0.604	1.66	0.234	3.42	0.247	1.18
1458636_at	2610206B13Rik	RIKEN cDNA 2610206B13 gene	-1.97	0.383	1.36	0.516	1.66	0.394	1.08	0.428	0.53
1440739_at	Vegfc	vascular endothelial growth factor C	1.04	0.795	1.24	0.22	1.24	0.259	-1.53	0.073	0.5
1416376_at	Tmem97	transmembrane protein 97	1.43	0.082	1.28	0.04	-1.24	0.094	1.62	0.258	0.77
1432378_at	C030004G16Rik	RIKEN cDNA C030004G16 gene	1.51	0.584	1.36	0.461	-1.53	0.368	1.4	0.698	0.68
1425671_at	Homer1	homer homolog 1 (Drosophila)	1.51	0.087	1.39	0.433	-1.61	0.318	1.42	0.366	0.68
1454174_a_at	C330007P06Rik	RIKEN cDNA C330007P06 gene	1.41	0.367	-1.3	0.498	1.34	0.517	1.94	0.241	0.85
1421529_a_at	Txnrd1	thioredoxin reductase 1	-1.11	0.07	1.27	0.046	1.35	0.004	1.41	0.041	0.73
1423790_at	Dap	death-associated protein	-1.17	0.401	1.42	0.168	1.25	0.056	1.32	0	0.71
1418270_at	Adamts8	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.25	0.709	-1.77	0.131	1.71	0.102	1.06	0.467	0.56
1460051_at	BC038613	cDNA sequence BC038613	-1.8	0.236	1.89	0.198	1.08	0.211	1.3	0.487	0.62
1435566_s_at	Araf	v-raf murine sarcoma 3611 viral oncogene homolog	1.02	0.952	-1.03	0.948	1.53	0.104	1.13	0.5	0.66
1423401_at	Etv6	ets variant gene 6 (TEL oncogene)	-1.13	0.578	1.02	0.87	1.62	0.218	1.29	0.241	0.7
1434917_at	Cobl	cordon-bleu	1.35	0.061	-1.05	0.858	1.23	0.459	1.83	0.165	0.84
1455007_s_at	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	1.12	0.482	-1.08	0.744	1.48	0.255	1.46	0.197	0.75
1447762_x_at	Car12	carbonic anyhydrase 12	-1.98	0.12	1.71	0.257	1.31	0.596	1	0.994	0.51
1416053_at	Lrrn1	leucine rich repeat protein 1, neuronal	1.45	0.336	-2.22	0.384	1.63	0.403	1.05	0.844	0.48
1452287_at	---	Mus musculus, clone IMAGE:4527696, mRNA	1.68	0.46	-1.36	0.268	1.11	0.772	1.09	0.646	0.63
1423614_at	Lrrc8c	leucine rich repeat containing 8 family, member C	1.09	0.75	-1.06	0.857	1.49	0.139	1.29	0.054	0.7
1434611_at	Rnf123	ring finger protein 123	1.12	0.608	-1.01	0.917	1.42	0.127	3.21	0.161	1.18
1443372_at	---	12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C53(	1.45	0.061	1.31	0.181	-1.3	0.299	1.01	0.942	0.62
1459614_at	Lama5	laminin, alpha 5	-1.56	0.578	1.11	0.774	1.78	0.093	1.72	0.49	0.76
1438433_at	Whdc1	WAS protein homology region 2 domain containing 1	1.42	0.403	-1.28	0.535	1.33	0.384	1.16	0.392	0.66
1434253_s_at	Tmcc3	transmembrane and coiled coil domains 3	1.18	0.397	1.2	0.05	1.15	0.278	-1.24	0.406	0.57
1435084_at	C730049O14Rik	RIKEN cDNA C730049O14 gene	1.34	0.428	1.11	0.676	1.08	0.389	-1.13	0.679	0.6
1439326_at	Lnpep	leucyl/cystinyl aminopeptidase	1.44	0.413	1.34	0.447	-1.35	0.121	1.13	0.696	0.64
1439630_x_at	Sbsn	suprabasin	1.07	0.615	1.14	0.599	1.32	0.362	-1.02	0.952	0.63
1450997_at	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	1.05	0.871	1.3	0.191	1.18	0.505	-1.89	0.048	0.41
1444629_at	Als2cr13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 13 (hum	1.66	0.42	1.28	0.611	-1.7	0.287	1.33	0.331	0.64
1417412_at	F8a	factor 8-associated gene A	1.09	0.714	1.14	0.405	1.3	0.413	-1.3	0.409	0.56
1417855_at	Fbxl15	F-box and leucine-rich repeat protein 15	-1.05	0.823	1.07	0.7	1.5	0.007	1.2	0.467	0.68
1450363_at	Asb7	ankyrin repeat and SOCS box-containing protein 7	1.41	0.539	-1.92	0.112	1.6	0.504	1.57	0.228	0.66
1445136_at	---	---	1.29	0.369	1.07	0.858	1.17	0.636	-1.25	0.726	0.57
1444008_at	H2afy2	H2A histone family, member Y2	1.37	0.484	1.12	0.744	1.04	0.845	-3.38	0.051	0.04
1436568_at	Jam2	junction adhesion molecule 2	1.29	0.173	1.13	0.63	1.11	0.279	-1.35	0.37	0.55
1450260_at	Grpr	gastrin releasing peptide receptor	1.25	0.067	1.22	0.626	1.05	0.705	-1.46	0.247	0.52
1451985_at	Lrrk1	leucine-rich repeat kinase 1	1.39	0.122	1.07	0.338	1.07	0.658	-1.46	0.342	0.52
1425997_a_at	Pign	phosphatidylinositol glycan anchor biosynthesis, class N	1.58	0.251	-1.17	0.806	1.09	0.811	1.04	0.948	0.64
1421217_a_at	Lgals9	lectin, galactose binding, soluble 9	1.27	0.536	-1.12	0.626	1.37	0.245	1.19	0.44	0.68
1417161_at	Cdk2ap2	CDK2-associated protein 2	1.22	0.24	1.03	0.848	1.28	0.157	-1.28	0.2	0.56
1450627_at	Ank	progressive ankylosis	1.19	0.249	-1.23	0.024	1.52	0.042	2.46	0.163	0.99
1416010_a_at	Ehd1	EH-domain containing 1	1.11	0.134	1.21	0.004	1.21	0.262	-1.3	0.337	0.56
1427164_at	Il13ra1	interleukin 13 receptor, alpha 1	1.03	0.897	1.4	0.283	1.11	0.837	-1.01	0.984	0.63
1433060_at	6230426I18Rik	RIKEN cDNA 6230426I18 gene	1.49	0.591	1.29	0.53	-1.32	0.383	1.43	0.188	0.72
1452943_at	Tmem65	transmembrane protein 65	1.44	0.283	-1.16	0.68	1.23	0.587	2.16	0.182	0.92
1436465_at	Klhl1	kelch-like 1 (Drosophila)	1.91	0.008	1.1	0.769	-1.91	0.32	2.38	0.14	0.87
1440389_at	---	---	-1.68	0.644	1.05	0.926	1.89	0.141	1.67	0.079	0.73
1433668_at	Pnrc1	proline-rich nuclear receptor coactivator 1	1.06	0.645	1.32	0.274	1.15	0.384	-1.36	0.217	0.54
1421869_at	Trim44	tripartite motif-containing 44	-1.02	0.882	1.36	0.653	1.19	0.572	1.28	0.345	0.7
1432376_at	3830403N18Rik	RIKEN cDNA 3830403N18 gene	1.34	0.286	1.64	0.547	-1.81	0.097	1.31	0.666	0.62
1434409_at	Armcx6	armadillo repeat containing, X-linked 6	1.09	0.537	1.48	0.412	-1.04	0.926	1.33	0.301	0.71
1448592_at	Crtap	cartilage associated protein	1.19	0.095	1.29	0.017	1.05	0.81	-1.02	0.904	0.63
1422348_at	LOC676708	similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor	1.07	0.923	1.03	0.906	1.43	0.21	-1.05	0.95	0.62

1454023_a_at	D1Bwg1363e	DNA segment, Chr 1, Brigham & Women's Genetics 1363 expressed	-1.05	0.578	1.34	0.258	1.25	0.4	1.09	0.478	0.65
1426642_at	Fn1	fibronectin 1	1.17	0.363	1.08	0.255	1.28	0.274	-1.04	0.735	0.62
1455834_x_at	Tacc3	transforming, acidic coiled-coil containing protein 3	-1.39	0.09	1.61	0.154	1.21	0.26	2.59	0.268	1
1434667_at	Col8a2	procollagen, type VIII, alpha 2	1.01	0.96	-1.89	0.335	1.99	0.015	1.27	0.42	0.6
1449005_at	Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	1.03	0.96	-1.63	0.612	1.89	0.142	1.18	0.592	0.62
1447541_s_at	Itgae	integrin, alpha E, epithelial-associated	1.06	0.856	1.81	0.081	-1.5	0.062	1.1	0.794	0.62
1426080_a_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	-1.97	0.343	1.55	0.51	1.47	0.281	1.55	0.405	0.65
1417401_at	Rai14	retinoic acid induced 14	1.12	0.557	1.19	0.47	1.22	0.577	-1.49	0.21	0.51
1418665_at	Impa2	inositol (myo)-1(or 4)-monophosphatase 2	1.04	0.793	-1.18	0.757	1.64	0.157	1.11	0.481	0.65
1421065_at	Jak2	Janus kinase 2	1.06	0.32	1.02	0.922	1.46	0.001	-1.25	0.156	0.57
1422063_a_at	Pex5	peroxisome biogenesis factor 5	-1.13	0.397	1.03	0.898	1.62	0.091	1.13	0.732	0.66
1451611_at	Hrasls3	HRAS like suppressor 3	-1.03	0.699	1.15	0.087	1.42	0.039	2.24	0.176	0.94
1458275_at	2310045A20Rik	RIKEN cDNA 2310045A20 gene	1.91	0.179	-1.78	0.353	1.06	0.851	1.66	0.392	0.71
1445476_at	---	Mus musculus, clone IMAGE:1313576, mRNA	1.48	0.076	1.01	0.972	1.04	0.942	-1.41	0.576	0.53
1424453_at	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	-1.06	0.762	1.14	0.716	1.45	0.346	3.76	0.229	1.32
1455603_at	---	Transcribed locus	1.36	0.638	1.32	0.522	-1.17	0.38	1.15	0.783	0.66
1427488_a_at	Birc6	baculoviral IAP repeat-containing 6	1.68	0.314	-1.5	0.38	1.18	0.497	1.03	0.73	0.6
1420594_at	Bard1	BRCA1 associated RING domain 1	-1.21	0.309	1.57	0.36	1.14	0.759	6.76	0.174	2.06
1431081_a_at	Plscr3	phospholipid scramblase 3	1.27	0.014	-1.07	0.695	1.33	0.066	1.29	0.24	0.71
1452306_at	Zfyve26	zinc finger, FYVE domain containing 26	1.13	0.258	1.04	0.791	1.37	0.018	-1.35	0.233	0.55
1443969_at	Irs2	insulin receptor substrate 2	-1.08	0.867	1.5	0.094	1.11	0.419	1.37	0.109	0.73
1455363_at	Bai1	brain-specific angiogenesis inhibitor 1	1.7	0.343	1.09	0.871	-1.34	0.28	1	0.999	0.61
1460337_at	Sh3kbp1	SH3-domain kinase binding protein 1	1.05	0.705	1.34	0.188	1.14	0.594	-1.58	0.175	0.49
1441174_a_at	Lmln	leishmanolysin-like (metallopeptidase M8 family)	1.53	0.026	-1.42	0.236	1.3	0.33	2.47	0.008	0.97
1443967_at	4930517K23Rik	RIKEN cDNA 4930517K23 gene	-1.43	0.143	1.16	0.754	1.68	0.298	1.55	0.488	0.74
1417772_at	Grhpr	glyoxylate reductase/hydroxypyruvate reductase	1	0.979	-1.15	0.373	1.66	0.019	1.03	0.848	0.64
1416554_at	Pdlim1	PDZ and LIM domain 1 (elfin)	1.24	0.341	1.24	0.26	1.06	0.606	-1.13	0.213	0.6
1428988_at	Abcc3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	1.67	0.069	-1.34	0.46	1.12	0.629	1.64	0.32	0.77
1435877_at	Stk38l	serine/threonine kinase 38 like	1.16	0.395	1.14	0.746	1.24	0.343	-1.16	0.171	0.59
1433857_at	Fath /// LOC672128	fat tumor suppressor homolog (Drosophila) /// similar to fat tumor suppressor hom	1.26	0.306	1.1	0.207	1.19	0.309	-1.5	0.137	0.51
1451935_a_at	Spint2	serine protease inhibitor, Kunitz type 2	1.09	0.567	1.2	0.181	1.25	0.486	-1.04	0.862	0.62
1449076_x_at	Adi1	acireductone dioxygenase 1	-1.16	0.74	1	1	1.68	0.225	1.28	0.181	0.7
1445604_at	---	Transcribed locus	1.1	0.704	1.26	0.074	1.18	0.353	-1.34	0.332	0.55
1434698_at	9130229H14Rik	RIKEN cDNA 9130229H14 gene	1.39	0.139	1.06	0.708	1.09	0.553	-1.2	0.303	0.59
1431127_at	Zfp297b	zinc finger protein 297B	1.06	0.734	-2	0.24	1.98	0.255	2.44	0.181	0.87
1422691_at	Sptlc1	serine palmitoyltransferase, long chain base subunit 1	1.65	0.249	-1.73	0.323	1.31	0.322	1.28	0.667	0.63
1448001_x_at	Cdca3	cell division cycle associated 3	1.37	0.608	1.47	0.232	-1.42	0.072	1.49	0.591	0.73
1432289_a_at	Jsrp1	junctional sarcoplasmic reticulum protein 1	1.54	0.533	-1.15	0.718	1.13	0.723	1.33	0.458	0.71
1445087_at	---	---	-1.55	0.243	1.86	0.082	1.03	0.92	1.27	0.494	0.65
1433685_a_at	C330011F01Rik ///	RIKEN cDNA C330011F01 gene /// RIKEN cDNA 6430706D22 gene	1.21	0.429	-1.03	0.853	1.36	0.111	1.77	0.073	0.83
1458381_at	Clic5	chloride intracellular channel 5	1.1	0.752	1.42	0.271	1.02	0.92	-1.51	0.008	0.51
1436352_at	Cep78	centrosomal protein 78	-1.19	0.482	1.52	0.128	1.18	0.007	1.12	0.746	0.66
1436939_at	Unc45b	unc-45 homolog B (C. elegans)	1.2	0.517	1.11	0.575	1.23	0.514	-1.04	0.915	0.62
1436077_a_at	Fcho1	FCH domain only 1	1.23	0.103	-1.04	0.908	1.35	0.345	1.3	0.164	0.71
1456135_s_at	Pxn	paxillin	1.12	0.008	1.09	0.041	1.33	0.02	-1.11	0.672	0.61
1437316_at	Fbxw19	F-box and WD-40 domain protein 19	1.01	0.988	-1.01	0.984	1.54	0.043	3.19	0.112	1.18
1452382_at	Dnm3os	dynamin 3, opposite strand	1.62	0.391	1.17	0.703	-1.31	0.115	1.04	0.899	0.63
1438661_a_at	Arf2	ADP-ribosylation factor 2	1.26	0.727	1.16	0.721	1.12	0.765	-1.17	0.716	0.59
1456796_at	Snai3	snail homolog 3 (Drosophila)	1.13	0.879	1.08	0.543	1.33	0.15	-1.57	0.259	0.49
1455690_at	---	---	-1.2	0.798	1.36	0.294	1.34	0.035	1.28	0.413	0.7
1420004_s_at	Pom121	nuclear pore membrane protein 121	-1.38	0.166	1.13	0.22	1.69	0.181	1.06	0.671	0.63
1431791_a_at	Ptpn13	protein tyrosine phosphatase, non-receptor type 13	1.14	0.738	-1.12	0.819	1.51	0.645	1.31	0.57	0.71
1418123_at	Unc119	unc-119 homolog (C. elegans)	1.06	0.671	-1.13	0.334	1.6	0.151	1.09	0.491	0.65

1435057_x_at	Polr1e	polymerase (RNA) I polypeptide E	1.14	0.387	1.05	0.741	1.36	0.126	-1.47	0.148	0.52
1425249_a_at	Tyro3	TYRO3 protein tyrosine kinase 3	1.8	0.101	-2.55	0.068	1.35	0.377	2.29	0.277	0.72
1432434_at	4930522N08Rik	RIKEN cDNA 4930522N08 gene	1.8	0.401	-1.38	0.182	1.02	0.963	1.35	0.471	0.7
1455453_at	Gemin5	gem (nuclear organelle) associated protein 5	-1.02	0.947	1.24	0.518	1.32	0.391	1.12	0.722	0.67
1455263_at	9030625A04Rik	RIKEN cDNA 9030625A04 gene	-1.22	0.377	1.33	0.028	1.39	0.438	1.12	0.324	0.66
1451755_a_at	Apobec1	apolipoprotein B editing complex 1	1.1	0.418	1.26	0.083	1.18	0.432	-1.3	0.52	0.56
1427014_at	Dennd4b	DENN/MADD domain containing 4B	1	0.96	1.14	0.229	1.39	0.216	-1.76	0.154	0.45
1449024_a_at	Hexa	hexosaminidase A	1.07	0.468	1.31	0.002	1.17	0.177	-1.01	0.983	0.63
1437234_x_at	Prmt2	protein arginine N-methyltransferase 2	1.08	0.124	1.46	0.503	1	0.994	-1.4	0.279	0.54
1446332_at	Pcdhgc3	Protocadherin gamma subfamily C, 3	1.56	0.134	1.23	0.554	-1.32	0.169	1.1	0.784	0.64
1433144_at	Alg2	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase	-1.47	0.622	1.6	0.112	1.27	0.554	1.24	0.283	0.66
1421284_at	Pign	phosphatidylinositol glycan anchor biosynthesis, class N	-1.07	0.716	1.33	0.173	1.28	0.232	1.06	0.745	0.65
1433332_at	C030004M13Rik	RIKEN cDNA C030004M13 gene	-2.46	0.018	1.32	0.33	1.81	0.166	1.5	0.314	0.54
1417299_at	Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	-1.38	0.122	1.22	0.483	1.6	0.054	3.7	0.199	1.28
1445324_s_at	Greb1	gene regulated by estrogen in breast cancer protein	-1.47	0.619	1.15	0.759	1.71	0.33	2.36	0.339	0.94
1440241_at	Trpm1	Transient receptor potential cation channel, subfamily M, member 1	-1.12	0.843	1.35	0.478	1.3	0.372	1.6	0.262	0.78
1450844_at	Stx6	syntaxin 6	1.03	0.81	1.02	0.895	1.5	0.099	-1.4	0.029	0.54
1432631_at	1190002C06Rik	RIKEN cDNA 1190002C06 gene	1.59	0.493	1.27	0.414	-1.45	0.065	1.17	0.216	0.64
1421660_at	Scn9a /// LOC6718	sodium channel, voltage-gated, type IX, alpha /// similar to sodium channel 25	-1.88	0.283	1.82	0.324	1.19	0.703	2.14	0.062	0.82
1424550_at	Zfyve27	zinc finger, FYVE domain containing 27	1.27	0.102	1.05	0.802	1.23	0.106	-1.34	0.014	0.55
1450470_at	---	---	1.45	0.447	1.22	0.696	-1.13	0.621	1.47	0.483	0.75
1429795_at	1700001L05Rik	RIKEN cDNA 1700001L05 gene	-1.01	0.979	1.35	0.435	1.2	0.615	2.74	0.274	1.07
1418550_x_at	Defcr-rs1	defensin related sequence cryptdin peptide (paneth cells)	1.33	0.563	-1.06	0.864	1.28	0.572	1.06	0.801	0.65
1427918_a_at	Rhoq	ras homolog gene family, member Q	1	0.97	1.4	0.006	1.14	0.17	-1.4	0.235	0.54
1420052_x_at	Psmb1	proteasome (prosome, macropain) subunit, beta type 1	1.51	0.452	-1.28	0.268	1.26	0.555	1.38	0.249	0.72
1460719_a_at	P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	1.25	0.054	-1.34	0.545	1.55	0.178	2.09	0.313	0.89
1448590_at	Col6a1	procollagen, type VI, alpha 1	1.44	0.27	1.18	0.38	-1.08	0.764	1.26	0.021	0.7
1429808_at	1110020C03Rik	RIKEN cDNA 1110020C03 gene	-1.31	0.677	1.56	0.085	1.22	0.327	1.6	0.368	0.77
1459664_at	Wdr31	WD repeat domain 31	1.01	0.967	1.55	0.326	-1.01	0.949	1.14	0.623	0.67
1448623_at	Tmem123	transmembrane protein 123	1.04	0.018	1.31	0.034	1.19	0.261	-1.39	0.152	0.54
1447901_x_at	Sfi1 /// LOC673420	Sfi1 homolog, spindle assembly associated (yeast) /// similar to spindle assembly	1.03	0.662	1.37	0.1	1.15	0.092	-1.26	0.567	0.57
1418671_at	Capn5	calpain 5	-1.22	0.456	1.31	0.634	1.42	0.099	2.68	0.13	1.05
1447285_at	---	---	1.7	0.527	1.07	0.734	-1.28	0.59	1.36	0.384	0.71
1435145_at	Igsf4d	immunoglobulin superfamily, member 4	1.08	0.924	1.41	0.506	1.06	0.775	-3.13	0.075	0.1
1446074_at	Mosc1	MOCO sulphurase C-terminal domain containing 1	1.71	0.064	-1.4	0.116	1.13	0.833	2.28	0.037	0.93
1431526_at	LOC672430	hypothetical protein LOC672430	-1.3	0.74	1.11	0.852	1.67	0.105	2.22	0.114	0.93
1454915_at	Rab3gap2	RAB3 GTPase activating protein subunit 2	1.16	0.119	-1.07	0.72	1.45	0.078	1.1	0.789	0.66
1442118_at	---	Transcribed locus	-1.27	0.069	1.06	0.706	1.7	0.089	1.53	0.255	0.75
1426144_x_at	Trdn	triadin	-2.1	0.538	1.1	0.823	1.97	0.367	2.6	0.005	0.9
1437266_at	Txndc2	thioredoxin domain containing 2 (spermatozoa)	1.43	0.321	1.49	0.308	-1.6	0.424	1.12	0.752	0.61
1452305_s_at	2610510J17Rik	RIKEN cDNA 2610510J17 gene	1.58	0.39	-1.11	0.825	1.07	0.797	3.06	0.227	1.15
1431420_s_at	2610524G07Rik	RIKEN cDNA 2610524G07 gene	1.18	0.504	1.08	0.575	1.29	0.328	-1.1	0.742	0.61
1426837_at	Metap1	methionyl aminopeptidase 1	1.26	0.511	-1.06	0.896	1.34	0.313	1.24	0.636	0.7
1424330_at	Senp1	SUMO1/sentrin specific peptidase 1	1.13	0.364	-1.09	0.693	1.5	0.145	1.21	0.425	0.69
1456598_at	LOC545761 /// AU0	similar to PRAME family member 8 /// expressed sequence AU018829 /// similar t	-1.04	0.867	1.18	0.727	1.41	0.121	1.1	0.827	0.66
1429011_x_at	Snrp70	U1 small nuclear ribonucleoprotein polypeptide A	1.05	0.904	1.18	0.786	1.32	0.34	-1.18	0.344	0.59
1450405_at	Mrpl19	mitochondrial ribosomal protein L19	1.32	0.317	-1.07	0.43	1.3	0.124	1.05	0.855	0.65
1439099_at	Nova2	neuro-oncological ventral antigen 2	-1.1	0.588	1.41	0.33	1.23	0.207	1.01	0.764	0.64
1433488_x_at	Gns	glucosamine (N-acetyl)-6-sulfatase	1.05	0.632	1.1	0.394	1.39	0.063	-1.14	0.713	0.6
1446049_at	---	---	1.66	0.256	1.01	0.981	-1.14	0.241	1.61	0.011	0.79
1443356_at	Arpp21	Cyclic AMP-regulated phosphoprotein, 21	-1	0.999	1.32	0.644	1.23	0.732	2.23	0.2	0.94
1450325_at	Angpt4	angiopoietin 4	1.19	0.388	1.28	0.406	1.07	0.723	-2.37	0.109	0.29
1426134_at	Trdn	triadin	1.38	0.615	1.07	0.905	1.1	0.746	-1.15	0.371	0.6

1428548_at	Pak4	p21 (CDKN1A)-activated kinase 4	-1.07	0.491	1.59	0.004	1.03	0.748	2.02	0.224	0.89
1418080_at	B4galt2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	1.39	0.253	1.18	0.767	-1.02	0.942	1.37	0.475	0.73
1450663_at	Thbs2	thrombospondin 2	1.37	0.002	1.05	0.943	1.13	0.773	-1.11	0.795	0.61
1443965_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420435E1	-1.14	0.766	1.56	0.544	1.11	0.622	1.2	0.544	0.68
1451861_at	4930519N16Rik	RIKEN cDNA 4930519N16 gene	-1.17	0.721	1.62	0.344	1.08	0.758	1.4	0.051	0.73
1425596_at	AI317395	expressed sequence AI317395	1.13	0.256	-1.01	0.933	1.43	0.103	1.8	0.21	0.84
1459121_at	---	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030	-1.01	0.953	1.47	0.459	1.1	0.683	1.12	0.348	0.67
1458437_at	---	Transcribed locus	-1.48	0.466	1.77	0.044	1.11	0.747	1.31	0.584	0.68
1453111_a_at	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed	1.01	0.923	-1.03	0.842	1.57	0.096	2.44	0.208	1
1448355_at	Prss16	protease, serine, 16 (thymus)	-2.31	0.261	1.96	0.163	1.16	0.577	1.2	0.719	0.5
1459699_at	---	Transcribed locus	1.22	0.744	1.29	0.358	1.04	0.786	-2.65	0.38	0.23
1445746_at	LOC630474 /// LOC	hypothetical protein LOC630474 /// hypothetical protein LOC630475 /// hypothetic	1.71	0.556	1.4	0.556	-2.27	0.092	1.55	0.357	0.6
1418295_s_at	Dgat1	diacylglycerol O-acyltransferase 1	1	1	-1.07	0.725	1.62	0.081	1.17	0.579	0.68
1453603_at	2700022O18Rik	RIKEN cDNA 2700022O18 gene	1.11	0.654	1.28	0.339	1.17	0.601	-1.04	0.899	0.63
1443832_s_at	Sdpr	serum deprivation response	1.4	0.058	1.39	0.264	-1.31	0.205	1.29	0.574	0.69
1443072_at	---	---	-1.46	0.178	1.58	0.236	1.29	0.529	1.29	0.599	0.67
1454509_at	4930444E06Rik	RIKEN cDNA 4930444E06 gene	-2.37	0.245	1.49	0.484	1.64	0.067	2.88	0.001	0.91
1432413_at	1810044A24Rik	RIKEN cDNA 1810044A24 gene	1.37	0.64	-1.72	0.058	1.61	0.183	1.04	0.879	0.57
1430687_at	6330545A04Rik	RIKEN cDNA 6330545A04 gene	1.42	0.144	-1.09	0.778	1.21	0.459	1.1	0.672	0.66
1453604_a_at	Hbs1l	Hbs1-like (S. cerevisiae)	1.21	0.695	-1.23	0.668	1.52	0.323	1.47	0.462	0.74
1422029_at	Ccl20	chemokine (C-C motif) ligand 20	1.08	0.115	1.42	0.284	1.06	0.926	-1.42	0.496	0.53
1439008_at	Zfp319	zinc finger protein 319	1.04	0.698	1.03	0.904	1.49	0.08	-1.27	0.331	0.57
1458721_at	Pcdhgc3	Protocadherin gamma subfamily C, 3	1.59	0.099	1.23	0.564	-1.36	0.138	1.16	0.105	0.66
1442969_at	---	---	-1.1	0.604	1	0.999	1.65	0.205	1.78	0.106	0.83
1425366_a_at	Hus1	Hus1 homolog (S. pombe)	-1.73	0.413	1.63	0.165	1.35	0.283	1.33	0.424	0.64
1415793_at	Pnpo	pyridoxine 5'-phosphate oxidase	-1.03	0.805	1.08	0.502	1.51	0.146	3.75	0.201	1.33
1432774_at	2610105M22Rik	RIKEN cDNA 2610105M22 gene	1.37	0.03	1.44	0.264	-1.34	0.252	1.33	0.197	0.7
1442108_at	Rnf25	Ring finger protein 25	1.4	0.318	1.09	0.834	1.06	0.69	-1.45	0.355	0.53
1416382_at	Ctsc	cathepsin C	1.24	0.44	1.24	0.13	1.07	0.314	-1.08	0.682	0.62
1432123_at	4930455H04Rik	RIKEN cDNA 4930455H04 gene	1.26	0.504	1.63	0.28	-1.49	0.187	1.2	0.69	0.65
1419522_at	Zmynd19	zinc finger, MYND domain containing 19	1.2	0.597	-1.19	0.396	1.52	0.275	1.94	0.324	0.87
1460291_at	Cdk6	cyclin-dependent kinase 6	1.26	0.232	1.95	0.289	-2.9	0.011	3.15	0.263	0.86
1447825_x_at	Pcdh8	protocadherin 8	1.51	0.335	1.29	0.646	-1.31	0.446	2.67	0.176	1.04
1427388_at	Lrrc2	leucine rich repeat containing 2	1.57	0.667	1.22	0.506	-1.3	0.467	1.48	0.48	0.74
1442199_at	Btnl2	butyrophilin-like 2	1.08	0.909	1.2	0.734	1.27	0.718	-1.51	0.441	0.51
1436363_a_at	Nfix	nuclear factor I/X	1.25	0.11	-1.49	0.051	1.64	0.038	1.92	0.107	0.83
1427889_at	Spna2 /// LOC3813	spectrin alpha 2 /// similar to Spectrin alpha chain, brain (Spectrin, non-erythroid a	1.22	0.128	1.23	0.008	1.1	0.426	-1.4	0.2	0.54
1431247_at	1300014J16Rik	RIKEN cDNA 1300014J16 gene	-1.03	0.977	1.37	0.315	1.22	0.641	1.14	0.317	0.68
1459717_at	Olfr1344	Olfactory receptor 1344	-1.55	0.562	1.43	0.571	1.48	0.588	1.22	0.197	0.65
1437313_x_at	Hmgb2 /// LOC678	high mobility group box 2 /// high mobility group box 2 /// high mobility group box 2	-1.22	0.441	1.53	0.04	1.21	0.583	1.64	0.297	0.79
1442172_at	Prickle1	Prickle like 1 (Drosophila)	1.62	0.662	1	0.995	-1.07	0.19	1.22	0.613	0.69
1430815_at	4930534B04Rik	RIKEN cDNA 4930534B04 gene	1.45	0.392	-1.44	0.196	1.41	0.478	1.12	0.812	0.64
1436772_at	Gria4	Glutamate receptor, ionotropic, AMPA4 (alpha 4)	1.01	0.98	1.53	0.496	1.02	0.959	-1.08	0.929	0.62
1417038_at	9-Sep	septin 9	1.03	0.771	1.13	0.556	1.41	0.124	-1.2	0.558	0.59
1448200_at	Tcn2	transcobalamin 2	-1.02	0.887	1.21	0.089	1.37	0.192	1.09	0.382	0.66
1425962_at	Klrb1f	killer cell lectin-like receptor subfamily B member 1F	1.06	0.762	1.05	0.902	1.44	0.255	-4.49	0.013	-0.23
1445274_at	BC024063	cDNA sequence BC024063	1.35	0.536	1.18	0.69	1.03	0.833	-1.82	0.102	0.43
1432701_at	2810403G07Rik	RIKEN cDNA 2810403G07 gene	-1.36	0.076	1.09	0.75	1.73	0.125	1.16	0.729	0.66
1456340_at	2610205E22Rik	RIKEN cDNA 2610205E22 gene	1.51	0.137	1.08	0.714	-1.03	0.918	1.16	0.502	0.68
1421224_a_at	Tcf2	transcription factor 2	1.04	0.953	1.4	0.455	1.13	0.452	-1.1	0.687	0.61
1426804_at	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.03	0.665	1.11	0.266	1.42	0.086	-1.03	0.756	0.63
1450050_at	Hira	histone cell cycle regulation defective homolog A (S. cerevisiae)	1.4	0.605	-2.11	0.215	1.68	0.266	1.22	0.833	0.55
1455480_s_at	Ube2d3	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	1.06	0.848	-1.09	0.662	1.59	0.31	1.04	0.915	0.65

1428345_at	Ppapdc2	phosphatidic acid phosphatase type 2 domain containing 2	1.17	0.27	1	0.995	1.39	0.124	-1.27	0.486	0.57
1444608_at	Ankrd17	Ankyrin repeat domain 17	1.42	0.564	1.78	0.157	-2.76	0.046	1.65	0.509	0.52
1416126_at	LOC671429	similar to DNA-directed RNA polymerase I 135 kDa polypeptide (RNA polymeras	1.19	0.349	-1.13	0.459	1.48	0.126	1.22	0.313	0.69
1441933_x_at	Pigz	phosphatidylinositol glycan anchor biosynthesis, class Z	-1.43	0.347	1.54	0.372	1.32	0.434	1.53	0.35	0.74
1441609_at	---	Transcribed locus	1.3	0.6	-1.01	0.984	1.27	0.654	1.08	0.9	0.66
1420013_s_at	Lss	lanosterol synthase	-1.07	0.3	1.57	0.045	1.06	0.781	1.23	0.187	0.7
1444484_at	A130009E19Rik	RIKEN cDNA A130009E19 gene	1.06	0.961	1.05	0.793	1.46	0.012	-1.16	0.718	0.6
1422914_at	Sp5	trans-acting transcription factor 5	1.1	0.747	1.56	0.586	-1.11	0.814	1.37	0.484	0.73
1438408_at	Ankrd56	ankyrin repeat domain 56	1.1	0.124	1.4	0.293	1.06	0.806	-1.35	0.518	0.55
1425647_at	Trim60	tripartite motif-containing 60	1.29	0.64	1.08	0.79	1.19	0.676	-2.24	0.139	0.33
1417611_at	Tmem37	transmembrane protein 37	1.22	0.462	1.26	0.137	1.08	0.713	-1.02	0.969	0.64
1416279_at	Ap1b1	adaptor protein complex AP-1, beta 1 subunit	-1.15	0.22	1.11	0.25	1.58	0.047	1.52	0.222	0.77
1446846_at	---	16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A13008	1.19	0.145	1.3	0.476	1.08	0.689	-1.31	0.192	0.56
1420745_a_at	Ccndbp1	cyclin D-type binding-protein 1	1.07	0.319	-1.02	0.776	1.52	0.097	1.65	0.276	0.8
1421035_a_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	1.24	0.618	1.23	0.667	1.09	0.809	-1.09	0.731	0.62
1442820_at	Ptpn22	Protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	1.32	0.597	1.12	0.771	1.13	0.854	-1.1	0.731	0.62
1418838_at	Abcd1	ATP-binding cassette, sub-family D (ALD), member 1	1.21	0.216	1.32	0.295	1.04	0.811	-1.41	0.309	0.54
1449185_at	Crx	cone-rod homeobox containing gene	1.09	0.803	1.49	0.268	-1.01	0.985	1.01	0.992	0.64
1422528_a_at	Zfp36l1	zinc finger protein 36, C3H type-like 1	1.05	0.722	1.2	0.326	1.32	0.327	-1.52	0.134	0.51
1420673_a_at	Acox2	acyl-Coenzyme A oxidase 2, branched chain	1.24	0.188	-1.05	0.36	1.38	0.367	1.58	0.414	0.79
1438070_at	Phf3	PHD finger protein 3	-1.2	0.622	1.27	0.748	1.47	0.574	1.04	0.936	0.64
1448812_at	Hpcal1	hippocalcin-like 1	1.06	0.297	1.28	0.115	1.22	0.122	-1.03	0.867	0.63
1421812_at	Tapbp	TAP binding protein	1.19	0.202	1.16	0.065	1.22	0.216	-1.21	0.425	0.59
1439803_at	6430526N21Rik	RIKEN cDNA 6430526N21 gene	1.02	0.963	1.43	0.636	1.12	0.82	-1.13	0.896	0.61
1438873_at	---	---	1.34	0.271	1.44	0.515	-1.27	0.509	1.13	0.872	0.66
1429148_at	Nfic	nuclear factor I/C	1.36	0.546	1.03	0.889	1.18	0.518	-1.12	0.592	0.61
1452280_at	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	1.13	0.395	1.53	0.038	-1.11	0.556	1.11	0.62	0.67
1449460_at	Asb13	ankyrin repeat and SOCS box-containing protein 13	1.25	0.542	1.17	0.633	1.15	0.449	-1.52	0.167	0.51
1434079_s_at	Mcm2	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	-1.24	0.138	1.32	0.315	1.44	0.279	2.98	0.17	1.13
1440029_at	St8sia3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	1.22	0.502	1.48	0.092	-1.15	0.643	1.17	0.585	0.68
1421949_a_at	2610507L03Rik	RIKEN cDNA 2610507L03 gene	1.06	0.674	-1.37	0.123	1.78	0.286	1.96	0.318	0.86
1430595_at	Gas2l1	growth arrest-specific 2 like 1	1.6	0.522	-2.15	0.199	1.51	0.478	1.13	0.47	0.52
1455731_at	Slc29a3	solute carrier family 29 (nucleoside transporters), member 3	1.04	0.761	1.35	0.113	1.17	0.461	-1.04	0.906	0.63
1451802_at	Mcpt6	mast cell protease 6	-2.04	0.484	1.66	0.242	1.42	0.472	1.46	0.407	0.63
1426295_at	Hapln1	hyaluronan and proteoglycan link protein 1	2	0.583	1.13	0.859	-2.26	0.268	2.26	0.112	0.78
1418421_at	Bcl6b	B-cell CLL/lymphoma 6, member B	1.23	0.088	1.69	0.508	-1.55	0.486	1.15	0.701	0.63
1421626_at	Tmc1	transmembrane channel-like gene family 1	1.36	0.419	1.11	0.77	1.1	0.795	-1.2	0.625	0.59
1452191_at	Prcp	prolylcarboxypeptidase (angiotensinase C)	-1.28	0.544	1.58	0.291	1.2	0.485	1.09	0.754	0.65
1421915_a_at	St3gal3	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	1.31	0.631	-1.07	0.875	1.32	0.57	2.46	0.129	1.01
1451409_at	2210021J22Rik	RIKEN cDNA 2210021J22 gene	1.08	0.786	1.46	0.002	1.04	0.873	-1.11	0.394	0.61
1442940_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.59	0.541	-1.2	0.51	1.15	0.685	1.07	0.905	0.65
1434588_x_at	Tbca /// LOC62031	tubulin cofactor a /// similar to Tubulin-specific chaperone A (Tubulin-folding cofac	-1.29	0.589	1.56	0.156	1.24	0.628	1.02	0.913	0.63
1427260_a_at	Tpm3	tropomyosin 3, gamma	1.13	0.343	1.29	0.033	1.15	0.062	-1.06	0.674	0.63
1420476_a_at	Nap1l1	nucleosome assembly protein 1-like 1	1.25	0.101	1.06	0.473	1.26	0.482	-1.04	0.796	0.63
1450223_at	Apaf1	apoptotic peptidase activating factor 1	1	0.993	-1.2	0.57	1.74	0.162	1.11	0.8	0.66
1417119_at	Zfpl1	zinc finger like protein 1	1.34	0.252	1.03	0.856	1.21	0.088	-1.06	0.525	0.63
1449352_at	Poll	polymerase (DNA directed), lambda	1.16	0.354	1.04	0.816	1.38	0.043	-1.48	0.184	0.52
1435297_at	Gja9	gap junction membrane channel protein alpha 9	1.6	0.014	1.33	0.512	-1.56	0.288	1.14	0.687	0.63
1451959_a_at	Vegfa	vascular endothelial growth factor A	1.17	0.323	-1.22	0.578	1.58	0.208	1.43	0.443	0.74
1419956_at	C77144	expressed sequence C77144	1.27	0.644	1.7	0.366	-1.64	0.023	1.15	0.795	0.62
1431524_at	4933427I22Rik	RIKEN cDNA 4933427I22 gene	1.15	0.281	1.73	0.241	-1.46	0.498	1.18	0.637	0.65
1445442_at	Mtap9	microtubule-associated protein 9	-1.56	0.488	1.93	0.256	1	0.996	2.2	0.057	0.89
1431291_at	2700071J12Rik	RIKEN cDNA 2700071J12 gene	1.26	0.185	-1	0.997	1.32	0.499	1.23	0.443	0.7

1426805_at	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	1.36	0.368	-1.05	0.742	1.26	0.607	1.34	0.01	0.73
1418405_at	Hgfac	hepatocyte growth factor activator	1.03	0.728	1.19	0.021	1.36	0.344	-1.22	0.762	0.59
1439548_at	Rap2b	RAP2B, member of RAS oncogene family	1.25	0.737	1.34	0.224	-1.02	0.946	1.25	0.157	0.71
1447493_at	A530088H08Rik	RIKEN cDNA A530088H08 gene	1.43	0.535	-1.55	0.034	1.5	0.215	1.34	0.532	0.68
1445563_at	---	---	1.33	0.17	1.49	0.361	-1.34	0.29	1.09	0.44	0.64
1449404_at	Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	1.02	0.771	1.45	0.014	1.1	0.48	-1.27	0.284	0.58
1416798_a_at	Nme4	expressed in non-metastatic cells 4, protein	-1.31	0.276	1.25	0.746	1.56	0.314	1.58	0.449	0.77
1445104_at	E230029C05Rik	RIKEN cDNA E230029C05 gene	1.21	0.351	1.66	0.017	-1.42	0.183	1.01	0.97	0.62
1438372_at	Myom2	myomesin 2	1.22	0.809	-1.52	0.172	1.69	0.297	1.38	0.236	0.69
1459138_at	---	---	1.56	0.177	1.08	0.843	-1.07	0.716	1.03	0.934	0.65
1420911_a_at	Mfge8	milk fat globule-EGF factor 8 protein	1.06	0.064	1.42	0.037	1.1	0.552	-2.33	0.121	0.31
1421520_at	Jph1	junctophilin 1	1.31	0.14	1.05	0.91	1.21	0.534	-1.42	0.158	0.54
1457088_at	Pldn	pallidin	1.39	0.422	1.03	0.944	1.16	0.43	-1.47	0.462	0.53
1431875_a_at	E2f1	E2F transcription factor 1	-1.84	0.078	1.8	0.081	1.23	0.26	3.34	0.181	1.13
1417706_at	Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	1.2	0.069	1.01	0.882	1.36	0.108	-1.08	0.816	0.62
1447710_at	1700019P21Rik	RIKEN cDNA 1700019P21 gene	1.06	0.599	1.46	0.242	1.05	0.896	-1.1	0.876	0.62
1431686_a_at	Gmfb	glia maturation factor, beta	1.37	0.573	-1.2	0.682	1.38	0.652	1.14	0.801	0.67
1435048_at	AI854703	expressed sequence AI854703	-1.11	0.264	1.4	0.62	1.28	0.593	1.45	0.313	0.75
1440625_at	D930015E06Rik	RIKEN cDNA D930015E06 gene	1.22	0.822	-1.17	0.788	1.5	0.249	1.17	0.279	0.68
1452496_at	Atp11c	Atpase, class VI, type 11C	1.55	0.162	-1.3	0.613	1.26	0.595	1.29	0.594	0.7
1452504_s_at	Ctbs	chitobiase, di-N-acetyl-	1	0.988	1.45	0.204	1.13	0.62	-1.03	0.881	0.64
1437936_at	6330534C20Rik	RIKEN cDNA 6330534C20 gene	-1.03	0.835	1.57	0.272	1.04	0.875	1.34	0.246	0.73
1451318_a_at	Lyn /// LOC676654	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog /// similar to Yamaguchi sa	1.12	0.592	1.12	0.219	1.34	0.292	-1.5	0.131	0.52
1436383_at	Cplx2	complexin 2	-1.03	0.871	1.61	0.398	1	0.978	1.38	0.121	0.74
1425930_a_at	Mlx	MAX-like protein X	1.35	0.474	1.02	0.956	1.22	0.649	-1.08	0.871	0.63
1442196_at	A930006K02Rik	RIKEN cDNA A930006K02 gene	1.14	0.626	1.65	0.196	-1.27	0.314	1.57	0.375	0.77
1440532_a_at	---	Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:933017	-1.01	0.967	1.45	0.244	1.15	0.82	1.44	0.587	0.75
1422082_a_at	Nfya	nuclear transcription factor-Y alpha	1.44	0.55	-1.01	0.982	1.15	0.657	1.54	0.332	0.78
1443108_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930002E	1.61	0.085	1.26	0.447	-1.4	0.278	1.19	0.634	0.66
1422945_a_at	Kif5c	kinesin family member 5C	1.37	0.242	1.41	0.497	-1.24	0.579	1.71	0.293	0.81
1419813_at	---	Transcribed locus	1.32	0.784	-1.35	0.638	1.52	0.416	3.01	0.153	1.12
1419688_at	Gpc6	glypican 6	1.55	0.029	1.12	0.797	-1.1	0.627	1.23	0.31	0.7
1430413_at	Tmem29	transmembrane protein 29	-1.71	0.071	1.17	0.528	1.82	0.327	1.15	0.592	0.61
1426010_a_at	Epb4.1l3	erythrocyte protein band 4.1-like 3	1.07	0.773	1.83	0.358	-1.48	0.645	1.17	0.249	0.65
1430878_at	2210406H18Rik	RIKEN cDNA 2210406H18 gene	-2.79	0.055	2.14	0.107	1.09	0.855	1.02	0.94	0.36
1455843_at	Fut4	fucosyltransferase 4	-1.35	0.346	1.68	0.131	1.16	0.227	1.08	0.84	0.64
1447742_at	Laptm5	lysosomal-associated protein transmembrane 5	-1.38	0.548	1.08	0.791	1.77	0.259	1.72	0.328	0.8
1428585_at	Actn1	actinin, alpha 1	1.11	0.653	1.11	0.412	1.36	0.112	-1.59	0.028	0.5
1431046_at	2410127E16Rik	RIKEN cDNA 2410127E16 gene	1.66	0.278	1.05	0.887	-1.15	0.765	1.47	0.599	0.76
1448988_at	Acadl	acyl-Coenzyme A dehydrogenase, long-chain	-1.04	0.774	1.62	0.352	1.01	0.961	1.01	0.978	0.65
1448661_at	Plcb3	phospholipase C, beta 3	1	0.983	1.44	0.085	1.15	0.56	-1.62	0.103	0.49
1435795_at	Glb1	galactosidase, beta 1	1.27	0.199	1.14	0.647	1.18	0.518	-1.24	0.416	0.59
1449573_at	Alpk3	alpha-kinase 3	-1.09	0.624	1.31	0.63	1.35	0.363	1.58	0.009	0.79
1422643_at	Moxd1	monooxygenase, DBH-like 1	1.53	0.595	1.47	0.516	-1.72	0.107	1.31	0.515	0.65
1429922_at	Scn9a	Sodium channel, voltage-gated, type IX, alpha	1.29	0.758	1.74	0.342	-1.81	0.31	2.04	0.324	0.82
1429249_at	4833424O15Rik	RIKEN cDNA 4833424O15 gene	1.02	0.906	1.55	0.309	1.02	0.921	-1.58	0.112	0.5
1419091_a_at	Anxa2	annexin A2	1.18	0.326	1.6	0.07	-1.24	0.018	1.09	0.156	0.66
1415829_at	Lbr	lamin B receptor	-1.03	0.814	1.3	0.172	1.31	0.062	1.6	0.164	0.8
1432727_at	Psmd11 /// LOC627	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 /// similar to 26S	-1.11	0.697	1.15	0.727	1.54	0.481	2.01	0.219	0.9
1441282_at	Ssu72	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	1.22	0.762	1.13	0.293	1.23	0.419	-1.24	0.427	0.59
1448383_at	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	1.54	0.198	1.22	0.355	-1.2	0.451	1.2	0.242	0.69
1446394_at	Oprk1	opioid receptor, kappa 1	-1.44	0.471	1.56	0.232	1.33	0.255	1.79	0.327	0.81
1450204_a_at	Mynn	myoneurin	1.03	0.885	1.19	0.359	1.37	0.162	-1.34	0.459	0.56

1443149_at	Nmnat3	Nicotinamide nucleotide adenylyltransferase 3	-1.32	0.709	1.83	0.244	1	0.997	1.95	0.226	0.87
1444412_at	Aim1	Absent in melanoma 1	1.12	0.689	1.05	0.902	1.42	0.377	-1.41	0.51	0.54
1420470_at	Sult1c1	sulfotransferase family, cytosolic, 1C, member 1	1.39	0.655	1.06	0.846	1.13	0.623	-1.38	0.011	0.55
1451523_a_at	Mif4gd	MIF4G domain containing	1.07	0.73	1.28	0.195	1.23	0.304	-1.51	0.208	0.52
1423306_at	2010002N04Rik	RIKEN cDNA 2010002N04 gene	-1.04	0.329	1.54	0.13	1.09	0.613	1.86	0.403	0.86
1426371_at	Mlstd2	male sterility domain containing 2	1.07	0.773	1.32	0.56	1.2	0.61	-1.01	0.979	0.65
1429850_x_at	Alkbh4	alkB, alkylation repair homolog 4 (E. coli)	1.31	0.165	1.15	0.474	1.12	0.272	-1.18	0.32	0.6
1432231_at	4930526H09Rik	RIKEN cDNA 4930526H09 gene	1.39	0.69	1.65	0.326	-1.8	0.499	2.77	0	1
1426343_at	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisia	1.06	0.666	-1.04	0.65	1.57	0.033	1.39	0.04	0.75
1419428_a_at	Gaa	glucosidase, alpha, acid	1	0.976	-1.07	0.165	1.65	0.047	1.19	0.098	0.69
1452236_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	1.34	0.328	-1.32	0.065	1.5	0.109	1.37	0.348	0.72
1455936_a_at	Rbpms	RNA binding protein gene with multiple splicing	1.07	0.585	1.04	0.755	1.48	0.06	-1.19	0.65	0.6
1447351_x_at	---	---	1.25	0.297	1.3	0.511	1.05	0.887	-1.35	0.447	0.56
1443348_at	D030028M11Rik	RIKEN cDNA D030028M11 gene	-1.09	0.894	1.2	0.625	1.48	0.538	1.01	0.989	0.65
1424565_at	Polr3d	polymerase (RNA) III (DNA directed) polypeptide D	1.04	0.832	-1.12	0.804	1.66	0.189	1.23	0.337	0.7
1420975_at	Baz1b	bromodomain adjacent to zinc finger domain, 1B	1.24	0.465	-1.03	0.939	1.38	0.461	1.44	0.584	0.76
1423392_at	Clic4	chloride intracellular channel 4 (mitochondrial)	1.05	0.79	-1.09	0.765	1.62	0.152	2.08	0.128	0.92
1425626_at	Gstm1 /// LOC4339	glutathione S-transferase, mu 1 /// similar to Glutathione S-transferase Mu 1 (GST	-1.12	0.518	1.07	0.775	1.63	0.057	1.02	0.93	0.65
1451715_at	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian)	1.53	0.453	-1.44	0.413	1.37	0.488	1.72	0.199	0.79
1446817_at	D10Ertd43e	DNA segment, Chr 10, ERATO Doi 43, expressed	1.12	0.693	1.22	0.701	1.25	0.16	-1.14	0.394	0.61
1422720_at	Isl1	ISL1 transcription factor, LIM/homeodomain	1.46	0.421	1.56	0.323	-1.74	0.14	1.04	0.955	0.58
1456671_at	Tbrg3	transforming growth factor beta regulated gene 3	1.4	0.444	1.05	0.641	1.14	0.56	-1.22	0.559	0.59
1444228_s_at	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	1.82	0.104	1.05	0.921	-1.39	0.177	1.33	0.457	0.7
1435063_at	LOC625638	similar to CG8312-PA, isoform A	1.78	0.284	-1.23	0.68	1	0.994	1.08	0.911	0.66
1431055_a_at	Snx10	sorting nexin 10	-1.16	0.161	1.42	0.263	1.31	0.027	1.06	0.821	0.66
1434827_at	Thoc6	THO complex 6 homolog (Drosophila)	-1.04	0.721	1.29	0.117	1.35	0.047	1.03	0.865	0.65
1424924_at	Sec63	SEC63-like (S. cerevisiae)	1.31	0.068	1.08	0.596	1.21	0.226	-1.32	0.324	0.57
1425787_a_at	Sytl3	synaptotagmin-like 3	1.04	0.805	1.4	0.437	1.16	0.498	-1.42	0.165	0.54
1423213_at	Plxnc1	plexin C1	1.25	0.393	1.21	0.403	1.13	0.376	-1.86	0.051	0.43
1417273_at	Pdk4	pyruvate dehydrogenase kinase, isoenzyme 4	1.11	0.826	1.06	0.763	1.42	0.26	-2.42	0.296	0.29
1416533_at	Egln2	EGL nine homolog 2 (C. elegans)	1.16	0.336	1.19	0.089	1.24	0.138	-1.35	0.09	0.56
1442141_at	BC028454	cDNA sequence BC028454	1.75	0.381	1.36	0.477	-2.03	0.203	2.13	0.13	0.8
1422618_x_at	Xmr /// LOC546272	Xmr protein /// similar to Xlr-related, meiosis regulated /// similar to Xlr-related, me	1.63	0.376	-1.48	0.566	1.29	0.454	2.17	0.46	0.9
1420224_at	---	---	1.02	0.985	-1.04	0.904	1.62	0.486	2.46	0.236	1.01
1445041_at	D16Ertd6e	DNA segment, Chr 16, ERATO Doi 6, expressed	1.74	0.116	1.1	0.873	-1.33	0.558	1.52	0.58	0.76
1430832_at	4930426I24Rik	RIKEN cDNA 4930426I24 gene	-1.21	0.758	1.49	0.347	1.27	0.348	1.07	0.784	0.66
1456852_at	Paip1	polyadenylate binding protein-interacting protein 1	-1.32	0.279	1.24	0.641	1.59	0.112	2.28	0.119	0.95
1442960_at	Muc20	mucin 20	1.85	0.197	1.12	0.895	-1.58	0.174	2.55	0.115	0.98
1449358_at	D6Mm5e	DNA segment, Chr 6, Miriam Meisler 5, expressed	1.5	0.298	-1.42	0.254	1.4	0.332	1.78	0.346	0.81
1440359_at	1700012H17Rik	RIKEN cDNA 1700012H17 gene	-1.12	0.907	1.29	0.369	1.41	0.493	1.53	0.248	0.78
1442529_at	Ogfrl1	Opioid growth factor receptor-like 1	1.6	0.452	1.15	0.794	-1.17	0.365	1.02	0.836	0.65
1460595_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130021L	-1.23	0.491	1.57	0.189	1.21	0.642	1.48	0.432	0.76
1442410_at	Depdc5	DEP domain containing 5	1.11	0.101	1.33	0.513	1.15	0.683	-1.36	0.333	0.56
1457152_at	---	---	1.7	0.291	1.23	0.699	-1.51	0.311	1.22	0.611	0.66
1454865_at	Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	1.44	0.285	1.05	0.804	1.11	0.33	-1.52	0.175	0.52
1450555_at	Tex13	testis expressed gene 13	1.61	0.331	1.15	0.766	-1.19	0.779	1.46	0.291	0.76
1437279_x_at	Sdc1	syndecan 1	1.35	0.337	1.34	0.087	-1.1	0.46	1.88	0.379	0.87
1443213_at	Gtdc1	glycosyltransferase-like domain containing 1	1.73	0.015	-1.2	0.575	1.03	0.873	1.23	0.563	0.7
1426614_at	Prkcbp1	protein kinase C binding protein 1	1.1	0.53	1.21	0.172	1.28	0.083	-1.03	0.684	0.64
1434455_at	Fbxo44	: F-box protein 44	1.17	0.076	1.2	0.225	1.23	0.329	-1.55	0.054	0.51
1447601_x_at	Nat10	N-acetyltransferase 10	2.05	0.393	-2.3	0.021	1.11	0.88	1.56	0.454	0.61
1451119_a_at	Fbln1	fibulin 1	1.53	0.165	1.25	0.762	-1.22	0.413	1.33	0.194	0.72
1447733_x_at	---	---	1.15	0.605	1.73	0.374	-1.39	0.168	1.86	0.124	0.84

1429985_at	5430439G13Rik	RIKEN cDNA 5430439G13 gene	1.1	0.892	1.45	0.32	1.05	0.904	-1.11	0.675	0.62
1449079_s_at	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	-1.67	0.073	1.89	0.021	1.11	0.721	1.18	0.615	0.63
1455980_a_at	Gas2l3	growth arrest-specific 2 like 3	1.47	0.279	1.42	0.37	-1.41	0.467	2.21	0.287	0.92
1443662_at	Ctnna1	Catenin (cadherin associated protein), alpha 1	1.17	0.176	1.42	0.417	1.01	0.981	-1.08	0.896	0.63
1437712_x_at	Exosc4	exosome component 4	1.1	0.846	1.29	0.654	1.21	0.67	-1.02	0.971	0.64
1430315_at	1700010N08Rik	RIKEN cDNA 1700010N08 gene	1.1	0.661	1.17	0.8	1.34	0.562	-1.33	0.713	0.57
1430514_a_at	Cd99	CD99 antigen	1.63	0.379	1.22	0.535	-1.32	0.269	1.06	0.897	0.65
1419585_at	Rp2h	retinitis pigmentosa 2 homolog (human)	1.12	0.77	-1.04	0.932	1.52	0.329	1.42	0.103	0.76
1447978_at	C80719	expressed sequence C80719	1.37	0.669	1.3	0.565	-1.07	0.879	1.43	0.687	0.76
1422468_at	Ppt1	palmitoyl-protein thioesterase 1	1.16	0.605	1.07	0.64	1.37	0.269	-1.09	0.55	0.63
1438322_x_at	Fdft1	farnesyl diphosphate farnesyl transferase 1	1.31	0.331	1.43	0.097	-1.16	0.129	1.23	0.451	0.7
1458933_at	A530052I06Rik	RIKEN cDNA A530052I06 gene	1.27	0.59	1.53	0.221	-1.26	0.168	1.12	0.392	0.67
1437795_at	---	---	-1.03	0.723	1.42	0.096	1.21	0.367	1.2	0.062	0.7
1425732_a_at	Mxi1	Max interacting protein 1	1.24	0.485	-1.56	0.263	1.73	0.247	2.53	0.315	0.98
1419648_at	Myo1c	myosin IC	1.16	0.441	1.33	0.031	1.12	0.515	-1.26	0.122	0.59
1440169_x_at	Ifnar2	interferon (alpha and beta) receptor 2	1.25	0.369	1.46	0.039	-1.11	0.427	1.01	0.93	0.65
1448686_at	Il16	interleukin 16	1.5	0.328	1.02	0.949	1.09	0.151	-1.84	0.187	0.44
1423743_at	Arcn1	archain 1	1.17	0.657	-1.08	0.837	1.51	0.425	1.01	0.985	0.65
1448918_at	Slco3a1	solute carrier organic anion transporter family, member 3a1	1.55	0.046	-1	0.981	1.06	0.772	1.1	0.641	0.68
1445572_at	Foxq1	forkhead box Q1	1.35	0.015	1.27	0.572	-1.02	0.949	1.11	0.794	0.68
1435618_at	Pnma2	paraneoplastic antigen MA2	1.14	0.831	1.52	0.477	-1.05	0.876	1.78	0.353	0.84
1433227_at	9430081G06Rik	RIKEN cDNA 9430081G06 gene	-1.17	0.431	1.52	0.151	1.23	0.435	1.23	0.462	0.7
1433546_at	Gns	glucosamine (N-acetyl)-6-sulfatase	1.03	0.399	1.09	0.108	1.48	0.066	-1.02	0.954	0.65
1454056_at	9030407P20Rik	RIKEN cDNA 9030407P20 gene	1.14	0.568	-1.53	0.165	1.81	0.041	1.28	0.434	0.67
1460498_a_at	Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	1.14	0.371	1.17	0.314	1.3	0.455	-1.08	0.863	0.63
1434685_at	D3Bwg0562e	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	-1.1	0.736	1.26	0.648	1.43	0.43	1.45	0.695	0.76
1431713_at	Sufu	suppressor of fused homolog (Drosophila)	1.1	0.842	-1.09	0.843	1.59	0.475	1.06	0.848	0.66
1447738_s_at	Ankrd13d	ankyrin repeat domain 13 family, member D	1.21	0.839	1.36	0.418	1.04	0.719	-1.23	0.018	0.59
1449171_at	Ttk	Ttk protein kinase	-1.82	0.494	1.29	0.719	1.77	0.292	3.23	0.257	1.12
1436146_at	4930481A15Rik	RIKEN cDNA 4930481A15 gene	1.12	0.666	1.38	0.482	1.1	0.628	-1.7	0.282	0.48
1425789_s_at	Anxa8	annexin A8	-2.54	0.082	1.81	0.273	1.4	0.476	1.58	0.328	0.56
1417155_at	Mycn	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	1.92	0.282	-1.73	0.546	1.11	0.669	2.08	0.118	0.85
1423433_at	Trove2	TROVE domain family, member 2	1.18	0.617	1.78	0.101	-1.56	0.074	1.14	0.507	0.64
1428734_at	3200002M19Rik	RIKEN cDNA 3200002M19 gene	-1.05	0.841	1.03	0.797	1.63	0.005	1.21	0.379	0.7
1456187_at	Slc7a14	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14	1.65	0.489	-2.24	0.291	1.51	0.356	1.09	0.897	0.5
1444721_at	---	---	1.23	0.552	1.22	0.466	1.16	0.503	-1.32	0.465	0.57
1455771_at	Bzrap1	benzodiazapine receptor associated protein 1	-1.02	0.94	1.1	0.607	1.53	0.03	1.33	0.296	0.73
1420908_at	Cd2ap	CD2-associated protein	1.04	0.904	1.3	0.397	1.27	0.444	-1.26	0.524	0.59
1438453_at	Rad51c	Rad51 homolog c (S. cerevisiae)	1.15	0.506	1.74	0.368	-1.4	0.435	2.89	0.331	1.1
1426745_at	D11Bwg0434e	DNA segment, Chr 11, Brigham & Women's Genetics 0434 expressed	-1.1	0.676	1.14	0.162	1.57	0.052	1.35	0.287	0.74
1456494_a_at	Trim30 /// AI451617	tripartite motif protein 30 /// expressed sequence AI451617	1.17	0.513	1.12	0.44	1.31	0.138	-1.62	0.165	0.5
1428727_at	4631422C13Rik	RIKEN cDNA 4631422C13 gene	1.2	0.339	-1.05	0.84	1.46	0.315	1.26	0.442	0.72
1450593_at	Ifna6	interferon alpha 6	1.67	0.448	1.08	0.913	-1.16	0.705	1.42	0.566	0.75
1432311_at	Tmem168	transmembrane protein 168	1.24	0.546	1.24	0.564	1.13	0.38	-1.27	0.387	0.58
1440449_at	Lrrc40	leucine rich repeat containing 40	-1.48	0.183	1.21	0.285	1.72	0.258	1.17	0.722	0.66
1445053_at	AU022537	expressed sequence AU022537	1.38	0.209	-1.08	0.507	1.3	0.636	1.36	0.64	0.74
1448638_at	Mtbp	Mdm2, transformed 3T3 cell double minute p53 binding protein	-1.49	0.364	1.74	0.408	1.2	0.096	1.31	0.295	0.69
1437150_at	1700012H17Rik	RIKEN cDNA 1700012H17 gene	1.19	0.016	1.21	0.826	1.21	0.324	-1.14	0.469	0.62
1458896_at	Gmeb1	glucocorticoid modulatory element binding protein 1	1.24	0.772	1.45	0.43	-1.08	0.836	1.32	0.619	0.73
1423531_a_at	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	-1.01	0.95	1.48	0.132	1.14	0.755	1.37	0.008	0.74
1458254_at	D330027H18Rik	RIKEN cDNA D330027H18 gene	-1.04	0.451	1.15	0.755	1.5	0.584	1.57	0.584	0.79
1447005_at	---	Transcribed locus	-1.61	0.486	1.56	0.604	1.43	0.453	2.39	0.105	0.94
1446192_at	Amph	Amphiphysin	1.44	0.395	1.61	0.478	-1.8	0.037	1.52	0.366	0.69

1426970_a_at	Ube1l /// D330022A	ubiquitin-activating enzyme E1-like /// RIKEN cDNA D330022A01 gene	1.29	0.143	1.13	0.076	1.19	0.091	-1.13	0.378	0.62
1442637_at	Itsn1	Intersectin 1 (SH3 domain protein 1A)	-1.08	0.797	1.37	0.382	1.31	0.068	1.71	0.226	0.83
1440829_x_at	Ttll11	tubulin tyrosine ligase-like family, member 11	1.16	0.842	1.64	0.065	-1.24	0.59	1.13	0.507	0.67
1418167_at	Tcfap4	transcription factor AP4	1.33	0.491	1.23	0.687	1.05	0.795	-1.24	0.391	0.59
1420172_at	Myh9	Myosin, heavy polypeptide 9, non-muscle	1.18	0.528	1.26	0.28	1.17	0.442	-1.1	0.552	0.63
1445227_at	Tnfsf13	Tumor necrosis factor (ligand) superfamily, member 13	1.23	0.784	1.57	0.204	-1.24	0.691	1.33	0.627	0.72
1416044_at	Fliih	flightless I homolog (Drosophila)	1.15	0.057	1.03	0.727	1.43	0.084	-1.18	0.391	0.61
1426580_at	Plk4	polo-like kinase 4 (Drosophila)	1.35	0.414	-1.32	0.494	1.51	0.085	4.66	0.193	1.55
1452198_at	Fbxl10	F-box and leucine-rich repeat protein 10	1.12	0.179	1.02	0.888	1.47	0.09	-1.05	0.204	0.64
1432044_a_at	4921504E06Rik	RIKEN cDNA 4921504E06 gene	1.34	0.348	1.52	0.598	-1.32	0.409	1.11	0.86	0.66
1425283_a_at	Mtl5	metallothionein-like 5, testis-specific (tesmin)	-1.14	0.64	1.68	0.339	1.06	0.808	1.74	0.181	0.83
1421759_a_at	Foxk1	forkhead box K1	1.89	0.145	1.1	0.804	-1.62	0.574	1.23	0.75	0.65
1422620_s_at	Ppap2a	phosphatidic acid phosphatase 2a	1.12	0.24	1.54	0.151	-1.05	0.698	1.06	0.778	0.67
1455606_at	BC004022	cDNA sequence BC004022	1.13	0.331	-1.03	0.884	1.51	0.077	1.41	0.289	0.75
1439733_at	---	13 days embryo stomach cDNA, RIKEN full-length enriched library, clone:D53002	1.98	0.408	1.1	0.636	-1.87	0.401	1.01	0.987	0.55
1420121_at	AA517858	expressed sequence AA517858	-1.26	0.381	1.42	0.607	1.4	0.534	1.84	0.229	0.85
1443282_at	Prpf38a	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	1.12	0.638	1.31	0.305	1.19	0.361	-1.42	0.263	0.55
1425267_a_at	3110045G13Rik	RIKEN cDNA 3110045G13 gene	1.29	0.371	1.09	0.699	1.23	0.25	-1.18	0.291	0.61
1446500_at	Lysmd4	LysM, putative peptidoglycan-binding, domain containing 4	1.15	0.626	1.02	0.963	1.44	0.555	-1.66	0.474	0.49
1458365_at	Scyl1bp1	SCY1-like 1 binding protein 1	-1.43	0.194	1.31	0.012	1.6	0.188	1.2	0.437	0.67
1436662_at	Sorcs1	VPS10 domain receptor protein SORCS 1	1.4	0.458	1.12	0.841	1.1	0.856	-1.88	0.33	0.43
1435681_s_at	Ddx49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	1.08	0.34	1.13	0.829	1.41	0.161	-1.27	0.383	0.59
1425206_a_at	Ube3a	Ubiquitin protein ligase E3A	1.14	0.725	1.08	0.903	1.39	0.524	-1.33	0.242	0.57
1422823_at	Eps8	epidermal growth factor receptor pathway substrate 8	-1.22	0.133	1.54	0.184	1.25	0.345	1.1	0.623	0.67
1440099_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.07	0.494	1.63	0.398	-1.09	0.71	1.04	0.897	0.66
1417691_at	Bin3	bridging integrator 3	1.09	0.361	1.28	0.025	1.25	0.246	-1.15	0.026	0.62
1416870_at	Dnalc4	dynein, axonemal, light chain 4	1.21	0.432	1.25	0.234	1.15	0.157	-1.01	0.966	0.65
1449327_at	1600015I10Rik	RIKEN cDNA 1600015I10 gene	1.61	0.278	1.42	0.658	-1.71	0.381	1.82	0.312	0.79
1458723_at	LOC544782	Similar to Poly(A) binding protein, cytoplasmic 4, isoform 1	1.01	0.98	1.63	0.107	-1.03	0.855	1.25	0.438	0.72
1453128_at	Xlkd1	extra cellular link domain-containing 1	1.29	0.064	1.38	0.198	-1.06	0.741	1.39	0.122	0.75
1430663_at	9430037O13Rik	RIKEN cDNA 9430037O13 gene	1.81	0.341	-1.35	0.513	1.07	0.544	2.13	0.193	0.91
1421046_a_at	Pabpc4 /// LOC432	poly A binding protein, cytoplasmic 4 /// similar to Poly(A) binding protein, cytopla	-1.18	0.291	1.31	0.079	1.45	0.049	2.25	0.213	0.96
1447783_x_at	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed	-1.06	0.766	1.17	0.004	1.51	0.336	2.36	0.2	0.99
1431096_at	Ints8	integrator complex subunit 8	1.09	0.8	-1.03	0.963	1.55	0.404	1.22	0.769	0.71
1447938_at	LOC545614	similar to 4933409K07Rik protein	1.42	0.022	1.26	0.436	-1.07	0.804	1.16	0.664	0.69
1417173_at	Crebl1	cAMP responsive element binding protein-like 1	1.21	0.211	1.13	0.446	1.28	0.086	-1.15	0.482	0.62
1460173_at	Lasp1	LIM and SH3 protein 1	1.16	0.164	1.04	0.636	1.42	0.013	-1.21	0.347	0.6
1419385_a_at	Ubqln1	ubiquilin 1	1.09	0.719	-1.12	0.726	1.64	0.179	1.02	0.938	0.66
1447986_at	D17892	expressed sequence D17892	-1.07	0.89	1.03	0.944	1.66	0.243	1.45	0.542	0.77
1427005_at	Plk2	polo-like kinase 2 (Drosophila)	1.49	0.243	1.19	0.496	-1.06	0.873	1.02	0.915	0.66
1418632_at	Ube2h	ubiquitin-conjugating enzyme E2H	1.86	0.499	-1.38	0.517	1.04	0.88	1.44	0.275	0.74
1427815_at	---	---	1.28	0.734	1.38	0.51	-1.04	0.915	1.67	0.394	0.82
1428532_at	Ints7	integrator complex subunit 7	1.23	0.433	-1.22	0.269	1.57	0.146	1.57	0.276	0.79
1448531_at	Lmnb2 /// LOC6715	lamin B2 /// similar to Lamin-B2	1.67	0.198	-1.75	0.092	1.38	0.391	1.56	0.278	0.71
1432783_at	4930556A17Rik	RIKEN cDNA 4930556A17 gene	1.04	0.891	1.34	0.445	1.24	0.797	-1.24	0.714	0.6
1449451_at	Serpinb11	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 11	1.06	0.919	1	0.994	1.55	0.059	-1.47	0.08	0.54
1433307_at	4930509E22Rik	RIKEN cDNA 4930509E22 gene	-2.51	0.444	2.19	0.155	1.03	0.931	1.07	0.89	0.44
1448603_at	Srpk2	serine/arginine-rich protein specific kinase 2	1.15	0.516	1.12	0.567	1.35	0.143	-1.05	0.609	0.64
1421996_at	Tcfap2a	transcription factor AP-2, alpha	1.17	0.328	1.63	0.171	-1.21	0.269	1.22	0.512	0.7
1439189_at	D630023B12Rik	RIKEN cDNA D630023B12 gene	1.52	0.34	1.14	0.754	-1.04	0.867	3.79	0.113	1.35
1423171_at	Gpr88 /// LOC6714	G-protein coupled receptor 88 /// similar to G-protein coupled receptor 88	-1.16	0.771	1.75	0.109	1	0.994	1.01	0.974	0.65
1432940_at	5730405N03Rik	RIKEN cDNA 5730405N03 gene	1.31	0.408	1.04	0.92	1.26	0.456	-2.23	0.039	0.35
1454448_at	2900018E21Rik	RIKEN cDNA 2900018E21 gene	1.57	0.303	-1.19	0.817	1.2	0.584	1.33	0.574	0.73

1441307_at	LOC665891 /// LOC	hypothetical protein LOC665891 /// hypothetical protein LOC670335	1.29	0.737	1.68	0.28	-1.52	0.465	1.69	0.549	0.78
1435476_a_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	-1.2	0.281	1.2	0.444	1.59	0.104	1.14	0.711	0.68
1450414_at	Pdgfb	platelet derived growth factor, B polypeptide	1.07	0.769	1.56	0.06	-1.01	0.965	1.3	0.096	0.73
1450691_at	Caskin2	cask-interacting protein 2	1.09	0.604	1.55	0.101	-1.02	0.878	1.23	0.501	0.71
1418138_at	Sult1d1	sulfotransferase family 1D, member 1	1.31	0.28	-1.22	0.103	1.49	0.535	1.02	0.944	0.65
1428584_a_at	Haghl	hydroxyacylglutathione hydrolase-like	1.06	0.783	1.14	0.568	1.43	0.045	-1.03	0.945	0.65
1441422_at	Gas2l1	growth arrest-specific 2 like 1	-1.33	0.729	1.69	0.565	1.18	0.56	1.59	0.368	0.78
1424756_at	Hip1	huntingtin interacting protein 1	1.35	0.033	-1.01	0.989	1.28	0.453	1.07	0.771	0.67
1428376_at	4932415G12Rik	RIKEN cDNA 4932415G12 gene	1.35	0.631	1.46	0.274	-1.23	0.322	1.03	0.902	0.65
1442101_at	A930017N06Rik	RIKEN cDNA A930017N06 gene	1.74	0.191	1.05	0.718	-1.2	0.558	1.07	0.678	0.66
1417498_at	Serpinf2	serine (or cysteine) peptidase inhibitor, clade F, member 2	-1.08	0.79	1.1	0.5	1.59	0.467	1.59	0.331	0.8
1436364_x_at	Nfix	nuclear factor I/X	1.1	0.669	-1.61	0.026	1.91	0.086	1.81	0.142	0.8
1433471_at	Tcf7	transcription factor 7, T-cell specific	1.51	0.359	1.08	0.734	1.04	0.912	-2	0.184	0.41
1422376_at	V1rb1	vomeronasal 1 receptor, B1	1.04	0.929	1.61	0.424	-1.03	0.948	2.46	0.033	1.02
1452336_at	BC027382	cDNA sequence BC027382	-1.04	0.834	1.11	0.797	1.55	0.055	1.04	0.825	0.67
1417259_a_at	Capzb	capping protein (actin filament) muscle Z-line, beta	1.12	0.663	1.16	0.369	1.34	0.237	-1.23	0.271	0.6
1460087_at	BC017643	cDNA sequence BC017643	-1.18	0.788	1.67	0.267	1.11	0.797	1	0.998	0.65
1459047_x_at	5430405G24Rik	RIKEN cDNA 5430405G24 gene	1.46	0.603	1.49	0.268	-1.48	0.183	1.74	0.14	0.8
1432501_at	1700092E16Rik	RIKEN cDNA 1700092E16 gene	-1.87	0.073	1.7	0.141	1.39	0.217	1.05	0.866	0.57
1451098_at	Pcoln3	procollagen (type III) N-endopeptidase	1.13	0.096	1.33	0.03	1.16	0.18	-1.3	0.206	0.58
1421027_a_at	Mef2c	myocyte enhancer factor 2C	1.35	0.269	1.22	0.574	1.06	0.864	-1.69	0.213	0.48
1459772_at	Hps3	Hermansky-Pudlak syndrome 3 homolog (human)	1.36	0.496	-1.08	0.881	1.34	0.536	1.24	0.54	0.72
1426444_at	Rhbdd2	rhomboid domain containing 2	1.2	0.777	1.2	0.719	1.22	0.462	-1.55	0.163	0.52
1453711_at	Rspo4	R-spondin family, member 4	1.19	0.292	1.16	0.389	1.27	0.49	-1.76	0.018	0.47
1447137_at	4632417K18Rik	RIKEN cDNA 4632417K18 gene	1.33	0.592	1.08	0.873	1.22	0.69	-1.09	0.735	0.63
1420839_at	Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specif	1	0.994	1.01	0.93	1.61	0.042	-1.23	0.103	0.6
1417031_at	2310028N02Rik	RIKEN cDNA 2310028N02 gene	1.07	0.755	1.31	0.219	1.25	0.479	-1.3	0.453	0.58
1448538_a_at	D4Wsu53e	DNA segment, Chr 4, Wayne State University 53, expressed	1.02	0.983	-1.03	0.941	1.64	0.252	1	1	0.66
1422844_a_at	Wdr77	WD repeat domain 77	1.12	0.164	-1.14	0.124	1.63	0.013	1.03	0.792	0.66
1428863_at	Ankrd39	ankyrin repeat domain 39	1.24	0.676	1.28	0.247	1.1	0.815	-1.28	0.406	0.59
1418645_at	Hal /// LOC638196	histidine ammonia lyase /// similar to Histidine ammonia-lyase (Histidase)	1.95	0.638	1.04	0.742	-1.57	0.403	3.72	0.155	1.28
1444153_at	---	16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830033E	1.02	0.98	1.49	0.448	1.11	0.825	-1.29	0.526	0.58
1457457_at	5033405K12Rik	RIKEN cDNA 5033405K12 gene	1.01	0.97	1.45	0.139	1.17	0.506	-1.09	0.789	0.63
1425735_at	Madd	MAP-kinase activating death domain	1.31	0.762	1.15	0.777	1.17	0.679	-1.84	0.215	0.45
1417384_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	1.05	0.631	1	0.995	1.58	0.047	-1.54	0.044	0.52
1437416_at	BC034902	cDNA sequence BC034902	-1.44	0.668	1.34	0.649	1.59	0.416	1.03	0.972	0.63
1421358_at	H2-M3	histocompatibility 2, M region locus 3	1.22	0.327	1.17	0.385	1.23	0.207	-1.67	0.184	0.49
1431725_at	Fmn2	formin 2	1.53	0.083	-1.11	0.552	1.2	0.39	1.17	0.392	0.7
1423363_at	Sort1	sortilin 1	-1.01	0.959	1.1	0.606	1.54	0.37	1.95	0.112	0.89
1435860_at	Slc5a6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	1.23	0.208	-1.05	0.842	1.45	0.045	1.26	0.251	0.72
1436717_x_at	Hbb-y	hemoglobin Y, beta-like embryonic chain	1.59	0.572	1.22	0.709	-1.21	0.766	5.14	0.056	1.68
1453422_a_at	1110020G09Rik	RIKEN cDNA 1110020G09 gene	1.01	0.914	-1.17	0.208	1.77	0.052	3.48	0.273	1.27
1447554_at	BC031781	cDNA sequence BC031781	1.03	0.948	1.79	0.076	-1.24	0.736	1.29	0.727	0.72
1431699_at	Fut4-ps1	fucosyltransferase 4, pseudogene 1	-1.84	0.436	2.03	0.041	1.05	0.926	2.7	0.174	0.99
1451746_a_at	Atg12	autophagy-related 12 (yeast)	1.51	0.24	-1.19	0.286	1.28	0.624	1.46	0.441	0.76
1419419_at	D0H6S2654E	DNA segment, human D6S2654E	-1.29	0.354	1.05	0.781	1.81	0.159	1.2	0.805	0.69
1420467_at	Psors1c2	psoriasis susceptibility 1 candidate 2 (human)	-1.04	0.919	1.32	0.574	1.35	0.239	1.1	0.674	0.68
1427265_at	Bcr	breakpoint cluster region homolog	-1.34	0.67	1.37	0.499	1.51	0.264	1.02	0.971	0.64
1440239_at	2310066E14Rik	RIKEN cDNA 2310066E14 gene	1.49	0.623	1.25	0.64	-1.12	0.525	1.11	0.829	0.68
1449986_at	2310034C09Rik	RIKEN cDNA 2310034C09 gene	1.06	0.677	1.61	0.193	-1.04	0.919	1.09	0.768	0.68
1428850_x_at	Cd99	CD99 antigen	1.66	0.19	1.22	0.516	-1.31	0.295	1.06	0.881	0.65
1450717_at	Ang1	angiogenin, ribonuclease A family, member 1	1.6	0.56	1.39	0.106	-1.57	0.067	1.31	0.201	0.68
1455656_at	Btla	B and T lymphocyte associated	1.17	0.552	1.22	0.385	1.24	0.552	-2.31	0.198	0.33

AFFX-TransRecMur	Tfrc	transferrin receptor	1.24	0.699	-1.19	0.493	1.55	0.546	3.91	0.255	1.38
1443641_at	---	---	1.34	0.716	1.15	0.8	1.14	0.665	-1.42	0.257	0.55
1452285_a_at	Eif3s5	eukaryotic translation initiation factor 3, subunit 5 (epsilon)	1.13	0.099	1.14	0.025	1.36	0.066	-1.35	0.131	0.57
1427115_at	Myh3	myosin, heavy polypeptide 3, skeletal muscle, embryonic	1.4	0.372	1.55	0.191	-1.46	0.617	2.29	0.162	0.95
1445378_at	---	---	1.84	0.323	-2.84	0.024	1.44	0.376	1.1	0.767	0.38
1432590_at	4930573O21Rik	RIKEN cDNA 4930573O21 gene	1.05	0.869	1.47	0.463	1.12	0.696	-1.11	0.781	0.63
1434164_s_at	AU024076	expressed sequence AU024076	1.46	0.551	1.3	0.646	-1.15	0.741	1.14	0.729	0.69
1426517_at	Gnaz	guanine nucleotide binding protein, alpha z subunit	1.1	0.792	-1.06	0.877	1.59	0.052	1.66	0.394	0.82
1456207_at	Mtcp1	mature T-cell proliferation 1	1.6	0.171	1.39	0.009	-1.55	0.035	1.84	0.059	0.82
1460388_at	4632408A20Rik	RIKEN cDNA 4632408A20 gene	1.6	0.254	1.22	0.617	-1.23	0.42	1.79	0.001	0.85
1460601_at	Myrip	myosin VIIA and Rab interacting protein	1.51	0.456	-1.13	0.752	1.24	0.516	1.9	0.137	0.88
1456978_s_at	D19Ertd652e	DNA segment, Chr 19, ERATO Doi 652, expressed	1.32	0.697	1.46	0.145	-1.17	0.095	1.26	0.492	0.72
1430310_at	Tspan11	tetraspanin 11	1.63	0.06	1.3	0.657	-1.43	0.276	1.07	0.866	0.65
1438825_at	Calm3	Calmodulin 3	1.05	0.874	1.32	0.391	1.26	0.463	-1.37	0.045	0.57
1455439_a_at	Lgals1	lectin, galactose binding, soluble 1	1.15	0.054	1.68	0.224	-1.24	0.27	1.13	0.762	0.68
1434780_at	C130038G02Rik	RIKEN cDNA C130038G02 gene	1.21	0.656	1.31	0.704	1.12	0.675	-1.18	0.591	0.61
1453222_at	Gse1	genetic suppressor element 1	1.3	0.676	-1	1	1.33	0.242	2.97	0.227	1.15
1418601_at	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7	1.83	0.022	1.07	0.648	-1.35	0.109	3.47	0.113	1.25
1436566_at	Rab40b	Rab40b, member RAS oncogene family	-1.14	0.602	1.44	0.485	1.32	0.368	1.33	0.367	0.74
1453556_x_at	Cd99	CD99 antigen	1.59	0.407	1.26	0.213	-1.27	0.339	1.14	0.785	0.68
1446339_at	Pdlim5	PDZ and LIM domain 5	1.52	0.624	1.06	0.858	1.06	0.638	-1.28	0.562	0.59
1447590_at	---	Adult male bone cDNA, RIKEN full-length enriched library, clone:9830167D18 prc	1.14	0.877	1.13	0.633	1.36	0.346	-2.3	0.213	0.33
1427217_at	Zfp455	zinc finger protein 455	1.19	0.747	1.41	0.204	1.04	0.444	-1.74	0.133	0.48
1430639_at	4930524L23Rik	RIKEN cDNA 4930524L23 gene	-1.42	0.14	1.32	0.449	1.61	0.2	1.02	0.9	0.63
1417395_at	Klf4	Kruppel-like factor 4 (gut)	-1.03	0.929	1.64	0.089	1.03	0.941	1.06	0.796	0.67
1435107_at	AW456874	expressed sequence AW456874	-1.23	0.042	1.26	0.563	1.57	0.02	1.65	0.044	0.81
1433172_at	3110049I03Rik	RIKEN cDNA 3110049I03 gene	-1.01	0.992	1.4	0.518	1.25	0.641	1.14	0.716	0.69
1452314_at	Kif11	kinesin family member 11	-1.01	0.983	1.27	0.653	1.38	0.065	5.46	0.19	1.78
1450201_at	---	---	-1.14	0.763	1.2	0.106	1.56	0.132	1.62	0.315	0.81
1422311_a_at	Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	1.86	0.403	-2.28	0.295	1.34	0.549	1.46	0.067	0.6
1422929_s_at	Atoh7	atonal homolog 7 (Drosophila)	1	0.996	1.8	0.146	-1.19	0.548	1	0.995	0.65
1428887_at	2610020C11Rik	RIKEN cDNA 2610020C11 gene	1.14	0.468	1.21	0.449	1.28	0.34	-1.44	0.024	0.55
1418895_at	Scap2	src family associated phosphoprotein 2	1.11	0.45	1.37	0.034	1.16	0.049	-1.12	0.468	0.63
1437858_at	Dpy19l3	dpy-19-like 3 (C. elegans)	1.11	0.645	1.17	0.809	1.36	0.277	-1.23	0.525	0.6
1416355_at	Rbmx	RNA binding motif protein, X chromosome	1.26	0.024	1.29	0.503	1.09	0.813	-1.3	0.439	0.59
1433496_at	Glt25d1	glycosyltransferase 25 domain containing 1	1.4	0.139	1.2	0.373	1.04	0.744	-1.34	0.302	0.57
1434814_x_at	Gpi1	glucose phosphate isomerase 1	1.06	0.332	1.04	0.535	1.54	0.004	-1.26	0.17	0.6
1458784_at	C78148	expressed sequence C78148	1.41	0.501	1.49	0.503	-1.35	0.62	1.3	0.766	0.71
1436821_at	Plcxd3	phosphatidylinositol-specific phospholipase C, X domain containing 3	1.05	0.743	1.56	0.262	1.03	0.866	-1.02	0.984	0.66
1424627_at	Cst12	cystatin 12	1.04	0.959	1.58	0.139	1.02	0.951	-1.18	0.756	0.62
1429936_at	2700059L22Rik	RIKEN cDNA 2700059L22 gene	1.35	0.484	1.27	0.619	1.02	0.957	-1.13	0.875	0.63
1428980_at	1110001M24Rik	RIKEN cDNA 1110001M24 gene	1.2	0.639	1.5	0.228	-1.05	0.738	1.15	0.68	0.7
1422478_a_at	Acss2	acyl-CoA synthetase short-chain family member 2	-1.15	0.349	1.37	0.075	1.41	0.244	1	0.996	0.66
1439581_at	6330403L08Rik	RIKEN cDNA 6330403L08 gene	1.63	0.446	1.45	0.442	-1.78	0.299	2.42	0.066	0.93
1419601_at	Kcnj10	potassium inwardly-rectifying channel, subfamily J, member 10	1.09	0.532	1.47	0.028	1.08	0.876	-1.02	0.937	0.65
1449110_at	Rhob	ras homolog gene family, member B	1.19	0.365	1.39	0.226	1.06	0.775	-1.05	0.835	0.65
1434334_at	Prkd2	protein kinase D2	1.12	0.228	1.47	0.279	1.05	0.764	-2.66	0.046	0.25
1453234_at	1300002K09Rik	RIKEN cDNA 1300002K09 gene	1.04	0.899	1.05	0.752	1.56	0.057	-2.41	0.083	0.31
1450564_x_at	Ifna1	interferon alpha 1	-1.33	0.78	1.7	0.071	1.19	0.832	4.12	0.166	1.42
1435172_at	Eomes	eomesodermin homolog (Xenopus laevis)	1.2	0.681	-1.77	0.067	1.88	0.221	1.53	0.539	0.71
1427338_at	Crocc	ciliary rootlet coiled-coil, rootletin	-1.15	0.415	1.3	0.564	1.48	0.498	2.57	0.265	1.05
1425227_a_at	Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	1.08	0.608	-1.55	0.458	1.92	0.354	2.89	0.193	1.08
1438833_at	Casc5 /// LOC6772	cancer susceptibility candidate 5 /// similar to cancer susceptibility candidate 5 isc	-2.17	0.148	1.42	0.409	1.77	0.268	3.13	0.205	1.04

1450503_at	Kcnj2	potassium inwardly-rectifying channel, subfamily J, member 2	-1.04	0.82	1.36	0.493	1.32	0.552	1.24	0.096	0.72
1428430_at	Rgmb	RGM domain family, member B	1.1	0.756	1.35	0.748	1.2	0.504	-1.41	0.271	0.56
1416936_at	Aatk	apoptosis-associated tyrosine kinase	-1.35	0.275	1.64	0.09	1.27	0.229	1.17	0.4	0.68
1433512_at	Fli1	Friend leukemia integration 1	1.05	0.537	1.53	0.094	1.07	0.795	-1.76	0.053	0.47
1419479_at	Sectm1	secreted and transmembrane 1	1.04	0.933	1.4	0.522	1.21	0.633	-1.44	0.653	0.55
1419189_at	Vti1a	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	1.02	0.942	-1.05	0.83	1.68	0.014	1.3	0.027	0.74
1438150_at	Fdps /// LOC54472	farnesyl diphosphate synthetase /// similar to farnesyl diphosphate synthetase ///	-1	0.989	1.53	0.521	1.12	0.841	1.17	0.79	0.7
1432348_at	4930524O07Rik	RIKEN cDNA 4930524O07 gene	-1.35	0.471	1.12	0.572	1.79	0.084	2.15	0.198	0.93
1459925_at	C78282	expressed sequence C78282	1.35	0.6	1.56	0.362	-1.35	0.584	1.76	0.198	0.83
1419712_at	Il3ra	interleukin 3 receptor, alpha chain	-1.11	0.617	1.15	0.774	1.59	0.152	1.02	0.882	0.66
1457151_at	---	Mus musculus, clone IMAGE:1527712, mRNA	1.49	0.475	1.34	0.073	-1.23	0.487	1.86	0.037	0.87
1436716_at	Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	-1.19	0.486	1.72	0.089	1.08	0.662	1.25	0.373	0.72
1458468_at	Coq10a	Coenzyme Q10 homolog A (yeast)	1.56	0.691	-1.06	0.759	1.15	0.736	2.71	0.298	1.09
1442797_x_at	Cmtm2a	CKLF-like MARVEL transmembrane domain containing 2A	1.18	0.566	1.66	0.222	-1.25	0.469	1.09	0.673	0.67
1442157_at	A930041H05Rik	RIKEN cDNA A930041H05 gene	1.55	0.122	1	0.999	1.1	0.61	-1.94	0.259	0.43
1431997_at	3000002C10Rik	RIKEN cDNA 3000002C10 gene	-1.41	0.368	1.09	0.516	1.85	0.102	1.08	0.777	0.65
1430464_at	9430021M05Rik	RIKEN cDNA 9430021M05 gene	1.41	0.399	1.62	0.356	-1.62	0.328	1.45	0.187	0.71
AFFX-b-ActinMur/M	Actb	actin, beta, cytoplasmic	1.31	0.674	1.02	0.955	1.31	0.446	-1.21	0.362	0.61
1451006_at	Xdh	xanthine dehydrogenase	1.36	0.352	-1.05	0.458	1.33	0.302	1.37	0.307	0.75
1424436_at	Gart	phosphoribosylglycinamide formyltransferase	-1.06	0.008	1.2	0.284	1.5	0.068	1.07	0.725	0.68
1445990_at	AU020096	expressed sequence AU020096	-1.3	0.426	1.75	0.353	1.13	0.798	1.35	0.6	0.73
1444868_at	4921529O18Rik	RIKEN cDNA 4921529O18 gene	1.35	0.515	1.14	0.818	1.16	0.692	-1.18	0.609	0.62
1417303_at	Mvd	mevalonate (diphospho) decarboxylase	1.14	0.56	1.5	0.092	1.01	0.956	-1.7	0.221	0.49
1432799_at	C030011G24Rik	RIKEN cDNA C030011G24 gene	-1.13	0.689	1.4	0.472	1.37	0.554	1.23	0.657	0.72
1431936_a_at	Neu2	neuraminidase 2	1.1	0.592	1.48	0.258	1.07	0.758	-1.8	0.338	0.46
1432751_at	4930403O18Rik	RIKEN cDNA 4930403O18 gene	1.57	0.324	1.62	0.043	-2.19	0.098	2.79	0.005	0.95
1448321_at	Smoc1	SPARC related modular calcium binding 1	-1.28	0.343	1.13	0.228	1.74	0.063	1.28	0.417	0.72
1459198_at	D4Ertd199e	DNA segment, Chr 4, ERATO Doi 199, expressed	1.03	0.907	1.79	0.403	-1.2	0.359	1.64	0.074	0.81
1457106_at	Thada	thyroid adenoma associated	1.34	0.645	1.05	0.927	1.27	0.364	-1.26	0.534	0.6
1452178_at	Plec1 /// LOC67153	plectin 1 /// similar to poly (ADP-ribose) polymerase family, member 10	1.07	0.691	1.2	0.091	1.38	0.059	-1.14	0.443	0.63
1450884_at	Cd36	CD36 antigen	1.61	0.202	1.45	0.046	-1.68	0.006	1.13	0.412	0.63
1424062_at	Ube2d1	ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog (yeast)	1.13	0.18	1.19	0.148	1.33	0.062	-1.26	0.554	0.6
1423454_a_at	Sema6c	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.6	0.607	1.04	0.843	1.99	0.136	1.36	0.271	0.7
1423542_at	Klk7	kallikrein 7 (chymotryptic, stratum corneum)	1.61	0.431	-1.03	0.957	1.07	0.907	1.13	0.688	0.7
1436497_at	Igf1	Insulin-like growth factor 1	1.07	0.876	1.39	0.541	1.19	0.518	-1.02	0.983	0.66
1449320_at	Pbsn	probasin	1.12	0.688	-2	0.014	2.04	0.181	5.14	0.004	1.57
1433538_at	Marveld1	MARVEL (membrane-associating) domain containing 1	1.38	0.031	1.07	0.797	1.2	0.434	-1.32	0.428	0.58
1418783_at	Trpm5	transient receptor potential cation channel, subfamily M, member 5	-1.38	0.531	1.83	0.037	1.1	0.378	1.08	0.754	0.66
1440795_x_at	Rabep2	rabaptin, RAB GTPase binding effector protein 2	1.03	0.767	1.26	0.03	1.36	0.051	-1.77	0.177	0.47
1425734_a_at	Ccdc77	coiled-coil domain containing 77	1.87	0.11	1.28	0.415	-2	0.271	1.44	0.474	0.65
1445006_at	---	---	-2.59	0.174	1.15	0.775	2.12	0.144	2.17	0.063	0.71
1449884_at	Efcab2	EF-hand calcium binding domain 2	1.18	0.492	1.22	0.555	1.25	0.302	-3.09	0.042	0.14
1426117_a_at	Slc19a2	solute carrier family 19 (thiamine transporter), member 2	1.44	0.449	-1.21	0.624	1.39	0.16	1.15	0.691	0.69
1442048_at	Rnf11	ring finger protein 11	1.1	0.8	1.75	0.018	-1.24	0.208	1.83	0.317	0.86
1438346_at	4930525G20Rik	RIKEN cDNA 4930525G20 gene	-1.04	0.727	1.12	0.816	1.57	0.337	1.04	0.891	0.67
1425008_a_at	Ifi203	interferon activated gene 203	1.28	0.161	1.14	0.715	1.24	0.146	-1.51	0.373	0.54
1433228_at	9430081G06Rik	RIKEN cDNA 9430081G06 gene	1.72	0.437	1.06	0.919	-1.13	0.802	1.5	0.448	0.79
1440710_at	Zfp706	zinc finger protein 706	1.7	0.048	1.05	0.821	-1.1	0.764	2.85	0.051	1.13
1454011_a_at	Rpa2	replication protein A2	1.26	0.26	-1.35	0.414	1.65	0.123	2.22	0.29	0.95
1454383_at	5430434G16Rik	RIKEN cDNA 5430434G16 gene	1.5	0.085	-1.08	0.892	1.22	0.574	1.57	0.363	0.81
1416157_at	Vcl	vinculin	1.03	0.928	-1.27	0.605	1.84	0.289	1.97	0.191	0.89
1425725_s_at	Ppp2r5c	Protein phosphatase 2, regulatory subunit B (B56), gamma isoform	-1.02	0.961	1.32	0.554	1.36	0.412	1.16	0.56	0.7
1423261_at	1500015O10Rik	RIKEN cDNA 1500015O10 gene	1.44	0.364	1.07	0.794	1.15	0.701	-1.53	0.324	0.53

1431210_at	Agbl3	ATP/GTP binding protein-like 3	-1.01	0.975	1.03	0.941	1.64	0.366	1.64	0.31	0.82
1427508_at	Arsi	arylsulfatase i	-1.27	0.392	1.76	0.178	1.1	0.692	1	0.979	0.65
1427211_at	Krtap8-1	keratin associated protein 8-1	-1.04	0.943	1.16	0.799	1.54	0.342	1.98	0.363	0.91
1437112_at	Pld1	phospholipase D1	-1.07	0.703	1.7	0.095	1.03	0.88	1.05	0.886	0.68
1446028_at	---	---	1.02	0.95	-1.13	0.677	1.76	0.016	1.1	0.508	0.69
1451970_at	E330036I19Rik	RIKEN cDNA E330036I19 gene	-1	0.994	1.24	0.351	1.43	0.097	1.41	0.232	0.77
1449615_s_at	Hdlbp	high density lipoprotein (HDL) binding protein	1.49	0.505	-1.14	0.828	1.29	0.714	1.3	0.649	0.74
1421269_at	Ugcg	UDP-glucose ceramide glucosyltransferase	1.14	0.36	-1.01	0.978	1.53	0.217	1.42	0.221	0.77
1416165_at	Rab31	RAB31, member RAS oncogene family	1.22	0.322	1.56	0.03	-1.14	0.206	1.22	0.131	0.72
1437314_a_at	Trmt1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	1.17	0.585	1.24	0.496	1.26	0.271	-1.38	0.419	0.57
1438686_at	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	1.24	0.56	-1.17	0.821	1.56	0.471	1.02	0.971	0.67
1454331_at	9430092D12Rik	RIKEN cDNA 9430092D12 gene	1.63	0.461	-1.44	0.57	1.34	0.264	1.55	0.133	0.77
1446536_at	Sema6d	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semapho	-1.47	0.476	1.89	0.297	1.09	0.736	1.06	0.784	0.64
1419191_at	Hipk3	homeodomain interacting protein kinase 3	1.12	0.554	1.09	0.835	1.45	0.478	-1.06	0.819	0.65
1433351_at	4933412L11Rik	RIKEN cDNA 4933412L11 gene	1.69	0.126	-1.3	0.387	1.2	0.524	1.04	0.847	0.66
1428690_at	Tysnd1	trypsin domain containing 1	1.4	0.302	-1.21	0.608	1.44	0.446	1.19	0.231	0.7
1433134_at	5830448L01Rik	RIKEN cDNA 5830448L01 gene	-1.63	0.493	1.96	0.144	1.09	0.87	4.64	0.315	1.51
1432787_at	6720420G18Rik	RIKEN cDNA 6720420G18 gene	1.76	0.097	1.13	0.607	-1.31	0.444	1.1	0.791	0.67
1431083_a_at	1810014B01Rik	RIKEN cDNA 1810014B01 gene	-1.09	0.768	1.47	0.041	1.27	0.158	1.12	0.517	0.69
1433096_at	4930473M17Rik	RIKEN cDNA 4930473M17 gene	1.44	0.455	-1.71	0.386	1.63	0.314	2.03	0.052	0.85
1455025_at	Paqr9	progestin and adipoQ receptor family member IX	-1.08	0.359	1.05	0.789	1.69	0.158	2.59	0.141	1.06
1457741_at	---	---	1.15	0.818	1.44	0.266	1.07	0.847	-1.8	0.457	0.47
1416921_x_at	Aldoa	aldolase 1, A isoform	1.02	0.787	1.15	0.219	1.49	0.003	-1.11	0.43	0.64
1441554_at	4833446K15Rik	RIKEN cDNA 4833446K15 gene	1.09	0.626	1.42	0.11	1.16	0.816	-1.97	0.039	0.42
1429104_at	Limd2	LIM domain containing 2	1.04	0.894	1.5	0.006	1.13	0.657	-2.13	0.101	0.38
1417869_s_at	Ctsz	cathepsin Z	1.02	0.847	1.35	0.042	1.3	0.185	-1.76	0.109	0.48
1449283_a_at	Mapk12	mitogen-activated protein kinase 12	1.12	0.473	1.36	0.21	1.19	0.045	-1.3	0.588	0.59
1448389_at	Wdr5	WD repeat domain 5	1.61	0.071	-1.31	0.481	1.29	0.35	1.81	0.144	0.85
1437324_x_at	Fmod	fibromodulin	-1.02	0.93	1.44	0.55	1.24	0.537	1.08	0.326	0.69
1437269_at	AW124722	expressed sequence AW124722	1.4	0.306	1.09	0.632	1.19	0.426	-1.5	0.461	0.54
1456768_a_at	Mmrn2	multimerin 2	1.24	0.03	1.29	0.018	1.13	0.584	-1.36	0.086	0.58
1429198_at	1810030O07Rik	RIKEN cDNA 1810030O07 gene	1.27	0.493	-1.13	0.536	1.51	0.336	1.22	0.552	0.72
1442233_at	Phb	Prohibitin	1.29	0.603	1.3	0.28	1.08	0.714	-1.36	0.329	0.58
1439104_at	C230081A13Rik	RIKEN cDNA C230081A13 gene	1.87	0.045	1.27	0.405	-1.9	0.002	1.04	0.838	0.57
1430054_at	1700030F18Rik	RIKEN cDNA 1700030F18 gene	1.61	0.14	1.51	0.427	-1.82	0.15	1.62	0.125	0.73
1421385_a_at	Myo7a	myosin VIIa	1.23	0.289	1.12	0.246	1.31	0.006	-1.1	0.755	0.64
1425329_a_at	Cyb5r3	cytochrome b5 reductase 3	1.41	0.579	-1.3	0.611	1.48	0.532	1.55	0.399	0.79
1453133_at	Slc25a31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), m	1.63	0.214	-1.01	0.986	1.05	0.926	1.11	0.774	0.69
1421559_at	Abo	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase, tr	1.04	0.896	1.75	0.419	-1.13	0.789	1.61	0.162	0.82
1460356_at	Esam1	endothelial cell-specific adhesion molecule	1.28	0.198	1.24	0.151	1.15	0.216	-1.01	0.964	0.66
1446966_at	AU042651	Expressed sequence AU042651	2.07	0.186	-1.73	0.467	1.03	0.951	2.75	0.246	1.03
1436354_at	Dzip1l	DAZ interacting protein 1-like	1.15	0.569	1.3	0.023	1.22	0.266	-1.64	0.186	0.51
1426801_at	8-Sep	septin 8	1.39	0.184	1.45	0.095	-1.19	0.368	3.47	0.138	1.28
1430933_at	5730433K22Rik	RIKEN cDNA 5730433K22 gene	1.06	0.843	1.26	0.621	1.34	0.553	-2.13	0.23	0.39
1420920_a_at	Arf1	ADP-ribosylation factor 1	1.35	0.631	1.15	0.719	1.18	0.734	-1	0.993	0.67
1453077_a_at	Snapc3	small nuclear RNA activating complex, polypeptide 3	1.35	0.394	1.33	0.329	-1.01	0.962	1.06	0.869	0.68
1448384_at	Pofut2	protein O-fucosyltransferase 2	1.19	0.272	1.15	0.324	1.34	0.128	-1.07	0.424	0.65
1450447_at	Hnf4a	hepatic nuclear factor 4, alpha	1.53	0.33	1.11	0.856	1.02	0.92	-1.54	0.268	0.53
1439660_at	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	1.39	0.511	1.51	0.319	-1.3	0.283	1.01	0.959	0.65
1425862_a_at	Pik3c2a	phosphatidylinositol 3-kinase, C2 domain containing, alpha polypeptide	1.34	0.623	1.16	0.687	1.17	0.682	-1.11	0.691	0.64
1430879_at	C030008P14Rik	RIKEN cDNA C030008P14 gene	1.28	0.55	1.47	0.191	-1.09	0.861	3.83	0.201	1.37
1450700_at	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3	1.22	0.457	1.54	0.037	-1.11	0.453	1.63	0.138	0.82
1449356_at	Asb5	ankyrin repeat and SOCs box-containing protein 5	1.13	0.277	1	0.998	1.55	0.11	-2.35	0.077	0.33

1452127_a_at	Ptpn13	protein tyrosine phosphatase, non-receptor type 13	1.06	0.607	1.26	0.712	1.35	0.074	-1.18	0.498	0.62
1427535_s_at	AW822216	expressed sequence AW822216	1.23	0.048	1.42	0.42	1.03	0.843	-1.31	0.41	0.59
1456735_x_at	Acpl2	acid phosphatase-like 2	1.22	0.233	1.14	0.497	1.32	0.312	-1.04	0.34	0.66
1427980_at	4933407C03Rik	RIKEN cDNA 4933407C03 gene	-1.14	0.532	1.18	0.091	1.62	0.058	1.17	0.119	0.71
1436310_at	Gemin5	gem (nuclear organelle) associated protein 5	1.02	0.928	1.08	0.553	1.57	0.087	-1.14	0.633	0.63
1446113_at	---	---	1.8	0.276	1.14	0.734	-1.35	0.568	1.38	0.478	0.74
1439831_at	LOC240327	Hypothetical LOC240327	1.71	0.31	-1.11	0.294	1.06	0.778	1.14	0.536	0.7
1428139_at	4930538D17Rik	RIKEN cDNA 4930538D17 gene	-1.07	0.883	1.04	0.63	1.7	0.057	1.98	0.449	0.91
1424338_at	Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	1.52	0.085	-1.09	0.103	1.23	0.754	2.35	0.153	1
1436867_at	Srl /// LOC669709	sarcalumenin /// similar to sarcalumenin	-1.52	0.261	1.29	0.668	1.73	0.254	1.02	0.97	0.63
1448043_x_at	Rnf2	ring finger protein 2	-1.45	0.277	1.03	0.923	1.95	0.293	1.45	0.615	0.75
1451681_at	BC089597	cDNA sequence BC089597	1.05	0.674	-1.06	0.595	1.69	0.4	2.91	0.019	1.14
1418192_at	Mnt	max binding protein	1.08	0.871	1.22	0.171	1.38	0.27	-1.49	0.295	0.55
1415943_at	Sdc1	syndecan 1	1.28	0.384	1.49	0.068	-1.1	0.496	1.81	0.2	0.87
1454312_at	2900097C17Rik	RIKEN cDNA 2900097C17 gene	1.06	0.871	1.14	0.832	1.48	0.65	-1.98	0.154	0.42
1419138_at	B3galt4	UDP-Gal:betaGalNAc beta 1,3-galactosyltransferase, polypeptide 4	1.38	0.327	1.09	0.819	1.21	0.148	-1.38	0.12	0.57
1425594_at	Lamc3	laminin gamma 3	1.08	0.837	1.05	0.878	1.55	0.302	-1.1	0.855	0.65
1417929_at	Slc7a8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	-1.53	0.265	1.75	0.004	1.27	0.006	1.42	0.232	0.73
1447068_at	Pik3r3	Phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	1.48	0.087	1.37	0.152	-1.21	0.402	1.6	0.273	0.81
1420749_a_at	Pou6f1	POU domain, class 6, transcription factor 1	1.92	0.46	-1.4	0.463	1.05	0.761	1.14	0.583	0.68
1441368_at	---	12 days embryo embryonic body between diaphragm region and neck cDNA, RIK	1.25	0.71	1.17	0.739	1.25	0.651	-1.33	0.658	0.59
1449375_at	Ces6	carboxylesterase 6	1.3	0.43	-1.54	0.203	1.73	0.138	3.34	0.034	1.21
1427256_at	Cspg2	chondroitin sulfate proteoglycan 2	-1.46	0.459	1.98	0.12	1.01	0.96	2.74	0.154	1.07
1460196_at	Cbr1	carbonyl reductase 1	1.63	0.006	-1.22	0.146	1.23	0.205	1.19	0.411	0.71
1433748_at	Zdhhc18	zinc finger, DHHC domain containing 18	1.34	0.219	1.2	0.05	1.14	0.474	-1.38	0.239	0.58
1419485_at	Foxc1	forkhead box C1	1.23	0.358	1.49	0.178	-1.05	0.719	1.26	0.66	0.73
1422809_at	Rims2	regulating synaptic membrane exocytosis 2	1.62	0.174	-1.02	0.842	1.08	0.627	1.88	0.257	0.89
1454337_at	6330571C24Rik	RIKEN cDNA 6330571C24 gene	-1.43	0.611	1.24	0.671	1.74	0.004	1.05	0.839	0.65
1459582_at	---	---	1.07	0.849	-1.05	0.864	1.66	0.325	1.85	0.33	0.88
1424667_a_at	Cutl1	cut-like 1 (Drosophila)	1.32	0.596	-1.05	0.78	1.41	0.112	1.38	0.109	0.76
1430036_at	2310015B20Rik	RIKEN cDNA 2310015B20 gene	-1.17	0.761	1.63	0.405	1.2	0.285	1.27	0.716	0.73
1425703_at	Ppard	peroxisome proliferator activator receptor delta	1.6	0.32	1.14	0.549	-1.07	0.572	1.18	0.534	0.71
1427422_at	LOC624219	similar to hepatocellular carcinoma-associated gene TD26	-1.48	0.038	1.04	0.86	1.96	0.007	1.3	0.654	0.71
1428174_x_at	Khsrp	KH-type splicing regulatory protein	1.36	0.016	-1.01	0.98	1.33	0.51	1.56	0.259	0.81
1436789_at	Ccnjl	cyclin J-like	1.1	0.848	1.95	0.305	-1.61	0.33	1.05	0.902	0.62
1448281_a_at	Ela2a	elastase 2A	-1.04	0.162	1.36	0.597	1.37	0.3	1.28	0.44	0.74
1416348_at	Men1	multiple endocrine neoplasia 1	1.07	0.883	1.08	0.667	1.53	0.085	-1.26	0.452	0.6
1432495_at	Sox7	SRY-box containing gene 7	1.45	0.396	1.71	0.291	-1.92	0.002	1.44	0.089	0.67
1459723_at	Zdhhc22	zinc finger, DHHC-type containing 22	1.63	0.183	1.33	0.563	-1.38	0.448	1.5	0.347	0.77
1426799_at	Rab8b	RAB8B, member RAS oncogene family	1.18	0.018	1.52	0.065	-1.02	0.881	1.33	0.155	0.75
1434944_at	Dmpk	dystrophia myotonica-protein kinase	-1.19	0.455	1.37	0.193	1.47	0.299	1.06	0.915	0.68
1453276_at	Kif13b	kinesin family member 13B	1.73	0.206	1.05	0.868	-1.12	0.77	1.38	0.203	0.76
1425529_s_at	D19Wsu162e	DNA segment, Chr 19, Wayne State University 162, expressed	1.1	0.39	-1.08	0.476	1.65	0.044	1.22	0.161	0.72
1422862_at	LOC669660	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ an	1.19	0.072	-1.13	0.766	1.61	0.471	1.11	0.784	0.7
1422603_at	Rnase4	ribonuclease, RNase A family 4	1.77	0.442	1.06	0.544	-1.17	0.177	1.32	0.146	0.75
1436621_at	P140	P140 gene	-1.26	0.267	1.84	0.061	1.05	0.52	2.13	0.131	0.94
1428098_a_at	Tm7sf3	transmembrane 7 superfamily member 3	-1.02	0.919	1.22	0.113	1.48	0.059	1.68	0.168	0.84
1424775_at	Oas1a	2'-5' oligoadenylate synthetase 1A	1.15	0.033	1.09	0.073	1.44	0.054	-1.5	0.127	0.55
1436329_at	Egr3	early growth response 3	1.12	0.802	1.42	0.274	1.15	0.852	-2.74	0.118	0.24
1449331_a_at	Rapsn	receptor-associated protein of the synapse	1.59	0.15	-1.07	0.818	1.16	0.579	1.28	0.668	0.74
1418805_at	Sct	secretin	1.2	0.243	1.48	0.61	1	0.99	-1.75	0.422	0.48
1436372_a_at	2210010A19Rik	RIKEN cDNA 2210010A19 gene	1.2	0.233	1.18	0.608	1.31	0.499	-1.26	0.267	0.61
1417231_at	Cldn2	claudin 2	1.26	0.041	1.19	0.407	1.23	0.315	-1.65	0.437	0.51

1448031_at	Gnao1	Guanine nucleotide binding protein, alpha o	1.34	0.669	1.02	0.93	1.32	0.392	-1.25	0.575	0.61
1421324_a_at	Akt2	thymoma viral proto-oncogene 2	1.46	0.328	-1.09	0.808	1.31	0.615	1.03	0.956	0.68
1447721_at	Zbtb26	zinc finger and BTB domain containing 26	1.76	0.209	-1.31	0.09	1.16	0.591	1.13	0.772	0.69
1448640_at	Slc14a1	solute carrier family 14 (urea transporter), member 1	1.09	0.861	-1.07	0.783	1.66	0.094	2.37	0.253	1.01
1435658_at	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	-1	0.998	1.06	0.817	1.63	0.231	1.1	0.828	0.7
1444098_at	1700010H15Rik	RIKEN cDNA 1700010H15 gene	1.76	0.376	1.05	0.916	-1.14	0.497	1.26	0.53	0.73
1430058_at	Slbp	stem-loop binding protein	-1.26	0.358	1.79	0.195	1.1	0.762	1.64	0.172	0.82
1451806_at	Fnbp1	formin binding protein 1	1.08	0.778	-1.56	0.034	1.96	0.323	1.53	0.272	0.75
1425169_at	Tessp2	testis serine protease 2	1.15	0.765	1.29	0.477	1.25	0.273	-1.26	0.39	0.61
1450644_at	Zfp36l1	zinc finger protein 36, C3H type-like 1	1.11	0.516	1.22	0.163	1.35	0.083	-1.72	0.084	0.49
1418280_at	Klf6	Kruppel-like factor 6	1.17	0.386	1.51	0.097	1	0.988	-1.11	0.559	0.64
1421337_at	Elf4	E74-like factor 4 (ets domain transcription factor)	1.08	0.891	1.2	0.477	1.4	0.4	-1.14	0.832	0.64
1440237_at	Ercc4	excision repair cross-complementing rodent repair deficiency, complementation g	1.06	0.809	1.43	0.127	1.2	0.249	-1.21	0.588	0.62
1450310_at	Grid2ip	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein 1	-1.75	0.195	1.95	0.156	1.17	0.672	1.16	0.507	0.63
1418967_a_at	St7	Suppression of tumorigenicity 7	-1.1	0.772	1.61	0.037	1.17	0.232	2.58	0.275	1.07
1418823_at	Arf6	ADP-ribosylation factor 6	-1.06	0.635	1.45	0.152	1.29	0.438	1.06	0.749	0.69
1457968_at	Tmem23	Transmembrane protein 23	1.32	0.138	1.02	0.969	1.35	0.258	-1.54	0.341	0.54
1441914_x_at	Fgf3	Fibroblast growth factor 3	1.18	0.63	1.78	0.493	-1.37	0.645	1.26	0.635	0.71
1417559_at	Sfxn1	sideroflexin 1	-1.07	0.578	1.16	0.113	1.59	0	1.57	0.296	0.81
1454294_at	2310061A09Rik	RIKEN cDNA 2310061A09 gene	1.72	0.493	-1.4	0.357	1.26	0.469	1.16	0.622	0.68
1417430_at	Cdr2	cerebellar degeneration-related 2	-1.01	0.989	1.44	0.263	1.26	0.526	4.73	0.198	1.61
1425610_s_at	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.35	0.398	-1.04	0.832	1.38	0.243	1.61	0.074	0.83
1436751_at	BC052883	cDNA sequence BC052883	1.87	0.604	-1.6	0.208	1.19	0.768	2.28	0.101	0.94
1433529_at	E430002G05Rik	RIKEN cDNA E430002G05 gene	1.63	0.119	1.45	0.044	-1.63	0.231	1.1	0.805	0.64
1429339_a_at	Acad10	acyl-Coenzyme A dehydrogenase family, member 10	1.15	0.492	1.09	0.787	1.45	0.054	-1.46	0.175	0.56
1435929_at	LOC677429	similar to RIKEN cDNA 9630033F20 gene	1.34	0.034	1.13	0.293	1.22	0.58	-1.11	0.732	0.65
1444732_at	---	---	1.42	0.372	1.19	0.35	1.08	0.855	-1.03	0.641	0.66
1447929_at	Ssh3	slingshot homolog 3 (Drosophila)	1.28	0.622	1.16	0.446	1.26	0.299	-1.11	0.728	0.65
1425158_at	Tbx20	T-box 20	1.26	0.604	1.33	0.538	1.11	0.78	-1.8	0.038	0.47
1433639_at	5730593F17Rik	RIKEN cDNA 5730593F17 gene	-1.11	0.735	1.3	0.458	1.49	0.086	2.25	0.161	0.98
1459839_x_at	Btbd11	BTB (POZ) domain containing 11	1.06	0.716	1.24	0.225	1.39	0.145	-1.25	0.157	0.61
1425704_at	BC022224	cDNA sequence BC022224	-1.12	0.38	1.03	0.734	1.77	0.288	4.13	0.168	1.45
1423228_at	B4galt6 /// LOC675	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 /// similar to E	-1.11	0.326	1.16	0.646	1.63	0.14	1.47	0.042	0.79
1417051_at	Pcdh8	protocadherin 8	-1.32	0.584	1.36	0.613	1.57	0.077	2.87	0.373	1.12
1432169_at	4930523O13Rik	RIKEN cDNA 4930523O13 gene	2.03	0.143	1.08	0.868	-1.71	0.398	1.25	0.701	0.66
1430080_at	Fcnb	ficolin B	-1.6	0.342	1.75	0.416	1.32	0.485	2.23	0.458	0.92
1421694_a_at	Cspg2	chondroitin sulfate proteoglycan 2	-3.1	0.019	1.5	0.554	1.88	0.276	1.62	0.264	0.47
1426942_at	Aim1	absent in melanoma 1	1.19	0.454	1.09	0.421	1.41	0.022	-1.38	0.404	0.58
1451978_at	Loxl1	lysyl oxidase-like 1	1.75	0.011	1.28	0.401	-1.5	0.051	1.33	0.079	0.71
1440328_at	Nasp	nuclear autoantigenic sperm protein (histone-binding)	-2.08	0.401	2.06	0.285	1.15	0.707	1.16	0.777	0.57
1455470_x_at	Lasp1	LIM and SH3 protein 1	1.06	0.049	1.12	0.452	1.52	0.042	-1.41	0.254	0.57
1430537_at	Trmt12	tRNA methyltranferase 12 homolog (S. cerevisiae)	1.08	0.86	-1.18	0.788	1.77	0.376	1.65	0.067	0.83
1435190_at	Chl1	cell adhesion molecule with homology to L1CAM	1.45	0.591	1.31	0.361	-1.07	0.862	1.62	0.036	0.83
1459848_x_at	Dbh	dopamine beta hydroxylase	-1.48	0.214	1.49	0.151	1.53	0.277	1.4	0.379	0.74
1440270_at	Fgf12	fibroblast growth factor 12	1.08	0.935	1.85	0.458	-1.3	0.233	1.03	0.971	0.66
1443708_at	BC068281	cDNA sequence BC068281	1.58	0.378	-1.14	0.392	1.24	0.691	1.01	0.99	0.67
1422543_at	Ropn1	ropporin, rhophilin associated protein 1	1.01	0.968	1.49	0.407	1.2	0.613	-1.33	0.288	0.59
1451534_at	Scgn	secretagogin, EF-hand calcium binding protein	1.23	0.611	1.03	0.918	1.43	0.137	-1.5	0.127	0.55
1415959_at	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4	1.02	0.963	-1.27	0.237	1.89	0.329	5.61	0.188	1.81
1425612_at	Cutl1	cut-like 1 (Drosophila)	-1.25	0.598	1.31	0.771	1.59	0.532	1.46	0.064	0.78
1444547_at	---	---	1.7	0.386	-1.41	0.253	1.29	0.649	1.88	0.362	0.87
1439855_at	BC023818	cDNA sequence BC023818	1.32	0.188	1.19	0.817	1.19	0.466	-2.01	0.171	0.42
1419451_at	Fzr1	fizzy/cell division cycle 20 related 1 (Drosophila)	1.23	0.424	-1.01	0.965	1.48	0.163	3.31	0.192	1.25

1422974_at	Nt5e	5' nucleotidase, ecto	1.1	0.86	-1.24	0.635	1.79	0.16	1.27	0.353	0.73
1454183_at	3100004P22Rik	RIKEN cDNA 3100004P22 gene	-1.73	0.213	1.84	0.177	1.28	0.53	1.27	0.765	0.66
1451932_a_at	Adamtsl4	ADAMTS-like 4	1.29	0.391	-1.05	0.816	1.46	0.025	1.06	0.784	0.69
1424704_at	Runx2	runt related transcription factor 2	1.29	0.446	1.14	0.745	1.27	0.188	-1.41	0.302	0.57
1418925_at	Celsr1	cadherin EGF LAG seven-pass G-type receptor 1	1.13	0.665	1.12	0.713	1.45	0.086	-1.14	0.554	0.64
1441559_at	LOC627626	similar to CG11212-PA	1.67	0.258	-1.02	0.97	1.05	0.899	1.27	0.708	0.74
1427705_a_at	Nfkb1	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	1.06	0.645	1.18	0.25	1.46	0.034	-1.7	0.082	0.5
1443864_at	Dtl	denticleless homolog (Drosophila)	1.34	0.737	-1.07	0.796	1.42	0.558	6.81	0.171	2.13
1443275_at	Cdgap	Cdc42 GTPase-activating protein	1.51	0.507	1.74	0.135	-2.25	0.014	1.56	0.196	0.64
1434830_at	Mxd1	MAX dimerization protein 1	-1.39	0.057	1.2	0.398	1.78	0.09	2.96	0.246	1.14
1447360_at	Tsc22d1	TSC22 domain family, member 1	1.36	0.722	1.63	0.391	-1.41	0.345	1.3	0.679	0.72
1445778_at	Elf4	E74-like factor 4 (ets domain transcription factor)	1.6	0.261	1.22	0.72	-1.14	0.014	1.2	0.661	0.72
1439622_at	Rassf4	Ras association (RalGDS/AF-6) domain family 4	-1.1	0.685	1.45	0.107	1.34	0.192	1.14	0.727	0.71
1458596_at	Dctn4	dynactin 4	1.28	0.699	1.01	0.978	1.4	0.3	-1.37	0.122	0.58
1440882_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1.31	0.229	-1.22	0.542	1.57	0.15	1.09	0.609	0.69
1442189_at	Pscd1	Pleckstrin homology, Sec7 and coiled-coil domains 1	-1.46	0.592	1.64	0.144	1.38	0.434	1.29	0.278	0.71
1444011_at	---	---	1.37	0.059	1.17	0.775	1.16	0.716	-2.06	0.111	0.41
1417489_at	Npy2r	neuropeptide Y receptor Y2	-1.06	0.814	1	0.996	1.76	0.367	1.14	0.59	0.71
1430882_at	---	---	1.49	0.509	1.27	0.442	-1.07	0.81	1.19	0.356	0.72
1419145_at	Smtnl1	smoothelin-like 1	-1.05	0.943	1.35	0.654	1.4	0.362	1.29	0.733	0.75
1428024_at	Map1lc3b	Microtubule-associated protein 1 light chain 3 beta	1.97	0.231	1.01	0.992	-1.37	0.324	1.84	0.299	0.86
1429682_at	4930431B09Rik	RIKEN cDNA 4930431B09 gene	1.21	0.772	-1.09	0.897	1.58	0.257	3.65	0.138	1.34
1445040_at	D7Ertd783e	DNA segment, Chr 7, ERATO Doi 783, expressed	-2.53	0.048	1.85	0.231	1.46	0.533	1.04	0.941	0.45
1449311_at	Bach1	BTB and CNC homology 1	1.74	0.214	1.17	0.595	-1.25	0.521	1.8	0.117	0.86
1441694_at	---	Transcribed locus	1.25	0.664	1.66	0.136	-1.27	0.547	1.16	0.809	0.7
1443962_at	Tfdp2	transcription factor Dp 2	1.19	0.056	-1.19	0.268	1.68	0.123	4.49	0.21	1.54
1439695_a_at	Mphosph1	M-phase phosphoprotein 1	1.1	0.564	1.78	0.164	-1.21	0.285	1.55	0.429	0.8
1426100_a_at	Tk2	thymidine kinase 2, mitochondrial	1.11	0.244	1.15	0.259	1.44	0.007	-1.74	0.132	0.49
1454349_at	2810487C13Rik	RIKEN cDNA 2810487C13 gene	1.5	0.378	1.09	0.63	1.11	0.295	-1.54	0.415	0.54
1429403_x_at	Glt8d2	glycosyltransferase 8 domain containing 2	-1.6	0.027	2	0.063	1.08	0.735	1.25	0.41	0.68
1434199_at	Gm323	gene model 323, (NCBI)	1.41	0.395	1.09	0.836	1.2	0.549	-1.01	0.974	0.67
1425850_a_at	Nek6 /// LOC67424	NIMA (never in mitosis gene a)-related expressed kinase 6 /// similar to NIMA (ne	1.08	0.129	1.26	0.424	1.37	0.153	-1.01	0.962	0.67
1449805_at	Prss29	Protease, serine, 29	-1.17	0.582	1.46	0.031	1.39	0.317	2.5	0.194	1.05
1436233_at	AI117581	expressed sequence AI117581	1.34	0.138	1.15	0.127	1.21	0.381	-1.01	0.982	0.67
1459621_at	Itsn1	intersectin 1 (SH3 domain protein 1A)	1.3	0.529	1.52	0.307	-1.13	0.799	1.81	0.356	0.88
1434871_at	Cox17	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	1.05	0.769	1.11	0.776	1.54	0.301	-1.66	0.19	0.51
1450715_at	Cyp1a2	cytochrome P450, family 1, subfamily a, polypeptide 2	1.5	0.625	-1.45	0.276	1.52	0.457	1.02	0.974	0.65
1426007_a_at	Ubxd3	UBX domain containing 3	-2.22	0.132	1.34	0.032	1.92	0.171	1.56	0.076	0.65
1428860_at	4930572J05Rik	RIKEN cDNA 4930572J05 gene	1.15	0.811	-1.13	0.565	1.67	0.389	1.03	0.837	0.68
1428319_at	Pdlim7	PDZ and LIM domain 7	1.49	0.06	1	0.991	1.22	0.452	-1	0.993	0.68
1418744_s_at	Tesc	tescalcin	1.06	0.54	1.27	0.708	1.38	0.126	-1.53	0.203	0.54
1437732_at	Omt2a /// LOC6408	oocyte maturation, alpha /// similar to oocyte maturation, beta	1.17	0.193	1.79	0.242	-1.34	0.599	1.13	0.798	0.69
1454796_at	D5Ertd40e	DNA segment, Chr 5, ERATO Doi 40, expressed	1.09	0.644	1.25	0.377	1.37	0.138	-1.04	0.674	0.67
1451860_a_at	Trim30	tripartite motif protein 30	1.13	0.522	1.55	0.001	1.03	0.792	-1.96	0.078	0.44
1436461_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.48	0.282	1.11	0.744	1.12	0.806	-1.32	0.453	0.6
1442064_at	AW556556	expressed sequence AW556556	1.15	0.378	2	0.004	-1.79	0.006	1.11	0.528	0.62
1446740_at	---	Transcribed locus	-1.05	0.883	1.66	0.239	1.1	0.869	1.55	0.238	0.81
1455902_x_at	Rhof	Ras homolog gene family, member f	1.26	0.09	1.58	0.451	-1.14	0.511	3.07	0.181	1.19
1416935_at	Trpv2	transient receptor potential cation channel, subfamily V, member 2	1.09	0.807	1.36	0.409	1.26	0.106	-1.34	0.116	0.59
1424495_a_at	Cklf	chemokine-like factor	1.13	0.526	1.48	0.144	1.1	0.706	-1.28	0.549	0.61
1443347_at	---	---	-1.93	0.373	1.67	0.392	1.52	0.387	1.11	0.792	0.59
1432137_at	4933434P08Rik	RIKEN cDNA 4933434P08 gene	1.2	0.689	1.13	0.83	1.38	0.434	-3.46	0.053	0.06
1458189_at	Emid2	EMI domain containing 2	1.26	0.734	1.21	0.746	1.24	0.588	-2.23	0.072	0.37

1452349_x_at	Ifi205 /// Mnda	interferon activated gene 205 /// myeloid cell nuclear differentiation antigen	1.22	0.304	1.36	0.133	1.13	0.593	-1.86	0.09	0.46
1450247_a_at	Scamp5	secretory carrier membrane protein 5	1.09	0.732	-1.17	0.647	1.77	0.249	1.93	0.1	0.9
1442741_at	Mcc	mutated in colorectal cancers	1.18	0.595	-2.04	0.203	2.05	0.339	1.88	0.328	0.77
1450781_at	Hmga2	high mobility group AT-hook 2	1.11	0.901	1.6	0.415	1.01	0.983	-1.91	0.149	0.45
1429038_at	1500034J01Rik	RIKEN cDNA 1500034J01 gene	1.01	0.984	-1.03	0.897	1.74	0.155	1.09	0.674	0.7
1446799_at	---	---	1.71	0.275	1.46	0.52	-1.83	0.032	1.05	0.802	0.6
1431870_at	4930463O16Rik	RIKEN cDNA 4930463O16 gene	-1.03	0.955	1.27	0.621	1.47	0.33	1.21	0.639	0.73
1434610_at	Plec1	plectin 1	1.06	0.803	1.19	0.253	1.46	0.005	-1.02	0.942	0.67
1425378_at	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	1.54	0.357	1.34	0.533	-1.2	0.458	1.46	0.146	0.79
1443910_at	6330408A02Rik	RIKEN cDNA 6330408A02 gene	1.46	0.424	1.11	0.26	1.14	0.719	-3.25	0.254	0.12
1418930_at	Cxcl10	chemokine (C-X-C motif) ligand 10	1.18	0.622	1.03	0.918	1.5	0.29	-1.36	0.278	0.59
1425949_at	Slc25a30	solute carrier family 25, member 30	1.59	0.348	1.03	0.956	1.09	0.848	-1.02	0.959	0.67
1427689_a_at	Tnip1	TNFAIP3 interacting protein 1	1.07	0.667	1.1	0.266	1.54	0.147	-1.37	0.249	0.59
1426943_at	Ints1	integrator complex subunit 1	1.15	0.408	1.11	0.303	1.45	0.058	-1.15	0.331	0.64
1418240_at	Gbp2	guanylate nucleotide binding protein 2	1.08	0.103	1.54	0.11	1.09	0.529	-1.26	0.178	0.61
1416777_at	Ceacam12	CEA-related cell adhesion molecule 12	1.05	0.907	1.38	0.12	1.28	0.503	-1.22	0.644	0.62
1451607_at	Klk1b21	kallikrein 1-related peptidase b21	1.92	0.497	1.14	0.748	-1.54	0.1	1.06	0.854	0.65
1432621_at	5730410E19Rik	RIKEN cDNA 5730410E19 gene	1.76	0.054	1.12	0.809	-1.2	0.726	1.05	0.862	0.68
1455577_at	Ccl28	Chemokine (C-C motif) ligand 28	1.34	0.723	1.12	0.549	1.25	0.421	-1.6	0.026	0.53
1452531_at	Runx1	runt related transcription factor 1	1.28	0.415	1.49	0.437	-1.07	0.611	1.26	0.452	0.74
1451881_at	---	---	-1.11	0.675	1.73	0.485	1.09	0.652	1.28	0.545	0.75
1455993_at	---	---	1.13	0.74	-1.72	0.149	2	0.192	1.3	0.249	0.68
1436941_at	Gm1752	gene model 1752, (NCBI)	1.03	0.858	1.03	0.928	1.65	0.077	-1.29	0.305	0.61
1426064_at	Cyp3a44	cytochrome P450, family 3, subfamily a, polypeptide 44	1.84	0.659	1.26	0.501	-1.63	0.274	1.01	0.986	0.62
1459741_x_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	-1.82	0.151	1.41	0.392	1.76	0.012	1.52	0.094	0.72
1426529_a_at	Tagln2	transgelin 2	-1.06	0.784	1.54	0.083	1.24	0.108	1.03	0.898	0.69
1441818_at	---	Transcribed locus	-1	0.967	1.58	0.467	1.15	0.786	1.69	0.139	0.85
1432871_at	4932429P19Rik	RIKEN cDNA 4932429P19 gene	1.22	0.605	1.4	0.124	1.1	0.678	-1.33	0.407	0.6
1452278_a_at	Hace1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	1.03	0.752	2.02	0.296	-1.5	0.022	3.09	0.148	1.16
1430835_at	5830436D01Rik	RIKEN cDNA 5830436D01 gene	1.27	0.058	1.18	0.607	1.27	0.236	-1.14	0.398	0.65
1455288_at	1110036O03Rik	RIKEN cDNA 1110036O03 gene	1.42	0.166	1.25	0.45	1.05	0.801	-1.32	0.359	0.6
1453433_at	2600001A11Rik	RIKEN cDNA 2600001A11 gene	1.22	0.475	1.12	0.638	1.38	0.002	-1.75	0.006	0.49
1432386_a_at	Phf7	PHD finger protein 7	1.27	0.415	-1.02	0.95	1.47	0.167	1.03	0.94	0.69
1448191_at	Plk1	polo-like kinase 1 (Drosophila)	1.22	0.258	-1.33	0.558	1.75	0.111	3.12	0.21	1.19
1426051_a_at	Cenpb	centromere protein B	1.6	0.425	1.22	0.38	-1.11	0.464	1.11	0.665	0.7
1450569_a_at	Rbm14	RNA binding motif protein 14	1.1	0.777	-1.04	0.342	1.66	0.05	1.53	0.188	0.81
1448412_a_at	Tsc22d4	TSC22 domain family 4	1.2	0.164	1.23	0.122	1.29	0.124	-1.03	0.791	0.67
1437736_at	Akt1s1	AKT1 substrate 1 (proline-rich)	1.54	0.533	1.49	0.432	-1.45	0.226	1.16	0.451	0.69
1427885_at	Pold4	polymerase (DNA-directed), delta 4	1.05	0.884	1.09	0.512	1.58	0.238	-2.05	0.248	0.42
1416321_s_at	Prelp	proline arginine-rich end leucine-rich repeat	1.37	0.155	1.18	0.044	1.17	0.643	-1.12	0.725	0.65
1429845_at	1700019L03Rik	RIKEN cDNA 1700019L03 gene	2.07	0.319	-1.68	0.405	1.05	0.739	1.76	0.195	0.8
1445076_at	---	---	1.7	0.083	1.2	0.439	-1.21	0.648	2.17	0.002	0.96
1419587_s_at	Rp2h	retinitis pigmentosa 2 homolog (human)	-1.04	0.735	1.49	0.097	1.27	0.461	1.17	0.154	0.72
1431645_a_at	Gdi2	guanosine diphosphate (GDP) dissociation inhibitor 2	1.03	0.885	1.06	0.806	1.63	0.176	-1.38	0.299	0.59
1427106_at	Zbtb3	zinc finger and BTB domain containing 3	1.42	0.148	1.19	0.739	1.11	0.682	-1.3	0.148	0.61
1447127_at	Abl2	V-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	1.67	0.07	-1.32	0.439	1.3	0.454	1.31	0.028	0.74
1437351_at	Cxxc4	CXXC finger 4	1.52	0.54	1.24	0.573	-1.03	0.88	1.11	0.839	0.71
1445942_at	AU015858	expressed sequence AU015858	1.64	0.59	1.53	0.213	-1.8	0.324	1.26	0.676	0.66
1436954_at	Waspip	Wiskott-Aldrich syndrome protein interacting protein	1.14	0.488	1.46	0.017	1.12	0.495	-1.47	0.346	0.56
1456512_at	Pdzrn4	PDZ domain containing RING finger 4	1.14	0.795	1.3	0.647	1.29	0.581	-3.09	0.182	0.16
1419990_at	A830082K12Rik	RIKEN cDNA A830082K12 gene	1.08	0.911	1.99	0.171	-1.53	0.438	1.77	0.204	0.83
1436090_at	Enpp6	ectonucleotide pyrophosphatase/phosphodiesterase 6	1.02	0.86	1.41	0.439	1.3	0.465	-1.2	0.518	0.63
1422479_at	Acss2	acyl-CoA synthetase short-chain family member 2	-1.04	0.716	1.35	0.191	1.41	0.17	1.21	0.179	0.73

1453956_a_at	Pftk1	PFTAIRE protein kinase 1	1.45	0.561	-1.29	0.282	1.5	0.509	1.45	0.402	0.78
1449302_at	Abca2	ATP-binding cassette, sub-family A (ABC1), member 2	1.29	0.533	1.01	0.942	1.43	0.114	-1.25	0.622	0.62
1443040_x_at	---	---	1.38	0.301	-1.1	0.489	1.44	0.597	1.96	0.471	0.92
1421845_at	Golph3	golgi phosphoprotein 3	1.22	0.677	-1.04	0.93	1.54	0.421	2.13	0.258	0.96
1432846_at	5033428C03Rik	RIKEN cDNA 5033428C03 gene	-2.82	0.353	1.75	0.201	1.62	0.153	1.42	0.22	0.49
1429869_at	1110020C03Rik	RIKEN cDNA 1110020C03 gene	1.04	0.924	1.68	0.455	1	0.991	-1.09	0.618	0.66
1453403_at	2210019I11Rik	RIKEN cDNA 2210019I11 gene	-1.11	0.737	1.78	0.388	1.05	0.9	1.91	0.125	0.91
1452429_s_at	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	1.46	0.293	-1.07	0.448	1.33	0.065	1.46	0.182	0.8
1453326_at	3300001A09Rik ///	RIKEN cDNA 3300001A09 gene /// similar to 3300001A09Rik protein	1.37	0.628	-2.1	0.093	1.89	0.156	1.84	0.304	0.75
1453370_at	Troap	trophinin associated protein	1.47	0.601	1.69	0.01	-1.74	0.356	2.24	0.337	0.91
1457614_at	---	Transcribed locus	1.04	0.878	1.28	0.21	1.4	0.025	-1.27	0.224	0.61
1440639_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	-1.43	0.458	1.88	0.038	1.15	0.709	1.54	0.33	0.78
1417392_a_at	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	-1.22	0.271	1.34	0.091	1.57	0.082	1.11	0.439	0.7
1443541_at	LOC381438	Hypothetical gene supported by AK039231; AK039519; AK039710; AK045832	1.21	0.495	1.67	0.555	-1.18	0.365	1.96	0.269	0.92
1434089_at	Synpo	synaptopodin	1.11	0.469	1.42	0.308	1.2	0.306	-1.04	0.816	0.67
1440340_at	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	1.35	0.317	-1.63	0.131	1.77	0.003	1.01	0.959	0.62
1453529_at	6330418B08Rik	RIKEN cDNA 6330418B08 gene	1.3	0.709	-3.36	0.087	2.13	0.233	4.82	0	1.22
1450481_at	---	---	1.87	0.456	1.26	0.714	-1.67	0.3	1.21	0.572	0.67
1460722_at	Soat2	sterol O-acyltransferase 2	1.13	0.873	-1.06	0.647	1.66	0.335	2.03	0.091	0.94
1460485_at	8430434A19Rik	RIKEN cDNA 8430434A19 gene	-1.99	0.215	1.48	0.314	1.75	0.261	1.85	0.101	0.77
1448885_at	Rap2b	RAP2B, member of RAS oncogene family	1.43	0.39	1.42	0.182	-1.13	0.694	1.53	0.125	0.81
1425205_at	Ddx19b	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19b	2.05	0.084	-1.68	0.029	1.08	0.837	1.21	0.321	0.67
1448249_at	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	1.1	0.71	-1.25	0.046	1.83	0.281	2.71	0.171	1.1
1449994_at	Epgn	epithelial mitogen	1.24	0.645	1.43	0.306	1.07	0.863	-1.14	0.763	0.65
1417375_at	Tuba4	tubulin, alpha 4	-1.86	0.581	1.54	0.5	1.65	0.421	2.29	0.1	0.91
1452742_at	Trak1	trafficking protein, kinesin binding 1	1.25	0.407	-1.02	0.949	1.5	0.158	1.06	0.64	0.7
1431003_a_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	1.04	0.8	1.35	0.202	1.34	0.06	-1.24	0.109	0.62
1422529_s_at	Casq2	calsequestrin 2	1.9	0.283	-1.6	0.25	1.2	0.55	1.13	0.328	0.66
1448951_at	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b	-2	0.047	1.26	0.579	1.98	0.167	1.07	0.85	0.58
1442583_a_at	AI854703	expressed sequence AI854703	1.01	0.953	1.68	0.34	1.04	0.793	-1.8	0.392	0.48
1432747_at	4933403J19Rik	RIKEN cDNA 4933403J19 gene	1.4	0.571	1.27	0.545	1.07	0.805	-1.01	0.981	0.68
1436350_at	D430039N05Rik	RIKEN cDNA D430039N05 gene	1.25	0.55	1.61	0.18	-1.14	0.35	1.05	0.835	0.69
1448852_at	Rgn	regucalcin	1.81	0.258	-1.17	0.401	1.07	0.84	2.46	0.298	1.04
1460307_at	Akt3	thymoma viral proto-oncogene 3	1.08	0.883	1.75	0.273	-1.1	0.814	1.11	0.774	0.71
1445141_at	Ikbkb	inhibitor of kappaB kinase beta	1.22	0.335	1.42	0.35	1.09	0.687	-1.66	0.275	0.52
1444036_at	Ppp2r5a	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform	1.06	0.857	1.3	0.303	1.38	0.108	-1.14	0.363	0.65
1451055_at	Slc45a2	solute carrier family 45, member 2	1.04	0.846	1.07	0.744	1.63	0.049	-1.12	0.655	0.65
1448890_at	Klf2	Kruppel-like factor 2 (lung)	1.11	0.058	1.25	0.144	1.38	0.328	-2.05	0.151	0.42
1416235_at	Lrrc59	leucine rich repeat containing 59	-1.04	0.928	1.21	0.506	1.57	0.219	1.2	0.587	0.73
1429021_at	Epha4	Eph receptor A4	1.15	0.258	1.63	0.183	-1.05	0.852	1.38	0.339	0.78
1417255_at	Ift140	intraflagellar transport 140 homolog (Chlamydomonas)	-1.07	0.108	1.06	0.288	1.75	0.062	2	0.233	0.93
1449165_at	Capn5	calpain 5	1.17	0.68	-1.73	0.104	1.99	0.129	2.04	0.12	0.87
1449957_at	Ptprv	protein tyrosine phosphatase, receptor type, V	1.07	0.802	-1.13	0.705	1.78	0.014	1.21	0.27	0.73
1424090_at	Sdcbp2	syndecan binding protein (syntenin) 2	1	0.995	1.53	0.385	1.2	0.614	-1.1	0.849	0.66
1457831_at	Trim61	tripartite motif-containing 61	1.28	0.554	1.7	0.595	-1.31	0.376	1.72	0.416	0.85
1435503_at	KIAA0415	KIAA0415 protein	1.13	0.166	1.26	0.406	1.35	0.322	-1.32	0.241	0.6
1424935_at	Gdap1l1	ganglioside-induced differentiation-associated protein 1-like 1	1.05	0.946	1.61	0.27	1.08	0.915	-1.15	0.63	0.65
1437812_x_at	Ganab	alpha glucosidase 2 alpha neutral subunit	1.3	0.367	1.71	0.076	-1.37	0.059	1.48	0.304	0.78
1436476_at	Dand5	DAN domain family, member 5	1.25	0.443	1.56	0.406	-1.08	0.818	1.82	0.211	0.89
1418978_at	Sap30bp /// LOC63	SAP30 binding protein /// similar to transcriptional regulator protein	1.03	0.857	1.64	0.272	1.07	0.201	-1.25	0.528	0.62
1417043_at	Lcat	lecithin cholesterol acyltransferase	1.77	0.43	1.05	0.229	-1.09	0.675	1.47	0.091	0.8
1418163_at	Tlr4	toll-like receptor 4	1.13	0.576	1.62	0.034	-1.01	0.974	1.08	0.507	0.7
1454463_at	5430402O13Rik	RIKEN cDNA 5430402O13 gene	1.5	0.125	1.19	0.578	1.05	0.74	-1	0.993	0.68

1455292_x_at	Rsl1	Regulator of sex limited protein-Slp 1	1.09	0.768	1.24	0.313	1.41	0.036	-1.53	0.154	0.55
1447877_x_at	Dnmt1	DNA methyltransferase (cytosine-5) 1	1.54	0.34	-1.23	0.214	1.39	0.376	2.06	0.203	0.94
1427311_at	Falz	fetal Alzheimer antigen	1.24	0.409	1.18	0.497	1.32	0.318	-1.09	0.86	0.66
1452021_a_at	Hes6	hairy and enhancer of split 6 (Drosophila)	1.35	0.363	1.08	0.757	1.31	0.127	-1.22	0.151	0.63
1418738_at	Scn1b	sodium channel, voltage-gated, type I, beta	1.1	0.679	-1.01	0.914	1.65	0.027	1.28	0.21	0.76
1448552_s_at	2310028N02Rik	RIKEN cDNA 2310028N02 gene	1.02	0.863	1.66	0.431	1.06	0.767	-1.42	0.117	0.58
1424829_at	A830007P12Rik	RIKEN cDNA A830007P12 gene	1.31	0.009	1.17	0.285	1.26	0.282	-1.38	0.221	0.59
1418864_at	Gata4	GATA binding protein 4	1.79	0.474	-1.22	0.665	1.14	0.682	1.03	0.867	0.68
1450594_at	Magea4	melanoma antigen, family A, 4	-1.07	0.905	1.08	0.887	1.73	0.116	1.06	0.804	0.7
1422137_at	9030623N16Rik	RIKEN cDNA 9030623N16 gene	1.11	0.866	1.83	0.173	-1.24	0.379	1.32	0.626	0.75
1458307_at	B230334C09Rik	RIKEN cDNA B230334C09 gene	1.94	0.426	1.13	0.836	-1.51	0.322	1.08	0.524	0.66
1448607_at	---	---	1.17	0.26	1.38	0.265	1.19	0.643	-1.02	0.838	0.68
1457277_at	BC038925	cDNA sequence BC038925	1.05	0.847	1.81	0.079	-1.14	0.425	1.04	0.887	0.69
1435449_at	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	1.3	0.227	1.31	0.205	1.13	0.672	-1.02	0.932	0.68
1423325_at	Pnn	pinin	1.22	0.629	-1.01	0.949	1.54	0.419	1.06	0.88	0.7
1436830_at	Marveld1	MARVEL (membrane-associating) domain containing 1	1.49	0.388	1.13	0.735	1.12	0.733	-1.26	0.448	0.62
1449146_at	Notch4	Notch gene homolog 4 (Drosophila)	1.08	0.737	1.26	0.43	1.41	0.103	-1.35	0.51	0.6
1450258_a_at	Elavl4	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	1.32	0.647	-1.15	0.79	1.55	0.299	1.12	0.826	0.71
1460617_s_at	Rab6b	RAB6B, member RAS oncogene family	1.38	0.059	1.19	0.235	1.17	0.366	-1.29	0.19	0.61
1427780_at	Defb35	defensin beta 35	1.01	0.978	1.15	0.694	1.58	0.406	-1.05	0.931	0.67
1457027_at	Dhtkd1	dehydrogenase E1 and transketolase domain containing 1	1.05	0.838	-1.14	0.294	1.82	0.06	1.25	0.529	0.74
1435932_at	Hps6	Hermansky-Pudlak syndrome 6	1.83	0.143	-1.46	0.293	1.23	0.587	1.14	0.408	0.68
1432130_a_at	Ttc14	tetratricopeptide repeat domain 14	1.58	0.174	1.05	0.925	1.11	0.767	-2.53	0.172	0.3
1420180_at	---	---	1.25	0.319	1.61	0.408	-1.13	0.623	1.82	0.23	0.89
1422533_at	Cyp51	cytochrome P450, family 51	1.11	0.48	1.55	0.18	1.08	0.768	-1.08	0.795	0.67
1446638_at	Ptpru	protein tyrosine phosphatase, receptor type, U	1.2	0.574	1.13	0.804	1.42	0.173	-1.23	0.389	0.63
1426012_a_at	2610301G19Rik	RIKEN cDNA 2610301G19 gene	1.15	0	1.12	0.407	1.48	0.037	-1.36	0.039	0.6
1446814_at	---	---	1.13	0.616	1.35	0.295	1.27	0.096	-1.16	0.491	0.65
1422772_at	C1galt1	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransfe	1.23	0.612	-1.25	0.744	1.71	0.429	1.54	0.579	0.81
1453712_a_at	Map2k5	mitogen activated protein kinase kinase 5	1.23	0.002	1.21	0.525	1.3	0.377	-1.51	0.269	0.56
1423539_at	Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	-1.05	0.882	1.74	0.317	1.06	0.603	1.13	0.501	0.72
1418317_at	Lhx2	LIM homeobox protein 2	2.01	0.369	1.24	0.474	-1.99	0.116	1.58	0.532	0.71
1443982_at	Rgnef	Rho-guanine nucleotide exchange factor	-2.08	0.346	1.01	0.984	2.26	0.121	1.3	0.458	0.62
1453250_at	4921511C04Rik	RIKEN cDNA 4921511C04 gene	1.31	0.289	-1	0.997	1.44	0.145	1.35	0.553	0.77
1431992_at	4930568K20Rik	RIKEN cDNA 4930568K20 gene	-1.37	0.474	1.12	0.76	1.9	0.07	1.11	0.731	0.69
1419408_at	Six6	sine oculis-related homeobox 6 homolog (Drosophila)	1.06	0.893	1.54	0.611	1.15	0.395	-2.84	0.159	0.23
1435855_x_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	-1.11	0.428	1.23	0.802	1.62	0.172	1.51	0.224	0.81
1442598_at	Prkrip1	Prkr interacting protein 1 (IL11 inducible)	-5.3	0.002	1.95	0.265	1.61	0.44	1.27	0.616	-0.12
1430996_at	Etnk1	ethanolamine kinase 1	-1.11	0.853	1.01	0.975	1.83	0.318	1.02	0.948	0.69
1442926_at	1700011B04Rik	RIKEN cDNA 1700011B04 gene	1.42	0.659	-1.38	0.559	1.61	0.386	1.18	0.827	0.71
1422793_at	Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	1.13	0.664	-1.17	0.767	1.77	0.382	1.66	0.337	0.85
1433345_s_at	4930448K20Rik	RIKEN cDNA 4930448K20 gene	1.47	0.658	1.39	0.67	-1.11	0.768	1.72	0.296	0.87
1456713_at	Pola2	polymerase (DNA directed), alpha 2	1.23	0.634	1.61	0.363	-1.09	0.796	2.05	0.425	0.95
1442631_at	2700070H01Rik	RIKEN cDNA 2700070H01 gene	1.04	0.776	1.66	0.052	1.05	0.841	-2.2	0.438	0.39
1451761_at	Hoxb4	homeo box B4	-1.04	0.886	1.64	0.202	1.15	0.478	1.83	0.048	0.89
1416564_at	Sox7	SRY-box containing gene 7	1.11	0.424	1.2	0.51	1.44	0.205	-1	0.994	0.69
1421185_at	Mettl7a	methyltransferase like 7A	1.03	0.954	1.83	0.219	-1.12	0.704	1.72	0.511	0.86
1421287_a_at	Pecam1	platelet/endothelial cell adhesion molecule 1	1.22	0.102	1.22	0.694	1.31	0.066	-1.41	0.153	0.59
1421926_at	Mapk11	mitogen-activated protein kinase 11	1.07	0.923	1.54	0.406	1.15	0.498	-2.94	0.014	0.2
1422146_at	Sema5b	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmeml	1.22	0.679	1.54	0.017	-1.01	0.982	1.01	0.966	0.69
1429792_at	9530048O09Rik	RIKEN cDNA 9530048O09 gene	1.05	0.781	-1.02	0.961	1.72	0.067	1.33	0.204	0.77
1416033_at	Tmem109	transmembrane protein 109	1.49	0.436	1.13	0.808	1.13	0.629	-1.44	0.652	0.58
1447118_at	Saps3	SAPS domain family, member 3	-2.75	0.06	2.13	0.041	1.26	0.349	2.82	0.244	0.86

1456569_x_at	Gsn	gelsolin	1.69	0.053	1.01	0.953	1.04	0.906	-1.3	0.599	0.61
1427771_x_at	Itgb1	integrin beta 1 (fibronectin receptor beta)	-1.11	0.676	1.18	0.677	1.67	0.095	1.21	0.328	0.74
1420928_at	St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	1.13	0.504	1.46	0.066	1.16	0.244	-1.49	0.426	0.57
1438602_s_at	Masp1	mannan-binding lectin serine peptidase 1	1.77	0.074	1.17	0.062	-1.23	0.237	1.08	0.877	0.7
1434845_at	AI195381	Expressed sequence AI195381	1.08	0.725	1.74	0.24	-1.07	0.823	1.31	0.249	0.76
1447962_at	---	PREDICTED: Mus musculus hypothetical protein LOC626765 (LOC626765), mR	1.15	0.566	1.41	0.579	1.19	0.466	-1.76	0.326	0.5
1417662_at	Elk3	ELK3, member of ETS oncogene family	1.25	0.666	1.28	0.297	1.22	0.556	-1.39	0.423	0.59
1430971_a_at	Aqr	aquarius	1.45	0.697	-1.86	0.358	1.77	0.094	1.11	0.871	0.62
1425017_at	Pcdhac1	protocadherin alpha subfamily C, 1	1.45	0.627	1.72	0.002	-1.73	0.328	1.02	0.98	0.62
1445801_at	AK129341	CDNA sequence AK129341	-1.8	0.103	2.19	0.36	1.01	0.977	1.22	0.637	0.65
1422853_at	Shc1	src homology 2 domain-containing transforming protein C1	1.39	0.182	-1.23	0.571	1.55	0.412	1.43	0.553	0.79
1453466_at	Rps6	ribosomal protein S6	1.2	0.607	1.75	0.098	-1.24	0.367	1.04	0.915	0.69
1438715_at	Ccdc102a	coiled-coil domain containing 102A	1.64	0.059	-2.85	0.115	1.77	0.427	1.52	0.328	0.52
1429864_at	Spatc1	spermatogenesis and centriole associated 1	1.5	0.415	1.12	0.775	1.14	0.576	-1.33	0.397	0.61
1450205_at	---	---	-2.14	0.301	1.33	0.511	1.96	0.434	1.16	0.332	0.58
1419455_at	Il10rb	interleukin 10 receptor, beta	1.03	0.801	1.61	0.007	1.12	0.204	-1.38	0.254	0.59
1458216_at	---	Transcribed locus	2.01	0.08	1.15	0.873	-1.67	0.11	1.04	0.878	0.63
1426322_a_at	Kcnmb2	potassium large conductance calcium-activated channel, subfamily M, beta meml	1.18	0.745	-1.06	0.69	1.64	0.407	1.14	0.726	0.72
1457351_at	Taf2	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.09	0.897	1.26	0.676	1.4	0.463	-1.21	0.77	0.64
1452242_at	Cep55	centrosomal protein 55	1.36	0.33	1.38	0.014	1.02	0.885	-1.26	0.415	0.63
1426397_at	Tgfbr2	transforming growth factor, beta receptor II	1.17	0.257	1.38	0.014	1.2	0.307	-1.7	0.153	0.51
1450587_at	H2-M10.1	histocompatibility 2, M region locus 10.1	-2.03	0.173	2.02	0.017	1.25	0.704	2.04	0.044	0.82
1459286_at	---	Transcribed locus	-1.33	0.646	1.83	0.064	1.17	0.702	1.35	0.564	0.76
1434885_at	Spty2d1	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	1.24	0.382	-1.43	0.385	1.82	0.211	1.26	0.454	0.72
1436920_at	Pcdh17	protocadherin 17	1.04	0.784	2.2	0.026	-1.93	0.109	1.03	0.93	0.59
1418706_at	Slc38a3	solute carrier family 38, member 3	1.61	0.095	1.06	0.782	1.09	0.754	-1.05	0.827	0.68
1416019_at	Dr1	down-regulator of transcription 1	1.08	0.386	-1.07	0.842	1.74	0.195	1.54	0.335	0.82
1429225_at	6330417K15Rik	RIKEN cDNA 6330417K15 gene	1.37	0.206	-1.03	0.948	1.42	0.439	1.02	0.868	0.7
1422403_at	Ifna1 /// Ifna2 /// Ifna	interferon alpha 1 /// interferon alpha 2 /// interferon alpha 4 /// interferon alpha 5 /	-1.01	0.941	1.31	0.487	1.46	0.322	1.08	0.762	0.71
1432200_at	C030044M21Rik	RIKEN cDNA C030044M21 gene	1.43	0.315	-1.29	0.433	1.55	0.008	1.66	0.227	0.84
1446282_at	LOC626082	hypothetical protein LOC626082	1.52	0.185	-1.42	0.476	1.54	0.322	1.45	0.539	0.77
1450802_at	Prss28	protease, serine, 28	1.47	0.542	-1.25	0.676	1.48	0.544	2.27	0.224	1
1456610_at	Jmjd3	jumonji domain containing 3	1.24	0.277	1.02	0.911	1.5	0.295	-1.03	0.93	0.68
1432096_at	Snrpn	small nuclear ribonucleoprotein N	1	0.997	1.38	0.298	1.38	0.544	-1.42	0.101	0.58
1451296_x_at	Pabpc4 /// LOC432	poly A binding protein, cytoplasmic 4 /// similar to Poly(A) binding protein, cytopla	-1.03	0.393	1.01	0.928	1.79	0.032	2.56	0.199	1.08
1431564_at	Bcar3	breast cancer anti-estrogen resistance 3	-1.68	0.601	1.46	0.08	1.7	0.153	1.24	0.555	0.68
1460505_at	8030442B05Rik	RIKEN cDNA 8030442B05 gene	1.22	0.472	-1.39	0.6	1.83	0.15	1.18	0.746	0.71
1450462_at	Crhr2	corticotropin releasing hormone receptor 2	1	0.991	1.43	0.306	1.33	0.143	-1.6	0.516	0.54
1422639_at	Calcb	calcitonin-related polypeptide, beta	1.35	0.592	1.41	0.454	1.01	0.967	-1.05	0.924	0.68
1453425_at	Ccdc83	coiled-coil domain containing 83	2.07	0.132	1.03	0.949	-1.51	0.3	1.19	0.222	0.69
1427748_at	Igk-V1	Immunoglobulin kappa chain variable 1 (V1)	1.35	0.422	1.61	0.318	-1.24	0.726	1.65	0.27	0.84
1453361_at	Hells	helicase, lymphoid specific	1.53	0.274	1.44	0.236	-1.26	0.252	1.03	0.912	0.69
1440393_at	Odz2	Odd Oz/ten-m homolog 2 (Drosophila)	1.81	0.487	1.13	0.629	-1.21	0.584	1.13	0.597	0.71
1457190_at	---	12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D23000	1.09	0.71	1.83	0.291	-1.19	0.58	1.65	0.428	0.85
1457998_at	---	Transcribed locus	1.86	0.321	1.13	0.842	-1.3	0.312	1.46	0.326	0.79
1436393_a_at	Trim37	tripartite motif protein 37	1.19	0.215	1.61	0.003	-1.03	0.771	2.86	0.197	1.16
1422318_at	Foxd4	forkhead box D4	1.31	0.505	-2.96	0.031	2.12	0.137	1.92	0.22	0.6
1457217_at	Palm	Paralemmin	2.1	0.153	-2.64	0.075	1.28	0.691	1.16	0.805	0.47
1431261_at	Clic5	chloride intracellular channel 5	1.46	0.452	-1.73	0.255	1.72	0.527	1.39	0.628	0.71
1440322_at	Cugbp2	CUG triplet repeat, RNA binding protein 2	1.41	0.636	1.64	0.407	-1.41	0.49	1.16	0.73	0.7
1418001_at	Itm2b	integral membrane protein 2B	1.92	0.414	1.12	0.772	-1.39	0.288	1.14	0.706	0.7
1434880_at	Etv6	ets variant gene 6 (TEL oncogene)	1.08	0.774	1.52	0.003	1.17	0.216	-1.03	0.849	0.68
1439956_at	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	1.09	0.792	1.48	0.046	1.2	0.47	-2.09	0.154	0.42

1430981_s_at	Gpbp1	GC-rich promoter binding protein 1	1.33	0.325	1.23	0.595	1.21	0.681	-1.03	0.947	0.68
1437092_at	Rsnl2	restin-like 2	1.79	0.532	-1.11	0.847	1.08	0.793	1.19	0.275	0.74
1452467_at	Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	1.21	0.693	1.1	0.782	1.46	0.232	-1.02	0.963	0.69
1451321_a_at	0610033I05Rik	RIKEN cDNA 0610033I05 gene	1.26	0.025	1.52	0.005	-1.01	0.915	1.04	0.794	0.7
1420455_at	Gcm2	glial cells missing homolog 2 (Drosophila)	1.08	0.889	-1.51	0.235	2.02	0.157	1.09	0.805	0.67
1418766_s_at	Timd2	T-cell immunoglobulin and mucin domain containing 2	1.01	0.989	-1.33	0.119	2.01	0.367	1.94	0.346	0.91
1425798_a_at	Recql	RecQ protein-like	1.45	0.148	1.04	0.821	1.28	0.374	-1.16	0.243	0.65
1459228_at	Mipol1	mirror-image polydactyly gene 1 homolog (human)	1.14	0.886	-1.17	0.711	1.77	0.181	2.31	0.074	1.01
1421403_at	Pi15	peptidase inhibitor 15	1.16	0.887	1.51	0.42	1.1	0.834	-2.33	0.343	0.36
1453768_a_at	5430432M24Rik	RIKEN cDNA 5430432M24 gene	-1.16	0.813	1.8	0.103	1.11	0.561	1.01	0.971	0.69
1431994_at	4930432B10Rik	RIKEN cDNA 4930432B10 gene	-1.07	0.943	1.67	0.146	1.17	0.466	1.1	0.393	0.71
AFFX-GapdhMur/M	LOC14433	similar to glyceraldehyde-3-phosphate dehydrogenase	1.08	0.834	-1.05	0.877	1.73	0.218	1.1	0.786	0.72
1438504_x_at	Tm7sf3	Transmembrane 7 superfamily member 3	-1.02	0.936	1.34	0.075	1.45	0.018	1.87	0.349	0.91
1433051_at	2610011I18Rik	RIKEN cDNA 2610011I18 gene	-1.5	0.079	1.97	0.093	1.13	0.684	1.57	0.24	0.79
1460692_at	Ehmt2	euchromatic histone lysine N-methyltransferase 2	1.11	0.41	1.26	0.033	1.39	0.171	-1.02	0.958	0.69
1421289_at	Hspb7	heat shock protein family, member 7 (cardiovascular)	-1.11	0.663	1.22	0.504	1.65	0.516	1.93	0.225	0.92
1451507_at	Mef2c	myocyte enhancer factor 2C	1.42	0.23	1.3	0.375	1.05	0.837	-2.12	0.098	0.41
1444770_at	1700095A13Rik	RIKEN cDNA 1700095A13 gene	1.47	0.043	1.21	0.79	1.09	0.872	-1.26	0.673	0.63
1457065_at	Upk1b	uroplakin 1B	-1.4	0.392	2.04	0.002	1.02	0.94	2.29	0.253	0.99
1426866_at	D4st1	dermatan 4 sulfotransferase 1	1.18	0.28	1.64	0.145	-1.05	0.841	1.12	0.202	0.72
1419573_a_at	Lgals1	lectin, galactose binding, soluble 1	1.2	0.208	1.68	0.193	-1.11	0.68	1.11	0.84	0.72
1431878_at	Grhl2	grainyhead-like 2 (Drosophila)	1.62	0.397	-1.93	0.376	1.64	0.349	1.32	0.597	0.66
1442368_at	Kctd12b	potassium channel tetramerisation domain containing 12b	1.5	0.029	1.46	0.153	-1.23	0.376	1.27	0.189	0.75
1436448_a_at	Ptgs1	prostaglandin-endoperoxide synthase 1	1.04	0.738	1.63	0.054	1.1	0.615	-1.15	0.361	0.66
1446425_at	4732418C07Rik	RIKEN cDNA 4732418C07 gene	1.39	0.156	1.35	0.036	1.04	0.864	-1.33	0.371	0.61
1437213_at	Nudt21	nudix (nucleoside diphosphate linked moiety X)-type motif 21	2.13	0.295	1.2	0.491	-2.25	0.032	1.52	0.458	0.65
1433783_at	Ldb3	LIM domain binding 3	1.16	0.153	-1.13	0.827	1.73	0.407	2	0.401	0.94
1448660_at	Arhgdig	Rho GDP dissociation inhibitor (GDI) gamma	-1.07	0.476	1.53	0.37	1.31	0.386	1.26	0.607	0.76
1435835_at	Mks1	Meckel syndrome, type 1	1.11	0.157	1.12	0.611	1.55	0.014	-1.35	0.304	0.61
1451955_a_at	Cacna2d2 /// LOC6	calcium channel, voltage-dependent, alpha 2/delta subunit 2 /// similar to calcium	-2.63	0.126	2.28	0.297	1.11	0.806	1.37	0.712	0.53
1423844_s_at	Cbs	cystathionine beta-synthase	-1.12	0.443	1.04	0.132	1.85	0.052	1.12	0.708	0.72
1422314_at	Clcn6	chloride channel 6	1.29	0.064	1.03	0.955	1.46	0.016	-1.44	0.3	0.58
1446899_at	---	---	1.04	0.835	1.91	0.223	-1.21	0.374	1.19	0.517	0.73
1421922_at	Sh3bp5	SH3-domain binding protein 5 (BTK-associated)	1.31	0.324	1.13	0.533	1.34	0.389	-1.83	0.099	0.49
1427970_at	Zfp689	zinc finger protein 689	1.67	0.031	1.29	0.568	-1.22	0.231	1.13	0.433	0.72
1433305_at	9530034D02Rik	RIKEN cDNA 9530034D02 gene	1.38	0.488	1.18	0.42	1.22	0.704	-2.03	0.368	0.44
1424194_at	Rcsd1	RCSD domain containing 1	1.19	0.07	1.36	0.058	1.22	0.505	-1.4	0.412	0.59
1446987_at	---	---	1.05	0.872	1.71	0.28	1.02	0.972	-1.27	0.453	0.63
1425623_a_at	Cbs	cystathionine beta-synthase	1.02	0.959	1.03	0.837	1.73	0.024	-1.05	0.938	0.68
1421248_at	Syn3	synapsin III	1.99	0.151	1.18	0.68	-1.64	0.467	1.65	0.48	0.79
1418848_at	Aqp7	aquaporin 7	-1.29	0.016	1.1	0.814	1.91	0.48	1.67	0.31	0.85
1420812_at	Hdac7a	histone deacetylase 7A	1.23	0.445	1.13	0.3	1.41	0.164	-1.06	0.88	0.68
1455416_at	C130021I20Rik	Riken cDNA C130021I20 gene	-1.11	0.809	1.47	0.26	1.41	0.441	1.53	0.317	0.82
1421264_at	Butr1	butyrophilin related 1	1.68	0.256	1.35	0.359	-1.32	0.486	4.2	0.164	1.48
1438370_x_at	Dos	downstream of Stk11	1.42	0.451	1.25	0.671	1.11	0.2	-1.09	0.833	0.67
1419731_at	Cyp2b19	cytochrome P450, family 2, subfamily b, polypeptide 19	-1.26	0.525	1.82	0.122	1.17	0.447	1.7	0.165	0.86
1439913_at	1810053B01Rik	RIKEN cDNA 1810053B01 gene	1.12	0.835	1.21	0.742	1.45	0.136	-1.11	0.771	0.67
1422075_at	Cdx2	caudal type homeo box 2	1.71	0.55	1.34	0.441	-1.36	0.576	1.02	0.952	0.68
1419674_a_at	Dpep1	dipeptidase 1 (renal)	-1.25	0.102	1.74	0.482	1.24	0.386	1.07	0.901	0.7
1452717_at	Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	1.49	0.125	1.45	0.007	-1.18	0.174	2	0.129	0.94
1431074_a_at	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	1.1	0.642	1.8	0.187	-1.14	0.656	1.53	0.009	0.82
1439766_x_at	Vegfc	vascular endothelial growth factor C	1.37	0.148	1.3	0.137	1.11	0.665	-1.87	0.221	0.48
1421796_a_at	Efna5	ephrin A5	-1.16	0.439	1.18	0.704	1.74	0.028	1.22	0.641	0.75

1449806_at	---	Transcribed locus	1.22	0.572	1.45	0.313	1.11	0.726	-1.72	0.028	0.52
1419201_at	Klk11	kallikrein 11	-1.5	0.518	1.92	0.05	1.2	0.384	2.02	0.38	0.91
1419638_at	Efnb2	ephrin B2	1.19	0.134	1.41	0.141	1.18	0.427	-1.53	0.273	0.56
1447770_at	Cib2	calcium and integrin binding family member 2	1.77	0.312	1.01	0.984	1.01	0.988	-1.57	0.446	0.55
1417897_at	Brms1	breast cancer metastasis-suppressor 1	1.75	0.057	1.09	0.359	-1.06	0.806	1.05	0.77	0.71
1446038_at	Hnrpa1	Heterogeneous nuclear ribonucleoprotein A1	1.23	0.585	-1.24	0.397	1.74	0.092	2.36	0.301	1.02
1455912_x_at	Unc45a	Unc-45 homolog A (C. elegans)	1.21	0.454	1.39	0.061	1.19	0.163	-1.39	0.243	0.6
1440924_at	Mphosph1	M-phase phosphoprotein 1	1.37	0.431	-1.27	0.707	1.62	0.346	2.19	0.39	0.98
1451425_a_at	Mkrn1	makorin, ring finger protein, 1	-1.13	0.472	1.22	0.203	1.68	0.339	2.52	0.234	1.07
1416525_at	Spop	speckle-type POZ protein	1.15	0.222	1.14	0.542	1.49	0.219	-1.05	0.618	0.68
1457102_at	A030001D16Rik	RIKEN cDNA A030001D16 gene	-1.43	0.693	1.02	0.956	2.07	0.138	1.32	0.223	0.74
1453746_at	Fnbp1	formin binding protein 1	-1.24	0.188	1.56	0.113	1.42	0.246	1	0.997	0.68
1423813_at	Kif22	kinesin family member 22	-1.55	0.449	1.98	0.344	1.17	0.524	2.93	0.208	1.13
1422055_at	Mid1	midline 1	-1.19	0.816	1.32	0.223	1.63	0.133	1.16	0.388	0.73
1421037_at	Npas2	neuronal PAS domain protein 2	1.06	0.956	1.48	0.632	1.24	0.553	-1.13	0.642	0.66
1442312_at	Tbl1xr1	transducin (beta)-like 1X-linked receptor 1	1.9	0.04	1	0.99	-1.14	0.599	1.37	0.513	0.79
1447953_at	Egfl8	EGF-like domain 8	1.09	0.72	1.46	0.082	1.23	0.699	-3.76	0.091	0.01
1452137_at	Acbd3	acyl-Coenzyme A binding domain containing 3	1.14	0.619	1.22	0.348	1.43	0.461	-1.12	0.836	0.67
1418768_at	Opa1	optic atrophy 1 homolog (human)	1.3	0.366	-1.12	0.645	1.59	0.414	1.05	0.81	0.71
1451655_at	Slfn8	schlafen 8	1.57	0.129	1.17	0.599	1.05	0.836	-1.83	0.14	0.49
1440512_at	AW048066	expressed sequence AW048066	1.54	0.109	-1.46	0.575	1.56	0.093	1.14	0.792	0.7
1448806_at	Mmp24	matrix metallopeptidase 24	-1.13	0.723	1.7	0.172	1.21	0.541	1.07	0.814	0.71
1450737_at	Polr3k	polymerase (RNA) III (DNA directed) polypeptide K	1.28	0.674	1.34	0.623	1.17	0.759	-1.05	0.821	0.68
1430466_at	2310005G13Rik	RIKEN cDNA 2310005G13 gene	1.79	0.072	-1.43	0.417	1.3	0.526	2.33	0.098	1
1439512_at	5830444B04Rik	RIKEN cDNA 5830444B04 gene	-1.19	0.771	1.13	0.645	1.82	0.008	2.24	0.058	1
1441567_at	Myo9a	Myosin IXa	1.06	0.771	2.16	0.009	-1.75	0.001	1.26	0.253	0.68
1424668_a_at	Cutl1	cut-like 1 (Drosophila)	1.04	0.946	-1.03	0.842	1.78	0.307	1.3	0.376	0.77
1432255_at	Mast1	microtubule associated serine/threonine kinase 1	1.06	0.9	-1.02	0.959	1.75	0.199	1.04	0.937	0.71
1429912_at	Spag4l	sperm associated antigen 4-like	-2.33	0.373	1.46	0.096	1.9	0.221	2.02	0.002	0.76
1438670_at	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	1.07	0.782	1.35	0.241	1.37	0.071	-1.11	0.656	0.67
1431442_at	2310047B19Rik	RIKEN cDNA 2310047B19 gene	-1.12	0.148	1.25	0.676	1.65	0.099	2.45	0.273	1.06
1443353_at	Zfr	Zinc finger RNA binding protein	2.09	0.291	1.16	0.614	-1.85	0.118	1.39	0.543	0.7
1431576_at	4933404K08Rik	RIKEN cDNA 4933404K08 gene	-1.03	0.967	1.28	0.51	1.54	0.068	1.12	0.826	0.73
1433652_at	Igsf1	immunoglobulin superfamily, member 1	1.67	0.221	-1.16	0.645	1.26	0.109	1.26	0.595	0.76
1424513_at	Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit A2	1.13	0.782	1.06	0.827	1.6	0.259	-1.18	0.626	0.65
1433032_at	2900064K03Rik	RIKEN cDNA 2900064K03 gene	-1.32	0.34	1.48	0.191	1.56	0.102	1.28	0.716	0.75
1444307_at	---	Transcribed locus	1.29	0.315	1.54	0.128	-1.04	0.89	1.11	0.627	0.72
1445735_at	Hapln1	Hyaluronan and proteoglycan link protein 1	1.39	0.749	1.01	0.981	1.39	0.506	-1.36	0.609	0.61
1451110_at	Egln1	EGL nine homolog 1 (C. elegans)	1.21	0.554	1.09	0.538	1.49	0.183	-1.02	0.945	0.69
1421794_at	Klrc3	killer cell lectin-like receptor subfamily C, member 3	1.11	0.205	1.57	0.008	1.12	0.805	-2.2	0.121	0.4
1439448_x_at	Tmed9	transmembrane emp24 protein transport domain containing 9	1.3	0.157	1.27	0.506	1.23	0.346	-1.51	0.415	0.57
1456525_at	AA881470	EST AA881470	-1.28	0.516	1.98	0.361	1.03	0.875	1.12	0.714	0.71
1456562_x_at	KIAA0415	KIAA0415 protein	-1.85	0.324	1.02	0.946	2.23	0.136	1.08	0.938	0.62
1421476_a_at	Cant1	calcium activated nucleotidase 1	1.08	0.512	1.16	0.61	1.55	0.308	-1.31	0.5	0.62
1458871_at	Tmprss11e	transmembrane protease, serine 11e	1.64	0.287	-1.04	0.958	1.19	0.489	1.61	0.506	0.85
1459279_at	Dock4	Dedicator of cytokinesis 4	-1.32	0.335	1.58	0.55	1.46	0.528	1.55	0.426	0.82
1426802_at	8-Sep	septin 8	-1.23	0.522	1.05	0.857	1.94	0.205	2.55	0.267	1.08
1417040_a_at	Bok	Bcl-2-related ovarian killer protein	1.08	0.796	1.29	0.121	1.43	0.147	-1.02	0.916	0.69
1460569_x_at	Cldn3	claudin 3	1.54	0.001	1.06	0.636	1.2	0.183	-1.02	0.958	0.69
1451048_at	Metap2	methionine aminopeptidase 2	1.84	0.12	-1.04	0.83	1	0.994	3.19	0.186	1.24
1449361_at	Tbx21	T-box 21	1.98	0.147	-1.22	0.678	1	0.999	1.54	0.426	0.82
1429575_at	---	---	1.79	0.003	1.31	0.506	-1.44	0.1	1.5	0.005	0.79
1445803_at	Diap3	Diaphanous homolog 3 (Drosophila)	-1.62	0.467	2.08	0.193	1.1	0.813	1.3	0.549	0.71

1446577_at	Pde4b	Phosphodiesterase 4B, cAMP specific	-1.51	0.671	1.33	0.719	1.8	0.27	1.14	0.485	0.69
1442833_at	D15Ertd30e	DNA segment, Chr 15, ERATO Doi 30, expressed	1.1	0.772	-1.05	0.912	1.75	0.16	1.26	0.562	0.76
1423828_at	Fasn	fatty acid synthase	-1.44	0.432	1.3	0.399	1.8	0.258	1.03	0.775	0.67
1427837_at	Igk-V32	Immunoglobulin kappa chain variable 32 (V32)	1.55	0.492	1.02	0.974	1.22	0.616	-2.63	0.005	0.29
1450168_at	Ankrd12	ankyrin repeat domain 12	1.37	0.19	1.45	0.061	-1.02	0.93	1.21	0.258	0.75
1417626_at	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)	1.1	0.155	-1.37	0.049	1.97	0.304	1.04	0.888	0.68
1444269_at	---	---	1.48	0.364	1.23	0.477	1.09	0.843	-1.55	0.378	0.56
1458305_at	---	---	1.9	0.028	1.47	0.272	-2.37	0.034	2.11	0.163	0.78
1456182_x_at	Mela	melanoma antigen	-1.32	0.031	1.5	0.343	1.54	0.336	2.78	0.424	1.13
1428613_at	Ldhd	lactate dehydrogenase D	1.24	0.343	1.33	0.197	1.23	0.459	-1.62	0.039	0.55
1455618_x_at	Tspan33	tetraspanin 33	1.15	0.165	-1.61	0.04	2.02	0.249	5.34	0.137	1.73
1446666_at	Adamts12	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	-1.15	0.286	1.67	0.301	1.25	0.555	1.09	0.824	0.72
1431768_a_at	Prmt3	protein arginine N-methyltransferase 3	1.2	0.575	-1.46	0.222	1.91	0.1	1.02	0.963	0.67
1440286_at	Fbxl16	F-box and leucine-rich repeat protein 16	-1.02	0.906	1.25	0.493	1.57	0.157	1.06	0.788	0.71
1427063_at	5330417C22Rik	RIKEN cDNA 5330417C22 gene	1.28	0.307	1.33	0.365	1.19	0.428	-1.18	0.701	0.66
1447639_x_at	---	---	-1.17	0.882	1.1	0.917	1.85	0.057	1.55	0.578	0.83
1458076_at	---	---	-1.53	0.558	1.97	0.121	1.18	0.261	4.58	0.208	1.55
1450073_at	Kif3b	kinesin family member 3B	1.34	0.189	-1.09	0.867	1.55	0.291	1.12	0.654	0.73
1452746_at	Atp13a2	ATPase type 13A2	-1.12	0.166	1.21	0.234	1.7	0.003	1.13	0.259	0.73
1457948_at	---	Transcribed locus	-1.14	0.765	1.33	0.488	1.6	0.17	1.01	0.983	0.7
1415997_at	Txnip	thioredoxin interacting protein	1.3	0.61	1.01	0.988	1.5	0.506	-1.46	0.549	0.59
1439593_s_at	C030010B13Rik	RIKEN cDNA C030010B13 gene	1.53	0.212	-1.04	0.935	1.31	0.047	1.11	0.806	0.73
1418972_at	Bcl10	B-cell leukemia/lymphoma 10	1	0.993	1.1	0.762	1.7	0.172	-1.04	0.925	0.69
1421890_at	St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	1.11	0.753	-1.07	0.882	1.76	0.279	2.44	0.304	1.06
1426441_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member	-1.01	0.98	1.64	0.286	1.17	0.081	2.58	0.118	1.1
1431640_at	4933431J24Rik	RIKEN cDNA 4933431J24 gene	-1.14	0.82	1.21	0.43	1.72	0.087	1.27	0.728	0.76
1450624_at	Bhmt	betaine-homocysteine methyltransferase	1.43	0.305	-1.16	0.521	1.52	0.198	2.77	0.174	1.14
1447275_at	Gm1805	gene model 1805, (NCBI)	-1.04	0.865	1.54	0.246	1.3	0.065	1.47	0.072	0.82
1420041_at	---	---	-3.69	0.016	1.57	0.329	1.97	0.004	1.36	0.415	0.3
1427776_a_at	Fgfr4	fibroblast growth factor receptor 4	-1	0.994	1.37	0.24	1.44	0.171	1.21	0.362	0.75
1449566_at	Nkx2-5	NK2 transcription factor related, locus 5 (Drosophila)	1.28	0.385	1.35	0.348	1.17	0.485	-1.2	0.509	0.65
1460483_at	2610034E01Rik	RIKEN cDNA 2610034E01 gene	-1.23	0.425	1.46	0.027	1.53	0.091	1.27	0.533	0.76
1446741_at	LOC432868	hypothetical gene supported by AK052160	1.91	0.45	-1.43	0.322	1.2	0.661	1.1	0.671	0.69
1435584_at	AI662791	expressed sequence AI662791	1.13	0.367	1.33	0.413	1.34	0.064	-1.27	0.461	0.63
1458715_at	Casp6	Caspase 6	1.72	0.234	-1.03	0.912	1.11	0.252	1.38	0.157	0.8
1458278_at	---	---	1.11	0.864	1.63	0.205	1.06	0.907	-1.29	0.489	0.63
1437186_at	BC055324	cDNA sequence BC055324	1.64	0.43	-1.58	0.327	1.54	0.444	1.43	0.323	0.76
1429214_at	Adamtsl2	ADAMTS-like 2	1.1	0.681	1.92	0.029	-1.27	0.084	1.03	0.905	0.7
1440477_at	---	---	1.05	0.88	1.72	0.017	1.04	0.857	-1.21	0.602	0.65
1459072_at	---	Transcribed locus	1.59	0.298	1.41	0.658	-1.24	0.652	1.17	0.762	0.73
1447837_x_at	---	---	1.62	0.199	1.26	0.255	-1.07	0.672	2.3	0.086	1.03
1420313_x_at	---	---	1.25	0.416	2.07	0.339	-2.02	0.011	1.02	0.942	0.58
1452163_at	Ets1	E26 avian leukemia oncogene 1, 5' domain	1.22	0.234	1.45	0.199	1.14	0.696	-2.14	0.113	0.42
1446820_at	Zfp182	zinc finger protein 182	1.6	0.175	1.26	0.378	-1.06	0.677	1.01	0.967	0.7
1460124_at	1190020J12Rik	RIKEN cDNA 1190020J12 gene	1.56	0.157	-1.01	0.966	1.27	0.195	1.17	0.623	0.75
1435281_at	Cpt1c	carnitine palmitoyltransferase 1c	1.66	0.294	-1.05	0.925	1.19	0.192	1.48	0.119	0.82
1451423_at	Tbcc	tubulin-specific chaperone c	1.18	0.5	1.48	0.128	1.15	0.809	-1.01	0.932	0.7
1425809_at	Fabp4	fatty acid binding protein 4, adipocyte	-1.03	0.949	1.4	0.463	1.44	0.559	1.62	0.098	0.86
1451506_at	Mef2c	myocyte enhancer factor 2C	1.12	0.223	1.52	0.117	1.16	0.399	-1.97	0.226	0.46
1434875_a_at	Hmgn3	high mobility group nucleosomal binding domain 3	1.02	0.936	1.78	0.045	1.01	0.914	-1.26	0.443	0.64
1441658_at	---	Transcribed locus	1.34	0.444	1.05	0.939	1.43	0.368	-1.32	0.552	0.62
1437187_at	E2f7	E2F transcription factor 7	-1.14	0.725	1.57	0.183	1.36	0.265	4.56	0.232	1.59
1436973_at	Cct8	chaperonin subunit 8 (theta)	1.14	0.698	1.51	0.2	1.16	0.757	-1.56	0.338	0.56

1421895_at	Eif2s3x /// LOC673	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked /// simi	1.44	0.216	-1.12	0.737	1.48	0.496	1.32	0.572	0.78
1448613_at	Ecm1	extracellular matrix protein 1	1.07	0.668	-1.02	0.871	1.76	0.016	1.04	0.686	0.71
1448732_at	Ctsb	cathepsin B	-1.03	0.912	1.28	0.297	1.55	0.087	1.04	0.581	0.71
1445751_at	Col12a1	Procollagen, type XII, alpha 1	1.57	0.01	1.14	0.849	1.11	0.885	-1.35	0.27	0.62
1459521_at	---	---	1.86	0.185	1.13	0.827	-1.21	0.534	1.23	0.315	0.75
1430031_at	Ipmk	inositol polyphosphate multikinase	1.29	0.192	-1.09	0.757	1.6	0.118	1.39	0.585	0.8
1436771_x_at	Pgd	phosphogluconate dehydrogenase	1.02	0.819	1.36	0.057	1.43	0.081	-1.47	0.015	0.59
1425239_at	Setd4	SET domain containing 4	1.51	0.104	1.14	0.323	1.16	0.701	-1.58	0.13	0.56
1429190_at	Arsb	arylsulfatase B	-1.13	0.695	1.12	0.456	1.81	0.023	1.43	0.075	0.81
1456483_at	Zfp9	zinc finger protein 9	1.93	0.401	1.1	0.75	-1.28	0.289	2.13	0.379	0.97
1457450_at	A830091I15Rik	RIKEN cDNA A830091I15 gene	-1.17	0.412	1.04	0.943	1.92	0.435	1.07	0.923	0.71
1457150_at	AI428301	expressed sequence AI428301	1.97	0.127	1.25	0.258	-1.7	0.005	1.26	0.544	0.7
1452142_at	Slc6a1	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	1.51	0.314	1.5	0.518	-1.24	0.307	2.76	0.164	1.13
1441728_at	Scn1a	sodium channel, voltage-gated, type I, alpha	1.35	0.603	1.73	0.549	-1.36	0.506	1.02	0.908	0.69
1428927_at	Shq1	SHQ1 homolog (S. cerevisiae)	1.65	0.477	1.02	0.932	1.14	0.692	-1.15	0.665	0.67
1416194_at	Cyp4b1	cytochrome P450, family 4, subfamily b, polypeptide 1	1.52	0.119	1.37	0.111	-1.09	0.195	2.25	0.092	1.01
1456361_at	2600003E23Rik	RIKEN cDNA 2600003E23 gene	2.15	0.064	1.12	0.589	-1.84	0.235	2.29	0.18	0.93
1430886_at	1700112E06Rik	RIKEN cDNA 1700112E06 gene	1.12	0.266	1.83	0.135	-1.15	0.313	1.13	0.458	0.73
1426913_at	Lss	lanosterol synthase	1.18	0.147	1.35	0.061	1.29	0.159	-1.65	0.042	0.54
1416134_at	Aplp1	amyloid beta (A4) precursor-like protein 1	1.1	0.822	1.07	0.763	1.64	0.393	-1.56	0.226	0.56
1443530_at	Msi2	Musashi homolog 2 (Drosophila)	1.43	0.047	1.4	0.135	-1.01	0.982	1.19	0.461	0.75
1434628_a_at	Rhpn2	rhophilin, Rho GTPase binding protein 2	1.12	0.484	-1.13	0.454	1.81	0.067	1.77	0.272	0.89
1451608_a_at	Tspan33	tetraspanin 33	1.07	0.799	-1.14	0.654	1.87	0.341	5.44	0.198	1.81
1438679_at	Trim8	Tripartite motif protein 8	-2.07	0.054	1.52	0.32	1.82	0.152	1.14	0.695	0.6
1447582_x_at	Adipoq	Adiponectin, C1Q and collagen domain containing	1.37	0.459	1.4	0.438	1.05	0.832	-2.69	0.219	0.28
1440991_at	Plekhg1	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	1.49	0.56	-2.83	0.012	1.98	0.112	1.1	0.841	0.43
1435200_at	6330419J24Rik	RIKEN cDNA 6330419J24 gene	1.41	0.582	-1.12	0.822	1.51	0.426	1.16	0.746	0.74
1446207_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	1.42	0.343	1.19	0.712	1.21	0.27	-1.55	0.47	0.57
1421348_a_at	Cend1	cell cycle exit and neuronal differentiation 1	1.3	0.761	-1.03	0.89	1.54	0.426	1.89	0.064	0.93
1453511_at	2310007B03Rik	RIKEN cDNA 2310007B03 gene	1.63	0.033	-1.05	0.904	1.24	0.239	1.95	0.133	0.94
1449925_at	Cxcr3	chemokine (C-X-C motif) receptor 3	1.25	0.218	-1.24	0.416	1.76	0.125	1.36	0.673	0.78
1456300_at	Ilvbl	ilvB (bacterial acetolactate synthase)-like	1.26	0.532	1.25	0.617	1.31	0.369	-1.75	0.12	0.52
1426363_x_at	H2afy2	H2A histone family, member Y2	1.18	0.609	1.41	0.316	1.22	0.385	-1.2	0.726	0.65
1447633_x_at	Ube2l6	Ubiquitin-conjugating enzyme E2L 6	1.38	0.607	1.82	0.272	-1.61	0.327	2.87	0.049	1.12
1418908_at	Pam	peptidylglycine alpha-amidating monooxygenase	1.69	0.679	1.22	0.336	-1.1	0.837	1.16	0.495	0.74
1421708_a_at	Stat6	signal transducer and activator of transcription 6	1.3	0.394	1.18	0.424	1.34	0.372	-1.7	0.22	0.53
1453922_at	4921539H07Rik	RIKEN cDNA 4921539H07 gene	-1.26	0.715	1.34	0.633	1.69	0.313	1.21	0.745	0.75
1418818_at	Aqp5	aquaporin 5	1.3	0.599	1.78	0.142	-1.35	0.177	1.09	0.821	0.71
1425807_at	BC021891	cDNA sequence BC021891	1.18	0.313	-1.25	0.768	1.85	0.082	1.46	0.551	0.81
1421933_at	Cbx5	chromobox homolog 5 (Drosophila HP1a)	1.76	0.454	1.38	0.455	-1.47	0.443	2.52	0.295	1.05
1432696_at	5830431M20Rik	RIKEN cDNA 5830431M20 gene	-2.92	0.265	1.77	0.214	1.71	0.078	1.26	0.688	0.46
1457729_at	---	Transcribed locus	1.81	0.24	-1.5	0.598	1.35	0.141	1.4	0.258	0.77
1460481_at	---	---	-1.09	0.885	1.79	0.53	1.12	0.609	2.08	0.068	0.97
1418063_at	Kera	keratocan	1.4	0.396	-1.06	0.838	1.48	0.202	1.1	0.73	0.73
1444680_at	Pcqap	Positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated protein	1.12	0.885	2.26	0.444	-2.25	0.183	1.99	0.214	0.78
1423770_at	Tmc6	transmembrane channel-like gene family 6	-1.14	0.339	1.39	0.016	1.56	0.016	1.27	0.273	0.77
1449218_at	Cox8b	cytochrome c oxidase, subunit VIIIb	-1.13	0.286	1.57	0.534	1.37	0.593	1.66	0.248	0.87
1423000_a_at	Dgke	diacylglycerol kinase, epsilon	1.24	0.613	1.26	0.534	1.32	0.371	-1.09	0.812	0.68
1434950_a_at	Armc8	armadillo repeat containing 8	-1.12	0.488	1.02	0.923	1.92	0.297	3.86	0.303	1.42
1439160_at	4732496O08Rik	RIKEN cDNA 4732496O08 gene	1.1	0.531	1.27	0.129	1.46	0.322	-1.46	0.085	0.59
1417389_at	Gpc1	glypican 1	1.56	0.079	-1.07	0.577	1.33	0.571	1.11	0.575	0.73
1439255_s_at	Gpr137b /// LOC66	G protein-coupled receptor 137B /// similar to transmembrane 7 superfamily mem	1	0.982	1.68	0.085	1.15	0.105	-1.39	0.326	0.61
1448894_at	Akr1b8	aldo-keto reductase family 1, member B8	1.07	0.653	1.36	0.156	1.4	0	-1.04	0.849	0.7

1449029_at	Mknk2	MAP kinase-interacting serine/threonine kinase 2	1.47	0.413	-1.06	0.799	1.41	0.188	1.07	0.867	0.72
1423326_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	1.17	0.653	1.32	0.088	1.34	0.425	-1.05	0.844	0.7
1442801_x_at	Tm7sf3	transmembrane 7 superfamily member 3	1.23	0.816	-1.38	0.043	1.88	0.401	1.58	0.391	0.83
1449705_x_at	Mcm3 /// LOC6719(	minichromosome maintenance deficient 3 (S. cerevisiae) /// similar to DNA replica	1.62	0.175	-1.29	0.54	1.44	0.14	1.97	0.303	0.93
1419084_a_at	Pcp2	Purkinje cell protein 2 (L7)	1.29	0.114	1.84	0.253	-1.43	0.116	1.61	0	0.83
1456435_at	Morn1	MORN repeat containing 1	1.14	0.729	1.29	0.505	1.4	0.205	-1.06	0.897	0.69
1422176_at	Fgf23	fibroblast growth factor 23	1.53	0.41	1.41	0.356	-1.12	0.536	1.38	0.317	0.8
1446648_at	Stxbp4	Syntaxin binding protein 4	1.19	0.635	2.02	0.304	-1.61	0.089	1.63	0.355	0.81
1438604_at	Atp8b3	ATPase, Class I, type 8B, member 3	1.38	0.631	1.62	0.179	-1.2	0.649	1.09	0.884	0.72
1439282_at	D930023I05Rik	RIKEN cDNA D930023I05 gene	1.31	0.153	1.2	0.399	1.33	0.304	-1.02	0.966	0.7
1459281_at	Npy2r	Neuropeptide Y receptor Y2	1.45	0.433	1.61	0.339	-1.3	0.679	1.18	0.811	0.74
1445790_at	Gipr	gastric inhibitory polypeptide receptor	1.72	0.513	1.21	0.651	-1.11	0.643	1.01	0.992	0.71
1440564_at	Prokr2	prokineticin receptor 2	1.3	0.551	1.15	0.819	1.39	0.62	-1.34	0.71	0.62
1456442_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	1.37	0.457	1.74	0.067	-1.37	0.181	3.06	0.123	1.2
1450004_at	Tslp	thymic stromal lymphopoietin	1.47	0.341	1.86	0.048	-1.98	0.07	1.48	0.453	0.71
1438115_a_at	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	1.13	0.268	1.18	0.03	1.52	0.166	-1.72	0.202	0.53
1454032_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	1.41	0.546	-1.68	0.034	1.83	0.297	1.42	0.593	0.74
1447580_at	---	Transcribed locus	-3.04	0.153	2.44	0.133	1.07	0.869	1.78	0.141	0.56
1454531_at	C030043A13Rik	RIKEN cDNA C030043A13 gene	-1.72	0.332	1.34	0.63	1.91	0.14	1.03	0.918	0.64
1426246_at	Pros1	protein S (alpha)	1.66	0.109	1.46	0.165	-1.4	0.051	1.01	0.963	0.68
1452652_at	Tmem158	transmembrane protein 158	1.34	0.687	-2.55	0.212	2.1	0.099	1.78	0.492	0.67
1432140_at	Gsdm2	gasdermin 2	1.32	0.634	-1.11	0.863	1.61	0.252	1.4	0.531	0.81
1441929_at	Mid1	Midline 1	1.69	0.465	1.11	0.853	1.04	0.887	-1.12	0.753	0.68
1450982_at	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	1.2	0.513	1.18	0.156	1.46	0.108	-1.12	0.655	0.68
1446439_at	Rpo1-4	RNA polymerase 1-4	2.25	0.031	-2.55	0.027	1.19	0.493	1.05	0.844	0.49
1454732_at	Mtap1s	microtubule-associated protein 1S	1.08	0.579	1.33	0.109	1.43	0.036	-1.02	0.814	0.7
1443776_at	---	---	1.6	0.352	1.73	0.459	-1.96	0.097	1.12	0.761	0.62
1430727_at	4930432O21Rik	RIKEN cDNA 4930432O21 gene	1.69	0.41	-1.05	0.82	1.19	0.645	1.02	0.972	0.71
1426843_at	1810013C15Rik	RIKEN cDNA 1810013C15 gene	1	0.983	-1.33	0.019	2.08	0.017	1.52	0.094	0.82
1449802_x_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630030	1.79	0.343	1.44	0.706	-1.67	0.29	1.28	0.211	0.71
1450037_at	Usp9x	ubiquitin specific peptidase 9, X chromosome	-1.04	0.928	1.69	0.237	1.18	0.498	1.33	0.181	0.79
1418334_at	Dbf4	DBF4 homolog (S. cerevisiae)	-1.03	0.946	1.75	0.076	1.11	0.372	2.34	0.173	1.04
1449554_at	Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	1.3	0.386	1.32	0.527	1.21	0.402	-1.13	0.755	0.68
1416959_at	Nr1d2	nuclear receptor subfamily 1, group D, member 2	1.46	0.388	1.01	0.986	1.37	0.665	-1.3	0.591	0.63
1432569_at	1700121K02Rik	RIKEN cDNA 1700121K02 gene	1.32	0.317	1.14	0.482	1.38	0.406	-1.09	0.709	0.69
1453085_at	Serpina1f	serine (or cysteine) peptidase inhibitor, clade A, member 1f	1.44	0.091	-2.49	0.236	2	0.124	1.25	0.508	0.55
1446180_at	Lamb1-1	laminin B1 subunit 1	1.19	0.503	-1.02	0.979	1.66	0.253	2.12	0.33	0.99
1451574_at	Bcl9	B-cell CLL/lymphoma 9	1.51	0.109	1.15	0.539	1.18	0.227	-1.44	0.433	0.6
1432638_at	Bag5	BCL2-associated athanogene 5	1.74	0.411	-1.28	0.637	1.31	0.593	1.56	0.573	0.83
1427267_at	Zfp469	zinc finger protein 469	-1.07	0.721	1.86	0.185	1.05	0.903	1.17	0.051	0.75
1460591_at	Esr1	estrogen receptor 1 (alpha)	-1.51	0.048	1.04	0.625	2.14	0.034	1.48	0.086	0.79
1421825_at	Bace1	beta-site APP cleaving enzyme 1	-1.18	0.278	1.89	0.023	1.1	0.603	1.27	0.586	0.77
1419807_at	D4Ertd335e	DNA segment, Chr 4, ERATO Doi 335, expressed	1.39	0.366	-1.26	0.08	1.65	0.338	1.05	0.932	0.71
1456647_a_at	Eya4	eyes absent 4 homolog (Drosophila)	1.39	0.505	1.06	0.899	1.39	0.383	-2.09	0.168	0.44
1420691_at	Il2ra	interleukin 2 receptor, alpha chain	-1.66	0.441	1.4	0.541	1.84	0.067	1.03	0.842	0.65
1425509_at	Mark1	MAP/microtubule affinity-regulating kinase 1	1.02	0.402	1.5	0.472	1.32	0.459	-1.23	0.641	0.65
1419249_at	Pftk1	PFTAIRE protein kinase 1	1.27	0.164	1.68	0.121	-1.13	0.466	1.01	0.98	0.71
1437247_at	Fosl2 /// LOC63441	fos-like antigen 2 /// similar to fos-like antigen 2	1.28	0.511	1.6	0.184	-1.04	0.877	1.39	0.341	0.81
1417472_at	Myh9	myosin, heavy polypeptide 9, non-muscle	-1.03	0.726	1.51	0.026	1.36	0.179	1.11	0.663	0.74
1441600_at	C920021A13	hypothetical protein C920021A13	1.64	0.426	1.59	0.452	-1.63	0.147	1.05	0.869	0.66
1458773_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	-1.98	0.144	2.2	0.048	1.13	0.66	1.2	0.532	0.64
1439214_a_at	Api5	apoptosis inhibitor 5	1.46	0.135	-1.09	0.837	1.47	0.519	1.49	0.566	0.83
1447971_at	A230061C15Rik	RIKEN cDNA A230061C15 gene	1.48	0.548	1.1	0.371	1.26	0.383	-1.29	0.55	0.64

1450779_at	Fabp7	fatty acid binding protein 7, brain	-1.59	0.039	1.89	0.031	1.32	0.343	1.08	0.807	0.68
1428268_at	Psd2	pleckstrin and Sec7 domain containing 2	1.3	0.727	1.46	0.544	1.08	0.69	-1.76	0.52	0.52
1439834_at	2400009B08Rik	RIKEN cDNA 2400009B08 gene	-1.89	0.184	1.95	0.179	1.36	0.345	1.18	0.386	0.65
1432031_at	4930563E18Rik	RIKEN cDNA 4930563E18 gene	1.02	0.974	1.67	0.586	1.15	0.702	-1.04	0.968	0.7
1427541_x_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	-1.78	0.033	1.74	0.065	1.54	0.333	4.91	0.214	1.6
1456342_at	Pax6	paired box gene 6	1.35	0.68	1.58	0.248	-1.09	0.871	1.16	0.585	0.75
1447107_at	Ddx55	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	-1.05	0.911	1.74	0.213	1.15	0.702	1.13	0.403	0.74
1435289_at	D230014K01Rik	RIKEN cDNA D230014K01 gene	-1.25	0.089	1.37	0.517	1.68	0.021	1.14	0.464	0.73
1418733_at	Twist1	twist gene homolog 1 (Drosophila)	1.11	0.047	-1.6	0.134	2.11	0.267	1.18	0.561	0.7
1459085_at	D1Ertd259e	DNA segment, Chr 1, ERATO Doi 259, expressed	-1.06	0.721	1.15	0.81	1.75	0.022	1.19	0.341	0.76
1428892_at	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	1.07	0.722	-1.12	0.227	1.89	0.107	1.22	0.393	0.76
1455924_at	Rab6b	RAB6B, member RAS oncogene family	1.03	0.915	1.17	0.537	1.66	0.266	-4.81	0.079	-0.24
1460713_at	BC048355	cDNA sequence BC048355	1.06	0.81	-1.08	0.579	1.86	0.255	2.33	0.113	1.04
1455506_at	Slc25a34	solute carrier family 25, member 34	1.12	0.64	1.01	0.978	1.72	0.203	-1.3	0.065	0.64
1438148_at	Gm1960	gene model 1960, (NCBI)	1.21	0.467	-1.11	0.612	1.74	0.019	1.24	0.135	0.77
1426983_at	Fnbp1	formin binding protein 1	1.15	0.495	1.19	0.165	1.51	0.176	-1.44	0.321	0.6
1433238_at	4930448E06Rik	RIKEN cDNA 4930448E06 gene	-1.92	0.2	1.54	0.517	1.79	0.329	1.55	0.487	0.74
1420764_at	Scrg1	scrapie responsive gene 1	-2.36	0.221	1.74	0.093	1.69	0.628	1.04	0.956	0.53
1447140_at	C130078N14	hypothetical protein C130078N14	1.82	0.006	-1.34	0.664	1.29	0.469	1.54	0.431	0.83
1445487_at	Rif1	Rap1 interacting factor 1 homolog (yeast)	-1.92	0.371	1.76	0.172	1.57	0.336	2.58	0.244	1
1451157_at	Rnf187	ring finger protein 187	1.55	0.427	-1.05	0.844	1.35	0.632	2.76	0.326	1.15
1454483_at	6330590E21Rik	RIKEN cDNA 6330590E21 gene	1.09	0.875	2.24	0.226	-1.92	0.02	1.24	0.492	0.66
1422701_at	Zap70	zeta-chain (TCR) associated protein kinase	1.23	0.711	1.04	0.819	1.58	0.007	-1.61	0.389	0.56
1423396_at	Agt	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1.63	0.146	-1.05	0.687	1.27	0.489	1.5	0.402	0.84
1446160_x_at	Tmem69	transmembrane protein 69	1.74	0.031	-1.2	0.627	1.28	0.48	1.26	0.546	0.77
1450426_at	Chrna6	cholinergic receptor, nicotinic, alpha polypeptide 6	1.43	0.534	1.08	0.87	1.35	0.461	-1.41	0.321	0.61
1441892_x_at	4933440H19Rik	RIKEN cDNA 4933440H19 gene	1.36	0.524	1.53	0.431	-1.03	0.947	1.08	0.664	0.73
1419767_at	Padi3	peptidyl arginine deiminase, type III	1.24	0.445	-1.48	0.537	1.94	0.133	1.28	0.273	0.75
1419417_at	Vegfc	vascular endothelial growth factor C	1.26	0.161	1.42	0.189	1.17	0.473	-1.84	0	0.5
1422754_at	---	---	-1.22	0.353	1.96	0.05	1.07	0.763	4.62	0.15	1.61
1419383_at	S100b	S100 protein, beta polypeptide, neural	-1.2	0.774	1.23	0.377	1.79	0.049	1.11	0.647	0.73
1429570_at	Mlkl	mixed lineage kinase domain-like	-1.06	0.932	1.51	0.026	1.4	0.001	1.21	0.486	0.76
1435628_x_at	2610305J24Rik /// I	RIKEN cDNA 2610305J24 gene /// cDNA sequence BC005512 /// hypothetical pr	1.91	0.005	-1.23	0.635	1.12	0.735	1.44	0.289	0.81
1417688_at	BC004044	cDNA sequence BC004044	1.1	0.364	1.18	0.413	1.57	0.148	-1.76	0.256	0.52
1451679_at	6530401D17Rik	RIKEN cDNA 6530401D17 gene	-1.17	0.552	1.21	0.406	1.78	0.493	1.28	0.572	0.78
1456111_at	D930028F11Rik	RIKEN cDNA D930028F11 gene	1.24	0.176	1.67	0.12	-1.06	0.709	2.01	0.186	0.96
1446980_at	---	Transcribed locus	1.47	0.191	-1.16	0.816	1.52	0.474	1.28	0.544	0.78
1417808_at	2310050C09Rik	RIKEN cDNA 2310050C09 gene	1.2	0.586	-2.18	0.212	2.19	0.222	1.33	0.421	0.64
1417000_at	Abtb1	ankyrin repeat and BTB (POZ) domain containing 1	1.07	0.793	-1.01	0.966	1.79	0.074	1.5	0.399	0.84
1430778_a_at	Nubp1	nucleotide binding protein 1	1.12	0.347	1	0.992	1.73	0.111	-1.13	0.759	0.68
1444196_at	AI662501	expressed sequence AI662501	1.18	0.702	1.28	0.419	1.39	0.267	-1.53	0.29	0.58
1441278_at	4930513N10Rik	RIKEN cDNA 4930513N10 gene	1.94	0.385	1.2	0.525	-1.41	0.532	1.09	0.871	0.71
1456176_x_at	D11Ertd333e	DNA segment, Chr 11, ERATO Doi 333, expressed	-1	0.959	1.05	0.172	1.82	0.08	2.12	0.187	1
1432659_at	4930402H05Rik	RIKEN cDNA 4930402H05 gene	1.61	0.385	-1.23	0.704	1.43	0.313	1.47	0.131	0.82
1441126_at	Farslb	Phenylalanine-tRNA synthetase-like, beta subunit	1.49	0.57	1.53	0.48	-1.2	0.621	1.09	0.75	0.73
1421355_at	Tgm3	transglutaminase 3, E polypeptide	-1.55	0.476	1.69	0.238	1.52	0.078	1.3	0.294	0.74
1451656_at	Clmn	calmin	1.06	0.796	1.09	0.07	1.71	0.235	-1.51	0.126	0.59
1431533_at	4921530D09Rik	RIKEN cDNA 4921530D09 gene	1.25	0.422	-1.23	0.308	1.8	0.299	1.95	0.173	0.94
1416527_at	Rab32	RAB32, member RAS oncogene family	-1.35	0.272	1.51	0.061	1.61	0.056	1.04	0.698	0.7
1418476_at	Crlf1	cytokine receptor-like factor 1	1.72	0.5	-1.12	0.456	1.25	0.208	4.48	0.2	1.58
1428132_at	Cdc42se1	CDC42 small effector 1	1.23	0.143	1.08	0.594	1.54	0.309	-1.33	0.342	0.63
1446951_at	---	---	1.52	0.592	1.16	0.542	1.18	0.7	-2.49	0.194	0.34
1422002_at	Mxd1	MAX dimerization protein 1	-1.08	0.579	1.67	0.3	1.26	0.727	4.58	0.285	1.61

1431286_at	---	---	1.94	0.461	1.1	0.69	-1.21	0.141	1.06	0.591	0.72
1423054_at	Wdr1	WD repeat domain 1	1.12	0.656	1.24	0.32	1.49	0.101	-1.23	0.29	0.66
1420527_s_at	Tcp10a /// Tcp10b /	t-complex protein 10a /// t-complex protein 10b /// t-complex protein 10c	-1.35	0.296	1.4	0.415	1.72	0.187	1.5	0.345	0.82
1447893_x_at	Slc39a6	solute carrier family 39 (metal ion transporter), member 6	1.53	0.215	1.25	0.694	1.08	0.744	-2.26	0.064	0.4
1456951_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4921513I01 pro	1.61	0.115	1.03	0.947	1.22	0.591	-1.01	0.97	0.71
1434007_at	Gyltl1b	glycosyltransferase-like 1B	1.23	0.356	1.46	0.369	1.17	0.682	-2	0.373	0.46
1433491_at	Epb4.1l2	erythrocyte protein band 4.1-like 2	1.04	0.933	1.65	0.144	1.18	0.569	-1.16	0.591	0.68
1441483_at	Slitrk2	SLIT and NTRK-like family, member 2	1.86	0.07	-1.05	0.92	1.05	0.828	2.48	0.03	1.09
1459907_a_at	Whsc1l1	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	1.31	0.162	-1.63	0.451	1.94	0.2	1.13	0.237	0.69
1426549_at	2410018C20Rik	RIKEN cDNA 2410018C20 gene	1.17	0.852	1.52	0.262	1.17	0.791	-1.05	0.888	0.7
1427919_at	Srpx2	sushi-repeat-containing protein, X-linked 2	1.28	0.036	1.84	0.063	-1.33	0.327	4.73	0.066	1.63
1415905_at	Reg1	regenerating islet-derived 1	1.27	0.778	1.45	0.369	1.14	0.642	-1.46	0.023	0.6
1426239_s_at	Arrb2	arrestin, beta 2	1.1	0.569	1.31	0.211	1.45	0.075	-1.12	0.677	0.69
1418794_at	Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	1.32	0.05	1.08	0.631	1.47	0.23	-1.01	0.964	0.71
1432522_s_at	Ccdc46	coiled-coil domain containing 46	1.46	0.363	1.58	0.621	-1.22	0.192	1.03	0.934	0.71
1429467_s_at	Slc26a3	solute carrier family 26, member 3	1.3	0.781	-1.11	0.824	1.67	0.368	1.02	0.918	0.72
1445511_at	Cetn4 /// LOC6328(	centrin 4 /// similar to centrin 4	-1.14	0.821	1.02	0.876	1.97	0.134	1.21	0.56	0.76
1436654_at	5830483C08Rik	RIKEN cDNA 5830483C08 gene	1.35	0.266	-1.06	0.811	1.57	0.237	4.21	0.227	1.52
1423853_at	6330527O06Rik	RIKEN cDNA 6330527O06 gene	1.6	0.198	1.44	0.486	-1.22	0.747	1.1	0.82	0.73
1430670_at	Ccdc91	coiled-coil domain containing 91	-1.26	0.468	1.46	0.334	1.61	0.342	1.27	0.463	0.77
1441453_at	8030453O22Rik	RIKEN cDNA 8030453O22 gene	1.12	0.731	1.84	0.223	-1.1	0.809	1.15	0.825	0.75
1421780_a_at	Cabp5	calcium binding protein 5	1.1	0.911	1.76	0.329	1.02	0.956	-1.29	0.201	0.64
1452527_a_at	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	1.14	0.717	1.18	0.571	1.55	0.276	-1.07	0.777	0.7
1437724_x_at	Pitpnm1	phosphatidylinositol membrane-associated 1	1.22	0.14	1.46	0.093	1.18	0.273	-1.28	0.34	0.65
1420508_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.01	0.927	1.65	0.121	1.21	0.242	-1.55	0.088	0.58
1438746_at	A530058N18Rik	RIKEN cDNA A530058N18 gene	-1.11	0.783	1.79	0.444	1.18	0.713	1.03	0.963	0.72
1422351_at	Olfr480	olfactory receptor 480	1.06	0.838	1.3	0.707	1.5	0.269	-1.17	0.766	0.68
1431338_at	Caskin1	CASK interacting protein 1	1.89	0.41	-1.54	0.018	1.33	0.457	1.26	0.559	0.73
1421300_at	Adarb2	adenosine deaminase, RNA-specific, B2	-2.81	0.095	1.48	0.468	2.04	0.053	2.59	0.033	0.82
1435097_at	Mmab	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	1.23	0.518	1.14	0.565	1.51	0.035	-1.05	0.808	0.7
1458270_at	---	---	1.67	0.26	-2.01	0.032	1.7	0.301	1.25	0.717	0.65
1418054_at	Neurod4	neurogenic differentiation 4	-1.04	0.863	1.62	0.335	1.29	0.426	1.13	0.845	0.75
1423452_at	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	1.16	0.382	1.32	0.134	1.4	0.207	-1.96	0.052	0.48
1429673_at	5830407E08Rik	RIKEN cDNA 5830407E08 gene	1.45	0.198	1.34	0.183	1.08	0.688	-2.43	0.035	0.36
1425396_a_at	Lck	lymphocyte protein tyrosine kinase	1.17	0.663	1.21	0.491	1.49	0.151	-1.73	0.261	0.54
1424065_at	Edem1	ER degradation enhancer, mannosidase alpha-like 1	-1.03	0.773	1.04	0.737	1.86	0.001	1.41	0.364	0.82
1425739_at	Pld1	phospholipase D1	1.1	0.628	1.57	0.27	1.2	0.378	-1.21	0.071	0.67
1424150_at	Gdpd5	glycerophosphodiester phosphodiesterase domain containing 5	1.26	0.303	1.34	0.598	1.27	0.281	-1.28	0.556	0.65
1416306_at	Clca3	chloride channel calcium activated 3	1.91	0.191	1.59	0.414	-2.72	0.066	1.33	0.335	0.53
1454205_at	4930448A20Rik	RIKEN cDNA 4930448A20 gene	1.48	0.652	-1.43	0.546	1.69	0.373	1.47	0.099	0.8
1423704_at	Lypla3	lysophospholipase 3	-1.03	0.892	1.67	0.001	1.23	0.177	1.09	0.399	0.74
1431103_at	1700003P14Rik	RIKEN cDNA 1700003P14 gene	1.03	0.954	1.79	0.299	1.05	0.762	-1.17	0.754	0.68
1443631_at	Dgkb	Diacylglycerol kinase, beta	1.06	0.819	1.9	0.128	-1.09	0.872	1.57	0.102	0.86
1424229_at	Dyrk3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	1.34	0.421	-1.26	0.562	1.74	0.193	5.54	0.185	1.84
1437813_at	Aim1l	absent in melanoma 1-like	1.45	0.565	1.14	0.426	1.29	0.109	-2.7	0.052	0.29
1448953_at	Blm	Bloom syndrome homolog (human)	-1.1	0.835	1.39	0.239	1.58	0.142	4.26	0.195	1.53
1422079_at	Prkch	protein kinase C, eta	1.26	0.086	1.21	0.55	1.41	0.179	-1.71	0.18	0.54
1441709_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member	-1.11	0.784	1.76	0.234	1.22	0.514	1.75	0.532	0.9
1460134_at	9330175E14Rik	RIKEN cDNA 9330175E14 gene	1.31	0.505	1.18	0.577	1.38	0.364	-1.32	0.507	0.64
1453428_at	2700045P11Rik	RIKEN cDNA 2700045P11 gene	1.37	0.752	1.67	0.415	-1.19	0.624	1.19	0.81	0.76
1441259_s_at	Ift122	intraflagellar transport 122 homolog (Chlamydomonas)	1.02	0.627	1.01	0.933	1.84	0.002	-1.2	0.588	0.67
1459909_at	Nfix	nuclear factor I/X	1.77	0.08	-1.45	0.051	1.42	0.099	1.83	0.183	0.89
1418819_at	Arl8b	ADP-ribosylation factor-like 8B	1.1	0.739	-1.02	0.811	1.8	0.09	1.53	0.096	0.85

1426119_at	Tyms-ps	thymidylate synthase, pseudogene	-1.12	0.668	1.43	0.543	1.56	0.398	1.18	0.647	0.76
1455825_s_at	Lnx1	ligand of numb-protein X 1	-1	0.996	1.86	0.099	1.02	0.927	1.75	0.262	0.91
1455161_at	AI504432	expressed sequence AI504432	1.77	0.102	1.08	0.751	1.03	0.816	-1.4	0.118	0.62
1429658_a_at	Smc2	structural maintenance of chromosomes 2	-1.27	0.607	1.68	0.231	1.41	0.356	3.91	0.202	1.43
1447979_at	Rutbc2	RUN and TBC1 domain containing 2	-1.2	0.61	1.96	0.293	1.09	0.366	1.68	0.451	0.88
1427601_at	9430022F06Rik	RIKEN cDNA 9430022F06 gene	1.3	0.732	1.55	0.367	1.03	0.942	-2.16	0.193	0.43
1455194_at	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	1.86	0.324	1.07	0.926	-1.05	0.844	3.86	0.006	1.43
1431700_at	Grin2b	glutamate receptor, ionotropic, NMDA2B (epsilon 2)	1.15	0.627	1.51	0.354	1.22	0.284	-1.64	0.344	0.56
1427299_at	Rps6ka3	ribosomal protein S6 kinase polypeptide 3	1.07	0.566	1.74	0.16	1.07	0.453	-1.01	0.943	0.72
1423311_s_at	Tpbg	trophoblast glycoprotein	1.92	0.112	1.21	0.665	-1.32	0.204	1.26	0.637	0.76
1439312_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	-1.89	0.311	1.79	0.293	1.57	0.469	1.16	0.783	0.65
1427813_at	Ids	iduronate 2-sulfatase	1.08	0.903	1.61	0.158	1.19	0.401	-2.09	0.414	0.45
1422707_at	Pik3cg	phosphoinositide-3-kinase, catalytic, gamma polypeptide	-1.02	0.719	1.63	0.11	1.27	0.322	1.03	0.89	0.73
1445156_at	C81001	expressed sequence C81001	1.89	0.243	1.35	0.633	-1.56	0.284	1.06	0.834	0.69
1419279_at	Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	1.27	0.195	1.17	0.35	1.44	0.17	-1.12	0.373	0.69
1433790_at	Troap	trophinin associated protein	-1.41	0.567	2.05	0.197	1.13	0.716	2.22	0.459	1
1455828_at	Gprin1	G protein-regulated inducer of neurite outgrowth 1	1.09	0.672	2.02	0.021	-1.3	0.43	1.32	0.41	0.78
1449996_a_at	Tpm3	tropomyosin 3, gamma	1.33	0.597	-1.3	0.558	1.78	0.179	1.14	0.772	0.74
1437072_at	Arhgap25	Rho GTPase activating protein 25	1.24	0.224	1.43	0.123	1.22	0.258	-1.81	0.223	0.52
1453290_at	Hmgb2l1	high mobility group box 2-like 1	1.7	0.258	1.5	0.193	-1.46	0.11	1.81	0.145	0.89
1449262_s_at	Lin7c	lin-7 homolog C (C. elegans)	1.21	0.462	1.09	0.825	1.58	0.464	-1.21	0.569	0.67
1446985_at	---	PREDICTED: Mus musculus similar to serine/threonine kinase (LOC626078), mR	1.25	0.637	1.62	0.423	1.02	0.97	-1.36	0.551	0.63
1417884_at	Slc16a6	solute carrier family 16 (monocarboxylic acid transporters), member 6	-1.51	0.021	1.07	0.817	2.15	0.122	1.81	0.258	0.88
1427646_a_at	Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	1.07	0.738	-1.32	0.342	2.05	0.277	1.31	0.272	0.78
1436425_at	Ankrd38	ankyrin repeat domain 38	1.3	0.384	1.29	0.586	1.29	0.348	-1.48	0.254	0.6
1417858_at	Rasal1	RAS protein activator like 1 (GAP1 like)	1.17	0.643	1.42	0.275	1.29	0.706	-1.19	0.547	0.67
1451764_at	Marveld3	MARVEL (membrane-associating) domain containing 3	1.4	0.195	1.24	0.585	1.25	0.473	-2.43	0.419	0.36
1418536_at	LOC630509 /// LOC	similar to H-2 class I histocompatibility antigen, Q7 alpha chain precursor (QA-2 a	1.24	0.071	1.14	0.441	1.51	0.055	-1.46	0.373	0.61
1431008_at	0610037M15Rik	RIKEN cDNA 0610037M15 gene	1.13	0.372	1.22	0.214	1.55	0.157	-1.56	0.321	0.58
1427742_a_at	Klf6	Kruppel-like factor 6	1.05	0.781	1.77	0.025	1.07	0.753	-1.03	0.933	0.71
1425071_s_at	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3	1.73	0.388	-1.16	0.79	1.3	0.011	1	0.988	0.72
1445127_at	Ccbe1	collagen and calcium binding EGF domains 1	-1.74	0.18	1.51	0.556	1.81	0.004	1.18	0.591	0.69
1431331_at	Mgll	monoglyceride lipase	1.5	0.007	1.1	0.873	1.28	0.328	-1	0.996	0.72
1451701_x_at	Cldn3	claudin 3	1.59	0.127	1.04	0.812	1.26	0.259	-1.42	0.477	0.62
1430513_at	1700055N04Rik	RIKEN cDNA 1700055N04 gene	-1.17	0.405	1.68	0.279	1.35	0.407	1.27	0.257	0.78
1459924_at	Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	-1.24	0.595	1.85	0.045	1.24	0.522	1.21	0.547	0.76
1445189_at	Gpatc2	G patch domain containing 2	1.24	0.397	1.27	0.387	1.38	0.249	-1.24	0.724	0.66
1454578_at	6030458A19Rik	RIKEN cDNA 6030458A19 gene	1.35	0.253	1.08	0.9	1.46	0.547	-1.04	0.926	0.71
1429277_at	---	---	-1.51	0.178	1.72	0.01	1.51	0.489	2.27	0.043	1
1460083_at	Adam10	A disintegrin and metallopeptidase domain 10	-3.05	0.325	2.3	0.261	1.26	0.427	4.02	0.021	1.13
1454622_at	Slc38a5	solute carrier family 38, member 5	1.27	0.786	2	0.245	-1.63	0.168	6.72	0.191	2.09
1453955_a_at	4930432H15Rik	RIKEN cDNA 4930432H15 gene	1.02	0.955	1.86	0.367	1.01	0.967	-1.27	0.431	0.65
1417292_at	Ifi47	interferon gamma inducible protein 47	1.6	0.469	1.25	0.399	1.04	0.805	-1.25	0.281	0.66
1443668_x_at	C79407	expressed sequence C79407	1.02	0.957	1.89	0.062	-1.03	0.787	1.36	0.454	0.81
1451750_at	---	---	1.08	0.747	1.43	0.094	1.38	0.205	-1.01	0.969	0.72
1460248_at	Cpxm2	carboxypeptidase X 2 (M14 family)	1.29	0.541	-1.09	0.813	1.68	0.232	1.14	0.746	0.75
1446551_at	---	Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library,	1.35	0.004	-2.35	0.369	2.12	0.156	1.48	0.429	0.65
1440714_at	---	Transcribed locus	2.18	0.28	1.35	0.726	-2.74	0.075	1.49	0.615	0.57
1451931_x_at	H2-L	histocompatibility 2, D region	1.58	0.043	1.08	0.403	1.23	0.039	-1.26	0.127	0.66
1448786_at	1100001H23Rik	RIKEN cDNA 1100001H23 gene	1.13	0.21	1.2	0.059	1.57	0.031	-1.07	0.847	0.71
1419253_at	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydr	-1.14	0.362	1.52	0.162	1.5	0.125	2.14	0.207	1
1446522_at	---	---	1.01	0.993	1.96	0.25	-1.07	0.751	1.48	0.057	0.84
1443442_at	AU022084	expressed sequence AU022084	1.72	0.583	1.42	0.592	-1.32	0.11	1.31	0.489	0.78

1416021_a_at	Fabp5 /// LOC6282	fatty acid binding protein 5, epidermal /// similar to Fatty acid-binding protein, epid	1.05	0.674	1.98	0.284	-1.15	0.053	1.13	0.462	0.75
1451010_at	Nol11	nucleolar protein 11	1.1	0.802	-1.05	0.837	1.84	0.161	1.04	0.895	0.73
1443979_at	A830021K08Rik	RIKEN cDNA A830021K08 gene	-1.1	0.835	1.88	0.463	1.11	0.629	1.87	0.342	0.94
1449608_a_at	---	---	1.04	0.837	1.54	0.175	1.32	0.304	-1.28	0.417	0.65
1425400_a_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	1.1	0.482	-1.2	0.723	1.96	0.269	6.04	0.193	1.98
1421290_at	Hspb7	heat shock protein family, member 7 (cardiovascular)	1.26	0.493	1.28	0.352	1.36	0.137	-1.17	0.498	0.68
1432448_at	2600006K01Rik	RIKEN cDNA 2600006K01 gene	-1.32	0.31	1.45	0.529	1.69	0.353	5.03	0.202	1.71
1428176_at	Edg5	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5	1.04	0.862	1.82	0.026	1.04	0.765	-1.43	0.355	0.62
1422526_at	Acsl1	acyl-CoA synthetase long-chain family member 1	1.19	0.675	-2.04	0.109	2.21	0.145	3.99	0.219	1.34
1460640_at	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	-1.97	0.228	1.65	0.463	1.74	0.115	1.46	0.617	0.72
1456077_x_at	---	---	-1.56	0.55	2.24	0.042	1.02	0.951	5.06	0.207	1.69
1433267_at	Ing1	inhibitor of growth family, member 1	1.14	0.71	1.68	0.335	1.08	0.823	-1.49	0.36	0.6
1416255_at	Gja4	gap junction membrane channel protein alpha 4	1.41	0.201	1.29	0.373	1.2	0.161	-1.71	0.127	0.55
1452426_x_at	Zfp236	Zinc finger protein 236 /// CDNA clone IMAGE:4009820	1.25	0.352	1.15	0.682	1.5	0.406	-1.37	0.498	0.63
1419434_at	Slc2a10	solute carrier family 2 (facilitated glucose transporter), member 10	1.49	0.447	1.19	0.772	1.21	0.456	-2.32	0.454	0.4
1417350_at	Pldn	pallidin	1.05	0.914	1.07	0.846	1.79	0.231	-1.17	0.78	0.68
1451097_at	Vasp	vasodilator-stimulated phosphoprotein	1.19	0.502	1.32	0.026	1.38	0.308	-1.22	0.49	0.67
1423446_at	Dapk3	death-associated kinase 3	1.42	0.252	1.01	0.955	1.46	0.27	-1.06	0.841	0.71
1437333_x_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	1.74	0.186	1.26	0.515	-1.11	0.526	1.68	0.065	0.89
1421220_at	Ankrd17	ankyrin repeat domain 17	1.68	0.197	1.05	0.903	1.18	0.696	-1.29	0.474	0.65
1437846_x_at	Bace2	beta-site APP-cleaving enzyme 2	1.31	0.661	1.39	0.49	1.19	0.539	-1.29	0.438	0.65
1442767_s_at	Ube1x	ubiquitin-activating enzyme E1, Chr X	1.18	0.261	1.77	0.024	-1.06	0.729	1.45	0.444	0.84
1422612_at	Hk2	hexokinase 2	-1.12	0.746	1.75	0.162	1.26	0.352	1.11	0.064	0.75
1436665_a_at	Ltbp4	latent transforming growth factor beta binding protein 4	1.33	0.083	1.12	0.677	1.46	0.193	-1.07	0.869	0.71
1449763_at	Dmrt3	Doublesex and mab-3 related transcription factor 3	1.12	0.889	1.58	0.117	1.21	0.103	-2.9	0.193	0.25
1419414_at	Gng13	guanine nucleotide binding protein 13, gamma	1.02	0.963	-1.35	0.723	2.14	0.364	2.07	0.167	0.97
1425469_a_at	9030208C03Rik	RIKEN cDNA 9030208C03 gene	1.7	0.327	-1.96	0.302	1.69	0.001	1.22	0.705	0.66
1431035_at	Daam1	dishevelled associated activator of morphogenesis 1	1.11	0.632	-1.43	0.211	2.1	0.069	1.7	0.406	0.87
1421937_at	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	1.26	0.299	1.35	0.216	1.29	0.201	-1.65	0.033	0.56
1439120_at	BC010304	cDNA sequence BC010304	1.18	0.405	-1.19	0.723	1.88	0.092	1.29	0.539	0.79
1458595_at	Pdzd6	PDZ domain containing 6	1.11	0.897	1.07	0.666	1.73	0.516	-1.34	0.662	0.64
1427777_x_at	Fgfr4	fibroblast growth factor receptor 4	1.29	0.011	1.32	0.486	1.3	0.273	-1.57	0.512	0.58
1428065_at	Slc44a2	solute carrier family 44, member 2	1.07	0.412	1.58	0.068	1.25	0.251	-1.93	0.019	0.5
1445110_at	Khdrbs2	KH domain containing, RNA binding, signal transduction associated 2	1.55	0.568	1.38	0.547	-1.03	0.972	4.71	0.013	1.66
1424335_at	Ppcdc	phosphopantothenoylcysteine decarboxylase	1.28	0.069	1.02	0.879	1.61	0.096	-1.72	0.086	0.55
1441675_at	---	---	1.65	0.474	-2.18	0.397	1.8	0.482	1.24	0.618	0.63
1423430_at	Mybbp1a	MYB binding protein (P160) 1a	1.06	0.629	1.04	0.703	1.81	0.031	-1.06	0.639	0.71
1431267_at	5430425J12Rik	RIKEN cDNA 5430425J12 gene	1.79	0.235	1.18	0.815	-1.06	0.895	1.12	0.717	0.76
1433469_at	Lrrn2	leucine rich repeat protein 2, neuronal	1.95	0.462	-1.21	0.733	1.14	0.631	1.08	0.483	0.74
1458128_at	1110028C15Rik	RIKEN cDNA 1110028C15 gene	1.51	0.223	1.71	0.458	-1.44	0.282	1.01	0.962	0.7
1416416_x_at	Gstm1	glutathione S-transferase, mu 1	1.16	0.299	-1.06	0.839	1.8	0.027	1.14	0.242	0.76
1452380_at	Epha7	Eph receptor A7	1.79	0.273	1.29	0.668	-1.21	0.504	2.61	0.315	1.12
1418417_at	Msc	musculin	1.12	0.603	1.32	0.422	1.47	0.105	-1.11	0.536	0.7
1431912_at	2700089I24Rik	RIKEN cDNA 2700089I24 gene	1.99	0.063	-1.62	0.376	1.3	0.355	1.72	0.33	0.85
1430791_at	6330415B21Rik	RIKEN cDNA 6330415B21 gene	1.23	0.403	1.85	0.371	-1.21	0.5	1.2	0.019	0.77
1438988_x_at	Hn1	hematological and neurological expressed sequence 1	-1.41	0.318	1.24	0.117	1.96	0.32	1.03	0.886	0.71
1447963_at	---	---	-1.56	0.592	2.05	0.148	1.22	0.686	1.32	0.692	0.76
1426210_x_at	Parp3	poly (ADP-ribose) polymerase family, member 3	1.41	0.041	1.45	0.017	1.05	0.589	-2.06	0.083	0.46
1418052_at	Mvk	mevalonate kinase	1.34	0.648	1.53	0.006	1.04	0.804	-1.66	0.345	0.56
1432823_at	Sypl2	synaptophysin-like 2	1.45	0.548	1.24	0.48	1.23	0.648	-1.47	0.531	0.61
1450604_at	Olfr140	olfactory receptor 140	1.19	0.515	1.8	0.306	-1.08	0.917	1.58	0.096	0.87
1443639_at	Apcdd1	Adenomatosis polyposis coli down-regulated 1	1.65	0.374	-1.12	0.858	1.37	0.59	1.18	0.799	0.77
1450852_s_at	F2r	coagulation factor II (thrombin) receptor	1.31	0.557	1.67	0.026	-1.07	0.575	1.02	0.97	0.73

1459471_at	---	---	1.99	0.51	1.24	0.672	-1.45	0.521	1.17	0.674	0.74
1452917_at	Rfc5	replication factor C (activator 1) 5	1.23	0.497	-1.01	0.939	1.69	0.241	1.67	0.278	0.9
1447262_at	---	Transcribed locus	1.22	0.805	1.84	0.066	-1.17	0.752	1.01	0.99	0.72
1420858_at	Pkia	protein kinase inhibitor, alpha	1.35	0.36	1.05	0.93	1.52	0.408	-1.49	0.307	0.61
1427558_s_at	Alg12	asparagine-linked glycosylation 12 homolog (yeast, alpha-1,6-mannosyltransfera	1.24	0.21	1.39	0.442	1.29	0.195	-1.06	0.718	0.71
1456310_a_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	1.05	0.243	1.61	0.16	1.26	0.011	-1.61	0.127	0.58
1423604_at	Cspg3	chondroitin sulfate proteoglycan 3	-1.16	0.453	1.92	0.286	1.14	0.833	1.55	0.091	0.86
1439723_at	5730590G19Rik	RIKEN cDNA 5730590G19 gene	1.65	0.35	-1.01	0.975	1.28	0.692	2.95	0.024	1.22
1450230_at	D17H6S56E-3	DNA segment, Chr 17, human D6S56E 3	1.07	0.829	1.45	0.353	1.41	0.475	-2.01	0.153	0.48
1449232_at	Gata1	GATA binding protein 1	1.23	0	-1.07	0.805	1.76	0.101	6.2	0.21	2.03
1454027_at	4930448N21Rik	RIKEN cDNA 4930448N21 gene	1.48	0.263	1.18	0.204	1.27	0.286	-1.98	0.399	0.49
1460662_at	Per3	period homolog 3 (Drosophila)	1.53	0.396	-1.11	0.861	1.49	0.391	2.31	0.078	1.05
1439852_at	---	---	-1.33	0.362	2.16	0.077	1	0.995	1.02	0.973	0.72
1451762_a_at	Kif1b	kinesin family member 1B	1.42	0.108	-1.04	0.813	1.53	0.166	1.29	0.489	0.8
1440269_at	Scyl2	SCY1-like 2 (S. cerevisiae)	-1.22	0.747	1.66	0.58	1.44	0.503	1.28	0.593	0.79
1450520_at	Cacng3	calcium channel, voltage-dependent, gamma subunit 3	1.24	0.552	1.46	0.512	1.23	0.683	-1.14	0.786	0.7
1438394_x_at	Krt4	keratin 4	-1.09	0.624	1.03	0.928	1.98	0.205	1.39	0.642	0.83
1435323_a_at	Mboat1	membrane bound O-acyltransferase domain containing 1	1.06	0.602	1.76	0.027	1.11	0.688	-1.27	0.584	0.66
1432540_at	5430433J05Rik	RIKEN cDNA 5430433J05 gene	1.44	0.232	-1.07	0.72	1.55	0.485	3.09	0.313	1.25
1445142_at	Ap2b1	Adaptor-related protein complex 2, beta 1 subunit	1.28	0.495	1.59	0.428	1.06	0.853	-1.06	0.881	0.72
1440570_at	Lhfpl3	Lipoma HMGIC fusion partner-like 3	2.06	0.351	-1.27	0.564	1.08	0.878	1.08	0.935	0.74
1460305_at	Itga3	integrin alpha 3	1.43	0.611	-1.12	0.857	1.6	0.506	1.16	0.824	0.77
1455575_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	1.45	0.283	1.04	0.926	1.44	0.177	-1.24	0.623	0.67
1417281_a_at	Mmp23	matrix metallopeptidase 23	1.14	0.033	1.76	0.099	1.02	0.724	-1.53	0.131	0.6
1427035_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	1.13	0.504	1.38	0.243	1.41	0.006	-1.37	0.348	0.64
1455464_x_at	---	---	1.03	0.525	2.27	0.248	-1.6	0.128	1.21	0.149	0.73
1418027_at	Exo1	exonuclease 1	1.38	0.642	1.8	0.032	-1.35	0.23	2.19	0.261	1.01
1455576_at	5830482F20Rik	RIKEN cDNA 5830482F20 gene	1.28	0.238	1.27	0.016	1.38	0.133	-1.21	0.464	0.68
1455921_at	---	Transcribed locus	2.2	0.386	-2.36	0.092	1.3	0.645	1.06	0.92	0.55
1418182_at	Ptp4a3	protein tyrosine phosphatase 4a3	1.34	0.536	1.32	0.328	1.26	0.012	-1.34	0.481	0.65
1416641_at	Lig1	ligase I, DNA, ATP-dependent	1.29	0.268	-1.02	0.911	1.66	0.167	2.83	0.181	1.19
1429243_at	1110054O05Rik	RIKEN cDNA 1110054O05 gene	1.32	0.211	1.36	0.456	1.25	0.217	-1.06	0.823	0.72
1426319_at	Pdgfd	platelet-derived growth factor, D polypeptide	1.12	0.445	1.45	0.187	1.36	0.251	-1.09	0.9	0.71
1451923_at	3222401M22Rik	RIKEN cDNA 3222401M22 gene	2.03	0.396	1.14	0.343	-1.33	0.388	1.35	0.55	0.8
1458639_at	Fnbp1	Formin binding protein 1	1.69	0.592	1.09	0.795	1.15	0.788	-1.59	0.469	0.58
1429770_at	Pggt1b	protein geranylgeranyltransferase type I, beta subunit	-1.05	0.775	1.62	0.099	1.35	0.501	1.27	0.384	0.8
1437230_at	---	Adult male corpus striatum cDNA, RIKEN full-length enriched library, clone:7630	-4.03	0.009	2.42	0.381	1.26	0.723	2.07	0.481	0.43
1447545_at	D7Ertd193e	DNA segment, Chr 7, ERATO Doi 193, expressed	2.05	0.272	-1.27	0.744	1.09	0.811	2.14	0.261	1
1423706_a_at	Pgd	phosphogluconate dehydrogenase	-1.17	0.274	1.46	0	1.62	0.035	1.09	0.716	0.75
1442077_at	2310076G05Rik	RIKEN cDNA 2310076G05 gene	1.45	0.448	1.03	0.957	1.45	0.119	-1.4	0.412	0.63
1447994_at	1700026B20Rik	RIKEN cDNA 1700026B20 gene	1.98	0.51	-1.23	0.605	1.14	0.716	1.1	0.573	0.75
1435945_a_at	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfamily	1	0.996	-1.06	0.908	1.98	0.062	1.88	0.314	0.95
1417904_at	Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	1.02	0.941	2.1	0.438	-1.23	0.134	1.97	0.222	0.97
1448124_at	Gusb	glucuronidase, beta	-1.03	0.359	1.57	0.007	1.4	0.036	1.12	0.455	0.76
1449239_at	1700045I19Rik	RIKEN cDNA 1700045I19 gene	-2.78	0.048	2.17	0.528	1.4	0.128	1.05	0.938	0.46
1416575_at	Cdc45l	cell division cycle 45 homolog (S. cerevisiae)-like	1.22	0.728	-1.13	0.362	1.83	0.005	2.23	0.281	1.04
1452415_at	Actn1	actinin, alpha 1	1.22	0.482	1.43	0.156	1.27	0.208	-1.18	0.465	0.69
1420016_at	Ppt1	Palmitoyl-protein thioesterase 1	1.43	0.036	1.71	0.485	-1.27	0.6	1.31	0.666	0.8
1456824_at	Zfp612	zinc finger protein 612	1.07	0.789	1.67	0.093	1.2	0.332	-1.91	0.347	0.51
1417218_at	2810048G17Rik	RIKEN cDNA 2810048G17 gene	1.48	0.008	1.09	0.77	1.35	0.06	-2.01	0.053	0.48
1417068_a_at	Ptpn1	protein tyrosine phosphatase, non-receptor type 1	1.08	0.571	1.3	0.184	1.55	0.12	-1.12	0.435	0.7
1456567_x_at	Grn	granulin	-1.07	0.208	1.45	0.033	1.55	0.016	1.09	0.731	0.76
1420371_at	Sntb2	syntrophin, basic 2	1.71	0.396	1.39	0.585	-1.2	0.727	3.07	0.014	1.24

1427092_at	---	---	1.5	0.18	1.19	0.621	1.24	0.783	-1.85	0.407	0.52
1439648_at	Anln	anillin, actin binding protein (scraps homolog, Drosophila)	-1.09	0.806	1.3	0.427	1.71	0.168	1.67	0.455	0.9
1446186_at	Usp15	ubiquitin specific peptidase 15	1.01	0.957	-1.92	0.3	2.4	0.013	1.86	0.203	0.84
1419791_at	Zhx3	zinc fingers and homeoboxes 3	1.09	0.81	1.69	0.258	1.16	0.312	-1.82	0.332	0.53
1445393_at	Slc24a2	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	1.17	0.782	-1.54	0.145	2.12	0.057	1.93	0.362	0.92
1420412_at	Tnfsf10	tumor necrosis factor (ligand) superfamily, member 10	1.17	0.723	2.02	0.185	-1.34	0.359	1.1	0.418	0.74
1449857_at	1200011I18Rik	RIKEN cDNA 1200011I18 gene	1.65	0.076	-1.07	0.796	1.35	0.325	1.05	0.758	0.75
1458380_at	Asxl1	additional sex combs like 1 (Drosophila)	1.58	0.659	1.04	0.885	1.32	0.012	-1.76	0.315	0.54
1431926_a_at	1300010M03Rik	RIKEN cDNA 1300010M03 gene	-1.1	0.65	1.34	0.409	1.69	0.051	1.37	0.284	0.83
1428680_at	Cds1	CDP-diacylglycerol synthase 1	1.15	0.014	1.7	0.224	1.09	0.478	-1.2	0.707	0.69
1438947_x_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.05	0.899	2.18	0.079	-1.42	0.129	1.36	0.009	0.79
1429393_at	Wdr40a	WD repeat domain 40A	-1	0.972	1.2	0.52	1.74	0.17	2.6	0.21	1.13
1451212_at	Ccdc21	coiled-coil domain containing 21	-1.04	0.787	1.45	0.014	1.52	0.109	2.21	0.283	1.04
1416645_a_at	Afp	alpha fetoprotein	1.72	0.069	-1.56	0.502	1.58	0.138	1.8	0.479	0.88
1459345_at	---	---	1.32	0.55	1.26	0.556	1.37	0.51	-1.61	0.378	0.58
1456223_at	Fbxl5	F-box and leucine-rich repeat protein 5	1.43	0.012	1.21	0.638	1.31	0.331	-1.43	0.05	0.63
1438293_at	Tchp	trichoplein, keratin filament binding	1.23	0.379	1.42	0.608	1.29	0.172	-1.06	0.757	0.72
1444053_at	Ssbp1	single-stranded DNA binding protein 1	1.64	0.509	-2.76	0.025	1.94	0.209	1.12	0.235	0.49
1450682_at	Fabp6	fatty acid binding protein 6, ileal (gastrotropin)	1.56	0.055	2.04	0.049	-2.98	0.014	1.09	0.839	0.43
1419125_at	Ptpn18	protein tyrosine phosphatase, non-receptor type 18	1.14	0.038	1.56	0.011	1.24	0.446	-2.02	0.143	0.48
1449477_s_at	Slc2a10	solute carrier family 2 (facilitated glucose transporter), member 10	-1.01	0.979	1.79	0.085	1.16	0.286	1.16	0.663	0.77
1422088_at	Mycl1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avia	-1.23	0.485	1.18	0.519	1.95	0.27	1.32	0.493	0.8
1434028_at	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	-1.05	0.573	1.84	0.352	1.15	0.655	1.19	0.548	0.78
1429316_at	Rasgef1a	RasGEF domain family, member 1A	1.58	0.187	1.28	0.629	1.08	0.846	-1.63	0.372	0.58
1443287_at	Gm1337	gene model 1337, (NCBI)	-1.23	0.78	1.91	0.294	1.23	0.61	2.21	0.13	1.03
1421737_at	Alx4	aristaless 4	1.26	0.714	1.13	0.287	1.56	0.119	-1.03	0.927	0.73
1430225_at	5730442G03Rik	RIKEN cDNA 5730442G03 gene	1.57	0.356	1.67	0.432	-1.42	0.461	1.77	0.22	0.9
1436196_at	C030046G05	hypothetical protein C030046G05	1.24	0.035	1.23	0.413	1.48	0.33	-2.38	0.036	0.39
1437611_x_at	Kif2c	kinesin family member 2C	-1.22	0.843	1.64	0.242	1.48	0.415	2.41	0.192	1.08
1437606_at	---	Transcribed locus, weakly similar to NP_808467.1 hypothetical protein LOC3278	1.24	0.176	1.12	0.698	1.59	0.164	-1.32	0.263	0.66
1425161_a_at	Trabd	TraB domain containing	1.5	0.325	-1.01	0.988	1.46	0.285	1.14	0.618	0.77
1423244_at	9030012A22Rik	RIKEN cDNA 9030012A22 gene	1.89	0.231	-1.55	0.094	1.41	0.374	1.49	0.458	0.81
1427869_at	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	1.24	0.404	1.41	0.346	1.3	0.536	-2.15	0.395	0.45
1432173_at	Serpinb12	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	1.26	0.315	1.12	0.733	1.58	0.287	-1.52	0.248	0.61
1453003_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	1.11	0.264	1.58	0.243	1.26	0.184	-2.02	0.255	0.48
1423463_a_at	D2Ertd750e	DNA segment, Chr 2, ERATO Doi 750, expressed	-1.01	0.955	1.41	0.455	1.55	0.146	1.69	0.266	0.91
1429236_at	Galntl2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.44	0.25	1.69	0.133	-1.23	0.561	1.21	0.548	0.78
1452040_a_at	Cdca3	cell division cycle associated 3	-1.5	0.521	1.1	0.36	2.18	0.156	4.16	0.167	1.49
1445661_at	4930406D18Rik	RIKEN cDNA 4930406D18 gene	1.69	0.111	-3.51	0.136	1.97	0.224	1.88	0.273	0.51
1452526_a_at	Pax6	paired box gene 6	1.42	0.142	1.81	0.096	-1.4	0.598	1.78	0.177	0.9
1421624_a_at	Enah	enabled homolog (Drosophila)	1.19	0.482	1.73	0.306	1.03	0.9	-2.35	0.37	0.4
1450946_at	Nrl	neural retina leucine zipper gene	2.12	0.249	-1.38	0.595	1.11	0.798	2.48	0.147	1.08
1419705_at	Car5b	carbonic anhydrase 5b, mitochondrial	-1.08	0.69	1.14	0.475	1.88	0.025	1.35	0.198	0.82
1456475_s_at	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	-1.3	0.474	1.28	0.205	1.91	0.001	4.15	0.203	1.51
1449544_a_at	Kcnh2	potassium voltage-gated channel, subfamily H (eag-related), member 2	1.19	0.154	1.61	0.149	1.15	0.185	-1.76	0.207	0.55
1455016_at	Prpf38b	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	1.59	0.023	1.61	0.2	-1.33	0.3	1.1	0.663	0.74
1427796_at	Zfp133	zinc finger protein 133	-1.2	0.793	1.49	0.577	1.62	0.43	1.01	0.992	0.73
1447125_at	Krtap5-5	Keratin associated protein 5-5	1.61	0.24	-1.33	0.592	1.6	0.211	1.32	0.391	0.8
1417910_at	Ccna2	cyclin A2	-1.18	0.573	1.8	0.108	1.31	0.314	4.39	0.171	1.58
1443036_at	C630007C17Rik	RIKEN cDNA C630007C17 gene	1.76	0.486	-1.03	0.962	1.23	0.693	1.1	0.915	0.76
1459048_s_at	Zfp142	zinc finger protein 142	-1.07	0.802	1.39	0.411	1.63	0.06	1.1	0.642	0.76
1456586_x_at	Mvp	major vault protein	1.09	0.437	1.56	0.073	1.3	0.031	-1.42	0.053	0.63
1441821_at	---	---	1.51	0.036	1.31	0.213	1.13	0.413	-1.01	0.981	0.74

1429269_at	BC068157	cDNA sequence BC068157	1.78	0.604	1.39	0.539	-1.29	0.311	1.13	0.78	0.76
1448324_at	Rnps1	ribonucleic acid binding protein S1	1.17	0.408	-1	0.998	1.79	0.003	1.18	0.303	0.78
1435455_at	C79267	expressed sequence C79267	1.67	0.079	1.06	0.861	1.23	0.293	-1.31	0.535	0.66
1449494_at	Rab3c	RAB3C, member RAS oncogene family	1.41	0.513	1.84	0.21	-1.4	0.502	1.4	0.485	0.81
1454648_s_at	D10Wsu102e	DNA segment, Chr 10, Wayne State University 102, expressed	1.02	0.875	1.09	0.428	1.84	0.191	-1.01	0.861	0.74
1441622_at	LOC433023	hypothetical gene supported by AK078896	1.72	0.103	1.26	0.298	-1.03	0.967	1.35	0.704	0.83
1437176_at	AI451557	expressed sequence AI451557	1.51	0.262	1.06	0.556	1.38	0.225	-1.44	0.239	0.63
1455215_at	C530028O21Rik	RIKEN cDNA C530028O21 gene	1.09	0.673	1.9	0.133	-1.03	0.907	1.01	0.911	0.74
1441382_at	Gpr101	G protein-coupled receptor 101	1.53	0.405	-1.04	0.94	1.46	0.38	1.77	0.452	0.93
1434431_x_at	Adora2b	adenosine A2b receptor	-1.18	0.313	1.89	0.235	1.22	0.592	1.13	0.777	0.76
1455704_at	Xkr8	X Kell blood group precursor related family member 8 homolog	1.21	0.373	1.32	0.024	1.43	0.052	-1.18	0.125	0.7
1422230_s_at	Cyp2a4 /// Cyp2a5	cytochrome P450, family 2, subfamily a, polypeptide 4 /// cytochrome P450, famil	1.31	0.03	-1.2	0.71	1.82	0.064	2.31	0.452	1.06
1458614_at	Dcp1b	DCP1 decapping enzyme homolog b (S. cerevisiae)	1.34	0.387	-2.31	0.173	2.18	0.137	1.17	0.727	0.6
1448618_at	Mvp	major vault protein	1.18	0.286	1.46	0.149	1.32	0.069	-1.12	0.702	0.71
1420355_at	Gprk2l	G protein-coupled receptor kinase 2, groucho gene related (Drosophila)	-1.07	0.82	1.76	0.508	1.27	0.234	1.94	0.137	0.97
1426538_a_at	Trp53	transformation related protein 53	1.12	0.77	1.19	0.54	1.65	0.033	-1.25	0.589	0.68
1429205_at	Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosopl	1.09	0.791	2.28	0.054	-1.71	0.046	1.52	0.235	0.8
1433452_at	B630019K06Rik	RIKEN cDNA B630019K06 gene	1.75	0.218	1.16	0.806	1.05	0.86	-1.2	0.589	0.69
1460500_at	5033421C21Rik	RIKEN cDNA 5033421C21 gene	1.23	0.606	1.67	0.491	1.06	0.735	-1.52	0.543	0.61
1421857_at	Adam17	a disintegrin and metallopeptidase domain 17	1.45	0.238	1.07	0.829	1.44	0.238	-1.09	0.513	0.72
1421588_at	Tnfsf14	tumor necrosis factor (ligand) superfamily, member 14	1.2	0.548	-1.24	0.522	1.96	0.499	1.35	0.702	0.81
1425941_a_at	BC025462	cDNA sequence BC025462	1.19	0.835	2	0.216	-1.31	0.458	1.05	0.916	0.74
1422822_at	Stard5	StAR-related lipid transfer (START) domain containing 5	1.09	0.497	-1.02	0.864	1.89	0.054	1.09	0.735	0.76
1459916_at	Pax5	Paired box gene 5	1.16	0.799	1.33	0.5	1.47	0.283	-3.01	0.298	0.24
1453800_at	2500002L14Rik	RIKEN cDNA 2500002L14 gene	1.41	0.239	1.44	0.459	1.11	0.751	-1.37	0.116	0.65
1458548_at	---	Transcribed locus	1.01	0.984	1.63	0.492	1.32	0.618	-1.07	0.918	0.72
1421232_at	Plxna1	plexin A1	1.15	0.863	1.47	0.449	1.34	0.62	-1.27	0.719	0.67
1419051_at	Ovol1	OVO homolog-like 1 (Drosophila)	1.31	0.48	1.7	0.376	-1.06	0.872	1.04	0.919	0.75
1445665_at	6-Sep	Septin 6	1.38	0.216	1.2	0.625	1.38	0.355	-2.43	0.165	0.38
1444230_at	2900046D03Rik	RIKEN cDNA 2900046D03 gene	1.64	0.451	1.65	0.085	-1.49	0.331	1.49	0.363	0.82
1425652_s_at	Rbpms	RNA binding protein gene with multiple splicing	1.22	0.506	1.24	0.483	1.5	0.185	-1.29	0.386	0.67
1453851_a_at	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	-1.36	0.467	2.16	0.269	1.07	0.812	1.26	0.204	0.78
1426423_at	Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)	1.09	0.829	-1.01	0.928	1.89	0.253	1.84	0.242	0.95
1417341_a_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.23	0.196	-1.14	0.487	1.86	0.219	1.6	0.254	0.89
1427932_s_at	1200003I10Rik /// 1	RIKEN cDNA 1200003I10 gene /// RIKEN cDNA 1200015M12 gene /// RIKEN cD	1.62	0.415	1.23	0.281	1.11	0.389	-1.7	0.113	0.57
1443866_at	Lrtm1	leucine-rich repeats and transmembrane domains 1	1.1	0.888	1.38	0.339	1.48	0.253	-1.4	0.621	0.64
1443477_at	Psmd2 /// LOC4324	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2 /// similar to prote	-1.11	0.887	1.41	0.534	1.65	0.284	1.11	0.711	0.77
1419520_at	Cml4	camello-like 4	1.15	0.71	1.43	0.36	1.39	0.301	-1.43	0.478	0.63
1425627_x_at	Gstm1 /// LOC4339	glutathione S-transferase, mu 1 /// similar to Glutathione S-transferase Mu 1 (GST	-1.04	0.886	1.11	0.695	1.89	0.061	1.05	0.77	0.75
1451800_at	Gcc2	GRIP and coiled-coil domain containing 2	1.03	0.959	1.06	0.891	1.89	0.431	-1.49	0.584	0.62
1431299_a_at	2310014H01Rik	RIKEN cDNA 2310014H01 gene	1.23	0.068	1.52	0.079	1.22	0.313	-1.45	0.223	0.63
1454204_at	4930442G10Rik	RIKEN cDNA 4930442G10 gene	1.93	0.461	-1.4	0.296	1.32	0.709	1.07	0.846	0.73
1437122_at	Bcl2	B-cell leukemia/lymphoma 2	1.02	0.96	1.82	0.403	1.12	0.647	-1.3	0.548	0.67
1460700_at	Stat3	signal transducer and activator of transcription 3	1.2	0.439	1.62	0.083	1.15	0.081	-1.21	0.394	0.69
1437453_s_at	Pcsk9	proprotein convertase subtilisin/kexin type 9	-1.12	0.698	1.81	0.014	1.27	0.21	1.57	0.47	0.88
1426200_at	---	Immunoglobulin kappa chain complex	1.02	0.939	1.43	0.359	1.52	0.121	-1.24	0.798	0.68
1446554_at	Gp6 /// LOC636242	glycoprotein 6 (platelet) /// similar to glycoprotein VI (platelet)	-1.48	0.515	1.47	0.253	1.83	0.324	1.92	0.297	0.93
1440868_at	Gabpb2	GA repeat binding protein, beta 2	1.81	0.383	1.55	0.099	-1.63	0.15	1.05	0.802	0.69
1430793_at	4931429I11Rik	RIKEN cDNA 4931429I11 gene	1.15	0.792	1.51	0.46	1.31	0.461	-2.09	0.355	0.47
1422160_at	H2-T24	histocompatibility 2, T region locus 24	2.02	0.172	1.16	0.671	-1.26	0.517	1.78	0.296	0.92
1436135_at	2900075N08Rik	RIKEN cDNA 2900075N08 gene	-1.08	0.755	1.73	0.361	1.32	0.645	1.59	0.118	0.89
1420638_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	1.26	0.49	1.25	0.319	1.47	0.29	-1.16	0.625	0.7
1419494_a_at	Tpd52	tumor protein D52	1.05	0.78	1.15	0.507	1.78	0.288	-1.12	0.627	0.71

1426599_a_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	1.06	0.437	1.12	0.494	1.79	0.119	-1.77	0.105	0.55
1454005_at	Fmo2	flavin containing monooxygenase 2	2.16	0.069	-1.23	0.709	1	0.993	1.22	0.694	0.79
1449224_at	Trpm5	transient receptor potential cation channel, subfamily M, member 5	1.8	0.545	-1.27	0.53	1.39	0.711	1.03	0.969	0.74
1426754_x_at	Ckap4	cytoskeleton-associated protein 4	-1.02	0.941	1.67	0.452	1.31	0.235	1.57	0.14	0.88
1420832_at	Qscn6	quiescin Q6	1.01	0.968	1.5	0.374	1.47	0.096	-1.01	0.958	0.74
1454584_at	2810034D10Rik	RIKEN cDNA 2810034D10 gene	1.06	0.883	1.95	0.141	-1.03	0.943	1.12	0.533	0.77
1442434_at	D8Ertd82e	DNA segment, Chr 8, ERATO Doi 82, expressed	1.09	0.321	1.77	0.161	1.11	0.574	-1.36	0.573	0.65
1424040_at	Rprc1	arginine/proline rich coiled-coil 1	1.19	0.437	1.62	0.123	1.16	0.338	-1.01	0.957	0.74
1455989_at	Gja12	gap junction membrane channel protein alpha 12	2.23	0.495	-1.72	0.438	1.16	0.589	2.66	0.125	1.08
1446513_at	Adamts19	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	2.02	0.55	-2.73	0.257	1.59	0.323	1.51	0.516	0.6
1451969_s_at	Parp3	poly (ADP-ribose) polymerase family, member 3	1.4	0.092	1.55	0.005	1.03	0.844	-1.66	0.186	0.58
1442374_at	D2Ertd127e	DNA segment, Chr 2, ERATO Doi 127, expressed	1.2	0.237	2.19	0.299	-1.7	0.066	3.25	0.01	1.23
1421154_at	Hcn2	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	1.03	0.972	2.12	0.161	-1.21	0.405	1.08	0.858	0.75
1451884_a_at	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	1.13	0.775	-1.2	0.331	2.01	0.205	2.1	0.174	1.01
1453103_at	Ablim1	actin-binding LIM protein 1	1.13	0.563	1.53	0.047	1.31	0.234	-1.96	0.26	0.5
1433727_at	BC038479	cDNA sequence BC038479	1.31	0.201	1.52	0.321	1.15	0.207	-1.23	0.692	0.69
1444016_at	C430014K04Rik	RIKEN cDNA C430014K04 gene	2.05	0.485	-1.26	0.691	1.13	0.715	1.14	0.793	0.77
1435115_at	Fndc5	fibronectin type III domain containing 5	-1.56	0.023	2.09	0.055	1.24	0.252	1.24	0.648	0.75
1430365_at	Nfxl1	nuclear transcription factor, X-box binding-like 1	2.28	0.487	-2.34	0.219	1.28	0.53	1.19	0.823	0.6
1415978_at	Tubb3	tubulin, beta 3	1.18	0.641	1.98	0.169	-1.23	0.531	1.13	0.568	0.77
1436882_at	Ubl5 /// LOC43533(	ubiquitin-like 5 /// similar to ubiquitin-like 5 /// similar to ubiquitin-like 5	1.49	0.525	1.31	0.093	1.18	0.475	-1.44	0.183	0.63
1422832_at	Rgr	retinal G protein coupled receptor	-1.24	0.396	1.92	0.168	1.25	0.618	1.25	0.57	0.8
1433297_at	1700039M15Rik	RIKEN cDNA 1700039M15 gene	1.55	0.451	1.72	0.241	-1.41	0.576	1.04	0.934	0.72
1450521_a_at	Tcrg /// LOC670271	T-cell receptor gamma chain /// region containing T-cell receptor gamma chain; T	1.7	0.22	-1.27	0.602	1.49	0.218	1.52	0.572	0.86
1449849_a_at	Fbxl6	F-box and leucine-rich repeat protein 6	1.2	0.131	-1.12	0.576	1.88	0.021	1.2	0.09	0.79
1423135_at	Thy1	thymus cell antigen 1, theta	1.13	0.534	1.56	0.071	1.3	0.41	-1.35	0.601	0.66
1438490_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	1.39	0.629	1.42	0.555	1.17	0.445	-1.36	0.483	0.66
1451034_at	Zfp36l2	zinc finger protein 36, C3H type-like 2	1.49	0.662	-1.09	0.872	1.57	0.439	1.79	0.292	0.94
1453550_a_at	Mlstd2	male sterility domain containing 2	1.51	0.412	1.42	0.496	1.05	0.903	-1.37	0.458	0.65
1422015_a_at	Abcb8	ATP-binding cassette, sub-family B (MDR/TAP), member 8	1.14	0.858	-1.19	0.613	2	0.229	1.14	0.828	0.77
1424680_at	BB146404	expressed sequence BB146404	2.01	0.305	1.16	0.735	-1.23	0.281	1.04	0.889	0.75
1420990_at	Chd1	chromodomain helicase DNA binding protein 1	1.11	0.707	-1.05	0.831	1.92	0.172	1.24	0.137	0.81
1431730_at	4921506M07Rik	RIKEN cDNA 4921506M07 gene	2.15	0.148	-1.41	0.439	1.13	0.824	1.73	0.433	0.9
1423603_at	Zfpm1	zinc finger protein, multitype 1	-1.25	0.716	1.05	0.893	2.14	0.118	6.28	0.209	2.05
1449524_at	Eda	ectodysplasin-A	-1.78	0.245	1.82	0.067	1.61	0.155	2.71	0.333	1.09
1425155_x_at	Csf1	colony stimulating factor 1 (macrophage)	1.37	0.043	1.23	0.568	1.39	0.324	-1.3	0.23	0.67
1423020_at	---	---	1.53	0.631	-1.8	0.313	1.9	0.213	1.25	0.602	0.72
1442116_at	Gpr176	G protein-coupled receptor 176	1.67	0.1	1.04	0.934	1.28	0.544	-1.58	0.046	0.6
1460381_at	BC023179	cDNA sequence BC023179	-1.12	0.235	1.98	0.17	1.12	0.493	1.13	0.706	0.78
1458260_at	Espn	Espin	-1.26	0.776	1.75	0.147	1.45	0.371	1.07	0.937	0.75
1423259_at	Id4	inhibitor of DNA binding 4	-1.04	0.84	1.85	0.192	1.18	0.577	1.25	0.009	0.81
1425551_at	Hip1r	huntingtin interacting protein 1 related	1.3	0.435	1.22	0.609	1.47	0.321	-1.3	0.612	0.67
1448330_at	Gstm1	glutathione S-transferase, mu 1	1.13	0.579	-1.04	0.9	1.9	0.043	1.19	0.073	0.79
1456653_a_at	Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1.12	0.489	-1.39	0.312	2.14	0.102	1.35	0.368	0.81
1451666_at	Acly	ATP citrate lyase	1.04	0.655	1.35	0.214	1.6	0.165	-1.04	0.695	0.74
1437517_x_at	Serpinb3a	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A	1.34	0.645	1.41	0.561	1.24	0.504	-1.34	0.671	0.66
1430019_a_at	Hnrpa1 /// LOC225	heterogeneous nuclear ribonucleoprotein A1 /// heterogeneous nuclear ribonucle	-1.07	0.72	1.07	0.387	1.98	0.141	1.22	0.182	0.8
1450368_a_at	Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	1.48	0.394	1.3	0.499	1.2	0.652	-1.75	0.21	0.56
1430140_at	1700017N19Rik	RIKEN cDNA 1700017N19 gene	1.85	0.51	1.39	0.351	-1.34	0.475	1.34	0.465	0.81
1459007_at	---	Transcribed locus	1.12	0.497	2.4	0.173	-2.12	0.237	1.56	0.401	0.74
1440686_at	Prss27	protease, serine 27	1.63	0.259	-1.08	0.861	1.44	0.159	1.39	0.609	0.84
1437385_at	Ccbe1	collagen and calcium binding EGF domains 1	1.57	0.187	1.33	0.058	1.09	0.624	-1.23	0.524	0.69
1449619_s_at	Arhgap9	Rho GTPase activating protein 9	1.32	0.095	1.07	0.75	1.6	0.11	-1.94	0.109	0.51

1432091_a_at	Rutbc3	RUN and TBC1 domain containing 3	1.4	0.681	-1.03	0.633	1.62	0.564	1.59	0.012	0.9
1444169_at	3110052M02Rik	RIKEN cDNA 3110052M02 gene	1.08	0.712	1.32	0.302	1.59	0.23	-1.53	0.335	0.62
1428304_at	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	1.84	0.431	1.34	0.516	-1.22	0.682	4.61	0.229	1.64
1422681_at	Ctr9	Ctr9, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	1.35	0.191	1.02	0.978	1.63	0.198	-1.19	0.654	0.7
1455527_at	E430002D04Rik	RIKEN cDNA E430002D04 gene	-1.67	0.618	1.99	0.217	1.41	0.365	1.22	0.745	0.74
1456814_at	1110014J01Rik	RIKEN cDNA 1110014J01 gene	1.07	0.933	2.47	0.318	-2.15	0.136	1.91	0.12	0.82
1448022_at	---	Transcribed locus	1.9	0.325	-2.06	0.186	1.61	0.322	1.39	0.424	0.71
1429495_at	1110004B13Rik	RIKEN cDNA 1110004B13 gene	-1.21	0.181	1.69	0.459	1.48	0.496	1.39	0.723	0.84
1425793_a_at	Rorc	RAR-related orphan receptor gamma	1.55	0.305	-1.11	0.563	1.55	0.056	1.16	0.827	0.79
1432883_at	4932431P20Rik	RIKEN cDNA 4932431P20 gene	1.53	0.578	1.06	0.889	1.4	0.01	-1.09	0.84	0.73
1449315_at	Odz3	odd Oz/ten-m homolog 3 (Drosophila)	1.56	0.245	1.01	0.929	1.43	0.431	-1.93	0.103	0.52
1421286_a_at	Atp4a	ATPase, H+/K+ exchanging, gastric, alpha polypeptide	1.74	0.067	1.51	0.407	-1.33	0.255	1.14	0.632	0.76
1440757_at	---	10 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:B93	1.72	0.256	-1.06	0.892	1.33	0.298	1.11	0.842	0.78
1453894_at	4933434C23Rik	RIKEN cDNA 4933434C23 gene	1.27	0.726	1.42	0.462	1.31	0.473	-1.39	0.63	0.65
1445608_at	9130204L05Rik	RIKEN cDNA 9130204L05 gene	-1.18	0.597	2.08	0.242	1.07	0.836	2.68	0.027	1.16
1457421_at	1700063D05Rik	RIKEN cDNA 1700063D05 gene	1.57	0.45	1.23	0.735	1.21	0.619	-2.04	0.067	0.49
1449111_a_at	Grb2	growth factor receptor bound protein 2	1.15	0.548	1.05	0.639	1.81	0.08	-1.63	0.113	0.59
1415784_at	Vps35	vacuolar protein sorting 35	1.14	0.806	-1.29	0.66	2.09	0.405	1.42	0.66	0.84
1448870_at	Ltbp1	latent transforming growth factor beta binding protein 1	1.01	0.761	2.07	0.133	-1.08	0.522	1.01	0.903	0.75
1442849_at	Lrp1	low density lipoprotein receptor-related protein 1	1.94	0.048	1.28	0.332	-1.28	0.292	1.37	0.253	0.83
1455231_s_at	---	---	1.01	0.99	1.26	0.53	1.73	0.336	-1.23	0.355	0.69
1449823_at	Dach2	dachshund 2 (Drosophila)	-1.05	0.941	1.38	0.592	1.68	0.396	1.25	0.779	0.81
1431274_a_at	---	---	1.54	0.624	-1.37	0.675	1.74	0.571	1.12	0.9	0.76
1432131_at	4930404N11Rik	RIKEN cDNA 4930404N11 gene	2.03	0.41	1.15	0.605	-1.2	0.422	1.13	0.611	0.78
1415922_s_at	Marcksl1	MARCKS-like 1	1.03	0.794	1.22	0.119	1.76	0.353	-1.39	0.349	0.66
1451925_at	Eda	ectodysplasin-A	1.22	0.605	1.67	0.287	1.12	0.871	-1.65	0.403	0.59
1418136_at	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	1.59	0.052	-1.24	0.271	1.62	0.073	1.42	0.129	0.85
1447788_s_at	Tspyl3	TSPY-like 3	1.47	0.346	1.41	0.217	1.13	0.335	-1.79	0.089	0.56
1459172_at	---	---	1.84	0.187	1.23	0.571	-1.06	0.73	1.7	0.233	0.93
1457239_at	Syk	Spleen tyrosine kinase	1.62	0.366	1.12	0.756	1.27	0.563	-1.21	0.559	0.7
1454062_at	4933402D24Rik	RIKEN cDNA 4933402D24 gene	1.74	0.453	-1.28	0.502	1.49	0.405	1.79	0.176	0.93
1435665_at	AI451617	expressed sequence AI451617	1.52	0.354	1.25	0.018	1.24	0.195	-2.04	0.04	0.49
1447332_at	C86896	expressed sequence C86896	1.62	0.482	1.33	0.029	1.06	0.763	-1.45	0.605	0.64
1419309_at	Pdpn	podoplanin	1.95	0.11	1.22	0.325	-1.18	0.279	1.29	0.344	0.82
1417289_at	Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specif	1.2	0.486	1.1	0.744	1.71	0.087	-1.8	0.169	0.55
1427308_at	Dab1	disabled homolog 1 (Drosophila)	1.33	0.298	1.16	0.758	1.52	0.361	-1.37	0.15	0.66
1456269_at	Pramel6	preferentially expressed antigen in melanoma like 6	1.48	0.609	1.87	0.209	-1.52	0.354	1.06	0.917	0.72
1423524_at	Mastl	microtubule associated serine/threonine kinase-like	1.51	0.442	1.66	0.408	-1.19	0.435	2.87	0.233	1.21
1437503_a_at	Scotin	scotin gene	1.14	0.408	1.67	0.149	1.2	0.065	-1.72	0.111	0.57
1427567_a_at	Tpm3	tropomyosin 3, gamma	1.32	0.44	1.34	0.254	1.35	0.29	-1.01	0.973	0.75
1428993_at	1110017I16Rik	RIKEN cDNA 1110017I16 gene	-3.74	0.388	1.11	0.86	2.63	0.022	1.3	0.576	0.33
1422172_x_at	2810408B13Rik	RIKEN cDNA 2810408B13 gene	1.53	0.365	1.87	0.186	-1.63	0.132	1.2	0.725	0.74
1453717_s_at	Ttll10	tubulin tyrosine ligase-like family, member 10	2.26	0.26	-2.84	0.209	1.4	0.529	1.04	0.866	0.47
1420214_at	1810012K16Rik	RIKEN cDNA 1810012K16 gene	2.36	0.119	-1.76	0.41	1.08	0.847	1.4	0.646	0.77
1441032_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730040K	-1.02	0.863	1.68	0.098	1.35	0.281	1.46	0.294	0.87
1425326_at	Acly	ATP citrate lyase	1.13	0.56	1.16	0.657	1.73	0.088	-1.41	0.189	0.65
1428387_at	Acsl3	acyl-CoA synthetase long-chain family member 3	-1.17	0.018	1.74	0.01	1.43	0.153	1.29	0.043	0.82
1440330_at	Hist1h1e	Histone 1, H1e	1.73	0.403	-1.45	0.614	1.6	0.301	1.56	0.591	0.86
1450001_a_at	Ush1c	Usher syndrome 1C homolog (human)	1.09	0.316	1.5	0.506	1.42	0.244	-2.63	0.372	0.35
1436065_at	A130091K22Rik	RIKEN cDNA A130091K22 gene	1.46	0.443	1.25	0.69	1.31	0.51	-1.32	0.282	0.67
1419618_at	Bbox1	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hy	1.21	0.574	-1.32	0.112	2.05	0.158	1.13	0.533	0.77
1443897_at	Ddit3	DNA-damage inducible transcript 3	2.09	0.395	-1.45	0.233	1.24	0.567	1.26	0.261	0.79
1439944_at	---	---	1.3	0.776	1.6	0.28	1.12	0.544	-1.37	0.237	0.66

1426025_s_at	Laptm5	lysosomal-associated protein transmembrane 5	1.34	0.1	1.55	0.022	1.14	0.646	-1.49	0.411	0.63
1457939_at	4930578N16Rik	RIKEN cDNA 4930578N16 gene	1.01	0.993	2.13	0.004	-1.13	0.744	1.59	0.059	0.9
1448110_at	Sema4a	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	-1.06	0.805	1.31	0.004	1.77	0.015	1.04	0.797	0.77
1437476_at	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)	1.12	0.297	1.46	0.055	1.44	0.164	-1.21	0.189	0.7
1458685_at	Garnl1	GTPase activating RANGAP domain-like 1	1.44	0.433	1.54	0.386	1.04	0.878	-2.56	0.159	0.37
1458143_at	Adamts3	ADAM metallopeptidase with thrombospondin type 1 motif, 3	1.23	0.322	1.66	0.367	1.14	0.835	-1.21	0.772	0.7
1448797_at	Elk3	ELK3, member of ETS oncogene family	1.2	0.154	1.45	0.059	1.37	0.241	-1.34	0.291	0.67
1420080_a_at	Gfpt1	glutamine fructose-6-phosphate transaminase 1	1.58	0.355	1.43	0.079	1.01	0.953	-1.09	0.86	0.73
1445772_at	D16Ertd550e	DNA segment, Chr 16, ERATO Doi 550, expressed	-1.29	0.587	1.9	0.223	1.35	0.642	2.78	0.263	1.18
1438924_x_at	Fibp	Fibroblast growth factor (acidic) intracellular binding protein	1.61	0.283	1.01	0.985	1.4	0.226	-2.45	0.132	0.39
1436819_at	6-Sep	septin 6	1.28	0.497	1.47	0.164	1.27	0.4	-1.92	0.12	0.53
1443104_at	---	---	1.37	0.091	1.41	0.365	1.25	0.697	-1.17	0.674	0.72
1417599_at	Cd276	CD276 antigen	2.55	0.493	-2.86	0.039	1.13	0.737	1.09	0.798	0.47
1421045_at	Mrc2	mannose receptor, C type 2	1.61	0.109	1.52	0.515	-1.12	0.714	1.25	0.2	0.82
1438204_at	Hist1h1c	histone 1, H1c	1.75	0.162	1.18	0.722	1.09	0.814	-2.55	0.326	0.37
1421063_s_at	Snrpn /// Snurf	small nuclear ribonucleoprotein N /// SNRPN upstream reading frame	1.26	0.599	1.14	0.717	1.63	0.377	-1.84	0.459	0.55
1450981_at	Cnn2	calponin 2	1.32	0.115	1.62	0.056	1.08	0.507	-1.69	0.097	0.59
1433324_at	9330154F10Rik	RIKEN cDNA 9330154F10 gene	1.71	0.087	-1.22	0.577	1.5	0.391	1.55	0.125	0.89
1417528_at	Spag6	sperm associated antigen 6	1.01	0.966	1.83	0.208	1.19	0.31	-1.45	0.419	0.64
1415972_at	Marcks	myristoylated alanine rich protein kinase C substrate	1.15	0.719	1.87	0.032	1	0.989	-1.17	0.712	0.72
1451452_a_at	Rgs16	regulator of G-protein signaling 16	1.84	0.252	-1.34	0.719	1.45	0.171	1.2	0.525	0.79
1429184_at	Gvin1	GTPase, very large interferon inducible 1	1.09	0.734	1.84	0.082	1.1	0.306	-1.19	0.602	0.71
1444727_at	---	---	1.27	0.548	1.98	0.121	-1.28	0.258	1.16	0.649	0.78
1460261_at	Dlgh4	discs, large homolog 4 (Drosophila)	1.36	0.48	-4.15	0.05	2.43	0.041	2.38	0.049	0.51
1421753_a_at	Lhx3	LIM homeobox protein 3	1.4	0.498	1.34	0.594	1.29	0.457	-1.82	0.317	0.55
1431245_at	1700063H04Rik	RIKEN cDNA 1700063H04 gene	1.53	0.562	-1.23	0.394	1.69	0.226	1.8	0.042	0.95
1424107_at	Kif18a	kinesin family member 18A	-1.05	0.826	2.05	0.192	1.04	0.862	5.53	0.16	1.89
1432318_at	Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	-1.09	0.647	1.91	0.079	1.21	0.731	1.15	0.704	0.79
1457471_at	Il17rc	interleukin 17 receptor C	2.21	0.383	-1.37	0.636	1.09	0.839	1.09	0.907	0.76
1434960_at	Taf9b	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.12	0.439	2.07	0.032	-1.18	0.254	1.23	0.228	0.81
1431982_at	Arhgap19	Rho GTPase activating protein 19	-1.97	0.462	1.61	0.176	1.92	0.365	1.07	0.914	0.66
1423509_a_at	Iapp	islet amyloid polypeptide	1.13	0.774	1.82	0.035	1.09	0.893	-1.56	0.671	0.62
1448071_at	---	---	-1.06	0.528	1.43	0.516	1.67	0.102	1.12	0.832	0.79
1415971_at	Marcks	myristoylated alanine rich protein kinase C substrate	1.11	0.741	1.79	0.001	1.14	0.293	-1.31	0.363	0.68
1420687_at	4932438H23Rik	RIKEN cDNA 4932438H23 gene	-1.64	0.349	1.17	0.705	2.26	0.154	1.18	0.799	0.74
1436729_at	2600003E23Rik	RIKEN cDNA 2600003E23 gene	1.22	0.254	1.75	0.233	1.07	0.831	-1.1	0.708	0.74
1418807_at	3110070M22Rik	RIKEN cDNA 3110070M22 gene	1.48	0.469	1.63	0.337	-1.08	0.803	1.2	0.511	0.81
1432730_at	5830415G21Rik	RIKEN cDNA 5830415G21 gene	-1.39	0.357	1.19	0.785	2.13	0.091	1.08	0.821	0.75
1417414_at	3-Sep	septin 3	1.63	0.253	1.78	0.014	-1.59	0.248	1.2	0.175	0.75
1453544_at	Dmrtc1c /// LOC66	DMRT-like family C1c /// similar to doublesex and mab-3 related transcription fact	1.27	0.061	1.45	0.244	1.33	0.34	-2.02	0.17	0.5
1430657_at	1810034E14Rik	RIKEN cDNA 1810034E14 gene	1.09	0.757	1.21	0.785	1.74	0.044	-1.06	0.932	0.74
1456666_at	2610020C07Rik	RIKEN cDNA 2610020C07 gene	2.2	0.409	1.11	0.781	-1.37	0.428	1.58	0.38	0.88
1450320_at	4931432E15Rik	RIKEN cDNA 4931432E15 gene	1.16	0.715	1.08	0.803	1.8	0.165	-1.91	0.025	0.53
1450392_at	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	1.14	0.806	1.03	0.971	1.87	0.295	-1.27	0.717	0.69
1451908_a_at	Sec14l1	SEC14-like 1 (S. cerevisiae)	1.37	0.259	1.08	0.482	1.59	0.371	-1.18	0.317	0.72
1428838_a_at	Dck	deoxycytidine kinase	1.55	0.411	-2.05	0.217	2	0.117	4.55	0.264	1.51
1438841_s_at	Arg2	arginase type II	1.81	0.038	1.33	0.398	-1.11	0.794	1.15	0.621	0.8
1420997_a_at	Gpi1 /// LOC67659	glucose phosphate isomerase 1 /// similar to Glucose-6-phosphate isomerase (GI	1.26	0.053	1.1	0.043	1.68	0.008	-1.25	0.206	0.7
1425832_a_at	Cxcr6	chemokine (C-X-C motif) receptor 6	1.1	0.64	1.28	0.495	1.67	0.053	-1.29	0.607	0.69
1446438_at	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	1.25	0.713	2.06	0.315	-1.36	0.456	1.06	0.853	0.75
1451775_s_at	Il13ra1	interleukin 13 receptor, alpha 1	-1.09	0.686	1.53	0.264	1.59	0.381	1.21	0.061	0.81
1454371_at	Sypl2	synaptophysin-like 2	1.36	0.563	1.21	0.543	1.48	0.49	-1.37	0.443	0.67
1454297_at	4631402F24Rik	RIKEN cDNA 4631402F24 gene	1.38	0.548	-2.14	0.197	2.2	0.037	2.27	0.433	0.93

1433067_at	6330582A15Rik	RIKEN cDNA 6330582A15 gene	1.36	0.633	1.62	0.184	1.06	0.886	-1.14	0.826	0.73
1442636_at	BC004636	CDNA sequence BC004636	1.01	0.981	1.77	0.219	1.27	0.692	-1.28	0.068	0.69
1452811_at	Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydr	1.18	0.787	1.03	0.949	1.84	0.384	-1.04	0.919	0.75
1418732_s_at	1500041N16Rik	RIKEN cDNA 1500041N16 gene	1.11	0.113	1.07	0.263	1.87	0.002	-1.17	0.365	0.72
1450762_s_at	Zfp191	zinc finger protein 191	1.86	0.107	-1.11	0.721	1.29	0.221	1.26	0.365	0.82
1423100_at	Fos	FBJ osteosarcoma oncogene	-1.98	0.158	2.08	0.234	1.46	0.07	1.12	0.631	0.67
1435477_s_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	-1.11	0.572	1.36	0.111	1.79	0.129	1.17	0.672	0.8
1420951_a_at	Son	Son cell proliferation protein	1.69	0.096	1.15	0.653	1.21	0.648	-1.04	0.89	0.75
1460365_a_at	Dnm1	dynamin 1	1.9	0.031	1.49	0.527	-1.5	0.465	1.1	0.913	0.74
1419666_x_at	Nupr1	nuclear protein 1	1.5	0.407	1.41	0.611	1.15	0.604	-1.07	0.747	0.75
1437341_x_at	Cnp1	cyclic nucleotide phosphodiesterase 1	1.23	0.312	1.15	0.339	1.67	0.204	-1.54	0.198	0.63
1430706_at	1700081D17Rik	RIKEN cDNA 1700081D17 gene	1.13	0.669	2.08	0.129	-1.19	0.714	1.31	0.308	0.83
1448220_at	Ctrb1	chymotrypsinogen B1	1.83	0.474	1.41	0.529	-1.24	0.6	1.09	0.863	0.77
1431920_a_at	2010004A03Rik	RIKEN cDNA 2010004A03 gene	1.42	0.332	1.29	0.259	1.34	0.099	-1.31	0.001	0.69
1443320_at	Clasp2	CLIP associating protein 2	1.03	0.734	2.37	0.198	-1.53	0.176	1.08	0.825	0.74
1449767_x_at	Syt6	synaptotagmin VI	1.22	0.675	1.98	0.142	-1.17	0.742	4.5	0.024	1.63
1450459_at	2010106G01Rik	RIKEN cDNA 2010106G01 gene	1.77	0.529	-1.07	0.87	1.35	0.635	1.23	0.751	0.82
1425138_at	Guca1b	guanylate cyclase activator 1B	1.07	0.909	-1.23	0.321	2.18	0.002	1.35	0.493	0.84
1425214_at	P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	1.57	0.169	1.38	0.138	1.11	0.497	-1.17	0.309	0.72
1432179_x_at	2810433K01Rik	RIKEN cDNA 2810433K01 gene	-1.08	0.838	1.63	0.149	1.5	0.536	1.51	0.483	0.89
1449011_at	Slc12a7	solute carrier family 12, member 7	1.18	0.681	-1.01	0.974	1.88	0.239	1.02	0.906	0.77
1457072_at	2410127E16Rik ///	RIKEN cDNA 2410127E16 gene /// B-cell CLL/lymphoma 11A (zinc finger protein	1.77	0.393	1.08	0.773	1.2	0.731	-1.64	0.146	0.6
1417483_at	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.03	0.93	1.94	0.024	1.09	0.775	-1.23	0.395	0.71
1451139_at	Slc39a4	solute carrier family 39 (zinc transporter), member 4	2.03	0.071	-1.47	0.097	1.35	0.044	1.82	0.109	0.93
1421003_at	Gmeb1	glucocorticoid modulatory element binding protein 1	2.7	0.225	-2.92	0.071	1.01	0.973	1.26	0.609	0.51
1441130_at	---	Transcribed locus	2.16	0.258	-1.28	0.758	1.11	0.781	2.23	0.072	1.06
1440920_at	---	Transcribed locus	1.7	0.33	1.21	0.522	1.15	0.59	-1.55	0.118	0.63
1429789_at	Arpm1	actin related protein M1	1.05	0.922	1.65	0.276	1.36	0.532	-1.12	0.688	0.74
1439778_at	Cables1	Cdk5 and Abl enzyme substrate 1	2	0.31	1.53	0.554	-1.91	0.5	1.8	0.246	0.86
1444994_at	A230038B01Rik	RIKEN cDNA A230038B01 gene	1.21	0.752	-1.37	0.639	2.12	0.025	1.16	0.75	0.78
1441950_s_at	2010109A12Rik	RIKEN cDNA 2010109A12 gene	1.09	0.914	1.84	0.31	1.13	0.738	-1.2	0.772	0.71
1448823_at	Cxcl12	chemokine (C-X-C motif) ligand 12	1.51	0.022	1.25	0.007	1.31	0.228	-1.26	0.568	0.7
1441582_at	---	---	1.76	0.426	-1.3	0.401	1.53	0.425	1.29	0.678	0.82
1443703_at	Cd28	CD28 antigen	1	0.998	1.97	0.402	1.09	0.737	-3	0.022	0.27
1425965_at	Ubc	ubiquitin C	-1.21	0.727	1.06	0.881	2.17	0.218	2.29	0.028	1.08
1449204_at	Gjb5	gap junction membrane channel protein beta 5	-1.18	0.247	1.68	0.415	1.53	0.569	1.1	0.885	0.78
1436199_at	---	---	1.22	0.075	1.03	0.83	1.81	0.051	-2.08	0.094	0.5
1459082_at	---	Transcribed locus	1.32	0.691	1.59	0.292	1.16	0.773	-2.34	0.263	0.43
1460007_at	Thyn1	thymocyte nuclear protein 1	2.01	0.096	-1.62	0.253	1.44	0.475	1.56	0.147	0.85
1424494_s_at	2810417J12Rik	RIKEN cDNA 2810417J12 gene	1.12	0.491	2.28	0.011	-1.52	0.424	1.38	0.34	0.82
1453490_at	Sass6	spindle assembly 6 homolog (C. elegans)	1.3	0.733	-1.44	0.55	2.07	0.065	1.38	0.45	0.83
1421112_at	Nkx2-2	NK2 transcription factor related, locus 2 (Drosophila)	1.62	0.313	-1.5	0.447	1.78	0.039	1.07	0.851	0.74
1450078_at	Nrk	Nik related kinase	1.71	0.261	1.73	0.286	-1.61	0.265	1.65	0.537	0.87
1454093_at	4933436I20Rik	RIKEN cDNA 4933436I20 gene	1.56	0.506	1.61	0.5	-1.12	0.782	1.04	0.959	0.77
1423155_at	Sri	sorcin	1.01	0.9	1.24	0.378	1.81	0.234	-1.11	0.604	0.74
1445671_at	---	Transcribed locus	1.06	0.7	1.78	0.153	1.23	0.251	-1.14	0.732	0.73
1421899_a_at	Mr1	major histocompatibility complex, class I-related	1.24	0.488	1.31	0.453	1.52	0.174	-1.23	0.131	0.71
1454893_at	1110013L07Rik	RIKEN cDNA 1110013L07 gene	1.23	0.461	1.58	0.065	1.26	0.122	-1.84	0.196	0.56
1417030_at	2310028N02Rik	RIKEN cDNA 2310028N02 gene	1.01	0.913	1.81	0.04	1.25	0.376	-1.34	0.17	0.68
1449330_at	Pdzd3	PDZ domain containing 3	-1.08	0.306	1.92	0.278	1.22	0.609	2.27	0.306	1.08
1449508_at	Il27ra	interleukin 27 receptor, alpha	1.85	0.493	1.22	0.592	1	0.991	-2.63	0.071	0.36
1421415_s_at	Gcnt2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.37	0.519	-1.38	0.474	1.97	0.402	1.09	0.663	0.76
1426615_s_at	Ndrg4	N-myc downstream regulated gene 4	-1.34	0.113	2.15	0.108	1.18	0.64	1.46	0.292	0.86

1432463_at	5730510P18Rik	RIKEN cDNA 5730510P18 gene	1.08	0.559	1.32	0.701	1.67	0.43	-1.56	0.503	0.63
1450189_at	Xkh	Kell blood group precursor (McLeod phenotype) homolog	1.92	0.445	-1.04	0.948	1.19	0.619	2.37	0.378	1.11
1432793_at	4930401B11Rik	RIKEN cDNA 4930401B11 gene	1.27	0.603	1.47	0.27	1.34	0.619	-1.02	0.969	0.76
1454278_at	A430105D02Rik	RIKEN cDNA A430105D02 gene	1.26	0.135	1.22	0.649	1.59	0.37	-2.12	0.363	0.49
1449154_at	Col11a1	procollagen, type XI, alpha 1	1.06	0.692	1.26	0.74	1.75	0.135	-1.26	0.31	0.7
1442338_at	---	Transcribed locus	1.75	0.247	1.48	0.037	-1.17	0.621	3.05	0.12	1.28
1442140_at	Tnn	tenascin N	1.61	0.249	1.25	0.509	1.21	0.569	-1.72	0.24	0.59
1453919_at	2610028H24Rik	RIKEN cDNA 2610028H24 gene	1.73	0.441	-1.01	0.989	1.35	0.226	2.17	0.289	1.06
1450565_at	Il9	interleukin 9	1.59	0.398	1.06	0.816	1.42	0.298	-1.02	0.929	0.76
1417600_at	Slc15a2	solute carrier family 15 (H+/peptide transporter), member 2	1.34	0.146	1.81	0.212	-1.08	0.655	1.68	0.303	0.94
1450314_at	Dqx1	DEAQ RNA-dependent ATPase	1.87	0.296	1.11	0.784	1.1	0.802	-1.62	0.256	0.61
1451235_at	Cend1	cell cycle exit and neuronal differentiation 1	1.97	0.001	-1.15	0.763	1.24	0.384	1.62	0.227	0.92
1445314_at	Etv1	ets variant gene 1	1.42	0.371	1.56	0.447	1.09	0.846	-1.11	0.731	0.74
1435496_at	5730469M10Rik	RIKEN cDNA 5730469M10 gene	2.25	0.336	1.1	0.862	-1.38	0.484	2.71	0.352	1.17
1422181_at	Cnga2	cyclic nucleotide gated channel alpha 2	1.14	0.533	1.47	0.472	1.46	0.336	-1.02	0.944	0.76
1421516_at	Nr6a1	nuclear receptor subfamily 6, group A, member 1	2.09	0.171	1.31	0.605	-1.49	0.34	1.53	0.374	0.86
1457319_at	A130038J17Rik	RIKEN cDNA A130038J17 gene	1.05	0.954	2.25	0.385	-1.28	0.619	2.41	0.353	1.11
1444442_at	Oraov1	oral cancer overexpressed 1	2.18	0.264	-1.33	0.464	1.14	0.656	1.3	0.674	0.82
1441261_at	---	---	-1.4	0.634	1.2	0.52	2.16	0.001	1.06	0.907	0.76
1430250_at	Sec24c	SEC24 related gene family, member C (S. cerevisiae)	1.41	0.565	1.99	0.113	-1.47	0.387	1.38	0.083	0.83
1445159_at	---	Transcribed locus	2.1	0.181	-1.27	0.616	1.2	0.522	1.35	0.48	0.84
1435192_at	LOC631901	similar to SRY (sex determining region Y)-box 3	1.99	0.513	1.05	0.798	1.04	0.955	-1.07	0.888	0.75
1430602_at	4930520K10Rik	RIKEN cDNA 4930520K10 gene	1.79	0.1	1.12	0.48	1.17	0.613	-1.4	0.61	0.67
1452337_at	4930427A07Rik	RIKEN cDNA 4930427A07 gene	-1.7	0.377	1.11	0.807	2.38	0.089	1.6	0.423	0.85
1427699_a_at	Ptpn11	protein tyrosine phosphatase, non-receptor type 11	1.74	0.155	1.29	0.589	1.05	0.764	-1.33	0.634	0.69
1451451_at	Gca	grancalcin	-1.32	0.475	2.32	0.179	1	0.984	1.78	0.259	0.95
1416753_at	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	-1.03	0.905	2.05	0.05	1.07	0.469	1.67	0.302	0.94
1450007_at	1500003O03Rik	RIKEN cDNA 1500003O03 gene	1.35	0.558	-1.18	0.682	1.88	0.35	2.08	0.35	1.04
1448197_at	Ceacam11	CEA-related cell adhesion molecule 11	1.35	0.067	1.71	0.32	1.03	0.871	-1.14	0.51	0.74
1430072_at	1700057K13Rik	RIKEN cDNA 1700057K13 gene	1.95	0.308	1.16	0.474	-1.03	0.949	1.69	0.188	0.94
1421978_at	Gad2	glutamic acid decarboxylase 2	1.62	0.387	1.66	0.196	-1.25	0.561	1.24	0.248	0.82
1450488_at	Ccl24	chemokine (C-C motif) ligand 24	-1.11	0.801	2.04	0.406	1.14	0.834	3.79	0.348	1.47
1422120_at	Eaf2	ELL associated factor 2	1.13	0.224	-1.32	0.404	2.2	0.013	1.14	0.808	0.79
1459404_at	4930583H14Rik	RIKEN cDNA 4930583H14 gene	1.98	0.42	1.13	0.86	-1.03	0.904	1.11	0.843	0.8
1446291_at	9330175H22Rik	RIKEN cDNA 9330175H22 gene	2.08	0.056	1.07	0.845	-1.07	0.8	1.46	0.401	0.88
1435697_a_at	Pscdbp	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	1.12	0.411	1.89	0.06	1.07	0.705	-1.97	0.08	0.53
1423318_at	Rad18	RAD18 homolog (S. cerevisiae)	-1.27	0.738	1.65	0.298	1.65	0.088	2.06	0.328	1.02
1434912_at	Ric3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	1.39	0.288	-2.03	0.227	2.21	0.068	1.83	0.434	0.85
1439489_at	Gpr120	G protein-coupled receptor 120	1.78	0.371	1.29	0.731	1.02	0.936	-1.24	0.556	0.71
1440519_at	Sp8	trans-acting transcription factor 8	2.06	0.271	-1.4	0.115	1.32	0.555	1.02	0.967	0.75
1426607_at	LOC633640	similar to CG10866-PA	1.24	0.306	1.18	0.216	1.67	0.018	-1.21	0.199	0.72
1431005_at	D10Wsu102e	DNA segment, Chr 10, Wayne State University 102, expressed	1.08	0.923	-1.13	0.694	2.12	0.126	1.25	0.667	0.83
1421700_at	Tex16	testis expressed gene 16	2.19	0.267	-5.7	0.122	1.72	0.171	1.17	0.803	-0.15
1455373_at	---	Transcribed locus	1.6	0.29	1.89	0.313	-1.68	0.248	1.53	0.311	0.84
1427181_at	D18Ertd653e	DNA segment, Chr 18, ERATO Doi 653, expressed	1.19	0.782	2.21	0.149	-1.44	0.307	1.23	0.407	0.8
1451643_a_at	Rab4b	RAB4B, member RAS oncogene family	1.23	0.474	1.42	0.207	1.43	0.266	-1.26	0.288	0.71
1436564_at	Rims4	Regulating synaptic membrane exocytosis 4	1.29	0.595	1.31	0.527	1.5	0.036	-1.1	0.819	0.75
1425016_at	Ephb2	Eph receptor B2	1.03	0.809	2.02	0.06	1.05	0.86	-1.02	0.895	0.77
1457068_at	Naaladl1	N-acetylated alpha-linked acidic dipeptidase-like 1	1.75	0.6	2	0.025	-2.93	0.148	7.42	0.228	2.06
1452358_at	Rai2	retinoic acid induced 2	1.44	0.204	1.36	0.243	1.29	0.398	-1.17	0.375	0.73
1434414_at	Foxred2	FAD-dependent oxidoreductase domain containing 2	1.33	0.277	1.44	0.582	1.32	0.161	-1.77	0.061	0.58
1447222_at	Hspa12a	heat shock protein 12A	1.44	0.472	-1.63	0.172	2.04	0.213	1.05	0.837	0.72
1433333_at	C030004M13Rik	RIKEN cDNA C030004M13 gene	1.28	0.618	1.25	0.499	1.56	0.321	-1.1	0.798	0.75

1448367_at	Sdf4	stromal cell derived factor 4	2.01	0.331	-1.97	0.466	1.57	0.615	1.18	0.435	0.7
1430486_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	1.08	0.859	-1.66	0.398	2.42	0.176	1.3	0.271	0.78
1455116_at	Tnfrsf19l /// LOC67	tumor necrosis factor receptor superfamily, member 19-like /// similar to GrpE pro	-1.67	0.443	1.78	0.154	1.72	0.095	1.32	0.253	0.79
1428786_at	Nckap1l	NCK associated protein 1 like	1.27	0.522	1.38	0.005	1.44	0.374	-1.6	0.232	0.62
1418977_at	Sap30bp	SAP30 binding protein	1.77	0.404	1.3	0.659	1.02	0.968	-1.61	0.138	0.62
1445243_at	D10Ertd533e	DNA segment, Chr 10, ERATO Doi 533, expressed	-1.37	0.7	2.13	0.221	1.23	0.645	1.25	0.606	0.81
1449220_at	Gimap3	GTPase, IMAP family member 3	1.39	0.074	1.22	0.551	1.49	0.211	-1.58	0.296	0.63
1439666_at	2010001J22Rik	RIKEN cDNA 2010001J22 gene	1.79	0.279	-1.19	0.424	1.47	0.214	1.77	0.163	0.96
1450862_at	Rad54l	RAD54 like (S. cerevisiae)	-1.07	0.91	1.72	0.166	1.44	0.061	2.89	0.235	1.25
1454430_at	Pde11a	phosphodiesterase 11A	1.07	0.707	1.51	0.493	1.51	0.326	-1.23	0.804	0.72
1427788_at	Nespas	neuroendocrine secretory protein antisense	1.68	0.416	-1.05	0.865	1.47	0.234	1.35	0.404	0.86
1446237_at	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	1.13	0.878	1.58	0.27	1.39	0.203	-1.04	0.956	0.77
1422175_at	Mmp1a /// LOC672	matrix metallopeptidase 1a (interstitial collagenase) /// similar to matrix metalloprc	2.22	0.099	1.12	0.854	-1.32	0.654	1.1	0.833	0.78
1433318_at	5430416B10Rik	RIKEN cDNA 5430416B10 gene	1.32	0.447	1.67	0.164	1.11	0.844	-1.61	0.603	0.62
1443582_at	RP23-249K18.2	similar to growth arrest-specific 2 like 2; GAS2-related protein	1.28	0.55	1.35	0.415	1.47	0.063	-1.03	0.947	0.77
1446231_at	---	Transcribed locus	1.57	0.14	-1.06	0.912	1.58	0.213	1.6	0.447	0.93
1452326_at	1810010G06Rik	RIKEN cDNA 1810010G06 gene	1.37	0.347	1.24	0.584	1.49	0.241	-1.4	0.471	0.68
1420740_at	Il25	interleukin 25	1.14	0.448	-1.05	0.884	2	0.347	2.04	0.285	1.03
1422430_at	Fignl1	fidgetin-like 1	-1.37	0.269	1.98	0.244	1.39	0.502	4.46	0.199	1.62
1432672_at	4933407A17Rik	RIKEN cDNA 4933407A17 gene	-1.07	0.883	1.57	0.405	1.6	0.098	1.04	0.72	0.78
1456270_s_at	Pramel6	preferentially expressed antigen in melanoma like 6	-1.02	0.984	1.09	0.9	2.03	0.332	1.77	0.442	0.97
1416405_at	Bgn	biglycan	1.65	0.081	1.47	0.118	-1.01	0.965	1.09	0.72	0.8
1422734_a_at	Myb	myeloblastosis oncogene	-1.14	0.519	1.77	0.356	1.46	0.053	1.51	0.314	0.9
1458523_at	Zfml	zinc finger, matrin-like	2.01	0.049	1.03	0.925	1.07	0.82	-1.84	0.166	0.57
1454577_at	LOC238896	similar to cell division cycle 20 homolog	1.12	0.875	-1.81	0.243	2.44	0.07	1.73	0.089	0.87
1434693_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	1.28	0.452	-1.02	0.863	1.84	0.118	1.15	0.787	0.81
1433699_at	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	1.07	0.683	1.54	0.05	1.49	0.224	-1.58	0.146	0.63
1422080_at	Il7	interleukin 7	1.06	0.923	1.86	0.308	1.19	0.481	-1.97	0.006	0.53
1425215_at	Ffar2	free fatty acid receptor 2	1.12	0.383	1.28	0.069	1.71	0.024	-1.45	0.209	0.66
1426816_at	Ccdc64	coiled-coil domain containing 64	1.09	0.694	1.28	0.437	1.74	0.081	-1.22	0.41	0.72
1448175_at	Ehd1	EH-domain containing 1	1.22	0.469	1.28	0.243	1.61	0.078	-1.21	0.231	0.72
1439018_at	6330505N24Rik	RIKEN cDNA 6330505N24 gene	-1.12	0.486	2.14	0.041	1.08	0.642	5.43	0.193	1.88
1425555_at	Crkrs	Cdc2-related kinase, arginine/serine-rich	1.08	0.872	1.26	0.519	1.77	0.193	-1.41	0.027	0.67
1422038_a_at	Tnfrsf22	tumor necrosis factor receptor superfamily, member 22	1.56	0.593	1.77	0.302	-1.29	0.392	1.21	0.674	0.81
1441714_at	---	Transcribed locus	2	0.356	1.26	0.662	-1.18	0.054	1.29	0.342	0.84
1458976_at	C230035I16Rik	RIKEN cDNA C230035I16 gene	-1.37	0.259	2.38	0.163	1	0.998	1.11	0.814	0.78
1443919_at	Prrt3	proline-rich transmembrane protein 3	1.96	0.133	1.02	0.879	1.13	0.623	-1.09	0.782	0.75
1418649_at	Egln3	EGL nine homolog 3 (C. elegans)	1.11	0.489	-1.73	0.019	2.42	0.009	1.83	0.098	0.91
1439576_at	---	Transcribed locus	-1.27	0.378	2.12	0.399	1.21	0.658	2.22	0.088	1.07
1459742_at	---	15 days embryo brain cDNA, RIKEN full-length enriched library, clone:G630032A	1.72	0.24	-1.03	0.886	1.42	0.301	1.1	0.515	0.8
1429668_at	Pou4f1	POU domain, class 4, transcription factor 1	1.98	0.451	-1.53	0.54	1.48	0.506	1.84	0.187	0.94
1422771_at	LOC670044	similar to Mothers against decapentaplegic homolog 6 (SMAD 6) (Mothers agains	1.27	0.094	1.43	0.358	1.42	0.126	-1.26	0.424	0.71
1431758_at	BC051628	cDNA sequence BC051628	1.16	0.413	2.51	0.087	-2.28	0.237	1.14	0.741	0.63
1431537_at	2010001E11Rik	RIKEN cDNA 2010001E11 gene	1.09	0.76	-1.62	0.406	2.41	0.054	2.06	0.314	0.98
1423600_a_at	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	1.01	0.865	1.13	0.564	1.98	0.023	-1.5	0.166	0.65
1436332_at	Hspb6	heat shock protein, alpha-crystallin-related, B6	1.19	0.433	-1.13	0.564	2.04	0.085	2.77	0.139	1.22
1439069_a_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	1	0.989	1.26	0.052	1.85	0.007	-1.01	0.986	0.78
1417358_s_at	Sorbs1	sorbin and SH3 domain containing 1	2.03	0.042	-1.19	0.732	1.24	0.563	1.53	0.393	0.9
1416881_at	Mcl1	myeloid cell leukemia sequence 1	1.25	0.134	1.23	0.354	1.63	0.246	-1.28	0.441	0.71
1449102_at	Ebf2	early B-cell factor 2	1.95	0.4	1.07	0.898	1.1	0.863	-3.16	0.215	0.24
1452661_at	Tfrc	transferrin receptor	1.34	0.544	2.02	0.339	-1.32	0.062	3.27	0.128	1.33
1458462_at	Arhgap30	Rho GTPase activating protein 30	1.23	0.299	1.37	0.258	1.52	0.214	-1.58	0.362	0.63
1431422_a_at	Dusp14	dual specificity phosphatase 14	1.12	0.555	1.71	0.168	1.29	0.369	-1.55	0.42	0.64

1432469_at	1700094E07Rik	RIKEN cDNA 1700094E07 gene	2.26	0.061	-1.3	0.468	1.09	0.824	1.12	0.798	0.79
1452233_at	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	1.04	0.497	1.75	0.026	1.33	0.003	-1.16	0.445	0.74
1427487_at	---	---	2.1	0.075	1.04	0.928	-1.02	0.933	1.17	0.386	0.82
1457937_at	A430088P11Rik	RIKEN cDNA A430088P11 gene	1.82	0.249	1.02	0.915	1.28	0.357	-1.47	0.321	0.66
1460281_at	Asb15	ankyrin repeat and SOCS box-containing protein 15	1.01	0.96	1.89	0.214	1.22	0.638	-1.28	0.628	0.71
1459766_x_at	---	---	1.77	0.386	1.74	0.385	-1.63	0.186	1.3	0.099	0.8
1427430_at	AI848100	expressed sequence AI848100	-1.16	0.77	1.5	0.494	1.77	0.281	1.46	0.591	0.89
1453329_s_at	Tcba1	T-cell lymphoma breakpoint associated target 1	1.2	0.637	1.69	0.139	1.23	0.566	-3.08	0.129	0.26
1442282_at	LOC625068	Similar to vomeronasal 2, receptor, 2	1.07	0.935	1.59	0.427	1.47	0.275	-2.39	0.116	0.43
1429365_at	1700016M24Rik	RIKEN cDNA 1700016M24 gene	1.64	0.53	1.1	0.853	1.39	0.437	-1.38	0.276	0.69
1443870_at	Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	-1.08	0.182	1.91	0.091	1.29	0.141	1.68	0.093	0.95
1416302_at	Ebf1	early B-cell factor 1	1.09	0.502	1.77	0.252	1.26	0.555	-2.51	0.111	0.4
1449887_at	2310010I16Rik	RIKEN cDNA 2310010I16 gene	2.07	0.116	-1.09	0.921	1.13	0.632	1.18	0.834	0.82
1419901_at	---	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library,	1.07	0.73	1.64	0.217	1.41	0.257	-1.72	0.022	0.6
1422544_at	Myo10	myosin X	-1.14	0.431	1.46	0.087	1.79	0.113	1.29	0.411	0.85
1453444_at	5730437C12Rik	RIKEN cDNA 5730437C12 gene	1.48	0.395	1.18	0.626	1.47	0.425	-1.53	0.498	0.65
1454467_at	LOC668894 /// LOC	similar to Vinculin CG3299-PA /// similar to Vinculin CG3299-PA	-1.06	0.472	1.81	0.391	1.38	0.294	3.05	0.004	1.29
1427710_at	BC013491	cDNA sequence BC013491	-1.06	0.907	1.95	0.321	1.23	0.143	1.38	0.257	0.88
1420226_x_at	Hoxa4	homeo box A4	1.2	0.058	2.19	0.038	-1.35	0.151	1.25	0.578	0.82
1446402_at	---	---	1.79	0.268	-1.26	0.528	1.54	0.238	1.2	0.661	0.82
1454694_a_at	Top2a	topoisomerase (DNA) II alpha	-1.05	0.771	1.73	0.02	1.45	0.415	2.9	0.17	1.26
1430173_x_at	Cyp4f16	cytochrome P450, family 4, subfamily f, polypeptide 16	-1.04	0.929	2.06	0.33	1.11	0.718	1.17	0.576	0.82
1452822_at	Ints7	integrator complex subunit 7	-1.47	0.152	1.53	0.433	1.92	0.005	1.87	0.233	0.96
1432127_at	4933401L05Rik	RIKEN cDNA 4933401L05 gene	1.2	0.782	1.72	0.414	1.21	0.652	-1.48	0.36	0.66
1422425_at	Sprr2k	small proline-rich protein 2K	1	0.992	2.26	0.418	-1.15	0.721	1.37	0.481	0.87
1450696_at	Psmb9	proteosome (prosome, macropain) subunit, beta type 9 (large multifunctional pep	1.34	0.142	1.14	0.193	1.65	0.115	-1.31	0.374	0.7
1432302_s_at	2410024N13Rik	RIKEN cDNA 2410024N13 gene	1.41	0.665	1.09	0.837	1.63	0.148	-1.34	0.561	0.7
1426333_a_at	Ikbkb	inhibitor of kappaB kinase beta	1.13	0.155	1.27	0.254	1.73	0.042	-1.29	0.108	0.71
1434055_at	Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.29	0.211	-2	0.22	2.34	0.145	1.86	0.316	0.87
1448188_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	-1	0.977	1.2	0.322	1.93	0.001	1.29	0.151	0.86
1460287_at	Timp2	tissue inhibitor of metalloproteinase 2	1.58	0.209	1.49	0.054	1.06	0.783	-1.06	0.831	0.77
1415988_at	Hdlbp	high density lipoprotein (HDL) binding protein	1.64	0.314	-1.03	0.961	1.53	0.538	1.1	0.857	0.81
1416226_at	Arpc1b	actin related protein 2/3 complex, subunit 1B	1.11	0.102	1.49	0.003	1.53	0.04	-1.68	0.091	0.61
1419331_at	Cdh17	cadherin 17	1.12	0.842	1.53	0.461	1.49	0.104	-2.15	0.033	0.5
1424705_at	Rbmx2	RNA binding motif protein, X-linked 2	1.46	0.512	1.84	0.425	-1.2	0.24	2.34	0.155	1.11
1452311_at	Dmgdh	dimethylglycine dehydrogenase precursor	1.08	0.68	1.03	0.855	2.02	0.313	-1.04	0.876	0.77
1418785_at	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	1.39	0.696	1.21	0.775	1.53	0.179	-2.04	0.059	0.52
1438205_at	1110014N23Rik	RIKEN cDNA 1110014N23 gene	1.47	0.547	1.09	0.869	1.57	0.395	-1.44	0.425	0.67
1451956_a_at	Oprs1	opioid receptor, sigma 1	1.21	0.704	1.04	0.936	1.89	0.236	-1.07	0.893	0.77
1453224_at	Zfand5	zinc finger, AN1-type domain 5	1.17	0.672	-1.07	0.903	2.03	0.176	1.37	0.317	0.87
1431648_at	4930528F23Rik	RIKEN cDNA 4930528F23 gene	1.2	0.773	-1.02	0.86	1.95	0.106	2.47	0.087	1.15
1443964_at	Tmie	transmembrane inner ear	1.3	0.754	1.28	0.476	1.56	0.517	-2.36	0.099	0.44
1426041_a_at	Fgd4	FYVE, RhoGEF and PH domain containing 4	-1.06	0.849	1.31	0.76	1.89	0.183	1.35	0.398	0.87
1429266_at	Tmhs	tetraspan transmembrane protein, hair cell stereocilia	-1.03	0.97	1.48	0.475	1.68	0.075	1.35	0.65	0.87
1426262_at	Zfp508	zinc finger protein 508	1.24	0.629	2.07	0.034	-1.21	0.063	1.19	0.501	0.82
1419556_at	Elf5	E74-like factor 5	1.16	0.832	2.11	0.098	-1.14	0.626	1.38	0.052	0.87
1457254_x_at	6330442E10Rik	RIKEN cDNA 6330442E10 gene	1.5	0.045	1.61	0.143	1.03	0.931	-1.94	0.108	0.55
1417527_at	Ap3m2	adaptor-related protein complex 3, mu 2 subunit	1.17	0.159	1.89	0.072	1.07	0.716	-1.75	0.176	0.6
1432112_at	4930589L23Rik	RIKEN cDNA 4930589L23 gene	2.43	0.28	-3.54	0.007	1.42	0.34	1.34	0.437	0.41
1427485_at	Lmod1	leiomodin 1 (smooth muscle)	2.45	0.387	1.05	0.843	-1.56	0.188	1.81	0.402	0.94
1445848_at	9630009C16	hypothetical protein 9630009C16	1.66	0.116	1.87	0.225	-1.63	0.116	1.28	0.467	0.79
1446862_at	---	---	1.49	0.143	-1.11	0.819	1.75	0.201	1.16	0.654	0.82
1460521_a_at	5830411E10Rik	RIKEN cDNA 5830411E10 gene	1.13	0.707	1.29	0.42	1.72	0.197	-2.34	0.137	0.45

1421961_a_at	Dnajb5	DnaJ (Hsp40) homolog, subfamily B, member 5	1.5	0.586	-1.11	0.853	1.74	0.331	1.28	0.67	0.85
1449564_at	Tpsg1	tryptase gamma 1	1.69	0.537	1.23	0.377	1.23	0.657	-2.62	0.009	0.38
1416715_at	Gjb3	gap junction membrane channel protein beta 3	2.22	0.273	-1.78	0.099	1.36	0.293	1.06	0.905	0.71
1420141_at	AA517023	expressed sequence AA517023	2.08	0.003	-1.06	0.912	1.12	0.523	1.04	0.949	0.79
1426734_at	BC022623	cDNA sequence BC022623	1.01	0.946	1.6	0.018	1.54	0.22	-1.39	0.126	0.69
1427312_at	Cmya5	cardiomyopathy associated 5	1.02	0.956	1.2	0.723	1.93	0.292	-1.2	0.624	0.73
1454474_at	4933433M23Rik	RIKEN cDNA 4933433M23 gene	1.38	0.702	-1.44	0.01	2.06	0.09	3.06	0.242	1.27
1451599_at	Sesn2	sestrin 2	1.88	0.213	-1.92	0.129	1.75	0.158	1.87	0.1	0.89
1450675_at	Smap1l	stromal membrane-associated protein 1-like	1.22	0.272	1.12	0.503	1.79	0.137	-1.27	0.332	0.72
1422683_at	Irak1bp1	interleukin-1 receptor-associated kinase 1 binding protein 1	-1.06	0.87	1.83	0.164	1.37	0.414	1.1	0.097	0.81
1437820_at	Fkhl18	forkhead-like 18 (Drosophila)	1.46	0.388	1.4	0.497	1.29	0.359	-1.32	0.385	0.71
1431592_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	1.25	0.502	1.39	0.47	1.5	0.009	-1.51	0.259	0.66
1421199_at	Dlgh2	discs, large homolog 2 (Drosophila)	1.06	0.86	1.14	0.825	1.95	0.091	-1.04	0.878	0.78
1446203_at	Mkln1	muskelin 1, intracellular mediator containing kelch motifs	1.18	0.475	1.69	0.239	1.27	0.568	-2.13	0.371	0.5
1436414_at	AW822216	expressed sequence AW822216	1.53	0.484	1.72	0.36	-1.11	0.737	1.04	0.916	0.79
1424084_at	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	-1.12	0.707	1.38	0.071	1.87	0.193	1.31	0.589	0.86
1418992_at	F10	coagulation factor X	-1.08	0.9	1.22	0.246	2	0.18	1.59	0.413	0.93
1416069_at	Pfkp	phosphofructokinase, platelet	1.06	0.616	1.87	0.034	1.22	0.163	-1.14	0.588	0.75
1450006_at	Ncoa4 /// LOC6275	nuclear receptor coactivator 4 /// similar to nuclear receptor coactivator 4	1.02	0.751	-1.09	0.796	2.2	0.049	2.6	0.277	1.18
1448731_at	Il10ra	interleukin 10 receptor, alpha	1.71	0.364	1.2	0.307	1.24	0.386	-1.91	0.135	0.56
1441223_at	4-Mar	membrane-associated ring finger (C3HC4) 4	1.28	0.716	1.17	0.729	1.7	0.05	-1.91	0.366	0.56
1429501_s_at	Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	1.99	0.074	-1.01	0.989	1.17	0.093	1.1	0.807	0.81
1439200_x_at	Rhox4b	Reproductive homeobox 4B	1.7	0.098	-1.03	0.926	1.48	0.402	1.33	0.527	0.87
1423166_at	Cd36	CD36 antigen	1.48	0.002	1.87	0.033	-1.25	0.418	1.13	0.611	0.81
1428479_at	Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.35	0.166	1.1	0.509	1.7	0.005	-1.5	0.379	0.66
1422534_at	Cyp51	cytochrome P450, family 51	1.18	0.404	1.37	0.525	1.6	0.123	-2.01	0.254	0.54
1417110_at	Man1a	mannosidase 1, alpha	-1.02	0.673	1.06	0.566	2.11	0.324	1.15	0.711	0.83
1428964_at	Slc25a18	solute carrier family 25 (mitochondrial carrier), member 18	1.14	0.624	1.8	0.302	1.22	0.31	-1.02	0.952	0.78
1438760_x_at	Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)	-1.17	0.637	2.1	0.019	1.2	0.319	1.02	0.872	0.79
1440361_at	---	16 days embryo head cDNA, RIKEN full-length enriched library, clone:C130014E	-1.84	0.299	2.48	0.021	1.13	0.759	1.51	0.588	0.82
1459006_a_at	LOC432938	Hypothetical gene supported by AK083927	1.08	0.841	1.15	0.717	1.93	0.123	-2.38	0.02	0.44
1425634_a_at	Tnk1	tyrosine kinase, non-receptor, 1	2.16	0.198	1.24	0.665	-1.33	0.48	1.99	0.177	1.02
1449807_x_at	---	---	1.36	0.271	1.92	0.425	-1.15	0.168	1.44	0.385	0.89
1453960_a_at	Capzb	capping protein (actin filament) muscle Z-line, beta	1.1	0.795	1.18	0.552	1.87	0.196	-1.17	0.654	0.75
1443130_at	LOC628951	hypothetical protein LOC628951	1.44	0.194	2.07	0.319	-1.53	0.256	1.29	0.669	0.82
1416188_at	Gm2a	GM2 ganglioside activator protein	1.31	0.561	1.04	0.889	1.8	0.223	-1.16	0.705	0.75
1457408_at	Pde4a	Phosphodiesterase 4A, cAMP specific	1.41	0.548	1.84	0.43	-1.1	0.859	1.72	0.145	0.97
1451805_at	Phip	pleckstrin homology domain interacting protein	1.3	0.159	1.35	0.484	1.51	0.425	-1.12	0.762	0.76
1441311_at	Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	1.68	0.076	1.76	0.346	-1.39	0.505	1.32	0.62	0.84
1460599_at	D19Wsu12e	DNA segment, Chr 19, Wayne State University 12, expressed	-1.01	0.969	1.14	0.682	2.02	0.133	1.04	0.832	0.8
1448348_at	Gpiap1	GPI-anchored membrane protein 1	1.31	0.568	-1.18	0.83	2	0.351	1.28	0.775	0.85
1419025_at	Sag	retinal S-antigen	1.51	0.474	1.49	0.417	1.17	0.437	-1.24	0.304	0.73
1450883_a_at	Cd36	CD36 antigen	1.44	0.119	1.91	0.002	-1.25	0.035	1.02	0.897	0.78
1447774_x_at	5730469M10Rik	RIKEN cDNA 5730469M10 gene	-1.2	0.422	1.17	0.173	2.16	0.045	3.56	0.152	1.42
1430829_s_at	Fto	fatso	1.69	0.187	-1.1	0.844	1.55	0.233	1.36	0.228	0.88
1430571_s_at	Armc6	armadillo repeat containing 6	1.53	0.516	-1.04	0.868	1.67	0.184	1.15	0.824	0.83
1439197_at	Pik4cb	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	2.1	0.03	1.28	0.398	-1.27	0.546	1.26	0.259	0.84
1449318_at	Tubg2	tubulin, gamma 2	1.01	0.964	1.6	0.299	1.55	0.424	-1.29	0.451	0.72
1434773_a_at	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	1.16	0.399	1.15	0.548	1.86	0.063	-1.67	0.121	0.62
1456412_a_at	RP23-136K12.4	putative phosphatase	1.56	0.171	1.4	0.277	1.2	0.54	-1.42	0.078	0.69
1420029_at	Mcm3	Minichromosome maintenance deficient 3 (S. cerevisiae)	2.08	0.106	1.16	0.669	-1.08	0.65	1.81	0.073	0.99
1456954_at	Kcna6	potassium voltage-gated channel, shaker-related, subfamily, member 6	-1.76	0.001	1.36	0.326	2.24	0.223	1.52	0.133	0.84
1427993_at	Rufy2	RUN and FYVE domain-containing 2	1.67	0.396	1.1	0.875	1.4	0.516	-1.98	0.032	0.55

1450430_at	Mrc1	mannose receptor, C type 1	1.81	0.242	1.41	0.017	-1.05	0.779	1.34	0.405	0.88
1446828_at	---	---	1.96	0.278	-1.01	0.989	1.22	0.643	1.69	0.281	0.97
1460582_x_at	a	Nonagouti	1.34	0.736	1.9	0.101	-1.08	0.811	1.26	0.457	0.86
1418181_at	Ptp4a3	protein tyrosine phosphatase 4a3	1.88	0.029	1.31	0.09	-1.02	0.941	1.05	0.63	0.8
1421086_at	Per3	period homolog 3 (Drosophila)	1.43	0.139	1.85	0.325	-1.13	0.775	1.83	0.518	1
1443627_at	---	---	-1.53	0.138	2.26	0.161	1.25	0.546	1.06	0.82	0.76
1424945_at	Chrdl1	chordin-like 1	1.58	0.473	1.38	0.626	1.21	0.595	-1.4	0.419	0.69
1426989_at	Clstn3	calsyntenin 3	-1.69	0.052	1.61	0.125	1.97	0.146	1.01	0.978	0.72
1450081_x_at	Gpi1	glucose phosphate isomerase 1	1.24	0.155	1.11	0.063	1.82	0.01	-1.23	0.329	0.74
1437905_at	Txnl1	thioredoxin-like 1	1.9	0.241	-3.25	0.184	1.96	0.165	1.21	0.83	0.46
1440509_at	Sox30	SRY-box containing gene 30	1.13	0.894	1.73	0.352	1.31	0.528	-1.09	0.639	0.77
1452537_at	Igk-V1	immunoglobulin kappa chain variable 1 (V1)	1.55	0.373	1.42	0.456	1.21	0.623	-4.23	0.231	-0.02
1449288_at	Gdf3	growth differentiation factor 3	1.27	0.385	2.06	0.043	-1.18	0.55	4.12	0.169	1.57
1446635_at	D13Ertd476e	DNA segment, Chr 13, ERATO Doi 476, expressed	1.59	0.022	1.38	0.672	1.2	0.378	-2.29	0.263	0.47
1417455_at	Tgfb3	transforming growth factor, beta 3	1.43	0.228	2.05	0.288	-1.44	0.248	1.01	0.969	0.76
1439471_at	2610305J24Rik	RIKEN cDNA 2610305J24 gene	1.46	0.169	-1.97	0.336	2.21	0.181	1.18	0.424	0.72
1458098_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	1.87	0.219	1.63	0.364	-1.47	0.575	2.55	0.112	1.14
1438596_at	Hectd2	HECT domain containing 2	1.76	0.64	-2.4	0.056	2	0.253	1.48	0.538	0.71
1425847_a_at	B230120H23Rik	RIKEN cDNA B230120H23 gene	-1.4	0.368	2.26	0.04	1.2	0.659	1.52	0.463	0.9
1437752_at	Lin28	lin-28 homolog (C. elegans)	-3.06	0.299	2.01	0.189	1.84	0.494	2	0.506	0.7
1431371_at	9030411M13Rik	RIKEN cDNA 9030411M13 gene	1.24	0.542	1.24	0.452	1.7	0.369	-1.33	0.438	0.71
1455220_at	Frat2	frequently rearranged in advanced T-cell lymphomas 2	2.4	0.459	1.08	0.743	-1.45	0.353	1.56	0.187	0.9
1430340_at	4930431B11Rik	RIKEN cDNA 4930431B11 gene	1.47	0.608	2.05	0.214	-1.55	0.071	1.89	0.125	0.97
1456444_at	Fbxo41	F-box protein 41	-1.32	0.239	2.28	0.033	1.14	0.654	1.35	0.249	0.86
1417971_at	Nrm	nurim (nuclear envelope membrane protein)	1.38	0.411	1.37	0.494	1.42	0.075	-1.32	0.202	0.71
1421916_at	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	1.33	0.396	1.67	0.272	1.17	0.52	-1.12	0.719	0.76
1460253_at	Cmtm7	CKLF-like MARVEL transmembrane domain containing 7	1.09	0.825	1.35	0.25	1.74	0.048	-1.35	0.166	0.71
1431130_at	2010110P09Rik	RIKEN cDNA 2010110P09 gene	1.77	0.511	1.49	0.078	-1.09	0.74	1.76	0.117	0.98
1420671_x_at	Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	1.12	0.582	1.62	0.217	1.44	0.234	-2.53	0.07	0.41
1431978_at	8430437L04Rik	RIKEN cDNA 8430437L04 gene	2.78	0.305	-2.88	0.04	1.05	0.935	2.57	0.019	0.88
1441412_s_at	Trim45	tripartite motif-containing 45	1.32	0.446	1.68	0.294	1.18	0.145	-1.68	0.001	0.62
1456907_at	Cxcl9	chemokine (C-X-C motif) ligand 9	2.07	0.232	-1.05	0.908	1.16	0.771	1.01	0.966	0.8
1427348_at	Zc3h12a	zinc finger CCCH type containing 12A	1.44	0.096	1.38	0.052	1.36	0.305	-1.67	0.081	0.63
1453008_at	2300002D11Rik	RIKEN cDNA 2300002D11 gene	1.89	0.06	1.02	0.973	1.27	0.152	-1.53	0.347	0.66
1455525_at	Endogl1	endonuclease G-like 1	1.88	0.336	1.14	0.768	1.16	0.606	-1.3	0.183	0.72
1456792_at	Tbc1d2	TBC1 domain family, member 2	1.72	0.278	-1.47	0.429	1.78	0.173	1.12	0.658	0.79
1448466_at	Cdca5	cell division cycle associated 5	-1.67	0.281	2.14	0.066	1.44	0.492	3.55	0.194	1.37
1451359_at	Aytl2	acyltransferase like 2	1.16	0.511	2.3	0.09	-1.39	0.174	1.55	0.331	0.91
1432694_at	4921527H02Rik	RIKEN cDNA 4921527H02 gene	1.21	0.75	1.45	0.44	1.52	0.262	-1.6	0.25	0.65
1430480_at	Nub1	negative regulator of ubiquitin-like proteins 1	1	0.948	2.05	0.253	1.13	0.784	-1.42	0.445	0.69
1417633_at	Sod3	superoxide dismutase 3, extracellular	1.21	0.545	1.58	0.06	1.38	0.231	-1.15	0.771	0.76
1422395_at	V1rc8 /// V1rc22	vomeronasal 1 receptor, C8 /// vomeronasal 1 receptor, C22	1.61	0.188	2.06	0.399	-1.94	0.256	1.28	0.667	0.75
1448469_at	Nid1 /// LOC63077	nidogen 1 /// similar to Nidogen precursor (Entactin)	1.2	0.75	1.66	0.259	1.32	0.099	-1.14	0.665	0.76
1443073_at	LOC545681	hypothetical protein LOC545681	1.22	0.352	2	0.467	-1.03	0.926	3.1	0.043	1.32
1427739_a_at	Trp53	transformation related protein 53	1.17	0.342	1.12	0.474	1.9	0.047	-1.01	0.985	0.79
1434992_at	9130206N08Rik	RIKEN cDNA 9130206N08 gene	1.27	0.576	1.3	0.753	1.62	0.171	-1.07	0.381	0.78
1423778_at	Usp20	ubiquitin specific peptidase 20	1.53	0.344	1.07	0.91	1.58	0.431	-1.34	0.542	0.71
1442336_at	---	---	1.39	0.357	2.23	0.074	-1.77	0.3	1.08	0.868	0.73
1435053_s_at	Plekhh1	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1	1.55	0.172	1.92	0.216	-1.4	0.077	1.46	0.337	0.88
1448833_at	Foxm1	forkhead box M1	-1.5	0.211	2.32	0.373	1.2	0.299	1.89	0.236	0.98
1430297_a_at	2010301N04Rik	RIKEN cDNA 2010301N04 gene	-1.16	0.048	1.58	0.633	1.75	0.145	2.19	0.269	1.09
1426572_at	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	-1.05	0.545	2.13	0.016	1.11	0.113	1.11	0.53	0.82
1460630_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	1.22	0.612	1.69	0.496	1.29	0.306	-1.39	0.406	0.7

1449888_at	Epas1	endothelial PAS domain protein 1	1.15	0.749	1.28	0.518	1.76	0.159	-1.33	0.512	0.72
1428184_at	3110035E14Rik	RIKEN cDNA 3110035E14 gene	1.78	0.324	1.24	0.6	1.17	0.388	-1.25	0.749	0.74
1449976_a_at	Gpr35	G protein-coupled receptor 35	1.27	0.732	1.47	0.325	1.45	0.288	-1.42	0.041	0.69
1433282_at	4930529H12Rik	RIKEN cDNA 4930529H12 gene	1.94	0.508	1.01	0.992	1.25	0.287	-1.38	0.27	0.7
1436366_at	Ppp1r15b	protein phosphatase 1, regulatory (inhibitor) subunit 15b	1.77	0.153	-1.6	0.22	1.79	0.169	1.32	0.561	0.82
1423017_a_at	Il1rn	interleukin 1 receptor antagonist	-1.52	0.547	1.49	0.142	2.05	0.303	1.07	0.907	0.77
1454768_at	Kcnf1	potassium voltage-gated channel, subfamily F, member 1	1.35	0.698	1.53	0.475	1.31	0.572	-1.07	0.917	0.78
1420234_at	---	---	-2.26	0.432	2.31	0.194	1.44	0.612	1.04	0.702	0.63
1434069_at	Setd6	SET domain containing 6	1.02	0.945	1.63	0.064	1.55	0.004	-1.26	0.328	0.73
1425811_a_at	Csrp1	cysteine and glycine-rich protein 1	1.23	0.185	1.91	0.047	1.05	0.729	-1.22	0.14	0.74
1430280_at	1810062G17Rik	RIKEN cDNA 1810062G17 gene	2.03	0.445	1.36	0.383	-1.23	0.305	1.3	0.513	0.86
1445587_at	---	---	1.96	0.496	1.03	0.965	1.21	0.596	-1.36	0.653	0.71
1421884_at	Sos1	Son of sevenless homolog 1 (Drosophila)	-1.11	0.711	1.01	0.966	2.29	0.058	1.02	0.928	0.8
1446728_at	D3Ertd797e	DNA segment, Chr 3, ERATO Doi 797, expressed	-1.27	0.699	2.32	0.189	1.09	0.875	1.97	0.24	1.03
1460566_at	Mtap1a	microtubule-associated protein 1 A	2.17	0.269	-1.35	0.498	1.28	0.282	1.27	0.539	0.84
1452459_at	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	1.86	0.331	1.35	0.42	-1.02	0.961	2.62	0.256	1.2
1434679_at	Cspg3	chondroitin sulfate proteoglycan 3	1.47	0.471	-1.1	0.813	1.82	0.08	1.1	0.389	0.82
1441570_at	2810021G02Rik	RIKEN cDNA 2810021G02 gene	1.11	0.776	2.04	0.034	1.04	0.853	-1.32	0.577	0.72
1453090_x_at	Obox1 /// LOC6664	oocyte specific homeobox 1 /// similar to oocyte specific homeobox 2	1.52	0.02	1.37	0.51	1.31	0.475	-1.34	0.636	0.72
1453505_a_at	Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	1.24	0.622	2.26	0.22	-1.43	0.572	2.07	0.351	1.03
1424890_at	Bnc1	basonuclin 1	1.08	0.905	-1.55	0.519	2.47	0.47	1.14	0.314	0.79
1421486_at	Egr3	early growth response 3	1.1	0.872	1.52	0.082	1.58	0.254	-1.1	0.867	0.77
1415854_at	Kitl	kit ligand	1.57	0.137	1.9	0.437	-1.37	0.268	1.23	0.179	0.83
1440047_at	Socs1	suppressor of cytokine signaling 1	1.68	0.403	1.3	0.571	1.23	0.253	-1.36	0.249	0.71
1457424_at	Eya1	eyes absent 1 homolog (Drosophila)	1.83	0.472	1.52	0.511	-1.17	0.513	1	0.989	0.8
1422512_a_at	Ogfr	opioid growth factor receptor	1.49	0.402	1.15	0.737	1.56	0.432	-1.06	0.933	0.79
1441458_at	Rasa4	RAS p21 protein activator 4	1.22	0.609	1.93	0.199	1.06	0.502	-1.64	0.164	0.64
1436694_s_at	Neurod4	neurogenic differentiation 4	1.28	0.688	1.78	0.385	1.15	0.786	-1.59	0.416	0.65
1437831_at	Zcchc4	zinc finger, CCHC domain containing 4	1.39	0.511	1.98	0.133	-1.2	0.804	1.64	0.242	0.95
1454359_at	9530023I19Rik	RIKEN cDNA 9530023I19 gene	1.13	0.519	1.84	0.443	1.24	0.667	-1.69	0.507	0.63
1422286_a_at	Tgif	TG interacting factor	1.35	0.206	1.04	0.751	1.82	0.051	-1.54	0.167	0.67
1422024_at	Fli1	Friend leukemia integration 1	1.83	0.085	1.17	0.505	1.21	0.673	-1.53	0.442	0.67
1460598_at	Il28ra	interleukin 28 receptor alpha	1.22	0.117	2.05	0.031	-1.07	0.613	1.11	0.696	0.83
1429858_at	1700011E24Rik	RIKEN cDNA 1700011E24 gene	1.92	0.513	-1.09	0.897	1.37	0.384	2.13	0.338	1.08
1437555_at	E130309B19Rik	RIKEN cDNA E130309B19 gene	1.49	0.613	1.42	0.573	1.3	0.157	-1.75	0.414	0.61
1439827_at	Adamts12	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	1.03	0.924	2.49	0.009	-1.47	0.12	1.44	0.135	0.87
1439853_at	B4galnt2	beta-1,4-N-acetyl-galactosaminyl transferase 2	2.57	0.304	1.09	0.808	-1.84	0.229	1.29	0.376	0.78
1420240_at	---	---	1.57	0.363	1.56	0.242	1.08	0.829	-1.19	0.831	0.75
1452525_a_at	Nf1	neurofibromatosis 1	1.24	0.785	2.16	0.033	-1.24	0.48	1.34	0.443	0.87
1432605_at	---	---	2.56	0.451	1.17	0.623	-2.09	0.242	1.69	0.208	0.83
1430987_s_at	Wbp11	WW domain binding protein 11	1.47	0.421	-1.08	0.784	1.81	0.366	1.43	0.336	0.91
1438953_at	---	---	1.81	0.037	-1.12	0.674	1.51	0.096	1.28	0.093	0.87
1449101_at	Ebf2	early B-cell factor 2	1.2	0.357	1.92	0.206	1.08	0.673	-1.14	0.79	0.77
1425681_a_at	Prnd	prion protein dublet	1.99	0.153	1.03	0.955	1.19	0.625	-1.48	0.549	0.68
1430952_at	3110039C02Rik	RIKEN cDNA 3110039C02 gene	-1.07	0.684	1.16	0.831	2.11	0.219	1.8	0.46	1
1422812_at	Cxcr6	chemokine (C-X-C motif) receptor 6	1.43	0.609	1.24	0.467	1.54	0.161	-1.32	0.607	0.72
1423714_at	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	-1.26	0.669	2.04	0.101	1.37	0.149	3.56	0.193	1.43
1429028_at	Dock11	dedicator of cytokinesis 11	1.29	0.208	1.84	0.035	1.09	0.488	-1.81	0.208	0.6
1456944_at	Kcnc1	potassium voltage gated channel, Shaw-related subfamily, member 1	1.73	0.521	1.38	0.552	1.1	0.785	-1.04	0.891	0.79
1450329_a_at	Arr3	arrestin 3, retinal	1.49	0.09	-1.17	0.769	1.87	0.05	1.14	0.852	0.83
1453211_at	Ccdc89	coiled-coil domain containing 89	2.4	0.097	-1.48	0.365	1.14	0.573	1.16	0.809	0.8
1429696_at	Gpr123	G protein-coupled receptor 123	1.4	0.587	-2.24	0.067	2.37	0.149	1.26	0.437	0.7
1436216_s_at	2610204M08Rik	RIKEN cDNA 2610204M08 gene	1.13	0.639	1.6	0.028	1.48	0.102	-1.07	0.805	0.78

1459524_at	Mcc	mutated in colorectal cancers	-1.08	0.647	2.28	0.201	1.01	0.99	1.65	0.448	0.96
1436953_at	Waspip	Wiskott-Aldrich syndrome protein interacting protein	1.03	0.795	1.65	0.049	1.54	0.02	-1.81	0.041	0.6
1433259_at	4930518C04Rik	RIKEN cDNA 4930518C04 gene	-1.7	0.373	2.44	0.238	1.19	0.552	1.64	0.103	0.89
1450123_at	Ryr2	ryanodine receptor 2, cardiac	1.68	0.314	1.36	0.618	1.17	0.554	-1.18	0.859	0.76
1440546_at	9630002D21Rik	RIKEN cDNA 9630002D21 gene	1.44	0.578	1.02	0.986	1.76	0.27	-1.63	0.494	0.65
1422400_a_at	Hemt1	hematopoietic cell transcript 1	1.16	0.019	1.79	0.337	1.27	0.464	-1.92	0.2	0.57
1446393_at	D5Ertd159e	DNA segment, Chr 5, ERATO Doi 159, expressed	1.23	0.197	1.14	0.803	1.85	0.301	-1.56	0.285	0.66
1421811_at	Thbs1 /// LOC6404	thrombospondin 1 /// similar to thrombospondin 1	1.03	0.628	2.33	0.251	-1.17	0.791	1.74	0.507	0.98
1451683_x_at	LOC547343	similar to H-2 class I histocompatibility antigen, L-D alpha chain precursor	1.24	0.291	1.25	0.207	1.73	0.02	-1.36	0.23	0.71
1448182_a_at	Cd24a	CD24a antigen	1.05	0.739	2.27	0.292	-1.12	0.44	1.29	0.304	0.87
1422415_at	Ang2	angiogenin, ribonuclease A family, member 2	-1.25	0.568	1.92	0.085	1.5	0.051	1.8	0.304	0.99
1423006_at	Pim1	proviral integration site 1	1.64	0.32	-1.09	0.776	1.66	0.361	3.04	0.293	1.31
1450367_at	---	---	1.08	0.921	1.94	0.038	1.2	0.697	-2.29	0.267	0.48
1454261_at	E130304I02Rik	RIKEN cDNA E130304I02 gene	1.18	0.701	1.93	0.065	1.11	0.754	-1.13	0.336	0.77
1457511_at	Rgs12	regulator of G-protein signaling 12	1.12	0.798	2.46	0.176	-1.56	0.09	2.16	0.209	1.04
1420250_at	---	---	2.1	0.527	1.2	0.757	-1.08	0.798	1.06	0.802	0.82
1421365_at	Fst	follistatin	1.45	0.492	1.98	0.088	-1.27	0.403	1.03	0.959	0.8
1434881_s_at	Kctd12	potassium channel tetramerisation domain containing 12	1.16	0.543	1.8	0.001	1.27	0.096	-1.32	0.409	0.73
1425164_a_at	Phkg1	phosphorylase kinase gamma 1	1.89	0.053	1.01	0.982	1.32	0.588	-1	0.986	0.8
1445554_at	---	---	1.16	0.204	-1.16	0.686	2.2	0.015	1.05	0.948	0.81
1422115_a_at	Flt3l	FMS-like tyrosine kinase 3 ligand	2.02	0.349	1.2	0.367	1	0.98	-1.56	0.264	0.67
1430268_at	9630005C17Rik	RIKEN cDNA 9630005C17 gene	2.46	0.433	1.04	0.945	-1.38	0.396	1.06	0.927	0.79
1455747_at	Ggtla1	gamma-glutamyltransferase-like activity 1	1.84	0.023	1.17	0.797	1.21	0.614	-1.24	0.62	0.74
1435654_at	G630039H03Rik	RIKEN cDNA G630039H03 gene	1.45	0.236	-1.04	0.899	1.81	0.383	1.49	0.109	0.93
1427514_at	LOC624295	hypothetical protein LOC624295	1.23	0.757	1.51	0.198	1.48	0.384	-1.63	0.546	0.65
1454437_at	---	---	1.69	0.432	-1.23	0.764	1.72	0.288	2.94	0.006	1.28
1449613_at	---	---	-1.34	0.777	2.12	0.202	1.36	0.458	1.12	0.871	0.81
1437937_at	Ccbp2	chemokine binding protein 2	2.09	0.114	1.12	0.592	1.01	0.955	-1.09	0.782	0.78
1421001_a_at	Car6	carbonic anhydrase 6	-1.2	0.718	2.2	0.014	1.19	0.376	1.25	0.158	0.86
1426149_at	Spi15	serine protease inhibitor 15	-1.25	0.455	2.28	0.077	1.14	0.696	1.01	0.963	0.79
1439151_at	Msrb3	methionine sulfoxide reductase B3	1.46	0.254	1.19	0.556	1.58	0.518	-1.11	0.782	0.78
1416969_at	Gtse1	G two S phase expressed protein 1	1.56	0.552	1.96	0.281	-1.43	0.184	3.17	0.186	1.32
1459750_s_at	Gpr123	G protein-coupled receptor 123	1.69	0.14	-1.11	0.835	1.63	0.272	1.13	0.347	0.84
1432072_at	Kif2a	kinesin family member 2A	2.51	0.064	-1.84	0.195	1.18	0.658	1.46	0.06	0.83
1443503_at	Ihpk3	inositol hexaphosphate kinase 3	-2.12	0.365	2.69	0.131	1.07	0.889	1.48	0.563	0.78
1450487_at	Vsx1	visual system homeobox 1 homolog (zebrafish)	1.27	0.586	2.28	0.183	-1.48	0.5	1.58	0.12	0.91
1427086_at	Slit3	slit homolog 3 (Drosophila)	1.92	0.186	1.38	0.201	-1.08	0.767	1.04	0.763	0.82
1435959_at	Arhgap15	Rho GTPase activating protein 15	1.27	0.315	1.61	0.064	1.35	0.249	-1.89	0.069	0.58
1454427_at	---	---	2.15	0.43	1.22	0.749	-1.16	0.419	1.5	0.566	0.93
1442601_at	Gmeb1	glucocorticoid modulatory element binding protein 1	1.71	0.047	1.19	0.744	1.33	0.278	-1.08	0.775	0.79
1416666_at	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	2.29	0.196	1.02	0.911	-1.09	0.601	1.69	0.343	0.98
1450798_at	Tnxb	tenascin XB	1.28	0.31	1.57	0.098	1.38	0.624	-1.44	0.303	0.7
1434673_at	Gpr22	G protein-coupled receptor 22	2.4	0.19	1.07	0.924	-1.3	0.484	1.4	0.109	0.89
1424077_at	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	1.22	0.063	2.19	0.01	-1.21	0.464	1.61	0.093	0.95
1446083_at	Hnrpd	Heterogeneous nuclear ribonucleoprotein D	-1.93	0.226	2.4	0.133	1.32	0.412	1.26	0.627	0.76
1452599_s_at	AI413582	expressed sequence AI413582	1.15	0.282	1.99	0.01	1.09	0.614	-1.66	0.065	0.64
1445497_at	Car10	Carbonic anhydrase 10	1.56	0.082	1.28	0.506	1.4	0.035	-1.15	0.458	0.77
1452789_at	Snn	stannin	1.06	0.438	1.79	0.099	1.38	0.357	-1.91	0.215	0.58
1428150_at	Coro7	coronin 7	1.1	0.785	1.41	0.316	1.72	0.06	-1.5	0.457	0.68
1451260_at	Aldh1b1	aldehyde dehydrogenase 1 family, member B1	1.37	0.072	1.13	0.401	1.74	0.072	-1.57	0.089	0.67
1431133_at	Arhgap18	Rho GTPase activating protein 18	1.03	0.954	-1.97	0.292	2.7	0.197	1.57	0.27	0.83
1434981_at	E130303B06Rik	RIKEN cDNA E130303B06 gene	-1.23	0.471	2.22	0.041	1.21	0.363	1.61	0.327	0.95
1441786_at	---	PREDICTED: Mus musculus similar to HYPOTHETICAL PROTEIN ORF-1137 (L	2.16	0.428	-1.58	0.147	1.44	0.125	1.46	0.437	0.87

1437436_s_at	Gprk6	G protein-coupled receptor kinase 6	1.18	0.489	1.28	0.023	1.78	0.132	-1.55	0.073	0.67
1460351_at	S100a11	S100 calcium binding protein A11 (calizzarin)	1.07	0.646	2.13	0.048	1.04	0.586	-1.05	0.688	0.8
1421123_at	Cdk5r1	cyclin-dependent kinase 5, regulatory subunit (p35) 1	-1.27	0.678	2.18	0.232	1.27	0.538	1.12	0.82	0.83
1454361_at	9230106L01Rik	RIKEN cDNA 9230106L01 gene	2.05	0.122	1.03	0.947	1.17	0.768	-3.14	0.16	0.27
1417939_at	Rad51ap1	RAD51 associated protein 1	-1.81	0.33	1.32	0.137	2.37	0.002	5.14	0.248	1.76
1451353_at	Tm6sf1	transmembrane 6 superfamily member 1	1.39	0.19	1.59	0.055	1.27	0.241	-1.88	0.077	0.59
1430698_a_at	D14Ertd581e	DNA segment, Chr 14, ERATO Doi 581, expressed	1.68	0.029	1.14	0.708	1.42	0.476	-1.67	0.192	0.64
1424940_s_at	BC022687	cDNA sequence BC022687	-1.02	0.832	1.93	0.142	1.33	0.147	1.3	0.222	0.88
1447368_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	1.47	0.54	1.82	0.374	-1.05	0.785	1.32	0.361	0.89
1449308_at	C6	complement component 6	1.92	0.116	1.3	0.359	1.02	0.736	-1.03	0.953	0.8
1432960_at	4930447I22Rik	RIKEN cDNA 4930447I22 gene	1.51	0.347	1.64	0.105	1.09	0.72	-1.03	0.949	0.8
1450533_a_at	Plagl1	pleiomorphic adenoma gene-like 1	-1.42	0.025	1.84	0.452	1.71	0.365	1.1	0.586	0.81
1432287_a_at	Sntg1	syntrophin, gamma 1	1.1	0.589	2.14	0.037	1.02	0.953	-1.2	0.762	0.76
1439636_at	Nalp9c	NACHT, LRR and PYD containing protein 9c	1.86	0.553	1.26	0.703	1.13	0.831	-2.4	0.377	0.46
1460114_at	1700123M08Rik	RIKEN cDNA 1700123M08 gene	1.88	0.508	1.61	0.183	-1.32	0.508	1.98	0.392	1.04
1452087_at	Epsti1	epithelial stromal interaction 1 (breast)	1.43	0.045	1.31	0.178	1.51	0.113	-1.64	0.286	0.65
1456222_at	Btbd1	BTB (POZ) domain containing 1	1.73	0.561	1.72	0.174	-1.25	0.663	1.66	0.224	0.97
1417492_at	Ctsb	cathepsin B	1.1	0.259	1.64	0.013	1.51	0.046	-1	0.95	0.81
1448260_at	Uchl1	ubiquitin carboxy-terminal hydrolase L1	1.37	0.473	1.08	0.888	1.8	0.006	-1.3	0.245	0.74
1435611_x_at	Ela3	elastase 3, pancreatic	1.4	0.566	1.6	0.455	1.25	0.458	-1.15	0.693	0.77
1431794_at	4932434E15Rik	RIKEN cDNA 4932434E15 gene	1.85	0.218	1.36	0.686	1.04	0.84	-1.47	0.639	0.69
1459779_s_at	Setd8	SET domain containing (lysine methyltransferase) 8	-1.04	0.923	2.02	0.107	1.27	0.497	2.19	0.041	1.11
1432886_at	5730488B01Rik	RIKEN cDNA 5730488B01 gene	-1.08	0.899	1.5	0.359	1.82	0.154	1	0.998	0.81
1453572_a_at	Plp2	proteolipid protein 2	1.19	0.301	1.85	0.05	1.21	0.266	-1.03	0.852	0.81
1439773_at	Ly6e	lymphocyte antigen 6 complex, locus E	1.27	0.337	1.95	0.094	1.03	0.918	-2.09	0.083	0.54
1421386_at	Ankrd6	ankyrin repeat domain 6	2.06	0.059	1.12	0.855	1.07	0.864	-2.19	0.026	0.52
1424265_at	Npl	N-acetylneuraminate pyruvate lyase	1.03	0.902	1.67	0.211	1.55	0.033	-1.37	0.276	0.72
1435327_at	AW112037	expressed sequence AW112037	1.23	0.05	1.87	0.111	1.16	0.193	-1.59	0.072	0.67
1451171_at	2310008H04Rik	RIKEN cDNA 2310008H04 gene	1.92	0.047	1.38	0.042	-1.04	0.628	1.49	0.263	0.94
1450718_at	Sh2b2	SH2B adaptor protein 2	1.2	0.748	1.54	0.229	1.52	0.071	-1.3	0.366	0.74
1429687_at	4930503B16Rik	RIKEN cDNA 4930503B16 gene	1.06	0.956	1.2	0.816	2	0.297	-3.46	0.205	0.2
1419284_at	Cyhr1	cysteine and histidine rich 1	1.74	0.41	1.4	0.584	1.12	0.724	-1.8	0.461	0.61
1423986_a_at	Scotin	scotin gene	1.15	0.399	1.75	0.138	1.36	0.074	-2.16	0.082	0.52
1449250_at	Prcc	papillary renal cell carcinoma (translocation-associated)	2.17	0.246	1.25	0.699	-1.2	0.516	1.71	0.199	0.98
1426056_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	1.96	0.179	-1.08	0.908	1.37	0.094	2.74	0.343	1.25
1459458_at	D9Ertd338e	DNA segment, Chr 9, ERATO Doi 338, expressed	1.48	0.445	1.73	0.395	1.04	0.792	-1.64	0.399	0.65
1424885_at	Klhdc8a	kelch domain containing 8A	1.06	0.863	1.78	0.278	1.42	0.098	-1.74	0.072	0.63
1445649_x_at	Zfp142	zinc finger protein 142	1.1	0.901	2.39	0.056	-1.29	0.145	1.78	0.213	0.99
1429577_at	Iqcf4	IQ motif containing F4	1.63	0.243	1.38	0.53	1.25	0.514	-2.19	0.182	0.52
1450617_at	---	---	-1.22	0.78	1.55	0.53	1.88	0.311	3.25	0.004	1.37
1429622_at	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	1.39	0.053	1.06	0.909	1.82	0.092	-1.19	0.147	0.77
1420948_s_at	4833408C14Rik	RIKEN cDNA 4833408C14 gene	1.54	0.335	1.26	0.59	1.46	0.454	-1	0.992	0.81
1431080_at	1700021K10Rik	RIKEN cDNA 1700021K10 gene	2.04	0.376	1.22	0.717	-1.01	0.983	1.26	0.1	0.88
1425733_a_at	Eps8	epidermal growth factor receptor pathway substrate 8	-1.02	0.731	1.92	0.139	1.36	0.182	1	0.994	0.81
1454478_at	3100002H20Rik	RIKEN cDNA 3100002H20 gene	-1.09	0.838	1.33	0.11	2.02	0.169	1.39	0.486	0.91
1451206_s_at	Pscdbp	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	1.09	0.067	2.12	0.088	1.05	0.796	-1.99	0.067	0.57
1445477_at	---	Transcribed locus	1.69	0.406	1.1	0.785	1.47	0.145	-1.53	0.306	0.68
1426324_at	H2-D1	histocompatibility 2, D region locus 1	1.36	0.295	1.41	0.051	1.49	0.151	-1.47	0.23	0.7
1431464_a_at	Pmm2	phosphomannomutase 2	1.42	0.488	1.22	0.668	1.63	0.326	-1.01	0.993	0.81
1441954_s_at	H1fnt	H1 histone family, member N, testis-specific	1.76	0.594	1.93	0.248	-1.76	0.091	2.28	0.081	1.05
1421098_at	AI586015	expressed sequence AI586015	1.22	0.589	1.28	0.107	1.76	0.105	-2.01	0.086	0.56
1447181_s_at	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	-1.11	0.845	1.28	0.401	2.08	0.138	1.14	0.702	0.85
1441322_at	Scap1	src family associated phosphoprotein 1	1.19	0.776	1.46	0.202	1.62	0.357	-2.95	0.005	0.33

1455937_at	Lrrtm4	leucine rich repeat transmembrane neuronal 4	2.06	0.437	1.39	0.643	-1.23	0.677	1.93	0.438	1.04
1441864_x_at	Cenpa	centromere protein A	1.92	0.166	1.41	0.245	-1.07	0.889	1.29	0.331	0.89
1432803_at	A230101C19Rik	RIKEN cDNA A230101C19 gene	1.86	0.388	1.24	0.545	1.17	0.587	-1.16	0.447	0.78
1416016_at	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.55	0.087	1.24	0.025	1.47	0.247	-1.43	0.287	0.71
1456228_x_at	Mbp	myelin basic protein	-1.4	0.104	2.15	0.272	1.4	0.423	1.52	0.098	0.92
1425963_at	Cabp7	calcium binding protein 7	1.35	0.639	1.71	0.415	1.21	0.659	-1.2	0.404	0.77
1456994_at	Rassf1	Ras association (RalGDS/AF-6) domain family 1	2.08	0.165	1.05	0.915	1.14	0.807	-1.29	0.462	0.75
1451484_a_at	Syn1	synapsin I	-1.58	0.488	1.78	0.343	1.86	0.028	1.49	0.499	0.89
1451965_at	---	Anti-human CD37 antibody WR17 kappa light chain variable region	1.66	0.075	1.08	0.773	1.52	0.141	-1.56	0.438	0.68
1422086_at	Tbx19	T-box 19	2	0.257	1.84	0.17	-2.31	0.043	1.44	0.224	0.74
1455954_x_at	Gpaa1	GPI anchor attachment protein 1	-1.05	0.857	1.67	0.012	1.65	0.131	1.28	0.422	0.89
1444949_at	---	---	-1.22	0.67	2.09	0.347	1.36	0.383	1.85	0.118	1.02
1433087_at	5330430C04Rik	RIKEN cDNA 5330430C04 gene	2.18	0.461	1.22	0.25	-1.14	0.281	1.11	0.783	0.84
1439547_at	A930007A09Rik	RIKEN cDNA A930007A09 gene	2.29	0.093	-1.43	0.55	1.29	0.503	3.16	0.003	1.33
1431522_at	A930001A20Rik	RIKEN cDNA A930001A20 gene	-2.21	0.444	1.97	0.315	1.85	0.261	1.37	0.001	0.74
1441387_at	BC030343	cDNA sequence BC030343	1.3	0.728	1	0.994	1.97	0.063	-3.25	0.012	0.25
1419193_a_at	Gmfg	glia maturation factor, gamma	1.08	0.711	1.44	0.234	1.75	0.226	-2.73	0.034	0.38
1450672_a_at	Trex1	three prime repair exonuclease 1	1.71	0.031	1.13	0.693	1.44	0.12	-1.24	0.525	0.76
1448619_at	Dhcr7	7-dehydrocholesterol reductase	1.26	0.352	1.87	0.008	1.15	0.277	-1.35	0.316	0.73
1434914_at	Rab6b	RAB6B, member RAS oncogene family	1.01	0.96	2.16	0.14	1.11	0.631	-1.29	0.541	0.75
1438211_s_at	Dbp	D site albumin promoter binding protein	1.46	0.683	1.13	0.911	1.69	0.59	-1.08	0.902	0.8
1421028_a_at	Mef2c	myocyte enhancer factor 2C	2.01	0.194	1.14	0.759	1.13	0.676	-1.87	0.197	0.6
1447311_at	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	1.25	0.444	-1.14	0.285	2.16	0.009	1.36	0.282	0.9
1438954_x_at	---	---	2.12	0.031	-1.19	0.439	1.31	0.339	1.13	0.567	0.84
1419718_at	4921530L21Rik	RIKEN cDNA 4921530L21 gene	1.65	0.485	-1.47	0.415	1.95	0.129	1.87	0.114	1
1440938_at	Treml2	triggering receptor expressed on myeloid cells-like 2	1.02	0.966	1.37	0.589	1.89	0.217	-2.45	0.017	0.46
1445286_at	6430701C03Rik	RIKEN cDNA 6430701C03 gene	2.14	0.127	1.04	0.956	1.1	0.848	-1.01	0.984	0.82
1428016_a_at	Rasip1	Ras interacting protein 1	1.41	0.319	1.26	0.452	1.62	0.05	-1.04	0.857	0.81
1422962_a_at	Psmb8	proteosome (prosome, macropain) subunit, beta type 8 (large multifunctional pep	1.53	0.079	1.21	0.128	1.53	0.201	-1.61	0.24	0.67
1448449_at	Ripk3	receptor-interacting serine-threonine kinase 3	1.39	0.393	1.72	0.117	1.17	0.405	-1.27	0.357	0.75
1442594_at	Ttk	Ttk protein kinase	2.47	0.098	1.09	0.894	-1.39	0.47	1.41	0.233	0.89
1416587_a_at	Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1	1.07	0.581	1.17	0.253	2.05	0.268	-1.17	0.47	0.78
1442974_at	D6Ertd160e	DNA segment, Chr 6, ERATO Doi 160, expressed	1.36	0.551	1.48	0.518	1.44	0.324	-1.91	0.061	0.59
1437866_at	Dusp18	dual specificity phosphatase 18	-1.31	0.345	2.51	0.237	1.01	0.948	3.03	0.325	1.31
1451620_at	C1ql3	C1q-like 3	1.15	0.741	2.5	0.018	-1.6	0.161	1.24	0.697	0.82
1427727_x_at	Psg19	pregnancy specific glycoprotein 19	2.16	0.08	-1.62	0.382	1.5	0.455	1.36	0.565	0.85
1422095_a_at	Tyki	thymidylate kinase family LPS-inducible member	1.46	0.22	-1.19	0.624	1.98	0.133	1.95	0.356	1.05
1435706_at	Btbd9	BTB (POZ) domain containing 9	1.36	0.263	1.39	0.357	1.53	0.181	-1.44	0.487	0.71
1427524_a_at	4930548G07Rik	RIKEN cDNA 4930548G07 gene	2.02	0.107	1.22	0.613	1.04	0.913	-1.09	0.583	0.8
1439745_at	Cacng7	calcium channel, voltage-dependent, gamma subunit 7	-1.22	0.44	2.37	0.254	1.1	0.812	1.23	0.404	0.87
1447981_at	C78441	expressed sequence C78441	2.03	0.125	-1.04	0.952	1.3	0.62	1.17	0.865	0.86
1444249_at	---	Transcribed locus	2.17	0.403	1.15	0.878	-1.03	0.924	1.19	0.809	0.87
1426186_a_at	Fgf5	fibroblast growth factor 5	1.24	0.327	2.31	0.347	-1.35	0.55	2.32	0.083	1.13
1457242_at	Ubox5	U box domain containing 5	1.06	0.94	1.03	0.928	2.19	0.093	-1.75	0.186	0.64
1425679_a_at	Mapk8ip1	mitogen activated protein kinase 8 interacting protein 1	-1.06	0.873	1.54	0.385	1.8	0.029	1.17	0.573	0.86
1437386_at	Lrrn6a	leucine rich repeat neuronal 6A	1.48	0.441	1.37	0.457	1.44	0.447	-1.13	0.748	0.79
1427180_at	Slc27a3	solute carrier family 27 (fatty acid transporter), member 3	2.43	0.199	1.04	0.837	-1.22	0.14	1.02	0.967	0.82
1439143_at	9.33E+12	hypothetical protein 9330167E06	1.98	0.185	1.52	0.458	-1.25	0.702	1.01	0.986	0.81
1446787_at	Commd1	COMM domain containing 1	1.71	0.394	1.8	0.308	-1.29	0.553	2.09	0.046	1.08
1432807_at	5830426K05Rik	RIKEN cDNA 5830426K05 gene	1.46	0.511	2.3	0.381	-1.91	0.046	1.78	0.311	0.91
1421738_at	Gabra2	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 2	1.28	0.779	2.15	0.165	-1.17	0.683	1.19	0.52	0.86
1422382_at	Olfr16	olfactory receptor 16	1.04	0.936	1.33	0.213	1.92	0.157	-1.21	0.074	0.77
1460686_at	Cntd1	cyclin N-terminal domain containing 1	1.1	0.675	2.25	0.31	-1.07	0.91	1.9	0.145	1.05

1432027_a_at	Tbc1d14	TBC1 domain family, member 14	1.1	0.897	1.85	0.348	1.34	0.579	-1.21	0.675	0.77
1440470_at	---	Transcribed locus	1.09	0.066	2.33	0.018	-1.15	0.263	1.93	0.301	1.05
1418554_at	Admr	adrenomedullin receptor	1.7	0.35	1.31	0.217	1.29	0.25	-1.11	0.624	0.8
1426677_at	Flna	filamin, alpha	1.31	0.012	1.68	0.009	1.3	0.141	-1.23	0.408	0.77
1456275_at	Mrpl21 /// LOC3849	mitochondrial ribosomal protein L21 /// hypothetical gene supported by AK00328	1.58	0.459	1.68	0.441	1.03	0.956	-2.06	0.297	0.56
1434322_at	A930021H16Rik	RIKEN cDNA A930021H16 gene	1.76	0.16	1.56	0.196	-1.02	0.759	3.61	0.193	1.48
1431955_at	4930453H23Rik	RIKEN cDNA 4930453H23 gene	-1.54	0.598	2.39	0.11	1.26	0.44	2.3	0.246	1.1
1451246_s_at	Aurkb	aurora kinase B	-1.06	0.939	1.77	0.188	1.58	0.379	3.62	0.193	1.48
1455332_x_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	-1.08	0.264	1.46	0.126	1.91	0.05	1.16	0.775	0.86
1430462_at	2310002L09Rik	RIKEN cDNA 2310002L09 gene	1.27	0.079	1.33	0.726	1.71	0.138	-1.62	0.305	0.67
1444274_at	---	---	1.06	0.861	2.71	0.45	-1.9	0.117	1	0.993	0.72
1421184_a_at	Mettl7a /// Ubie /// L	methyltransferase like 7A /// UbiE-YGHL1 fusion protein /// UbiE-YGHL1 fusion pr	1.12	0.449	-1.63	0.41	2.57	0.304	2.31	0.223	1.09
1438885_at	BB182387	expressed sequence BB182387	-1.13	0.874	2.18	0.213	1.24	0.491	1.07	0.862	0.84
1446045_at	AU024581	expressed sequence AU024581	2.1	0.213	-1.03	0.895	1.24	0.554	2.19	0.17	1.12
1458733_at	Gpr149	G protein-coupled receptor 149	-1.35	0.474	1.97	0.22	1.59	0.34	1.56	0.252	0.94
1416811_s_at	Ctla2a /// Ctla2b	cytotoxic T lymphocyte-associated protein 2 alpha /// cytotoxic T lymphocyte-assc	1.29	0.407	2.1	0.008	-1.1	0.413	1.01	0.976	0.83
1433827_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	1.18	0.167	2.25	0.034	-1.15	0.491	1.36	0.313	0.91
1432092_a_at	Gulp1	GULP, engulfment adaptor PTB domain containing 1	1.7	0.601	1.37	0.263	1.24	0.802	-1.9	0.241	0.6
1439264_x_at	Lasp1	LIM and SH3 protein 1	1.01	0.935	1.56	0.078	1.73	0.115	-1.37	0.541	0.73
1417813_at	Ikbke	inhibitor of kappaB kinase epsilon	1.61	0.299	1.64	0.158	1.05	0.764	-2.1	0.019	0.55
1433130_at	8430418B16Rik	RIKEN cDNA 8430418B16 gene	1.47	0.311	-1.24	0.462	2.03	0.062	1.12	0.436	0.84
1451850_at	Prlr	prolactin receptor	1.61	0.593	-1.46	0.365	2.01	0.305	1.02	0.955	0.8
1430128_a_at	Reep6	receptor accessory protein 6	1.75	0.03	-1.24	0.419	1.75	0.158	8.56	0.211	2.71
1420700_s_at	Folr4	folate receptor 4 (delta)	1.74	0.548	1.4	0.405	1.17	0.566	-1.21	0.666	0.77
1435495_at	Adora1	adenosine A1 receptor	1.34	0.009	1.93	0.003	1.04	0.866	-1.65	0.362	0.66
1419673_at	Spock1 /// LOC671	sparc/osteonectin, cwcv and kazal-like domains proteoglycan 1 /// similar to sparc	1.72	0.411	1.48	0.561	1.11	0.592	-2.59	0.013	0.43
1436847_s_at	Cdca8	cell division cycle associated 8	-1.37	0.616	1.49	0.122	2.09	0.024	3.25	0.171	1.37
1434726_at	Tmem146	transmembrane protein 146	1.33	0.574	-1.01	0.982	1.98	0.134	1.1	0.417	0.85
1437918_at	4930539E08Rik	RIKEN cDNA 4930539E08 gene	2.67	0.043	-2.03	0.146	1.15	0.803	1.66	0.138	0.86
1450214_at	Adora2b	adenosine A2b receptor	1.2	0.059	1.91	0.018	1.21	0.274	-1.13	0.65	0.8
1438822_at	Dmt2	dorso-medial telencephalon gene 2	1.41	0.395	1.9	0.239	1.01	0.989	-1.1	0.879	0.8
1431196_at	Atp2c1	ATPase, Ca++-sequestering	1.43	0.215	-1.46	0.142	2.2	0.162	1.07	0.741	0.81
1418398_a_at	Tspan32	tetraspanin 32	1.06	0.807	1.52	0.384	1.73	0.268	-1.57	0	0.69
1439327_at	Ccbe1	collagen and calcium binding EGF domains 1	1.39	0.137	1.56	0.14	1.37	0.18	-1.48	0.248	0.71
1434321_at	6620401K05Rik	RIKEN cDNA 6620401K05 gene	1.1	0.683	1.6	0.491	1.62	0.06	-1.99	0.124	0.58
1430903_at	4933416O17Rik	RIKEN cDNA 4933416O17 gene	1	0.999	1.15	0.514	2.17	0.155	-1.15	0.83	0.79
1457411_at	---	---	2.15	0.315	-1.16	0.626	1.31	0.443	1.64	0.32	0.98
1432128_at	4930455B06Rik	RIKEN cDNA 4930455B06 gene	-1.03	0.955	2.21	0.075	1.13	0.793	1.47	0.468	0.95
1429380_at	Rgs12	regulator of G-protein signaling 12	1.35	0.396	-1.6	0.339	2.34	0.325	1.13	0.835	0.8
1418050_at	Gpld1	glycosylphosphatidylinositol specific phospholipase D1	2	0.179	-1.01	0.841	1.33	0.073	1.74	0.074	1.01
1457769_at	H60	histocompatibility 60	1.71	0.466	1.9	0.141	-1.41	0.48	1.05	0.777	0.81
1422864_at	Runx1	runt related transcription factor 1	2.22	0.043	1.29	0.344	-1.24	0.457	1.22	0.15	0.87
1434388_at	Mobkl2a	MOB1, Mps One Binder kinase activator-like 2A (yeast)	1.37	0.023	1.72	0.008	1.23	0.326	-1.55	0.194	0.69
1428135_a_at	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange pro	-1.34	0.587	2.12	0.497	1.45	0.492	1.97	0.459	1.05
1419486_at	Foxc1	forkhead box C1	1.14	0.411	1.52	0.174	1.65	0.018	-1.64	0.301	0.67
1440257_at	Obox6	oocyte specific homeobox 6	-2.31	0.245	2.65	0.045	1.24	0.352	1.15	0.756	0.68
AFFX-b-ActinMur/M	Actb	actin, beta, cytoplasmic	1.42	0.65	1.12	0.784	1.77	0.253	-1.15	0.633	0.79
1431296_at	Gpr15	G protein-coupled receptor 15	1.32	0.723	-1.59	0.077	2.38	0.121	1.84	0.424	0.98
1423186_at	Tiam2	T-cell lymphoma invasion and metastasis 2	1.39	0.014	1.21	0.273	1.72	0.187	-1.41	0.103	0.73
1421179_at	Ttyh2	tweety homolog 2 (Drosophila)	1.58	0.024	1.68	0.525	1.07	0.848	-1.19	0.637	0.78
1445701_at	Atp2b4	ATPase, Ca++ transporting, plasma membrane 4	2.3	0.371	1.44	0.348	-1.71	0.153	4.02	0.205	1.51
1451937_at	Glra4	glycine receptor, alpha 4 subunit	1.49	0.605	2.14	0.402	-1.44	0.201	1.74	0.46	0.98
1457331_at	Rtbdn	Retbindin	1.42	0.344	2.31	0.013	-1.69	0.272	1.3	0.636	0.83

1417249_at	Polm	polymerase (DNA directed), mu	1.07	0.877	1.59	0.289	1.66	0.146	-1.34	0.409	0.75
1437697_at	Rad23a	RAD23a homolog (S. cerevisiae)	2.45	0.102	1.09	0.9	-1.27	0.555	1.9	0.339	1.04
1425092_at	Cdh10	cadherin 10	2.11	0.467	1.34	0.69	-1.15	0.457	1.8	0.151	1.03
1443387_at	BB045044	expressed sequence BB045044	1.55	0.095	1.82	0.02	-1.04	0.847	1.08	0.583	0.85
1433007_at	5430430B14Rik	RIKEN cDNA 5430430B14 gene	1.96	0.082	1.17	0.652	1.2	0.565	-1.04	0.932	0.82
1442105_at	4831416G18Rik	RIKEN cDNA 4831416G18 gene	-1.44	0.118	1.04	0.895	2.6	0.021	1.54	0.282	0.93
1420544_at	Gcet2	germinal center expressed transcript 2	1.58	0.167	1.94	0.091	-1.24	0.456	1.15	0.632	0.86
1449496_at	2010109I03Rik	RIKEN cDNA 2010109I03 gene	-1.63	0.639	2.32	0.24	1.39	0.621	1.6	0.287	0.92
1438716_at	AI451617	expressed sequence AI451617	1.2	0.782	1.67	0.03	1.46	0.085	-1.81	0.156	0.63
1423530_at	Stk32c	serine/threonine kinase 32C	1.19	0.823	1.91	0.384	1.23	0.695	-1.86	0.021	0.62
1421237_at	Tmpo	thymopoietin	-1.21	0.739	1.22	0.782	2.28	0.254	3.45	0.154	1.44
1435723_at	A530089L17	hypothetical protein A530089L17	1.16	0.541	1.81	0.182	1.36	0.163	-1.03	0.812	0.83
1435353_a_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	1.28	0.156	1.18	0.101	1.87	0.002	-1.33	0.543	0.75
1420877_at	6-Sep	septin 6	2.06	0.229	1.14	0.336	1.14	0.671	-2.24	0.079	0.52
1434095_at	Unc5a	unc-5 homolog A (C. elegans)	1.62	0.438	1.28	0.648	1.44	0.421	-1.11	0.596	0.81
1423909_at	0610011I04Rik	RIKEN cDNA 0610011I04 gene	1.1	0.365	2.22	0.088	1	0.983	-1.23	0.536	0.78
1427610_at	Dsp	desmoplakin	1.01	0.982	-1.55	0.613	2.67	0.29	2.87	0.155	1.25
1456180_at	LOC380843 /// LOC	similar to RNA binding motif protein 24 /// similar to RNA binding motif protein 24	1.73	0.652	1.24	0.419	1.36	0.145	-1.05	0.879	0.82
1459199_at	---	---	1.46	0.197	1.07	0.86	1.81	0.127	-1.29	0.201	0.76
1431824_at	Cdh13	cadherin 13	2.02	0.549	1.04	0.938	1.27	0.654	-2.12	0.46	0.55
1428027_at	---	BIC noncoding mRNA, complete sequence	1.74	0.37	1.27	0.61	1.32	0.528	-1.16	0.802	0.79
1450743_s_at	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	1.63	0.039	1.28	0.322	1.43	0.354	-1.06	0.906	0.82
1459594_at	Zfp294	zinc finger protein 294	-1.08	0.57	1.59	0.5	1.82	0.036	1.17	0.428	0.87
1418110_a_at	Inpp5d	inositol polyphosphate-5-phosphatase D	1.27	0.432	1.64	0.026	1.43	0.102	-1.51	0.209	0.71
1456498_at	Itga4	integrin alpha 4	1.8	0.225	-1	1	1.53	0.328	1.28	0.628	0.9
1455405_at	Pstpip2	proline-serine-threonine phosphatase-interacting protein 2	-1.19	0.214	1.24	0.307	2.25	0.216	1.94	0.01	1.06
1448375_at	Tm9sf3	transmembrane 9 superfamily member 3	1.44	0.692	-1.01	0.972	1.91	0.381	1.51	0.362	0.96
1455881_at	Ier5l	immediate early response 5-like	1.06	0.82	1.96	0.286	1.32	0.523	-1.5	0.409	0.71
1444133_at	Wnk4	WNK lysine deficient protein kinase 4	2.32	0.14	1.3	0.654	-1.39	0.008	2.54	0.05	1.19
1444866_at	E230006M18Rik	RIKEN cDNA E230006M18 gene	1.38	0.514	-1.47	0.161	2.28	0.006	1.17	0.657	0.84
1424998_at	Emr4	EGF-like module containing, mucin-like, hormone receptor-like sequence 4	-1.29	0.664	1.68	0.087	1.88	0.08	1.24	0.499	0.88
1437463_x_at	Tgfbi	transforming growth factor, beta induced	1.48	0.187	1.17	0.088	1.68	0.135	-1.23	0.264	0.78
1425490_a_at	Wdr13	WD repeat domain 13	1.64	0.206	1.12	0.791	1.58	0.435	-1.06	0.887	0.82
1418872_at	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	1.38	0.179	1.21	0.56	1.75	0.13	-1.13	0.677	0.8
1453513_at	---	---	1.04	0.578	2.02	0.105	1.28	0.373	-1.06	0.906	0.82
1438361_at	2310035C23Rik	RIKEN cDNA 2310035C23 gene	1.21	0.86	1.84	0.425	1.29	0.701	-1.69	0.471	0.66
1429386_at	Wdr68	WD repeat domain 68	-1.17	0.836	1.23	0.433	2.26	0.058	1.9	0.045	1.05
1428909_at	A130040M12Rik	RIKEN cDNA A130040M12 gene	1.73	0.307	1.22	0.309	1.39	0.504	-1.86	0.177	0.62
1417450_a_at	Tacc3	transforming, acidic coiled-coil containing protein 3	1.14	0.676	2.41	0.019	-1.25	0.639	3.37	0.204	1.42
1448575_at	Il7r	interleukin 7 receptor	1.45	0.419	1.68	0.126	1.23	0.548	-1.53	0.503	0.7
1418097_a_at	Tpte2	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	1.22	0.078	1.56	0.125	1.56	0.059	-1.45	0.229	0.72
1432574_at	4930548F15Rik	RIKEN cDNA 4930548F15 gene	1.62	0.426	1.76	0.238	-1.03	0.916	1.65	0.365	1
1452492_a_at	Slc37a2	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	1.58	0.133	1.67	0.247	1.1	0.609	-1.13	0.375	0.81
1422352_at	Mcpt1	mast cell protease 1	1.04	0.903	-1.73	0.417	2.73	0.09	1.79	0.459	0.96
1459066_at	Zfp612	zinc finger protein 612	1.47	0.566	1.72	0.38	1.16	0.828	-2.14	0.411	0.55
1420589_at	Has3	hyaluronan synthase 3	1.87	0.573	1.67	0.274	-1.22	0.793	1.53	0.636	0.96
1441500_at	---	---	1.92	0.266	1.22	0.687	1.21	0.741	-1.43	0.577	0.73
1420170_at	Myh9	myosin, heavy polypeptide 9, non-muscle	1.15	0.372	1.63	0.046	1.57	0.154	-1.08	0.777	0.82
1449175_at	Gpr65	G-protein coupled receptor 65	1.42	0.509	1.45	0.035	1.48	0.145	-1.28	0.45	0.77
1453587_at	Ggt6	gamma-glutamyltransferase 6	1.13	0.349	2.02	0.009	1.21	0.641	-1.55	0.293	0.7
1452641_at	BC028663	cDNA sequence BC028663	2.94	0.03	-2.59	0.012	1.03	0.949	1.43	0.302	0.7
1425432_at	Oprm1	opioid receptor, mu 1	1.34	0.564	-1.05	0.911	2.06	0.169	2.01	0.058	1.09
1417780_at	Lass4	longevity assurance homolog 4 (S. cerevisiae)	1.48	0.155	1.73	0.111	1.14	0.643	-2	0.118	0.59

1456827_at	AA987161	expressed sequence AA987161	1.42	0.411	1.18	0.75	1.75	0.432	-1.75	0.507	0.65
1439440_x_at	Ptk9l	protein tyrosine kinase 9-like (A6-related protein)	1.04	0.685	2.14	0.018	1.18	0.276	-1.76	0.051	0.65
1454786_at	5031439G07Rik	RIKEN cDNA 5031439G07 gene	1.35	0.043	1	0.985	2	0.026	-1.45	0.439	0.73
1444946_at	---	Transcribed locus	1.16	0.302	2.15	0.121	1.04	0.832	-1.41	0.595	0.74
1451099_at	Mbc2	membrane bound C2 domain containing protein	1.35	0.053	1.3	0.041	1.71	0.046	-1.47	0.14	0.72
1422344_s_at	Tnfrsf10b	tumor necrosis factor receptor superfamily, member 10b	1.47	0.188	1.67	0.221	1.22	0.537	-1.02	0.943	0.84
1450563_at	Mgst3	microsomal glutathione S-transferase 3	-1.02	0.779	1.94	0.191	1.44	0.275	2.07	0.445	1.11
1443702_at	Mtap4	microtubule-associated protein 4	1.45	0.643	2.52	0.422	-2.57	0.231	1.07	0.671	0.62
1441548_at	Frmd4b	FERM domain containing 4B	2.27	0.321	1.4	0.355	-1.46	0.225	1.4	0.328	0.9
1439649_at	Adc	arginine decarboxylase	2.07	0.198	1.46	0.613	-1.21	0.538	2.09	0.278	1.1
1434677_at	Hps5	Hermansky-Pudlak syndrome 5 homolog (human)	1.32	0.194	1.58	0.103	1.47	0.069	-1.73	0.015	0.66
1444260_at	---	Transcribed locus, weakly similar to XP_573711.1 PREDICTED: similar to ORF2	1.65	0.202	1.22	0.699	1.5	0.287	-1.63	0.371	0.68
1441899_x_at	Bcan	Brevican	2.28	0.25	1.24	0.63	-1.19	0.634	1.22	0.706	0.89
1450961_a_at	Tceal6 /// Tceal5 ///	transcription elongation factor A (SII)-like 6 /// transcription elongation factor A (SI	-1.05	0.893	2.1	0.302	1.31	0.708	2.45	0.169	1.2
1415983_at	Lcp1	lymphocyte cytosolic protein 1	1.55	0.07	1.23	0.033	1.58	0.073	-1.47	0.192	0.72
1443845_x_at	1700012P22Rik	RIKEN cDNA 1700012P22 gene	2.21	0.234	1.19	0.78	-1.04	0.928	1.13	0.848	0.87
1431069_at	4930544G21Rik	RIKEN cDNA 4930544G21 gene	1.67	0.023	1.87	0.176	-1.21	0.548	1.66	0.503	1
1418296_at	Fxyd5	FXYD domain-containing ion transport regulator 5	1.65	0.044	1.42	0.096	1.29	0.298	-1.21	0.477	0.79
1459112_at	---	Adult male testis cDNA, RIKEN full-length enriched library, clone:4930558M01 pr	-1.89	0.127	2.66	0.148	1.18	0.319	1.51	0.101	0.87
1460145_at	---	---	2	0.235	1.46	0.027	-1.11	0.835	1.17	0.618	0.88
1425251_at	Ptger3	prostaglandin E receptor 3 (subtype EP3)	-1.43	0.48	2.53	0.313	1.14	0.826	2.05	0.33	1.07
1449328_at	Ly75	lymphocyte antigen 75	1.17	0.558	1.31	0.434	1.89	0.026	-1.57	0.078	0.7
1425792_a_at	Rorc	RAR-related orphan receptor gamma	1.31	0.516	1.2	0.144	1.86	0.134	-1.1	0.098	0.82
1453416_at	Gas2l3	growth arrest-specific 2 like 3	1.21	0.211	2.26	0.02	-1.11	0.607	1.91	0.343	1.07
1454728_s_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	1.36	0.071	2.21	0.018	-1.24	0.149	1.38	0.278	0.93
1455224_at	Angptl1	angiopoietin-like 1	-1.06	0.663	1.99	0.383	1.44	0.399	1.27	0.698	0.91
1459334_at	---	---	1.54	0.187	-1.63	0.199	2.22	0.062	1.26	0.632	0.85
1426430_at	Jag2	jagged 2	1.34	0.494	1.68	0.314	1.35	0.249	-2.77	0.037	0.4
1458264_at	4930412F12Rik	RIKEN cDNA 4930412F12 gene	2.43	0.325	1.21	0.706	-1.38	0.521	1.45	0.062	0.93
1455948_x_at	Matn3	matrilin 3	1.44	0.656	1.68	0.175	1.25	0.586	-1.3	0.666	0.77
1426434_at	Tmem43	transmembrane protein 43	1.57	0.161	1.38	0.07	1.43	0.118	-1.13	0.148	0.81
1432304_a_at	9030624J02Rik	RIKEN cDNA 9030624J02 gene	1.43	0.496	1.01	0.983	1.93	0.352	-1.04	0.93	0.83
1442888_at	Inadl	InaD-like (Drosophila)	1.59	0.542	2.1	0.265	-1.46	0.254	1.31	0.596	0.89
1446289_at	Stk3	Serine/threonine kinase 3 (Ste20, yeast homolog)	1.12	0.797	2.83	0.15	-2.32	0.002	1.01	0.981	0.66
1420380_at	Ccl2	chemokine (C-C motif) ligand 2	1.22	0.73	1.53	0.515	1.62	0.008	-1.42	0.642	0.74
1434798_at	Atp6v0d2	ATPase, H+ transporting, lysosomal V0 subunit D2	-1.57	0.007	2.4	0.013	1.34	0.318	3.15	0.083	1.33
1424409_at	Cldn23	claudin 23	1.5	0.414	1.98	0.364	-1.12	0.725	1.04	0.947	0.85
1425504_at	Mylk	myosin, light polypeptide kinase	2.16	0.366	1.04	0.831	1.18	0.683	-1.26	0.501	0.78
1452981_at	Cntn1	contactin 1	2.01	0.111	1.31	0.468	1.06	0.852	-2.69	0.14	0.42
1438266_at	Adamtsl5	ADAMTS-like 5	2.24	0.199	-1.07	0.542	1.21	0.535	1.09	0.721	0.87
1450960_at	Igfbpl1	insulin-like growth factor binding protein-like 1	1.9	0.047	-1.05	0.923	1.52	0.34	1.47	0.329	0.96
1441653_at	D030022P06Rik	RIKEN cDNA D030022P06 gene	2.56	0.33	1.15	0.641	-1.5	0.227	1.17	0.401	0.85
1430249_at	4930473A02Rik	RIKEN cDNA 4930473A02 gene	-1.25	0.538	1.99	0.069	1.58	0.155	1.46	0.204	0.95
1446582_at	Poln	DNA polymerase N	-1.47	0.225	2.45	0.179	1.25	0.407	1.37	0.67	0.9
1432668_at	2210411G17Rik	RIKEN cDNA 2210411G17 gene	2.2	0.54	1.47	0.587	-1.41	0.451	1.05	0.894	0.83
1453892_at	A930007I19Rik	RIKEN cDNA A930007I19 gene	2.08	0.354	1.55	0.071	-1.33	0.364	1	0.994	0.83
1453272_at	4930579F01Rik	RIKEN cDNA 4930579F01 gene	1.74	0.506	1.15	0.491	1.49	0.202	-1.59	0.428	0.7
1430839_at	9430076G02Rik	RIKEN cDNA 9430076G02 gene	1.35	0.101	2.08	0.374	-1.05	0.634	10.48	0.219	3.21
1452376_at	Zfp444	zinc finger protein 444	2.19	0.191	1.19	0.588	-1	0.99	1.22	0.432	0.9
1427474_s_at	Gstm3	glutathione S-transferase, mu 3	-1.26	0.511	1.71	0.107	1.88	0.113	1.09	0.705	0.86
1415994_at	Cyp2e1	cytochrome P450, family 2, subfamily e, polypeptide 1	1.6	0.122	-1.19	0.474	1.95	0.514	4.87	0.216	1.81
1422189_x_at	Tcrg /// LOC670271	T-cell receptor gamma chain /// region containing T-cell receptor gamma chain; T	-1.09	0.753	1.93	0.109	1.53	0.11	1.32	0.59	0.92
1437554_at	Plec1	plectin 1	1.12	0.577	1.38	0.552	1.88	0.451	-1.65	0.365	0.68

1448477_at	Chst12	carbohydrate sulfotransferase 12	-1.01	0.986	1.66	0.259	1.73	0.021	1.27	0.231	0.91
1453677_a_at	Derl3	Der1-like domain family, member 3	-1.36	0.435	1.2	0.615	2.45	0.101	2	0.23	1.07
1430550_at	Lipl3	lipase-like, ab-hydrolase domain containing 3	-1.38	0.592	2.46	0.145	1.21	0.644	3.94	0.004	1.56
1440694_at	---	---	1.65	0.129	1.77	0.374	-1.03	0.959	1.12	0.876	0.88
1429828_at	1700024P04Rik	RIKEN cDNA 1700024P04 gene	1.08	0.812	1.92	0.412	1.39	0.533	-1.13	0.521	0.82
1417426_at	Prg1	proteoglycan 1, secretory granule	1.35	0.289	1.79	0.01	1.25	0.204	-1.26	0.088	0.78
1424317_at	Slc25a19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19	-1.04	0.757	1.76	0.076	1.66	0.23	1.13	0.475	0.88
1459602_at	Ccni	cyclin I	2.18	0.108	-1.48	0.439	1.54	0.234	1.22	0.015	0.87
1417383_at	Entpd5	ectonucleoside triphosphate diphosphohydrolase 5	1.34	0.169	1.04	0.872	2.01	0.235	-1.08	0.667	0.83
1419726_at	Adam18	a disintegrin and metallopeptidase domain 18	-1.1	0.856	1.81	0.358	1.67	0.289	1.87	0.005	1.06
1440913_at	BC037704	cDNA sequence BC037704	1.76	0.166	1.27	0.268	1.37	0.35	-1.52	0.065	0.72
1424349_a_at	Lpgat1	lysophosphatidylglycerol acyltransferase 1	1.36	0.112	1.86	0.114	1.17	0.462	-1.5	0.437	0.72
1458759_at	Mtap4	Microtubule-associated protein 4	2	0.176	1	0.996	1.39	0.408	-1.42	0.05	0.74
1422010_at	Tlr7	toll-like receptor 7	1.17	0.355	1.54	0.49	1.69	0.028	-1.38	0.308	0.75
1454488_at	4930534I15Rik	RIKEN cDNA 4930534I15 gene	1.61	0.363	1.35	0.276	1.44	0.3	-1.94	0.214	0.61
1423851_a_at	Tmem46	transmembrane protein 46	1.35	0.114	1.91	0.351	1.14	0.711	-2.6	0.038	0.45
1442584_at	---	---	1.81	0.269	1.05	0.919	1.54	0.504	-2.41	0.213	0.5
1421648_at	Nlgn1	neuroligin 1	1.6	0.411	1.14	0.467	1.66	0.33	-1.22	0.803	0.79
1450557_at	Scn4a	sodium channel, voltage-gated, type IV, alpha	-1.37	0.623	1.06	0.91	2.61	0.272	1.11	0.58	0.85
1454106_a_at	Cxxc1	CXXC finger 1 (PHD domain)	1.47	0.449	-1.09	0.859	2.01	0.451	1.07	0.904	0.86
1439206_at	Gna12	Guanine nucleotide binding protein, alpha 12	2.13	0.462	1.22	0.357	1.04	0.847	-1.36	0.309	0.76
1452711_at	Spg3a	spastic paraplegia 3A homolog (human)	2.37	0.164	1.18	0.775	-1.18	0.407	2.97	0.205	1.33
1456424_s_at	Pltp	phospholipid transfer protein	2.01	0.009	1.47	0.057	-1.09	0.466	1.33	0.338	0.93
1436524_at	4833438C02Rik	RIKEN cDNA 4833438C02 gene	1.27	0.087	1.92	0.161	1.21	0.478	-1.58	0.128	0.7
1449803_x_at	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.22	0.295	1.35	0.635	2.23	0.058	1.99	0.035	1.09
1431000_at	2310002B06Rik	RIKEN cDNA 2310002B06 gene	1.09	0.83	2.12	0.238	1.19	0.773	-2.64	0.018	0.44
1419872_at	Csf1r	colony stimulating factor 1 receptor	1.44	0.038	1.74	0.003	1.22	0.134	-1.43	0.121	0.74
1447318_at	Galnt4	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.96	0.333	1.01	0.993	1.43	0.48	-2.3	0.133	0.53
1423049_a_at	Tpm1	tropomyosin 1, alpha	1.87	0.132	1.57	0.214	-1.03	0.913	1.07	0.877	0.87
1425756_at	Rab40b	Rab40b, member RAS oncogene family	1.46	0.248	1.5	0.234	1.45	0.4	-1.45	0.573	0.74
1449911_at	Lag3	lymphocyte-activation gene 3	-1.69	0.534	1.04	0.947	2.77	0.013	1.3	0.004	0.85
1451581_at	Saps2	SAPS domain family, member 2	2.32	0.235	-1.63	0.266	1.47	0.5	1.51	0.483	0.92
1444358_at	Fbxl11	F-box and leucine-rich repeat protein 11	1.4	0.567	1.93	0.251	1.08	0.735	-1.09	0.849	0.83
1447632_at	Fancc	Fanconi anemia, complementation group C	2.45	0.412	1.37	0.262	-1.71	0.026	1.52	0.433	0.91
1447543_at	Wdfy1	WD repeat and FYVE domain containing 1	1.49	0.662	2.33	0.217	-1.73	0.29	1.03	0.881	0.78
1429229_s_at	4930534B04Rik	RIKEN cDNA 4930534B04 gene	-1	0.999	2.01	0.462	1.39	0.15	1.61	0.446	1
1450076_at	4933411K20Rik	RIKEN cDNA 4933411K20 gene	2.33	0.465	-2.63	0.394	1.69	0.561	1.06	0.837	0.61
1452913_at	Pcp4l1	Purkinje cell protein 4-like 1	1.1	0.786	1.34	0.209	1.97	0.281	-1.11	0.431	0.82
1449501_a_at	Gzmm	granzyme M (lymphocyte met-ase 1)	-1.31	0.356	1.82	0.222	1.82	0.291	4.61	0.311	1.74
1445817_at	BB168181	expressed sequence BB168181	-1.3	0.637	1.58	0.627	2.06	0.044	1.13	0.634	0.87
1419561_at	Ccl3	chemokine (C-C motif) ligand 3	-1.14	0.862	1.92	0.326	1.61	0.389	2.03	0.086	1.1
1451883_at	LOC620316	hypothetical LOC620316	1.06	0.893	1.92	0.294	1.43	0.215	-1.96	0.005	0.61
1440242_at	C030014K22Rik	RIKEN cDNA C030014K22 gene	-1.11	0.1	1.21	0.712	2.29	0.026	1.69	0.306	1.02
1440613_at	Perld1	Per1-like domain containing 1	-1.31	0.727	1.07	0.347	2.58	0.319	1.9	0.057	1.06
1458783_at	---	---	2.22	0.488	-1.25	0.638	1.39	0.308	1.17	0.853	0.88
1443403_at	4933428G09Rik	RIKEN cDNA 4933428G09 gene	1.09	0.689	2.37	0.078	-1.05	0.899	2.85	0.055	1.32
1427854_x_at	Hspb1	heat shock protein 1	2.15	0.37	-1.05	0.941	1.31	0.415	1.33	0.237	0.93
1436381_at	Dlgap3	discs, large (Drosophila) homolog-associated protein 3	1.17	0.258	2.04	0.019	1.2	0.669	-2.35	0.237	0.52
1452484_at	Car7	carbonic anhydrase 7	1.25	0.212	2.33	0.17	-1.21	0.694	1.32	0.704	0.92
1427864_at	Hist2h3c1 /// Hist1h	histone 2, H3c1 /// histone1, H3d /// histone 1, H3b /// histone 1, H3e /// histone 2,	-1.1	0.772	2.08	0.03	1.42	0.37	1.22	0.669	0.91
1450637_a_at	Aebp1	AE binding protein 1	1.13	0.262	1.35	0.571	1.93	0.103	-1.27	0.653	0.79
1421229_at	Dffb	DNA fragmentation factor, beta subunit	1.13	0.438	1.67	0.189	1.62	0.017	-1.37	0.32	0.76
1421044_at	Mrc2	mannose receptor, C type 2	2.14	0.257	1.28	0.463	-1	0.995	1.55	0.276	0.99

1422789_at	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	1.67	0.085	1.47	0.504	1.28	0.68	-1.19	0.78	0.81
1456490_at	Cdk2ap2	CDK2-associated protein 2	1.99	0.228	-1	0.998	1.43	0.295	2.38	0.044	1.2
1452539_a_at	Cd247	CD247 antigen	1.68	0.509	1.23	0.744	1.51	0.373	-3.7	0.293	0.18
1428301_at	LOC544988 /// B93	hypothetical protein LOC544988 /// RIKEN cDNA B930046C15 gene /// hypotheti	1.21	0.549	2.41	0.448	-1.25	0.315	1.02	0.961	0.85
1415801_at	Gja1	gap junction membrane channel protein alpha 1	-1.07	0.762	2.08	0.345	1.4	0.408	1.09	0.738	0.88
1439241_x_at	Srd5a2l	steroid 5 alpha-reductase 2-like	2.47	0.056	-1.72	0.042	1.37	0.307	1.03	0.856	0.79
1451371_at	Mrap	melanocortin 2 receptor accessory protein	-1.76	0.428	1.23	0.219	2.62	0.457	2.54	0.192	1.16
1449235_at	Fasl	Fas ligand (TNF superfamily, member 6)	2.19	0.103	-1.11	0.805	1.33	0.147	1.33	0.591	0.93
1437407_at	9930039A11Rik	RIKEN cDNA 9930039A11 gene	1.67	0.253	1.27	0.673	1.47	0.005	-1.35	0.041	0.77
1430883_at	4933402C05Rik	RIKEN cDNA 4933402C05 gene	-1.16	0.672	2.18	0.227	1.38	0.325	1.2	0.752	0.9
1458236_at	---	12 days embryo eyeball cDNA, RIKEN full-length enriched library, clone:D23001	2.43	0.118	1.23	0.614	-1.32	0.281	1.41	0.579	0.94
1442709_at	Zfp521	Zinc finger protein 521	2.37	0.184	-1.11	0.866	1.15	0.648	1.85	0.405	1.06
1426512_at	Olfm3	olfactomedin 3	1.03	0.925	2	0.111	1.39	0.579	-1.6	0.274	0.71
1417601_at	Rgs1	regulator of G-protein signaling 1	1.51	0.076	1.43	0.279	1.49	0.166	-1.46	0.217	0.74
1451702_at	Cmtm7	CKLF-like MARVEL transmembrane domain containing 7	1.34	0.508	1.82	0.036	1.26	0.399	-1.4	0.072	0.76
1451698_at	Psrc1	proline/serine-rich coiled-coil 1	1.63	0.069	1.97	0.219	-1.22	0.625	1.94	0.105	1.08
1421508_at	Odz1	odd Oz/ten-m homolog 1 (Drosophila)	1.32	0.607	1.64	0.392	1.46	0.332	-2.45	0.421	0.49
1447467_at	Ptpra	protein tyrosine phosphatase, receptor type, A	2.1	0.366	1.66	0.328	-1.51	0.477	1.35	0.485	0.9
1428711_at	Mon1b	MON1 homolog b (yeast)	1.1	0.748	1.57	0.095	1.75	0.08	-2.01	0.175	0.6
1415836_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	-1.14	0.432	1.64	0.307	1.9	0.008	1.48	0.046	0.97
1453238_s_at	3930401B19Rik ///	RIKEN cDNA 3930401B19 gene /// RIKEN cDNA 1200016E24 gene /// RIKEN cD	1.89	0.418	1.33	0.189	1.21	0.292	-1.5	0.2	0.73
1429224_at	Pnma1	paraneoplastic antigen MA1	2.07	0.251	-1.61	0.387	1.73	0.104	2.91	0.267	1.28
1427187_at	6030413G23Rik	RIKEN cDNA 6030413G23 gene	1.81	0.439	1.28	0.508	1.33	0.115	-1.49	0.143	0.73
1443532_at	---	---	1.54	0.164	1.06	0.801	1.83	0.249	-1.18	0.736	0.81
1451672_at	Gprk6	G protein-coupled receptor kinase 6	1.1	0.357	1.23	0.489	2.09	0.136	-1.53	0.04	0.73
1435647_at	Ikbkg	inhibitor of kappaB kinase gamma	1.54	0.176	-1.11	0.641	1.99	0.223	1.25	0.644	0.92
1449843_at	St8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-1.24	0.786	2.18	0.161	1.45	0.144	1.63	0.426	1
1437716_x_at	Kif22	kinesin family member 22	-1.17	0.613	1.56	0.097	2.01	0.134	3.04	0.097	1.36
1431651_at	C330001K17Rik	RIKEN cDNA C330001K17 gene	2.39	0.129	-1.59	0.292	1.41	0.271	1.03	0.958	0.81
1442813_at	Dgki	Diacylglycerol kinase, iota	2.04	0.015	1.73	0.012	-1.5	0.532	1.83	0.13	1.02
1448566_at	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	-1.03	0.916	1.24	0.329	2.22	0.295	1.18	0.387	0.9
1459087_at	---	---	1.76	0.456	1.9	0.152	-1.31	0.498	1.31	0.528	0.92
1423365_at	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subunit	2.36	0.529	1.51	0.475	-1.77	0.116	2.17	0.216	1.07
1442474_at	---	---	1.94	0.52	-1.18	0.782	1.65	0.225	1.19	0.797	0.9
1455338_at	A4galt	alpha 1,4-galactosyltransferase	1.3	0.342	2.32	0.401	-1.22	0.659	1.23	0.815	0.91
1419843_at	Calr4	Calreticulin 4	1.37	0.268	2.12	0.292	-1.05	0.916	1.34	0.133	0.94
1421719_at	V2r1b	vomeronasal 2, receptor, 1b	1.2	0.48	2.1	0.409	1.14	0.821	-1.21	0.804	0.81
1439211_at	Umodl1	uromodulin-like 1	-2.11	0.078	2.85	0.197	1.11	0.801	1.23	0.603	0.77
1453006_at	2610306H15Rik	RIKEN cDNA 2610306H15 gene	1.33	0.394	1.92	0.125	1.19	0.081	-1.23	0.485	0.8
1439231_at	---	---	2.01	0.351	1.43	0.419	-1	0.994	1.28	0.404	0.93
1457296_at	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	1.2	0.785	1.3	0.394	1.94	0.285	-1.59	0.346	0.71
1433523_at	D930005D10Rik	RIKEN cDNA D930005D10 gene	2.22	0.311	1.14	0.695	1.08	0.852	-2.83	0.252	0.4
1458767_at	Gbe1	Glucan (1,4-alpha-), branching enzyme 1	2.44	0.4	-1.48	0.382	1.32	0.531	1.41	0.459	0.92
1419593_at	Greb1	gene regulated by estrogen in breast cancer protein	1.25	0.795	1.8	0.127	1.39	0.478	-2.32	0.262	0.53
1449282_at	Cysltr1	cysteinyl leukotriene receptor 1	-1.3	0.597	2.58	0.086	1.09	0.702	1.79	0.415	1.04
1449391_at	Zfp37	zinc finger protein 37	2.53	0.445	1	0.997	-1.09	0.821	1.78	0.101	1.05
1420045_at	---	---	1.58	0.544	1.65	0.276	1.21	0.384	-3.88	0.198	0.14
1421034_a_at	Il4ra	interleukin 4 receptor, alpha	1.87	0.068	1.17	0.368	1.41	0.093	-1.75	0.07	0.67
1458720_at	D9Ertd356e	DNA segment, Chr 9, ERATO Doi 356, expressed	1.37	0.189	1.72	0.508	1.36	0.444	-1.15	0.561	0.83
1431136_at	Rab36	RAB36, member RAS oncogene family	1.11	0.859	-1.23	0.076	2.52	0.029	1.23	0.163	0.91
1424443_at	Hdgfrp3 /// Tm6sf1	hepatoma-derived growth factor, related protein 3 /// transmembrane 6 superfami	1.04	0.879	2.19	0.005	1.22	0.285	-1.86	0.067	0.65
1454405_at	4930453J04Rik	RIKEN cDNA 4930453J04 gene	1.46	0.678	1.54	0.444	1.45	0.344	-2.07	0.197	0.6
1441917_s_at	Tmem40	transmembrane protein 40	-1.57	0.024	1.31	0.25	2.51	0.145	2.7	0.367	1.24

1453348_at	1700085D22Rik	RIKEN cDNA 1700085D22 gene	1.77	0.419	1.44	0.304	1.24	0.102	-1.1	0.683	0.84
1459342_at	C230029M16	hypothetical protein C230029M16	-1.66	0.068	2.52	0.18	1.33	0.148	1.21	0.577	0.85
1420693_at	Myom1	myomesin 1	1.89	0.043	-1.1	0.847	1.65	0.217	1.19	0.488	0.91
1447350_at	---	---	2.15	0.424	1.39	0.648	-1.1	0.723	1.38	0.692	0.95
1438884_at	D830007B15Rik	RIKEN cDNA D830007B15 gene	1.26	0.302	2.26	0.182	-1.08	0.676	1.24	0.667	0.92
1452535_at	Igh-1a	Immunoglobulin heavy chain 1a (serum IgG2a)	1.73	0.27	1.35	0.392	1.38	0.2	-1.53	0.524	0.73
1418648_at	Egln3	EGL nine homolog 3 (C. elegans)	1.55	0.179	-1.77	0.038	2.34	0.088	1.73	0.439	0.96
1459668_at	Tank	TRAF family member-associated Nf-kappa B activator	2.16	0.2	1.17	0.792	1.13	0.597	-1.05	0.85	0.85
1422253_at	Col10a1	procollagen, type X, alpha 1	1.6	0.273	1.49	0.521	1.37	0.291	-2.26	0.318	0.55
1418099_at	Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b	1.44	0.039	1.16	0.45	1.85	0.04	-1.28	0.407	0.79
1419306_at	Ccdc96	coiled-coil domain containing 96	-1.61	0.338	2.42	0.204	1.42	0.33	1.87	0.248	1.02
1439372_at	Sumo3	SMT3 suppressor of mif two 3 homolog 3 (yeast)	1.28	0.657	1.92	0.443	1.25	0.575	-1.57	0.417	0.72
1432948_at	4921519G19Rik	RIKEN cDNA 4921519G19 gene	1.57	0.105	-1.24	0.562	2.08	0.054	1.35	0.287	0.94
1421004_at	Cep110	centrosomal protein 110	2.83	0.099	-1.62	0.356	1.02	0.97	1.06	0.865	0.82
1430600_at	Cmtm5	CKLF-like MARVEL transmembrane domain containing 5	2.13	0.454	1.56	0.508	-1.3	0.446	1.3	0.675	0.92
1428484_at	Osbpl3	oxysterol binding protein-like 3	-1.11	0.197	1.99	0.072	1.57	0.061	1.45	0.166	0.97
1451644_a_at	H2-Q1 /// 0610037M	histocompatibility 2, Q region locus 1 /// RIKEN cDNA 0610037M15 gene	1.19	0.325	1.45	0.113	1.82	0.02	-1.57	0.297	0.72
1435996_at	Card11	caspase recruitment domain family, member 11	1.82	0.384	1.16	0.601	1.49	0.346	-1.88	0.19	0.65
1442542_at	Eya4	eyes absent 4 homolog (Drosophila)	1.43	0.431	2.13	0.099	-1.11	0.702	3.79	0.01	1.56
1419697_at	Cxcl11	chemokine (C-X-C motif) ligand 11	1.12	0.628	-1.03	0.911	2.37	0.037	1.39	0.596	0.96
1440423_at	Zbtb37	zinc finger and BTB domain containing 37	1.79	0.212	1.07	0.743	1.6	0.072	-2.32	0.097	0.54
1426587_a_at	Stat3	signal transducer and activator of transcription 3	1.34	0.517	1.6	0.104	1.52	0.141	-1.12	0.7	0.84
1438309_at	---	Transcribed locus	1.05	0.914	-2.84	0.039	3.06	0.407	1.14	0.867	0.6
1434763_at	Tmem142b	transmembrane protein 142B	1.47	0.187	1.5	0.481	1.5	0.13	-1.94	0.245	0.63
1430087_at	Nkpd1	NTPase, KAP family P-loop domain containing 1	1.12	0.497	1.95	0.37	1.4	0.358	-2.79	0.411	0.42
1417788_at	Sncg	synuclein, gamma	1.74	0.288	-1.59	0.274	2.09	0.163	1.51	0.58	0.94
1439034_at	Spn	sialophorin	1.32	0.267	1.43	0.277	1.72	0.002	-1.18	0.302	0.82
1427912_at	Cbr3	carbonyl reductase 3	2.09	0.09	1.26	0.454	1.11	0.581	-1.52	0.079	0.74
1450913_at	B4galt6 /// LOC675	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6 /// similar to E	-1.3	0.335	1.66	0.123	2.04	0.123	2.33	0.146	1.18
1440832_at	Ang4	angiogenin, ribonuclease A family, member 4	1.21	0.151	-1.12	0.886	2.36	0.226	1.19	0.759	0.91
1424208_at	Ptger4	prostaglandin E receptor 4 (subtype EP4)	1.55	0.204	1.41	0.037	1.51	0.195	-1.14	0.29	0.83
1452824_at	D1Bwg0212e	DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed	1.07	0.818	1.41	0.63	1.99	0.103	-1.27	0.631	0.8
1445090_at	Grik2	Glutamate receptor, ionotropic, kainate 2 (beta 2)	1.78	0.39	1.14	0.81	1.55	0.209	-2.31	0.297	0.54
1432922_at	4933416E14Rik	RIKEN cDNA 4933416E14 gene	1.89	0.512	1.58	0.509	-1.01	0.974	1.02	0.978	0.87
1434421_at	Islr2	immunoglobulin superfamily containing leucine-rich repeat 2	1.99	0.4	1.55	0.511	-1.08	0.842	2.73	0.149	1.3
1436171_at	Arhgap30	Rho GTPase activating protein 30	1.18	0.374	1.44	0.009	1.85	0.083	-1.58	0.252	0.72
1449432_a_at	Mmel1	membrane metallo-endopeptidase-like 1	1.83	0.469	2.2	0.274	-2.32	0.126	3.93	0.309	1.41
1417121_at	Gabra6	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6	-2.35	0.131	1.5	0.145	2.54	0.047	1.42	0.469	0.78
1429881_at	Arhgap15	Rho GTPase activating protein 15	1.52	0.367	1.23	0.379	1.73	0.145	-2.28	0.128	0.55
1416528_at	Sh3bgrl3	SH3 domain binding glutamic acid-rich protein-like 3	1.17	0.231	1.66	0.008	1.64	0.08	-1.4	0.307	0.77
1417025_at	H2-Eb1	histocompatibility 2, class II antigen E beta	1.73	0.077	1.41	0.213	1.34	0.322	-1.51	0.162	0.74
1421909_at	Tcf20	transcription factor 20	1.75	0.205	1.19	0.6	1.54	0.204	-2.57	0.238	0.48
1416588_at	Ptprn /// LOC66906	protein tyrosine phosphatase, receptor type, N /// similar to Receptor-type tyrosin	-1.83	0.427	1.71	0.462	2.22	0.008	1.95	0.505	1.02
1445356_at	---	---	-1.72	0.502	1.65	0.585	2.24	0.175	1.36	0.637	0.88
1422267_at	Foxb2	forkhead box B2	1.93	0.552	1.52	0.541	1.03	0.937	-1.09	0.633	0.85
1441188_at	---	---	1.47	0.635	1.58	0.502	1.43	0.324	-1.37	0.315	0.78
1420153_at	---	---	2.1	0.166	1.05	0.892	1.33	0.283	-1.22	0.663	0.81
1437257_at	Wdr47	WD repeat domain 47	1.61	0.489	1.02	0.962	1.85	0.51	-1.16	0.861	0.83
1456556_at	A230009B12Rik	RIKEN cDNA A230009B12 gene	2.05	0.116	-1.07	0.868	1.49	0.425	1.23	0.765	0.93
1458750_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930028N	1.32	0.298	1.76	0.161	1.41	0.272	-2.07	0.036	0.6
1451924_a_at	Edn1	endothelin 1	1.88	0.026	1.32	0.695	1.28	0.47	-2.06	0.302	0.61
1455920_x_at	Lyzl6	lysozyme-like 6	1.29	0.742	1.31	0.54	1.88	0.152	-1.16	0.771	0.83
1419646_a_at	Mbp	myelin basic protein	-1.49	0.539	1.96	0.186	1.86	0.203	1.17	0.273	0.87

1456452_at	BC107230	cDNA sequence BC107230	2.12	0.261	1.63	0.322	-1.35	0.488	1.89	0.349	1.07
1421924_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	-1.2	0.084	1.31	0.509	2.35	0.533	1.92	0.519	1.1
1425888_at	Klra17	killer cell lectin-like receptor, subfamily A, member 17	-1.92	0.209	1.39	0.435	2.58	0.358	1.5	0.122	0.89
1418765_at	Timd2	T-cell immunoglobulin and mucin domain containing 2	1.3	0.482	-1.16	0.23	2.33	0.384	1.93	0.121	1.1
1436565_at	Ceacam10	CEA-related cell adhesion molecule 10	1.85	0.008	1.22	0.745	1.42	0.649	-1.45	0.607	0.76
1450338_x_at	V2r8 /// V2r9	vomeronasal 2, receptor, 8 /// vomeronasal 2, receptor, 9	1.47	0.553	2.26	0.078	-1.32	0.396	1.41	0.003	0.95
1418771_a_at	Cpb2	carboxypeptidase B2 (plasma)	1.95	0.501	1.47	0.202	1.07	0.593	-1.25	0.686	0.81
1421682_a_at	Tcte3	t-complex-associated testis expressed 3	2.08	0.317	-1.13	0.508	1.53	0.263	1.78	0.476	1.06
1452575_at	Krtap6-3	keratin associated protein 6-3	2.29	0.328	1.02	0.962	1.18	0.61	-2.22	0.273	0.57
1450480_a_at	Gprk6	G protein-coupled receptor kinase 6	1.51	0.347	1.19	0.604	1.79	0.139	-1.35	0.418	0.79
1450905_at	Plxnc1	plexin C1	1.46	0.145	1.5	0.322	1.53	0.147	-1.68	0.085	0.7
1438042_at	Shox2	short stature homeobox 2	2.35	0.218	-1.14	0.754	1.26	0.592	1.44	0.044	0.98
1441861_at	1700018G05Rik	RIKEN cDNA 1700018G05 gene	1.55	0.325	1.53	0.495	1.41	0.515	-1.29	0.608	0.8
1431185_at	4930503B20Rik	RIKEN cDNA 4930503B20 gene	-1.34	0.074	1.75	0.45	2	0.108	1.81	0.275	1.05
1420604_at	Hesx1	homeo box gene expressed in ES cells	1.16	0.66	1.72	0.118	1.62	0.086	-2.05	0.017	0.61
1422212_at	Foxh1	forkhead box H1	1.73	0.519	1.26	0.709	1.51	0.037	-1.17	0.38	0.83
1454124_at	1700067K01Rik	RIKEN cDNA 1700067K01 gene	-1.34	0.052	1.29	0.213	2.46	0.02	1.8	0.158	1.05
1451372_a_at	Art1	ADP-ribosyltransferase 1	1.35	0.531	1.64	0.067	1.5	0.357	-1.1	0.844	0.85
1453304_s_at	Ly6e	lymphocyte antigen 6 complex, locus E	1.44	0.154	1.78	0.08	1.28	0.068	-1.33	0.229	0.79
1450165_at	Slfn2	schlafen 2	1.6	0.193	1.8	0.061	1.1	0.833	-2.28	0.114	0.55
1451704_at	Abpd	androgen binding protein delta	1.82	0.374	1.35	0.283	1.33	0.527	-2.14	0.159	0.59
1450227_at	Ankrd6	ankyrin repeat domain 6	-1.01	0.947	2.08	0.095	1.42	0.235	1.49	0.203	1
1444058_at	2310047C04Rik	RIKEN cDNA 2310047C04 gene	-1.29	0.559	2.68	0.095	1.04	0.902	1.22	0.623	0.91
1441187_at	E330037M01Rik	RIKEN cDNA E330037M01 gene	2.74	0.345	-1.43	0.349	1.06	0.926	1.21	0.722	0.9
1421816_at	LOC630729	similar to Glutathione reductase, mitochondrial precursor (GR) (GRase)	-1.01	0.949	1.01	0.919	2.5	0.101	1.49	0.314	1
1440902_at	A330104H05Rik	RIKEN cDNA A330104H05 gene	-1.23	0.63	1.78	0.01	1.91	0.083	1.75	0.11	1.05
1418920_at	Cldn15	claudin 15	-1.11	0.229	1.4	0.447	2.2	0.151	2.16	0.299	1.16
1426855_at	D10Ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed	2.53	0.047	1.03	0.934	-1.06	0.839	1.02	0.907	0.88
1442919_at	Sh3pxd2b	SH3 and PX domains 2B	2.44	0.483	1.14	0.73	-1.08	0.797	1.58	0.272	1.02
1437107_at	Rab6b	RAB6B, member RAS oncogene family	1.2	0.397	1.18	0.76	2.13	0.07	-1.58	0.334	0.73
1454327_at	4933430H06Rik	RIKEN cDNA 4933430H06 gene	1.99	0.383	1.37	0.463	1.15	0.554	-1.06	0.916	0.86
1458488_at	Dcamkl2	doublecortin and CaM kinase-like 2	-1.34	0.584	1.87	0.246	1.89	0.147	1.21	0.719	0.91
1452431_s_at	H2-Aa /// H2-Ea	histocompatibility 2, class II antigen A, alpha /// histocompatibility 2, class II antige	1.74	0.166	1.6	0.224	1.16	0.549	-1.64	0.176	0.72
1433465_a_at	AI467606	expressed sequence AI467606	1.38	0.099	1.77	0.105	1.35	0.093	-2.17	0.042	0.58
1419614_at	Pla2g12b	phospholipase A2, group XIIB	2.62	0.068	1.04	0.595	-1.18	0.286	1.29	0.651	0.94
1430347_at	4930524J08Rik	RIKEN cDNA 4930524J08 gene	-1.18	0.436	2.17	0.256	1.49	0.149	1.51	0.303	1
1427359_at	A630082K20Rik	RIKEN cDNA A630082K20 gene	1.39	0.304	-1.07	0.835	2.19	0.28	1.89	0.384	1.1
1427368_x_at	Fes	feline sarcoma oncogene	1.22	0.07	1.54	0.026	1.75	0.081	-1.14	0.418	0.84
1435876_at	C86350	expressed sequence C86350	1.3	0.391	2.71	0.11	-2	0.014	1.6	0.258	0.9
1441511_at	Kcnt1	potassium channel, subfamily T, member 1	1.17	0.559	1.8	0.295	1.54	0.146	-1.05	0.876	0.87
1417089_a_at	Ckmt1	creatine kinase, mitochondrial 1, ubiquitous	-1.07	0.649	2.34	0.06	1.24	0.47	2.21	0.311	1.18
1451358_a_at	Racgap1	Rac GTPase-activating protein 1	-1.17	0.729	1.64	0.362	2.02	0.023	2.65	0.173	1.28
1429319_at	Rhoh	ras homolog gene family, member H	1.25	0.772	1.39	0.567	1.87	0.332	-2.08	0.088	0.61
1442133_at	Gm237	gene model 237, (NCBI)	1.44	0.203	2.14	0.205	-1.07	0.846	1.29	0.651	0.95
1438645_x_at	Bace2	beta-site APP-cleaving enzyme 2	2.08	0.417	1.03	0.94	1.4	0.323	-1.42	0.423	0.77
1419835_s_at	Plec1	plectin 1	1.69	0.002	1.4	0.017	1.42	0.117	-1.39	0.292	0.78
1437268_at	Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	-1.09	0.885	1.52	0.484	2.07	0.002	2.36	0.155	1.22
1436829_at	Trim67	tripartite motif-containing 67	2.02	0.465	1.46	0.501	1.03	0.938	-1.31	0.437	0.8
1434975_x_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	1.18	0.176	1.48	0.01	1.86	0.002	-1.21	0.65	0.83
1425948_a_at	Slc25a30	solute carrier family 25, member 30	1.25	0.773	-6	0.102	3.1	0.224	1.57	0.535	-0.02
1439608_at	---	Transcribed locus	1.15	0.804	1.19	0.312	2.18	0.093	-1.65	0.561	0.72
1428599_at	Kndc1	kinase non-catalytic C-lobe domain (KIND) containing 1	1.86	0.328	-1.42	0.639	1.96	0.002	1.85	0.212	1.06
1423768_at	Unc93b1	unc-93 homolog B1 (C. elegans)	1.1	0.333	1.5	0.014	1.91	0.221	-1.39	0.18	0.78

1444666_at	Bxdc1	brix domain containing 1	1.5	0.666	1.6	0.086	1.41	0.272	-1.02	0.962	0.87
1441888_x_at	---	---	2.26	0.165	-1.22	0.603	1.43	0.501	1.97	0.451	1.11
1436194_at	C330008K14Rik	RIKEN cDNA C330008K14 gene	1.26	0.127	2.38	0.038	-1.14	0.489	1.44	0.195	0.98
1436245_at	Usp20	ubiquitin specific peptidase 20	1.03	0.943	2.09	0.025	1.4	0.49	-1.13	0.796	0.85
1453033_at	2010003O02Rik	RIKEN cDNA 2010003O02 gene	2.52	0.138	1.07	0.748	-1.08	0.868	1.2	0.689	0.93
1416287_at	Rgs4	regulator of G-protein signaling 4	1.05	0.915	2.51	0.069	-1.04	0.918	2.28	0.222	1.2
1421146_at	Rapgef1	Rap guanine nucleotide exchange factor (GEF) 1	1.56	0.556	1.31	0.742	1.66	0.427	-1.95	0.331	0.64
1431680_a_at	Ptprk	protein tyrosine phosphatase, receptor type, K	1.58	0.514	-1.04	0.94	1.98	0.337	1.31	0.316	0.96
1426184_a_at	Pdcd6ip	programmed cell death 6 interacting protein	1.21	0.752	1.03	0.963	2.29	0.442	-1.03	0.967	0.87
1459174_at	---	---	2.39	0.059	1.38	0.626	-1.33	0.365	1.73	0.227	1.04
1457091_at	4930526D03Rik	RIKEN cDNA 4930526D03 gene	1.61	0.135	2.03	0.025	-1.13	0.745	1.14	0.836	0.91
1447727_at	Aqp3	Aquaporin 3	1.02	0.948	2.25	0.137	1.25	0.547	-1.52	0.472	0.75
1435425_at	4933439C20Rik ///	RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	1.44	0.003	1.23	0.523	1.85	0.041	-1.24	0.651	0.82
1460390_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	1.23	0.493	1.62	0.287	1.67	0.172	-1.66	0.135	0.72
1445599_at	Fndc7	fibronectin type III domain containing 7	-1.6	0.444	2.56	0.315	1.34	0.559	1.49	0.433	0.95
1436791_at	Wnt5a	wingless-related MMTV integration site 5A	1.03	0.813	2.69	0.225	-1.25	0.312	1.12	0.452	0.9
1450808_at	Fpr1	formyl peptide receptor 1	-1.12	0.495	1.59	0.027	2.05	0.31	1.59	0.228	1.03
1448558_a_at	Pla2g4a	phospholipase A2, group IVA (cytosolic, calcium-dependent)	-1.02	0.945	2.41	0.001	1.14	0.275	1.18	0.388	0.93
1439252_at	---	---	-1.56	0.502	2.59	0.032	1.3	0.077	3.24	0.163	1.39
1437760_at	Galnt12	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.28	0.338	1.06	0.75	2.18	0.052	-1.94	0.089	0.65
1418166_at	Il12rb1	interleukin 12 receptor, beta 1	-1.19	0.589	1.07	0.924	2.62	0.004	1.27	0.598	0.94
1450834_at	Fut4	fucosyltransferase 4	1.4	0.649	-3.32	0.255	2.83	0.147	1.27	0.637	0.54
1415798_at	Ddr1	discoidin domain receptor family, member 1	1.28	0.568	2.02	0.446	1.23	0.564	-1.65	0.389	0.72
1438618_at	AI507597	expressed sequence AI507597	-1.44	0.694	1.81	0.342	2.02	0.185	2.02	0.047	1.1
1459115_at	---	Transcribed locus	-1.13	0.844	1.8	0.279	1.85	0.146	1.09	0.883	0.9
1428392_at	Rassf2	Ras association (RalGDS/AF-6) domain family 2	2.44	0.118	1.04	0.838	1.05	0.889	-1.63	0.357	0.73
1430744_at	Napsa	napsin A aspartic peptidase	1.11	0.665	2.27	0.265	1.16	0.751	-2.37	0.039	0.54
1439914_at	4932416H05Rik	RIKEN cDNA 4932416H05 gene	1.25	0.435	2.48	0.063	-1.25	0.373	1.65	0.278	1.03
1424292_at	Depdc1a	DEP domain containing 1a	-1.67	0.432	2.67	0.075	1.27	0.052	5.21	0.197	1.87
1443225_at	Acvr1c	activin A receptor, type IC	1	0.999	-1.09	0.884	2.62	0.14	1.27	0.693	0.95
1457737_at	E130012K09	hypothetical protein E130012K09	2.58	0.044	-1.24	0.725	1.15	0.821	1.78	0.479	1.07
1459294_at	Mipep	mitochondrial intermediate peptidase	1.17	0.782	1.05	0.947	2.32	0.12	-1.44	0.6	0.78
1459737_s_at	Ttr	transthyretin	1.16	0.804	-1.15	0.464	2.51	0.231	5.25	0.301	1.94
1415850_at	Rasa3	RAS p21 protein activator 3	1.6	0.318	1.28	0.128	1.66	0.03	-1.78	0.084	0.69
1445354_at	---	Transcribed locus	1.75	0.182	1.79	0.299	1	0.993	-1.35	0.34	0.8
1421628_at	Il18r1	interleukin 18 receptor 1	1.55	0.114	2.07	0.224	-1.08	0.794	2.38	0.392	1.23
1458310_at	A230056J06Rik	RIKEN cDNA A230056J06 gene	1.49	0.133	2.4	0.298	-1.53	0.255	1.05	0.944	0.85
1425478_x_at	Ube2i	ubiquitin-conjugating enzyme E2I	1.3	0.4	2.6	0.363	-1.55	0.333	1.13	0.829	0.87
1448407_at	4632428N05Rik	RIKEN cDNA 4632428N05 gene	-1.02	0.879	1.83	0.06	1.74	0.134	1.14	0.254	0.92
1431513_at	4921537P18Rik	RIKEN cDNA 4921537P18 gene	1.62	0.351	2.06	0.23	-1.15	0.752	1.45	0.264	1
1447558_at	---	---	1.1	0.841	-1.14	0.664	2.58	0	2.06	0.237	1.15
1428242_at	Hmha1	histocompatibility (minor) HA-1	1.57	0.343	1.32	0.23	1.67	0.036	-2.19	0.046	0.59
1442313_at	4933400E14Rik	RIKEN cDNA 4933400E14 gene	-1.14	0.858	2.52	0.259	1.16	0.808	1.11	0.886	0.91
1455774_at	Jund1	Jun proto-oncogene related gene d1	1.43	0.441	2.06	0.279	1.07	0.759	-1.53	0.414	0.76
1454764_s_at	Slc38a1	solute carrier family 38, member 1	1.14	0.437	1.98	0.124	1.44	0.207	-1.4	0.231	0.79
1437794_at	Cabin1	calcineurin binding protein 1	-1.39	0.669	1.69	0.539	2.15	0.174	1.58	0.272	1.01
1442063_at	5930437A14Rik	RIKEN cDNA 5930437A14 gene	1.26	0.336	2.25	0.316	1.05	0.829	-1.2	0.013	0.84
1452437_at	1110021J02Rik	RIKEN cDNA 1110021J02 gene	1.5	0.722	1.86	0.214	1.2	0.53	-2.06	0.235	0.62
1459260_at	---	---	1.68	0.591	1.67	0.226	1.21	0.624	-1.43	0.394	0.78
1421070_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	1.47	0.38	1.15	0.78	1.94	0.086	-1.2	0.561	0.84
1453973_s_at	2900057H02Rik	RIKEN cDNA 2900057H02 gene	1.19	0.617	-1.09	0.895	2.46	0.115	1.18	0.51	0.93
1459266_at	---	---	1.52	0.225	2.02	0.188	1.02	0.832	-1.37	0.441	0.8
1425598_a_at	LOC676654	similar to Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	1.21	0.165	1.31	0.231	2.05	0.035	-1.26	0.296	0.83

1419655_at	Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	1.02	0.834	1.88	0.027	1.67	0.011	-1.36	0.303	0.8
1430984_at	Azin1	antizyme inhibitor 1	1.51	0.391	-1.46	0.567	2.37	0.405	1.91	0.468	1.08
1436285_at	Ccdc113	coiled-coil domain containing 113	1.92	0.425	1.78	0.265	-1.16	0.591	1.9	0.365	1.11
1449504_at	Kpna1	karyopherin (importin) alpha 1	1.62	0.294	-1.17	0.794	2.09	0.253	1.59	0.405	1.03
1456911_at	Clasp2	CLIP associating protein 2	1.28	0.741	1.93	0.381	1.36	0.352	-1.34	0.68	0.81
1418650_at	Spata6	spermatogenesis associated 6	1.11	0.654	2.43	0.085	1.04	0.855	-1.91	0.127	0.67
1436470_at	Rims2	regulating synaptic membrane exocytosis 2	-1.11	0.233	1.7	0.374	1.97	0.079	1.83	0.358	1.1
1455755_at	Gm88	gene model 88, (NCBI)	-1.13	0.891	2.13	0.125	1.55	0.289	1.36	0.737	0.98
1428306_at	Ddit4	DNA-damage-inducible transcript 4	1.15	0.757	1.88	0.185	1.55	0.271	-1.73	0.079	0.71
1452534_a_at	Hmgb2 /// LOC433	high mobility group box 2 /// similar to High mobility group protein 2 (HMG-2) /// hi	-1.12	0.056	1.97	0.161	1.72	0.051	1.81	0.297	1.09
1422959_s_at	Zfp313	zinc finger protein 313	1.25	0.684	1.31	0.499	2.01	0.289	-1.21	0.724	0.84
1416702_at	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1	1.16	0.799	1.43	0.536	1.99	0.042	-1.52	0.114	0.76
1431138_at	Armc9	armadillo repeat containing 9	1.42	0.204	-1.1	0.721	2.24	0.057	1.69	0.381	1.06
1452352_at	Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta	1.68	0.03	1.92	0.015	-1.03	0.875	1.34	0.195	0.98
1442902_at	Qrich2	glutamine rich 2	2.73	0.455	-1.82	0.348	1.29	0.158	1.23	0.649	0.86
1459214_at	Odz2	Odd Oz/ten-m homolog 2 (Drosophila)	-1.11	0.576	1.15	0.812	2.52	0.02	1.49	0.57	1.01
1434353_at	Sfmbt2	Scm-like with four mbt domains 2	1.74	0.352	1.24	0.687	1.6	0.555	-1.52	0.039	0.76
1429338_a_at	Nol9	nucleolar protein 9	2.05	0.318	1.2	0.674	1.33	0.624	-1.03	0.922	0.89
1450281_a_at	1700021K02Rik	RIKEN cDNA 1700021K02 gene	2.65	0.023	-1.45	0.489	1.24	0.482	1.17	0.728	0.9
1457280_at	---	---	1.14	0.492	2.75	0.087	-1.45	0.281	1.03	0.958	0.87
1419933_at	Pdrg1	p53 and DNA damage regulated 1	1.56	0.571	1.48	0.448	1.54	0.466	-1.77	0.347	0.7
1453414_at	Ypel2	yippee-like 2 (Drosophila)	2.39	0.144	1.2	0.701	-1	0.997	1.17	0.457	0.94
1419220_at	Cmya1	cardiomyopathy associated 1	1.7	0.259	2.22	0.034	-1.52	0.584	1.02	0.964	0.86
1434959_at	Dhh	desert hedgehog	1.11	0.886	2.29	0.297	1.18	0.482	-1.86	0.061	0.68
1437355_at	Zcchc5	zinc finger, CCHC domain containing 5	1.57	0.334	2.07	0.087	-1.06	0.739	1.13	0.618	0.93
1450032_at	Slco2a1	solute carrier organic anion transporter family, member 2a1	1.56	0.33	1.14	0.705	1.88	0.168	-1.16	0.623	0.86
1422557_s_at	Mt1	metallothionein 1	-1.01	0.946	2.45	0.026	1.14	0.487	3.64	0.029	1.56
1445214_at	LOC195531	Similar to reduced expression 2	1.95	0.056	2.05	0.324	-1.71	0.092	1.33	0.363	0.91
1417928_at	Pdlim4	PDZ and LIM domain 4	1.44	0.13	1.62	0.299	1.53	0.151	-1.45	0.339	0.78
1459165_at	D4Ertd179e	DNA segment, Chr 4, ERATO Doi 179, expressed	-1.27	0.834	2.26	0.155	1.54	0.542	1.22	0.623	0.94
1424158_at	LOC673251	similar to EH-domain containing 2	1.95	0.19	1.09	0.885	1.55	0.406	-3.11	0.302	0.37
1435022_at	Cart1	cartilage homeo protein 1	1.11	0.649	1.39	0.263	2.09	0.377	-1.94	0.046	0.66
1447879_x_at	Dalrd3 /// Wdr6	DALR anticodon binding domain containing 3 /// WD repeat domain 6	2.57	0.375	-1.04	0.855	1.05	0.869	1.01	0.968	0.9
1449621_s_at	Thsd1	thrombospondin, type I, domain 1	1.77	0.377	1.72	0.154	1.1	0.515	-1.14	0.804	0.86
1430062_at	1600002O04Rik	RIKEN cDNA 1600002O04 gene	-1.19	0.796	1.88	0.275	1.87	0.052	1.26	0.084	0.96
1447192_at	---	---	1.54	0.707	1.21	0.431	1.84	0.223	-1.22	0.658	0.84
1444407_at	---	Transcribed locus	-3	0.07	3.02	0.306	1.24	0.486	1.07	0.909	0.58
1426387_x_at	4933439C20Rik ///	RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	1.48	0.288	1.24	0.13	1.88	0.017	-1.25	0.631	0.84
1426170_a_at	Cd8b1	CD8 antigen, beta chain 1	1.15	0.316	1.88	0.447	1.56	0.412	-1.63	0.538	0.74
1457014_x_at	Slc16a8	Solute carrier family 16 (monocarboxylic acid transporters), member 8	1.25	0.681	1.68	0.426	1.67	0.297	-1.06	0.822	0.88
1447799_x_at	1700001P01Rik	RIKEN cDNA 1700001P01 gene	2.09	0.074	1.07	0.885	1.44	0.323	-1.12	0.904	0.87
1447133_at	---	---	2.05	0.341	1.51	0.476	1.04	0.936	-1.39	0.643	0.8
1422903_at	Ly86	lymphocyte antigen 86	1.3	0.306	1.54	0.001	1.76	0.315	-1.7	0.157	0.72
1418162_at	Tlr4	toll-like receptor 4	1.82	0.02	1.81	0.015	-1.04	0.683	1.16	0.402	0.94
1459297_at	Cdc91l1	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	1.12	0.768	1.47	0.57	2.01	0.132	-1.68	0.518	0.73
1432382_at	4930434B07Rik	RIKEN cDNA 4930434B07 gene	3.01	0.147	-2.17	0.2	1.13	0.755	1.01	0.894	0.75
1421168_at	Abcg3	ATP-binding cassette, sub-family G (WHITE), member 3	1.3	0.391	1.86	0.042	1.44	0.242	-1.55	0.357	0.76
1420565_at	Hoxa1	homeo box A1	1.18	0.123	2.64	0.028	-1.27	0.361	1.44	0.212	1
1454266_at	Cldnd2	claudin domain containing 2	2.19	0.21	-1.02	0.958	1.44	0.123	1.22	0.393	0.96
1454420_at	5730420F10Rik	RIKEN cDNA 5730420F10 gene	1.75	0.407	1.44	0.58	1.42	0.461	-1.37	0.495	0.81
1429964_at	5031420N21Rik	RIKEN cDNA 5031420N21 gene	1.16	0.517	1.44	0.373	2	0.294	-1.49	0.555	0.78
1440437_at	Herc1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	2.56	0.318	-1.52	0.568	1.39	0.415	2.11	0.063	1.13
1430373_at	5430427O19Rik	RIKEN cDNA 5430427O19 gene	1.32	0.054	1.62	0.25	1.66	0	-1.12	0.697	0.87

1449461_at	Rbp7	retinol binding protein 7, cellular	1.39	0.595	-2.42	0.172	2.8	0.192	1.96	0.264	0.93
1431546_at	4930509K18Rik	RIKEN cDNA 4930509K18 gene	1.44	0.489	1.74	0.24	1.43	0.288	-1.15	0.717	0.87
1444335_at	Edem2	ER degradation enhancer, mannosidase alpha-like 2	1.77	0.366	1.02	0.946	1.82	0.109	-2.19	0.369	0.6
1430396_at	5730403I07Rik	RIKEN cDNA 5730403I07 gene	1.2	0.7	1.98	0.327	1.44	0.56	-1.27	0.419	0.83
1447707_s_at	Pde2a	phosphodiesterase 2A, cGMP-stimulated	1.09	0.64	1.1	0.301	2.42	0	-1.36	0.406	0.81
1430615_at	4921517B04Rik	RIKEN cDNA 4921517B04 gene	1.08	0.382	1.81	0.196	1.73	0.269	-1.77	0.347	0.71
1420337_at	Gbx2	gastrulation brain homeobox 2	1.29	0.354	2.08	0.294	1.24	0.533	-1.74	0.218	0.72
1439133_at	4930524O07Rik	RIKEN cDNA 4930524O07 gene	1.7	0.32	2.04	0.261	-1.15	0.674	1.02	0.974	0.9
1458496_at	Cyb561	Cytochrome b-561	1.47	0.248	2.4	0.4	-1.36	0.489	1.99	0.038	1.13
1441826_x_at	Ubtd1	Ubiquitin domain containing 1	1.24	0.811	1.27	0.769	2.11	0.07	-1.84	0.231	0.69
1453516_at	4931431F19Rik	RIKEN cDNA 4931431F19 gene	1.25	0.036	1.34	0.64	2.03	0.328	-1.09	0.898	0.88
1425667_at	Acot11	acyl-CoA thioesterase 11	-1.03	0.822	2.24	0.284	1.41	0.106	1.41	0.559	1.01
1439835_x_at	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2	1.72	0.583	-1.7	0.435	2.31	0.066	1.5	0.286	0.96
1456230_at	4933422H20Rik	RIKEN cDNA 4933422H20 gene	1.66	0.418	2.33	0.017	-1.6	0.367	1.86	0.178	1.06
1445023_at	---	Transcribed locus	2.91	0.135	-2.32	0.216	1.28	0.653	2.25	0.41	1.03
1438102_at	Senp8	SUMO/sentrin specific peptidase 8	-1.03	0.974	2.15	0.107	1.5	0.319	1.15	0.443	0.94
1452202_at	Pde2a	phosphodiesterase 2A, cGMP-stimulated	1.21	0.372	1.12	0.667	2.29	0.006	-1.18	0.693	0.86
1432254_at	C030013D06Rik	RIKEN cDNA C030013D06 gene	1.22	0.848	2.72	0.191	-1.47	0.41	1.01	0.981	0.87
1450195_at	Ndst4	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	2.62	0.292	1.25	0.377	-1.33	0.151	1.91	0.099	1.11
1433263_at	---	---	1.5	0.417	2.37	0.049	-1.33	0.574	2.04	0.367	1.14
1433046_at	4930535F04Rik	RIKEN cDNA 4930535F04 gene	1.28	0.796	1.91	0.095	1.44	0.384	-1.26	0.658	0.84
1441650_at	Arhgap15	Rho GTPase activating protein 15	1.66	0.076	1.74	0.053	1.22	0.799	-4.03	0.441	0.15
1445581_at	---	---	1.43	0.413	1.65	0.298	1.54	0.4	-1.39	0.337	0.81
1450828_at	Synpo2	synaptopodin 2	1.35	0.588	1.54	0.088	1.73	0.098	-1.16	0.734	0.86
1446259_at	---	---	1.43	0.551	-1.5	0.184	2.53	0.234	1.21	0.723	0.92
1419288_at	Jam2	junction adhesion molecule 2	-1.19	0.437	1.43	0.4	2.35	0.311	1.04	0.801	0.91
1458599_at	---	---	1.13	0.161	2.49	0.126	-1	0.993	1.57	0.211	1.05
1417756_a_at	Lsp1	lymphocyte specific 1	1.4	0.029	1.76	0.013	1.46	0.2	-1.71	0.221	0.73
1425510_at	Mark1	MAP/microtubule affinity-regulating kinase 1	1.51	0.288	1.99	0.107	1.13	0.742	-1.34	0.545	0.82
1440382_at	BC051628	cDNA sequence BC051628	2.33	0.238	-1.36	0.711	1.57	0.179	1.04	0.919	0.89
1450790_at	Tgn	thyroglobulin	1.1	0.898	-1.22	0.514	2.71	0.035	3.3	0.032	1.47
1456949_at	Fchsd2	FCH and double SH3 domains 2	1.58	0.088	1.68	0.44	1.37	0.3	-2.34	0.137	0.57
1445481_at	AI317158	expressed sequence AI317158	1.08	0.773	2.86	0.01	-1.45	0.116	1.2	0.708	0.92
1426547_at	Gc	group specific component	1.02	0.935	-1.2	0.323	2.78	0.041	2.78	0.434	1.35
1425657_at	1700016D06Rik	RIKEN cDNA 1700016D06 gene	1.73	0.571	-1.22	0.654	2.09	0.116	1.17	0.8	0.94
1422017_s_at	4833439L19Rik	RIKEN cDNA 4833439L19 gene	1.25	0.746	-1.46	0.541	2.7	0.278	1.66	0.467	1.04
1427763_a_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	1.14	0.696	1.58	0.276	1.92	0.148	-1.2	0.581	0.86
1416529_at	Emp1	epithelial membrane protein 1	1.31	0.314	2.68	0.045	-1.54	0.018	1.33	0.362	0.94
1417612_at	Ier5	immediate early response 5	1.25	0.028	1.74	0.033	1.66	0.044	-1.88	0.094	0.69
1456426_at	---	---	1.32	0.722	2.11	0.244	1.22	0.064	-4.31	0.095	0.08
1417634_at	Sod3	superoxide dismutase 3, extracellular	1.62	0.333	1.71	0.176	1.32	0.518	-1.53	0.583	0.78
1438044_at	1700047M11Rik	RIKEN cDNA 1700047M11 gene	-1.31	0.208	1.16	0.78	2.72	0.188	2.6	0.217	1.29
1440709_at	C130081A10Rik	RIKEN cDNA C130081A10 gene	2.34	0.101	1.41	0.329	-1.12	0.802	1.08	0.911	0.93
1430084_at	Tlcd1	TLC domain containing 1	2.28	0.397	-1.65	0.262	1.76	0.369	3.71	0.312	1.52
1449454_at	Bst1	bone marrow stromal cell antigen 1	1.21	0.212	2.1	0.245	1.34	0.295	-1.23	0.388	0.85
1450196_s_at	Gys1	glycogen synthase 1, muscle	1.3	0.388	-1.25	0.681	2.54	0.243	1.04	0.951	0.91
1437344_x_at	---	---	1.37	0.429	2.25	0.331	1.03	0.875	-1.41	0.455	0.81
1419541_at	4930403L05Rik	RIKEN cDNA 4930403L05 gene	1.18	0.833	2.42	0.039	1.05	0.937	-1.3	0.545	0.84
1446798_at	---	---	1.78	0.197	2.51	0.174	-2.79	0.077	1.58	0.412	0.77
1417887_at	Ints5	integrator complex subunit 5	1.32	0.497	-1.03	0.943	2.36	0.284	1.48	0.47	1.03
1430459_at	4632428C04Rik	RIKEN cDNA 4632428C04 gene	2.91	0.433	-1.48	0.117	1.07	0.901	1.01	0.991	0.88
1425603_at	0610011I04Rik	RIKEN cDNA 0610011I04 gene	1.42	0.154	2.22	0.124	1.01	0.924	-1.45	0.234	0.8
1437292_at	A330019N05Rik	RIKEN cDNA A330019N05 gene	1.82	0.537	-1.75	0.416	2.25	0.173	1.51	0.616	0.96

1419882_at	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	2.25	0.358	1.25	0.179	1.15	0.782	-1.17	0.813	0.87
1443019_at	---	---	3.04	0.052	1.03	0.901	-1.74	0.514	1.37	0.621	0.93
1422573_at	Ampd3	AMP deaminase 3	-1.18	0.385	2.27	0.006	1.54	0.055	2.69	0.181	1.33
1421192_a_at	Itsn1	intersectin 1 (SH3 domain protein 1A)	1.15	0.486	2.68	0.267	-1.21	0.601	2.49	0.023	1.28
1424249_a_at	Arhgap9	Rho GTPase activating protein 9	1.09	0.749	1.54	0.249	2.03	0.067	-1.67	0.107	0.75
1446881_at	AU022749	expressed sequence AU022749	1.64	0.261	1.72	0.117	1.29	0.254	-1.41	0.497	0.81
1443973_at	Dact2	dapper homolog 2, antagonist of beta-catenin (xenopus)	2.28	0.047	1.24	0.652	1.13	0.664	-1.07	0.894	0.9
1420297_at	---	---	1.74	0.598	1.34	0.627	1.58	0.524	-1.11	0.722	0.89
1439555_at	Rlf	rearranged L-myc fusion sequence	1.23	0.777	1	0.996	2.42	0.405	-1.26	0.801	0.85
1438584_at	4932411G14Rik	RIKEN cDNA 4932411G14 gene	2.93	0.053	-1.92	0.22	1.21	0.613	1.87	0.115	1.02
1450970_at	Got1	glutamate oxaloacetate transaminase 1, soluble	1.02	0.807	1.03	0.834	2.62	0.018	-1.43	0.114	0.81
1438280_at	1700023L04Rik	RIKEN cDNA 1700023L04 gene	1.28	0.264	1.64	0.29	1.75	0.365	-1.41	0.199	0.81
1453912_at	Zfp558	zinc finger protein 558	1.33	0.604	1.57	0.471	1.77	0.373	-1.84	0.164	0.71
1457617_at	---	---	1	0.972	2.83	0.025	-1.2	0.646	1.35	0.598	1
1433741_at	Cd38	CD38 antigen	1.15	0.361	2.01	0	1.5	0.349	-1.19	0.639	0.87
1420864_at	Zfp161	zinc finger protein 161	2.35	0.037	-1.5	0.302	1.65	0.245	2.14	0.106	1.16
1459510_at	Tmprss2	transmembrane protease, serine 2	1.46	0.693	2.88	0.035	-3.09	0.224	1.01	0.955	0.57
1453628_s_at	Lrrc2	leucine rich repeat containing 2	1.2	0.383	2.19	0.154	1.28	0.44	-1.02	0.892	0.91
1457204_at	Zdhhc2	Zinc finger, DHHC domain containing 2	1.76	0.396	-1.55	0.448	2.27	0.004	1.07	0.855	0.89
1448561_at	Ncf2	neutrophil cytosolic factor 2	1.31	0.183	1.54	0.01	1.82	0.17	-1.95	0.101	0.68
1460501_at	4930521G14Rik	RIKEN cDNA 4930521G14 gene	1.78	0.476	1.66	0.25	1.23	0.768	-2	0.367	0.67
1432661_at	0610042E11Rik	RIKEN cDNA 0610042E11 gene	1.61	0.456	1.88	0.138	1.19	0.666	-1.55	0.578	0.78
1417104_at	Emp3	epithelial membrane protein 3	1.43	0.522	2.15	0.009	1.1	0.634	-1.51	0.362	0.79
1457863_at	---	---	2.9	0.451	-1.6	0.46	1.15	0.653	1.5	0.477	0.99
1425607_at	Hlcs	holocarboxylase synthetase (biotin- [propriony-Coenzyme A-carboxylase (ATP-h	1.1	0.859	1.36	0.342	2.22	0.129	-1.1	0.708	0.89
1420065_at	Tktl1	Transketolase-like 1	1.08	0.88	2.85	0.259	-1.34	0.61	1.12	0.872	0.93
1453281_at	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	1.15	0.667	1.44	0.04	2.09	0.027	-1.4	0.363	0.82
1454028_at	4931402H11Rik	RIKEN cDNA 4931402H11 gene	-1.49	0.421	2.04	0.326	1.97	0.059	2.09	0.444	1.15
1432917_at	4933408M05Rik	RIKEN cDNA 4933408M05 gene	1.67	0.351	1.71	0.346	1.3	0.311	-1.45	0.545	0.81
1453164_a_at	Ptdss2	phosphatidylserine synthase 2	1.62	0.543	-1.89	0.345	2.54	0.392	26.62	0.236	7.22
1423029_at	Hes2	hairy and enhancer of split 2 (Drosophila)	-1.16	0.502	2.09	0.136	1.73	0.379	1.43	0.012	1.02
1423026_at	Rad51c	Rad51 homolog c (S. cerevisiae)	1.78	0.122	-1.54	0.428	2.25	0.182	2.66	0.214	1.29
1418655_at	B4galnt1	beta-1,4-N-acetyl-galactosaminyl transferase 1	1.9	0.051	1.29	0.083	1.5	0.022	-1.58	0.343	0.78
1444063_at	5430435G22Rik	RIKEN cDNA 5430435G22 gene	1.78	0.256	2.03	0.197	-1.15	0.702	1.04	0.928	0.92
1417312_at	Dkk3	dickkopf homolog 3 (Xenopus laevis)	1.65	0.119	2.16	0.212	-1.15	0.462	1.09	0.508	0.94
1445014_at	AU019157	expressed sequence AU019157	3.04	0.314	-3.08	0.152	1.32	0.607	1.46	0.648	0.68
1448213_at	Anxa1	annexin A1	1.16	0.341	2.53	0.041	-1	0.977	1.36	0.63	1.01
1416752_at	Ldb3	LIM domain binding 3	-1.03	0.949	1.49	0.309	2.22	0.19	1.39	0.629	1.02
1427694_at	Gnrhr	gonadotropin releasing hormone receptor	-1.51	0.372	2.07	0.044	1.96	0.351	1.18	0.768	0.92
1427770_a_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	1.47	0.478	1.02	0.975	2.2	0.315	-1.18	0.781	0.88
1430811_a_at	Cdca1	cell division cycle associated 1	-1.45	0.054	1.93	0.305	2.07	0.069	4.72	0.163	1.82
1452487_x_at	Pira2	paired-Ig-like receptor A2	-1.38	0.003	2.29	0.377	1.68	0.302	1.23	0.287	0.95
1457310_x_at	Scrt2	scratch homolog 2, zinc finger protein (Drosophila)	-1.3	0.105	1.78	0.5	2.14	0.015	1.41	0.6	1.01
1422963_at	Sprr2i	small proline-rich protein 2I	-1.13	0.611	1.58	0.549	2.23	0.247	1.17	0.152	0.96
1420719_at	Tex15	testis expressed gene 15	1.71	0.223	2.4	0.109	-1.72	0.028	1.14	0.654	0.88
1426258_at	Sorl1	sortilin-related receptor, LDLR class A repeats-containing	1.02	0.773	2.37	0.027	1.3	0.016	-2.18	0.115	0.63
1428111_at	Slc38a4	solute carrier family 38, member 4	2.71	0.087	-1.03	0.773	1.02	0.943	1.47	0.44	1.04
1434295_at	Rasgrp1	RAS guanyl releasing protein 1	1.16	0.378	1.52	0.07	2.02	0.116	-1.69	0.258	0.75
1436264_at	BC025920	cDNA sequence BC025920	1.1	0.721	2.49	0.037	1.12	0.364	-1.08	0.766	0.91
1460329_at	LOC675709	similar to Beta-1,4-galactosyltransferase 6 (Beta-1,4-GalTase 6) (Beta4Gal-T6) (I	-1.01	0.934	2.22	0.026	1.5	0.05	1.75	0.041	1.11
1416737_at	---	---	-1.02	0.919	2.21	0.077	1.51	0.03	1.14	0.553	0.96
1423829_at	0910001A06Rik	RIKEN cDNA 0910001A06 gene	1.3	0.308	1.9	0.015	1.5	0.186	-1.26	0.404	0.86
1444176_at	Atp6v0d2	ATPase, H+ transporting, lysosomal V0 subunit D2	-1.56	0.042	2.64	0.084	1.42	0.079	2.01	0.315	1.13

1448506_at	Serpina6	serine (or cysteine) peptidase inhibitor, clade A, member 6	2.28	0.134	-1.26	0.639	1.63	0.251	2.21	0.103	1.21
1453946_a_at	Sdccag8	serologically defined colon cancer antigen 8	1.78	0.092	1.15	0.52	1.77	0.264	-1.64	0.047	0.77
1449265_at	Casp1	caspase 1	1.23	0.745	1.29	0.1	2.19	0.013	-1.43	0.277	0.82
1442221_at	Sergef	Secretion regulating guanine nucleotide exchange factor	2.62	0.099	1.04	0.926	1.05	0.945	-2.22	0.212	0.62
1440741_at	Htr1d	5-hydroxytryptamine (serotonin) receptor 1D	1.4	0.546	2.6	0.179	-1.42	0.027	1.83	0.228	1.1
1434458_at	Fst	Follistatin	1.09	0.62	2.69	0.171	-1.09	0.769	1.36	0.525	1.01
1434929_at	BC035044	cDNA sequence BC035044	1.48	0.301	1.9	0.026	1.33	0.291	-1.75	0.167	0.74
1448827_s_at	Myh6 /// Myh7 /// LC	myosin, heavy polypeptide 6, cardiac muscle, alpha /// myosin, heavy polypeptide	-1.04	0.86	1.4	0.401	2.35	0.286	1.2	0.279	0.98
1424067_at	Icam1	intercellular adhesion molecule	1.54	0.139	1.99	0.038	1.18	0.354	-1.51	0.244	0.8
1425863_a_at	Ptpro	protein tyrosine phosphatase, receptor type, O	1.37	0.269	2.29	0.069	1.05	0.895	-1.3	0.31	0.85
1438749_at	Fuz	fuzzy homolog (Drosophila)	2.29	0.375	1.18	0.742	1.24	0.556	-2.88	0.02	0.46
1419064_a_at	Ugt8a	UDP galactosyltransferase 8A	2.33	0.416	1.85	0.374	-1.87	0.138	1.41	0.675	0.93
1428959_at	5830405N20Rik	RIKEN cDNA 5830405N20 gene	2.11	0.398	1.18	0.773	1.42	0.505	-2.84	0.035	0.47
1434110_x_at	Mup1	major urinary protein 1	2.17	0.565	-1.41	0.243	1.83	0.069	1.51	0.123	1.03
1442156_at	E030030I06Rik	RIKEN cDNA E030030I06 gene	2.09	0.034	1.56	0.336	1.06	0.78	-2.41	0.005	0.58
1418396_at	Gpsm3	G-protein signalling modulator 3 (AGS3-like, C. elegans)	1.7	0.03	1.6	0.007	1.41	0.196	-1.59	0.179	0.78
1447907_x_at	Apba2bp	Amyloid beta (A4) precursor protein-binding, family A, member 1 binding protein	1.49	0.364	1.74	0.122	1.49	0.489	-2.09	0.31	0.66
1459545_at	---	---	2.8	0.418	1.11	0.852	-1.24	0.57	1.52	0.048	1.05
1449840_at	Sntb2	syntrophin, basic 2	-1.12	0.746	2.32	0.021	1.5	0.286	1.06	0.795	0.94
1458560_at	Aspm	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	-1.07	0.759	1.32	0.299	2.46	0.137	7.9	0.23	2.66
1446208_at	Tdrd5	Tudor domain containing 5	1.29	0.797	2.23	0.238	1.2	0.68	-2.12	0.381	0.65
1438119_at	Itgb1	Integrin beta 1 (fibronectin receptor beta)	2.6	0.041	1.05	0.931	1.08	0.797	-1.31	0.686	0.85
1454601_at	8030497O21Rik	RIKEN cDNA 8030497O21 gene	2.83	0.14	-1.38	0.372	1.17	0.825	1.67	0.179	1.07
1452557_a_at	---	---	1.5	0.275	1.49	0.195	1.73	0.044	-1.2	0.488	0.88
1421475_at	Ms4a2	membrane-spanning 4-domains, subfamily A, member 2	1.43	0.519	-2.37	0.188	2.88	0.249	1.31	0.72	0.81
1427586_at	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	-1.12	0.673	1.18	0.311	2.66	0.053	1.68	0.114	1.1
1425295_at	Ear11	eosinophil-associated, ribonuclease A family, member 11	-1.9	0.064	2.33	0.207	1.88	0.544	3.85	0.3	1.54
1424629_at	Brca1	breast cancer 1	-1.35	0.644	2.59	0.019	1.4	0.04	3.52	0.208	1.54
1441601_at	Orc5l	Origin recognition complex, subunit 5-like (S. cerevisiae)	2.89	0.142	-1.26	0.659	1.05	0.92	1.15	0.806	0.96
1421067_a_at	Phf2	PHD finger protein 2	1.03	0.97	1.68	0.503	2.03	0.351	-1.78	0.41	0.74
1433492_at	Epb4.1l2	erythrocyte protein band 4.1-like 2	1.85	0.197	1.08	0.707	1.81	0.457	-1.66	0.478	0.77
1455162_at	4922503N01Rik	RIKEN cDNA 4922503N01 gene	-2.27	0.065	2.91	0.176	1.39	0.295	1.15	0.476	0.79
1432758_at	2900011L18Rik	RIKEN cDNA 2900011L18 gene	2.75	0.05	1.08	0.906	-1.1	0.701	1.01	0.983	0.94
1433373_at	Supt7l	suppressor of Ty 7 (S. cerevisiae)-like	1.6	0.395	2.09	0.039	1.04	0.937	-1.15	0.774	0.9
1436321_at	B3gnt7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7	1.11	0.845	2.46	0.067	1.17	0.153	-1.71	0.392	0.76
1449396_at	Aoc3	amine oxidase, copper containing 3	-1.49	0.182	1.46	0.436	2.6	0.333	1.57	0.003	1.04
1435640_x_at	A130040M12Rik	RIKEN cDNA A130040M12 gene	1.2	0.775	1.64	0.141	1.89	0.409	-1.54	0.181	0.8
1435426_s_at	4933439C20Rik ///	RIKEN cDNA 4933439C20 gene /// phosphatidylserine decarboxylase	1.49	0.011	1.28	0.286	1.97	0.029	-1.15	0.695	0.9
1457364_at	---	---	1.1	0.224	1.54	0.351	2.11	0.256	-1.01	0.989	0.93
1448889_at	Slc38a4	solute carrier family 38, member 4	2.62	0.271	-1.01	0.924	1.14	0.81	2.04	0.429	1.2
1458325_x_at	Bmf	Bcl2 modifying factor	-1.4	0.56	2.71	0.153	1.32	0.61	1.91	0.242	1.14
1449846_at	Ear2	eosinophil-associated, ribonuclease A family, member 2	1.86	0.17	2.25	0.018	-1.57	0.058	1.26	0.407	0.95
1440165_at	Ptprc	Protein tyrosine phosphatase, receptor type, C	1.52	0.039	2.22	0.02	1.01	0.969	-2.33	0.203	0.6
1422637_at	Rassf5	Ras association (RalGDS/AF-6) domain family 5	1.55	0.026	1.01	0.925	2.19	0.022	-1.69	0.19	0.76
1438718_at	Fgf9	fibroblast growth factor 9	-1.12	0.664	1.73	0.397	2.12	0.043	1.73	0.441	1.12
1427707_a_at	---	---	2.65	0.426	-1.11	0.8	1.21	0.638	3.88	0.193	1.65
1439070_x_at	4933439C20Rik ///	RIKEN cDNA 4933439C20 gene /// RIKEN cDNA D030013I16 gene	1.23	0.106	1.39	0.092	2.13	0.133	-1.43	0.348	0.83
1460273_a_at	Birc1b	baculoviral IAP repeat-containing 1b	1.52	0.063	1.77	0	1.46	0.017	-1.13	0.563	0.9
1419978_s_at	D10Ertd610e	DNA segment, Chr 10, ERATO Doi 610, expressed	1.34	0.084	2.65	0.023	-1.32	0.225	1.1	0.234	0.94
1432102_at	Rims2	regulating synaptic membrane exocytosis 2	2.08	0.35	1.09	0.833	1.58	0.419	-1.3	0.66	0.86
1417759_at	Pfpl	pore forming protein-like	-1.14	0.229	2.71	0.242	1.16	0.651	1.65	0.366	1.1
1458785_at	Ss18l1	Synovial sarcoma translocation gene on chromosome 18-like 1	1.2	0.052	2.38	0.234	1.17	0.809	-1.77	0.002	0.75
1433049_at	5730478J17Rik	RIKEN cDNA 5730478J17 gene	2.46	0.503	2	0.097	-3.44	0.11	1.43	0.518	0.61

1424307_at	Arhgap1	Rho GTPase activating protein 1	1.36	0.663	1.68	0.135	1.72	0.353	-1.16	0.757	0.9
1451667_at	C530043G21Rik	RIKEN cDNA C530043G21 gene	1.87	0.204	-1.32	0.626	2.13	0.328	2.16	0.501	1.21
1435772_at	Kif21b	kinesin family member 21B	1.58	0.043	1.32	0.208	1.86	0.044	-1.72	0.157	0.76
1418569_at	Fblim1	filamin binding LIM protein 1	2.09	0.09	1.73	0.267	-1.06	0.78	1.14	0.537	0.97
1435569_at	D630029K05Rik	RIKEN cDNA D630029K05 gene	1.4	0.589	1.85	0.198	1.51	0.331	-1.05	0.949	0.93
1453940_at	2810404M03Rik	RIKEN cDNA 2810404M03 gene	2.01	0.37	1.28	0.64	1.46	0.299	-1.28	0.5	0.87
1421129_a_at	Atp2a3	ATPase, Ca++ transporting, ubiquitous	1.46	0.003	1.66	0.157	1.64	0.177	-1.13	0.746	0.91
1431559_at	6430710C18Rik	RIKEN cDNA 6430710C18 gene	1.97	0.265	-1.15	0.748	1.93	0.262	1.52	0.507	1.07
1444090_at	Pram1	PML-RAR alpha-regulated adaptor molecule 1	-1.38	0.09	1.33	0.64	2.71	0.287	1.53	0.389	1.05
1418252_at	Padi2 /// LOC63893	peptidyl arginine deiminase, type II /// similar to peptidyl arginine deiminase, type	1.75	0.141	1.75	0.178	1.26	0.036	-1.06	0.698	0.92
1427829_at	Abcd4	ATP-binding cassette, sub-family D (ALD), member 4	2.05	0.366	1.72	0.468	-1.01	0.957	1.16	0.747	0.98
1425587_a_at	Ptprj	protein tyrosine phosphatase, receptor type, J	1.06	0.739	1.03	0.943	2.68	0.2	-1.28	0.085	0.87
1451941_a_at	Fcgr2b	Fc receptor, IgG, low affinity IIb	-1.2	0.316	1.53	0.17	2.4	0.053	1.26	0.539	1
1458924_at	D430013B06Rik	RIKEN cDNA D430013B06 gene	1.58	0.018	2.44	0.319	-1.35	0.069	1.04	0.897	0.93
1426321_at	Tbx4	T-box 4	1.27	0.607	2.33	0.255	1.17	0.533	-1.6	0.363	0.79
1456406_at	---	---	1.26	0.211	2.28	0.193	1.23	0.243	-1.2	0.565	0.89
1446590_at	---	---	2.24	0.077	1.06	0.913	1.47	0.562	-1.05	0.939	0.93
1451878_a_at	Jmy	junction-mediating and regulatory protein	1.62	0.042	1.04	0.907	2.11	0.248	-1.72	0.473	0.76
1427911_at	2610307O08Rik	RIKEN cDNA 2610307O08 gene	1.28	0.327	2.05	0.008	1.44	0.097	-1.35	0.281	0.85
1459177_at	AU015741	expressed sequence AU015741	1.55	0.544	1.48	0.51	1.74	0.202	-1.23	0.397	0.88
1449858_at	Cd86	CD86 antigen	1.64	0.316	1.93	0.093	1.2	0.309	-1.34	0.246	0.86
1442646_at	Bank1	B-cell scaffold protein with ankyrin repeats 1	1.92	0.58	1.4	0.533	1.45	0.6	-2.75	0.113	0.51
1454127_at	1010001I08Rik	RIKEN cDNA 1010001I08 gene	2.49	0.424	1.13	0.785	1.15	0.786	-1.53	0.648	0.81
1454191_at	A030007E19Rik	RIKEN cDNA A030007E19 gene	2.54	0.44	1.11	0.558	1.13	0.608	-1.69	0.175	0.77
1416759_at	Mical1	microtubule associated monoxygenase, calponin and LIM domain containing 1	1.53	0.288	2.11	0.199	1.13	0.484	-1.81	0.153	0.74
1460271_at	Trem3	triggering receptor expressed on myeloid cells 3	-1.32	0.21	1.32	0.459	2.69	0.219	2.02	0.381	1.18
1450471_at	Smad3	MAD homolog 3 (Drosophila)	1.32	0.715	1.84	0.396	1.61	0.582	-1.04	0.794	0.93
1454633_at	Etnk1	ethanolamine kinase 1	1.86	0.124	1.51	0.477	1.4	0.494	-1.55	0.53	0.81
1439412_at	Arpp21	Cyclic AMP-regulated phosphoprotein, 21	1.24	0.611	2.41	0.013	1.13	0.606	-2.14	0.276	0.66
1418276_at	Elf2	E74-like factor 2	1.05	0.951	2.84	0.041	-1.12	0.807	1.6	0.304	1.09
1425122_at	ORF9	open reading frame 9	1.22	0.548	2.99	0.232	-1.74	0.224	1.43	0.494	0.97
1459610_at	C87490	expressed sequence C87490	-1.05	0.944	1.21	0.589	2.62	0.018	1.95	0.338	1.18
1460092_at	Lsamp	Limbic system-associated membrane protein	2.04	0.026	-1.08	0.873	1.81	0.116	1.57	0.326	1.09
1424316_at	Slc25a19	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19	-1.11	0.417	1.7	0.131	2.18	0.186	1.41	0.013	1.05
1421944_a_at	Asgr1	asialoglycoprotein receptor 1	2.65	0.517	1	0.988	1.13	0.776	-1.24	0.787	0.89
1420954_a_at	Add1	adducin 1 (alpha)	1.29	0.457	-1.25	0.457	2.7	0.22	2.35	0.309	1.27
1418734_at	BE136769	expressed sequence BE136769	1.37	0.371	1.8	0.253	1.61	0.103	-1.2	0.7	0.9
1416707_a_at	Pmf1	polyamine-modulated factor 1	2.16	0.147	-1.44	0.449	1.93	0.337	1.5	0.255	1.04
1428444_at	Asb2	ankyrin repeat and SOCS box-containing protein 2	1.23	0.501	1.63	0.143	1.93	0.064	-1.34	0.362	0.86
1441396_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	1.22	0.782	3.17	0.223	-2.55	0.117	2.79	0.121	1.16
1457590_at	P2rx1	Purinergic receptor P2X, ligand-gated ion channel, 1	2.42	0.153	-1.13	0.699	1.48	0.511	2.18	0.092	1.24
1430176_at	5430433E21Rik	RIKEN cDNA 5430433E21 gene	1.42	0.033	2.64	0.289	-1.36	0.093	1.44	0.403	1.03
1427942_at	Pamci	peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor	1.37	0.285	2.42	0.153	1	0.985	-3.04	0.393	0.44
1440370_at	Abca13 /// LOC672	ATP-binding cassette, sub-family A (ABC1), member 13 /// similar to ATP binding	1.1	0.571	-1.03	0.963	2.72	0.248	2.28	0.432	1.27
1436529_at	Gpr123	G protein-coupled receptor 123	1.53	0.592	1.88	0.132	1.38	0.529	-1.5	0.662	0.82
1437226_x_at	Marcksl1	MARCKS-like 1	1.48	0.269	1.62	0.103	1.7	0.488	-1.46	0.25	0.83
1449830_at	Prlpj	prolactin-like protein J	1.08	0.85	1.89	0.202	1.82	0.204	-1.78	0.364	0.75
1448354_at	G6pdx	glucose-6-phosphate dehydrogenase X-linked	-1.03	0.889	2.1	0.001	1.73	0.151	1.62	0.148	1.1
1417160_s_at	Expi	extracellular proteinase inhibitor	-1.14	0.669	1.58	0.348	2.33	0.125	3.01	0.059	1.45
1439002_s_at	Csh1	chorionic somatomammotropin hormone 1	2.19	0.426	1.35	0.612	1.26	0.397	-2.6	0.333	0.55
1416342_at	Tnc	tenascin C	-1.03	0.891	2.8	0.026	1.02	0.945	1.73	0.115	1.13
1420286_at	---	Transcribed locus	-1.39	0.735	1.85	0.233	2.23	0.113	1	0.988	0.92
1442630_at	---	Transcribed locus	2.76	0.452	-1.25	0.454	1.24	0.598	1.55	0.235	1.08

1416196_at	Rpsa	ribosomal protein SA	1.88	0.518	1.56	0.114	1.37	0.38	-1.08	0.897	0.93
1432098_a_at	Olfr701	olfactory receptor 701	1.43	0.357	1.78	0.351	1.59	0.084	-1.26	0.688	0.88
1417856_at	Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	1.14	0.189	1.82	0.125	1.84	0.153	-2.1	0.077	0.68
1420445_at	Slc16a8	solute carrier family 16 (monocarboxylic acid transporters), member 8	1.49	0.229	2.54	0.324	-1.3	0.621	1.3	0.645	1.01
1420782_at	Tnfrsf17	tumor necrosis factor receptor superfamily, member 17	-1.23	0.526	1.84	0.337	2.15	0.044	1.03	0.887	0.95
1433310_at	D530031A16Rik	RIKEN cDNA D530031A16 gene	1.27	0.314	1.99	0.286	1.55	0.313	-1.18	0.848	0.91
1441424_at	Mfn2	Mitofusin 2	1.23	0.797	2.78	0.097	-1.25	0.588	1.28	0.343	1.01
1450453_a_at	Pde6g	phosphodiesterase 6G, cGMP-specific, rod, gamma	1.78	0.593	1.14	0.675	1.89	0.095	-1.36	0.51	0.86
1438149_at	AI449441	Expressed sequence AI449441	2.12	0.021	2.37	0.163	-3.07	0.104	3.51	0.324	1.23
1456941_at	Tert	telomerase reverse transcriptase	1.44	0.009	1.64	0.391	1.73	0.363	-1.27	0.482	0.89
1433809_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1.07	0.87	1.47	0.344	2.27	0.016	-1.08	0.195	0.93
1419542_at	Dazl	deleted in azoospermia-like	1.29	0.302	1.04	0.705	2.48	0.212	-1.08	0.366	0.93
1427798_x_at	---	Envelope protein, mRNA sequence	1.4	0.555	-1.2	0.692	2.58	0.077	2.43	0.18	1.3
1427926_at	Maml2 /// LOC4343	mastermind like 2 (Drosophila) /// similar to mastermind-like 2; mastermind (Dros	1.77	0.19	-1.13	0.849	2.16	0.345	1.84	0.317	1.16
1416206_at	Sipa1	signal-induced proliferation associated gene 1	1.92	0.238	1.46	0.314	1.44	0.022	-2.04	0.007	0.69
1434399_at	Galnt6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.29	0.754	2.08	0.144	1.45	0.224	-1.93	0.137	0.72
1418278_at	Apoc3	apolipoprotein C-III	2.05	0.452	-1.18	0.488	1.92	0.243	2.02	0.402	1.2
1435365_at	4732415M23Rik	RIKEN cDNA 4732415M23 gene	2.37	0.122	1.42	0.568	1.04	0.885	-1.27	0.123	0.89
1429734_at	4632434I11Rik	RIKEN cDNA 4632434I11 gene	1.99	0.532	-1.52	0.326	2.17	0.105	3.64	0.226	1.57
1450648_s_at	H2-Ab1	histocompatibility 2, class II antigen A, beta 1	2.05	0.022	1.38	0.207	1.39	0.305	-1.65	0.257	0.79
1430027_at	1810028F09Rik	RIKEN cDNA 1810028F09 gene	2.29	0.111	-1.12	0.888	1.64	0.268	1.01	0.993	0.95
1453223_s_at	Dppa2	developmental pluripotency associated 2	2.19	0.349	1.64	0.056	-1	0.974	1.19	0.811	1
1417680_at	Kcna5	potassium voltage-gated channel, shaker-related subfamily, member 5	1.01	0.946	1.77	0.361	2.04	0.068	-1.04	0.865	0.95
1448730_at	Cpa3	carboxypeptidase A3, mast cell	-2.59	0.348	1.49	0.497	2.95	0.092	2.17	0.261	1.01
1419983_at	Zfp644	zinc finger protein 644	1.91	0.432	1.61	0.198	1.3	0.687	-1.31	0.783	0.88
1431973_at	6-Sep	septin 6	1.83	0.439	1.31	0.1	1.69	0.328	-2.08	0.07	0.69
1421371_at	---	---	1.19	0.8	1.04	0.834	2.6	0.045	-1.86	0.422	0.74
1430172_a_at	Cyp4f16 /// LOC623	cytochrome P450, family 4, subfamily f, polypeptide 16 /// similar to cytochrome P	1.17	0.521	2.34	0.045	1.31	0.163	-1.34	0.547	0.87
1442965_at	---	---	1.28	0.774	2.77	0.157	-1.28	0.621	1.19	0.715	0.99
1445358_at	Tnks	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	2.09	0.467	1.47	0.405	1.27	0.704	-1.28	0.555	0.89
1458619_at	---	Transcribed locus, moderately similar to XP_576460.1 PREDICTED: similar to hy	-1.47	0.607	2.36	0.108	1.79	0.134	1.38	0.163	1.02
1460136_at	AW047481	expressed sequence AW047481	1.65	0.397	1.31	0.756	1.87	0.287	-4.13	0.2	0.18
1455532_at	Atxn7l2	ataxin 7-like 2	1.57	0.416	1.07	0.661	2.2	0.328	-1.69	0.215	0.79
1418641_at	Lcp2	lymphocyte cytosolic protein 2	1.32	0.048	1.62	0.006	1.89	0.019	-1.14	0.571	0.92
1446300_at	---	Adult male epididymis cDNA, RIKEN full-length enriched library, clone:9230007L	1.2	0.459	2.14	0.368	1.5	0.267	-1.34	0.117	0.87
1420653_at	Tgfb1	transforming growth factor, beta 1	1.48	0.148	1.85	0.026	1.51	0.061	-1.14	0.67	0.92
1458609_at	---	Adult male bone cDNA, RIKEN full-length enriched library, clone:9830162N06 pro	1.47	0.412	-1.04	0.96	2.4	0.205	8.56	0.214	2.85
1435944_s_at	Cenpb	centromere protein B	1.46	0.356	-1.46	0.593	2.69	0.36	1.25	0.501	0.99
1433169_at	5830456J23Rik	RIKEN cDNA 5830456J23 gene	1.03	0.937	1.35	0.149	2.46	0.387	-1.34	0.51	0.87
1448591_at	Ctss	cathepsin S	1.67	0.216	1.82	0.012	1.35	0.152	-1.24	0.307	0.9
1430608_at	4930535I16Rik	RIKEN cDNA 4930535I16 gene	2.06	0.098	1.61	0.398	1.17	0.715	-1.27	0.715	0.89
1450065_at	Adcy7	adenylate cyclase 7	1.5	0.179	2.2	0.007	1.14	0.617	-1.66	0.201	0.79
1432453_a_at	Ms4a10	membrane-spanning 4-domains, subfamily A, member 10	1.43	0.278	2.05	0.385	1.36	0.614	-1.74	0.571	0.77
1421145_at	Slc26a2	solute carrier family 26 (sulfate transporter), member 2	2.06	0.112	1.92	0.325	-1.16	0.261	1.21	0.559	1.01
1454289_at	Zhx3	zinc fingers and homeoboxes 3	1.51	0.449	1.08	0.907	2.26	0.439	-1.25	0.706	0.9
1459161_at	AU015777	expressed sequence AU015777	1.36	0.591	1.18	0.648	2.31	0.149	-1.05	0.899	0.95
1437319_at	Unc13c	unc-13 homolog C (C. elegans)	-1.59	0.447	3.13	0.026	1.09	0.847	1.69	0.575	1.08
1437485_at	Nos1ap	nitric oxide synthase 1 (neuronal) adaptor protein	-1.28	0.029	3.07	0.085	1	0.986	1.37	0.508	1.04
1458761_at	Ubox5	U box domain containing 5	1.34	0.645	2.33	0.182	1.19	0.735	-2.54	0.132	0.58
1439615_at	Gan	giant axonal neuropathy	1.32	0.552	2.55	0.258	-1.02	0.927	1.03	0.952	0.97
1447369_at	1190005F20Rik	RIKEN cDNA 1190005F20 gene	1.19	0.468	-1.58	0.383	3.03	0.056	1.38	0.19	1
1424011_at	Aqp9	aquaporin 9	2.34	0.507	-1.21	0.009	1.69	0.37	4.18	0.032	1.75
1449253_at	Smc1b	structural maintenace of chromosomes 1B	-1.18	0.352	2.84	0.048	1.18	0.318	1.93	0.498	1.19

1421956_at	Rbpsuhl	recombining binding protein suppressor of hairless-like (Drosophila)	3.11	0.237	1.06	0.872	-1.44	0.215	1.36	0.237	1.02
1430532_at	Dym	dymeclin	2.56	0.035	1.87	0.279	-2.32	0.07	1.02	0.907	0.78
1430235_at	4933424G06Rik	RIKEN cDNA 4933424G06 gene	2.82	0.112	-1.08	0.845	1.12	0.857	1.01	0.993	0.97
1421042_at	Arhgef2	rho/rac guanine nucleotide exchange factor (GEF) 2	-1.01	0.947	2.06	0.015	1.82	0.019	1.14	0.678	1
1431636_at	4930558K02Rik	RIKEN cDNA 4930558K02 gene	1.03	0.96	1.62	0.366	2.21	0.158	-2	0.231	0.72
1453404_at	2900002H16Rik	RIKEN cDNA 2900002H16 gene	-1.16	0.585	1.82	0.141	2.18	0.008	1.97	0.037	1.2
1418652_at	Cxcl9	chemokine (C-X-C motif) ligand 9	1.28	0.352	1.2	0.622	2.38	0.186	-1.23	0.317	0.91
1456250_x_at	Tgfbi	transforming growth factor, beta induced	1.88	0.079	1.29	0.019	1.69	0.131	-1.17	0.467	0.93
1441672_at	D3Ertd547e	DNA segment, Chr 3, ERATO Doi 547, expressed	1.75	0.496	1.23	0.722	1.89	0.068	-1.43	0.517	0.86
1443264_at	Ms4a2	membrane-spanning 4-domains, subfamily A, member 2	1.4	0.079	-1.49	0.714	2.8	0.141	1.43	0.154	1.03
1426072_at	Cmklr1	chemokine-like receptor 1	1.01	0.863	2.34	0.141	1.52	0.411	-1.09	0.732	0.94
1431404_at	Tmem56	transmembrane protein 56	2.08	0.206	-1	0.996	1.79	0.203	2.19	0.091	1.26
1455615_at	Cklf	chemokine-like factor	1.84	0.108	1.62	0.308	1.4	0.347	-1.27	0.353	0.9
1426137_at	Rex2	reduced expression 2	1.29	0.555	1.77	0.39	1.81	0.087	-1.32	0.569	0.89
1452114_s_at	Igfbp5	insulin-like growth factor binding protein 5	1.19	0.535	1.58	0.397	2.1	0.323	-1.83	0.285	0.76
1444736_at	Cdh7	cadherin 7, type 2	2.32	0.498	-2.03	0.07	2.06	0.347	1.53	0.662	0.97
1450472_s_at	Smad3	MAD homolog 3 (Drosophila)	1.83	0.065	1.14	0.674	1.91	0.2	-1.01	0.984	0.97
1416111_at	Cd83	CD83 antigen	1.57	0.002	1.18	0.645	2.12	0.442	-2.01	0.104	0.72
1418747_at	Sfpi1	SFFV proviral integration 1	1.01	0.961	1.68	0.021	2.19	0.114	-1.25	0.415	0.91
1457650_x_at	Atg4a /// LOC66647	autophagy-related 4A (yeast) /// similar to Cysteine protease ATG4A (Autophagy-	-1.3	0.034	2.42	0.131	1.68	0.094	1.33	0.542	1.03
1431796_at	2810430I11Rik	RIKEN cDNA 2810430I11 gene	1.11	0.573	3.04	0.125	-1.37	0.225	1.24	0.405	1
1432581_at	3110054G05Rik	RIKEN cDNA 3110054G05 gene	2.57	0.079	1.06	0.914	1.24	0.631	-1.14	0.805	0.93
1451854_a_at	Shroom3	shroom family member 3	1.06	0.871	2.29	0.213	1.52	0.213	-1.06	0.93	0.95
1440462_at	B930068K11Rik	RIKEN cDNA B930068K11 gene	1.66	0.19	2.66	0.001	-1.77	0.206	2.06	0.22	1.15
1460185_at	Krt85	keratin 85	1.41	0.555	1.31	0.672	2.16	0.026	-1.42	0.429	0.87
1430888_at	4930535E21Rik	RIKEN cDNA 4930535E21 gene	1.88	0.014	1.47	0.306	1.54	0.516	-1.63	0.046	0.81
1434980_at	Pik3r5	phosphoinositide-3-kinase, regulatory subunit 5, p101	1.43	0.319	1.76	0.111	1.69	0.138	-1.35	0.517	0.88
1451661_at	Akap4	A kinase (PRKA) anchor protein 4	1.69	0.234	1.6	0.421	1.6	0.218	-1.83	0.168	0.76
1447148_at	---	Transcribed locus	3.44	0.073	-3.15	0.333	1.13	0.575	1.02	0.979	0.61
1421366_at	Clec5a	C-type lectin domain family 5, member a	-1.15	0.518	1.79	0.124	2.22	0.307	1.69	0.365	1.14
1417597_at	Cd28	CD28 antigen	1.2	0.617	2.09	0.004	1.6	0.113	-1.88	0.227	0.75
1421167_at	Atp11a	ATPase, class VI, type 11A	1.05	0.888	2.46	0.241	1.39	0.65	-1.12	0.855	0.94
1431001_at	9030624J02Rik	RIKEN cDNA 9030624J02 gene	2.09	0.386	2.09	0.193	-1.41	0.086	1.24	0.676	1
1431759_at	Zbed4 /// 4930529C	zinc finger, BED domain containing 4 /// RIKEN cDNA 4930529C04 gene /// simila	-1.27	0.018	2.69	0.147	1.41	0.513	1.82	0.211	1.16
1449765_at	C76628	expressed sequence C76628	2.13	0.414	1.73	0.45	1.03	0.946	-2.71	0.209	0.55
1449176_a_at	Dck	deoxycytidine kinase	-1.16	0.741	1.68	0.024	2.35	0.184	1.84	0.291	1.18
1434411_at	---	---	1.56	0.206	2.72	0.092	-1.61	0.394	1.09	0.79	0.94
1443140_at	LOC627777	hypothetical protein LOC627777	-1.12	0.876	2.99	0.014	1.01	0.976	3	0.073	1.47
1431057_a_at	Prss23	protease, serine, 23	1.15	0.019	2.39	0.023	1.35	0.143	-1.37	0.52	0.88
1453989_at	Stxbp4	syntaxin binding protein 4	2.81	0.005	1.32	0.595	-1.31	0.511	1.02	0.97	0.96
1437522_x_at	Gh	growth hormone	2.14	0.555	1.65	0.229	1.11	0.843	-2.11	0.122	0.7
1455448_at	Nt5dc3	5'-nucleotidase domain containing 3	-1.11	0.414	2.47	0.236	1.54	0.017	1.98	0.039	1.22
1433330_at	4933401J01Rik	RIKEN cDNA 4933401J01 gene	-1.35	0.561	1.68	0.372	2.49	0.059	2.49	0.025	1.33
1438893_at	5530601H04Rik	RIKEN cDNA 5530601H04 gene	2.57	0.321	1.19	0.7	1.14	0.55	-1.01	0.971	0.97
1443306_at	---	0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C2300	2.34	0.112	1.94	0.355	-1.59	0.224	1.75	0.321	1.11
1420838_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-1.01	0.984	2.25	0.041	1.66	0.012	1.18	0.493	1.02
1425248_a_at	Tyro3	TYRO3 protein tyrosine kinase 3	1.25	0.343	2.56	0.02	1.1	0.613	-2.02	0.339	0.72
1446718_at	Nfkbib	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, beta	2.05	0.024	1.82	0.257	1.03	0.946	-1.05	0.941	0.96
1455893_at	Rspo2	R-spondin 2 homolog (Xenopus laevis)	1.61	0.4	1.91	0.406	1.39	0.352	-1.56	0.514	0.84
1438671_at	Ppp2r2c	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamma isofor	1.01	0.986	-1.17	0.502	3.05	0.019	1.32	0.476	1.05
1459943_at	A030012G06Rik	RIKEN cDNA A030012G06 gene	1.54	0.097	1.39	0.538	1.98	0.071	-1.38	0.408	0.88
1433987_at	Hpcal4	hippocalcin-like 4	1.4	0.111	2.24	0.184	1.28	0.096	-1.85	0.252	0.77
1451589_at	Gats	opposite strand transcription unit to Stag3	-1.24	0.387	3.02	0.001	1.09	0.685	1.17	0.531	1.01

1452410_a_at	Fes	feline sarcoma oncogene	1.2	0.187	2.18	0.023	1.54	0.013	-1.24	0.151	0.92
1449246_at	Rap2ip	Rap2 interacting protein	1.13	0.596	2.03	0.086	1.76	0.448	-1.16	0.542	0.94
1439935_at	Tmem122	transmembrane protein 122	-1.56	0.649	1.2	0.636	3.08	0.33	2.19	0.015	1.23
1448581_at	Zfp346	zinc finger protein 346	1.27	0.33	2.21	0.019	1.45	0.087	-1.18	0.708	0.94
1450518_at	Hnf4g	hepatocyte nuclear factor 4, gamma	2.78	0.013	-1.24	0.661	1.34	0.575	1.17	0.814	1.01
1422090_a_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	-2.06	0.48	1.34	0.218	3.1	0.188	1.48	0.463	0.96
1433515_s_at	Etnk1	ethanolamine kinase 1	1.4	0.378	1.32	0.673	2.21	0.322	-1.31	0.67	0.9
1459102_at	Myo1d	Myosin ID	2.63	0.046	1.21	0.807	1.09	0.555	-1.42	0.411	0.88
1425519_a_at	Cd74	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II a	1.81	0.028	1.74	0.136	1.38	0.161	-1.25	0.279	0.92
1435421_at	Fsd1	fibronectin type 3 and SPRY domain-containing protein	2.69	0.302	-1.07	0.926	1.31	0.611	1.77	0.248	1.17
1457745_at	Gpr4	G protein-coupled receptor 4	1.83	0.009	1.95	0.342	1.16	0.758	-1.83	0.456	0.77
1431426_at	4930535B03Rik	RIKEN cDNA 4930535B03 gene	1.2	0.809	1.87	0.406	1.86	0.401	-1.88	0.259	0.76
1418677_at	Actn3	actinin alpha 3	-1.14	0.381	1.33	0.553	2.72	0.291	1.6	0.112	1.13
1452565_x_at	LOC641050	hypothetical protein LOC641050	-1.16	0.873	1.63	0.29	2.45	0.311	1.34	0.376	1.06
1452480_at	BC024760	cDNA sequence BC024760	2.29	0.239	-1.52	0.375	1.99	0.251	2.5	0.003	1.31
1428682_at	Zc3h6	zinc finger CCCH type containing 6	1.11	0.342	2.22	0.052	1.6	0.016	-1.07	0.861	0.97
1418959_at	Tmprss5	transmembrane protease, serine 5 (spinesin)	1.8	0.062	1.77	0.169	1.37	0.46	-1.38	0.315	0.89
1434034_at	Cerk	ceramide kinase	1.3	0.215	2.13	0.042	1.51	0.384	-1.45	0.296	0.87
1439568_at	Greb1	gene regulated by estrogen in breast cancer protein	1.58	0.455	1.93	0.322	1.44	0.067	-1.04	0.906	0.98
1420283_at	---	---	-1.06	0.931	2.65	0.242	1.35	0.534	1.53	0.41	1.12
1435939_s_at	AI987662	expressed sequence AI987662	-1.52	0.218	2.16	0.341	2.13	0.392	1.66	0.36	1.11
1454207_at	C430039J16Rik	RIKEN cDNA C430039J16 gene	-1.04	0.973	1.38	0.34	2.61	0.044	1.01	0.909	0.99
1448816_at	Ptgis	prostaglandin I2 (prostacyclin) synthase	1.79	0.064	2.02	0.005	1.14	0.489	-2.33	0.169	0.66
1425344_at	Narf	nuclear prelamin A recognition factor	1.46	0.133	-1.06	0.879	2.55	0.019	4.49	0.244	1.86
1449877_s_at	Kifc1	kinesin family member C1	2.37	0.054	-1.38	0.46	1.87	0.099	4.57	0.211	1.86
1430387_at	1810073O08Rik	RIKEN cDNA 1810073O08 gene	-1.02	0.974	1.06	0.918	2.92	0.292	1.02	0.883	1
1460295_s_at	Il6st	interleukin 6 signal transducer	1.56	0.44	1.69	0.326	1.71	0.3	-1.29	0.591	0.92
1451906_at	Ubxd3	UBX domain containing 3	-2.87	0.145	2.33	0.018	2.29	0.15	1.66	0.46	0.85
1416296_at	Il2rg	interleukin 2 receptor, gamma chain	1.57	0.002	1.57	0.082	1.82	0.025	-1.58	0.328	0.85
1427041_at	BC013712	cDNA sequence BC013712	1.38	0.24	1.47	0.027	2.12	0.069	-1.42	0.219	0.89
1431499_at	4933436F18Rik	RIKEN cDNA 4933436F18 gene	2.25	0.434	2.09	0.213	-1.59	0.276	1.11	0.857	0.97
1433027_at	5830485P09Rik	RIKEN cDNA 5830485P09 gene	2.5	0.073	1.72	0.27	-1.32	0.596	1.43	0.261	1.08
1419132_at	Tlr2	toll-like receptor 2	1.15	0.49	2.67	0.015	1.16	0.352	-1.05	0.6	0.98
1437356_at	Ebi2	Epstein-Barr virus induced gene 2	1.98	0.391	1.09	0.758	1.9	0.027	-2.34	0.128	0.66
1429598_at	2310042D19Rik	RIKEN cDNA 2310042D19 gene	-1.69	0.414	1.95	0.316	2.44	0.105	1.26	0.141	0.99
1434346_at	---	---	2.69	0.39	-1.36	0.555	1.56	0.357	1.13	0.718	1
1419018_at	Rhox6	reproductive homeobox 6	2.58	0.005	1.29	0.657	1.11	0.747	-3.12	0.277	0.46
1434594_at	Dnahc1	dynein, axonemal, heavy chain 1	-1.06	0.928	2.5	0.144	1.54	0.034	1.21	0.723	1.05
1452796_at	Def6	differentially expressed in FDCP 6	1.71	0.09	1.41	0.382	1.86	0.121	-1.8	0.102	0.79
1436430_at	B430105G09Rik	RIKEN cDNA B430105G09 gene	-1.16	0.842	3.1	0.118	1.02	0.917	1.21	0.559	1.04
1426120_a_at	Cd244 /// LOC6770	CD244 natural killer cell receptor 2B4 /// similar to Natural killer cell receptor 2B4	1.55	0.417	2.33	0.11	1.1	0.763	-1.32	0.373	0.91
1454385_at	1700018P08Rik	RIKEN cDNA 1700018P08 gene	1.39	0.432	2.43	0.293	1.16	0.799	-1.69	0.386	0.82
1450261_a_at	Slc10a1	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	2.12	0.521	-1.36	0.074	2.13	0.097	1.44	0.45	1.08
1420685_at	Grap2 /// LOC6740	GRB2-related adaptor protein 2 /// similar to GRB2-related adaptor protein 2 (GAI	1.06	0.843	-1.16	0.602	3.06	0.026	1.07	0.245	1.01
1426470_at	---	---	2.89	0.46	1.49	0.594	-1.64	0.513	1.96	0.383	1.18
1422710_a_at	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	2	0.165	-1.57	0.232	2.36	0.065	1.94	0.106	1.18
1420893_a_at	Tgfbr1	transforming growth factor, beta receptor I	1.3	0.408	1.8	0.047	1.89	0.244	-1.37	0.196	0.9
1441761_at	Sla	Src-like adaptor	2.32	0.109	1.33	0.437	1.33	0.525	-1.47	0.209	0.88
1451174_at	Lrrc33	leucine rich repeat containing 33	1.66	0.114	1.57	0.007	1.76	0.025	-1.83	0.013	0.79
1432278_at	4930471M09Rik	RIKEN cDNA 4930471M09 gene	1.87	0.556	2.4	0.313	-1.38	0.01	1.92	0.283	1.2
1416871_at	Adam8	a disintegrin and metallopeptidase domain 8	1.14	0.841	1.44	0.585	2.41	0.131	-1.1	0.686	0.97
1449334_at	Timp3	tissue inhibitor of metalloproteinase 3	-1.03	0.597	2.68	0.051	1.34	0.215	1.29	0.386	1.07
1436271_at	BC085284 /// LOC6	cDNA sequence BC085284 /// similar to apolipoprotein L, 3 (predicted)	1.13	0.811	2.28	0.129	1.59	0.288	-1.3	0.473	0.92

1439469_at	Lrrc8c	Leucine rich repeat containing 8 family, member C	1.12	0.6	1.77	0.018	2.1	0.074	-1.76	0.426	0.81
1425727_at	Cldn19	claudin 19	1.16	0.696	1.58	0.154	2.25	0.203	-1.06	0.923	0.98
1438142_s_at	1700021K14Rik	RIKEN cDNA 1700021K14 gene	-1.08	0.911	2.62	0.393	1.45	0.034	1.34	0.14	1.08
1442219_at	Ms4a4b	Membrane-spanning 4-domains, subfamily A, member 4B	1.58	0.23	1.11	0.804	2.31	0.322	-1.98	0.206	0.75
1452060_a_at	Limk2	LIM motif-containing protein kinase 2	1.16	0.64	2.78	0.234	1.06	0.714	-1.19	0.277	0.95
1460188_at	Ptpn6	protein tyrosine phosphatase, non-receptor type 6	1.22	0.198	1.38	0.001	2.4	0.123	-1.62	0.272	0.85
1444786_at	Nol3	nucleolar protein 3 (apoptosis repressor with CARD domain)	1.06	0.772	-1.56	0.168	3.3	0.041	1.2	0.599	1
1454039_at	4921517D16Rik	RIKEN cDNA 4921517D16 gene	-1.08	0.8	2.95	0.048	1.13	0.77	1.52	0.237	1.13
1433072_at	4933425E08Rik	RIKEN cDNA 4933425E08 gene	2.82	0.379	1.53	0.515	-1.52	0.145	1.04	0.901	0.97
1457274_at	E330017N17	hypothetical protein E330017N17	1.56	0.353	1.6	0.501	1.84	0.166	-2.09	0.141	0.73
1431826_a_at	Brsk2	BR serine/threonine kinase 2	1.92	0.307	2.33	0.101	-1.3	0.672	1.16	0.804	1.03
1449551_at	Myo1c	myosin IC	1.94	0.24	1.53	0.311	1.55	0.431	-1.39	0.644	0.91
1453559_a_at	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	1.76	0.431	-1.32	0.605	2.5	0.253	1.3	0.253	1.06
1445160_at	9630020C08Rik ///	RIKEN cDNA 9630020C08 gene /// region containing RIKEN cDNA 9630020C08	1.04	0.958	1.83	0.29	2.16	0.197	-1.75	0.251	0.82
1455490_at	Ubtf	upstream binding transcription factor, RNA polymerase I	2.87	0.006	-1.12	0.476	1.27	0.264	1.5	0.563	1.13
1449817_at	Abcb11	ATP-binding cassette, sub-family B (MDR/TAP), member 11	1.85	0.602	-1.19	0.015	2.34	0.079	2.04	0.115	1.26
1427774_at	Defb7	defensin beta 7	2.26	0.355	1.89	0.164	-1.14	0.796	1.99	0.108	1.25
1455790_at	E2f2	E2F transcription factor 2	-1.05	0.921	2.68	0.02	1.4	0.409	3.17	0.16	1.55
1420664_s_at	Procr	protein C receptor, endothelial	1.32	0.249	1.61	0.228	2.09	0.006	-1.9	0.173	0.78
1429475_at	2810457I06Rik	RIKEN cDNA 2810457I06 gene	-1.03	0.908	2.01	0.062	2.05	0.116	1.48	0.107	1.13
1457295_at	Tnrc6a	trinucleotide repeat containing 6a	1.09	0.816	1.64	0.392	2.31	0.327	-1.24	0.618	0.95
1437093_at	Dnaic1	dynein, axonemal, intermediate chain 1	1.17	0.785	2.38	0.417	1.49	0.337	-2	0.021	0.76
1419418_a_at	Morc1	microrchidia 1	2.64	0.243	1.03	0.677	1.36	0.362	-1.35	0.225	0.92
1421180_at	Lix1	limb expression 1 homolog (chicken)	1.06	0.77	2.65	0.215	1.34	0.584	-1.49	0.397	0.89
1423593_a_at	Csf1r	colony stimulating factor 1 receptor	1.57	0.001	1.92	0.004	1.55	0.031	-1.05	0.865	1
1440209_at	1-Mar	membrane-associated ring finger (C3HC4) 1	1.43	0.026	2.24	0.052	1.38	0.337	-1.86	0.153	0.8
1440319_at	Gm817	gene model 817, (NCBI)	2.74	0.13	-2.14	0.262	1.84	0.025	1.88	0.402	1.08
1417439_at	Cd248	CD248 antigen, endosialin	2.12	0.018	1.79	0.229	1.14	0.833	-1.36	0.475	0.92
1460241_a_at	St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	3.11	0.131	-1.31	0.473	1.18	0.622	8.84	0.158	2.95
1457235_at	Lrp1b	low density lipoprotein-related protein 1B (deleted in tumors)	1.42	0.559	2.41	0.093	1.22	0.743	-1.16	0.865	0.97
1421515_at	Nr6a1	nuclear receptor subfamily 6, group A, member 1	1.65	0.419	1.04	0.935	2.37	0.109	-1.98	0.378	0.77
1420756_at	Fut7	fucosyltransferase 7	1.4	0.45	2.63	0.287	1.03	0.968	-1.99	0.481	0.76
1422112_at	Ccbp2	chemokine binding protein 2	-1.03	0.938	2.3	0.259	1.78	0.139	1.02	0.941	1.02
1450283_at	Atp7b	ATPase, Cu++ transporting, beta polypeptide	1.59	0.347	-1.26	0.172	2.67	0.051	1.03	0.962	1.01
1443743_at	1700054O13Rik	RIKEN cDNA 1700054O13 gene	1.87	0.351	1.39	0.276	1.8	0.227	-1.92	0.493	0.78
1431705_a_at	Mcoln2	mucolipin 2	1.16	0.316	1.46	0.19	2.43	0.236	-1.68	0.154	0.84
1435045_s_at	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	1.13	0.055	2.46	0.01	1.46	0.451	-1.24	0.596	0.95
1425427_at	LOC639910	hypothetical protein LOC639910	1.21	0.813	-1.55	0.476	3.2	0.328	1.02	0.935	0.97
1450457_at	Cbl	Casitas B-lineage lymphoma	1.15	0.85	1.17	0.72	2.74	0.115	-1.9	0.123	0.79
1421166_at	Atrn	attractin	1.2	0.488	-1.57	0.527	3.22	0.121	1.04	0.958	0.97
1435216_a_at	Odf2	outer dense fiber of sperm tails 2	-1.13	0.847	1.9	0.23	2.27	0.152	2.67	0.158	1.43
1429757_at	1700094C09Rik	RIKEN cDNA 1700094C09 gene	2.3	0.273	1.66	0.303	1.1	0.84	-1.04	0.966	1.01
1426808_at	Lgals3	lectin, galactose binding, soluble 3	1.23	0.492	2.73	0.006	1.11	0.439	-1.19	0.245	0.97
1433893_s_at	Spag5	sperm associated antigen 5	-1.13	0.67	2.21	0.046	1.97	0.452	4.03	0.175	1.77
1446452_at	Tcf7l2	Transcription factor 7-like 2, T-cell specific, HMG-box	2.29	0.226	2.17	0.098	-1.67	0.083	1.6	0.349	1.1
1422602_a_at	Wnt5b	wingless-related MMTV integration site 5B	1.6	0.281	2.5	0.147	-1.03	0.958	1.22	0.137	1.07
1419094_at	Cyp2c37 /// Cyp2c5	cytochrome P450, family 2. subfamily c, polypeptide 37 /// cytochrome P450, fam	2.98	0.436	-1.15	0.572	1.22	0.727	2.36	0.189	1.35
1449555_a_at	Fetub	fetuin beta	2.51	0.398	1.15	0.405	1.4	0.241	-1.02	0.839	1.01
1425407_s_at	Clec4a2 /// Clec4b1	C-type lectin domain family 4, member a2 /// C-type lectin domain family 4, memb	-1.05	0.767	2.93	0.023	1.19	0.607	1.81	0.334	1.22
1423630_at	Cygb	cytoglobin	2.66	0.171	1.74	0.038	-1.49	0.038	1.28	0.29	1.05
1454009_at	1700008O03Rik	RIKEN cDNA 1700008O03 gene	1.9	0.482	1.59	0.385	1.58	0.435	-1.72	0.074	0.84
1453825_at	---	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library,	-1.53	0.657	3.08	0.043	1.34	0.416	1.55	0.325	1.11
1441975_at	Acpp	acid phosphatase, prostate	1.14	0.4	2.92	0.064	1.02	0.945	-1.28	0.367	0.95

1432085_at	4930425O10Rik	RIKEN cDNA 4930425O10 gene	1.59	0.534	1.61	0.292	1.87	0.304	-1.25	0.284	0.96
1432927_at	4921507K24Rik	RIKEN cDNA 4921507K24 gene	1.05	0.954	2.6	0.013	1.43	0.568	-1.42	0.231	0.92
1457527_at	---	---	1.6	0.492	2.96	0.167	-1.93	0.255	1.13	0.877	0.94
1449393_at	Sh2d1a	SH2 domain protein 1A	2.29	0.035	1.45	0.681	1.35	0.28	-1.04	0.944	1.01
1460530_at	4933416A02Rik	RIKEN cDNA 4933416A02 gene	1.36	0.735	2.95	0.021	-1.28	0.659	1.79	0.32	1.2
1447496_s_at	Fank1	fibronectin type 3 and ankyrin repeat domains 1	1.07	0.938	2.88	0.152	1.13	0.618	-1.11	0.745	0.99
1416613_at	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	1.9	0.12	1.04	0.921	2.15	0.154	-1.34	0.01	0.94
1441384_at	---	Transcribed locus	2.57	0.036	1.02	0.963	1.49	0.379	-3.48	0.134	0.4
1434810_a_at	Cage1	cancer antigen 1	-1.28	0.659	2.4	0.035	1.91	0.169	1.02	0.973	1.01
1440912_at	Rnf39	ring finger protein 39	1.84	0.45	1.84	0.502	1.41	0.616	-1.04	0.921	1.01
1431146_a_at	Cpne8	copine VIII	1.23	0.468	2.91	0.134	-1.05	0.781	1.24	0.272	1.08
1440141_at	Kcnq2	potassium voltage-gated channel, subfamily Q, member 2	1.45	0.472	-1.15	0.848	2.77	0.013	1.39	0.567	1.12
1421625_a_at	Tmc1	transmembrane channel-like gene family 1	-1.3	0.464	2.89	0.111	1.44	0.122	1.09	0.694	1.03
1449757_x_at	Dntt	deoxynucleotidyltransferase, terminal	1.47	0.435	2.4	0.012	1.22	0.435	-2.05	0.249	0.76
1424137_at	Gprin1	G protein-regulated inducer of neurite outgrowth 1	1.68	0.102	1.94	0.122	1.48	0.396	-1.65	0.205	0.86
1427611_at	Ghrhr	growth hormone releasing hormone receptor	1.42	0.449	1.86	0.414	1.83	0.127	-1.64	0.493	0.87
1458448_at	AA408296	expressed sequence AA408296	1.63	0.126	2.47	0.297	1	0.999	-1.5	0.439	0.9
1422009_at	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide	-1.04	0.835	1.63	0.309	2.52	0.07	2.42	0.198	1.38
1417905_at	Prlpf	prolactin-like protein F	1.89	0.445	2.57	0.235	-1.53	0.274	1.34	0.703	1.07
1437591_a_at	Wdr1	WD repeat domain 1	1.39	0.521	1.41	0.362	2.31	0.201	-1.19	0.698	0.98
1433678_at	Pld4	phospholipase D family, member 4	1.25	0.161	1.78	0.007	2.08	0.054	-1.05	0.91	1.01
1457460_at	Acss2	acyl-CoA synthetase short-chain family member 2	1.2	0.737	3.08	0.217	-1.2	0.389	1.17	0.847	1.06
1440224_at	9330133O14Rik	RIKEN cDNA 9330133O14 gene	1.52	0.178	2.49	0.012	1.1	0.866	-1.06	0.883	1.01
1447352_at	---	8 days neonate male testis cDNA, RIKEN full-length enriched library, clone:G630	2.44	0.107	1.18	0.659	1.5	0.462	-1.35	0.76	0.94
1418060_a_at	Mapk7	mitogen activated protein kinase 7	2.5	0.12	1.14	0.694	1.47	0.009	-1.71	0.286	0.85
1450132_at	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	2.16	0.389	1.68	0.436	1.27	0.662	-2.18	0.023	0.73
1425445_a_at	Cldn18	claudin 18	2.12	0.102	2.06	0.132	-1.07	0.829	1.49	0.346	1.15
1425736_at	Cd37	CD37 antigen	1.71	0.526	1.13	0.421	2.28	0.299	-1.97	0.156	0.79
1446730_at	C79267	Expressed sequence C79267	2.62	0.127	1.08	0.908	1.42	0.548	-1.87	0.25	0.81
1450243_a_at	Dscr1l1	Down syndrome critical region gene 1-like 1	1.36	0.457	2.34	0.194	1.42	0.288	-1.42	0.654	0.92
1452846_at	Ppfia4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting pı	1.72	0.014	2.37	0.034	1.03	0.814	-1.79	0.143	0.83
1426431_at	Jag2	jagged 2	1.01	0.975	2.56	0.03	1.55	0.164	-1.87	0.158	0.81
1456440_s_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	1.08	0.685	1.45	0.532	2.6	0.29	-1.48	0.25	0.91
1425761_a_at	Nfatc1	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	1.2	0.556	-1.28	0.512	3.15	0.122	1.28	0.437	1.09
1436442_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	1.39	0.63	1.61	0.484	2.13	0.107	-1.63	0.391	0.87
1442798_x_at	Hk3	hexokinase 3	-1.06	0.844	1.81	0.051	2.38	0.139	1.31	0.301	1.11
1440337_at	---	Transcribed locus	1.96	0.56	-1.47	0.445	2.49	0.154	2.24	0.07	1.3
1430447_a_at	Lair1	leukocyte-associated Ig-like receptor 1	1.63	0.188	2.21	0.002	1.29	0.37	-1.07	0.043	1.01
1420798_s_at	Pcdha4 /// Pcdha6 ,	protocadherin alpha 4 /// protocadherin alpha 6 /// protocadherin alpha 7 /// protoc	2.36	0.184	2.33	0.103	-2.27	0.015	1.74	0.321	1.04
1439098_at	E230013L22Rik	RIKEN cDNA E230013L22 gene	1.02	0.821	3.04	0.244	1.07	0.852	-1.73	0.22	0.85
1427007_at	1200013B08Rik	RIKEN cDNA 1200013B08 gene	1.39	0.091	1.77	0.011	1.97	0.03	-1.66	0.234	0.87
1458392_at	C87414	Expressed sequence C87414	1.32	0.687	2.82	0.161	-1	0.997	1	1	1.03
1449225_a_at	Mapk8ip2	mitogen-activated protein kinase 8 interacting protein 2	1.8	0.335	1.65	0.383	1.69	0.164	-1.04	0.949	1.02
1419985_s_at	Ccdc69	coiled-coil domain containing 69	1.87	0.051	1.41	0.428	1.87	0.128	-1.81	0.16	0.83
1440335_at	---	---	1.78	0.37	1.99	0.159	1.37	0.435	-1.07	0.93	1.02
1459128_at	Nmnat3	Nicotinamide nucleotide adenylyltransferase 3	3.32	0.085	-2.26	0.318	1.38	0.426	1.54	0.543	0.99
1417256_at	Mmp13	matrix metallopeptidase 13	-1.08	0.68	2.26	0.375	1.95	0.207	1.7	0.229	1.21
1451688_s_at	Cant1	calcium activated nucleotidase 1	1.52	0.511	1.71	0.363	1.91	0.481	-1.59	0.463	0.89
1430617_at	Oip5	Opa interacting protein 5	1.56	0.62	2.96	0.158	-1.62	0.169	4.75	0.241	1.91
1427867_at	Myh1	Myosin, heavy polypeptide 1, skeletal muscle, adult	1.28	0.476	-1.39	0.632	3.14	0.23	1.16	0.447	1.05
1452815_at	P2ry10	purinergic receptor P2Y, G-protein coupled 10	1.79	0.434	2.08	0.144	1.27	0.561	-2.35	0.111	0.7
1439301_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	1.27	0.38	3.24	0.102	-1.58	0.022	1.4	0.197	1.08
1442167_at	Cyfip2	cytoplasmic FMR1 interacting protein 2	1	0.974	-1.09	0.826	3.22	0.348	1.02	0.937	1.04

1453220_at	4432416J03Rik	RIKEN cDNA 4432416J03 gene	1.39	0.723	-1.05	0.703	2.81	0.236	4.26	0.179	1.85
1425067_at	Celsr3	cadherin EGF LAG seven-pass G-type receptor 3	-2.15	0.079	2.59	0.286	2.09	0.239	1.41	0.61	0.99
1445095_at	Il31ra	Interleukin 31 receptor A	2.67	0.155	1.17	0.841	1.32	0.519	-1.24	0.764	0.98
1418498_at	Fgf13	fibroblast growth factor 13	1.23	0.776	2.2	0.312	1.73	0.079	-1.07	0.94	1.02
1419675_at	Ngfb	nerve growth factor, beta	1.32	0.229	1.12	0.411	2.72	0.011	-1.44	0.275	0.93
1459561_at	---	---	2.21	0.431	-1.35	0.368	2.21	0.109	1.17	0.689	1.06
1460227_at	Timp1	tissue inhibitor of metalloproteinase 1	3.47	0.082	1.19	0.509	-1.97	0.014	1.4	0.112	1.02
1454516_at	4930424E08Rik	RIKEN cDNA 4930424E08 gene	1.73	0.565	1.19	0.638	2.24	0.176	-2.16	0.145	0.75
1429761_at	Rtn1	reticulon 1	1.76	0.095	1.71	0.079	1.69	0.209	-2.24	0.034	0.73
1448099_at	---	PREDICTED: Mus musculus hypothetical LOC432995 (LOC432995), mRNA	1.25	0.499	2.83	0.055	1.1	0.844	-1.42	0.162	0.94
1436472_at	Slfn9	schlafen 9	1.62	0.342	1.15	0.876	2.4	0.219	-1.04	0.711	1.03
1429385_at	Wdr68	WD repeat domain 68	1.44	0.28	-1.01	0.987	2.74	0.17	2.08	0.196	1.31
1458104_a_at	BC038167	cDNA sequence BC038167	1.36	0.537	2.9	0.146	-1.09	0.755	1.73	0.477	1.22
1439544_at	Tbc1d5	TBC1 domain family, member 5	1.18	0.795	2.87	0.082	1.12	0.752	-1.12	0.672	1.01
1415857_at	Emb	embigin	1.05	0.675	2.93	0.057	1.2	0.544	-1.57	0.077	0.9
1454040_at	5730591J02Rik	RIKEN cDNA 5730591J02 gene	2.51	0.045	1.36	0.712	1.32	0.605	-1.34	0.731	0.96
1448845_at	Rpp25	ribonuclease P 25 subunit (human)	2.87	0.478	1.13	0.652	1.17	0.791	-2.07	0.363	0.78
1430213_at	Rcbtb1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containir	2.87	0.062	1.01	0.959	1.31	0.546	-1.05	0.889	1.03
1460618_x_at	1700001J11Rik	RIKEN cDNA 1700001J11 gene	-3.01	0.222	3.82	0.006	1.03	0.912	1.49	0.106	0.83
1425757_a_at	Impg1	interphotoreceptor matrix proteoglycan 1	-1.93	0.405	1.51	0.501	3.16	0.286	3.44	0.023	1.54
1421603_a_at	Ceacam2	CEA-related cell adhesion molecule 2	2.52	0.155	-1.36	0.574	1.93	0.224	1.69	0.465	1.19
1424823_s_at	9630044O09Rik	RIKEN cDNA 9630044O09 gene	1.1	0.744	1.5	0.454	2.58	0.069	-1.36	0.091	0.95
1423467_at	Ms4a4b	membrane-spanning 4-domains, subfamily A, member 4B	2.19	0.012	1.55	0.368	1.45	0.188	-1.75	0.327	0.86
1419768_at	Cd22	CD22 antigen	1.95	0.27	1.17	0.264	2.06	0.204	-1.57	0.312	0.9
1447540_at	Tigd3	tigger transposable element derived 3	3.6	0.003	1.07	0.939	-1.93	0.213	2.82	0.218	1.39
1430005_a_at	Batf2	basic leucine zipper transcription factor, ATF-like 2	-1.22	0.789	2.14	0.174	2.22	0.043	3.12	0.053	1.57
1446553_at	Hck	Hemopoietic cell kinase	2.03	0.438	1.41	0.214	1.74	0.196	-1.27	0.44	0.98
1452965_at	Ankrd13d	ankyrin repeat domain 13 family, member D	1.97	0.475	1.35	0.67	1.88	0.173	-2.05	0.193	0.79
1431733_at	Alpk1	alpha-kinase 1	1.45	0.581	2.55	0.129	1.19	0.336	-1.15	0.672	1.01
1427851_x_at	Igh-VJ558	immunoglobulin heavy chain (J558 family)	1.08	0.85	-1.4	0.234	3.4	0.02	1.03	0.965	1.03
1434497_at	---	---	-1.04	0.868	2.51	0.053	1.72	0.085	2.04	0.424	1.31
1424583_at	Farp2	FERM, RhoGEF and pleckstrin domain protein 2	1.6	0.182	-1.05	0.838	2.64	0.004	1.06	0.932	1.06
1421582_a_at	Creb1	cAMP responsive element binding protein 1	2.65	0.086	-1.25	0.647	1.75	0.308	1.16	0.75	1.08
1429688_at	Arntl2	aryl hydrocarbon receptor nuclear translocator-like 2	1.84	0.398	2.46	0.091	-1.12	0.833	1.61	0.041	1.2
1443285_at	Gria4	Glutamate receptor, ionotropic, AMPA4 (alpha 4)	2.53	0.195	1.34	0.465	1.32	0.564	-2.2	0.322	0.75
1430640_a_at	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	-1.78	0.22	2.04	0.391	2.6	0.027	5.89	0.182	2.19
1443894_at	Evi2a	Ecotropic viral integration site 2a	2.2	0.074	1.7	0.051	1.31	0.447	-1.66	0.191	0.88
1458245_at	LOC634731	similar to sushi domain containing 1	-1.01	0.958	1.26	0.056	2.95	0.214	1.08	0.495	1.07
1439711_at	---	---	2.84	0.022	-1.03	0.96	1.4	0.339	1.37	0.14	1.14
1446423_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	3.35	0.052	1.17	0.821	-1.45	0.033	1.06	0.928	1.03
1427783_at	Erbb4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	1.18	0.805	2.96	0.006	1.07	0.816	-1.37	0.573	0.96
1442769_at	8030451F13Rik	RIKEN cDNA 8030451F13 gene	2.33	0.496	-1.76	0.043	2.31	0.245	1.03	0.951	0.98
1450234_at	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	1.19	0.311	1.68	0.07	2.35	0.17	-1.16	0.301	1.01
1445995_at	Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)	3.07	0.364	1.33	0.515	-1.23	0.791	1.56	0.025	1.18
1452412_at	Hoxc8	homeo box C8	-1.15	0.46	1.05	0.838	3.3	0.074	1.75	0.161	1.24
1436139_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	1.72	0.398	2.5	0.348	1	0.995	-1.03	0.974	1.05
1459351_at	Adra1a	adrenergic receptor, alpha 1a	2.02	0.167	2.09	0.064	1.1	0.847	-1.53	0.507	0.92
1452948_at	Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2	2.42	0.179	1.41	0.008	1.4	0.353	-2.54	0.131	0.67
1455883_a_at	Lrrtm1	leucine rich repeat transmembrane neuronal 1	1.7	0.31	1.24	0.78	2.3	0.131	-1.58	0.622	0.91
1434794_at	Rhof	ras homolog gene family, member f	1.17	0.314	2.48	0.042	1.58	0.21	-1.88	0.185	0.84
1422542_at	Gpr34	G protein-coupled receptor 34	-1.1	0.528	2.53	0.093	1.79	0.355	1.99	0.398	1.3
1420697_at	Slc15a3	solute carrier family 15, member 3	1.93	0.291	2.08	0.005	1.22	0.236	-1.09	0.765	1.04
1421137_a_at	Pkib	protein kinase inhibitor beta, cAMP dependent, testis specific	1.17	0.474	2.95	0.02	1.12	0.179	-2.42	0.026	0.7

1424484_at	Mobk1b	MOB1, Mps One Binder kinase activator-like 1B (yeast)	2.39	0.298	1.13	0.828	1.72	0.53	-1.02	0.984	1.06
1449743_a_at	BC021438	CDNA sequence BC021438	2.41	0.221	1.43	0.447	1.4	0.593	-1.96	0.212	0.82
1421255_a_at	Cabp1	calcium binding protein 1	-1.69	0.3	3.47	0.059	1.18	0.619	1.19	0.505	1.04
1417466_at	---	---	1.35	0.037	1.64	0.117	2.25	0.226	-1.01	0.955	1.06
1445249_at	---	---	1.43	0.415	1.34	0.568	2.47	0.105	-1.68	0.372	0.89
1448058_s_at	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	3.18	0.053	1.14	0.696	-1.08	0.735	1.32	0.497	1.14
1443612_at	AI838058	Expressed sequence AI838058	1.58	0.338	2.46	0.184	1.2	0.733	-1.41	0.645	0.96
1447433_at	Wdfy3	WD repeat and FYVE domain containing 3	-1.52	0.338	3.32	0.053	1.27	0.541	1.41	0.445	1.12
1420020_at	Suz12	suppressor of zeste 12 homolog (Drosophila)	1.4	0.586	1.17	0.782	2.68	0.002	-1.07	0.91	1.04
1452928_at	Abi3	ABI gene family, member 3	1.63	0.381	2.37	0.169	1.26	0.203	-2.04	0.309	0.8
1460491_at	Invs	inversin	1.49	0.027	2.58	0.02	1.18	0.302	-1.57	0.205	0.92
1458315_at	Epc1	enhancer of polycomb homolog 1 (Drosophila)	1.29	0.625	1.3	0.731	2.66	0.038	-1.44	0.544	0.95
1419497_at	Cdkn1b	cyclin-dependent kinase inhibitor 1B	-1.18	0.803	2.54	0.122	1.87	0.101	1.22	0.678	1.11
1437370_at	Sgol2	shugoshin-like 2 (S. pombe)	2.83	0.039	-1.23	0.696	1.62	0.136	2.8	0.162	1.5
1456772_at	Ncf1	neutrophil cytosolic factor 1	1.22	0.147	2.02	0.01	2.02	0.161	-1.7	0.032	0.89
1428009_a_at	Abcc10	ATP-binding cassette, sub-family C (CFTR/MRP), member 10	2.01	0.01	1.89	0.43	1.36	0.638	-2.23	0.131	0.76
1418113_at	Cyp2d10	cytochrome P450, family 2, subfamily d, polypeptide 10	3.53	0.421	-1.44	0.116	1.03	0.929	1.74	0.487	1.22
1422875_at	Cd84	CD84 antigen	1.67	0.192	1.64	0.008	1.94	0.134	-1.47	0.203	0.95
1450536_s_at	Krtap12-1	keratin associated protein 12-1	3.33	0.337	1.28	0.094	-1.53	0.559	1.11	0.853	1.05
1430704_at	Irak3	interleukin-1 receptor-associated kinase 3	2.16	0.4	1.42	0.337	1.68	0.34	-2.09	0.316	0.79
1429379_at	Xlkd1	extra cellular link domain-containing 1	2.37	0.384	1.99	0.061	-1.1	0.585	3.49	0.171	1.69
1436944_x_at	4933439C20Rik	RIKEN cDNA 4933439C20 gene	1.29	0.24	1.63	0.007	2.35	0.004	-1.33	0.507	0.98
1440045_at	Cryzl1	Crystallin, zeta (quinone reductase)-like 1	3.29	0.003	-1.2	0.793	1.14	0.512	1.13	0.338	1.09
1427797_s_at	Ctse /// LOC622147	cathepsin E /// similar to melanoma antigen /// similar to melanoma antigen /// sim	1.5	0.571	-1.16	0.781	2.91	0.213	2.71	0.253	1.49
1416118_at	LOC630539	similar to mouse RING finger 1	2.28	0.153	2.06	0.278	-1.08	0.709	2.21	0.222	1.37
1454017_at	4921509O07Rik	RIKEN cDNA 4921509O07 gene	1.48	0.71	-1.25	0.464	2.99	0.025	1.01	0.962	1.06
1427645_a_at	Il1rapl2	interleukin 1 receptor accessory protein-like 2	2.18	0.479	-1.25	0.522	2.29	0.119	1.35	0.55	1.14
1437374_at	6430526N21Rik	RIKEN cDNA 6430526N21 gene	1.81	0.317	1.37	0.381	2.1	0.064	-1.24	0.534	1.01
1444624_at	Ubap1	ubiquitin-associated protein 1	1.72	0.557	2.84	0.069	-1.42	0.116	1.7	0.247	1.21
1451976_s_at	Cmtm2a	CKLF-like MARVEL transmembrane domain containing 2A	3.95	0.033	-3.77	0.008	1.05	0.927	3.97	0.006	1.3
1441502_at	Lrfn5	Leucine rich repeat and fibronectin type III domain containing 5	2.21	0.126	1.33	0.673	1.73	0.229	-1.26	0.76	1
1457435_x_at	Myom2	myomesin 2	-1.14	0.667	1.61	0.343	2.78	0.251	1.17	0.763	1.11
1444513_at	Cnksr2	connector enhancer of kinase suppressor of Ras 2	-1.29	0.75	3	0.031	1.5	0.544	2.01	0.39	1.31
1418638_at	H2-DMb1	histocompatibility 2, class II, locus Mb1	1.9	0.121	1.86	0.074	1.51	0.302	-1.44	0.376	0.96
1421457_a_at	Samsn1	SAM domain, SH3 domain and nuclear localization signals, 1	1.99	0.13	1.47	0.087	1.82	0.102	-1.3	0.079	1
1421553_at	Epm2a	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	-2.54	0.051	2.91	0.021	1.98	0.07	1.73	0.082	1.02
1441637_at	F730047E07Rik	RIKEN cDNA F730047E07 gene	2.56	0.286	1.75	0.129	-1.02	0.961	1.59	0.332	1.22
1434279_at	Mtm1	X-linked myotubular myopathy gene 1	-1.22	0.73	2.3	0.086	2.17	0.317	1.25	0.266	1.12
1420942_s_at	---	---	1.81	0.32	1.93	0.144	1.55	0	-1.07	0.85	1.05
1428696_at	2310015N21Rik	RIKEN cDNA 2310015N21 gene	1.4	0.185	1.61	0.011	2.28	0.126	-1.58	0.127	0.93
1444837_at	---	---	2.44	0.017	1.95	0.381	-1.11	0.614	1.45	0.196	1.18
1438355_at	Tmem90a	transmembrane protein 90a	1.41	0.554	3.23	0.157	-1.53	0.162	1.22	0.514	1.08
1448183_a_at	Hif1a	hypoxia inducible factor 1, alpha subunit	1.72	0.354	-1.03	0.961	2.61	0.3	1.15	0.644	1.11
1444420_at	E230032D23Rik	RIKEN cDNA E230032D23 gene	2.96	0.046	1.25	0.357	1.09	0.605	-1.88	0.178	0.86
1454347_at	4930540E01Rik	RIKEN cDNA 4930540E01 gene	2.96	0.023	1.15	0.686	1.19	0.775	-1.14	0.815	1.04
1457108_at	Il1r2	Interleukin 1 receptor, type II	-2.2	0.287	1.43	0.455	3.42	0.159	2.4	0.302	1.26
1459217_at	Osmr	oncostatin M receptor	2.33	0.039	1.67	0.544	1.3	0.423	-2.49	0.002	0.7
1457140_s_at	4632411J06Rik	RIKEN cDNA 4632411J06 gene	1.46	0.111	2.35	0.314	1.5	0.11	-2.91	0.369	0.6
1433494_at	Dos	downstream of Stk11	2.96	0.056	1.17	0.531	1.18	0.455	-1.85	0.101	0.86
1459940_at	---	---	2.83	0.184	1.42	0.353	1.05	0.913	-1.36	0.652	0.99
1457665_x_at	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	3.1	0.415	1.06	0.903	1.15	0.626	-1.4	0.598	0.98
1460000_at	D830007B15Rik	RIKEN cDNA D830007B15 gene	-1.01	0.975	3.01	0.205	1.32	0.134	1.07	0.864	1.1
1442988_at	A630001O12Rik	RIKEN cDNA A630001O12 gene	-1.05	0.864	1.23	0.466	3.14	0.222	1.54	0.26	1.22

1442376_at	Ablim1	actin-binding LIM protein 1	2.37	0.194	-1.04	0.898	1.98	0.308	1.07	0.887	1.1
1455660_at	Csf2rb1	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage	1.09	0.873	1.86	0.032	2.38	0.023	-1.05	0.759	1.07
1439141_at	Gpr18	G protein-coupled receptor 18	1.92	0.095	1.02	0.933	2.38	0.189	-1.93	0.128	0.85
1428700_at	P2ry13	purinergic receptor P2Y, G-protein coupled 13	1.69	0.058	1.88	0.027	1.76	0.097	-1.13	0.638	1.05
1448160_at	Lcp1	lymphocyte cytosolic protein 1	1.69	0.196	1.19	0.495	2.44	0.095	-1.32	0.467	1
1420699_at	Clec7a	C-type lectin domain family 7, member a	2.11	0.109	1.93	0.005	1.28	0.135	-1.42	0.089	0.98
1418918_at	Igfbp1	insulin-like growth factor binding protein 1	1.23	0.366	1.67	0.389	2.43	0.001	-1.59	0.531	0.93
1426511_at	Susd2	sushi domain containing 2	-1.15	0.388	2.96	0.015	1.5	0.18	1.49	0.089	1.2
1428942_at	Mt2	metallothionein 2	1.19	0.506	3.38	0.068	-1.32	0.336	5.31	0.127	2.14
1450170_x_at	H2-K1	Histocompatibility 2, K1, K region	2.5	0.294	1.05	0.603	1.78	0.108	-1.52	0.217	0.95
1456915_at	D930005D10Rik	RIKEN cDNA D930005D10 gene	2.02	0.2	2.18	0.075	1.12	0.77	-1.32	0.367	1
1457253_at	Trim40	tripartite motif-containing 40	-1.99	0.367	1.05	0.917	3.78	0.243	2.24	0.194	1.27
1456283_at	Neto1	neuropilin (NRP) and tolloid (TLL)-like 1	-1.01	0.847	1	0.998	3.35	0.017	2.49	0.036	1.45
1437502_x_at	Cd24a	CD24a antigen	-1.07	0.657	3.33	0.217	1.07	0.725	1.43	0.197	1.19
1445538_at	Auts2	Autism susceptibility candidate 2	2.87	0.069	-1.15	0.803	1.6	0.312	1.14	0.677	1.12
1450297_at	Il6	interleukin 6	2.49	0.24	2.06	0.315	-1.28	0.676	2.25	0.239	1.38
1418770_at	Cd2	CD2 antigen	1.53	0.683	1.91	0.314	1.9	0.133	-1.89	0.322	0.86
1449455_at	Hck	hemopoietic cell kinase	1.51	0.421	2.27	0.001	1.55	0.109	-1.08	0.58	1.06
1419679_at	Lats2	large tumor suppressor 2	1.78	0.563	1.76	0.312	1.8	0.554	-1.64	0.679	0.93
1454850_at	Tbc1d10c	TBC1 domain family, member 10c	1.83	0.18	1.06	0.925	2.45	0.145	-2.31	0.079	0.76
1452631_at	Rufy2	RUN and FYVE domain-containing 2	2.99	0.35	1.17	0.815	1.19	0.729	-1.85	0.208	0.87
1430332_a_at	Gusb	glucuronidase, beta	1.61	0.072	1.67	0.349	2.06	0.195	-1.04	0.908	1.08
1451721_a_at	H2-Ab1	histocompatibility 2, class II antigen A, beta 1	1.96	0.033	1.78	0.154	1.61	0.166	-1.64	0.269	0.93
1439076_at	Dhx29	DEAH (Asp-Glu-Ala-His) box polypeptide 29	1.18	0.073	2.26	0.316	1.9	0.479	-1.16	0.843	1.05
1455234_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	1.56	0.586	2.85	0.182	-1.07	0.812	1.23	0.327	1.14
1422124_a_at	Ptprc	protein tyrosine phosphatase, receptor type, C	1.79	0.149	1.71	0.003	1.85	0.001	-1.66	0.135	0.92
1438448_at	Otop1	otopetrin 1	1.2	0.721	2.77	0.004	1.38	0.509	-1.74	0.296	0.9
1419656_at	Slc25a36	solute carrier family 25, member 36	1.05	0.743	3.26	0.01	1.04	0.884	-1.04	0.632	1.08
1416572_at	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	2.8	0.116	1.64	0.273	-1.09	0.759	1.11	0.723	1.11
1446523_at	---	---	2.61	0.197	-1.79	0.448	2.19	0.084	2.97	0.036	1.49
1425578_a_at	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	3.12	0.376	-1.59	0.439	1.61	0.308	1.7	0.171	1.21
1435146_s_at	Igsf4d	immunoglobulin superfamily, member 4	1.78	0.146	1.77	0.251	1.81	0.265	-2.19	0.198	0.79
1433969_at	AU067824	expressed sequence AU067824	3.19	0.174	-1.14	0.824	1.29	0.191	2.22	0.111	1.39
1452912_at	2600005O03Rik	RIKEN cDNA 2600005O03 gene	1.04	0.846	3.4	0.025	-1.09	0.809	3.55	0.174	1.73
1441667_s_at	Smyd1	SET and MYND domain containing 1	2.47	0.083	1.47	0.208	1.42	0.473	-1.06	0.945	1.08
1460028_at	Grip2	glutamate receptor interacting protein 2	1.05	0.876	2.89	0.014	1.43	0.246	-1.08	0.884	1.07
1423760_at	Cd44	CD44 antigen	2.23	0.121	1.94	0.055	1.19	0.374	-1.25	0.248	1.03
1436212_at	Tmem71	transmembrane protein 71	1.51	0.109	2.79	0.024	1.07	0.445	-2.07	0.056	0.82
1417890_at	Pdxp	pyridoxal (pyridoxine, vitamin B6) phosphatase	3.01	0.16	1.17	0.678	1.19	0.615	-1.14	0.473	1.06
1448612_at	Sfn	stratifin	2.07	0.246	2.1	0.122	1.19	0.507	-1.42	0.279	0.99
1440196_at	---	---	2.12	0.038	1.61	0.069	1.65	0.296	-1.86	0.183	0.88
1439118_at	Slc35e4	solute carrier family 35, member E4	1.19	0.863	1.77	0.475	2.42	0.214	-1.1	0.824	1.07
1458401_at	4932438A13Rik ///	RIKEN cDNA 4932438A13 gene /// similar to CG15133-PA /// similar to CG15133	2.59	0.184	1.1	0.886	1.68	0.554	-2.7	0.447	0.67
1433236_at	3830422I06Rik	RIKEN cDNA 3830422I06 gene	1.32	0.225	2.01	0.068	2.05	0.315	-1.35	0.686	1.01
1419202_at	Cst7	cystatin F (leukocystatin)	-1.04	0.832	2.52	0.199	1.89	0.046	1.8	0.212	1.3
1432329_a_at	Matk	megakaryocyte-associated tyrosine kinase	1.12	0.378	1.3	0.311	2.96	0.151	-1.24	0.389	1.04
1445564_at	---	Transcribed locus	-1.15	0.77	2.95	0.188	1.57	0.24	1.64	0.49	1.25
1438664_at	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	-1.48	0.305	2.87	0.117	1.85	0	3.8	0.176	1.76
1450774_at	Ly6g6d	lymphocyte antigen 6 complex, locus G6D	2.01	0.169	2.46	0.344	-1.09	0.626	1.02	0.971	1.1
1427325_s_at	AI597013	expressed sequence AI597013	1.69	0.083	1.43	0.229	2.26	0.017	-1.65	0.145	0.93
1425864_a_at	Sorcs1	VPS10 domain receptor protein SORCS 1	2.55	0.395	1.92	0.345	-1.09	0.873	3.26	0.145	1.66
1426454_at	Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	1.26	0.235	1.98	0.034	2.16	0.075	-1.56	0.085	0.96
1424379_at	Car11	carbonic anhydrase 11	-1.32	0.082	2.57	0.025	2.06	0.064	2.04	0.039	1.34

1425664_at	Klhl20	kelch-like 20 (Drosophila)	1.93	0.391	1.67	0.447	1.79	0.261	-1.85	0.407	0.89
1429683_at	5830472M02Rik	RIKEN cDNA 5830472M02 gene	2.04	0.397	1.44	0.491	1.92	0.294	-1.14	0.619	1.06
1425885_a_at	Kcnab2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	1.75	0.033	1.06	0.831	2.58	0.344	-4.53	0.295	0.22
1437310_at	Bbs1	Bardet-Biedl syndrome 1 homolog (human)	-1.21	0.298	2.71	0.201	1.86	0.007	1.18	0.476	1.14
1429889_at	Faim3	Fas apoptotic inhibitory molecule 3	1.16	0.525	1.51	0.498	2.72	0.152	-1.84	0.227	0.89
1440684_at	Aytl1	acyltransferase like 1	1.85	0.593	2.33	0.063	1.23	0.392	-1.01	0.973	1.1
1435871_at	2600009P04Rik	RIKEN cDNA 2600009P04 gene	-1.04	0.957	3.35	0.146	1.09	0.89	1.66	0.346	1.26
1444287_at	AI853106	expressed sequence AI853106	1.45	0.117	2.87	0.187	1.08	0.816	-1.15	0.531	1.06
1434364_at	Map3k14	mitogen-activated protein kinase kinase kinase 14	1.43	0.023	2.8	0.24	1.17	0.54	-1.99	0.152	0.85
1450355_a_at	Capg	capping protein (actin filament), gelsolin-like	1.3	0.11	2.3	0.011	1.81	0.074	-1.73	0.338	0.92
1424927_at	Glipr1	GLI pathogenesis-related 1 (glioma)	1.3	0.001	2.76	0.001	1.34	0.233	-1	0.992	1.1
1419973_at	Oxsm	3-oxoacyl-ACP synthase, mitochondrial	3.77	0.002	-1.62	0.329	1.02	0.949	1.09	0.761	1.06
1458085_at	---	---	-1.08	0.705	2.86	0.124	1.63	0.159	1.14	0.802	1.14
1436097_x_at	Arhgap9	Rho GTPase activating protein 9	1.22	0.435	1.77	0.001	2.43	0.008	-2	0.096	0.86
1419720_at	Gp9	glycoprotein 9 (platelet)	1.03	0.915	-1.03	0.951	3.42	0.184	1.99	0.425	1.35
1418826_at	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	1.83	0.229	1.69	0.022	1.91	0.005	-1.66	0.295	0.94
1418281_at	Rad51	RAD51 homolog (S. cerevisiae)	2.51	0.442	-1.24	0.716	2.11	0.089	2.39	0.206	1.44
1448123_s_at	Tgfbi	transforming growth factor, beta induced	2.33	0.084	1.44	0.016	1.66	0.111	-1.17	0.605	1.06
1435853_at	9030605E09Rik	RIKEN cDNA 9030605E09 gene	3.04	0.054	1.42	0.134	-1.04	0.949	1.78	0.206	1.3
1419658_at	C920025E04Rik	RIKEN cDNA C920025E04 gene	1.13	0.62	2.21	0.025	2.08	0.028	-1.49	0.01	0.98
1450641_at	Vim	vimentin	2.09	0.008	2.26	0.009	1.08	0.76	-1.47	0.389	0.99
1447473_at	---	Transcribed locus	3.56	0.007	1.04	0.914	-1.2	0.757	1.03	0.952	1.11
1439589_at	Cd53	CD53 antigen	2.39	0.128	1.85	0.129	1.2	0.292	-2.11	0.098	0.83
1417990_at	Ppp1r14d	protein phosphatase 1, regulatory (inhibitor) subunit 14D	1.02	0.98	3.59	0.156	-1.22	0.509	2.19	0.091	1.4
1429801_at	2310028H24Rik	RIKEN cDNA 2310028H24 gene	3.44	0.013	1.3	0.642	-1.44	0.531	2.55	0.073	1.46
1445777_at	Upf2	UPF2 regulator of nonsense transcripts homolog (yeast)	1.79	0.31	2.69	0.028	-1.04	0.922	1.19	0.552	1.16
1455859_at	A330021E22Rik	RIKEN cDNA A330021E22 gene	-1.29	0.135	3.67	0.292	1	0.981	1.06	0.874	1.11
1450241_a_at	Evi2a	ecotropic viral integration site 2a	1.82	0.091	1.58	0.011	2.04	0.06	-1.33	0.406	1.03
1417297_at	Itpr3	inositol 1,4,5-triphosphate receptor 3	1.88	0.041	1.95	0.264	1.62	0.014	-1.85	0.159	0.9
1444822_at	Sgcd	Sarcoglycan, delta (dystrophin-associated glycoprotein)	1.09	0.914	3.49	0.386	-1.15	0.13	1.13	0.584	1.14
1427836_at	Sr278	stretch responsive protein 278	2.5	0.135	1.55	0.281	1.39	0.493	-1.29	0.315	1.04
1445030_at	---	PREDICTED: Mus musculus similar to Glyceraldehyde-3-phosphate dehydrogena	-1.9	0.294	3.7	0.094	1.22	0.537	1.01	0.985	1.01
1449277_at	Ccl19	chemokine (C-C motif) ligand 19	2.1	0.003	1.52	0.375	1.83	0.317	-1.84	0.078	0.9
1449240_at	Gsbs	G substrate	2.89	0.102	1.94	0.208	-1.61	0.209	1.11	0.79	1.08
1444197_at	9930116N10Rik	RIKEN cDNA 9930116N10 gene	3.3	0.049	1.04	0.925	1.11	0.738	-1.23	0.549	1.06
1422066_x_at	Klrb1d	killer cell lectin-like receptor subfamily B member 1D	3.56	0.025	1.17	0.704	-1.38	0.183	1.13	0.512	1.12
1437438_x_at	Pnliprp2	pancreatic lipase-related protein 2	1.18	0.6	3.13	0.071	1.16	0.617	-1.05	0.896	1.1
1426112_a_at	Cd72	CD72 antigen	1.67	0.423	2.01	0.014	1.78	0.338	-1.31	0.446	1.04
1422527_at	H2-DMa	histocompatibility 2, class II, locus DMa	2.1	0.002	1.41	0.096	1.95	0.189	-1.63	0.183	0.96
1425284_a_at	Rab27a	RAB27A, member RAS oncogene family	1.39	0.173	2.55	0.193	1.52	0.419	-1.18	0.445	1.07
1444661_at	Gpr26	G protein-coupled receptor 26	-1.39	0.628	2.97	0.344	1.78	0.323	1.11	0.867	1.12
1457207_at	Attp	Signaling molecule ATTP	1.38	0.006	3.22	0.009	-1.16	0.627	2.69	0.212	1.53
1430730_at	9430024F10Rik	RIKEN cDNA 9430024F10 gene	1.99	0.11	2.42	0.181	1.06	0.935	-2.02	0.216	0.86
1458286_at	0610007P14Rik	RIKEN cDNA 0610007P14 gene	3.64	0.011	-2	0.091	1.33	0.439	1.1	0.433	1.02
1426766_at	6330403K07Rik	RIKEN cDNA 6330403K07 gene	2.18	0.045	2.43	0.083	-1.16	0.522	1.08	0.875	1.13
1436538_at	Ankrd37	ankyrin repeat domain 37	2.07	0.387	1.58	0.303	1.83	0.014	-1.71	0.071	0.94
1425477_x_at	H2-Ab1	histocompatibility 2, class II antigen A, beta 1	1.86	0.054	1.71	0.097	1.9	0.168	-1.51	0.373	0.99
1420970_at	Adcy7	adenylate cyclase 7	2.52	0.066	1.88	0.196	1.08	0.527	-1.58	0.198	0.97
1419631_at	Was	Wiskott-Aldrich syndrome homolog (human)	1.54	0.032	1.84	0.001	2.1	0.126	-1.13	0.733	1.09
1441782_at	Aak1	AP2 associated kinase 1	3.01	0.453	1.51	0.511	-1.04	0.913	1.33	0.373	1.2
1434376_at	Cd44	CD44 antigen	2.19	0.072	2.03	0.042	1.27	0.182	-1.14	0.547	1.09
1419099_x_at	Stom	stomatin	1.83	0.4	-1.24	0.702	2.85	0.327	4.98	0.216	2.1
1435560_at	Itgal /// LOC671163	integrin alpha L /// similar to Integrin alpha-L precursor (Leukocyte adhesion glycc	1.61	0.249	1.55	0.006	2.33	0.021	-1.37	0.434	1.03

1419526_at	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	1.36	0.074	1.71	0.027	2.42	0.152	-1.05	0.699	1.11
1438875_at	RP23-221M24.3	KRAB box containing protein	2.89	0.446	1.81	0.394	-1.27	0.641	2.3	0.129	1.43
1418051_at	Ephb6	Eph receptor B6	3.17	0.021	-1.02	0.978	1.34	0.498	1.03	0.966	1.13
1427801_at	Krtap16-2	keratin associated protein 16-2	-1.15	0.741	2.17	0.435	2.46	0.331	2.01	0.324	1.37
1457596_at	Son	Son cell proliferation protein	1.62	0.265	2.55	0.057	1.32	0.267	-1.04	0.886	1.11
1442817_at	A730091E23Rik	RIKEN cDNA A730091E23 gene	2.54	0.308	1.41	0.608	1.54	0.284	-2.06	0.222	0.86
1444546_at	BC027057	cDNA sequence BC027057	2.22	0.006	2.01	0.008	1.27	0.442	-1.15	0.323	1.09
1430371_x_at	Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	1.38	0.737	1.82	0.338	2.31	0.218	-6.52	0.045	-0.25
1417786_a_at	Rgs19	regulator of G-protein signaling 19	1.35	0.103	2.17	0.033	1.98	0.074	-1.74	0.091	0.94
1421317_x_at	Myb	myeloblastosis oncogene	1.49	0.147	3.14	0.079	-1.16	0.498	1.19	0.651	1.17
1432033_at	Ntng2	netrin G2	1.87	0.201	1.06	0.88	2.57	0.02	-1.13	0.608	1.09
1439874_at	9330102E08Rik	RIKEN cDNA 9330102E08 gene	2.83	0.011	1.59	0.339	1.08	0.851	-1.28	0.284	1.06
1420338_at	Alox15	arachidonate 15-lipoxygenase	-1.41	0.557	1.28	0.642	3.52	0.223	2.46	0.145	1.46
1456064_at	AI504432	expressed sequence AI504432	2.79	0.079	1.61	0.062	1.1	0.529	-1.74	0.037	0.94
1441610_at	N28178	expressed sequence N28178	3.28	0.343	1.15	0.65	1.08	0.801	-1.31	0.517	1.05
1425434_a_at	Msr1	macrophage scavenger receptor 1	-1.31	0.389	2.69	0.031	2.06	0.102	1.68	0.545	1.28
1452450_at	Atp8b2	Atpase, class I, type 8B, member 2	2.16	0.425	1.64	0.379	1.72	0.148	-2.02	0.186	0.87
1424254_at	Ifitm1	interferon induced transmembrane protein 1	2.04	0.109	1.99	0.04	1.49	0.432	-1.08	0.636	1.11
1449962_at	Pramel3 /// AV3208	preferentially expressed antigen in melanoma-like 3 /// expressed sequence AV32	2.08	0.018	1.8	0.326	1.64	0.328	-1.08	0.858	1.11
1427580_a_at	Rian	RNA imprinted and accumulated in nucleus	1.16	0.636	3.69	0.001	-1.49	0.605	1.66	0.359	1.26
1436397_at	BC027057	cDNA sequence BC027057	1.08	0.783	2.96	0.026	1.48	0.27	-1.64	0.069	0.97
1434716_at	Havcr1	hepatitis A virus cellular receptor 1	2.43	0.056	-1.52	0.495	2.44	0.312	1.11	0.49	1.11
1458374_at	C79407	expressed sequence C79407	-1.62	0.637	3.5	0.103	1.41	0.344	3.79	0.17	1.77
1457035_at	AI607873	expressed sequence AI607873	2.23	0.216	1.59	0.068	1.71	0.024	-1.28	0.444	1.06
1442555_at	Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	1.76	0.251	1.44	0.298	2.34	0.142	-1.79	0.225	0.94
1424046_at	Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	2.33	0.251	2.35	0.342	-1.17	0.265	3.74	0.195	1.81
1456319_at	LOC665081	hypothetical protein LOC665081	2.67	0.249	-1.59	0.123	2.24	0.367	2.62	0.133	1.48
1459073_x_at	Fgf14	Fibroblast growth factor 14	1.57	0.65	1.47	0.529	2.5	0.094	-1.72	0.606	0.96
1415945_at	Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	-1.09	0.217	2.76	0.017	1.86	0.154	2.8	0.203	1.58
1439258_at	Atf4	activating transcription factor 4	2.4	0.277	1.95	0.123	1.21	0.64	-1.05	0.816	1.13
1458398_at	1700027F06Rik	RIKEN cDNA 1700027F06 gene	3.44	0.173	1.39	0.511	-1.39	0.216	1.43	0.596	1.22
1420572_at	Ms4a3	membrane-spanning 4-domains, subfamily A, member 3	-1.23	0.519	2.24	0.272	2.5	0.181	3.43	0.367	1.74
1435367_at	Mapk4	mitogen-activated protein kinase 4	-1.2	0.164	3.17	0.106	1.56	0.324	1.26	0.769	1.2
1434940_x_at	Rgs19	regulator of G-protein signaling 19	1.58	0.099	2.12	0.006	1.86	0.078	-2.08	0.111	0.87
1421211_a_at	C2ta	class II transactivator	2.4	0.167	1.53	0.325	1.63	0.161	-1.98	0.183	0.9
1419851_at	---	---	1.48	0.634	2	0.533	2.09	0.166	-2.2	0.423	0.84
1452445_at	Slc41a2	solute carrier family 41, member 2	1.16	0.452	3.35	0.12	1.06	0.745	-1.49	0.278	1.02
1446879_at	Grid2	Glutamate receptor, ionotropic, delta 2	3.33	0.085	-1.7	0.609	1.66	0.452	1.32	0.581	1.15
1421378_s_at	Abcc1	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	1.24	0.562	2.29	0.202	2.05	0.138	-1.4	0.562	1.04
1417936_at	Ccl9	chemokine (C-C motif) ligand 9	2.63	0.283	1.12	0.237	1.84	0.19	-1.29	0.221	1.07
1451604_a_at	Acvrl1	activin A receptor, type II-like 1	2.09	0.163	2.58	0.025	-1.09	0.612	1.28	0.461	1.21
1427787_at	Sp6	trans-acting transcription factor 6	2.92	0.415	1.09	0.862	1.57	0.178	-3.09	0.422	0.62
1438135_at	E130114P18Rik	RIKEN cDNA E130114P18 gene	3.37	0.007	-1.03	0.885	1.25	0.555	1.05	0.9	1.16
1442403_at	B130034C11Rik	RIKEN cDNA B130034C11 gene	1.66	0.356	2.93	0.319	1	0.992	-1.16	0.762	1.11
1417523_at	Plek	pleckstrin	1.25	0.637	1.51	0.441	2.83	0.156	-1.06	0.9	1.13
1422628_at	4632417K18Rik	RIKEN cDNA 4632417K18 gene	2.26	0.221	1.88	0.003	1.44	0.145	-1.13	0.238	1.12
1421936_at	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	1.63	0.343	2	0.053	1.97	0.096	-1.29	0.234	1.08
1419604_at	Zbp1	Z-DNA binding protein 1	1.05	0.89	1.55	0.565	2.99	0.006	-3.18	0.115	0.6
1422150_at	Hmx3	H6 homeo box 3	2.37	0.033	1.23	0.679	2	0.041	-1.59	0.045	1
1417903_at	Dfna5h	deafness, autosomal dominant 5 homolog (human)	-1.47	0.16	1.15	0.399	3.77	0.18	1.78	0.267	1.31
1427967_at	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	2.24	0.254	-1.1	0.912	2.46	0.376	1.22	0.712	1.2
1421309_at	Mgmt	O-6-methylguanine-DNA methyltransferase	1.03	0.932	-1.51	0.025	3.92	0.294	1.55	0.384	1.25
1430562_at	Zfp95	zinc finger protein 95	1.74	0.414	1.67	0.421	2.21	0.065	-1.88	0.063	0.94

1421741_at	Cyp3a16	cytochrome P450, family 3, subfamily a, polypeptide 16	3.16	0.443	1.24	0.827	1.23	0.201	-2.09	0.512	0.88
1451497_at	Csnk1a1	casein kinase 1, alpha 1	2.68	0.219	1.56	0.445	1.38	0.43	-1.13	0.579	1.12
1422813_at	Cacng1	calcium channel, voltage-dependent, gamma subunit 1	3.34	0.259	1.34	0.541	-1.04	0.907	4.11	0.004	1.94
1416286_at	Rgs4	regulator of G-protein signaling 4	1.29	0.335	3.52	0.201	-1.2	0.613	2.85	0.121	1.62
1450298_at	Tnfsf14	tumor necrosis factor (ligand) superfamily, member 14	1.02	0.922	1.76	0.302	2.86	0.014	-1.01	0.984	1.16
1419297_at	H2-Oa	histocompatibility 2, O region alpha locus	3.05	0.004	1.03	0.946	1.56	0.424	-2.41	0.11	0.81
1422121_at	Oprd1	opioid receptor, delta 1	-1.02	0.98	3.27	0.044	1.4	0.233	1.06	0.911	1.18
1441934_at	---	---	1.25	0.836	2.55	0.001	1.86	0.073	-1.46	0.556	1.05
1452695_at	1810033M07Rik	RIKEN cDNA 1810033M07 gene	1.18	0.821	3.47	0.169	1	0.993	-1.85	0.247	0.95
1448576_at	Il7r	interleukin 7 receptor	1.81	0.435	2.75	0.016	1.09	0.736	-2.21	0.124	0.86
1448617_at	Cd53	CD53 antigen	2.22	0.214	1.84	0.004	1.6	0.049	-1.68	0.135	0.99
1457891_at	C230011H18Rik	RIKEN cDNA C230011H18 gene	1.77	0.598	1.51	0.552	2.39	0.178	-1.16	0.798	1.12
1459675_at	---	---	3.46	0.06	-1.17	0.754	1.34	0.58	1.32	0.698	1.24
1449609_at	---	Transcribed locus	1.1	0.492	3.75	0.031	-1.22	0.39	1.08	0.624	1.18
1424965_at	Lpxn	leupaxin	1.62	0.133	1.68	0.044	2.38	0.113	-1.61	0.253	1.02
1427301_at	Cd48	CD48 antigen	2.03	0.219	2.28	0.001	1.37	0.166	-1.66	0.205	1
1431043_at	Kbtbd5	kelch repeat and BTB (POZ) domain containing 5	1.04	0.934	1.65	0.401	3	0.006	-1.08	0.836	1.15
1418803_a_at	Fasl	Fas ligand (TNF superfamily, member 6)	-1.17	0.662	2.99	0.241	1.84	0.003	1.02	0.96	1.17
1430076_at	Ccdc116	coiled-coil domain containing 116	1.24	0.76	3.38	0.026	1.06	0.752	-1.64	0.04	1.01
1435783_at	B230112C05Rik	RIKEN cDNA B230112C05 gene	2.3	0.063	2.25	0.363	1.14	0.839	-1.33	0.631	1.09
1429511_at	4933402E13Rik	RIKEN cDNA 4933402E13 gene	3.14	0.012	-1.1	0.89	1.65	0.424	1.5	0.491	1.3
1418811_at	Barhl1	BarH-like 1 (Drosophila)	3.79	0.247	1.26	0.739	-1.55	0.266	2.15	0.212	1.41
1435724_at	4933400N17Rik	RIKEN cDNA 4933400N17 gene	2.13	0.474	2.66	0.021	-1.11	0.793	1.12	0.811	1.2
1417308_at	Pkm2	pyruvate kinase, muscle	1.21	0.272	2.86	0.026	1.63	0.011	-1.21	0.077	1.12
1432993_at	4930403L11Rik	RIKEN cDNA 4930403L11 gene	2.7	0.007	2.18	0.197	-1.23	0.36	1.11	0.499	1.19
1417268_at	Cd14	CD14 antigen	1.25	0.508	2.63	0.118	1.82	0.16	-1.06	0.88	1.16
1425258_at	Cst11	cystatin 11	1.13	0.815	3.25	0.03	1.32	0.311	-1.23	0.708	1.12
1431303_at	Stk38	serine/threonine kinase 38	2.86	0.185	1.13	0.83	1.71	0.389	-1.54	0.195	1.04
1446997_at	Eif3s7	eukaryotic translation initiation factor 3, subunit 7 (zeta)	1.2	0.766	3.6	0.07	-1.11	0.652	2.25	0.013	1.49
1455471_at	1500012D20Rik	RIKEN cDNA 1500012D20 gene	3.67	0.044	-1.3	0.581	1.27	0.69	1.76	0.206	1.35
1460220_a_at	Csf1	colony stimulating factor 1 (macrophage)	1.82	0.184	2	0.023	1.9	0.015	-1.36	0.332	1.09
1418133_at	Bcl3	B-cell leukemia/lymphoma 3	1.79	0.126	1.23	0.354	2.71	0.14	-1.09	0.813	1.16
1427652_x_at	Synj2	synaptojanin 2	1.33	0.625	1.4	0.088	2.99	0.321	-1.01	0.99	1.18
1417950_a_at	Apoa2	apolipoprotein A-II	3.53	0.45	-1.22	0.488	1.38	0.469	2.52	0.372	1.55
1431292_a_at	Ptk9l	protein tyrosine kinase 9-like (A6-related protein)	1.41	0.131	3.07	0.004	1.25	0.157	-1.99	0.043	0.94
1458504_at	Zc3h12d	zinc finger CCCH type containing 12D	1.08	0.898	1.4	0.047	3.26	0.127	-1.58	0.343	1.04
1417758_at	Itga2b	integrin alpha 2b	-1.17	0.2	1.04	0.688	3.84	0.051	1.53	0.541	1.31
1460238_at	Msln	mesothelin	-1.76	0.36	1.11	0.796	4.06	0.4	1.15	0.759	1.14
1444587_at	AI481207	expressed sequence AI481207	3.07	0.301	1.72	0.345	-1.05	0.911	1.33	0.462	1.27
1438425_at	Gtf3c1	general transcription factor III C 1	1.81	0.029	1.8	0.165	2.14	0.302	-1.72	0.399	1.01
1449484_at	Stc2	stanniocalcin 2	2.47	0.397	1.74	0.358	1.53	0.189	-1.25	0.01	1.12
1439019_at	Fras1	Fraser syndrome 1 homolog (human)	-1.38	0.077	1.55	0.291	3.47	0.309	2.32	0.016	1.49
1441978_at	Aqp6	aquaporin 6	-1.07	0.685	3.31	0.386	1.51	0.216	1.6	0.444	1.34
1429105_at	Dlgap1	discs, large (Drosophila) homolog-associated protein 1	2.04	0.343	1.66	0.01	2.07	0.136	-1.14	0.667	1.16
1451940_x_at	Trdn	triadin	2.03	0.432	2.29	0.117	1.44	0.374	-1.75	0.42	1
1459357_at	Nfasc	Neurofascin	3.06	0.34	1.52	0.366	1.19	0.771	-2.13	0.127	0.91
1419148_at	Avil	advillin	-1.54	0.313	2.12	0.413	3	0.314	2.69	0.397	1.57
1450512_at	Ntn4	netrin 4	-1.31	0.127	3.73	0.207	1.28	0.024	2.07	0.25	1.44
1428347_at	Cyfip2	cytoplasmic FMR1 interacting protein 2	1.05	0.257	1.53	0.142	3.19	0.068	-1.21	0.534	1.14
1418797_at	Ms4a8a	membrane-spanning 4-domains, subfamily A, member 8A	-1.79	0.317	3.73	0.006	1.49	0.184	3.71	0.291	1.78
1428670_at	2610305J24Rik /// I	RIKEN cDNA 2610305J24 gene /// similar to melanoma antigen /// hypothetical pı	2.85	0.02	-1.07	0.85	1.99	0.438	3.37	0.002	1.78
1415871_at	Tgfbi	transforming growth factor, beta induced	2.28	0.067	1.51	0.005	1.99	0.092	-1.01	0.977	1.19
1451416_a_at	Tgm1	transglutaminase 1, K polypeptide	1.33	0.41	2.96	0.071	1.5	0.202	-1.11	0.785	1.17

1457645_at	C130079G13Rik	RIKEN cDNA C130079G13 gene	3.67	0.063	-1.42	0.714	1.42	0.128	1.31	0.578	1.24
1441116_at	---	---	1.06	0.799	3.71	0.047	1.03	0.904	-1.02	0.978	1.19
1434427_a_at	Rnf157	ring finger protein 157	3.25	0.116	1.11	0.516	1.42	0.034	-1.09	0.762	1.17
1445052_at	Pcdh9	Protocadherin 9	2	0.165	1.71	0.157	2.08	0.01	-5.91	0.179	-0.03
1446468_at	Csmd1 /// LOC670	CUB and Sushi multiple domains 1 /// similar to CUB and Sushi multiple domains	2.71	0.445	1.08	0.898	2	0.129	-1.75	0.414	1.01
1436806_at	Trim62	tripartite motif-containing 62	3.9	0.209	1.18	0.721	-1.4	0.247	2.28	0.148	1.49
1435108_at	Arhgap22	Rho GTPase activating protein 22	2.39	0.431	2.22	0.246	1.2	0.516	-2.32	0.115	0.87
1449580_s_at	H2-DMb1 /// H2-DM	histocompatibility 2, class II, locus Mb1 /// histocompatibility 2, class II, locus Mb2	1.57	0.144	2.4	0.081	1.83	0.199	-1.38	0.559	1.1
1452245_at	Nova1 /// LOC6648	neuro-oncological ventral antigen 1 /// similar to neuro-oncological ventral antigen	-1.14	0.875	3.49	0.005	1.43	0.246	1.91	0.161	1.42
1459685_at	C77683	expressed sequence C77683	1.29	0.732	2.97	0.192	1.54	0.46	-1.76	0.432	1.01
1434759_at	Lrrtm3	leucine rich repeat transmembrane neuronal 3	3.74	0.023	1.06	0.946	-1	0.999	1.07	0.852	1.22
1422562_at	Rrad	Ras-related associated with diabetes	2.91	0.104	1.59	0.105	1.31	0.394	-2.49	0.14	0.83
1426410_at	Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	-1.04	0.053	3.78	0.003	1.06	0.471	1.94	0.061	1.44
1456940_at	Slc43a2	solute carrier family 43, member 2	1.28	0.171	1.34	0.483	3.19	0.011	-1.39	0.653	1.1
1460162_at	LOC640559	similar to Serine/threonine-protein kinase Nek1 (NimA-related protein kinase 1)	3.72	0.058	1.11	0.797	-1.02	0.931	1.33	0.577	1.28
1429481_at	4833426I10Rik	RIKEN cDNA 4833426I10 gene	1.72	0.371	3.04	0.158	1.07	0.822	-1.51	0.532	1.08
1443632_at	Obscn	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF	1.01	0.974	1.51	0.558	3.32	0.107	-1.08	0.721	1.19
1449905_at	Clec4f	C-type lectin domain family 4, member f	1.2	0.528	1.53	0.007	3.11	0.142	-1.56	0.426	1.07
1422188_s_at	Tcrg /// LOC670271	T-cell receptor gamma chain /// T cell receptor gamma chain /// region containing	3.28	0.175	-1.33	0.544	1.81	0.021	1.08	0.825	1.21
1448955_s_at	Cadps	Ca<2+>dependent activator protein for secretion	3.05	0.217	1.5	0.421	1.3	0.654	-1.52	0.082	1.08
1427892_at	Myo1g	myosin IG	2.21	0.101	1.81	0.243	1.83	0.038	-1.65	0.127	1.05
1435144_at	Phb	Prohibitin	2.56	0.25	1.6	0.013	1.69	0.156	-1.17	0.56	1.17
1438475_at	AB124611	cDNA sequence AB124611	1.6	0.524	1.73	0.129	2.52	0.142	-1.53	0.091	1.08
1423520_at	Lmnb1	lamin B1	2.71	0.189	-1.05	0.913	2.19	0.174	1.6	0.361	1.36
1433657_at	A130092J06Rik	RIKEN cDNA A130092J06 gene	2.01	0.232	2.84	0.055	1.01	0.977	-1.31	0.102	1.14
1430521_s_at	Cpne8	copine VIII	1.51	0.424	3.39	0.144	-1.04	0.687	1.15	0.371	1.25
1416754_at	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	1.81	0.19	-1.4	0.186	3.33	0.143	1.32	0.68	1.27
1435955_at	Siglecg	sialic acid binding Ig-like lectin G	1.63	0.668	1.85	0.266	2.38	0.353	-2.19	0.12	0.92
1454408_at	4930544L18Rik	RIKEN cDNA 4930544L18 gene	1.13	0.687	3.32	0.008	1.41	0.43	-1.14	0.486	1.18
1424624_at	2900011O08Rik	RIKEN cDNA 2900011O08 gene	-1.43	0.058	3.51	0.013	1.66	0.094	1.31	0.578	1.26
1431106_a_at	9530053H05Rik	RIKEN cDNA 9530053H05 gene	1.01	0.954	1.75	0.204	3.12	0.154	-1.6	0.236	1.07
1439254_at	Akap13	A kinase (PRKA) anchor protein 13	1.08	0.876	2.74	0.161	2.06	0.398	-1.39	0.51	1.12
1449835_at	Pdcd1	programmed cell death 1	-1.75	0.616	2.76	0.263	2.55	0.098	1.33	0.399	1.22
1429179_at	Colec11	collectin sub-family member 11	1.63	0.189	1.14	0.28	3.11	0.006	-1.71	0.408	1.04
1418907_at	---	---	1.09	0.729	-1.03	0.737	3.82	0.08	2.16	0.396	1.51
1420704_at	Csf2ra /// LOC6713	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	1.11	0.889	3.51	0.006	1.27	0.459	-1.35	0.399	1.14
1436370_at	Gucy2c	guanylate cyclase 2c	1.35	0.502	3.3	0.091	1.24	0.35	-1.43	0.187	1.12
1443687_x_at	H2-DMb1	Histocompatibility 2, class II, locus Mb1	2.25	0.193	1.6	0.221	2.05	0.394	-1.79	0.294	1.03
1418757_at	Rnf36	ring finger protein 36	2.75	0.008	1.47	0.09	1.69	0.141	-1.05	0.933	1.21
1436905_x_at	Laptm5	lysosomal-associated protein transmembrane 5	2.12	0.092	2.19	0.001	1.59	0.03	-1.41	0.194	1.12
1447513_at	Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	1	0.995	3.78	0.012	1.13	0.72	-2.17	0.378	0.94
1434945_at	Aytl1	acyltransferase like 1	2.34	0.129	1.51	0.276	2.07	0.038	-1.15	0.693	1.19
1426936_at	2610305J24Rik /// E	RIKEN cDNA 2610305J24 gene /// cDNA sequence BC005512 /// hypothetical pr	2.51	0.068	-1.26	0.554	2.61	0.296	1.72	0.145	1.4
1420066_s_at	Cd160	CD160 antigen	1.84	0.087	2.32	0.009	1.77	0.296	-1.61	0.32	1.08
1460657_at	Wnt10a	wingless related MMTV integration site 10a	1.41	0.365	1.59	0.436	2.92	0.289	-1.12	0.791	1.2
1434984_at	6330514A18Rik	RIKEN cDNA 6330514A18 gene	2.26	0.069	2.39	0.009	1.27	0.648	-1.29	0.678	1.16
1418617_x_at	Clgn	calmegin	3.49	0.467	1.73	0.223	-1.42	0.375	2.65	0.37	1.61
1422779_at	Smpd3	sphingomyelin phosphodiesterase 3, neutral	1.02	0.965	2.78	0.173	2.12	0.009	-1.57	0.333	1.09
1453242_x_at	2810047C21Rik	RIKEN cDNA 2810047C21 gene	2.65	0.026	1.55	0.452	1.72	0.003	-1.99	0.311	0.98
1429677_at	1700056E22Rik	RIKEN cDNA 1700056E22 gene	1.29	0.483	3.34	0.044	1.3	0.05	-1.1	0.871	1.21
1417391_a_at	Il16	interleukin 16	2.02	0.09	1.81	0.023	2.11	0.117	-1.76	0.131	1.04
1428664_at	Vip	vasoactive intestinal polypeptide	2.99	0.341	1.52	0.508	1.43	0.528	-1.42	0.644	1.13
1435582_at	Wdfy4	WD repeat and FYVE domain containing 4	2.17	0.031	2.08	0.015	1.69	0.37	-1.63	0.232	1.07

1432269_a_at	Sh3kbp1	SH3-domain kinase binding protein 1	2.06	0.373	1.57	0.336	2.31	0.054	-2.13	0.252	0.95
1431532_at	4931400O07Rik	RIKEN cDNA 4931400O07 gene	1.11	0.813	2.92	0.158	1.9	0.06	-1.42	0.593	1.13
1418147_at	Tcfap2c	transcription factor AP-2, gamma	1.41	0.5	1.58	0.321	2.95	0.029	-1.04	0.957	1.22
1420667_at	Doc2b	double C2, beta	1.1	0.744	1.1	0.876	3.74	0.064	-1	0.992	1.23
1438406_at	Scarf2	scavenger receptor class F, member 2	3.96	0.019	-1.91	0.271	1.46	0.177	1.04	0.88	1.14
1429235_at	Galntl2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.83	0.382	3.32	0.045	-1.26	0.581	2.35	0.144	1.56
1443994_at	6030407O03Rik	RIKEN cDNA 6030407O03 gene	2.93	0.009	2.62	0.286	-2.46	0.169	1.97	0.296	1.26
1418944_at	Cysltr1	cysteinyl leukotriene receptor 1	4.03	0.212	1.01	0.976	-1.11	0.636	1.61	0.246	1.39
1442590_at	Tnfrsf23	tumor necrosis factor receptor superfamily, member 23	1.38	0.432	3.47	0.044	1.1	0.656	-1.09	0.72	1.21
1425423_at	Glis1	GLIS family zinc finger 1	1.01	0.95	4.08	0.066	-1.17	0.803	1.07	0.821	1.25
1450273_at	Il1rl2	interleukin 1 receptor-like 2	1.06	0.894	3.54	0.048	1.35	0.64	-1.06	0.917	1.22
1435040_at	Irak3	interleukin-1 receptor-associated kinase 3	1.68	0.132	2.98	0.05	1.31	0.08	-1.57	0.048	1.1
1418868_at	En2	engrailed 2	3.72	0.015	1.17	0.743	1.07	0.903	-1.71	0.044	1.07
1416295_a_at	Il2rg	interleukin 2 receptor, gamma chain	2.33	0.144	1.93	0.044	1.71	0.045	-1.45	0.373	1.13
1449191_at	Wfdc12	WAP four-disulfide core domain 12	3.53	0.036	-1.72	0.363	1.87	0.058	3.91	0.243	1.9
1452117_a_at	Fyb	FYN binding protein	2.01	0.17	2.03	0.004	1.95	0.042	-1.24	0.169	1.18
1435532_at	4933426K21Rik	RIKEN cDNA 4933426K21 gene	1.22	0.563	3.2	0.199	1.57	0.381	-1.63	0.598	1.09
1430499_at	1700058M13Rik	RIKEN cDNA 1700058M13 gene	3.45	0.021	1.24	0.759	1.3	0.301	-1.71	0.502	1.07
1449399_a_at	Il1b	interleukin 1 beta	1.13	0.722	1.38	0.402	3.49	0.108	-1.4	0.48	1.15
1426231_at	Vit	vitrin	1.84	0.244	2.44	0.25	1.72	0.098	-1.57	0.321	1.11
1442437_at	Ptk2b	PTK2 protein tyrosine kinase 2 beta	3.5	0.012	1.44	0.386	1.06	0.93	-1.64	0.255	1.09
1450284_at	Pde3a	phosphodiesterase 3A, cGMP inhibited	2.66	0.155	1.32	0.629	2.02	0.134	-1.98	0.065	1.01
1445949_at	Tnfrsf19	Tumor necrosis factor receptor superfamily, member 19	3.2	0.061	-1.03	0.947	1.83	0.162	1.18	0.531	1.29
1445687_at	Gm885	gene model 885, (NCBI)	2.67	0.092	2.3	0.103	1.04	0.868	-1.39	0.17	1.15
1416298_at	Mmp9	matrix metallopeptidase 9	-1.45	0.321	2.02	0.135	3.31	0.208	2.14	0.336	1.51
1418075_at	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide	1.01	0.983	3.97	0.017	1.04	0.721	-1.02	0.872	1.25
1442891_at	AU023386	expressed sequence AU023386	1.04	0.961	2.93	0.116	2.05	0.083	-1.15	0.555	1.22
1448713_at	Stat4	signal transducer and activator of transcription 4	2.57	0.016	2.32	0.396	1.13	0.522	-2.32	0.07	0.93
1442162_at	---	---	2.65	0.088	2.68	0.007	-1.44	0.094	1.03	0.961	1.23
1422417_at	---	---	2.85	0.067	2	0.222	1.18	0.301	-1.93	0.092	1.03
1436590_at	Ppp1r3b	protein phosphatase 1, regulatory (inhibitor) subunit 3B	3.09	0.183	-1.21	0.362	2.11	0.002	1.43	0.492	1.36
1418853_at	Apon	apolipoprotein N	4.02	0.465	1.13	0.368	-1.13	0.657	1.25	0.192	1.32
1422412_x_at	Ear3	eosinophil-associated, ribonuclease A family, member 3	1.1	0.869	4.22	0.002	-1.38	0.038	1.14	0.344	1.27
1429621_at	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	1.82	0.032	2.05	0.276	2.17	0.102	-1.33	0.206	1.18
1425902_a_at	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	1.3	0.231	3.32	0.002	1.43	0.18	-1.74	0.22	1.08
1425032_at	Abpb	androgen binding protein beta	4.58	0.219	-2.27	0.027	1.03	0.941	1.18	0.734	1.13
1460021_at	LOC626231	hypothetical protein LOC626231	3.96	0.035	1.05	0.897	1.04	0.857	-1.63	0.244	1.1
1431248_at	5031426D15Rik	RIKEN cDNA 5031426D15 gene	3.66	0.103	1.99	0.125	-2.46	0.049	1.3	0.206	1.12
1450792_at	Tyrobp	TYRO protein tyrosine kinase binding protein	2.3	0.118	2.28	0	1.48	0.273	-1.27	0.21	1.2
1422190_at	C5ar1	complement component 5a receptor 1	1.97	0.038	1.58	0.533	2.51	0.074	-1.75	0.169	1.08
1436592_at	---	12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010015L(	1.36	0.677	-1.44	0.555	4.02	0.285	1.15	0.7	1.27
1457646_at	Hoxa11os	homeo box A11, opposite strand transcript	4.26	0.272	-1.69	0.316	1.22	0.655	3.31	0.037	1.78
1435217_at	LOC666185 /// LOC	hypothetical protein LOC666185 /// hypothetical protein LOC666222 /// hypothetic	1.51	0.094	3.45	0.088	1.14	0.698	-1.25	0.387	1.21
1417776_at	Azgp1	alpha-2-glycoprotein 1, zinc	2.96	0.035	-1.12	0.537	2.23	0.128	4.03	0.013	2.03
1452957_at	Krtap3-3	keratin associated protein 3-3	1.02	0.932	2.02	0.019	3.06	0.11	-1.43	0.478	1.17
1420515_a_at	Pglyrp2	peptidoglycan recognition protein 2	3.54	0.414	1.22	0.26	1.33	0.378	-2.44	0.15	0.91
1459921_at	Nxph1	neurexophilin 1	1.71	0.475	-1.35	0.193	3.64	0.065	2.22	0.099	1.55
1440610_at	Casd1	CAS1 domain containing 1	1.81	0.391	2.71	0.203	1.58	0.375	-1.69	0.541	1.1
1424902_at	Plxdc1	plexin domain containing 1	1.92	0.061	3.37	0.062	-1.23	0.561	1.14	0.445	1.3
1451849_a_at	Lmnb2	lamin B2	3.23	0.007	1.32	0.556	1.55	0.214	-1.15	0.801	1.24
1435990_at	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	2.2	0.286	3.59	0.108	-3.12	0.055	1.08	0.504	0.94
1442238_a_at	Kif6	kinesin family member 6	-1.67	0.075	4.14	0.056	1.37	0.345	1.01	0.979	1.21
1424722_at	1300017J02Rik	RIKEN cDNA 1300017J02 gene	3.98	0.404	-1.11	0.204	1.23	0.569	4.29	0.198	2.1

1444179_at	A530023O14Rik	RIKEN cDNA A530023O14 gene	1.26	0.624	2.64	0.245	2.22	0.124	-2.06	0.065	1.01
1427757_at	Igk-V21	immunoglobulin kappa chain variable 21 (V21)	2	0.306	-1.21	0.35	3.29	0.431	1.24	0.67	1.33
1427625_a_at	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (	1.55	0.158	3.79	0.204	-1.28	0.713	1.39	0.519	1.36
1450060_at	Pigr	polymeric immunoglobulin receptor	3.72	0.037	-1.06	0.634	1.46	0.128	1.09	0.857	1.31
1425546_a_at	Trf	transferrin	4.12	0.337	-1.18	0.492	1.16	0.22	1.36	0.244	1.37
1449127_at	Selpl	selectin, platelet (p-selectin) ligand	2.1	0.036	2.18	0.004	1.86	0.082	-1.11	0.696	1.26
1425958_at	Il1f9	interleukin 1 family, member 9	-1.03	0.934	1.03	0.87	4.14	0.247	1.98	0.433	1.53
1427076_at	Mpeg1 /// LOC6713	macrophage expressed gene 1 /// similar to macrophage expressed gene 1	2.62	0.226	2.09	0.01	1.44	0.066	-1.21	0.414	1.23
1457123_at	Nrg4	neuregulin 4	-4	0.03	1.67	0.175	4.22	0.185	2.18	0.212	1.02
1448458_at	Top2b	topoisomerase (DNA) II beta	2.44	0.403	1.69	0.411	2.01	0.581	-1.5	0.768	1.16
1424032_at	Hvcn1	hydrogen voltage-gated channel 1	1.55	0.215	3.13	0.03	1.48	0.393	-2.44	0.069	0.93
1422316_at	Gp1ba	glycoprotein 1b, alpha polypeptide	-1.2	0.003	2.14	0.16	3.18	0.125	2.31	0.393	1.61
1429745_at	LOC434795 /// LOC	similar to melanoma ubiquitous mutated protein /// similar to UBE-1C2 protein /// s	2.52	0.473	2.44	0.311	1.2	0.441	-1.25	0.803	1.23
1418741_at	Itgb7	integrin beta 7	3.05	0.017	1.61	0.094	1.5	0.128	-1.64	0.273	1.13
1444233_at	Gpr132	G protein-coupled receptor 132	2.86	0.062	2.01	0.062	1.29	0.075	-2	0.056	1.04
1450974_at	Timp4	tissue inhibitor of metalloproteinase 4	-1.09	0.925	2.24	0.251	3.01	0.02	3.03	0.051	1.8
1451335_at	Plac8	placenta-specific 8	1.35	0.346	1.94	0.067	2.89	0.132	-1.51	0.028	1.17
1453813_at	Cd200r3	CD200 receptor 3	-3.01	0.136	1.52	0.394	4.32	0.095	1.39	0.62	1.06
1421073_a_at	Ptger4	prostaglandin E receptor 4 (subtype EP4)	2.57	0.015	2.05	0.323	1.57	0.044	-1.02	0.729	1.29
1455269_a_at	Coro1a	coronin, actin binding protein 1A	2.24	0.168	2.15	0.019	1.79	0.202	-2.07	0.064	1.03
1420600_at	Tpo	thyroid peroxidase	2.93	0.066	2.86	0.233	-2.53	0.002	1.34	0.454	1.15
1436861_at	Il7	interleukin 7	1.32	0.278	3.65	0.011	1.22	0.117	-1.68	0.126	1.13
1427472_a_at	C8b	complement component 8, beta subunit	4.15	0.41	-1.15	0.722	1.17	0.468	1.14	0.594	1.33
1454139_at	4930405N21Rik	RIKEN cDNA 4930405N21 gene	-1.08	0.547	1.86	0.412	3.41	0.012	1.61	0.143	1.45
1448152_at	Igf2	insulin-like growth factor 2	3.88	0.014	1.27	0.756	1.05	0.696	-1.41	0.309	1.2
1454280_at	4931406H21Rik	RIKEN cDNA 4931406H21 gene	1.64	0.375	2.95	0.249	1.6	0.209	-1.24	0.635	1.24
1428114_at	Slc14a1	solute carrier family 14 (urea transporter), member 1	-1.48	0.081	3.23	0.111	2.3	0.029	3.04	0.195	1.77
1442531_at	D12Ertd123e	DNA segment, Chr 12, ERATO Doi 123, expressed	1.03	0.976	4.76	0.069	-2.38	0.04	2.06	0.156	1.37
1458512_at	Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	-1.1	0.808	4.22	0.187	1.08	0.828	1.02	0.963	1.3
1449751_at	---	---	1.72	0.202	2.09	0.29	2.4	0.29	-1.55	0.502	1.16
1417496_at	Cp	ceruloplasmin	3.33	0.3	1.7	0.289	1.18	0.764	-1.31	0.382	1.23
1421263_at	Gabra3	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 3	2.03	0.443	1.22	0.656	2.97	0.091	-1.65	0.102	1.14
1422201_at	---	---	2.02	0.488	1.04	0.896	3.15	0.382	-3.22	0.176	0.75
1442758_at	Hnrpa1	Heterogeneous nuclear ribonucleoprotein A1	2.95	0.155	1.4	0.546	1.87	0.034	-1.78	0.047	1.11
1460027_at	BC061194	cDNA sequence BC061194	2.82	0.326	2.26	0.23	1.14	0.843	-1.31	0.71	1.23
1460509_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	1.73	0.483	3.14	0.172	1.35	0.633	-1.09	0.864	1.28
1424870_at	Osbpl10	oxysterol binding protein-like 10	3.47	0.006	1.47	0.637	1.3	0.556	-1.07	0.878	1.29
1426792_s_at	Rusc2	RUN and SH3 domain containing 2	3.43	0.106	1.87	0.071	-1.06	0.819	1.02	0.966	1.32
1423852_at	Tmem46	transmembrane protein 46	1.26	0.64	3.84	0.123	1.14	0.735	-2.73	0.049	0.88
1456619_at	Liph	Lipase, member H	-1.64	0.606	4.62	0.041	1.02	0.91	1.11	0.88	1.28
1431707_a_at	Pscd3	pleckstrin homology, Sec7 and coiled-coil domains 3	1.33	0.37	3.95	0.09	-1	0.994	1.33	0.634	1.4
1421239_at	Il6st	interleukin 6 signal transducer	2.28	0.433	1.34	0.63	2.67	0.444	-1.31	0.735	1.24
1429788_at	Arpm1	actin related protein M1	2.02	0.106	2.77	0.306	1.5	0.3	-1.54	0.451	1.19
1436176_at	Syt11	synaptotagmin XI	3.58	0.067	1.5	0.579	1.21	0.589	-1.88	0.068	1.1
1429684_at	5830472M02Rik	RIKEN cDNA 5830472M02 gene	3.13	0.209	1.53	0.435	1.63	0.217	-1.58	0.432	1.18
1451948_at	Gm1409	gene model 1409, (NCBI)	2.14	0.162	3.05	0.12	1.11	0.612	-1.02	0.957	1.32
1432004_a_at	Dnm2	dynamin 2	1.56	0.527	-1.03	0.966	3.78	0.257	1.11	0.888	1.36
1430313_at	Adamtsl1	ADAMTS-like 1	2.28	0.419	3.37	0.138	-1.49	0.438	1.38	0.257	1.38
1421973_at	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	-1.3	0.274	1.36	0.553	4.22	0.388	1.15	0.736	1.35
1427655_a_at	A630038E17Rik	RIKEN cDNA A630038E17 gene	2.83	0.372	2.05	0.244	1.47	0.086	-4.36	0.004	0.5
1435424_x_at	---	Transcribed locus	1.27	0.678	3.08	0.223	1.99	0.137	-1.02	0.982	1.33
1456014_s_at	BC032204	cDNA sequence BC032204	1.68	0.141	1.64	0	3.02	0.086	-1.18	0.054	1.29
1420525_a_at	Otc	ornithine transcarbamylase	4.31	0.406	-1.21	0.267	1.21	0.603	2.15	0.178	1.62

1460042_at	Slc23a3	solute carrier family 23 (nucleobase transporters), member 3	2.14	0.022	2.29	0.13	1.92	0.203	-1.12	0.749	1.31
1418957_at	Stac	src homology three (SH3) and cysteine rich domain	4.39	0.015	-1.32	0.29	1.2	0.681	1.92	0.018	1.55
1440921_at	Nalp12	NACHT, LRR and PYD containing protein 12	3.24	0.295	-1.16	0.735	2.25	0.321	1.02	0.98	1.34
1429860_at	LOC677447	similar to RIKEN cDNA 5730590G19-like	2.67	0.094	-1.65	0.002	3.08	0.036	1.4	0.285	1.38
1458846_at	---	---	1.25	0.658	3.38	0.015	1.74	0.129	-1.66	0.427	1.17
1456147_at	St8sia6	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	1.08	0.677	2.64	0.285	2.64	0.271	-1.49	0.293	1.22
1429525_s_at	Myo1f	myosin IF	1.91	0.196	1.98	0.143	2.48	0.071	-1.03	0.857	1.34
1421851_at	Mtap1b	microtubule-associated protein 1 B	2.06	0.403	3.17	0.02	1.15	0.709	-1.1	0.82	1.32
1424279_at	Fga	fibrinogen, alpha polypeptide	3.22	0.389	-1.25	0.351	2.35	0.026	3.33	0.377	1.91
1449591_at	Casp4	caspase 4, apoptosis-related cysteine peptidase	3.03	0.05	1.93	0.006	1.41	0.156	-1.18	0.561	1.3
1440815_x_at	LOC624112	hypothetical protein LOC624112	3.19	0.103	1.55	0.32	1.64	0.291	-1	0.996	1.34
1426552_a_at	Bcl11a	B-cell CLL/lymphoma 11A (zinc finger protein)	1.53	0.552	1.07	0.898	3.79	0.144	-1.19	0.101	1.3
1419853_a_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	1.76	0.022	3	0.244	1.63	0.058	-1.15	0.69	1.31
1460218_at	Cd52	CD52 antigen	2.24	0.128	2.07	0.002	2.08	0.18	-1.64	0.124	1.19
1450136_at	Cd38	CD38 antigen	1.79	0.261	1.97	0.075	2.64	0.159	-1.03	0.939	1.34
1457433_x_at	Zfp120	Zinc finger protein 120	-1.2	0.047	4.5	0.14	1.07	0.746	1.53	0.155	1.48
1429524_at	Myo1f	myosin IF	1.55	0.147	2.47	0.006	2.39	0.093	-1.27	0.446	1.28
1431724_a_at	P2ry12	purinergic receptor P2Y, G-protein coupled 12	1.4	0.011	2.36	0.051	2.65	0.07	-1.04	0.635	1.34
1448573_a_at	Ceacam10	CEA-related cell adhesion molecule 10	-1.13	0.883	1.75	0.319	3.78	0.335	1.98	0.396	1.59
1416246_a_at	Coro1a	coronin, actin binding protein 1A	1.93	0.083	2.48	0.037	2.01	0.11	-2.09	0.048	1.08
1458071_at	---	Transcribed locus	2.34	0.185	2.48	0.207	1.59	0.198	-1.3	0.556	1.28
1430796_at	Trim14	tripartite motif-containing 14	3.03	0.012	1.89	0.105	1.5	0.414	-1.39	0.67	1.26
1421718_at	Strm	striamin	1.81	0.477	2.95	0.104	1.67	0.388	-1.23	0.64	1.3
1444627_at	P2ry5	Purinergic receptor P2Y, G-protein coupled, 5	2.32	0.338	3.4	0.355	-1.42	0.543	2.75	0.319	1.76
1438672_at	Parvb	parvin, beta	-1.07	0.19	3.71	0.019	1.79	0.044	3.05	0.219	1.87
1425062_at	Fcrl1	Fc receptor-like 1	2.93	0.422	1.49	0.109	2.02	0.352	-3.04	0.036	0.85
1451846_at	Nebl	nebulette	2.6	0.31	1.05	0.948	2.79	0.465	-1.1	0.889	1.33
1458922_at	Map3k9	mitogen-activated protein kinase kinase kinase 9	2.37	0.053	2.38	0.336	1.69	0.241	-1.14	0.853	1.33
1445678_at	---	---	3.19	0.001	-1.1	0.827	2.34	0.085	1.12	0.456	1.39
1439517_at	Mysm1	myb-like, SWIRM and MPN domains 1	3.06	0.112	1.09	0.863	2.31	0.52	-2.16	0.469	1.07
1460419_a_at	Prkcb1	protein kinase C, beta 1	1.67	0.386	1.79	0.007	3	0.248	-1.61	0.213	1.21
1450330_at	Il10	interleukin 10	2.02	0.3	-1.03	0.873	3.48	0.206	2.24	0.011	1.68
1421620_at	Il5ra	interleukin 5 receptor, alpha	3.04	0.083	-1.29	0.481	2.66	0.235	1.36	0.161	1.44
1432189_a_at	Sox5	SRY-box containing gene 5	3.88	0.036	-1.6	0.082	1.98	0.244	2.99	0.11	1.81
1429330_at	Gabra4	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	-1.22	0.171	4.6	0.209	1.08	0.907	1.83	0.382	1.57
1433466_at	AI467606	expressed sequence AI467606	1.07	0.928	3.81	0.013	1.61	0.029	-2.07	0.101	1.1
1458833_at	C130076O07Rik	RIKEN cDNA C130076O07 gene	3.09	0.037	1.68	0.085	1.72	0.297	-1.74	0.377	1.19
1422411_s_at	Ear1 /// Ear2 /// Ear	eosinophil-associated, ribonuclease A family, member 1 /// eosinophil-associated	2.78	0.01	3.04	0.008	-1.48	0.116	1.2	0.392	1.39
1416558_at	Melk	maternal embryonic leucine zipper kinase	-5.5	0.091	5.1	0.003	1.21	0.704	2.87	0.167	0.92
1460282_at	Trem1	triggering receptor expressed on myeloid cells 1	-1.06	0.952	1.37	0.596	4.2	0.395	3.02	0.256	1.88
1445652_at	Stag1	Stromal antigen 1	1.68	0.539	2.99	0.013	1.86	0.13	-1.09	0.873	1.36
1436778_at	Cybb	cytochrome b-245, beta polypeptide	1.8	0.24	2.13	0	2.59	0.02	-1.14	0.561	1.35
1460693_a_at	Col9a3	procollagen, type IX, alpha 3	1.24	0.121	4.37	0.001	-1.08	0.891	1.17	0.721	1.42
1453615_at	---	---	1.97	0.532	4.02	0.007	-1.84	0.163	1.92	0.343	1.52
1433930_at	Hpse	Heparanase	1.64	0.121	1.52	0.075	3.39	0.057	-1.39	0.246	1.29
1446378_at	D2Ertd357e	DNA segment, Chr 2, ERATO Doi 357, expressed	1.57	0.524	2.59	0.144	2.4	0.241	-1.11	0.869	1.36
1437056_x_at	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	1.75	0.312	4.11	0.124	-1.43	0.208	1.51	0.057	1.48
1421734_at	---	---	-1.38	0.397	2.17	0.105	3.67	0.177	1.64	0.447	1.52
1436576_at	A630077B13Rik	RIKEN cDNA A630077B13 gene	1.89	0.35	1.88	0.017	2.79	0.054	-1.03	0.949	1.38
1415823_at	Scd2	stearoyl-Coenzyme A desaturase 2	1.06	0.889	3.9	0.041	1.61	0.127	-1.18	0.501	1.35
1424302_at	Lilrb3 /// LOC61960	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains)	1.57	0.293	1.79	0.069	3.23	0.133	-1.32	0.521	1.32
1420407_at	Ltb4r1	leukotriene B4 receptor 1	-1.12	0.828	1.32	0.44	4.37	0.322	1.35	0.703	1.48
1457973_at	Pcdh9	Protocadherin 9	3.95	0.034	1.78	0.468	-1.16	0.794	1.31	0.314	1.47

1416576_at	Socs3	suppressor of cytokine signaling 3	2.96	0.277	2.32	0.186	1.31	0.05	-1.05	0.745	1.39
1419098_at	Stom	stomatin	2.87	0.114	-1.05	0.931	2.77	0.312	5.73	0.203	2.58
1434015_at	Slc2a6	solute carrier family 2 (facilitated glucose transporter), member 6	2.84	0.372	1.04	0.915	2.72	0.082	-1.79	0.011	1.2
1455015_at	Tbc1d9	TBC1 domain family, member 9	1.31	0.4	3.99	0.047	1.33	0.504	-1.06	0.902	1.39
1450379_at	Msn	moesin	1.68	0.376	2.22	0.048	2.74	0.222	-1.43	0.621	1.3
1424758_s_at	Serpina10	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsi	3.41	0.2	1.7	0.145	1.53	0.286	-1.52	0.215	1.28
1456304_at	Gm996	gene model 996, (NCBI)	-1.1	0.873	2.12	0.036	3.61	0.02	2.25	0.162	1.72
1427387_a_at	Itgb4	integrin beta 4	2	0.218	1.46	0.479	3.18	0.02	-1.62	0.129	1.25
1453670_at	Usp50	ubiquitin specific peptidase 50	5.01	0.155	1.33	0.488	-3.23	0.128	3.22	0.034	1.58
1421546_a_at	Racgap1	Rac GTPase-activating protein 1	-1.25	0.045	3.95	0.005	1.9	0.128	2.74	0.174	1.84
1427292_at	Igl-V1	immunoglobulin lambda chain, variable 1	1.78	0.229	1.31	0.629	3.57	0.143	-1.55	0.378	1.28
1437075_at	Frmd3	FERM domain containing 3	2.4	0.094	1.93	0.336	2.33	0.056	-1.45	0.166	1.3
1423427_at	Adcyap1	adenylate cyclase activating polypeptide 1	2.83	0.053	2.55	0.365	1.29	0.655	-1.9	0.498	1.19
1434535_at	Krt222	keratin 222	1	0.994	-1.01	0.985	4.68	0.201	1.58	0.027	1.56
1422583_at	Rab3b	RAB3B, member RAS oncogene family	-1.22	0.244	2.47	0.244	3.38	0.106	1.21	0.786	1.46
1459974_x_at	2700008N14Rik	RIKEN cDNA 2700008N14 gene	4.58	0.01	1.53	0.545	-1.77	0.207	1.28	0.629	1.41
1449112_at	Slc27a5	solute carrier family 27 (fatty acid transporter), member 5	4.66	0.323	-1.15	0.35	1.16	0.741	1.75	0.325	1.6
1458673_at	1700093J21Rik	RIKEN cDNA 1700093J21 gene	4.64	0.044	1.19	0.84	-1.14	0.708	1.43	0.511	1.53
1433008_at	6330526H18Rik	RIKEN cDNA 6330526H18 gene	2.72	0.153	2.14	0.251	1.86	0.154	-1.67	0.081	1.26
1433047_at	5330430B06Rik	RIKEN cDNA 5330430B06 gene	5.24	0	-2.5	0.095	1.08	0.888	1.1	0.9	1.23
1449049_at	Tlr1	toll-like receptor 1	1.22	0.775	2.61	0.015	2.89	0.189	-2.18	0.069	1.13
1419744_at	H2-DMb2	histocompatibility 2, class II, locus Mb2	1.55	0.313	1.18	0.483	4	0.213	-1.62	0.504	1.28
1449498_at	Marco	macrophage receptor with collagenous structure	1.74	0.118	2.36	0.104	2.63	0.016	-5.82	0.003	0.23
1450440_at	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	2.65	0.094	1.58	0.413	2.51	0.347	-1.13	0.861	1.4
1457790_at	Asb3	Ankyrin repeat and SOCS box-containing protein 3	4.81	0.083	1.03	0.905	-1.1	0.722	1.19	0.751	1.48
1441805_at	---	Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A2300	3.83	0.093	2.16	0.168	-1.31	0.279	1.02	0.939	1.42
1448748_at	Plek	pleckstrin	2.47	0.1	2.5	0.002	1.79	0.154	-1.03	0.862	1.43
1445084_at	---	---	3.48	0.044	2.89	0.089	-2.58	0.141	1.18	0.784	1.24
1421174_at	Irf4	interferon regulatory factor 4	1.94	0.387	2.99	0.218	1.85	0.057	-1.21	0.66	1.39
1425128_at	B3gnt8	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	4.26	0.087	1.13	0.723	1.38	0.502	-3.11	0.044	0.92
1423528_at	Bcas3	breast carcinoma amplified sequence 3	4.04	0.009	-2.14	0.297	2.27	0.136	1.05	0.925	1.31
1420819_at	Sla	src-like adaptor	1.69	0.48	2.68	0.034	2.42	0.129	-1.33	0.319	1.37
1441326_at	Cp	ceruloplasmin	2.97	0.316	2.34	0.256	1.5	0.481	-1.05	0.75	1.44
1432763_at	Prrg2	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	3.77	0.009	2.12	0.167	-1.09	0.851	1.46	0.655	1.57
1419910_at	Mphosph9	M-phase phosphoprotein 9	1.12	0.812	5.22	0.039	-2.07	0.206	1.08	0.498	1.34
1442049_at	Trf	Transferrin	4.02	0.3	1.82	0.171	-1.01	0.984	2.14	0.214	1.74
1440837_at	H2-Ob	histocompatibility 2, O region beta locus	1.82	0.509	1.85	0.27	3.18	0.374	-2.15	0.103	1.17
1444177_at	---	PREDICTED: Mus musculus hypothetical protein LOC626058 (LOC626058), mR	2.31	0.338	1.68	0.324	2.88	0.338	-2	0.123	1.22
1417613_at	Ier5	immediate early response 5	1.02	0.983	3.76	0.139	2.11	0.316	-2.09	0.311	1.2
1428784_at	Gmip	Gem-interacting protein	2.56	0.052	2.22	0.279	2.09	0.046	-1.8	0.151	1.27
1445272_at	Rnf38	Ring finger protein 38	3.72	0.315	1.93	0.096	1.25	0.713	-3.06	0.207	0.96
1419832_s_at	Acpp	acid phosphatase, prostate	1.11	0.882	3.89	0.182	1.91	0.317	-1.21	0.749	1.43
1420434_at	Cldn16	claudin 16	1.05	0.42	4.17	0.047	1.69	0.131	-2.19	0.336	1.18
1418778_at	Ccdc109b	coiled-coil domain containing 109B	1.42	0.252	4.11	0.168	1.4	0.194	-1.01	0.953	1.48
1426653_at	Mcm3	minichromosome maintenance deficient 3 (S. cerevisiae)	3.97	0.023	-1.02	0.946	1.97	0.077	3.23	0.229	2.04
1450829_at	Tnfaip3	tumor necrosis factor, alpha-induced protein 3	1.48	0.714	2.83	0.102	2.62	0.104	-1.74	0.062	1.3
1456328_at	Bank1	B-cell scaffold protein with ankyrin repeats 1	2.61	0.294	1.57	0.004	2.76	0.174	-1.73	0.228	1.3
1438609_x_at	Tnni2	troponin I, skeletal, fast 2	1.36	0.396	1.21	0.827	4.38	0.177	-1.56	0.589	1.35
1443852_at	---	Transcribed locus	4.51	0.169	1.56	0.555	-1.12	0.708	1.06	0.912	1.5
1440188_at	---	---	1.37	0.61	4.01	0.05	1.59	0.366	-2.02	0.171	1.24
1456966_at	BC028528	CDNA sequence BC028528	4.16	0.089	2	0.336	-1.22	0.405	1.4	0.596	1.58
1453072_at	Gpr160	G protein-coupled receptor 160	-1.1	0.358	4.99	0.062	1.09	0.788	1.36	0.148	1.59
1449153_at	Mmp12	matrix metallopeptidase 12	1.14	0.437	3.37	0.187	2.48	0.086	-3.12	0.06	0.97

1430700_a_at	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	1.04	0.819	2.42	0.149	3.54	0.11	-1.33	0.254	1.42
1434955_at	1-Mar	membrane-associated ring finger (C3HC4) 1	1.68	0.125	3.3	0.01	2.03	0.09	-2.43	0.055	1.14
1454211_a_at	Shroom3	shroom family member 3	1.11	0.724	4.38	0.005	1.52	0.115	-1.37	0.516	1.41
1439323_a_at	Map4k1 /// LOC672	mitogen activated protein kinase kinase kinase kinase 1 /// similar to Mitogen-acti	1.77	0.421	2.95	0.065	2.31	0.243	-1.77	0.093	1.31
1431214_at	1300007C21Rik	RIKEN cDNA 1300007C21 gene	2.44	0.315	1.76	0.48	2.83	0.446	-1.17	0.776	1.46
1422206_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	-1.35	0.715	5.25	0.239	1.04	0.696	2.48	0.306	1.86
1425137_a_at	H2-Q10	histocompatibility 2, Q region locus 10	3.26	0.452	-1	0.962	2.79	0.036	1.22	0.739	1.57
1418674_at	Osmr	oncostatin M receptor	2.43	0.163	3.85	0.086	-1.3	0.077	1.25	0.357	1.56
1425710_a_at	Homer1	homer homolog 1 (Drosophila)	1.69	0.403	3.15	0.233	2.22	0.225	-1.58	0.31	1.37
1449031_at	Cited1	Cbp/p300-interacting transactivator with Glu/Asp-rich carboxy-terminal domain 1	4.01	0.288	1.91	0.265	1.15	0.472	-1.17	0.586	1.47
1416120_at	Rrm2	ribonucleotide reductase M2	-1.08	0.649	1.06	0.926	5.08	0.031	5.37	0.123	2.61
1447498_at	Edar /// LOC66900	ectodysplasin-A receptor /// similar to Tumor necrosis factor receptor superfamily	2.6	0.304	3.1	0.162	1.37	0.481	-1.67	0.537	1.35
1419168_at	Mapk6	mitogen-activated protein kinase 6	4.36	0.007	1.15	0.486	1.55	0.536	-1.06	0.881	1.5
1460415_a_at	Cd40	CD40 antigen	1.51	0.582	4.39	0.103	1.17	0.363	-2.54	0.142	1.13
1437487_at	Myst3	MYST histone acetyltransferase (monocytic leukemia) 3	2.44	0.187	3.5	0.03	1.13	0.807	-1.09	0.836	1.5
1445567_at	Gap43	Growth associated protein 43	3.32	0.339	3.08	0.287	-1.46	0.248	2.05	0.116	1.75
1418243_at	Fcna	ficolin A	1.55	0.601	1.48	0.008	4.08	0.108	-1.35	0.307	1.44
1424630_a_at	Brca1	breast cancer 1	-2.24	0.193	5.19	0.083	1.48	0.437	3.81	0.185	2.06
1448201_at	Sfrp2	secreted frizzled-related protein 2	1.02	0.884	-1.22	0.304	5.29	0.315	1.09	0.876	1.54
1432516_at	4930447F04Rik	RIKEN cDNA 4930447F04 gene	2.01	0.462	4.1	0.139	1.02	0.794	-2.05	0.165	1.27
1452483_a_at	Cd44	CD44 antigen	2.32	0.293	2.76	0.089	2.06	0.283	-1.02	0.96	1.53
1451538_at	Sox9	SRY-box containing gene 9	3.35	0.027	2.3	0.078	1.5	0.516	-1.16	0.784	1.5
1450020_at	Cx3cr1	chemokine (C-X3-C) receptor 1	1.71	0.259	3.99	0.105	1.46	0.1	-1.26	0.245	1.48
1430612_at	1810033B17Rik	RIKEN cDNA 1810033B17 gene	1.39	0.499	2.64	0.099	3.17	0.159	-1.47	0.325	1.43
1443807_x_at	Ccnf	cyclin F	1.63	0.508	-1.08	0.73	4.65	0.004	4.7	0.248	2.47
1448759_at	Il2rb	interleukin 2 receptor, beta chain	2.61	0.232	2.57	0.133	2.02	0.104	-1.12	0.767	1.52
1420287_at	---	Transcribed locus	3.08	0.046	2.72	0.078	1.41	0.55	-1.21	0.727	1.5
1443298_at	Fbxw13	F-box and WD-40 domain protein 13	1.09	0.735	1.39	0.213	4.74	0.293	-1.73	0.52	1.37
1427167_at	AI448196	expressed sequence AI448196	1.37	0.59	4.74	0.145	1.13	0.502	-1.34	0.387	1.47
1456895_at	Cd209b	CD209b antigen	1.12	0.482	4.23	0	1.92	0.214	-3.9	0.001	0.84
1431843_a_at	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilo	1.8	0.23	2.18	0.017	3.3	0.245	-1.47	0.286	1.45
1419149_at	Serpine1	serine (or cysteine) peptidase inhibitor, clade E, member 1	2.89	0.227	3.2	0.289	1.2	0.595	-1.38	0.676	1.48
1417909_at	Serpinc1	serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	5.28	0.41	-1.12	0.504	1.14	0.424	1.68	0.284	1.74
1429492_x_at	Ptdss2	phosphatidylserine synthase 2	4.78	0.082	1.69	0.309	-1.18	0.791	4.13	0.217	2.36
1449577_x_at	Tpm2	tropomyosin 2, beta	1.18	0.231	1.28	0.765	4.86	0.266	-1.45	0.137	1.47
1457869_at	---	---	-1.02	0.863	2.33	0.08	4.03	0.185	1.85	0.021	1.8
1436312_at	Zfpn1a1	zinc finger protein, subfamily 1A, 1 (Ikaros)	2.89	0.062	1.93	0.009	2.52	0.065	-1.29	0.019	1.51
1422604_at	Uox	urate oxidase	4.97	0.432	-1.06	0.778	1.43	0.271	1.44	0.485	1.7
1417023_a_at	Fabp4	fatty acid binding protein 4, adipocyte	-1.37	0.203	3.19	0.157	3.42	0.366	3.71	0.063	2.24
1426505_at	Evi2b	ecotropic viral integration site 2b	2.8	0.055	2.7	0.008	1.87	0.054	-1.47	0.299	1.47
1418612_at	Slfn1	schlafen 1	2.27	0.31	2.17	0.313	2.92	0.118	-1.68	0.057	1.42
1429381_x_at	Igh-VJ558 /// LOC2	immunoglobulin heavy chain (J558 family) /// similar to immunoglobulin heavy cha	5.15	0.015	1.07	0.728	1.15	0.752	-2.26	0.063	1.28
1450240_a_at	Sytl1	synaptotagmin-like 1	1.71	0.442	4.11	0.016	1.57	0.453	-1.58	0.624	1.45
1440531_at	Rbm11	RNA binding motif protein 11	5.78	0.259	1.02	0.973	-1.65	0.069	2.05	0.253	1.8
1447756_x_at	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisi	1.21	0.802	4.77	0.062	1.43	0.477	-1.29	0.726	1.53
1449829_at	Itgb2l	integrin beta 2-like	-1.22	0.577	1.63	0.417	4.98	0.265	2.42	0.451	1.95
1417074_at	Ceacam10	CEA-related cell adhesion molecule 10	-3.57	0.166	1.13	0.766	6.05	0.361	1.58	0.484	1.3
1460407_at	Spib	Spi-B transcription factor (Spi-1/PU.1 related)	1.61	0.297	1.39	0.35	4.49	0.28	-2.01	0.138	1.37
1449134_s_at	Spic	Spi-C transcription factor (Spi-1/PU.1 related)	3.34	0.001	2.06	0.141	2.12	0.162	-1	1	1.63
1416322_at	Prelp	proline arginine-rich end leucine-rich repeat	5.02	0.065	1.05	0.906	1.47	0.417	-1.23	0.756	1.58
1450530_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	2.14	0.506	3.02	0.258	2.38	0.218	-1.32	0.5	1.56
1443686_at	H2-DMb1	Histocompatibility 2, class II, locus Mb1	3.22	0.094	1.33	0.637	3.01	0.268	-1.82	0.34	1.43
1449499_at	Hoxa7	homeo box A7	1.05	0.483	1.01	0.961	5.53	0.104	-1.44	0.132	1.54

1425871_a_at	LOC384413	Similar to immunoglobulin light chain variable region	2.3	0.214	1.76	0.413	3.56	0.117	-1.08	0.899	1.63
1417548_at	Sart3	squamous cell carcinoma antigen recognized by T-cells 3	3.26	0.295	1.91	0.417	2.45	0.43	-1.65	0.641	1.49
1425609_at	Ncf1	neutrophil cytosolic factor 1	2.35	0.513	1.99	0.116	3.28	0.272	-1.69	0.471	1.48
1422981_at	Dgcr8	DiGeorge syndrome critical region gene 8	4.62	0.074	1.06	0.931	1.95	0.323	-1.09	0.871	1.64
1435648_at	B430119L13Rik	RIKEN cDNA B430119L13 gene	1.72	0.155	-1.97	0.14	5.41	0.342	1.13	0.63	1.57
1448303_at	Gpnmb	glycoprotein (transmembrane) nmb	-1.79	0.427	3.79	0.172	3.3	0.089	1.34	0.473	1.66
1428790_at	Nfam1	Nfat activating molecule with ITAM motif 1	-3.71	0.023	4.34	0.06	3.05	0.026	1.26	0.35	1.24
1425574_at	Epha3	Eph receptor A3	2.81	0.456	3.86	0.122	1.01	0.987	-1.56	0.557	1.53
1419318_at	Saa4	serum amyloid A 4	5.48	0.47	1.39	0.296	-1.23	0.747	1.93	0.246	1.89
1418465_at	Ncf4	neutrophil cytosolic factor 4	1.51	0.545	2.48	0.011	3.7	0.109	-1.56	0.11	1.53
1422214_at	Npffr2	neuropeptide FF receptor 2	1.25	0.442	3.5	0.002	2.94	0.029	-2.42	0.456	1.32
1425367_at	Itgal /// LOC671163	integrin alpha L /// similar to Integrin alpha-L precursor (Leukocyte adhesion glycc	1.89	0.288	2.74	0.162	3.1	0.105	-1.06	0.891	1.67
1460449_at	Anks1b /// LOC544	ankyrin repeat and sterile alpha motif domain containing 1B /// similar to AIDA-1b	-1.32	0.509	1.96	0.296	5.01	0.102	2.45	0.215	2.03
1455497_at	Leng9	leukocyte receptor cluster (LRC) member 9	5.04	0.253	1.26	0.781	1.44	0.264	-2.15	0.202	1.4
1417640_at	Cd79b	CD79B antigen	3.36	0.373	1.43	0.375	2.94	0.322	-2.39	0.087	1.34
1452543_a_at	Scgb1a1	secretoglobin, family 1A, member 1 (uteroglobin)	3.31	0.138	3.66	0.122	-1.29	0.001	3.01	0.269	2.17
1451843_a_at	Ggta1	glycoprotein galactosyltransferase alpha 1, 3	3.36	0.039	2.01	0.266	2.38	0.248	-1.21	0.778	1.63
1451633_a_at	Gngt1	guanine nucleotide binding protein (G protein), gamma transducing activity polype	4.07	0.039	1.7	0.346	1.99	0.376	-1.67	0.246	1.52
1460568_at	Trim46	tripartite motif protein 46	4.5	0.115	-1.13	0.618	2.38	0.157	1.06	0.819	1.7
1422991_at	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	1.27	0.217	1.19	0.769	5.3	0.017	-1.16	0.776	1.65
1423478_at	Prkcb1	protein kinase C, beta 1	3.77	0.337	1.99	0.028	2	0.45	-1.95	0.089	1.45
1419481_at	Sell	selectin, lymphocyte	1.4	0.678	3.71	0.032	2.66	0.116	-2.85	0.032	1.23
1460437_at	Pscd4	pleckstrin homology, Sec7 and coiled/coil domains 4	3.09	0.065	2.85	0.004	1.84	0.02	-1.35	0.37	1.61
1422808_s_at	Dock2	dedicator of cyto-kinesis 2	3.33	0.085	2.12	0.011	2.33	0.116	-1.53	0.331	1.56
1417017_at	Cyp17a1	cytochrome P450, family 17, subfamily a, polypeptide 1	5.49	0.342	1.47	0.157	-1.22	0.365	2.7	0.349	2.11
1419319_at	Saa4	serum amyloid A 4	5.68	0.374	1.66	0.334	-2.24	0.102	1.87	0.185	1.74
1437121_at	Dennd1c	DENN/MADD domain containing 1C	2.81	0.014	2.86	0.013	2.21	0.108	-1.74	0.29	1.53
1451537_at	Chi3l1	chitinase 3-like 1	1.09	0.924	5.98	0.155	-1.24	0.055	1.76	0.546	1.9
1418830_at	Cd79a	CD79A antigen (immunoglobulin-associated alpha)	2.52	0.325	2.15	0.251	3.25	0.327	-1.95	0.176	1.49
1422873_at	Prg2	proteoglycan 2, bone marrow	-1.43	0.705	3.92	0.043	3.3	0.001	4.9	0.067	2.67
1420804_s_at	Clec4d	C-type lectin domain family 4, member d	1.84	0.494	3.48	0.007	2.62	0.244	-1.07	0.919	1.72
1431294_at	Speer8-ps1 /// Spe	spermatogenesis associated glutamate (E)-rich protein 8, pseudogene 1 /// sperm	6.23	0.092	-1.66	0.123	1.12	0.754	1.4	0.337	1.77
1449184_at	Pglyrp1	peptidoglycan recognition protein 1	-1.97	0.26	4.31	0.232	3.18	0.273	1.39	0.636	1.73
1423996_a_at	Il4ra	interleukin 4 receptor, alpha	3.77	0.085	1.82	0.069	2.42	0.173	-1.33	0.575	1.67
1418897_at	F2	coagulation factor II	5.72	0.413	-1.11	0.516	1.4	0.242	2.02	0.066	2.01
1451263_a_at	Fabp4	fatty acid binding protein 4, adipocyte	-1.65	0.008	4.35	0.14	3.08	0.329	3.41	0.06	2.3
1419178_at	Cd3g	CD3 antigen, gamma polypeptide	5.34	0.045	1.03	0.942	1.67	0.01	-1.77	0.289	1.57
1418261_at	Syk	spleen tyrosine kinase	2.71	0.312	1.54	0.023	3.8	0.163	-1.35	0.417	1.67
1428787_at	Nckap1l	NCK associated protein 1 like	3.3	0.157	2.21	0.01	2.54	0.072	-1.54	0.134	1.63
1419769_at	Cd22	CD22 antigen	2.87	0.304	2.02	0.253	3.18	0.059	-1.7	0.225	1.59
1448409_at	Lrmp	lymphoid-restricted membrane protein	3.35	0.241	1.48	0.087	3.27	0.241	-1.53	0.159	1.64
1420818_at	Sla	src-like adaptor	2.55	0.457	2.73	0.038	2.86	0.139	-1.17	0.568	1.74
1417973_at	Itih1	inter-alpha trypsin inhibitor, heavy chain 1	6.26	0.227	1.16	0.396	-1.41	0.235	1.29	0.451	1.82
1432856_at	---	---	3.17	0.403	3.76	0.015	1.21	0.667	-1.26	0.336	1.72
1421463_at	Siglece	sialic acid binding Ig-like lectin E	-1.02	0.962	1.91	0.212	5.25	0.244	1.38	0.109	1.88
1425666_at	LOC624168	similar to zinc finger protein of the cerebellum 5	3.73	0.192	2.37	0.208	2.07	0.02	-2.05	0.015	1.53
1425479_at	Smyd5	SET and MYND domain containing 5	2.49	0.127	3.02	0.021	2.7	0.033	-1.29	0.197	1.73
1433964_s_at	BC032204	cDNA sequence BC032204	1.45	0.365	2.95	0.056	3.83	0.062	-1.13	0.513	1.78
1422775_at	Blk	B lymphoid kinase	1.12	0.866	1.44	0.307	5.68	0.222	-1.75	0.162	1.62
1455098_a_at	Vtn	vitronectin	6.75	0.466	1.01	0.947	-2.1	0.137	2.12	0.288	1.95
1452393_at	AI597013	expressed sequence AI597013	3.51	0.13	2.32	0.125	2.42	0.039	-1.58	0.194	1.67
1422003_at	Blr1	Burkitt lymphoma receptor 1	2.01	0.286	1.25	0.043	4.99	0.252	-2.92	0.046	1.33
1425444_a_at	Tgfbr2	transforming growth factor, beta receptor II	4.49	0.007	1.17	0.481	2.61	0.356	-2.34	0.461	1.48

1452536_s_at	Igk-V1	immunoglobulin kappa chain variable 1 (V1)	1.73	0.34	1.83	0.197	4.74	0.134	-1.19	0.688	1.78
1438742_at	Zfp629	zinc finger protein 629	4.57	0.036	2.07	0.168	1.7	0.415	-1.1	0.926	1.81
1433963_a_at	BC032204	cDNA sequence BC032204	2.54	0.169	2.7	0.008	3.11	0.053	-1.18	0.059	1.79
1455965_at	---	---	2.91	0.087	4.55	0.062	-1.11	0.715	1.38	0.458	1.93
1457668_x_at	Ebna1bp2	EBNA1 binding protein 2	3.97	0.429	1.46	0.556	2.94	0.108	-1.02	0.978	1.84
1436074_at	AY078069	cDNA sequence AY078069	1.29	0.413	1.96	0.094	5.2	0.257	-1.67	0.21	1.7
1416025_at	Fgg	fibrinogen, gamma polypeptide	4.78	0.411	-1.22	0.271	2.85	0.006	2.83	0.32	2.31
1456936_at	Cabp4	calcium binding protein 4	2.69	0.091	3.41	0.095	2.38	0.432	-1.14	0.632	1.83
1451008_at	St8sia3	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	4.15	0.076	2.67	0.004	1.68	0.32	-1.08	0.911	1.85
1451767_at	Ncf1	neutrophil cytosolic factor 1	1.44	0.653	3.1	0.107	4	0.192	-1.57	0.338	1.74
1424076_at	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	1.23	0.384	6.48	0.011	-1.21	0.455	1.21	0.079	1.93
1417620_at	Rac2	RAS-related C3 botulinum substrate 2	1.84	0.244	2.16	0.02	4.54	0.078	-1.35	0.315	1.8
1455540_at	Cps1	carbamoyl-phosphate synthetase 1	6.38	0.423	-1.25	0.372	1.4	0.33	1.96	0.079	2.12
1451332_at	Zfp521	zinc finger protein 521	1.06	0.731	6.56	0.04	-1	0.991	1.17	0.245	1.95
1441887_x_at	LOC622976	hypothetical protein LOC622976	5.5	0.003	1.19	0.592	1.93	0.117	-1.87	0.154	1.69
1458299_s_at	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilo	2.63	0.196	2.39	0.083	3.61	0.261	-1.63	0.284	1.75
1435355_at	Neb	nebulin	1.93	0.412	1.49	0.146	5.24	0.384	-1.85	0.23	1.7
1423182_at	Tnfrsf13b	tumor necrosis factor receptor superfamily, member 13b	3.1	0.236	1.58	0.38	3.99	0.224	-1.97	0.143	1.67
1422755_at	Btk	Bruton agammaglobulinemia tyrosine kinase	3.49	0.332	3.52	0.004	1.75	0.133	-1.35	0.02	1.85
1424973_at	Cyp3a25 /// LOC62	cytochrome P450, family 3, subfamily a, polypeptide 25 /// similar to cytochrome P	6.69	0.453	-1.06	0.597	1.17	0.384	4.24	0.234	2.76
1454881_s_at	Upk3b	uroplakin 3B	-1.21	0.551	1.97	0.325	6.06	0.41	5.91	0	3.18
1417995_at	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	1.57	0.427	1.99	0.16	5.36	0.146	-1.13	0.845	1.95
1442023_at	A530030E21Rik	RIKEN cDNA A530030E21 gene	2.71	0.275	2.57	0.116	3.64	0.274	-1.29	0.573	1.91
1416464_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	-1.2	0.381	3.71	0.393	4.43	0.332	3.48	0.13	2.61
1425951_a_at	Clec4n	C-type lectin domain family 4, member n	2.19	0.417	5.73	0.001	1.08	0.775	-1.02	0.943	2
1417614_at	Ckm	creatine kinase, muscle	-1.07	0.944	3.78	0.002	4.31	0.208	1.53	0.628	2.14
1460212_at	Gnat1	guanine nucleotide binding protein, alpha transducing 1	3.29	0.025	4.37	0.04	1.36	0.343	-2.4	0.321	1.65
1436503_at	BC048546	cDNA sequence BC048546	3.98	0.442	3.33	0.032	1.72	0.008	-1.79	0.48	1.81
1452793_at	Dzip1	DAZ interacting protein 1	4.62	0.048	3.64	0.021	-1.23	0.568	1.24	0.677	2.07
1447918_x_at	LOC207685 /// LOC	hypothetical protein LOC207685 /// similar to Ig lambda-3 chain C region - mouse	2.56	0.05	1.35	0.521	5.16	0.319	-2.24	0.124	1.71
1416930_at	Ly6d	lymphocyte antigen 6 complex, locus D	1.65	0.272	3.2	0.253	4.24	0.342	-2.58	0.065	1.63
1454608_x_at	Ttr	transthyretin	1.17	0.81	-1.17	0.475	7.08	0.119	5.61	0.347	3.17
1450639_at	Slc28a2 /// LOC381	solute carrier family 28 (sodium-coupled nucleoside transporter), member 2 /// sin	1.22	0.821	4.97	0.012	2.95	0.138	-2.39	0.053	1.69
1436615_a_at	Otc	ornithine transcarbamylase	6.84	0.274	-1.02	0.892	1.37	0.389	1.77	0.125	2.24
1428396_at	Smurf1 /// LOC640	SMAD specific E3 ubiquitin protein ligase 1 /// similar to Smad ubiquitination regu	2.13	0.32	2.52	0.045	4.58	0.117	-2.7	0.134	1.63
1422978_at	Cybb	cytochrome b-245, beta polypeptide	2.38	0.051	2.08	0.027	4.85	0.044	-1.05	0.878	2.07
1421408_at	Igsf6	immunoglobulin superfamily, member 6	4.92	0.165	1.87	0.025	2.55	0.148	-1.17	0.564	2.04
1418821_at	Cyp2a12	cytochrome P450, family 2, subfamily a, polypeptide 12	7.25	0.392	-1.27	0.194	1.3	0.655	2.53	0.307	2.45
1447651_x_at	Mrpl30 /// LOC6215	mitochondrial ribosomal protein L30 /// similar to mitochondrial ribosomal protein l	1.69	0.27	6.1	0.137	1.6	0.333	-1.07	0.931	2.08
1424737_at	Thrsp	thyroid hormone responsive SPOT14 homolog (Rattus)	-1.56	0.436	1.07	0.907	7.73	0.348	2.05	0.166	2.32
1419005_at	Crybb3	crystallin, beta B3	2.59	0.024	5.96	0.092	-1.12	0.603	1.11	0.851	2.14
1417751_at	Stk10	serine/threonine kinase 10	4.48	0.021	3.41	0.024	1.56	0.063	-1.69	0.288	1.94
1450009_at	Ltf	lactotransferrin	-1.87	0.317	3.99	0.178	4.93	0.232	3.03	0.422	2.52
1416875_at	Parvg	parvin, gamma	1.27	0.529	6	0.001	2.28	0.074	-1.17	0.601	2.09
1422932_a_at	Vav1	vav 1 oncogene	3.82	0.079	2.91	0.009	2.84	0.129	-1.72	0.054	1.96
1420331_at	Clec4e	C-type lectin domain family 4, member e	4	0.259	-1.13	0.787	4.72	0.167	2.15	0.243	2.44
1442339_at	Stfa2l1	stefin A2 like 1	-1.2	0.428	3.17	0.172	5.64	0.158	1.79	0.527	2.35
1422992_s_at	Pik3cd	phosphatidylinositol 3-kinase catalytic delta polypeptide	1.58	0.607	2.27	0.153	5.8	0.06	-1.7	0.418	1.99
1425170_a_at	Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)	6.69	0.011	1.06	0.789	1.94	0.356	-2.64	0.162	1.76
1418262_at	Syk	spleen tyrosine kinase	2.89	0.294	2.21	0.048	4.61	0.184	-1.33	0.421	2.09
1416957_at	Pou2af1	POU domain, class 2, associating factor 1	2.6	0.324	2.1	0.28	5.07	0.151	-1.44	0.327	2.08
1424923_at	Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G	4.87	0.275	1.82	0.058	3.11	0.1	-1.18	0.566	2.16
1455913_x_at	Ttr	transthyretin	1.24	0.737	-1.14	0.516	7.7	0.079	4.21	0.366	3

1455899_x_at	Socs3	suppressor of cytokine signaling 3	3.66	0.2	4.69	0.129	1.47	0.257	-1.08	0.715	2.19
1422044_at	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	2.67	0.48	1.03	0.967	6.17	0.343	-4.16	0.211	1.43
1443984_at	Lin9	lin-9 homolog (C. elegans)	2.29	0.308	6.71	0.096	-1.14	0.485	2.04	0.034	2.48
1418842_at	Hcls1	hematopoietic cell specific Lyn substrate 1	5.01	0.001	2.14	0.049	2.75	0.024	-1.93	0.129	2
1426154_s_at	Mup1 /// Mup3	major urinary protein 1 /// major urinary protein 3	4.84	0.488	-1.28	0.33	4.45	0.096	1.24	0.844	2.31
1427870_x_at	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	1.99	0.174	1.44	0.434	6.69	0.192	-1.11	0.894	2.25
1455068_at	Psd4	pleckstrin and Sec7 domain containing 4	1.62	0.265	3.35	0.053	5.2	0.01	-1.87	0.268	2.08
1460423_x_at	Igh-V7183 /// Igk-V1	immunoglobulin heavy chain (V7183 family) /// immunoglobulin kappa chain varia	5.35	0.004	2.26	0.06	2.59	0.065	-1.12	0.851	2.27
1420652_at	Ate1	arginine-tRNA-protein transferase 1	7.43	0.172	-1.55	0.614	2.4	0.405	1.46	0.466	2.44
1448859_at	Cxcl13	chemokine (C-X-C motif) ligand 13	2.12	0.315	1.72	0.057	6.69	0.23	-2.31	0.101	2.06
1416677_at	Apoh	apolipoprotein H	8.05	0.399	-1.23	0.343	1.71	0.098	2.1	0.414	2.66
1448680_at	Serpina1c	serine (or cysteine) peptidase inhibitor, clade A, member 1c	8.19	0.379	-1.26	0.418	1.59	0.3	2.12	0.433	2.66
1419334_at	Ctla4	cytotoxic T-lymphocyte-associated protein 4	2.87	0.491	-1.33	0.517	7.01	0.325	1.72	0.19	2.57
1417651_at	Cyp2c29	cytochrome P450, family 2, subfamily c, polypeptide 29	7.45	0.417	-1.11	0.669	2.3	0.085	2.69	0.01	2.83
1443930_at	BC052046	cDNA sequence BC052046	3.24	0.074	-1.17	0.871	6.62	0.3	1.41	0.647	2.53
1456635_at	---	---	1.54	0.416	3.26	0.029	5.94	0.03	-1.21	0.385	2.38
1427860_at	Igkv6-23 /// Igk-V19	immunoglobulin kappa chain variable 6-23 /// immunoglobulin kappa chain variab	8.04	0.053	1.39	0.195	1.31	0.434	-2.39	0.077	2.09
1448371_at	Mylpf	myosin light chain, phosphorylatable, fast skeletal muscle	1.53	0.333	-1.27	0.134	8.52	0.125	1.82	0.305	2.65
1435196_at	Ntrk2	neurotrophic tyrosine kinase, receptor, type 2	-1.54	0.414	6.94	0.009	3.34	0.001	1.26	0.537	2.5
1430986_at	Farslb	phenylalanine-tRNA synthetase-like, beta subunit	5.41	0.002	1.09	0.831	4.5	0.142	-1.58	0.101	2.35
1416809_at	Cyp3a11	cytochrome P450, family 3, subfamily a, polypeptide 11	9.43	0.41	-1.65	0.039	1.04	0.757	1.22	0.748	2.51
1436453_at	BB144871	expressed sequence BB144871	-2.02	0.293	2.43	0.059	8.21	0.382	4.02	0.269	3.16
1419219_at	Cyp4f18	cytochrome P450, family 4, subfamily f, polypeptide 18	2.63	0.429	5.69	0.004	2.82	0.088	-1.43	0.209	2.43
1419135_at	Ltb	lymphotoxin B	4.38	0.23	2.14	0.269	4.65	0.109	-2.52	0.132	2.16
1449321_x_at	Serpina1a /// Serpir	serine (or cysteine) peptidase inhibitor, clade A, member 1a /// serine (or cysteine	9.49	0.185	1.07	0.366	-1.19	0.61	1.1	0.891	2.62
1450570_a_at	Cd19	CD19 antigen	4.42	0.373	3.06	0.174	4.01	0.321	-2.08	0.177	2.35
1419206_at	Cd37	CD37 antigen	2.85	0.367	1.29	0.188	7.46	0.206	-1.86	0.271	2.44
1425247_a_at	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	2.66	0.091	1.2	0.731	7.82	0.155	-1.2	0.832	2.62
1420465_s_at	Mup1 /// Mup2	major urinary protein 1 /// major urinary protein 2	6.22	0.473	-1.13	0.585	4.61	0.137	2.12	0.566	2.95
1417835_at	Mug1 /// LOC66934	murinoglobulin 1 /// similar to murinoglobulin 1	9.85	0.433	-1.44	0.113	1.18	0.792	1.82	0.316	2.85
1449965_at	Mcpt8	mast cell protease 8	-1.96	0.045	2.75	0.165	8.48	0.343	2.27	0.367	2.89
1416473_a_at	Nope	neighbor of Punc E11	1.06	0.943	9.25	0.263	1.48	0.34	-1.41	0.215	2.59
1420553_x_at	Serpina1a	serine (or cysteine) peptidase inhibitor, clade A, member 1a	9.19	0.252	-1.15	0.427	1.75	0.384	2.52	0.414	3.08
1415960_at	Mpo	myeloperoxidase	-1.76	0.428	5.65	0.118	5.84	0.207	2.79	0.437	3.13
1424542_at	S100a4	S100 calcium binding protein A4	1.45	0.258	9.48	0.067	1.17	0.536	-3.15	0.016	2.24
1430770_at	3110080E11Rik	RIKEN cDNA 3110080E11 gene	6.29	0.007	3.6	0.069	2.32	0.271	-1.95	0.224	2.57
1423226_at	Ms4a1	membrane-spanning 4-domains, subfamily A, member 1	6.66	0.452	2.03	0.399	3.84	0.229	-2.05	0.133	2.62
1447108_at	Rad51l1	RAD51-like 1 (S. cerevisiae)	1	1	10.72	0.135	-1.19	0.799	1.72	0.316	3.06
1452963_at	9530077C05Rik	RIKEN cDNA 9530077C05 gene	-1.46	0.381	10.86	0.133	1.1	0.679	3.37	0.277	3.47
1428947_at	2010001M09Rik	RIKEN cDNA 2010001M09 gene	3.01	0.177	1.12	0.78	8.8	0.162	-1.42	0.255	2.88
1434502_x_at	Slc4a1	solute carrier family 4 (anion exchanger), member 1	-1.15	0.045	6.71	0.303	5.43	0.323	2.21	0.183	3.3
1453391_at	Speer7-ps1	spermatogenesis associated glutamate (E)-rich protein 7, pseudogene 1	10.71	0.052	1.49	0.332	-1.05	0.34	1.27	0.691	3.1
1440792_x_at	Oprs1	opioid receptor, sigma 1	11.65	0.167	-2.14	0.366	1.06	0.833	1.25	0.718	2.96
1451858_at	Mrgpra2 /// LOC668	MAS-related GPR, member A2 /// similar to MAS-related GPR, member A2	-2.7	0.255	4.52	0.073	8.78	0.248	3.58	0.325	3.54
1458297_s_at	Marco	macrophage receptor with collagenous structure	1.95	0.274	3.04	0.054	8.78	0.003	-5.99	0.06	1.95
1419560_at	Lipc	lipase, hepatic	3.03	0.139	-1.65	0.026	10.17	0.22	2.67	0.124	3.55
1417085_at	Akr1c6	aldo-keto reductase family 1, member C6	11.08	0.4	-1.48	0.076	2.16	0.31	3.3	0.312	3.76
1427660_x_at	Igk-C /// Igk-V28 ///	immunoglobulin kappa chain, constant region /// immunoglobulin kappa chain var	7.73	0.001	4.67	0.003	1.64	0.016	-1.13	0.157	3.23
1452417_x_at	Igk-C /// Igk-V28 ///	immunoglobulin kappa chain, constant region /// immunoglobulin kappa chain var	7.37	0.028	5.37	0.003	1.42	0.108	-1.1	0.258	3.26
1428719_at	2010309G21Rik ///	RIKEN cDNA 2010309G21 gene /// hypothetical protein LOC207685	6.58	0.329	3.28	0.076	4.61	0.252	-1.97	0.077	3.13
1419681_a_at	Prok2	prokineticin 2	-1.09	0.869	1.77	0.097	11.84	0.245	5.19	0.249	4.43
1450912_at	Ms4a1	membrane-spanning 4-domains, subfamily A, member 1	6.25	0.357	3.91	0.276	4.61	0.282	-2.42	0.083	3.09
1457644_s_at	Cxcl1	chemokine (C-X-C motif) ligand 1	-1.28	0.336	12.98	0.083	1.05	0.532	1.22	0.426	3.49

1428079_at	Fgb	fibrinogen, B beta polypeptide	13.32	0.418	-1.22	0.336	1.06	0.583	2.46	0.396	3.9
1424931_s_at	Igl-V1	immunoglobulin lambda chain, variable 1	6.06	0.04	2.21	0.124	7.46	0.193	-1.14	0.804	3.65
1454713_s_at	Hdc	histidine decarboxylase	13.36	0.066	1.27	0.612	1.15	0.691	-1.2	0.763	3.65
1421946_at	Crp	C-reactive protein, pentraxin-related	14.13	0.439	1.02	0.868	-1.19	0.736	1.76	0.251	3.93
1419100_at	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	12.36	0.419	2.52	0.149	1.19	0.51	-1.06	0.573	3.75
1422928_at	Ela2	elastase 2, neutrophil	-2	0.3	9.28	0.082	6.85	0.263	3.09	0.395	4.31
1416649_at	Ambp	alpha 1 microglobulin/bikunin	13.72	0.432	-1.06	0.737	2.13	0.361	2.11	0.462	4.23
1427756_x_at	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	3.76	0.168	1.83	0.436	11.33	0.183	-1.31	0.777	3.9
1419209_at	Cxcl1	chemokine (C-X-C motif) ligand 1	1.03	0.902	14.59	0.066	1.33	0.015	-1.18	0.515	3.94
1418531_at	Oosp1	oocyte secreted protein 1	1.22	0.639	-1.03	0.865	14.81	0.253	2.59	0.05	4.4
1425260_at	Alb1	albumin 1	12.05	0.402	-1.17	0.481	4.53	0.133	4.51	0.362	4.98
1416913_at	Es1	esterase 1	13.89	0.405	-1.24	0.365	2.8	0.253	1.53	0.671	4.24
1424305_at	Igj	immunoglobulin joining chain	6.27	0.001	2.51	0.001	8.89	0.01	-1.25	0.369	4.11
1418653_at	Cyp2c37 /// Cyp2c5	cytochrome P450, family 2. subfamily c, polypeptide 37 /// cytochrome P450, fam	15.84	0.399	-1.31	0.329	1.22	0.526	2.41	0.444	4.54
1430523_s_at	Igl-V1	immunoglobulin lambda chain, variable 1	7.19	0.022	4.29	0.014	6.6	0.133	-1.22	0.684	4.21
1428720_s_at	Igl-V1 /// 2010309G	immunoglobulin lambda chain, variable 1 /// RIKEN cDNA 2010309G21 gene /// h	13.59	0.278	1.86	0.09	4.27	0.26	-1.96	0.114	4.44
1419549_at	Arg1	arginase 1, liver	17.27	0.421	-1.12	0.602	1.86	0.079	3.26	0.347	5.32
1459989_at	---	Transcribed locus	18.85	0.001	-1.07	0.88	1.05	0.92	1.33	0.648	5.04
1425324_x_at	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	3.84	0.042	2.2	0.4	15.51	0.17	-1.29	0.802	5.06
1419093_at	Tdo2	tryptophan 2,3-dioxygenase	19.72	0.396	-1.29	0.225	1.18	0.723	3.31	0.047	5.73
1417851_at	Cxcl13	chemokine (C-X-C motif) ligand 13	8.2	0.223	2.07	0.098	11.42	0.226	-2.24	0.132	4.86
1427455_x_at	Igk-C /// Igk-V28 ///	immunoglobulin kappa chain, constant region /// immunoglobulin kappa chain var	13.26	0	5.73	0.003	4.13	0	-1.14	0.076	5.49
1438840_x_at	Apoa1	apolipoprotein A-I	19	0.416	-1.3	0.3	3.84	0.036	1.69	0.297	5.81
1425220_x_at	AF067061 /// LOC6	cDNA sequence AF067061 /// hypothetical protein LOC639910 /// similar to 2-cell	2.53	0.191	-2.55	0.163	21	0.347	1.92	0.145	5.73
1455201_x_at	Apoa1	apolipoprotein A-I	27.3	0.424	-1.33	0.277	3.16	0.136	1.02	0.99	7.54
1427329_a_at	Igh-6	immunoglobulin heavy chain 6 (heavy chain of IgM)	15.09	0.002	6.66	0.002	10.69	0.001	-1.12	0.29	7.83
1420438_at	Orm2	orosomucoid 2	25.26	0.421	6.59	0.112	1.04	0.92	-3.55	0.073	7.34
1417246_at	Pzp	pregnancy zone protein	31.47	0.407	-1.25	0.353	1.43	0.346	2.81	0.33	8.62
1449326_x_at	Saa2	serum amyloid A 2	17.66	0.398	14.87	0.061	1.55	0.22	-1.04	0.951	8.26
1416729_at	Plg	plasminogen	31.46	0.429	-1.17	0.475	3.57	0.04	1.68	0.555	8.89
1427868_x_at	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	2.39	0.056	2.32	0.171	33.86	0.317	-1.07	0.928	9.37
1418282_x_at	Serpina1b	serine (or cysteine) preptidase inhibitor, clade A, member 1b	31.62	0.367	-1.14	0.628	7.84	0.005	1.09	0.921	9.85
1427735_a_at	Acta1	actin, alpha 1, skeletal muscle	2.06	0.316	-2.49	0.248	39.05	0.18	1.68	0.429	10.07
1423147_at	Mat1a	methionine adenosyltransferase I, alpha	40.09	0.421	-1.07	0.66	1.18	0.461	1.53	0.499	10.43
1427520_a_at	Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	2.92	0.021	1.58	0.164	44.31	0.303	-1.1	0.882	11.93
1455093_a_at	Ahsg	alpha-2-HS-glycoprotein	50.32	0.368	-1.12	0.565	1.35	0.534	2.74	0.426	13.32
1419233_x_at	Apoa1	apolipoprotein A-I	59.82	0.421	-1.35	0.277	1.38	0.189	1.39	0.73	15.31
1451513_x_at	Serpina1a /// Serpir	serine (or cysteine) peptidase inhibitor, clade A, member 1a /// serine (or cysteine	54.75	0.355	-1.21	0.458	7.09	0.02	1.31	0.76	15.48
1419232_a_at	Apoa1	apolipoprotein A-I	81.82	0.402	-1.34	0.304	1.92	0.198	1.96	0.479	21.09
1450788_at	Saa1	serum amyloid A 1	210.11	0.412	6.52	0.046	1.85	0.191	-1.41	0.621	54.27
1427351_s_at	Igh-6	immunoglobulin heavy chain 6 (heavy chain of IgM)	370.86	0	11.91	0.004	7.56	0.001	-1.21	0.038	97.28
1416138_at	Anxa7	annexin A7	1.02	0.909	1.01	0.839	1.01	0.927	1.01	0.945	1.01
1436047_at	Gm672	gene model 672, (NCBI)	1.01	0.933	1.04	0.766	1	1	1.23	0.443	1.07
1452841_at	Pgm2l1	phosphoglucomutase 2-like 1	1.04	0.937	1	0.992	1.01	0.931	1.34	0.383	1.1
1450276_a_at	Scin	scinderin	1.04	0.736	1.01	0.949	1.01	0.944	1	0.995	1.02
1443500_at	Mllt10	Myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosop	1.01	0.953	1.02	0.964	1.03	0.892	1.14	0.461	1.05
1448476_at	Nap1l4	nucleosome assembly protein 1-like 4	1.05	0.569	1.01	0.88	1.02	0.828	1.14	0.507	1.05
1454961_at	Synj1	synaptojanin 1	1	0.998	1	0.955	1.08	0.327	1.31	0.299	1.1
1432710_at	4930505O19Rik	RIKEN cDNA 4930505O19 gene	1.01	0.979	1.01	0.99	1.07	0.873	1.52	0.337	1.15
1426753_at	Phf17	PHD finger protein 17	1.02	0.922	1.04	0.884	1.02	0.897	1.19	0.414	1.07
1453199_at	Acbd6	acyl-Coenzyme A binding domain containing 6	1.02	0.726	1.04	0.787	1.03	0.802	1.2	0.251	1.07
1444783_at	Abi2	Abl-interactor 2	1	0.993	1.05	0.842	1.03	0.874	1.52	0.397	1.15
1426669_at	C530044N13Rik	RIKEN cDNA C530044N13 gene	1.01	0.906	1.01	0.921	1.07	0.587	1.04	0.831	1.03

1423074_at	Lman2	lectin, mannose-binding 2	1.02	0.855	1.03	0.666	1.05	0.464	1.06	0.498	1.04
1441720_at	4921530L18Rik	RIKEN cDNA 4921530L18 gene	1.02	0.543	1.05	0.504	1.03	0.921	1.26	0.045	1.09
1450705_at	Rdbp	RD RNA-binding protein	1.02	0.642	1.01	0.945	1.08	0.429	1.03	0.575	1.03
1436635_at	Ube2z	ubiquitin-conjugating enzyme E2Z (putative)	1.04	0.621	1.02	0.911	1.05	0.722	1.01	0.946	1.03
1421557_x_at	Txn2	thioredoxin 2	1.02	0.927	1.03	0.748	1.06	0.776	1.13	0.007	1.06
1436869_at	Shh	sonic hedgehog	1.01	0.903	1.1	0.72	1.01	0.966	1.38	0.381	1.12
1449066_a_at	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	1	0.996	1.11	0.583	1.01	0.954	1.04	0.817	1.04
1447829_x_at	Taf9b	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor	1.08	0.927	1.01	0.992	1.03	0.953	1.02	0.977	1.04
1450677_at	Chek1	checkpoint kinase 1 homolog (S. pombe)	1.03	0.973	1.07	0.897	1.02	0.917	3.08	0.241	1.55
1441328_at	Picalm	Phosphatidylinositol binding clathrin assembly protein	1.04	0.664	1.08	0.737	1.01	0.979	1.53	0.213	1.16
1451197_s_at	Gatad2a	GATA zinc finger domain containing 2A	1.05	0.733	1.05	0.595	1.02	0.827	1.16	0.219	1.07
1421830_at	Ak3l1	adenylate kinase 3 alpha-like 1	1.03	0.952	1.03	0.92	1.07	0.76	1.39	0.556	1.13
1427781_at	Usmg2	upregulated during skeletal muscle growth 2	1.01	0.92	1.07	0.905	1.04	0.936	1.78	0.384	1.23
1460446_at	Wrb	tryptophan rich basic protein	1.04	0.354	1.06	0.579	1.03	0.666	1.15	0.197	1.07
1449114_at	Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	1.01	0.972	1.12	0.677	1	0.999	1.16	0.322	1.07
1432759_at	6330571C24Rik	RIKEN cDNA 6330571C24 gene	1.04	0.868	1.08	0.747	1.01	0.981	1.17	0.614	1.07
1434599_a_at	Tjp2	tight junction protein 2	1.02	0.921	1.02	0.812	1.08	0.608	1.04	0.859	1.04
1460395_at	Nudcd3	NudC domain containing 3	1.01	0.904	1.1	0.314	1.02	0.889	1.04	0.773	1.05
1416878_at	Mrpl51	mitochondrial ribosomal protein L51	1.07	0.001	1.03	0.828	1.04	0.761	1.17	0.395	1.08
1436735_at	Nsun3	NOL1/NOP2/Sun domain family 3	1.02	0.836	1.05	0.455	1.07	0.302	1.16	0.599	1.07
1452919_a_at	1700012G19Rik	RIKEN cDNA 1700012G19 gene	1.09	0.577	1.02	0.877	1.02	0.899	2.33	0.158	1.37
1421891_at	St3gal2	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	1.07	0.782	1.02	0.955	1.06	0.755	2.45	0.157	1.4
1436215_at	Ipmk	inositol polyphosphate multikinase	1.09	0.244	1.02	0.855	1.04	0.44	1.45	0.165	1.15
1435659_a_at	Tpi1	triosephosphate isomerase 1	1.02	0.857	1.05	0.542	1.08	0.609	1.56	0.19	1.18
1418292_at	Asna1	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	1.12	0.801	1.01	0.972	1.03	0.908	1.12	0.75	1.07
1422848_a_at	Pabpn1	poly(A) binding protein, nuclear 1	1.05	0.871	1.11	0.395	1	0.994	1.21	0.247	1.09
1456478_at	Pgm2l1	phosphoglucomutase 2-like 1	1.03	0.923	1.11	0.718	1.01	0.957	1.33	0.467	1.12
1418605_at	Nr2c1	nuclear receptor subfamily 2, group C, member 1	1.06	0.819	1.03	0.841	1.06	0.642	1	0.99	1.04
1424261_at	Zfp672	zinc finger protein 672	1.07	0.32	1.06	0.644	1.03	0.752	1.43	0.35	1.15
1426694_at	9030624J02Rik	RIKEN cDNA 9030624J02 gene	1.14	0.129	1.01	0.942	1.01	0.818	1.02	0.719	1.04
1436906_at	Rnf166	ring finger protein 166	1.01	0.82	1.03	0.824	1.12	0.549	1.06	0.776	1.05
1456113_at	Oatl1	ornithine aminotransferase-like 1	1.09	0.758	1.07	0.833	1	0.988	1.01	0.976	1.04
1417077_at	Bcap29	B-cell receptor-associated protein 29	1.02	0.725	1.03	0.734	1.1	0.354	1.1	0.558	1.07
1420879_a_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	1.03	0.824	1.07	0.48	1.06	0.755	1.02	0.695	1.05
1417914_at	Rap2b	RAP2B, member of RAS oncogene family	1.1	0.525	1.06	0.825	1	0.99	1.29	0.091	1.11
1433911_at	Smg6	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	1.01	0.983	1.04	0.814	1.12	0.148	1.22	0.303	1.1
1452115_a_at	Plk4	polo-like kinase 4 (Drosophila)	1.05	0.825	1.02	0.942	1.09	0.373	3.25	0.271	1.6
1420679_a_at	Aig1	androgen-induced 1	1.01	0.928	1.04	0.637	1.12	0.647	1.25	0.062	1.1
1441645_s_at	Ipo9	importin 9	1.03	0.714	1	1	1.14	0.409	1.2	0.349	1.09
1447227_at	Slc40a1	Solute carrier family 40 (iron-regulated transporter), member 1	1.01	0.905	1.13	0.334	1.03	0.945	1.06	0.775	1.06
1428684_at	1500001M20Rik	RIKEN cDNA 1500001M20 gene	1.02	0.865	1.12	0.325	1.03	0.829	1.31	0.423	1.12
1449046_a_at	Josd2	Josephin domain containing 2	1.06	0.835	1.09	0.415	1.02	0.931	2.75	0.154	1.48
1422414_a_at	Calm2	calmodulin 2	1.02	0.626	1.14	0.312	1.01	0.933	1.17	0.12	1.09
1449491_at	Card10	caspase recruitment domain family, member 10	1.02	0.862	1.01	0.958	1.15	0.177	1.19	0.163	1.09
1416868_at	Cdkn2c	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.05	0.718	1.11	0.031	1.02	0.882	2.93	0.151	1.53
1419745_at	Arhgap23	Rho GTPase activating protein 23	1	0.974	1.05	0.832	1.13	0.381	2.91	0.137	1.52
1450478_a_at	Ptpn12	protein tyrosine phosphatase, non-receptor type 12	1.04	0.883	1.07	0.286	1.07	0.551	1.15	0.388	1.08
1426898_at	Map3k7ip1	mitogen-activated protein kinase kinase kinase 7 interacting protein 1	1.06	0.501	1.04	0.887	1.08	0.398	1.13	0.552	1.08
1427718_a_at	Mdm2	transformed mouse 3T3 cell double minute 2	1.05	0.828	1.08	0.815	1.05	0.858	1.22	0.431	1.1
1456464_x_at	---	---	1.06	0.785	1.05	0.831	1.07	0.455	1.08	0.663	1.07
1422870_at	Hoxc4	homeo box C4	1.07	0.343	1.05	0.927	1.06	0.717	1.77	0.148	1.24
1438445_at	Lrrc8e	leucine rich repeat containing 8 family, member E	1.12	0.35	1.02	0.945	1.05	0.873	1.81	0.3	1.25
1423916_s_at	Mlf2	myeloid leukemia factor 2	1.09	0.752	1.01	0.965	1.09	0.306	1.21	0.303	1.1

1456251_x_at	Tspo	translocator protein	1.11	0.122	1.04	0.744	1.04	0.808	1.29	0.449	1.12
1426972_at	Sec24d	SEC24 related gene family, member D (S. cerevisiae)	1.07	0.141	1.02	0.867	1.1	0.093	1.1	0.569	1.07
1435439_at	Dgcr8	DiGeorge syndrome critical region gene 8	1.13	0.354	1.01	0.957	1.05	0.762	1.45	0.432	1.16
1424419_at	Lrrc14	leucine rich repeat containing 14	1.01	0.957	1.02	0.835	1.16	0.254	1.11	0.473	1.08
1450650_at	Myo10	myosin X	1.01	0.915	1.04	0.689	1.14	0.689	1.4	0.092	1.15
1445900_at	Kalrn	Kalirin, RhoGEF kinase	1.02	0.971	1.04	0.823	1.14	0.305	1.11	0.74	1.08
1428200_a_at	2210010A19Rik	RIKEN cDNA 2210010A19 gene	1.08	0.32	1.11	0.701	1.01	0.923	1.03	0.883	1.06
1452174_at	Srebf2	sterol regulatory element binding factor 2	1.04	0.871	1.02	0.914	1.14	0.323	1.06	0.359	1.07
1451012_a_at	Csda	cold shock domain protein A	1.06	0.437	1.02	0.939	1.12	0.303	2.52	0.173	1.43
1456097_a_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	1.01	0.443	1.05	0.831	1.13	0.358	1	0.98	1.05
1431077_at	Alpi	alkaline phosphatase, intestinal	1.01	0.913	1.03	0.91	1.17	0.659	1.07	0.866	1.07
1456709_at	Ophn1	oligophrenin 1	1.11	0.588	1.09	0.816	1.01	0.984	1.08	0.883	1.07
1416203_at	Aqp1	aquaporin 1	1.12	0.519	1.02	0.944	1.07	0.283	4.33	0.103	1.89
1435469_at	Qscn6l1	quiescin Q6-like 1	1.08	0.529	1.04	0.838	1.09	0.416	1.09	0.511	1.08
1416928_at	Rbm12	RNA binding motif protein 12	1.04	0.724	1.13	0.322	1.05	0.826	1.08	0.713	1.07
1460586_at	Megf8	multiple EGF-like-domains 8	1.05	0.814	1.01	0.919	1.16	0.536	1.01	0.881	1.06
1435020_at	Sdccag1	serologically defined colon cancer antigen 1	1.03	0.738	1.04	0.784	1.15	0.497	1.39	0.338	1.15
1435866_s_at	Hist3h2a	histone 3, H2a	1.04	0.828	1.12	0.465	1.06	0.377	1.11	0.424	1.08
1424038_a_at	2310044H10Rik	RIKEN cDNA 2310044H10 gene	1.03	0.836	1.08	0.561	1.11	0.173	1.14	0.464	1.09
1440133_x_at	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	1.1	0.674	1.06	0.85	1.06	0.856	2.62	0.254	1.46
1433908_a_at	Cttn	cortactin	1.02	0.906	1.14	0.116	1.07	0.546	1.23	0.63	1.11
1430276_at	1700003I16Rik	RIKEN cDNA 1700003I16 gene	1.15	0.84	1.06	0.928	1.02	0.978	2.29	0.372	1.38
1447816_x_at	Oxnad1	oxidoreductase NAD-binding domain containing 1	1.09	0.588	1.08	0.578	1.05	0.802	1.05	0.792	1.07
1451284_at	Yipf3	Yip1 domain family, member 3	1.14	0.351	1.05	0.653	1.03	0.825	1.05	0.766	1.07
1423332_at	Sdcbp	syndecan binding protein	1.04	0.731	1.19	0.179	1	0.992	1.24	0.257	1.12
1428108_x_at	Tmcc2	transmembrane and coiled-coil domains 2	1.12	0.13	1.02	0.906	1.08	0.682	4.83	0.105	2.01
1443563_at	---	---	1.02	0.741	1.18	0.622	1.02	0.843	1.46	0.2	1.17
1434882_at	Mtdh	Metadherin	1.05	0.659	1.07	0.745	1.11	0.562	1.27	0.124	1.13
1460333_at	Ddx59	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	1.14	0.238	1.02	0.854	1.06	0.646	1.21	0.388	1.11
1452207_at	Cited2 /// LOC6714	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1.04	0.847	1.09	0.298	1.1	0.294	1.22	0.105	1.11
1445380_at	A230072C01Rik	RIKEN cDNA A230072C01 gene	1.02	0.726	1.17	0.244	1.04	0.875	1.07	0.273	1.08
1449622_s_at	Atp6ap1	ATPase, H+ transporting, lysosomal accessory protein 1	1	0.996	1.2	0.087	1.03	0.651	1.05	0.788	1.07
1426930_at	Brunol4	bruno-like 4, RNA binding protein (Drosophila)	1.13	0.644	1.03	0.917	1.08	0.611	1.27	0.63	1.13
1425845_a_at	Shoc2	soc-2 (suppressor of clear) homolog (C. elegans)	1.2	0.444	1	0.996	1.04	0.94	1.03	0.923	1.07
1456013_x_at	Slc35a4	solute carrier family 35, member A4	1.14	0.448	1.02	0.888	1.08	0.603	1.17	0.412	1.1
1420715_a_at	Pparg	peroxisome proliferator activated receptor gamma	1.05	0.941	1.18	0.698	1.01	0.98	1.18	0.656	1.1
1420813_at	Hdac7a	histone deacetylase 7A	1.03	0.906	1	0.985	1.2	0.387	1.12	0.726	1.09
1437859_x_at	Eif5a	eukaryotic translation initiation factor 5A	1.06	0.854	1.05	0.821	1.13	0.635	1.37	0.28	1.15
1453687_at	Slc4a3	solute carrier family 4 (anion exchanger), member 3	1.04	0.935	1	0.995	1.2	0.748	1.84	0.138	1.27
1425188_s_at	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	1.09	0.726	1	0.986	1.14	0.466	1.35	0.144	1.15
1419321_at	F7	coagulation factor VII	1.05	0.93	1.11	0.373	1.08	0.498	1.09	0.717	1.08
1417916_a_at	Fxc1	fractured callus expressed transcript 1	1.02	0.884	1.15	0.361	1.07	0.725	1.01	0.951	1.06
1452447_at	0610007P08Rik	RIKEN cDNA 0610007P08 gene	1.03	0.838	1.19	0.551	1.02	0.902	1.09	0.637	1.08
1424984_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	1.13	0.511	1.06	0.816	1.06	0.722	1.27	0.137	1.13
1423629_at	Dnm2	dynamin 2	1.03	0.881	1.04	0.595	1.17	0.425	1.07	0.617	1.08
1418512_at	Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	1.1	0.406	1.1	0.4	1.05	0.913	2.03	0.012	1.32
1420529_at	Neud4	neuronal d4 domain family member	1.04	0.808	1.13	0.739	1.08	0.766	1.14	0.567	1.1
1435505_at	Dmwd	dystrophia myotonica-containing WD repeat motif	1.07	0.79	1.04	0.5	1.14	0.381	1.52	0.325	1.19
1446351_at	D430034N21	hypothetical protein D430034N21	1.14	0.775	1.01	0.993	1.11	0.529	1.04	0.852	1.07
1426974_at	4632413K17Rik	RIKEN cDNA 4632413K17 gene	1.07	0.725	1.12	0.031	1.07	0.258	1.05	0.814	1.08
1417322_at	Dohh	deoxyhypusine hydroxylase/monooxygenase	1.15	0.432	1.05	0.779	1.06	0.745	1.02	0.912	1.07
1432892_at	5730564L20Rik	RIKEN cDNA 5730564L20 gene	1.11	0.548	1.03	0.959	1.12	0.809	1.24	0.524	1.13
1426690_a_at	Srebf1	sterol regulatory element binding factor 1	1.17	0.702	1.03	0.883	1.06	0.57	1.02	0.784	1.07

1416050_a_at	Scarb1	scavenger receptor class B, member 1	1.18	0.472	1.01	0.96	1.07	0.561	1.61	0.006	1.22
1426458_at	Slmap	sarcolemma associated protein	1.09	0.726	1.1	0.789	1.07	0.855	1.21	0.625	1.12
1433638_s_at	Hoxd8	homeo box D8	1.01	0.819	1.22	0.563	1.02	0.967	1.09	0.754	1.09
1426386_at	Rpl7l1	ribosomal protein L7-like 1	1.07	0.79	1.07	0.693	1.12	0.656	1.13	0.769	1.1
1448549_a_at	Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransf	1.01	0.951	1.09	0.362	1.16	0.024	1.27	0.285	1.13
1439616_at	---	Transcribed locus	1.01	0.955	1.08	0.694	1.17	0.373	1.06	0.808	1.08
1444137_at	A430108G06Rik	RIKEN cDNA A430108G06 gene	1.02	0.982	1.08	0.905	1.16	0.641	1.3	0.681	1.14
1418010_a_at	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	1.03	0.809	1.1	0.188	1.13	0.312	1.64	0.119	1.23
1424840_at	Rbks	ribokinase	1.1	0.762	1.07	0.428	1.1	0.724	1.45	0.426	1.18
1417205_at	Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.02	0.796	1.15	0.343	1.1	0.717	1.35	0.168	1.15
1424638_at	Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	1.25	0.683	1.01	0.987	1.01	0.985	1.11	0.582	1.09
1449506_a_at	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange pro	1.08	0.591	1.04	0.62	1.15	0.516	1.03	0.806	1.07
1417639_at	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	1.02	0.961	1.09	0.882	1.16	0.694	5.22	0.18	2.12
1448219_a_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	1.12	0.487	1.09	0.613	1.06	0.811	1.02	0.932	1.07
1424805_a_at	1110039B18Rik	RIKEN cDNA 1110039B18 gene	1.17	0.544	1.08	0.652	1.02	0.865	1.14	0.561	1.1
1455481_at	Ids	iduronate 2-sulfatase	1.1	0.122	1.06	0.534	1.11	0.384	1.04	0.924	1.08
1416329_at	Cyfip1	cytoplasmic FMR1 interacting protein 1	1.01	0.892	1.18	0.018	1.08	0.291	1.07	0.755	1.09
1449333_at	Sf3a1	splicing factor 3a, subunit 1	1.01	0.454	1.03	0.602	1.23	0.067	1.19	0.183	1.12
1416352_s_at	Gpsn2	glycoprotein, synaptic 2	1.01	0.942	1.06	0.465	1.19	0.102	1.23	0.328	1.13
1436511_at	BC031781	cDNA sequence BC031781	1.02	0.897	1.1	0.169	1.16	0.323	1.51	0.199	1.2
1433998_at	4933427D14Rik	RIKEN cDNA 4933427D14 gene	1.14	0.688	1.07	0.828	1.06	0.697	1.05	0.759	1.08
1428642_at	Slc35d3	solute carrier family 35, member D3	1.03	0.963	1.02	0.965	1.22	0.329	2.36	0.338	1.41
1417274_at	Snrpa	small nuclear ribonucleoprotein polypeptide A	1.01	0.929	1.07	0.567	1.19	0.142	1.09	0.665	1.09
1426248_at	Stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	1	1	1.07	0.359	1.21	0.245	1.46	0.192	1.18
1438016_at	BC068171	cDNA sequence BC068171	1.17	0.29	1.05	0.714	1.06	0.782	1.46	0.058	1.18
1416479_a_at	Tmem14c	transmembrane protein 14C	1.09	0.546	1.13	0.208	1.07	0.515	2.72	0.14	1.5
1430079_at	5033406O09Rik	RIKEN cDNA 5033406O09 gene	1.13	0.802	1.06	0.498	1.09	0.757	1.29	0.313	1.14
1418198_a_at	Tm9sf1	transmembrane 9 superfamily member 1	1.02	0.891	1.03	0.335	1.23	0.264	1.33	0.097	1.15
1459786_at	---	Transcribed locus	1.05	0.807	1.19	0.706	1.04	0.88	1.41	0.65	1.17
1424416_at	Nkiras2	NFKB inhibitor interacting Ras-like protein 2	1.03	0.835	1.17	0.165	1.09	0.453	1.03	0.857	1.08
1460440_at	Lphn3	latrophilin 3	1.04	0.93	1.08	0.826	1.17	0.659	1.01	0.951	1.07
1425988_a_at	Hipk1 /// LOC63403	homeodomain interacting protein kinase 1 /// similar to homeodomain-interacting	1	0.999	1.03	0.939	1.26	0.345	2.96	0.184	1.56
1440942_at	Dact2	dapper homolog 2, antagonist of beta-catenin (xenopus)	1.02	0.928	1.11	0.676	1.15	0.464	1.28	0.411	1.14
1437946_x_at	Rapgef3	Rap guanine nucleotide exchange factor (GEF) 3	1.17	0.519	1.11	0.507	1.01	0.949	1.97	0.248	1.32
1455143_at	Nlgn2	neuroligin 2	1.09	0.779	1.18	0.77	1.02	0.93	1.14	0.375	1.11
1416427_at	Ccni	cyclin I	1.15	0.222	1.01	0.937	1.14	0.334	1.12	0.368	1.1
1416182_at	Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	1.06	0.817	1	0.975	1.22	0.018	1.16	0.258	1.11
1438659_x_at	Chchd6	coiled-coil-helix-coiled-coil-helix domain containing 6	1.03	0.044	1.17	0.649	1.1	0.546	1.23	0.278	1.13
1426366_at	Eif2c2	eukaryotic translation initiation factor 2C, 2	1.17	0.467	1.03	0.899	1.09	0.836	2.69	0.145	1.5
1448688_at	Podxl	podocalyxin-like	1.12	0.334	1.13	0.516	1.05	0.776	1.94	0.316	1.31
1436915_x_at	Laptm4b	lysosomal-associated protein transmembrane 4B	1.1	0.003	1.15	0.109	1.05	0.709	1.06	0.775	1.09
1455060_at	RP23-336J1.4	Ras-GTPase-activating protein SH3-domain binding protein	1.04	0.623	1.08	0.763	1.17	0.47	1.05	0.811	1.09
1425406_at	Clec4a2	C-type lectin domain family 4, member a2	1.28	0.711	1.02	0.978	1	0.988	1.54	0.191	1.21
1448369_at	Pola2	polymerase (DNA directed), alpha 2	1.03	0.747	1.04	0.856	1.23	0.195	1.73	0.227	1.26
1427360_at	4930507D05Rik	RIKEN cDNA 4930507D05 gene	1.05	0.947	1.21	0.401	1.04	0.922	1.84	0.062	1.29
1433606_at	Dcp1a	decapping enzyme	1.02	0.689	1.18	0.203	1.1	0.446	1.05	0.785	1.09
1423862_at	Plekhf2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	1.05	0.753	1.04	0.896	1.22	0.499	1.85	0.331	1.29
1436824_x_at	Rnf26 /// LOC66815	ring finger protein 26 /// similar to ring finger protein 26 /// similar to ring finger pro	1.17	0.507	1.04	0.775	1.09	0.42	2.33	0.14	1.41
1456518_at	4930422I07Rik	RIKEN cDNA 4930422I07 gene	1.17	0.257	1.07	0.859	1.07	0.774	1.59	0.459	1.22
1423574_s_at	Srd5a2l	steroid 5 alpha-reductase 2-like	1.01	0.846	1.01	0.942	1.29	0.039	1.02	0.938	1.08
1423116_at	Dom3z	DOM-3 homolog Z (C. elegans)	1.08	0.334	1.09	0.429	1.13	0.3	1.02	0.799	1.08
1415755_a_at	Ube2v1 /// LOC666	ubiquitin-conjugating enzyme E2 variant 1 /// similar to ubiquitin-conjugating enzy	1.07	0.564	1.07	0.55	1.17	0.396	1.3	0.221	1.15
1448551_a_at	Trim2	tripartite motif protein 2	1.08	0.644	1.19	0.557	1.03	0.784	1.69	0.319	1.25

1420491_at	Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	1.01	0.985	1.29	0.586	1.01	0.971	2.55	0.158	1.46
1415874_at	Spry1	sprouty homolog 1 (Drosophila)	1.06	0.509	1.08	0.517	1.16	0.503	1.69	0.124	1.25
1439422_a_at	C1qdc2	C1q domain containing 2	1.12	0.288	1.18	0.039	1.01	0.966	3.98	0.119	1.82
1418513_at	Stk3	serine/threonine kinase 3 (Ste20, yeast homolog)	1.04	0.089	1.06	0.846	1.21	0.557	1.97	0.208	1.32
1422007_at	Aqp3	aquaporin 3	1.14	0.822	1.07	0.829	1.1	0.663	1.18	0.441	1.12
1423718_at	Ak3	adenylate kinase 3	1.06	0.811	1.01	0.976	1.25	0.478	1.27	0.385	1.14
1449518_at	Qpctl	glutaminyl-peptide cyclotransferase-like	1.22	0.357	1.09	0.595	1	0.972	1.53	0.166	1.21
1419516_at	D0HXS9928E	DNA segment, human DXS9928E	1.05	0.674	1.15	0.07	1.11	0.467	1.29	0.187	1.15
1450409_a_at	4930570C03Rik	RIKEN cDNA 4930570C03 gene	1.03	0.847	1.19	0.097	1.09	0.491	1.93	0.177	1.31
1449117_at	Jund1	Jun proto-oncogene related gene d1	1.04	0.713	1.17	0.283	1.1	0.807	1.16	0.502	1.12
1417238_at	Ewsr1	Ewing sarcoma breakpoint region 1	1.04	0.798	1.04	0.61	1.23	0.308	1.04	0.808	1.09
1455835_at	Rps16	Ribosomal protein S16	1.19	0.259	1.01	0.92	1.11	0.459	1.25	0.365	1.14
1449050_at	Recc1	replication factor C 1	1.07	0.306	1.19	0.519	1.06	0.673	1.18	0.392	1.12
1460619_at	4931419K03Rik	RIKEN cDNA 4931419K03 gene	1.08	0.627	1.09	0.779	1.14	0.404	1.17	0.726	1.12
1447939_a_at	4933409K07Rik ///	RIKEN cDNA 4933409K07 gene /// similar to 4933409K07Rik protein /// hypotheti	1.08	0.769	1.24	0.692	1	0.997	1.77	0.17	1.27
1449448_at	Med9	mediator of RNA polymerase II transcription, subunit 9 homolog (yeast)	1.12	0.116	1.02	0.9	1.19	0.444	1.56	0.213	1.22
1425524_at	2600011C06Rik	RIKEN cDNA 2600011C06 gene	1.03	0.921	1.05	0.756	1.23	0.413	1.02	0.927	1.09
1417931_at	Ndst2	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	1.08	0.497	1.05	0.559	1.18	0.141	1.2	0.338	1.13
1434664_at	2410129H14Rik	RIKEN cDNA 2410129H14 gene	1.01	0.917	1.06	0.678	1.24	0.308	2.26	0.178	1.39
1427226_at	Epn2	epsin 2	1.21	0.406	1.08	0.635	1.02	0.884	1.01	0.963	1.08
1427091_at	AI481105	expressed sequence AI481105	1.02	0.853	1.08	0.553	1.22	0.067	1.1	0.481	1.1
1449861_at	Nek4	NIMA (never in mitosis gene a)-related expressed kinase 4	1	0.995	1.1	0.559	1.22	0.06	1.32	0.276	1.16
1429842_at	Mdh1b	malate dehydrogenase 1B, NAD (soluble)	1.08	0.651	1.02	0.954	1.21	0.486	1.57	0.481	1.22
1421380_at	Insr	insulin receptor	1.16	0.627	1.1	0.489	1.06	0.839	1.02	0.965	1.08
1424291_at	Nup93	nucleoporin 93	1.06	0.689	1.07	0.518	1.19	0.189	1.26	0.336	1.15
1456181_at	9530020G05Rik	RIKEN cDNA 9530020G05 gene	1.03	0.869	1	0.983	1.29	0.042	1.19	0.352	1.13
1435806_at	---	---	1.02	0.862	1.16	0.4	1.14	0.44	1.14	0.132	1.12
1423051_at	Hnrpu	heterogeneous nuclear ribonucleoprotein U	1.17	0.125	1.08	0.453	1.07	0.733	1.18	0.17	1.13
1437733_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	1.1	0.8	1.04	0.753	1.18	0.181	1.09	0.714	1.1
1417764_at	Ssr1 /// LOC63653	signal sequence receptor, alpha /// similar to signal sequence receptor, alpha	1.08	0.739	1.2	0.462	1.04	0.891	1.92	0.072	1.31
1427357_at	Cda	cytidine deaminase	1.05	0.81	1.01	0.963	1.27	0.416	4.46	0.202	1.95
1422688_a_at	Nras	neuroblastoma ras oncogene	1.14	0.734	1.03	0.893	1.16	0.27	1.11	0.646	1.11
1418865_at	Zfp385	zinc finger protein 385	1.04	0.663	1.28	0.005	1.01	0.98	1.02	0.95	1.09
1426950_at	Parp16	poly (ADP-ribose) polymerase family, member 16	1.06	0.621	1.21	0.242	1.05	0.702	1.88	0.322	1.3
1434813_x_at	Wars	tryptophanyl-tRNA synthetase	1.05	0.791	1.06	0.784	1.21	0.179	1.11	0.331	1.11
1417097_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	1.04	0.771	1.05	0.621	1.24	0.276	1.17	0.429	1.13
1416433_at	Rpa2	replication protein A2	1.06	0.383	1.18	0.34	1.09	0.459	1.64	0.235	1.24
1460358_s_at	Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	1.01	0.901	1	0.977	1.32	0.012	1.64	0.197	1.24
1431574_at	4930465M20Rik	RIKEN cDNA 4930465M20 gene	1	0.993	1.05	0.902	1.27	0.116	1.43	0.484	1.19
1434061_at	Rp2h	retinitis pigmentosa 2 homolog (human)	1.02	0.853	1.29	0.144	1.02	0.873	1.34	0.365	1.17
1435122_x_at	Dnmt1	DNA methyltransferase (cytosine-5) 1	1.12	0.212	1.13	0.306	1.07	0.725	2.14	0.192	1.37
1421606_a_at	Sult4a1	sulfotransferase family 4A, member 1	1.06	0.607	1.14	0.796	1.13	0.749	1.16	0.168	1.12
1435009_at	Slc9a6	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	1.06	0.691	1.26	0.048	1.02	0.863	1.17	0.441	1.12
1424669_at	Zfyve21	zinc finger, FYVE domain containing 21	1.09	0.457	1.22	0.158	1.02	0.923	1.57	0.144	1.23
1418264_at	Cenpk	centromere protein K	1.02	0.919	1.02	0.931	1.29	0.178	4.4	0.206	1.93
1450847_at	Ncbp2	nuclear cap binding protein subunit 2	1.07	0.601	1.2	0.267	1.07	0.775	1.28	0.468	1.15
1459714_at	6330545A04Rik	RIKEN cDNA 6330545A04 gene	1.18	0.744	1	0.995	1.16	0.26	1.1	0.657	1.11
1418985_at	Cttnbp2nl	CTTNBP2 N-terminal like	1.07	0.79	1.21	0.653	1.05	0.82	1.19	0.529	1.13
1451768_a_at	Slc20a2	solute carrier family 20, member 2	1.08	0.812	1.07	0.756	1.19	0.726	1.1	0.642	1.11
1416234_at	Lrrc59	leucine rich repeat containing 59	1.05	0.56	1.16	0.319	1.13	0.23	1.32	0.135	1.16
1449194_at	Mrps25	mitochondrial ribosomal protein S25	1.2	0.356	1.09	0.463	1.05	0.686	1.17	0.553	1.13
1456754_at	Zfyve20	zinc finger, FYVE domain containing 20	1.16	0.555	1.11	0.42	1.07	0.505	1.17	0.047	1.13
1433608_at	Scfd2	sec1 family domain containing 2	1.06	0.729	1.09	0.654	1.19	0.469	1.17	0.398	1.13

1439541_at	4930414L22Rik	RIKEN cDNA 4930414L22 gene	1.13	0.677	1.05	0.868	1.17	0.447	1.39	0.035	1.18
1437537_at	Casp9	caspase 9	1.08	0.676	1.06	0.837	1.2	0.375	1.1	0.655	1.11
1436608_at	BC038822	cDNA sequence BC038822	1.12	0.748	1.1	0.721	1.12	0.467	1.02	0.882	1.09
1434216_a_at	Nudt19	nudix (nucleoside diphosphate linked moiety X)-type motif 19	1.03	0.891	1.01	0.956	1.3	0.064	1.24	0.299	1.15
1416537_at	Creld1	cysteine-rich with EGF-like domains 1	1.01	0.94	1.09	0.554	1.23	0.217	1.05	0.841	1.1
1450841_at	Stt3a	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisia	1.01	0.918	1.33	0.082	1.01	0.848	1.21	0.187	1.14
1459256_at	Nrp2	Neuropilin 2	1.07	0.939	1.22	0.513	1.05	0.785	1.42	0.078	1.19
1435834_at	Gas2	growth arrest specific 2	1.21	0.13	1.01	0.975	1.13	0.445	1.5	0.305	1.21
1423121_at	Ide	insulin degrading enzyme	1.06	0.655	1.04	0.827	1.24	0.501	1.22	0.502	1.14
1436174_at	Atad2	ATPase family, AAA domain containing 2	1.13	0.73	1.1	0.647	1.11	0.571	2.28	0.238	1.41
1419029_at	Ero1l	ERO1-like (S. cerevisiae)	1.06	0.723	1.15	0.639	1.14	0.635	1.58	0.288	1.23
1415930_a_at	Map1lc3b	microtubule-associated protein 1 light chain 3 beta	1.07	0.614	1.2	0.405	1.08	0.589	1.35	0.262	1.17
1416914_s_at	Mtvr2	mammary tumor virus receptor 2	1.1	0.631	1.12	0.413	1.13	0.418	1.12	0.533	1.12
1444397_at	Spef1	sperm flagellar 1	1.12	0.732	1.07	0.906	1.15	0.541	1.32	0.633	1.17
1436081_a_at	Zfp414	zinc finger protein 414	1.11	0.531	1.06	0.754	1.17	0.348	1.03	0.856	1.09
1426981_at	Pcsk6	proprotein convertase subtilisin/kexin type 6	1.13	0.078	1.01	0.945	1.21	0.482	1.24	0.666	1.15
1415907_at	Ccnd3	cyclin D3	1.15	0.524	1.06	0.68	1.14	0.428	2.17	0.195	1.38
1455818_at	4930427A07Rik	RIKEN cDNA 4930427A07 gene	1.09	0.691	1.12	0.778	1.14	0.236	1.42	0.161	1.19
1424236_at	Tbc1d10b	TBC1 domain family, member 10b	1.03	0.391	1.04	0.642	1.29	0.192	1.44	0.136	1.2
1427060_at	Mapk3	mitogen activated protein kinase 3	1.13	0.416	1.21	0.13	1.01	0.945	1.07	0.704	1.11
1423265_at	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	1.13	0.556	1.08	0.549	1.15	0.418	3.58	0.158	1.73
1416695_at	Tspo	translocator protein	1.12	0.699	1.16	0.106	1.08	0.763	1.96	0.174	1.33
1422491_a_at	Bnip2	BCL2/adenovirus E1B interacting protein 1, NIP2	1.15	0.503	1.11	0.304	1.1	0.569	1.07	0.761	1.11
1439934_at	Slc30a10	solute carrier family 30, member 10	1.16	0.865	1.13	0.692	1.06	0.862	2.52	0.16	1.47
1416925_at	Kpnb1	karyopherin (importin) beta 1	1.05	0.755	1.23	0.092	1.08	0.641	1.34	0.002	1.18
1433517_at	Myeov2	myeloma overexpressed 2	1.18	0.718	1.17	0.807	1.01	0.98	1.42	0.605	1.2
1424708_at	Tmed10	transmembrane emp24-like trafficking protein 10 (yeast)	1.03	0.542	1.11	0.418	1.21	0.133	1.24	0.096	1.15
1427199_at	Fryl	furry homolog-like (Drosophila)	1.2	0.137	1.07	0.67	1.1	0.639	1.65	0.075	1.25
1429348_at	Sema3c	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.03	0.857	1.22	0.015	1.11	0.522	1.15	0.771	1.13
1429296_at	Rab10	RAB10, member RAS oncogene family	1.02	0.741	1.02	0.87	1.32	0.057	1.39	0.18	1.19
1457159_at	Gm101	gene model 101, (NCBI)	1.06	0.609	1.21	0.661	1.09	0.681	1.77	0.372	1.28
1435671_at	Mipol1	mirror-image polydactyly gene 1 homolog (human)	1.01	0.972	1.23	0.348	1.13	0.584	1.13	0.748	1.12
1420411_a_at	Pi4k2b	phosphatidylinositol 4-kinase type 2 beta	1.36	0.069	1	0.982	1	1	4.79	0.272	2.04
1417822_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	1.23	0.573	1.09	0.672	1.04	0.851	1.16	0.453	1.13
1455852_at	4833432M17Rik	RIKEN cDNA 4833432M17 gene	1.21	0.562	1.08	0.826	1.08	0.748	3.41	0.187	1.69
1456630_x_at	Son	Son cell proliferation protein	1.09	0.756	1.18	0.656	1.1	0.178	1.49	0.267	1.21
1433864_at	Lrp12	low density lipoprotein-related protein 12	1.03	0.817	1.1	0.383	1.25	0.175	1.44	0.242	1.2
1455164_at	Cdgap	Cdc42 GTPase-activating protein	1.16	0.208	1.2	0.124	1.01	0.972	1.02	0.92	1.1
1426631_at	Pus7	pseudouridylate synthase 7 homolog (S. cerevisiae)	1.08	0.672	1.03	0.902	1.26	0.067	1.39	0.377	1.19
1417342_at	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.05	0.625	1.1	0.694	1.21	0.28	1.19	0.288	1.14
1436143_at	4933425L03Rik	RIKEN cDNA 4933425L03 gene	1.02	0.129	1.09	0.264	1.26	0.039	1.01	0.918	1.09
1425136_x_at	Dnm2	dynamin 2	1.01	0.972	1.07	0.398	1.3	0.296	1.15	0.506	1.13
1453532_at	4933415A04Rik	RIKEN cDNA 4933415A04 gene	1.07	0.753	1.06	0.749	1.24	0.572	1.52	0.49	1.22
1421143_at	Diap1	diaphanous homolog 1 (Drosophila)	1.2	0.57	1.01	0.973	1.16	0.709	1.43	0.386	1.2
1417501_at	Fbxo6b	F-box only protein 6b	1.01	0.965	1.23	0.508	1.13	0.478	1	0.924	1.09
1449221_a_at	Rrbp1	ribosome binding protein 1	1.16	0.224	1.04	0.799	1.18	0.034	1.36	0.197	1.18
1431415_a_at	Tbpl1	TATA box binding protein-like 1	1.07	0.506	1.04	0.847	1.27	0.021	1.25	0.302	1.16
1449141_at	Fblim1	filamin binding LIM protein 1	1.31	0.264	1.04	0.893	1.03	0.897	1.3	0.451	1.17
1430127_a_at	Ccnd2	cyclin D2	1.13	0.578	1.05	0.89	1.2	0.349	1.05	0.862	1.11
1456523_at	C77713	expressed sequence C77713	1.19	0.492	1.14	0.815	1.05	0.913	2.26	0.19	1.41
1423448_at	Rab11b	RAB11B, member RAS oncogene family	1.03	0.891	1.05	0.695	1.3	0.137	1.31	0.352	1.17
1450967_at	Ptplad2	protein tyrosine phosphatase-like A domain containing 2	1.1	0.617	1.13	0.338	1.15	0.542	1.71	0.153	1.27
1436158_at	Eif4ebp2	eukaryotic translation initiation factor 4E binding protein 2	1.1	0.332	1.03	0.702	1.25	0.393	1.12	0.42	1.13

1449700_at	Igbp1	Immunoglobulin (CD79A) binding protein 1	1.07	0.695	1.06	0.771	1.25	0.345	1.19	0.009	1.14
1448335_s_at	Ccni	cyclin I	1.08	0.392	1.05	0.6	1.26	0.062	1.12	0.051	1.13
1431306_at	Nt5c3	5'-nucleotidase, cytosolic III	1.22	0.16	1.08	0.772	1.08	0.857	2.39	0.258	1.44
1442047_at	Rreb1	ras responsive element binding protein 1	1.13	0.779	1.04	0.951	1.22	0.259	1.46	0.633	1.21
1453581_at	Cep170	centrosomal protein 170	1.07	0.352	1.13	0.628	1.18	0.135	1.03	0.754	1.1
1425142_a_at	Hnrpd	heterogeneous nuclear ribonucleoprotein D	1.04	0.714	1.08	0.442	1.27	0.28	1.25	0.285	1.16
1460465_at	A930038C07Rik	RIKEN cDNA A930038C07 gene	1.15	0.177	1.2	0.379	1.03	0.917	1.54	0.164	1.23
1436126_at	Dnali1	dynein, axonemal, light intermediate polypeptide 1	1.05	0.326	1.04	0.853	1.3	0.516	1.04	0.893	1.11
1436269_s_at	Htra2	HtrA serine peptidase 2	1.15	0.128	1.2	0.023	1.04	0.679	1.4	0.242	1.2
1429254_at	Aqp11	aquaporin 11	1.09	0.521	1.03	0.587	1.27	0.537	1.88	0.351	1.32
1419329_at	Sorbs3	sorbin and SH3 domain containing 3	1.05	0.91	1.25	0.498	1.09	0.091	1.13	0.715	1.13
1451382_at	Chac1	ChaC, cation transport regulator-like 1 (E. coli)	1	0.992	1.07	0.884	1.32	0.127	2.92	0.022	1.58
1434725_at	Gramd1c	GRAM domain containing 1C	1.07	0.659	1.08	0.588	1.24	0.103	1.15	0.693	1.14
1417311_at	Crip2	cysteine rich protein 2	1.19	0.406	1.01	0.972	1.2	0.09	1.67	0.131	1.27
1427234_at	Vangl1	vang-like 1 (van gogh, Drosophila)	1.01	0.95	1.36	0.132	1.02	0.788	3.68	0.149	1.77
1418901_at	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	1.03	0.934	1.09	0.733	1.28	0.336	1.05	0.776	1.11
1452600_at	Taf6l	TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated fa	1.02	0.958	1.11	0.475	1.26	0.052	1.3	0.13	1.17
1423075_at	Lman2	lectin, mannose-binding 2	1.15	0.069	1.02	0.909	1.23	0.38	1.07	0.743	1.12
1424570_at	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1.01	0.968	1.09	0.724	1.3	0.436	1.08	0.808	1.12
1438948_x_at	Tspo	translocator protein	1.13	0.073	1.15	0.331	1.12	0.466	1.36	0.303	1.19
1428419_at	5430411K18Rik	RIKEN cDNA 5430411K18 gene	1.06	0.774	1.13	0.339	1.21	0.103	1.2	0.154	1.15
1425166_at	Rbl1	retinoblastoma-like 1 (p107)	1.03	0.852	1.07	0.883	1.29	0.238	2.17	0.193	1.39
1435077_at	Asxl1	additional sex combs like 1 (Drosophila)	1.1	0.537	1	0.981	1.3	0.192	1.14	0.152	1.14
1424072_at	2010107G23Rik	RIKEN cDNA 2010107G23 gene	1.01	0.918	1.11	0.515	1.28	0.196	1.27	0.404	1.17
1416493_at	Ddost	dolichyl-di-phosphooligosaccharide-protein glycotransferase	1.05	0.721	1.09	0.39	1.26	0.124	1.43	0.038	1.21
1428154_s_at	Ppapdc1	phosphatidic acid phosphatase type 2 domain containing 1	1.05	0.664	1.18	0.275	1.17	0.051	1.83	0.002	1.31
1458703_at	---	---	1.06	0.209	1.25	0.172	1.1	0.648	1.15	0.683	1.14
1425874_at	Hoxc13	homeo box C13	1.15	0.315	1.23	0.21	1.02	0.912	1.73	0.343	1.28
1423947_at	1110008P14Rik	RIKEN cDNA 1110008P14 gene	1.14	0.721	1.15	0.386	1.12	0.696	1.14	0.433	1.14
1420874_at	Ptk9	protein tyrosine kinase 9	1.26	0.171	1.13	0.501	1.01	0.976	1.45	0.325	1.21
1424772_at	H2afj /// LOC63240	H2A histone family, member J /// similar to H2A histone family, member J isoform	1.24	0.567	1.12	0.501	1.05	0.626	1.48	0.236	1.22
1459842_x_at	Nubp2	nucleotide binding protein 2	1.19	0.303	1.05	0.728	1.17	0.408	1.48	0.314	1.22
1448475_at	Olfml3	olfactomedin-like 3	1.16	0.616	1.22	0.336	1.02	0.924	1.2	0.385	1.15
1451862_a_at	Prf1	perforin 1 (pore forming protein)	1.15	0.492	1.06	0.858	1.19	0.159	1.82	0.4	1.31
1439502_at	4930573I19Rik	RIKEN cDNA 4930573I19 gene	1.06	0.652	1.16	0.593	1.19	0.103	1.34	0.138	1.19
1450669_at	Map3k11	mitogen activated protein kinase kinase kinase 11	1.05	0.916	1.13	0.56	1.22	0.267	1.04	0.838	1.11
1418377_a_at	Siva	Cd27 binding protein (Hindu God of destruction)	1.02	0.78	1.38	0.014	1	0.993	1.53	0.243	1.23
1452719_at	---	---	1.09	0.724	1.22	0.301	1.1	0.587	1.29	0.336	1.17
1416457_at	Ddah2	dimethylarginine dimethylaminohydrolase 2	1.36	0.083	1.03	0.892	1.02	0.907	1.12	0.444	1.13
1444504_at	Dhrs7c	dehydrogenase/reductase (SDR family) member 7C	1.04	0.426	1.15	0.382	1.22	0.715	1.06	0.757	1.12
1443305_at	---	13 days embryo heart cDNA, RIKEN full-length enriched library, clone:D330014J(	1	0.985	1.38	0.084	1.03	0.952	1.66	0.321	1.27
1428330_at	Dopey2	dopey family member 2	1	0.962	1.33	0.011	1.07	0.516	1.36	0.204	1.19
1451680_at	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	1.19	0.283	1.05	0.779	1.17	0.602	1.95	0.267	1.34
1422706_at	LOC637870	similar to Nedd4 WW binding protein 4	1.02	0.926	1.3	0.229	1.08	0.167	1.07	0.466	1.12
1427103_at	Plekhq1	pleckstrin homology domain containing, family Q member 1	1.07	0.882	1.11	0.614	1.23	0.42	1.64	0.035	1.26
1458417_at	Jmjd1b	jumonji domain containing 1B	1.15	0.501	1.06	0.908	1.2	0.241	1.1	0.671	1.13
1451198_at	Gatad2a	GATA zinc finger domain containing 2A	1.11	0.685	1.01	0.955	1.29	0.282	1.45	0.3	1.21
1417201_at	Nt5c2	5'-nucleotidase, cytosolic II	1.16	0.47	1.12	0.585	1.13	0.473	1.45	0.308	1.22
1426545_at	Tnrc6b	trinucleotide repeat containing 6b	1.09	0.56	1.09	0.511	1.23	0.537	1.46	0.163	1.22
1418175_at	Vdr	vitamin D receptor	1.04	0.865	1.1	0.86	1.27	0.085	1.7	0.015	1.28
1457227_at	AI843755	expressed sequence AI843755	1.31	0.719	1.04	0.903	1.07	0.888	1.25	0.604	1.17
1452545_a_at	Itgb1	integrin beta 1 (fibronectin receptor beta)	1.19	0.201	1.09	0.552	1.13	0.336	1.82	0.046	1.31
1421994_a_at	Hs1bp3	HCLS1 binding protein 3	1.06	0.909	1.03	0.913	1.33	0.646	1.01	0.976	1.11

1423544_at	Ptpn5	protein tyrosine phosphatase, non-receptor type 5	1.32	0.106	1.08	0.825	1.02	0.958	1.1	0.727	1.13
1417533_a_at	Itgb5	integrin beta 5	1.18	0.122	1.23	0.021	1.01	0.934	1.36	0.189	1.2
1452750_at	5530601H04Rik	RIKEN cDNA 5530601H04 gene	1.13	0.315	1.25	0.362	1.05	0.796	1.15	0.587	1.14
1418999_at	2310033P09Rik	RIKEN cDNA 2310033P09 gene	1.04	0.632	1.21	0.291	1.17	0.303	1.12	0.436	1.14
1429234_s_at	11-Sep	septin 11	1.02	0.749	1.36	0.08	1.04	0.768	1.03	0.875	1.11
1435948_at	Gpr178	G protein-coupled receptor 178	1.02	0.837	1.26	0.131	1.14	0.265	1.42	0.27	1.21
1448580_at	Glg1	golgi apparatus protein 1	1.03	0.896	1.26	0.153	1.13	0.258	1.16	0.319	1.14
1416929_at	Rbm12	RNA binding motif protein 12	1.32	0.485	1.01	0.975	1.1	0.599	1.1	0.796	1.13
1450516_a_at	Rab17	RAB17, member RAS oncogene family	1.01	0.99	1.04	0.829	1.38	0.566	2.26	0.012	1.42
1437629_at	Arhgef19	Rho guanine nucleotide exchange factor (GEF) 19	1.2	0.495	1.22	0.178	1.01	0.899	1.07	0.785	1.12
1455614_at	Tomm40l	translocase of outer mitochondrial membrane 40 homolog-like (yeast)	1	0.987	1.09	0.592	1.34	0.069	1.03	0.854	1.11
1418773_at	Fads3	fatty acid desaturase 3	1.19	0.401	1.23	0.71	1.01	0.948	1.88	0.17	1.33
1450522_a_at	H1f0	H1 histone family, member 0	1.13	0.522	1.07	0.772	1.23	0.427	1.49	0.132	1.23
1421654_a_at	Lmna	lamin A	1.19	0.202	1.17	0.002	1.06	0.559	6.67	0.16	2.52
1423650_at	Rnf26	ring finger protein 26	1.11	0.694	1.15	0.43	1.17	0.492	1.89	0.2	1.33
1448994_at	Sp1	trans-acting transcription factor 1	1.12	0.679	1.28	0.242	1.03	0.933	1.09	0.718	1.13
1456033_at	Tbx4	T-box 4	1.16	0.647	1.22	0.662	1.05	0.861	2.01	0.016	1.36
1427094_at	Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	1.25	0.129	1.15	0.471	1.03	0.808	2	0.235	1.36
1431431_a_at	Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	1.01	0.981	1.01	0.988	1.41	0.389	1.25	0.679	1.17
1420865_at	Zfp161	zinc finger protein 161	1.1	0.759	1.28	0.185	1.05	0.77	1.41	0.049	1.21
1425940_a_at	Ssbp3	single-stranded DNA binding protein 3	1.14	0.575	1.16	0.552	1.13	0.607	2.64	0.208	1.52
1433858_at	Lrrc28	leucine rich repeat containing 28	1.12	0.29	1.02	0.943	1.29	0.04	1.07	0.748	1.12
1417958_at	Tspan1	tetraspanin 1	1.16	0.503	1.13	0.771	1.15	0.514	1.69	0.53	1.28
1423411_at	BC013481	cDNA sequence BC013481	1.39	0.369	1.01	0.966	1.03	0.848	1.14	0.517	1.14
1434853_x_at	Mkrn1	makorin, ring finger protein, 1	1	0.981	1.27	0.174	1.16	0.522	1.66	0.298	1.27
1451726_at	Mtmr6	myotubularin related protein 6	1.08	0.115	1.02	0.875	1.33	0.242	1.11	0.339	1.14
1457780_at	Stx11	syntaxin 11	1.12	0.582	1.3	0.356	1.02	0.935	1.82	0.055	1.31
1418924_at	Rassf7	Ras association (RalGDS/AF-6) domain family 7	1.25	0.22	1.13	0.5	1.05	0.695	1.2	0.398	1.16
1416545_at	Zdhhc7	zinc finger, DHHC domain containing 7	1.08	0.795	1.15	0.075	1.2	0.23	1.02	0.85	1.11
1452430_s_at	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	1.02	0.969	1.03	0.911	1.39	0.249	1.51	0.341	1.24
1419251_at	Eps15	epidermal growth factor receptor pathway substrate 15	1.08	0.696	1.05	0.866	1.3	0.304	1.78	0.151	1.3
1459130_at	Hace1	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	1.16	0.355	1.25	0.385	1.03	0.925	1.83	0.304	1.32
1426534_a_at	Arfgap3	ADP-ribosylation factor GTPase activating protein 3	1.19	0.412	1.16	0.436	1.09	0.445	1.43	0.11	1.22
1436909_at	B430110G05Rik	RIKEN cDNA B430110G05 gene	1.15	0.421	1.14	0.285	1.15	0.424	1.88	0.223	1.33
1415918_a_at	Tpi1	triosephosphate isomerase 1	1.04	0.649	1.18	0.064	1.22	0.115	1.1	0.464	1.14
1417986_at	Nrarp	Notch-regulated ankyrin repeat protein	1.03	0.779	1.3	0.371	1.11	0.706	2.16	0.015	1.4
1443733_x_at	Pold3	polymerase (DNA-directed), delta 3, accessory subunit	1.05	0.662	1.2	0.107	1.19	0.285	1.17	0.406	1.15
1421790_a_at	Kcnab3	potassium voltage-gated channel, shaker-related subfamily, beta member 3	1.17	0.408	1.27	0.13	1.01	0.93	2.41	0.297	1.46
1417571_at	Mpg	N-methylpurine-DNA glycosylase	1.18	0.487	1.05	0.657	1.22	0.258	1.31	0.436	1.19
1423658_at	Sppl3	signal peptide peptidase 3	1.01	0.926	1.25	0.098	1.18	0.43	1.82	0.09	1.32
1428190_at	Slc25a1	solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1	1.06	0.904	1.09	0.62	1.3	0.066	1.39	0.261	1.21
1425403_at	Dnm3	dynamin 3	1.08	0.79	1.21	0.523	1.15	0.385	2.07	0.039	1.38
1448315_a_at	Pycr2	pyrroline-5-carboxylate reductase family, member 2	1.16	0.125	1.04	0.532	1.24	0.036	1.76	0.29	1.3
1450157_a_at	Hmmr	hyaluronan mediated motility receptor (RHAMM)	1.11	0.921	1.16	0.873	1.18	0.684	6.13	0.232	2.39
1418231_at	Lims1	LIM and senescent cell antigen-like domains 1	1.12	0.751	1.1	0.871	1.23	0.657	1.36	0.568	1.2
1423612_at	AI462438	expressed sequence AI462438	1.01	0.909	1.2	0.492	1.24	0.076	1.25	0.6	1.17
1445229_at	Dgat1	diacylglycerol O-acyltransferase 1	1.13	0.793	1.13	0.733	1.19	0.475	1.04	0.869	1.12
1456405_at	Dido1	death inducer-obliterator 1	1.11	0.196	1.08	0.514	1.27	0.207	1.21	0.23	1.16
1440503_at	---	3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630095	1.02	0.837	1.04	0.951	1.39	0.529	1.23	0.085	1.17
1450057_at	2610042O14Rik	RIKEN cDNA 2610042O14 gene	1.01	0.969	1.3	0.014	1.14	0.535	1.17	0.565	1.16
1428291_at	Exosc8	exosome component 8	1.03	0.894	1.1	0.518	1.32	0.394	1.1	0.645	1.14
1438416_at	Thrap5	thyroid hormone receptor associated protein 5	1.14	0.621	1.19	0.493	1.12	0.633	1.23	0.054	1.17
1444052_at	---	Transcribed locus	1.24	0.439	1.12	0.484	1.1	0.367	1.23	0.086	1.17

1451458_at	Tmem2	transmembrane protein 2	1.28	0.292	1	0.989	1.18	0.21	1.4	0.242	1.22
1425381_a_at	Trfr2	transferrin receptor 2	1.28	0.433	1.15	0.105	1.03	0.888	4	0.211	1.86
1432282_a_at	2010305C02Rik	RIKEN cDNA 2010305C02 gene	1.11	0.166	1.18	0.251	1.17	0.402	1.38	0.476	1.21
1426790_at	Ssrp1	structure specific recognition protein 1	1.07	0.575	1.17	0.412	1.22	0.215	1.12	0.572	1.15
1453060_at	Rgs8	regulator of G-protein signaling 8	1.35	0.514	1.1	0.842	1.02	0.929	1.62	0.217	1.27
1458584_at	4832406H04Rik	RIKEN cDNA 4832406H04 gene	1.12	0.886	1.15	0.81	1.19	0.268	1.3	0.6	1.19
1436605_at	Tkt	transketolase	1.2	0.555	1.01	0.967	1.25	0.103	1.22	0.552	1.17
1437904_at	Drbp1	developmentally regulated RNA binding protein 1	1.2	0.703	1.14	0.509	1.13	0.783	1.6	0.145	1.27
1422845_at	Canx	calnexin	1.16	0.374	1.08	0.622	1.22	0.299	1.53	0.045	1.25
1448233_at	Prnp	prion protein	1.23	0.204	1.19	0.026	1.05	0.708	1.47	0.036	1.23
1421971_a_at	Mrps34	mitochondrial ribosomal protein S34	1.02	0.89	1.03	0.616	1.42	0.05	1.08	0.398	1.14
1451016_at	Ifrd2	interferon-related developmental regulator 2	1.18	0.149	1.16	0.316	1.13	0.27	4.83	0.176	2.07
1431339_a_at	Efhd2	EF hand domain containing 2	1.31	0.366	1.05	0.847	1.11	0.404	1.18	0.496	1.16
1427461_at	BC005561	cDNA sequence BC005561	1.05	0.785	1.02	0.963	1.4	0.167	1.79	0.302	1.31
1435015_at	2210018M03Rik	RIKEN cDNA 2210018M03 gene	1.03	0.917	1.24	0.354	1.19	0.358	1	1	1.12
1452036_a_at	Tmpo	thymopoietin	1.04	0.609	1.07	0.467	1.36	0.078	1.81	0.131	1.32
1444520_at	Fryl	furry homolog-like (Drosophila)	1.03	0.875	1.09	0.659	1.35	0.199	2.78	0.245	1.56
1431015_at	Tmem129	transmembrane protein 129	1.05	0.896	1.09	0.815	1.34	0.518	1.44	0.225	1.23
1416102_at	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta	1.13	0.586	1.19	0.28	1.14	0.552	1.04	0.802	1.13
1423475_at	Cnnm2	cyclin M2	1.17	0.036	1.05	0.729	1.25	0.23	2.69	0.149	1.54
1454091_at	Psg21	pregnancy-specific glycoprotein 21	1.25	0.467	1.16	0.591	1.06	0.792	1.45	0.22	1.23
1429332_at	4632427E13Rik	RIKEN cDNA 4632427E13 gene	1.33	0.462	1.02	0.944	1.12	0.688	1.03	0.951	1.13
1427376_a_at	Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	1.16	0.501	1.11	0.708	1.2	0.373	2.91	0.227	1.6
1421397_a_at	Lrdd	leucine-rich and death domain containing	1.1	0.698	1.26	0.454	1.11	0.593	2.01	0.175	1.37
1431721_a_at	Proz	protein Z, vitamin K-dependent plasma glycoprotein	1.06	0.83	1.02	0.934	1.39	0.453	3.61	0.015	1.77
1432157_at	4930515G13Rik	RIKEN cDNA 4930515G13 gene	1.43	0.48	1.03	0.932	1.02	0.96	1.1	0.829	1.14
1445597_s_at	Hrasls3	HRAS like suppressor 3	1.14	0.458	1.16	0.307	1.18	0.142	1.97	0.157	1.36
1429502_at	Stch	stress 70 protein chaperone, microsome-associated, human homolog	1.03	0.879	1.27	0.547	1.18	0.537	1.09	0.527	1.14
1426947_x_at	Col6a2	procollagen, type VI, alpha 2	1.16	0.395	1.31	0.112	1.01	0.961	1.39	0.083	1.22
1418952_at	Txlnb	taxilin beta	1.02	0.908	1.15	0.778	1.32	0.248	1.31	0.047	1.2
1427979_at	4732418C07Rik	RIKEN cDNA 4732418C07 gene	1.09	0.878	1.19	0.689	1.21	0.693	1.18	0.676	1.17
1437084_at	Padi6	peptidyl arginine deiminase, type VI	1.13	0.539	1.19	0.765	1.17	0.743	1.34	0.351	1.21
1454843_at	Prps2	phosphoribosyl pyrophosphate synthetase 2	1.02	0.929	1.19	0.053	1.29	0.376	1.03	0.936	1.13
1450975_at	Cacng4	calcium channel, voltage-dependent, gamma subunit 4	1.2	0.712	1.19	0.664	1.1	0.824	1.12	0.265	1.15
1422439_a_at	Cdk4 /// LOC64061	cyclin-dependent kinase 4 /// similar to Cell division protein kinase 4 (Cyclin-depe	1.03	0.909	1.43	0.006	1.03	0.847	1.27	0.377	1.19
1453044_at	C030014I23Rik	RIKEN cDNA C030014I23 gene	1.25	0.454	1.06	0.85	1.18	0.416	1.41	0.22	1.22
1433935_at	AU020206	expressed sequence AU020206	1.2	0.395	1.09	0.584	1.2	0.618	1.34	0.215	1.21
1429007_at	Slc35b2	solute carrier family 35, member B2	1.11	0.05	1.22	0.012	1.16	0.599	1.1	0.802	1.15
1460684_at	Tm7sf2	transmembrane 7 superfamily member 2	1.14	0.592	1.17	0.48	1.19	0.19	1.21	0.449	1.18
1452427_s_at	Ptplad1	protein tyrosine phosphatase-like A domain containing 1	1.16	0.666	1.02	0.952	1.32	0.528	1.42	0.319	1.23
1431020_a_at	Fgfr1op2	FGFR1 oncogene partner 2	1.21	0.515	1.05	0.758	1.23	0.36	1.33	0.397	1.21
1460278_a_at	D15Wsu75e	DNA segment, Chr 15, Wayne State University 75, expressed	1.03	0.795	1.14	0.335	1.32	0.098	1.47	0.197	1.24
1442217_at	Dnajb6	DnaJ (Hsp40) homolog, subfamily B, member 6	1.18	0.304	1.05	0.929	1.26	0.302	1.05	0.787	1.14
1416786_at	Acvr1	activin A receptor, type 1	1.08	0.586	1.22	0.306	1.2	0.524	1.25	0.205	1.19
1434363_x_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	1.17	0.683	1.09	0.841	1.24	0.259	1.45	0.224	1.24
1445945_at	AU021880	expressed sequence AU021880	1.03	0.861	1.44	0.05	1.03	0.967	2.59	0.097	1.52
1443937_at	AI790276	Expressed sequence AI790276	1.2	0.283	1.14	0.825	1.16	0.686	1.23	0.748	1.18
1424323_at	Noc2l	nucleolar complex associated 2 homolog (S. cerevisiae)	1.14	0.242	1.08	0.599	1.28	0.345	1.01	0.901	1.13
1428120_at	Fbxw9	F-box and WD-40 domain protein 9	1.07	0.694	1.12	0.028	1.32	0.146	1.01	0.942	1.13
1421912_at	Slc23a1	solute carrier family 23 (nucleobase transporters), member 1	1.2	0.073	1.11	0.312	1.19	0.218	1.41	0.449	1.23
1439984_at	Ptdss2	phosphatidylserine synthase 2	1.27	0.402	1.13	0.635	1.1	0.608	2.08	0.169	1.4
1425187_at	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	1.16	0.281	1.12	0.597	1.23	0.498	1.57	0.199	1.27
1452904_at	1700026L06Rik	RIKEN cDNA 1700026L06 gene	1.36	0.018	1.13	0.433	1.02	0.948	1.02	0.957	1.13

1425456_a_at	Map2k3	mitogen activated protein kinase kinase 3	1.17	0.649	1.08	0.632	1.25	0.325	3.73	0.226	1.81
1421339_at	Extl3	exostoses (multiple)-like 3	1.14	0.838	1.11	0.67	1.26	0.675	1.27	0.566	1.2
1456184_at	Tmem63c	transmembrane protein 63c	1.24	0.631	1.05	0.917	1.23	0.29	1.39	0.087	1.23
1423449_a_at	Actn4	actinin alpha 4	1.11	0.53	1.12	0.068	1.29	0.026	1.18	0.23	1.17
1439802_at	Stk35	serine/threonine kinase 35	1.17	0.788	1.1	0.646	1.25	0.504	1.32	0.091	1.21
1429176_at	Lrsam1	leucine rich repeat and sterile alpha motif containing 1	1.06	0.651	1.43	0.054	1.02	0.957	1.24	0.524	1.19
1429716_at	Zcchc4	zinc finger, CCHC domain containing 4	1.2	0.406	1.22	0.262	1.09	0.47	1.13	0.447	1.16
1427203_at	Myo15b	myosin XVB	1.16	0.443	1.01	0.983	1.34	0.204	1.1	0.751	1.15
1435760_at	Csta	cystatin A	1.02	0.97	1.04	0.954	1.45	0.464	1.32	0.671	1.21
1416256_a_at	Tubb5	tubulin, beta 5	1.24	0.149	1.02	0.875	1.26	0.174	1.6	0.138	1.28
1441923_s_at	Edn3	endothelin 3	1.36	0.242	1.1	0.8	1.05	0.655	1.92	0.291	1.36
1417114_at	Gmcl1	germ cell-less homolog 1 (Drosophila)	1.12	0.609	1.06	0.735	1.35	0.198	1.04	0.664	1.14
1430528_at	Sdcbp	syndecan binding protein	1.24	0.567	1.08	0.845	1.2	0.162	1.35	0.47	1.22
1422629_s_at	Shroom3	shroom family member 3	1.18	0.108	1.27	0.351	1.07	0.756	1.14	0.622	1.16
1417120_at	D4Wsu114e	DNA segment, Chr 4, Wayne State University 114, expressed	1.3	0.375	1.08	0.732	1.14	0.459	1.01	0.965	1.13
1419030_at	Ero1l	ERO1-like (S. cerevisiae)	1.07	0.709	1.05	0.877	1.41	0.301	1.43	0.328	1.24
1442393_at	Zfhx1b	Zinc finger homeobox 1b	1.19	0.389	1.28	0.102	1.05	0.875	1.08	0.681	1.15
1453406_a_at	Rab28	RAB28, member RAS oncogene family	1.01	0.959	1.12	0.512	1.4	0.287	1.13	0.592	1.16
1425160_at	AF067063	cDNA sequence AF067063	1.29	0.351	1.14	0.825	1.1	0.309	1.3	0.506	1.21
1455178_at	Rutbc1	RUN and TBC1 domain containing 1	1.49	0.29	1.02	0.941	1.02	0.907	1.96	0.062	1.37
1452043_at	2310011J03Rik	RIKEN cDNA 2310011J03 gene	1.34	0.443	1.1	0.363	1.09	0.458	1.06	0.788	1.15
1432579_at	Rshl2a	radial spokehead-like 2A	1.09	0.709	1.18	0.221	1.26	0.421	1.18	0.539	1.18
1416229_at	Rfk	riboflavin kinase	1.24	0.121	1.05	0.741	1.23	0.45	1.23	0.61	1.19
1426822_at	Rhot2	ras homolog gene family, member T2	1.08	0.111	1.15	0.385	1.3	0.08	1.32	0.152	1.21
1440771_at	Zkscan1	zinc finger with KRAB and SCAN domains 1	1.36	0.155	1.07	0.82	1.1	0.836	1.47	0.077	1.25
1419402_at	Mns1	meiosis-specific nuclear structural protein 1	1.26	0.65	1.24	0.636	1.03	0.914	4.38	0.187	1.98
1457143_at	---	PREDICTED: Mus musculus hypothetical protein LOC625121 (LOC625121), mR	1.07	0.934	1.42	0.547	1.05	0.932	1.38	0.293	1.23
1423333_at	1200007D18Rik	RIKEN cDNA 1200007D18 gene	1.13	0.404	1.01	0.922	1.39	0.264	1.27	0.321	1.2
1438422_at	Lrrc20	leucine rich repeat containing 20	1.33	0.189	1.19	0.078	1.01	0.955	1.78	0.151	1.33
1426069_s_at	Slc7a4	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	1.14	0.311	1.17	0.764	1.22	0.128	1.15	0.684	1.17
1416504_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	1.34	0.21	1.05	0.919	1.15	0.635	2.16	0.246	1.42
1424337_at	Snx15	sorting nexin 15	1.12	0.205	1.18	0.236	1.24	0.267	1.75	0.331	1.32
1451340_at	Arid5a	AT rich interactive domain 5A (Mrf1 like)	1.2	0.468	1.01	0.98	1.33	0.335	1.12	0.608	1.16
1426916_at	Scrn3	secernin 3	1.35	0.041	1.05	0.217	1.15	0.595	4.04	0.22	1.9
1426123_a_at	Rrbp1	ribosome binding protein 1	1.13	0.251	1.1	0.508	1.31	0.112	1.26	0.045	1.2
1438040_a_at	Hsp90b1	heat shock protein 90kDa beta (Grp94), member 1	1.18	0.376	1.12	0.717	1.24	0.53	1.03	0.916	1.14
1448138_at	Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	1.41	0.358	1.01	0.963	1.13	0.645	1.97	0.094	1.38
1459665_s_at	Mrvi1	MRV integration site 1	1.05	0.462	1.13	0.672	1.37	0.104	1.52	0.437	1.27
1449144_at	Gna11	guanine nucleotide binding protein, alpha 11	1.28	0.522	1.04	0.818	1.23	0.392	1.34	0.288	1.22
1423421_at	Ankrd49	ankyrin repeat domain 49	1.18	0.129	1.17	0.575	1.19	0.486	1.16	0.569	1.18
1427240_at	Dock6 /// LOC6700	dedicator of cytokinesis 6 /// similar to Dedicator of cytokinesis protein 6	1.12	0.457	1.32	0.217	1.11	0.719	1.1	0.747	1.16
1426310_at	Zdhhc5	zinc finger, DHHC domain containing 5	1.18	0.564	1.01	0.947	1.36	0.211	1.99	0.21	1.38
1431038_at	Rassf4	Ras association (RalGDS/AF-6) domain family 4	1.28	0.197	1	0.998	1.27	0.277	1.1	0.437	1.16
1417789_at	Ccl11	small chemokine (C-C motif) ligand 11	1.51	0.364	1.04	0.877	1	0.995	3.07	0.098	1.65
1451257_at	Acsl6	acyl-CoA synthetase long-chain family member 6	1.06	0.606	1.22	0.61	1.26	0.595	3.89	0.166	1.86
1429522_at	Ankrd42	ankyrin repeat domain 42	1.01	0.976	1.44	0.436	1.1	0.115	1.3	0.714	1.21
1436207_at	Tcf3	transcription factor 3	1.27	0.511	1	0.988	1.28	0.3	1.18	0.801	1.18
1451888_a_at	Odz4	odd Oz/ten-m homolog 4 (Drosophila)	1.17	0.607	1.23	0.662	1.15	0.328	1.53	0.42	1.27
1437138_at	Foxm1	forkhead box M1	1.11	0.829	1.24	0.676	1.2	0.747	1.45	0.517	1.25
1450629_at	Lima1	LIM domain and actin binding 1	1.22	0.014	1.31	0.037	1.02	0.908	1.11	0.75	1.17
1439194_at	C030048H21Rik	RIKEN cDNA C030048H21 gene	1.39	0.577	1.06	0.859	1.11	0.354	1.42	0.61	1.24
1448054_at	Ing4	Inhibitor of growth family, member 4	1.09	0.902	1.07	0.896	1.39	0.512	1.96	0.151	1.38
1431922_at	Isx	intestine specific homeobox	1.05	0.958	1.45	0.507	1.06	0.892	1.23	0.618	1.2

1417514_at	Ssx2ip	synovial sarcoma, X breakpoint 2 interacting protein	1.42	0.345	1.07	0.919	1.07	0.88	17.28	0.217	5.21
1418705_at	Crx	cone-rod homeobox containing gene	1.2	0.816	1.1	0.834	1.26	0.551	1.3	0.66	1.22
1420959_at	Asph	aspartate-beta-hydroxylase	1.06	0.688	1.18	0.49	1.31	0.301	1.79	0.226	1.34
1435727_s_at	Lima1	LIM domain and actin binding 1	1.14	0.213	1.17	0.151	1.25	0.132	1.09	0.832	1.16
1450134_at	Loxl4	lysyl oxidase-like 4	1.27	0.796	1.05	0.936	1.24	0.691	1.11	0.557	1.17
1419678_at	Lats2	large tumor suppressor 2	1.01	0.945	1.09	0.553	1.45	0.164	1.1	0.73	1.17
1439573_at	Rtn4rl2	reticulon 4 receptor-like 2	1.23	0.345	1.16	0.467	1.18	0.655	1.02	0.93	1.15
1418600_at	Klf1	Kruppel-like factor 1 (erythroid)	1.09	0.812	1.3	0.486	1.18	0.733	7.2	0.127	2.69
1453497_a_at	Piga	phosphatidylinositol glycan anchor biosynthesis, class A	1.39	0.075	1.13	0.666	1.05	0.916	2.45	0.311	1.5
1433662_s_at	Timp2	tissue inhibitor of metalloproteinase 2	1.33	0.319	1.23	0.201	1.01	0.974	1.14	0.682	1.18
1416311_s_at	Tuba3 /// Tuba7 ///	tubulin, alpha 3 /// tubulin, alpha 7 /// similar to tubulin, alpha 1	1.08	0.86	1.04	0.945	1.45	0.011	2.09	0.324	1.41
1416308_at	Ugdh	UDP-glucose dehydrogenase	1.19	0.211	1.29	0.071	1.09	0.338	1.07	0.422	1.16
1434157_at	Txlna	taxilin alpha	1.2	0.302	1.01	0.988	1.36	0.132	1.25	0.551	1.21
1420397_a_at	Spen	SPEN homolog, transcriptional regulator (Drosophila)	1.05	0.805	1.05	0.819	1.47	0.027	1.8	0.05	1.34
1450354_a_at	Ptdss2	phosphatidylserine synthase 2	1.15	0.679	1.31	0.337	1.11	0.482	7.95	0.193	2.88
1423695_at	Edem2	ER degradation enhancer, mannosidase alpha-like 2	1.08	0.725	1.08	0.614	1.41	0.088	1.27	0.503	1.21
1430440_at	4930442J19Rik	RIKEN cDNA 4930442J19 gene	1.05	0.958	1.49	0.473	1.03	0.913	1.1	0.719	1.17
1435100_at	A130042E20Rik	RIKEN cDNA A130042E20 gene	1.28	0.527	1.04	0.923	1.24	0.408	1.21	0.015	1.2
1446824_at	Pgm1	Phosphoglucomutase 1	1.27	0.729	1.12	0.777	1.18	0.645	2.04	0.085	1.4
1451619_at	Golph3l	golgi phosphoprotein 3-like	1.07	0.849	1.21	0.501	1.29	0.522	1.74	0.382	1.33
1424906_at	Pqlc3	PQ loop repeat containing	1.04	0.869	1.23	0.209	1.3	0.057	1.21	0.111	1.19
1437340_x_at	Gkn1	gastrokine 1	1.04	0.955	1.36	0.342	1.17	0.556	1.36	0.629	1.23
1417115_at	Map3k12	mitogen activated protein kinase kinase kinase 12	1.21	0.174	1.2	0.487	1.16	0.454	1.37	0.319	1.24
1445670_at	---	---	1.28	0.533	1.07	0.678	1.23	0.375	2.48	0.022	1.51
1448127_at	Rrm1	ribonucleotide reductase M1	1.12	0.524	1.09	0.723	1.37	0.424	3.91	0.242	1.87
1426710_at	Calm3	calmodulin 3	1.18	0.488	1.23	0.311	1.16	0.39	1.73	0.066	1.33
1451503_at	Nol3	nucleolar protein 3 (apoptosis repressor with CARD domain)	1.11	0.391	1.37	0.457	1.1	0.541	1.39	0.153	1.24
1458532_at	Mtr	5-methyltetrahydrofolate-homocysteine methyltransferase	1.12	0.78	1.05	0.931	1.4	0.315	1.15	0.694	1.18
1450384_at	Bace1	beta-site APP cleaving enzyme 1	1.01	0.96	1.05	0.886	1.52	0.349	1.24	0.689	1.21
1427841_at	Krt14 /// Krt17	keratin 14 /// keratin 17	1.07	0.887	1.16	0.53	1.35	0.651	1.05	0.88	1.16
1450288_at	Cdh6	cadherin 6	1.44	0.474	1.09	0.617	1.05	0.925	1.02	0.974	1.15
1432765_at	C030007D22Rik	RIKEN cDNA C030007D22 gene	1.28	0.78	1.23	0.592	1.07	0.834	1.23	0.342	1.2
1417131_at	Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)	1.1	0.073	1.1	0.733	1.38	0.153	1.58	0.351	1.29
1456407_a_at	Tlk1	tousled-like kinase 1	1.27	0.141	1.19	0.277	1.12	0.629	1.7	0.178	1.32
1420629_a_at	Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	1.15	0.622	1.02	0.938	1.42	0.104	1.11	0.813	1.17
1428260_at	Spg3a	spastic paraplegia 3A homolog (human)	1.05	0.717	1.21	0.265	1.33	0.081	2.02	0.212	1.4
1429999_at	4933403M19Rik	RIKEN cDNA 4933403M19 gene	1.26	0.405	1.03	0.943	1.31	0.293	1.25	0.501	1.21
1427592_at	Pcdh7	protocadherin 7	1.04	0.914	1.31	0.516	1.24	0.192	1.05	0.864	1.16
1450074_at	Kif3b	kinesin family member 3B	1.04	0.849	1.16	0.399	1.39	0.258	1.01	0.958	1.15
1425668_a_at	St3gal4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	1.16	0.572	1.23	0.319	1.2	0.423	2.62	0.206	1.55
1435828_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	1.18	0.139	1.21	0.021	1.21	0.539	1.31	0.56	1.23
1456348_x_at	Paqr5	progestin and adipoQ receptor family member V	1.14	0.713	1.31	0.243	1.14	0.618	1.25	0.385	1.21
1450332_s_at	Fmo5	flavin containing monooxygenase 5	1.31	0.062	1.1	0.529	1.2	0.091	1.25	0.375	1.21
1431187_s_at	Dlg5	discs, large homolog 5 (Drosophila)	1.03	0.958	1.36	0.531	1.21	0.701	2.13	0.401	1.43
1426090_a_at	Fert2	fer (fms/fps related) protein kinase, testis specific 2	1.32	0.614	1.15	0.797	1.13	0.691	2.42	0.028	1.51
1429244_at	2610524H06Rik	RIKEN cDNA 2610524H06 gene	1.2	0.326	1.27	0.345	1.13	0.633	1.05	0.853	1.16
1425349_a_at	Myef2	myelin basic protein expression factor 2, repressor	1.08	0.167	1.31	0.349	1.21	0.677	2.31	0.173	1.48
1418591_at	Dnaja4	DnaJ (Hsp40) homolog, subfamily A, member 4	1.26	0.145	1.16	0.612	1.18	0.694	4.37	0.228	1.99
1429227_x_at	Nap1l1	nucleosome assembly protein 1-like 1	1.12	0.005	1.05	0.624	1.43	0.239	1.1	0.247	1.17
1437478_s_at	Efhd2	EF hand domain containing 2	1.4	0.064	1.06	0.687	1.15	0.2	1	0.986	1.15
1445437_at	2310015A05Rik	RIKEN cDNA 2310015A05 gene	1.42	0.571	1.18	0.461	1	0.994	2.41	0.125	1.5
1436246_at	---	Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:63	1.29	0.508	1.31	0.284	1	0.992	2.64	0.062	1.56
1427671_a_at	Fmn1	formin 1	1.08	0.869	1.51	0.433	1.01	0.98	1.14	0.752	1.18

1418154_at	BC004022	cDNA sequence BC004022	1.04	0.698	1.02	0.758	1.54	0.081	1.16	0.529	1.19
1419449_a_at	Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	1.22	0.141	1.17	0.061	1.22	0.163	1.04	0.738	1.16
1435751_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	1.25	0.207	1.31	0.078	1.05	0.842	1.1	0.607	1.18
1431474_at	4833414L08Rik	RIKEN cDNA 4833414L08 gene	1.33	0.595	1.02	0.956	1.26	0.431	1	0.997	1.15
1436614_at	AI843639	expressed sequence AI843639	1.05	0.768	1.2	0.431	1.36	0.388	3.72	0.15	1.83
1436833_x_at	Ttll1	tubulin tyrosine ligase-like 1	1.17	0.21	1.3	0.158	1.14	0.242	1.18	0.12	1.2
1436160_at	Krt26	keratin 26	1.1	0.839	1.37	0.462	1.15	0.688	2.68	0.328	1.57
1421642_a_at	Cysltr2	cysteinyl leukotriene receptor 2	1.23	0.747	1.35	0.557	1.02	0.921	1.39	0.071	1.25
1423589_at	Arpc4	actin related protein 2/3 complex, subunit 4	1.28	0.319	1.22	0.127	1.12	0.563	1.01	0.969	1.15
1423082_at	Derl1	Der1-like domain family, member 1	1.07	0.763	1.05	0.707	1.48	0.197	1.45	0.077	1.27
1442378_x_at	---	In vitro fertilized eggs cDNA, RIKEN full-length enriched library, clone:7420405G1	1.23	0.079	1.26	0.184	1.12	0.588	1.14	0.694	1.19
1429204_at	Camk2n2	calcium/calmodulin-dependent protein kinase II inhibitor 2	1.06	0.59	1.34	0.277	1.21	0.318	1.92	0.038	1.38
1416214_at	Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	1.04	0.8	1.43	0.028	1.15	0.268	2.26	0.157	1.47
1454142_a_at	Pwp1	PWP1 homolog (S. cerevisiae)	1.01	0.95	1.1	0.764	1.51	0.102	1.02	0.958	1.16
1421087_at	Per3	period homolog 3 (Drosophila)	1.04	0.962	1.43	0.687	1.14	0.835	1.15	0.713	1.19
1417976_at	Ada	adenosine deaminase	1.34	0.077	1.27	0.393	1.01	0.984	1.39	0.025	1.25
1438402_at	9630050M13Rik	RIKEN cDNA 9630050M13 gene	1.08	0.439	1.22	0.408	1.31	0.303	1.43	0.202	1.26
1420953_at	Add1	adducin 1 (alpha)	1.1	0.856	1.07	0.784	1.45	0.189	1.31	0.513	1.23
1435463_s_at	Myo1d	myosin ID	1.07	0.71	1.15	0.352	1.4	0.013	2.83	0.15	1.61
1443731_at	---	Transcribed locus	1.28	0.67	1.08	0.883	1.26	0.64	1.31	0.45	1.23
1423618_at	Bin1	bridging integrator 1	1.14	0.572	1.42	0.137	1.06	0.709	1.03	0.953	1.16
1453985_at	0610007P08Rik	RIKEN cDNA 0610007P08 gene	1.48	0.227	1.02	0.965	1.12	0.558	1.21	0.08	1.21
1430873_at	---	---	1.34	0.599	1.15	0.172	1.13	0.591	1.13	0.492	1.19
1428544_at	0610007L01Rik	RIKEN cDNA 0610007L01 gene	1.22	0.211	1.17	0.376	1.23	0.341	1.9	0.007	1.38
1427110_at	Raver1	ribonucleoprotein, PTB-binding 1	1.1	0.766	1.11	0.604	1.4	0.137	1.13	0.609	1.19
1422885_at	Snrpd3	small nuclear ribonucleoprotein D3	1.13	0.632	1.34	0.111	1.14	0.572	1	0.994	1.16
1450287_at	Npas3	neuronal PAS domain protein 3	1.16	0.833	1.26	0.546	1.21	0.562	1.47	0.396	1.27
1416916_at	Elf3	E74-like factor 3	1.05	0.582	1.27	0.336	1.31	0.168	1.61	0.24	1.31
1431143_x_at	Amid	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death	1.42	0.128	1.03	0.885	1.17	0.666	1.31	0.135	1.24
1427844_a_at	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	1.23	0.585	1.18	0.53	1.22	0.469	1.54	0.138	1.29
1457330_at	Gipc2	GIPC PDZ domain containing family, member 2	1.1	0.377	1.24	0.547	1.28	0.638	1.63	0.373	1.32
1455466_at	Gpr133 /// LOC669	G protein-coupled receptor 133 /// similar to G protein-coupled receptor 133	1.51	0.744	1.02	0.946	1.11	0.811	1.49	0.3	1.28
1460444_at	Arrb1	arrestin, beta 1	1.18	0.206	1.43	0.026	1.01	0.949	2.98	0.2	1.65
1453315_at	Wibg	within bgcn homolog (Drosophila)	1.2	0.592	1.13	0.609	1.3	0.318	1.77	0.203	1.35
1450171_x_at	Gzme	granzyme E	1.11	0.838	1.25	0.661	1.27	0.626	1.7	0.181	1.33
1416955_at	Slc25a10	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member	1.13	0.764	1.07	0.804	1.43	0.366	1.33	0.455	1.24
1451616_at	Psg-ps1	pregnancy specific glycoprotein pseudogene 1	1.44	0.533	1.13	0.805	1.06	0.871	1.04	0.949	1.17
1451918_a_at	Loh12cr1	loss of heterozygosity, 12, chromosomal region 1 homolog (human)	1.14	0.678	1.01	0.883	1.48	0.133	1.17	0.389	1.2
1439479_at	Lct	lactase	1.06	0.826	1.33	0.674	1.25	0.614	1.32	0.456	1.24
1431082_a_at	Rabl3	RAB, member of RAS oncogene family-like 3	1.36	0.471	1.06	0.814	1.21	0.384	1.53	0.259	1.29
1425131_at	Ptpn5	protein tyrosine phosphatase, non-receptor type 5	1.08	0.671	1.41	0.167	1.15	0.408	1.35	0.135	1.25
1452716_at	5730469M10Rik	RIKEN cDNA 5730469M10 gene	1.02	0.797	1.06	0.513	1.56	0.131	3.23	0.238	1.72
1441258_at	AF529169	cDNA sequence AF529169	1.33	0.653	1.15	0.819	1.15	0.779	1.44	0.01	1.27
1417959_at	Pdlim7	PDZ and LIM domain 7	1.14	0.654	1.01	0.981	1.49	0.271	1.12	0.68	1.19
1450991_at	Dnajb7	DnaJ (Hsp40) homolog, subfamily B, member 7	1.12	0.697	1.45	0.28	1.07	0.869	1.63	0.34	1.32
1427324_at	BC022593	cDNA sequence BC022593	1.06	0.678	1.02	0.918	1.55	0.309	3.04	0.258	1.67
1454462_at	6430605C03Rik	RIKEN cDNA 6430605C03 gene	1.05	0.949	1.53	0.329	1.07	0.871	1.45	0.059	1.27
1455114_at	Ung2	uracil DNA glycosylase 2	1.05	0.844	1.57	0.15	1.02	0.913	1.36	0.66	1.25
1453619_at	Efcab1	EF hand calcium binding domain 1	1.14	0.617	1.3	0.47	1.19	0.15	1.03	0.912	1.17
1452258_at	Phf20	PHD finger protein 20	1.11	0.519	1.48	0.085	1.06	0.815	1.09	0.403	1.18
1417127_at	Msx1	homeo box, msh-like 1	1.01	0.992	1.57	0.357	1.07	0.873	1.13	0.786	1.19
1447758_x_at	Myst4	MYST histone acetyltransferase monocytic leukemia 4	1.36	0.358	1.27	0.76	1.02	0.965	1.13	0.865	1.19
1457915_at	4833442J19Rik	RIKEN cDNA 4833442J19 gene	1.16	0.334	1.43	0.22	1.06	0.716	1.26	0.292	1.23

1448433_a_at	Pcolce	procollagen C-endopeptidase enhancer protein	1.1	0.009	1.45	0.186	1.09	0.759	1.02	0.933	1.17
1436625_at	Fcgr1	Fc receptor, IgG, high affinity I	1.05	0.38	1.27	0.172	1.32	0.329	1.24	0.145	1.22
1416410_at	Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	1.02	0.898	1.29	0.11	1.33	0.225	1.03	0.931	1.17
1431400_a_at	Gas7	growth arrest specific 7	1.48	0.078	1.08	0.88	1.08	0.862	1.05	0.912	1.17
1460466_at	1700047I17Rik /// L	RIKEN cDNA 1700047I17 gene /// similar to signal recognition particle 54	1.15	0.809	1.19	0.024	1.3	0.604	1.09	0.867	1.18
1424133_at	Tmem98	transmembrane protein 98	1.26	0.22	1.16	0.275	1.23	0.137	1.16	0.405	1.2
1420899_at	Rab18	RAB18, member RAS oncogene family	1.03	0.891	1.07	0.823	1.54	0.339	1.39	0.567	1.26
1451168_a_at	Arhgdia	Rho GDP dissociation inhibitor (GDI) alpha	1.03	0.907	1.28	0.03	1.34	0.044	1.03	0.876	1.17
1449625_at	---	Transcribed locus, weakly similar to NP_570953.1 CAMP [Mus musculus]	1.07	0.79	1.44	0.347	1.14	0.588	1.6	0.286	1.31
1452490_a_at	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	1.03	0.892	1.05	0.814	1.56	0.262	2.5	0.151	1.54
1421861_at	Clstn1	calsyntenin 1	1.17	0.084	1.45	0.143	1.03	0.881	1.68	0.003	1.33
1435905_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	1.11	0.48	1.22	0.364	1.32	0.196	1.03	0.683	1.17
1449675_at	Ccnb1-rs1 /// LOC2	cyclin B1, related sequence 1 /// similar to G2/mitotic-specific cyclin B1 /// cyclin B	1.06	0.924	1.16	0.765	1.43	0.545	7.08	0.183	2.68
1423221_at	Tubb4	tubulin, beta 4	1.19	0.668	1.38	0.356	1.08	0.726	1.55	0.424	1.3
1459596_at	---	---	1.07	0.856	1.58	0.466	1.01	0.866	1.08	0.784	1.18
1421712_at	Sele	selectin, endothelial cell	1.22	0.409	1.1	0.854	1.33	0.244	2.7	0.045	1.59
1416903_at	Nucb1	nucleobindin 1	1.19	0.463	1.06	0.546	1.4	0.016	2.11	0.026	1.44
1425139_at	Sesn2	sestrin 2	1.19	0.545	1.38	0.216	1.08	0.69	1.54	0.185	1.3
1425649_at	Slc39a14	solute carrier family 39 (zinc transporter), member 14	1.4	0.085	1.2	0.688	1.05	0.872	1.76	0.024	1.35
1445762_at	Spint1	Serine protease inhibitor, Kunitz type 1	1.15	0.823	1.41	0.573	1.09	0.633	1.2	0.513	1.21
1452110_at	Mtrr	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	1.09	0.582	1.02	0.941	1.54	0.124	1.64	0.141	1.32
1419644_at	Cstf2	cleavage stimulation factor, 3' pre-RNA subunit 2	1.04	0.359	1.21	0.498	1.41	0.078	1.07	0.816	1.18
1436104_a_at	2310015A05Rik	RIKEN cDNA 2310015A05 gene	1.06	0.868	1.33	0.585	1.27	0.216	2.38	0.106	1.51
1420886_a_at	Xbp1	X-box binding protein 1	1.2	0.083	1.31	0.379	1.15	0.526	1.38	0.21	1.26
1428816_a_at	Gata2	GATA binding protein 2	1.04	0.582	1.53	0.379	1.09	0.589	1.02	0.965	1.17
1453971_at	2610015P09Rik	RIKEN cDNA 2610015P09 gene	1.04	0.938	1.13	0.733	1.5	0.347	1.74	0.354	1.35
1432583_at	2900042E19Rik	RIKEN cDNA 2900042E19 gene	1.18	0.625	1.22	0.683	1.26	0.223	1.26	0.203	1.23
1458357_x_at	Ptov1	Prostate tumor over expressed gene 1	1.07	0.898	1.08	0.887	1.52	0.422	1	0.992	1.17
1418810_at	Crhr1	corticotropin releasing hormone receptor 1	1.07	0.939	1.1	0.801	1.5	0.297	1.06	0.626	1.18
1457625_s_at	Cdkl2	cyclin-dependent kinase-like 2 (CDC2-related kinase)	1.28	0.549	1.07	0.877	1.32	0.488	1.52	0.448	1.3
1445553_at	Ric3	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	1.46	0.235	1.11	0.65	1.1	0.676	1.2	0.223	1.22
1443944_at	C530005A16Rik	RIKEN cDNA C530005A16 gene	1.05	0.935	1.5	0.517	1.11	0.714	1.4	0.5	1.27
1416573_at	Pofut2	protein O-fucosyltransferase 2	1.2	0.697	1.22	0.629	1.25	0.277	1.11	0.751	1.19
1426229_s_at	Kras	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	1	0.999	1.16	0.713	1.51	0.467	1.05	0.932	1.18
1426427_at	Ttll1	tubulin tyrosine ligase-like 1	1.05	0.714	1.18	0.552	1.44	0.146	1.23	0.443	1.22
1452244_at	6330406I15Rik	RIKEN cDNA 6330406I15 gene	1.2	0.111	1.34	0.59	1.13	0.717	2.35	0.112	1.51
1418855_at	1110008K04Rik	RIKEN cDNA 1110008K04 gene	1.38	0.474	1.19	0.782	1.1	0.842	1.96	0.442	1.41
1446667_at	---	---	1.11	0.9	1.32	0.461	1.24	0.53	1.06	0.855	1.18
1442694_at	---	---	1.46	0.053	1.2	0.735	1.01	0.712	1.22	0.468	1.22
1457684_at	1700037H04Rik	RIKEN cDNA 1700037H04 gene	1.05	0.909	1.38	0.399	1.24	0.45	1	0.993	1.17
1421338_at	Elf4 /// LOC676319	E74-like factor 4 (ets domain transcription factor) /// hypothetical protein LOC676	1.15	0.43	1.4	0.568	1.12	0.595	1.16	0.625	1.21
1421747_at	Esrrg	estrogen-related receptor gamma	1.05	0.175	1.61	0.212	1.02	0.921	1.31	0.57	1.25
1449107_at	Nudt4	nudix (nucleoside diphosphate linked moiety X)-type motif 4	1.11	0.269	1.03	0.84	1.53	0.247	3.86	0.243	1.88
1445250_at	Hephl1	Hephaestin-like 1	1.17	0.193	1.44	0.559	1.07	0.9	1.13	0.846	1.2
1424917_a_at	Wipi1	WD repeat domain, phosphoinositide interacting 1	1.1	0.618	1.24	0.584	1.34	0.409	3.63	0.227	1.83
1419826_at	Kif17	kinesin family member 17	1.12	0.19	1.1	0.741	1.45	0.506	1.55	0.39	1.31
1429392_at	Wdr40a	WD repeat domain 40A	1.09	0.526	1.15	0.504	1.44	0.152	2.44	0.248	1.53
1440053_at	Ccbe1	Collagen and calcium binding EGF domains 1	1.34	0.239	1.19	0.575	1.16	0.589	1.08	0.72	1.19
1454962_at	Spire1	spire homolog 1 (Drosophila)	1.32	0.265	1	1	1.36	0.28	3.97	0.178	1.91
1443122_at	---	15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930037A	1.33	0.434	1.11	0.786	1.23	0.572	1.06	0.78	1.19
1423627_at	Nqo1	NAD(P)H dehydrogenase, quinone 1	1.37	0.119	1.28	0.245	1.03	0.707	2.86	0.125	1.64
1418389_at	2810453I06Rik	RIKEN cDNA 2810453I06 gene	1.29	0.329	1.03	0.784	1.37	0.585	1.99	0.399	1.42
1424874_a_at	Ptbp1	polypyrimidine tract binding protein 1	1.23	0.63	1.17	0.408	1.29	0.325	1.21	0.435	1.22

1449219_at	Fads3	fatty acid desaturase 3	1.18	0.593	1.24	0.545	1.26	0.56	3.38	0.311	1.77
1425351_at	Srxn1	sulfiredoxin 1 homolog (S. cerevisiae)	1.07	0.849	1.06	0.866	1.56	0.176	2.36	0.257	1.51
1451329_at	Nudt22	nudix (nucleoside diphosphate linked moiety X)-type motif 22	1.03	0.843	1.37	0.328	1.28	0.041	1.18	0.249	1.22
1429970_at	Spaca3	sperm acrosome associated 3	1.21	0.676	1.35	0.493	1.12	0.813	1.53	0.272	1.3
1433707_at	Gabra4	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	1.4	0.277	1.17	0.745	1.12	0.47	2.02	0.061	1.43
1417078_at	Lgals2	lectin, galactose-binding, soluble 2	1.16	0.797	1.19	0.553	1.34	0.554	1.34	0.678	1.26
1423573_at	Srd5a2l	steroid 5 alpha-reductase 2-like	1.04	0.504	1.19	0.204	1.46	0.037	1.14	0.501	1.21
1431748_a_at	Rffl	ring finger and FYVE like domain containing protein	1.08	0.863	1.13	0.736	1.47	0.544	7.85	0.273	2.89
1429315_at	Syt11	synaptotagmin XI	1.11	0.599	1.56	0.308	1.02	0.938	1.15	0.605	1.21
1438434_at	Arhgap11a	Rho GTPase activating protein 11A	1.13	0.763	1.35	0.373	1.21	0.6	2.12	0.17	1.45
1418969_at	Skp2	S-phase kinase-associated protein 2 (p45)	1.2	0.317	1.37	0.27	1.12	0.708	2.33	0.003	1.51
1452078_a_at	Slc11a2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member	1.12	0.514	1.41	0.38	1.16	0.261	2.65	0.228	1.58
1435663_at	Esr1	estrogen receptor 1 (alpha)	1.05	0.923	1.4	0.072	1.24	0.529	1.03	0.934	1.18
1420548_a_at	2310008H09Rik	RIKEN cDNA 2310008H09 gene	1.38	0.045	1.1	0.647	1.21	0.455	1.1	0.549	1.2
1437772_s_at	Fuca1	fucosidase, alpha-L- 1, tissue	1.31	0.449	1.04	0.868	1.35	0.286	1.09	0.656	1.2
1441065_at	---	---	1.02	0.933	1.21	0.582	1.46	0.436	1.41	0.309	1.28
1453622_s_at	Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog (Drosoph	1.29	0.135	1.24	0.415	1.16	0.393	2.76	0.207	1.61
1453269_at	Unc5b	unc-5 homolog B (C. elegans)	1.12	0.64	1.31	0.588	1.27	0.36	1.12	0.559	1.2
1452461_a_at	Gnptab	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	1.12	0.68	1.04	0.904	1.53	0.121	1.04	0.911	1.18
1427998_at	2600001B17Rik	RIKEN cDNA 2600001B17 gene	1.15	0.42	1.22	0.286	1.33	0.359	1.41	0.199	1.28
1420857_at	Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	1.15	0.632	1.1	0.754	1.45	0.14	1.93	0.344	1.41
1444655_at	---	---	1.28	0.64	1.23	0.602	1.19	0.624	1.96	0.299	1.41
1454721_at	1110018G07Rik	RIKEN cDNA 1110018G07 gene	1.23	0.345	1.1	0.781	1.36	0.495	2.04	0.243	1.44
1421193_a_at	Pbx3	pre B-cell leukemia transcription factor 3	1.14	0.812	1.2	0.597	1.36	0.439	2.21	0.289	1.48
1456970_at	Cdh7	Cadherin 7, type 2	1.31	0.49	1.29	0.688	1.1	0.707	1.28	0.409	1.25
1426998_at	Zfand3	zinc finger, AN1-type domain 3	1.22	0.438	1.26	0.28	1.22	0.399	1.09	0.547	1.2
1429352_at	Mocos	molybdenum cofactor sulfurase	1.24	0.131	1.01	0.899	1.46	0.015	1.45	0.066	1.29
1421308_at	Car13	carbonic anhydrase 13	1.05	0.709	1.6	0.369	1.04	0.688	1.79	0.062	1.37
1453092_at	2300002G24Rik	RIKEN cDNA 2300002G24 gene	1.08	0.585	1.57	0.35	1.06	0.865	1.84	0.18	1.38
1424268_at	Smox	spermine oxidase	1.15	0.082	1.09	0.612	1.46	0.25	4.31	0.196	2
1448404_at	Scamp2	secretory carrier membrane protein 2	1.26	0.497	1.13	0.445	1.31	0.285	1.06	0.813	1.19
1460302_at	Thbs1 /// LOC6404	thrombospondin 1 /// similar to thrombospondin 1	1.04	0.741	1.39	0.445	1.28	0.685	2.64	0.357	1.59
1416676_at	Kng1	kininogen 1	1.23	0.018	1	0.969	1.47	0.522	2.67	0.398	1.59
1452103_at	2600005N12Rik	RIKEN cDNA 2600005N12 gene	1.34	0.48	1.01	0.983	1.36	0.297	1.2	0.556	1.23
1450914_at	Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	1.26	0.346	1.33	0.025	1.11	0.701	1.16	0.466	1.22
1450246_at	Fut2	fucosyltransferase 2	1.54	0.23	1.1	0.769	1.06	0.912	1.17	0.194	1.22
1424203_at	Ncln	nicalin homolog (zebrafish)	1.16	0.648	1.05	0.675	1.5	0.046	1.16	0.483	1.22
1425093_at	P2rx3	purinergic receptor P2X, ligand-gated ion channel, 3	1.32	0.421	1.36	0.53	1.03	0.926	1.23	0.432	1.23
1420868_s_at	Tmed2	transmembrane emp24 domain trafficking protein 2	1.21	0.508	1.25	0.36	1.25	0.464	2.13	0.029	1.46
1459867_x_at	Unc45a	unc-45 homolog A (C. elegans)	1.21	0.508	1.19	0.56	1.31	0.25	1.14	0.494	1.21
1450199_a_at	Stab1	stabilin 1	1.52	0.06	1.06	0.446	1.12	0.643	1.33	0	1.26
1455587_at	BC030183	cDNA sequence BC030183	1.19	0.157	1.14	0.358	1.38	0.45	1.42	0.226	1.28
1433696_at	D17Ertd441e	DNA segment, Chr 17, ERATO Doi 441, expressed	1.16	0.645	1.08	0.627	1.47	0.17	1.33	0.211	1.26
1440339_at	4833416E15Rik	RIKEN cDNA 4833416E15 gene	1.33	0.08	1.16	0.444	1.22	0.366	1.33	0.558	1.26
1418890_a_at	Rab3d	RAB3D, member RAS oncogene family	1.15	0.086	1.04	0.66	1.52	0.241	1.53	0.031	1.31
1449893_a_at	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1	1.28	0.437	1.27	0.427	1.16	0.623	1.01	0.975	1.18
1427071_at	Fbxo42	F-box protein 42	1.07	0.784	1.09	0.287	1.55	0.114	1.91	0.195	1.41
1445466_at	Map6d1	MAP6 domain containing 1	1.16	0.651	1.52	0.281	1.03	0.851	1.2	0.735	1.23
1420505_a_at	Stxbp1	syntaxin binding protein 1	1.2	0.146	1.17	0.416	1.34	0.256	1.38	0.039	1.27
1437028_at	Sftpb	surfactant associated protein B	1.41	0.382	1.22	0.792	1.09	0.596	1.03	0.892	1.19
1452952_at	9030418K01Rik	RIKEN cDNA 9030418K01 gene	1.07	0.321	1.34	0.305	1.3	0.064	1.39	0.397	1.28
1434799_x_at	Aldoa	aldolase 1, A isoform	1.09	0.325	1.16	0.389	1.47	0.032	1.01	0.951	1.18
1444066_at	Gapvd1	GTPase activating protein and VPS9 domains 1	1.18	0.476	1.28	0.575	1.25	0.591	1.53	0.453	1.31

1454547_at	2310045N14Rik	RIKEN cDNA 2310045N14 gene	1.35	0.492	1.34	0.274	1.03	0.934	1.04	0.907	1.19
1423554_at	Ggcx	gamma-glutamyl carboxylase	1.4	0.017	1.13	0.436	1.19	0.272	1.37	0.433	1.27
1422423_at	Magea7	melanoma antigen, family A, 7	1.07	0.896	1.16	0.729	1.49	0.407	2.39	0.031	1.53
1424619_at	Sf3b4 /// LOC63441	splicing factor 3b, subunit 4 /// similar to splicing factor 3b, subunit 4 (predicted) //	1.14	0.598	1.12	0.097	1.46	0.094	1.38	0.103	1.28
1445845_at	---	Transcribed locus	1.3	0.417	1.02	0.964	1.4	0.166	5.03	0.206	2.19
1437232_at	Bpil2	bactericidal/permeability-increasing protein-like 2	1.15	0.896	1.41	0.567	1.16	0.711	1.52	0.262	1.31
1450377_at	LOC640441	similar to thrombospondin 1	1.1	0.377	1.35	0.014	1.27	0.677	2.03	0.392	1.44
1422660_at	LOC671237	similar to Putative RNA-binding protein 3 (RNA-binding motif protein 3)	1.15	0.236	1.49	0.103	1.09	0.719	1.14	0.347	1.22
1456248_at	2310002A05Rik ///	RIKEN cDNA 2310002A05 gene /// hypothetical protein LOC630971	1.34	0.675	1.26	0.599	1.13	0.684	1.01	0.986	1.18
1456778_at	Nrp2	Neuropilin 2	1.24	0.255	1.39	0.068	1.1	0.725	1.13	0.638	1.22
1440251_s_at	Zfp64	zinc finger protein 64	1.16	0.793	1.07	0.836	1.49	0.557	1.05	0.594	1.2
1451109_a_at	Nedd4	neural precursor cell expressed, developmentally down-regulted gene 4	1.27	0.541	1.02	0.957	1.44	0.385	1.25	0.545	1.24
1418570_at	Ncstn	nicastrin	1.19	0.689	1.22	0.342	1.32	0.129	1.41	0.154	1.29
1438037_at	Herc5	hect domain and RLD 5	1.44	0.047	1.14	0.637	1.15	0.208	1.19	0.333	1.23
1424817_at	Spef1	sperm flagellar 1	1.29	0.149	1.34	0.413	1.1	0.477	1.36	0.469	1.27
1449020_at	Plscr3	phospholipid scramblase 3	1.09	0.632	1.5	0.02	1.15	0.381	1.55	0.144	1.32
1450769_s_at	Stard5	StAR-related lipid transfer (START) domain containing 5	1.06	0.747	1.01	0.907	1.66	0.152	1.18	0.621	1.23
1439154_at	Nup98	nucleoporin 98	1.01	0.959	1.37	0.284	1.36	0.017	1.02	0.911	1.19
1446998_at	Gprk5	G protein-coupled receptor kinase 5	1.63	0.513	1	0.995	1.1	0.835	1.37	0.432	1.28
1416933_at	Por	P450 (cytochrome) oxidoreductase	1.33	0.449	1.04	0.894	1.37	0.224	1.25	0.191	1.25
1439039_at	Tmem104	transmembrane protein 104	1.11	0.854	1.08	0.895	1.55	0.196	1.53	0.566	1.32
1454529_at	4930518C04Rik	RIKEN cDNA 4930518C04 gene	1.02	0.968	1.49	0.1	1.22	0.386	1.33	0.6	1.27
1429300_at	Ankrd9	ankyrin repeat domain 9	1.17	0.643	1.16	0.8	1.41	0.456	7.72	0.229	2.87
1437627_at	Rkhd1	ring finger (C3HC4 type) and KH domain containing 1	1.04	0.866	1.4	0.12	1.29	0.49	1.43	0.336	1.29
1445565_at	Hist1h1e	Histone 1, H1e	1.2	0.529	1.51	0.281	1.03	0.896	1.15	0.667	1.22
1437945_x_at	Nap1l1	nucleosome assembly protein 1-like 1	1.16	0.146	1.18	0.412	1.4	0.302	1.04	0.53	1.19
1447834_at	Copz1	Coatomer protein complex, subunit zeta 1	1.06	0.939	1.54	0.452	1.14	0.806	1.6	0.524	1.34
1455678_at	Sema4b	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and sh	1.05	0.707	1.17	0.335	1.53	0.213	1.28	0.286	1.26
1422152_at	Hmx1	H6 homeo box 1	1.03	0.875	1.7	0.15	1.01	0.936	1.38	0.223	1.28
1429843_at	Grrp1	glycine/arginine rich protein 1	1.56	0.049	1.08	0.929	1.1	0.427	1.12	0.437	1.22
1425730_at	Cacng6	calcium channel, voltage-dependent, gamma subunit 6	1.38	0.564	1.03	0.958	1.34	0.014	2.35	0.247	1.53
1426812_a_at	9130404D14Rik	RIKEN cDNA 9130404D14 gene	1.13	0.668	1.56	0.344	1.06	0.683	1.29	0.062	1.26
1424762_at	C1qtnf5 /// Mfrp	C1q and tumor necrosis factor related protein 5 /// membrane-type frizzled-relatec	1.54	0.015	1.15	0.243	1.06	0.657	1.59	0.262	1.34
1455691_at	Cyp21a1	cytochrome P450, family 21, subfamily a, polypeptide 1	1.16	0.75	1.03	0.94	1.56	0.318	1.67	0.268	1.36
1424031_at	Snx11	sorting nexin 11	1.31	0.331	1.3	0.267	1.14	0.321	1.16	0.059	1.23
1457347_at	Ryr1	ryanodine receptor 1, skeletal muscle	1.3	0.4	1.16	0.654	1.29	0.731	4.11	0	1.97
1453704_at	---	---	1.04	0.709	1.12	0.776	1.59	0.399	1.05	0.893	1.2
1459320_at	---	Transcribed locus	1.53	0.138	1.03	0.96	1.2	0.73	1.55	0.389	1.33
1427537_at	Eppk1	epiplakin 1	1.17	0.672	1.14	0.417	1.44	0.005	1.38	0.37	1.28
1442183_at	LOC236069	similar to carnitine deficiency-associated gene expressed in ventricle 3 isoform C	1.19	0.034	1.45	0.413	1.12	0.645	1.36	0.284	1.28
1451007_at	Cnnm2	cyclin M2	1.17	0.322	1.19	0.753	1.4	0.388	1.12	0.648	1.22
1450029_s_at	Itga9	integrin alpha 9	1.65	0.209	1.02	0.935	1.09	0.78	1.19	0.278	1.24
1421024_at	Agpat1	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransf	1.08	0.834	1.52	0.111	1.16	0.524	1.36	0.246	1.28
1460675_at	Igsf8	immunoglobulin superfamily, member 8	1.14	0.407	1.37	0.118	1.25	0.168	1.24	0.322	1.25
1437631_at	Kcnip4	Kv channel interacting protein 4	1.44	0.645	1.21	0.727	1.11	0.776	1	1	1.19
1458440_at	Specc1	spectrin domain with coiled-coils 1	1.08	0.815	1.56	0.352	1.13	0.485	3.73	0.241	1.87
1453760_at	Mier1	mesoderm induction early response 1 homolog (Xenopus laevis	1.42	0.492	1.02	0.967	1.33	0.543	2.43	0.219	1.55
1442877_at	---	---	1.03	0.905	1.71	0.101	1.03	0.901	1.2	0.518	1.24
1425911_a_at	Fgfr1	fibroblast growth factor receptor 1	1.34	0.52	1.36	0.257	1.07	0.774	1.34	0.33	1.28
1430055_at	1700080G18Rik	RIKEN cDNA 1700080G18 gene	1.03	0.965	1.04	0.961	1.7	0.01	1.04	0.881	1.2
1420878_a_at	Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta	1.11	0.765	1.09	0.678	1.56	0.261	1.16	0.571	1.23
1454733_at	Card4	caspase recruitment domain 4	1.13	0.165	1.31	0.125	1.33	0.201	1.16	0.796	1.23
1454495_at	4930432H08Rik	RIKEN cDNA 4930432H08 gene	1.07	0.922	1.37	0.573	1.32	0.695	1.04	0.954	1.2

1453972_x_at	Pparbp	peroxisome proliferator activated receptor binding protein	1.12	0.747	1.11	0.787	1.54	0.124	1.46	0.126	1.31
1418237_s_at	Col18a1	procollagen, type XVIII, alpha 1	1.34	0.414	1.04	0.524	1.39	0.093	1.29	0.017	1.26
1450939_at	Entpd1	ectonucleoside triphosphate diphosphohydrolase 1	1.15	0.562	1.03	0.88	1.59	0.068	1.01	0.975	1.19
1436334_at	Synj1	synaptojanin 1	1.23	0.481	1.2	0.288	1.35	0.087	1.62	0.098	1.35
1446944_at	D1Ertd84e	DNA segment, Chr 1, ERATO Doi 84, expressed	1.44	0.126	1.07	0.837	1.26	0.572	1.72	0.173	1.37
1427662_at	Svil	Supervillin	1.65	0.38	1.07	0.898	1.05	0.846	1.22	0.772	1.25
1438571_at	Bub1	Budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	1.22	0.527	1.5	0.297	1.05	0.608	2.45	0.297	1.55
1421499_a_at	Ptpn14	protein tyrosine phosphatase, non-receptor type 14	1.07	0.43	1.56	0.271	1.14	0.269	1.36	0.393	1.28
1446498_at	Il20ra	interleukin 20 receptor, alpha	1.25	0.773	1.01	0.984	1.52	0.237	1.28	0.405	1.26
1420761_at	Chrnd	cholinergic receptor, nicotinic, delta polypeptide	1.49	0.672	1.01	0.977	1.27	0.581	1.61	0.084	1.35
1443660_at	Nrg3	Neuregulin 3	1.68	0.62	1.05	0.838	1.04	0.913	1.33	0.675	1.28
1416847_s_at	Oas1d /// Oas1e	2'-5' oligoadenylate synthetase 1D /// 2'-5' oligoadenylate synthetase 1E	1.56	0.371	1.16	0.484	1.06	0.892	1.89	0.352	1.42
1422810_at	Zfp191	zinc finger protein 191	1.44	0.351	1.26	0.642	1.08	0.856	1.1	0.719	1.22
1449708_s_at	Chek1	checkpoint kinase 1 homolog (S. pombe)	1.05	0.181	1.2	0.771	1.52	0.37	2.47	0.21	1.56
1449230_at	Idua	iduronidase, alpha-L-	1.05	0.637	1.28	0.36	1.44	0.003	1.09	0.67	1.22
1415919_at	Npdc1	neural proliferation, differentiation and control gene 1	1.16	0.52	1.32	0.18	1.29	0.107	1.05	0.648	1.21
1422178_a_at	Rab17	RAB17, member RAS oncogene family	1.01	0.963	1.14	0.257	1.64	0.095	1.44	0.116	1.3
1426873_s_at	Jup	junction plakoglobin	1.13	0.656	1.42	0.066	1.22	0.1	1.51	0.021	1.32
1451355_at	Asah3l	N-acylsphingosine amidohydrolase 3-like	1.2	0.349	1.51	0.08	1.07	0.691	2.82	0.224	1.65
1420621_a_at	App	amyloid beta (A4) precursor protein	1.03	0.715	1.26	0.048	1.5	0.094	1.12	0.306	1.22
1426244_at	Mapre2	microtubule-associated protein, RP/EB family, member 2	1.04	0.7	1.37	0.017	1.37	0.199	1.26	0.297	1.26
1426066_a_at	Dtna	dystrobrevin alpha	1.4	0.679	1.24	0.499	1.13	0.721	1.15	0.682	1.23
1449344_s_at	2210409E12Rik	RIKEN cDNA 2210409E12 gene	1.08	0.828	1.64	0.098	1.06	0.871	1.61	0.04	1.35
1448932_at	Krt16	keratin 16	1.29	0.387	1.43	0.512	1.07	0.918	1.34	0.059	1.28
1451897_a_at	Nbr1	neighbor of Brca1 gene 1	1.24	0.365	1.05	0.865	1.48	0.317	1.46	0.328	1.31
1423420_at	Adrb1	adrenergic receptor, beta 1	1.05	0.767	1.63	0.14	1.1	0.479	1.14	0.575	1.23
1423686_a_at	Prr13	proline rich 13	1.17	0.183	1.15	0.16	1.46	0.14	1.1	0.543	1.22
1435872_at	---	Transcribed locus	1.16	0.721	1.12	0.606	1.5	0.267	1.88	0.231	1.42
1449135_at	Sox18	SRY-box containing gene 18	1.18	0.088	1.04	0.861	1.56	0.052	1.04	0.823	1.21
1444769_at	Tex9	Testis expressed gene 9	1.06	0.943	1.44	0.376	1.28	0.454	4.65	0.193	2.11
1416130_at	Prnp	prion protein	1.18	0.381	1.2	0.199	1.4	0.134	2.01	0.109	1.45
1425005_at	Klrc1 /// Klrc2	killer cell lectin-like receptor subfamily C, member 1 /// killer cell lectin-like recepto	1.49	0.44	1.26	0.574	1.04	0.931	1.89	0.505	1.42
1439349_at	Stno	strawberry notch homolog (Drosophila)	1.35	0.295	1.2	0.397	1.23	0.592	1.23	0.325	1.25
1416584_at	Man2b2	mannosidase 2, alpha B2	1.11	0.663	1.17	0.301	1.5	0.135	1.25	0.301	1.26
1448624_at	Cd2bp2	CD2 antigen (cytoplasmic tail) binding protein 2	1.01	0.966	1.15	0.485	1.63	0.142	1.07	0.771	1.22
1435518_at	Rap1b	RAS related protein 1b	1.12	0.58	1.11	0.544	1.56	0.143	1.07	0.626	1.21
1441788_s_at	BC068171	cDNA sequence BC068171	1.22	0.334	1.28	0.058	1.29	0.401	1.36	0.313	1.29
1418760_at	Rdh11	retinol dehydrogenase 11	1.03	0.772	1.5	0.099	1.25	0.285	1.44	0.14	1.31
1423812_s_at	AW146242	expressed sequence AW146242	1.23	0.309	1.47	0.132	1.09	0.635	2.42	0.091	1.55
1450747_at	Keap1	kelch-like ECH-associated protein 1	1.23	0.701	1.11	0.736	1.45	0.258	1.44	0.329	1.31
1449226_at	Hic1	hypermethylated in cancer 1	1.15	0.738	1.62	0.049	1.02	0.906	1.41	0.133	1.3
1436805_at	2810457I06Rik	RIKEN cDNA 2810457I06 gene	1.17	0.119	1.35	0.285	1.27	0.257	1.28	0.324	1.27
1458232_at	Dkk1	dickkopf homolog 1 (Xenopus laevis)	1.29	0.337	1.46	0.5	1.04	0.846	2.03	0.425	1.45
1439732_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	1.66	0.026	1.13	0.847	1.01	0.963	1.43	0.371	1.31
1448871_at	Mapk13	mitogen activated protein kinase 13	1.22	0.325	1.31	0.612	1.26	0.644	2.71	0.335	1.62
1435349_at	Nrp2	neuropilin 2	1.15	0.129	1.34	0.179	1.31	0.315	1.31	0.598	1.28
1450920_at	Ccnb2	cyclin B2	1.11	0.642	1.24	0.68	1.44	0.026	5.11	0.153	2.23
1425794_at	Pola2	polymerase (DNA directed), alpha 2	1.22	0.443	1.31	0.317	1.26	0.478	1.47	0.219	1.32
1426055_a_at	Pigq	phosphatidylinositol glycan anchor biosynthesis, class Q	1.22	0.671	1.09	0.692	1.49	0.213	4.21	0.211	2
1416691_at	Gtpbp2	GTP binding protein 2	1.23	0.565	1	0.995	1.56	0.219	2.26	0.223	1.51
1426297_at	Tcfe2a	transcription factor E2a	1.19	0.231	1.13	0.584	1.48	0.127	1.07	0.648	1.22
1417460_at	Ifitm2	interferon induced transmembrane protein 2	1.23	0.218	1.45	0.144	1.13	0.486	1.21	0.178	1.25
1445901_at	Lrp2	low density lipoprotein receptor-related protein 2	1.19	0.66	1.26	0.52	1.35	0.295	1.06	0.866	1.22

1417144_at	Tubg1	tubulin, gamma 1	1.29	0.318	1.29	0.072	1.22	0.22	1.7	0.151	1.37
1421889_a_at	Aplp2	amyloid beta (A4) precursor-like protein 2	1.39	0.414	1.06	0.805	1.35	0.39	2.03	0.08	1.46
1434448_at	Txlna	taxilin alpha	1.06	0.81	1.19	0.7	1.55	0.301	1.06	0.852	1.22
1460479_at	A330094K24Rik	RIKEN cDNA A330094K24 gene	1.1	0.788	1.55	0.091	1.16	0.676	3.12	0.33	1.73
1428440_at	Slc25a12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	1.02	0.955	1.37	0.186	1.42	0.031	1.1	0.564	1.22
1426313_at	Bre	brain and reproductive organ-expressed protein	1.08	0.885	1.01	0.965	1.71	0.204	1.09	0.801	1.22
1452383_at	---	---	1.1	0.323	1.13	0.814	1.57	0.532	1.06	0.759	1.22
1432947_at	4921519G19Rik	RIKEN cDNA 4921519G19 gene	1.13	0.816	1.31	0.623	1.36	0.586	1.42	0.576	1.31
1418860_a_at	Letmd1	LETM1 domain containing 1	1.09	0.716	1.09	0.419	1.63	0.041	1.38	0.066	1.3
1446738_at	D7Wsu130e	DNA segment, Chr 7, Wayne State University 130, expressed	1.37	0.499	1.18	0.535	1.25	0.16	1.73	0.057	1.38
1421313_s_at	Cttn	cortactin	1.41	0.469	1.17	0.691	1.23	0.698	1.23	0.67	1.26
1448205_at	Ccnb1-rs1 /// Ccnb1	cyclin B1, related sequence 1 /// cyclin B1	1.31	0.805	1.27	0.668	1.23	0.379	3.75	0.147	1.89
1449209_a_at	Rdh11	retinol dehydrogenase 11	1.28	0.408	1.39	0.246	1.14	0.469	1.31	0.473	1.28
1417022_at	Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3	1.15	0.655	1.4	0.168	1.26	0.096	2	0.011	1.45
1422946_a_at	Dnmt1	DNA methyltransferase (cytosine-5) 1	1.2	0.282	1.06	0.474	1.55	0.046	2.12	0.15	1.48
1417446_at	Slc12a4	solute carrier family 12, member 4	1.32	0.055	1.26	0.366	1.23	0.082	1.19	0.29	1.25
1426519_at	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha	1.05	0.918	1.25	0.266	1.5	0.517	1.12	0.737	1.23
1421960_at	Adcy3	adenylate cyclase 3	1.16	0.616	1.5	0.151	1.15	0.457	1.07	0.847	1.22
1421977_at	Mmp19	matrix metallopeptidase 19	1.39	0.735	1.34	0.351	1.08	0.598	1.66	0.367	1.37
1433158_at	Kif13b	kinesin family member 13B	1.48	0.379	1.28	0.619	1.04	0.923	2.28	0.04	1.52
1431342_at	---	---	1.32	0.59	1.07	0.925	1.42	0.48	1.28	0.389	1.27
1434815_a_at	Mapkapk3	mitogen-activated protein kinase-activated protein kinase 3	1.1	0.541	1.67	0.125	1.05	0.586	1.02	0.808	1.21
1416550_at	Slc35b4	solute carrier family 35, member B4	1.21	0.048	1.11	0.739	1.5	0.222	1.17	0.488	1.25
1458903_at	A230057G18Rik	RIKEN cDNA A230057G18 gene	1.39	0.461	1.21	0.654	1.22	0.579	1.3	0.466	1.28
1449310_at	Ptger2	prostaglandin E receptor 2 (subtype EP2)	1.56	0.301	1.21	0.465	1.04	0.805	1.06	0.895	1.22
1416062_at	Tbc1d15	TBC1 domain family, member 15	1.33	0.622	1.09	0.873	1.41	0.557	1.06	0.886	1.22
1419238_at	Abca7	ATP-binding cassette, sub-family A (ABC1), member 7	1.2	0.092	1.11	0.726	1.51	0.095	1.22	0.601	1.26
1437865_at	Spata13	spermatogenesis associated 13	1.08	0.581	1.09	0.587	1.64	0.046	1.21	0.512	1.26
1417940_s_at	Rad51ap1	RAD51 associated protein 1	1.26	0.331	1.47	0.497	1.09	0.777	3.05	0.171	1.72
1416251_at	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisi	1.11	0.653	1.46	0.066	1.25	0.293	2.28	0.13	1.52
1448782_at	Txndc11	thioredoxin domain containing 11	1.4	0.285	1.24	0.351	1.18	0.019	1.27	0.338	1.27
1449395_at	4921520G13Rik	RIKEN cDNA 4921520G13 gene	1.33	0.751	1.13	0.447	1.36	0.33	4.16	0.076	2
1422462_at	Ube2t	ubiquitin-conjugating enzyme E2T (putative)	1.65	0.183	1.16	0.517	1.02	0.851	2.58	0.18	1.6
1437473_at	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog	1.3	0.674	1.44	0.084	1.08	0.853	1.15	0.606	1.25
1431760_a_at	Sdccag3	serologically defined colon cancer antigen 3	1.63	0.186	1.05	0.915	1.15	0.8	1.38	0.497	1.3
1456554_at	7530414M10Rik	RIKEN cDNA 7530414M10 gene	1.08	0.79	1.17	0.611	1.58	0.05	1.72	0.06	1.39
1456929_at	BC042782	CDNA sequence BC042782	1.2	0.707	1.4	0.388	1.22	0.302	1.21	0.513	1.26
1459084_at	---	PREDICTED: Mus musculus similar to cyclin-dependent kinase 10 isoform 2 (LO	1.23	0.652	1.5	0.239	1.1	0.846	2.26	0.028	1.52
1426667_a_at	Unc84a	unc-84 homolog A (C. elegans)	1.2	0.409	1.19	0.505	1.44	0.404	1.37	0.388	1.3
1422504_at	Glrb	glycine receptor, beta subunit	1.03	0.959	1.31	0.723	1.5	0.522	1.37	0.196	1.3
1421758_at	Nat1	N-acetyltransferase 1 (arylamine N-acetyltransferase)	1.53	0.327	1.15	0.513	1.15	0.753	1.75	0.063	1.39
1456481_at	D9Ertd280e	DNA segment, Chr 9, ERATO Doi 280, expressed	1.66	0.005	1.1	0.329	1.07	0.706	1.09	0.845	1.23
1417461_at	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	1.26	0.225	1.29	0.421	1.29	0.379	1.17	0.404	1.25
1451814_a_at	Htatip2	HIV-1 tat interactive protein 2, homolog (human)	1.28	0.067	1.22	0.02	1.34	0.062	1.89	0.136	1.43
1425654_a_at	Lima1	LIM domain and actin binding 1	1.09	0.366	1.12	0.644	1.62	0.285	1.19	0.596	1.26
1426528_at	Nrp2	neuropilin 2	1.02	0.863	1.63	0.014	1.19	0.365	1.04	0.882	1.22
1453979_at	Rbm12b	RNA binding motif protein 12B	1.39	0.683	1.37	0.626	1.08	0.763	1.48	0.536	1.33
1448118_a_at	Ctsd	cathepsin D	1.01	0.953	1.33	0.012	1.51	0.009	1.15	0.047	1.25
1452170_at	2010209O12Rik	RIKEN cDNA 2010209O12 gene	1.05	0.772	1.23	0.449	1.57	0.009	1.1	0.03	1.24
1426237_at	Sp2	Sp2 transcription factor	1.01	0.977	1.36	0.066	1.47	0.221	1.22	0.465	1.27
1437829_s_at	Eef2k	eukaryotic elongation factor-2 kinase	1.05	0.848	1.01	0.939	1.79	0.002	2.22	0.187	1.52
1451945_at	---	---	1.02	0.917	1.07	0.633	1.76	0.355	1.1	0.695	1.24
1441009_at	4732491K20Rik	RIKEN cDNA 4732491K20 gene	1.15	0.714	1.57	0.098	1.13	0.609	1.13	0.776	1.24

1456311_x_at	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	1.32	0.1	1.3	0.735	1.22	0.701	2.77	0.404	1.65
1439322_at	Pcdh9	Protocadherin 9	1.13	0.727	1.47	0.539	1.24	0.553	1.26	0.669	1.28
1456741_s_at	Gpm6a	glycoprotein m6a	1.12	0.197	1.65	0.358	1.08	0.828	2.91	0.02	1.69
1452830_s_at	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorot	1.08	0.826	1.14	0.531	1.63	0.105	1.46	0.07	1.33
1448559_at	Flot1	flotillin 1	1.13	0.374	1.38	0.113	1.34	0.006	1.35	0.162	1.3
1453309_at	9330179D12Rik	RIKEN cDNA 9330179D12 gene	1.15	0.763	1.25	0.668	1.45	0.269	1.03	0.961	1.22
1439575_at	E130009J12Rik	RIKEN cDNA E130009J12 gene	1.26	0.787	1.28	0.728	1.32	0.559	1.88	0.273	1.43
1424947_at	Dync1li1	dynein cytoplasmic 1 light intermediate chain 1	1.64	0.401	1.09	0.631	1.13	0.545	1.46	0.414	1.33
1443060_at	2810003K23Rik	RIKEN cDNA 2810003K23 gene	1.31	0.426	1.1	0.78	1.45	0.245	1.11	0.861	1.24
1445750_at	---	Transcribed locus	1.09	0.1	1.33	0.195	1.44	0.561	1.25	0.378	1.28
1448180_a_at	Hn1	hematological and neurological expressed sequence 1	1	0.993	1.47	0.02	1.39	0.367	1.06	0.151	1.23
1429294_at	Trip13	thyroid hormone receptor interactor 13	1.12	0.819	1.17	0.52	1.58	0.416	2.76	0.132	1.65
1425064_at	Arnt	aryl hydrocarbon receptor nuclear translocator	1.01	0.981	1.38	0.465	1.47	0.155	1.95	0.278	1.45
1416038_at	AL033314	expressed sequence AL033314	1.29	0.357	1.16	0.375	1.41	0.163	1.07	0.742	1.23
1416263_at	Abcb9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	1.37	0.351	1.29	0.436	1.21	0.285	1.4	0.276	1.31
1453699_at	4930448D08Rik	RIKEN cDNA 4930448D08 gene	1.09	0.808	1.28	0.505	1.5	0.348	1.51	0.416	1.34
1458438_at	4933415L06Rik	RIKEN cDNA 4933415L06 gene	1.28	0.259	1.46	0.099	1.12	0.645	1.18	0.63	1.26
1432436_a_at	Ak3	adenylate kinase 3	1.1	0.892	1.01	0.987	1.76	0.495	1.18	0.674	1.26
1418025_at	Bhlhb2	basic helix-loop-helix domain containing, class B2	1.09	0.734	1.14	0.507	1.64	0.234	1.31	0.241	1.29
1436879_x_at	Afp	alpha fetoprotein	1.18	0.748	1.01	0.985	1.67	0.03	1.06	0.922	1.23
1435154_at	LOC245128	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), men	1.44	0.117	1.33	0.5	1.1	0.844	1.59	0.289	1.36
1453865_a_at	Otud5	OTU domain containing 5	1.17	0.36	1	0.971	1.69	0.046	1.94	0.22	1.45
1451408_at	Trub2	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	1.12	0.334	1.29	0.401	1.46	0.026	1.17	0.645	1.26
1458671_at	LOC669460	hypothetical protein LOC669460	1.24	0.753	1.21	0.712	1.43	0.488	1.28	0.474	1.29
1459241_at	---	Transcribed locus	1.23	0.618	1.43	0.276	1.21	0.399	1.02	0.918	1.22
1427900_at	Pip5kl1	phosphatidylinositol-4-phosphate 5-kinase-like 1	1.53	0.104	1.19	0.757	1.15	0.785	1.22	0.359	1.27
1458408_at	Samd8	sterile alpha motif domain containing 8	1.51	0.393	1.19	0.678	1.17	0.648	1.35	0.415	1.31
1424428_at	Ccdc95	coiled-coil domain containing 95	1.11	0.384	1.69	0.205	1.08	0.363	1.13	0.429	1.25
1431914_at	Pde3a	phosphodiesterase 3A, cGMP inhibited	1.03	0.965	1.79	0.013	1.05	0.827	1.61	0.504	1.37
1457322_at	C1qb	Complement component 1, q subcomponent, beta polypeptide	1.27	0.719	1.28	0.205	1.32	0.134	1.08	0.794	1.24
1417644_at	Sspn	sarcospan	1.16	0.067	1.61	0.105	1.1	0.722	1.27	0.688	1.29
1454968_at	1110034A24Rik	RIKEN cDNA 1110034A24 gene	1.06	0.65	1.03	0.908	1.78	0.027	1.46	0.399	1.33
1429208_at	5730408K05Rik	RIKEN cDNA 5730408K05 gene	1.76	0.334	1.08	0.899	1.03	0.784	1.32	0.053	1.3
1423588_at	Arpc4	actin related protein 2/3 complex, subunit 4	1.18	0.583	1.27	0.206	1.43	0.322	1.07	0.744	1.24
1425899_a_at	Itsn1	intersectin 1 (SH3 domain protein 1A)	1.03	0.878	1.19	0.48	1.66	0.084	6.75	0.224	2.66
1453479_at	1700086P04Rik	RIKEN cDNA 1700086P04 gene	1.29	0.363	1.52	0.053	1.07	0.809	1.09	0.667	1.24
1429527_a_at	Plscr1 /// LOC4333	phospholipid scramblase 1 /// hypothetical LOC433328 /// hypothetical protein LO	1.09	0.585	1.36	0.284	1.43	0.166	1.61	0.017	1.37
1416644_a_at	Sema3b	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	1.03	0.623	1.29	0.378	1.56	0.073	1.1	0.861	1.24
1421360_at	Inpp4a	inositol polyphosphate-4-phosphatase, type I	1.18	0.816	1.43	0.038	1.27	0.634	1.08	0.882	1.24
1435758_at	LOC675709	similar to Beta-1,4-galactosyltransferase 6 (Beta-1,4-GalTase 6) (Beta4Gal-T6) (b	1.1	0.362	1.45	0.168	1.32	0.146	1.81	0.012	1.42
1436434_at	9230110J10	hypothetical protein 9230110J10	1.57	0.538	1.11	0.858	1.21	0.616	4.06	0.181	1.99
1450652_at	Ctsk	cathepsin K	1.01	0.937	1.65	0.303	1.23	0.227	1.06	0.633	1.24
1424831_at	Cpne2	copine II	1.18	0.255	1.03	0.873	1.67	0.247	2.69	0.244	1.64
1436708_x_at	Mcm4	minichromosome maintenance deficient 4 homolog (S. cerevisiae)	1.25	0.465	1.32	0.302	1.31	0.164	2.4	0.139	1.57
1439899_at	Galnt13	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfer	1.26	0.792	1.26	0.672	1.36	0.218	1.01	0.986	1.22
1460523_at	---	---	1.34	0.514	1.37	0.573	1.17	0.782	1.17	0.704	1.26
1434577_at	BC052040	cDNA sequence BC052040	1.55	0.098	1.11	0.631	1.23	0.383	1.35	0.038	1.31
1431629_at	9130221D24Rik	RIKEN cDNA 9130221D24 gene	1.1	0.798	1.6	0.558	1.2	0.266	1.3	0.574	1.3
1422565_s_at	Nfic	nuclear factor I/C	1.58	0.612	1.15	0.743	1.15	0.686	1.9	0.141	1.45
1448715_x_at	Sgip1	SH3-domain GRB2-like (endophilin) interacting protein 1	1.22	0.472	1.53	0.068	1.14	0.49	1.06	0.447	1.24
1417240_at	Zyx	zyxin	1.16	0.5	1.03	0.804	1.7	0.067	1.2	0.287	1.27
1441111_at	---	15 days embryo embryonic body below diaphragm cDNA, RIKEN full-length enric	1.28	0.643	1.21	0.712	1.4	0.19	1.05	0.826	1.24
1451342_at	Spon1	spondin 1, (f-spondin) extracellular matrix protein	1.51	0.093	1.19	0.765	1.18	0.445	1.86	0.028	1.44

1460650_at	Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	1.04	0.959	1.12	0.812	1.73	0.46	2.1	0.11	1.5
1455476_a_at	Gse1	genetic suppressor element 1	1.22	0.39	1.31	0.181	1.36	0.14	1.68	0.209	1.39
1454686_at	C330011F01Rik ///	RIKEN cDNA C330011F01 gene /// RIKEN cDNA 6430706D22 gene	1.4	0.383	1.05	0.855	1.44	0.4	1.99	0.25	1.47
1429390_at	Acpl2	acid phosphatase-like 2	1.38	0.037	1.14	0.348	1.38	0.241	1.18	0.532	1.27
1453054_at	Scamp1	secretory carrier membrane protein 1	1.18	0.562	1.2	0.671	1.52	0.482	1.41	0.256	1.33
1426507_at	Il1f5	interleukin 1 family, member 5 (delta)	1.65	0.216	1.21	0.734	1.03	0.925	1.32	0.373	1.31
1444893_at	---	---	1.26	0.52	1.31	0.229	1.33	0.534	1.51	0.399	1.35
1421233_at	Pknox1	Pbx/knotted 1 homeobox	1.52	0.576	1.06	0.919	1.32	0.587	1.17	0.772	1.27
1416409_at	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	1.25	0.245	1.08	0.573	1.58	0.19	1.34	0.212	1.31
1434891_at	Ptgfrn	prostaglandin F2 receptor negative regulator	1.08	0.256	1.62	0.075	1.2	0.45	1.03	0.891	1.23
1442935_at	C81452	expressed sequence C81452	1.05	0.916	1.8	0.141	1.05	0.859	1.09	0.841	1.25
1457452_at	AA407782	expressed sequence AA407782	1.43	0.109	1.44	0.407	1.03	0.909	1.2	0.706	1.28
1450040_at	Timp2	tissue inhibitor of metalloproteinase 2	1.2	0.514	1.51	0.548	1.19	0.344	1.23	0.215	1.28
1448302_at	Kctd20	potassium channel tetramerisation domain containing 20	1.09	0.626	1.29	0.318	1.52	0.151	1.54	0.414	1.36
1423102_a_at	Rnf10	ring finger protein 10	1.28	0.116	1.05	0.666	1.57	0.114	2.47	0.173	1.59
1433031_at	2900064K03Rik	RIKEN cDNA 2900064K03 gene	1.01	0.958	1.32	0.62	1.58	0.1	1.06	0.915	1.24
1436668_at	5730409G15Rik	RIKEN cDNA 5730409G15 gene	1.24	0.315	1.22	0.359	1.45	0.225	1.24	0.128	1.29
1422677_at	Dgat2	diacylglycerol O-acyltransferase 2	1.08	0.595	1.02	0.952	1.81	0.123	1.17	0.493	1.27
1426247_at	Stk24	serine/threonine kinase 24 (STE20 homolog, yeast)	1.14	0.531	1.08	0.704	1.7	0.045	1.05	0.441	1.24
1448662_at	Fzd6	frizzled homolog 6 (Drosophila)	1.04	0.567	1.21	0.655	1.66	0.135	1.2	0.819	1.28
1450541_at	Pvt1	plasmacytoma variant translocation 1	1.63	0.149	1.11	0.616	1.18	0.757	1.85	0.182	1.44
1435762_at	Pacs1	phosphofurin acidic cluster sorting protein 1	1.25	0.303	1.29	0.184	1.39	0.294	1.31	0.069	1.31
1451189_at	Zswim1	zinc finger, SWIM domain containing 1	1.32	0.313	1.09	0.684	1.5	0.003	1.12	0.07	1.26
1421102_a_at	Vamp3	vesicle-associated membrane protein 3	1.16	0.581	1.34	0.375	1.42	0.554	1.49	0.416	1.35
1457579_at	D11Ertd717e	DNA segment, Chr 11, ERATO Doi 717, expressed	1.54	0.171	1.1	0.429	1.28	0.138	1.11	0.719	1.26
1457368_at	2310033K02Rik	RIKEN cDNA 2310033K02 gene	1.5	0.232	1.31	0.212	1.11	0.48	1.5	0.336	1.35
1439158_at	Tlk1	tousled-like kinase 1	1.39	0.235	1.09	0.771	1.43	0.28	2.17	0.258	1.52
1421160_a_at	Rfng	radical fringe gene homolog (Drosophila)	1.32	0.419	1.19	0.61	1.41	0.037	1.28	0.327	1.3
1451060_at	Gpr146	G protein-coupled receptor 146	1.76	0.287	1.07	0.85	1.09	0.772	1.94	0.225	1.47
1451306_at	Cdca7l	cell division cycle associated 7 like	1.01	0.954	1.53	0.344	1.38	0.049	1.41	0.096	1.33
1425025_at	Tmem106a	transmembrane protein 106A	1.01	0.956	1.48	0.093	1.44	0.006	1.54	0.244	1.37
1421963_a_at	Cdc25b	cell division cycle 25 homolog B (S. cerevisiae)	1.13	0.526	1.3	0.237	1.49	0.198	2.79	0.2	1.68
1440918_at	---	---	1.01	0.774	1.85	0.202	1.07	0.771	1.19	0.848	1.28
1434601_at	Amigo2	adhesion molecule with Ig like domain 2	1.53	0.321	1.21	0.489	1.19	0.523	1.04	0.886	1.24
1459598_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	1.35	0.712	1.12	0.752	1.46	0.523	1.02	0.952	1.24
1420665_at	Itgb3bp	integrin beta 3 binding protein (beta3-endonexin)	1.41	0.359	1.21	0.228	1.31	0.053	1.04	0.681	1.24
1429312_s_at	Ror1	receptor tyrosine kinase-like orphan receptor 1	1.61	0.072	1.17	0.727	1.15	0.468	2.05	0.104	1.5
1454070_a_at	Ddhd1	DDHD domain containing 1	1.02	0.962	1.49	0.262	1.42	0.002	1.07	0.539	1.25
1446823_at	D4Ertd103e	DNA segment, Chr 4, ERATO Doi 103, expressed	1.05	0.925	1.64	0.359	1.24	0.647	2.09	0.168	1.51
1429681_a_at	Gpsn2	glycoprotein, synaptic 2	1.11	0.718	1.11	0.517	1.71	0.026	1.43	0.266	1.34
1447265_at	AI848615	expressed sequence AI848615	1.05	0.96	1.69	0.26	1.2	0.707	1.85	0.446	1.44
1428241_at	2310035K24Rik	RIKEN cDNA 2310035K24 gene	1.11	0.606	1.35	0.011	1.48	0.045	1.17	0.542	1.28
1455428_at	A930008G19Rik	RIKEN cDNA A930008G19 gene	1.11	0.588	1.81	0.009	1.02	0.897	2.5	0.148	1.61
1436124_at	Pcyt1b	phosphate cytidylyltransferase 1, choline, beta isoform	1.01	0.956	1.5	0.158	1.42	0.146	4.31	0.261	2.06
1443745_s_at	Dmp1	dentin matrix protein 1	1.24	0.52	1.57	0.491	1.12	0.872	1.02	0.973	1.24
1421329_a_at	Smyd1	SET and MYND domain containing 1	1.27	0.76	1.15	0.712	1.51	0.398	1.93	0.145	1.47
1425640_at	Aff1	AF4/FMR2 family, member 1	1.32	0.709	1.05	0.922	1.58	0.023	1.34	0.181	1.32
1450027_at	Sdc3	syndecan 3	1.16	0.458	1.69	0.003	1.09	0.729	1.56	0.217	1.37
1439578_at	Lsm11	U7 snRNP-specific Sm-like protein LSM11	1.05	0.866	1.67	0.062	1.22	0.277	1.14	0.179	1.27
1442932_at	C79709	expressed sequence C79709	1.11	0.774	1.24	0.665	1.6	0.218	1.51	0.337	1.36
1419586_at	Rp2h	retinitis pigmentosa 2 homolog (human)	1.03	0.909	1.36	0.439	1.56	0.109	1.4	0.089	1.34
1433604_x_at	Aldoa	aldolase 1, A isoform	1.13	0.381	1.18	0.169	1.64	0.007	1.09	0.48	1.26
1439015_at	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	1.24	0.588	1.21	0.555	1.5	0.141	1.2	0.56	1.29

1449369_at	Tmprss2	transmembrane protease, serine 2	1.04	0.889	1.9	0.16	1.01	0.962	1.57	0.267	1.38
1449353_at	Zmat3	zinc finger matrin type 3	1.44	0.076	1.11	0.406	1.4	0.178	1.08	0.61	1.26
1450105_at	---	---	1.13	0.687	1.31	0.428	1.52	0.297	2.68	0.248	1.66
1449002_at	Phlda3	pleckstrin homology-like domain, family A, member 3	1.29	0.225	1.45	0.03	1.21	0.033	1.17	0.075	1.28
1418961_at	Necap2	NECAP endocytosis associated 2	1.16	0.624	1.16	0.598	1.63	0.171	2.16	0.152	1.53
1459546_s_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	1.23	0.146	1.19	0.056	1.54	0.396	1.16	0.421	1.28
1457148_at	Csmd2	CUB and Sushi multiple domains 2	1.08	0.124	1.86	0.099	1.01	0.982	1.14	0.69	1.27
1453181_x_at	Plscr1	phospholipid scramblase 1	1.09	0.602	1.4	0.18	1.47	0.143	1.69	0.019	1.41
1419303_at	Heyl	hairy/enhancer-of-split related with YRPW motif-like	1.62	0.316	1.22	0.683	1.11	0.609	1.48	0.455	1.36
1421321_a_at	Net1	neuroepithelial cell transforming gene 1	1.13	0.74	1.18	0.569	1.65	0.173	2.12	0.303	1.52
1450088_a_at	Mobp	myelin-associated oligodendrocytic basic protein	1.16	0.645	1.23	0.719	1.56	0.339	1.02	0.888	1.25
1432520_at	Igh-VJ558	immunoglobulin heavy chain (J558 family)	1.68	0.23	1.08	0.864	1.2	0.765	1.01	0.969	1.24
1450495_a_at	Klrk1	killer cell lectin-like receptor subfamily K, member 1	1.71	0.096	1.14	0.588	1.11	0.639	1.78	0.415	1.44
1418852_at	Chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	1.28	0.07	1.37	0.29	1.31	0.442	1.24	0.624	1.3
1427219_at	---	---	1.47	0.695	1.29	0.765	1.22	0.482	1.15	0.586	1.28
1421809_at	Dgcr2	DiGeorge syndrome critical region gene 2	1.14	0.677	1.16	0.318	1.67	0.135	1.36	0.475	1.33
1439787_at	P2rx7	purinergic receptor P2X, ligand-gated ion channel, 7	1.27	0.217	1.59	0.083	1.11	0.624	1.11	0.663	1.27
1454931_at	Cri2	CREBBP/EP300 inhibitory protein 2	1.24	0.308	1.61	0.026	1.12	0.25	1.03	0.841	1.25
1418059_at	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	1.37	0.085	1.55	0.142	1.05	0.752	1.07	0.581	1.26
1451095_at	Asns	asparagine synthetase	1.05	0.816	1.66	0.195	1.27	0.308	5.99	0.147	2.49
1433836_a_at	8430408G22Rik	RIKEN cDNA 8430408G22 gene	1.37	0.496	1.39	0.196	1.22	0.564	1.14	0.821	1.28
1451461_a_at	Aldoc	aldolase 3, C isoform	1.15	0.366	1.34	0.178	1.48	0.165	1.01	0.973	1.25
1416683_at	Plxnb2	plexin B2	1.15	0.439	1.12	0.08	1.71	0.01	1.16	0.568	1.28
1418360_at	Zfp179	zinc finger protein 179	1.05	0.953	1.28	0.54	1.64	0.406	2.52	0.132	1.63
1416028_a_at	Hn1	hematological and neurological expressed sequence 1	1.13	0.157	1.26	0.062	1.58	0.19	1.06	0.748	1.26
1451617_at	Rho	rhodopsin	1.13	0.849	1.84	0.12	1.01	0.978	1.06	0.926	1.26
1453757_at	Herc5	hect domain and RLD 5	1.43	0.359	1.23	0.564	1.32	0.317	1.06	0.828	1.26
1428867_at	4933417E01Rik	RIKEN cDNA 4933417E01 gene	1.04	0.789	1.47	0.036	1.46	0.227	1.18	0.421	1.29
1435458_at	Pim1	proviral integration site 1	1.11	0.746	1.29	0.201	1.58	0.123	2.37	0.115	1.59
1457234_at	---	Transcribed locus	1.12	0.835	1.35	0.56	1.51	0.206	1.7	0.235	1.42
1427471_at	Fbxl3	F-box and leucine-rich repeat protein 3	1.12	0.336	1.34	0.467	1.52	0.226	1.1	0.803	1.27
1451803_a_at	Vegfb	vascular endothelial growth factor B	1.26	0.414	1.09	0.651	1.64	0.045	1.76	0.06	1.44
1448562_at	Upp1	uridine phosphorylase 1	1.24	0.529	1.18	0.416	1.57	0.377	1.96	0.228	1.49
1459038_at	---	Transcribed locus	1.16	0.438	1.32	0.292	1.5	0.435	1.22	0.256	1.3
1444689_at	Wdr67	WD repeat domain 67	1.09	0.877	1.35	0.556	1.54	0.234	1.35	0.17	1.33
1445681_at	Cdca7	Cell division cycle associated 7	1.47	0.562	1.38	0.597	1.13	0.841	1.46	0.574	1.36
1422111_at	Ccbp2	chemokine binding protein 2	1.32	0.478	1.24	0.508	1.43	0.219	1.01	0.981	1.25
1421604_a_at	Klf3	Kruppel-like factor 3 (basic)	1.3	0.435	1.1	0.531	1.58	0.279	1.89	0.211	1.47
1448907_at	Thop1	thimet oligopeptidase 1	1.01	0.907	1.14	0.768	1.83	0.037	1.85	0.177	1.46
1438239_at	Mid1	midline 1	1.28	0.421	1.65	0.198	1.05	0.875	1.71	0.21	1.43
1424446_at	Armc7	armadillo repeat containing 7	1.17	0.309	1.33	0.118	1.49	0.056	1.28	0.596	1.32
1437764_at	A730011L01Rik	RIKEN cDNA A730011L01 gene	1.6	0.34	1.02	0.974	1.37	0.097	1.09	0.29	1.27
1422922_at	Recql4	RecQ protein-like 4	1.24	0.757	1.37	0.383	1.39	0.194	2.05	0.309	1.51
1430071_at	Brp44	brain protein 44	1.64	0.107	1.18	0.487	1.17	0.674	2.35	0.203	1.59
1417338_at	Epb4.2	erythrocyte protein band 4.2	1.03	0.788	1.45	0.283	1.52	0.412	12.48	0.209	4.12
1422399_a_at	Rab23	RAB23, member RAS oncogene family	1.28	0.408	1.12	0.848	1.59	0.224	1.66	0.295	1.41
1423209_at	---	---	1.25	0.806	1.55	0.343	1.2	0.326	1.04	0.886	1.26
1459065_at	Kalrn	Kalirin, RhoGEF kinase	1.09	0.705	1.71	0.44	1.2	0.414	1.17	0.751	1.29
1440897_at	---	Mus musculus, clone IMAGE:4458738, mRNA	1.45	0.495	1.07	0.534	1.48	0.481	1.18	0.572	1.3
1456971_at	Slc1a7	solute carrier family 1 (glutamate transporter), member 7	1.6	0.446	1.27	0.736	1.14	0.715	1.14	0.399	1.29
1453367_a_at	Abhd12	abhydrolase domain containing 12	1.32	0.201	1.17	0.621	1.51	0.267	1.04	0.871	1.26
1421710_at	Zfp92	zinc finger protein 92	1.49	0.561	1.04	0.912	1.47	0.315	2.02	0.008	1.5
1429605_at	4930532L20Rik	RIKEN cDNA 4930532L20 gene	1.07	0.703	1.68	0.43	1.24	0.318	1.67	0.098	1.42

1425146_at	2410075B13Rik	RIKEN cDNA 2410075B13 gene	1.14	0.812	1.09	0.862	1.78	0.011	1.4	0.049	1.35
1424648_at	Rabl4	RAB, member of RAS oncogene family-like 4	1.03	0.762	1.1	0.05	1.87	0.074	1.1	0.554	1.28
1426226_at	Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	1.26	0.546	1.13	0.526	1.62	0.173	1.72	0.354	1.43
1427198_at	BC022960	cDNA sequence BC022960	1.44	0.348	1.17	0.81	1.39	0.229	1.06	0.803	1.27
1426014_a_at	Mucdhl	mucin and cadherin like	1.24	0.474	1.14	0.581	1.63	0.138	1.08	0.767	1.27
1452295_at	LOC637870 /// LOC	similar to Nedd4 WW binding protein 4 /// similar to Nedd4 WW binding protein 4	1.48	0.224	1.48	0.573	1.05	0.606	1.25	0.504	1.32
1421459_a_at	Lrp8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	1.16	0.862	1.66	0.166	1.2	0.515	1.08	0.546	1.27
1416013_at	Pld3	phospholipase D family, member 3	1.37	0.461	1.33	0.125	1.31	0.068	1.31	0.439	1.33
1434169_at	9030409G11Rik	RIKEN cDNA 9030409G11 gene	1.23	0.458	1.59	0.545	1.2	0.35	1.03	0.926	1.26
1441516_a_at	C130050O18Rik	RIKEN cDNA C130050O18 gene	1.35	0.235	1.27	0.299	1.39	0.177	1.1	0.541	1.28
1423425_at	1300012G16Rik	RIKEN cDNA 1300012G16 gene	1.18	0.645	1.15	0.28	1.69	0.023	1.19	0.396	1.3
1418090_at	Plvap	plasmalemma vesicle associated protein	1.37	0.263	1.33	0.061	1.32	0.154	1.03	0.901	1.26
1415694_at	Wars	tryptophanyl-tRNA synthetase	1.24	0.554	1.22	0.255	1.56	0.124	1.29	0.197	1.33
1419483_at	C3ar1	complement component 3a receptor 1	1.38	0.152	1.48	0.277	1.16	0.486	1.34	0.369	1.34
1417631_at	Mknk1	MAP kinase-interacting serine/threonine kinase 1	1.27	0.489	1.06	0.677	1.69	0.024	1.42	0.401	1.36
1422183_a_at	Adra1b	adrenergic receptor, alpha 1b	1.7	0.539	1.26	0.706	1.06	0.842	1.08	0.84	1.27
1438552_x_at	Zyx	zyxin	1.01	0.964	1.98	0.409	1.03	0.939	1.01	0.99	1.26
1456592_at	Vps13a	Vacuolar protein sorting 13A (yeast)	1.24	0.36	1.55	0.344	1.23	0.161	1.16	0.328	1.3
1445841_at	Lrrc39	leucine rich repeat containing 39	1.3	0.807	1.37	0.529	1.36	0.286	1.45	0.367	1.37
1415806_at	Plat	plasminogen activator, tissue	1.14	0.287	1.43	0.382	1.45	0.249	1.64	0.041	1.42
1455546_s_at	Sf3a2	splicing factor 3a, subunit 2	1.06	0.773	1.02	0.796	1.95	0.01	1.02	0.827	1.26
1425799_at	Fmo4	flavin containing monooxygenase 4	1.25	0.373	1.27	0.388	1.51	0.399	2.02	0.461	1.51
1433477_at	Abr	active BCR-related gene	1.06	0.371	1.27	0.478	1.7	0.01	1.38	0.077	1.35
1455342_at	A230083H22Rik	RIKEN cDNA A230083H22 gene	1.21	0.748	1.34	0.468	1.49	0.267	1.31	0.227	1.33
1427354_at	Hoxa4	homeo box A4	1.43	0.615	1.34	0.223	1.26	0.57	1	0.996	1.26
1421744_at	Tnfsf4	tumor necrosis factor (ligand) superfamily, member 4	1.12	0.794	1.51	0.478	1.4	0.293	1.91	0.156	1.48
1448899_s_at	Rad51ap1	RAD51 associated protein 1	1.05	0.865	1.51	0.388	1.48	0.258	3.85	0.185	1.97
1421492_at	Ptgds2	prostaglandin D2 synthase 2, hematopoietic	1.23	0.618	1.47	0.394	1.34	0.274	1.12	0.486	1.29
1458345_s_at	Colec11	collectin sub-family member 11	1.15	0.455	1.26	0.008	1.63	0.347	1.02	0.959	1.26
1421304_at	Klra2	killer cell lectin-like receptor, subfamily A, member 2	1.05	0.93	1.72	0.009	1.27	0.534	2.08	0.006	1.53
1436297_a_at	Grina	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutam	1.02	0.922	1.33	0.043	1.69	0.027	2.2	0.105	1.56
1440655_at	---	Transcribed locus	1.18	0.85	1.67	0.435	1.18	0.588	1.57	0.458	1.4
1451975_at	2810453I06Rik	RIKEN cDNA 2810453I06 gene	1.18	0.572	1.07	0.642	1.79	0.361	2.7	0.257	1.69
1417332_at	Rfx2	regulatory factor X, 2 (influences HLA class II expression)	1.11	0.62	1.53	0.473	1.4	0.316	7.32	0.131	2.84
1451987_at	Arrb2	arrestin, beta 2	1.07	0.831	1.25	0.103	1.72	0.058	1.02	0.932	1.27
1436707_x_at	Brrn1	barren homolog (Drosophila)	1.28	0.304	1.68	0.334	1.09	0.466	2.91	0.174	1.74
1436355_at	Fads6	fatty acid desaturase domain family, member 6	1.13	0.631	1.24	0.232	1.67	0.035	1	0.99	1.26
1428018_a_at	Cd300d	Cd300D antigen	1.25	0.119	1.74	0.002	1.05	0.781	1.02	0.926	1.27
1441109_at	5430414B12Rik	RIKEN cDNA 5430414B12 gene	1.82	0.503	1.1	0.827	1.13	0.704	1.09	0.809	1.29
1451203_at	Mb	myoglobin	1.42	0.66	1.1	0.782	1.53	0.459	1.35	0.243	1.35
1429362_a_at	Sf3b2	splicing factor 3b, subunit 2	1.22	0.32	1.06	0.741	1.77	0.073	1.22	0.339	1.32
1430431_at	4933407H18Rik	RIKEN cDNA 4933407H18 gene	1.46	0.558	1.13	0.842	1.47	0.464	1.3	0.636	1.34
1421495_a_at	1700052N19Rik	RIKEN cDNA 1700052N19 gene	1.06	0.746	1.06	0.905	1.95	0.234	1.18	0.727	1.31
1455122_at	Ptchd2	patched domain containing 2	1.39	0.612	1.52	0.539	1.15	0.751	1.07	0.716	1.28
1454254_s_at	1600029D21Rik	RIKEN cDNA 1600029D21 gene	1.33	0.327	1.1	0.8	1.63	0.254	1.1	0.883	1.29
1448655_at	Lrp1	low density lipoprotein receptor-related protein 1	1.61	0.099	1.28	0.043	1.17	0.297	1.35	0.094	1.35
1418174_at	Dbp	D site albumin promoter binding protein	1.62	0.635	1.09	0.936	1.35	0.7	1.06	0.916	1.28
1450096_at	Gna12	guanine nucleotide binding protein, alpha 12	1.09	0.871	1.24	0.516	1.73	0.203	1.74	0.197	1.45
1419315_at	Slamf9	SLAM family member 9	1.18	0.374	1.77	0.192	1.11	0.529	1.72	0.154	1.45
1427489_at	Itga8	integrin alpha 8	1.53	0.282	1.2	0.758	1.33	0.614	1.59	0.259	1.41
1422951_at	Pcdhb4	protocadherin beta 4	1.19	0.768	1.41	0.579	1.46	0.331	2.7	0.003	1.69
1444272_at	Pdzd6	PDZ domain containing 6	1.77	0.27	1.06	0.892	1.23	0.445	1.19	0.269	1.31
1449936_at	8430419L09Rik	RIKEN cDNA 8430419L09 gene	1.47	0.486	1.29	0.511	1.3	0.472	3.98	0.271	2.01

1452847_at	2410008K03Rik	RIKEN cDNA 2410008K03 gene	1.18	0.39	1.78	0.422	1.11	0.362	1.03	0.69	1.28
1442094_at	Ing5	inhibitor of growth family, member 5	1.14	0.501	1.89	0.001	1.04	0.878	1.24	0.43	1.33
1449519_at	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	1.19	0.146	1.42	0.41	1.46	0.08	3.2	0.208	1.82
1445700_at	2310047M15Rik	RIKEN cDNA 2310047M15 gene	1.48	0.462	1.28	0.7	1.3	0.456	1.89	0.039	1.49
1427238_at	Fbxo15	F-box protein 15	1.51	0.397	1.3	0.301	1.26	0.086	1.67	0.393	1.44
1434282_at	Ibtk	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1.48	0.363	1.17	0.756	1.42	0.411	2.99	0.31	1.76
1419436_at	Cfhr1	complement factor H-related 1	1.48	0.637	1.08	0.502	1.51	0.38	2.12	0.154	1.55
1421165_at	Mycbp	c-myc binding protein	1.17	0.662	1.75	0.392	1.15	0.483	1.13	0.813	1.3
1448482_at	Slc39a8	solute carrier family 39 (metal ion transporter), member 8	1.76	0.058	1.01	0.981	1.3	0.51	5.12	0.255	2.3
1418184_at	Cenpm	centromere protein M	1.74	0.455	1.08	0.743	1.26	0.559	1.93	0.338	1.5
1419121_at	Tpmt	thiopurine methyltransferase	1.2	0.676	1.13	0.554	1.75	0.233	1.9	0.507	1.49
1422191_at	Cd200r1	CD200 receptor 1	1.16	0.73	1.59	0.272	1.33	0.123	1.35	0.501	1.36
1430452_at	Cyp20a1	cytochrome P450, family 20, subfamily A, polypeptide 1	1.51	0.402	1.12	0.747	1.46	0.434	1.77	0.303	1.46
1421412_at	Gsc	goosecoid	1.1	0.68	1.8	0.294	1.17	0.307	2.04	0.357	1.53
1443710_s_at	Spats1	spermatogenesis associated, serine-rich 1	1.07	0.893	1.58	0.369	1.42	0.294	1.38	0.605	1.37
1448777_at	Mcm2	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	1.08	0.644	1.5	0.212	1.51	0.258	2.35	0.211	1.61
1450886_at	Gsg2	germ cell-specific gene 2	1.66	0.155	1.34	0.623	1.08	0.857	2.35	0.138	1.61
1430015_at	Pxt1	peroxisomal, testis specific 1	1.07	0.642	1.51	0.151	1.51	0.258	1.02	0.945	1.28
1418719_at	2410004L22Rik	RIKEN cDNA 2410004L22 gene	1.34	0.034	1.51	0.149	1.23	0.169	1.04	0.79	1.28
1435189_at	Frmpd1 /// LOC669	FERM and PDZ domain containing 1 /// similar to FERM and PDZ domain contair	1.55	0.208	1.21	0.586	1.33	0.229	1.31	0.648	1.35
1416746_at	H2afx	H2A histone family, member X	1.34	0.07	1.03	0.904	1.72	0.123	2.67	0.162	1.69
1435059_at	Ddef1	development and differentiation enhancing	1.18	0.443	1.53	0.045	1.38	0.102	1.5	0.039	1.4
1457115_at	---	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C63000	1.34	0.673	1.6	0.436	1.16	0.374	1.04	0.948	1.28
1449297_at	Casp12	caspase 12	1.59	0.177	1.48	0.193	1.03	0.833	1.16	0.439	1.31
1447495_at	Fank1	fibronectin type 3 and ankyrin repeat domains 1	1.66	0.489	1.13	0.419	1.3	0.249	1.15	0.817	1.31
1446558_at	F730015K02Rik	RIKEN cDNA F730015K02 gene	1.67	0.07	1.34	0.144	1.08	0.797	2.19	0.257	1.57
1417960_at	Cpeb1	cytoplasmic polyadenylation element binding protein 1	1.08	0.634	1.3	0.252	1.72	0.244	1.02	0.926	1.28
1430530_s_at	Nmral1	NmrA-like family domain containing 1	1.74	0.268	1.34	0.308	1.03	0.941	1.74	0.232	1.46
1434928_at	Gas2l1	growth arrest-specific 2 like 1	1.15	0.076	1.46	0.205	1.49	0.093	1.67	0.27	1.44
1424994_at	6230410P16Rik	RIKEN cDNA 6230410P16 gene	1.15	0.641	1.06	0.859	1.89	0.185	1.11	0.857	1.3
1423847_at	2810406C15Rik	RIKEN cDNA 2810406C15 gene	1.11	0.068	1.22	0.279	1.77	0.148	2.94	0.169	1.76
1449383_at	Adssl1	adenylosuccinate synthetase like 1	1.27	0.493	1.04	0.805	1.8	0.002	1.73	0.005	1.46
1450370_a_at	Kcnip4	Kv channel interacting protein 4	1.19	0.606	1.14	0.57	1.78	0.201	1.27	0.614	1.34
1422572_at	Rhog	ras homolog gene family, member G	1.33	0.328	1.27	0.073	1.5	0.157	1.14	0.497	1.31
1437974_a_at	Hk1	hexokinase 1	1.13	0.395	1.34	0.195	1.64	0.012	2.87	0.177	1.74
1446123_at	B230396O12Rik	RIKEN cDNA B230396O12 gene	1.49	0.269	1.16	0.742	1.46	0.233	1.13	0.804	1.31
1416619_at	4632428N05Rik	RIKEN cDNA 4632428N05 gene	1.3	0.002	1.33	0.067	1.48	0.026	1.45	0.065	1.39
1446517_at	Car12	Carbonic anyhydrase 12	1.06	0.449	2	0.514	1.05	0.677	1.47	0.42	1.4
1446077_at	4833446K15Rik	RIKEN cDNA 4833446K15 gene	1.1	0.902	1.03	0.952	1.98	0.429	2.21	0.259	1.58
1421983_s_at	Hnf4a	hepatic nuclear factor 4, alpha	1.23	0.503	1.05	0.853	1.83	0.373	1.16	0.831	1.32
1423294_at	Mest	mesoderm specific transcript	1.02	0.959	1.36	0.09	1.74	0.16	1.63	0.331	1.44
1452772_at	Tnks2	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	1.59	0.36	1.01	0.98	1.52	0.5	1.11	0.882	1.31
1459963_at	Pola1	Polymerase (DNA directed), alpha 1	1.23	0.587	1.87	0.288	1.02	0.968	1.25	0.783	1.34
1417632_at	Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit A1	1.41	0.387	1.37	0.03	1.34	0.046	2.28	0.161	1.6
1451161_a_at	Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	1.1	0.742	1.69	0.024	1.34	0.027	1.74	0.295	1.47
1440030_at	---	---	1.69	0.001	1.43	0.586	1.01	0.987	1.97	0.045	1.52
1430442_at	Nos1ap	nitric oxide synthase 1 (neuronal) adaptor protein	1.24	0.612	1.75	0.376	1.14	0.725	1.75	0.267	1.47
1425294_at	Slamf8	SLAM family member 8	1.14	0.775	1.64	0.197	1.35	0.59	1.06	0.887	1.3
1444369_at	2310016D23Rik	RIKEN cDNA 2310016D23 gene	1.95	0.23	1.11	0.55	1.07	0.667	1.06	0.942	1.3
1416273_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	1.03	0.906	1.32	0.201	1.78	0.066	3.21	0.163	1.84
1421441_at	Angpt1	angiopoietin 1	1.57	0.555	1.2	0.689	1.37	0.701	2.99	0.337	1.78
1418129_at	Dhcr24	24-dehydrocholesterol reductase	1.28	0.584	1.57	0.054	1.29	0.506	2.01	0.284	1.54
1430628_at	Jmjd2c	jumonji domain containing 2C	1.32	0.573	1.2	0.831	1.62	0.162	1.7	0.105	1.46

1453307_a_at	Anapc5	anaphase-promoting complex subunit 5	1.42	0.504	1.14	0.681	1.58	0.295	1.93	0.334	1.52
1433275_at	4933401B01Rik	RIKEN cDNA 4933401B01 gene	1.26	0.774	1.66	0.254	1.22	0.76	1.98	0.14	1.53
1424060_at	Neil3	nei like 3 (E. coli)	1.23	0.767	1.15	0.777	1.77	0.372	3.89	0.182	2.01
1423788_at	Nup133	nucleoporin 133	1.11	0.736	1.46	0.431	1.58	0.203	3.98	0.097	2.03
1451691_at	Ednra	endothelin receptor type A	1.61	0.082	1.44	0.391	1.1	0.811	1.23	0.255	1.34
1453713_s_at	4930546H06Rik	RIKEN cDNA 4930546H06 gene	1.06	0.927	1.81	0.28	1.27	0.458	1.15	0.621	1.32
1427414_at	Prkar2a	protein kinase, cAMP dependent regulatory, type II alpha	1.5	0.519	1.38	0.489	1.27	0.581	1.3	0.678	1.36
1419482_at	C3ar1	complement component 3a receptor 1	1.26	0.344	1.3	0.287	1.59	0.151	2.26	0.212	1.6
1424961_at	Tapbpl	TAP binding protein-like	1.18	0.523	1.62	0.144	1.35	0.196	1.04	0.875	1.3
1426680_at	Sepn1	selenoprotein N, 1	1.25	0.294	1.64	0.08	1.26	0.12	1.37	0.028	1.38
1426442_at	Gpm6a	glycoprotein m6a	1.08	0.631	1.65	0.109	1.42	0.435	2.16	0.069	1.58
1417291_at	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	1.25	0.119	1.64	0.034	1.26	0.064	1.18	0.291	1.33
1415865_s_at	Bpgm	2,3-bisphosphoglycerate mutase	1.29	0.319	1.19	0.559	1.67	0.386	2.3	0.298	1.61
1419106_at	2210409E12Rik	RIKEN cDNA 2210409E12 gene	1.16	0.515	1.75	0.474	1.24	0.519	1.6	0.548	1.44
1430777_a_at	Golph3	golgi phosphoprotein 3	1.11	0.819	1.08	0.842	1.95	0.22	1.55	0.246	1.43
1432371_a_at	1700109K24Rik	RIKEN cDNA 1700109K24 gene	1.08	0.814	1.03	0.8	2.05	0.286	2.52	0.138	1.67
1442705_at	C76938	expressed sequence C76938	1.22	0.503	1.59	0.156	1.35	0.535	1.02	0.961	1.29
1434325_x_at	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	1.5	0.1	1.55	0.128	1.11	0.501	1.95	0.425	1.53
1430557_at	4930434J08Rik	RIKEN cDNA 4930434J08 gene	1.84	0.152	1.1	0.869	1.22	0.666	1.25	0.619	1.35
1435722_at	Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)	1.11	0.213	1.47	0.324	1.58	0.063	1.48	0.187	1.41
1425711_a_at	Akt1	thymoma viral proto-oncogene 1	1.35	0.512	1.56	0.278	1.25	0.579	1.24	0.637	1.35
1428278_at	Zdhhc24	zinc finger, DHHC domain containing 24	1.29	0.442	1.34	0.186	1.53	0.021	1.31	0.403	1.37
1436945_x_at	Stim1	stromal interaction molecule 1	1.36	0.346	1.63	0.186	1.17	0.632	1.4	0.164	1.39
1432616_at	4833422B07Rik	RIKEN cDNA 4833422B07 gene	1.01	0.981	1.71	0.117	1.43	0.382	1.04	0.947	1.3
1425753_a_at	Ung	uracil DNA glycosylase	1.17	0.541	1.4	0.206	1.59	0.235	1.41	0.43	1.39
1423414_at	Ptgs1	prostaglandin-endoperoxide synthase 1	1.25	0.135	1.72	0.008	1.19	0.345	1.59	0.014	1.44
1435802_at	Zfp499	zinc finger protein 499	1.12	0.308	1.53	0.439	1.51	0.02	1.44	0.022	1.4
1427483_at	Slc25a24	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 24	1.87	0.028	1.24	0.543	1.06	0.882	3.12	0.231	1.82
1453880_s_at	1700041C02Rik	RIKEN cDNA 1700041C02 gene	1.25	0.834	1.34	0.63	1.57	0.369	1.08	0.924	1.31
1417323_at	Psrc1	proline/serine-rich coiled-coil 1	1.52	0.034	1.34	0.459	1.31	0.099	2.96	0.114	1.78
1443063_at	A330019N05Rik	RIKEN cDNA A330019N05 gene	1.44	0.237	1.03	0.92	1.7	0.089	1.96	0.011	1.53
1425192_at	Klhl25	kelch-like 25 (Drosophila)	1.24	0.325	1.1	0.736	1.83	0.126	2.48	0.286	1.66
1425547_a_at	Klc4	kinesin light chain 4	1.06	0.901	1.22	0.373	1.9	0.235	1.79	0.253	1.49
1427457_a_at	Bmp1	bone morphogenetic protein 1	1.69	0.232	1.43	0.317	1.06	0.814	1.4	0.356	1.4
1451091_at	Txndc5	thioredoxin domain containing 5	1.31	0.012	1.1	0.18	1.76	0.02	1.33	0.46	1.38
1458647_at	6430553K19Rik	RIKEN cDNA 6430553K19 gene	1.8	0.427	1.25	0.692	1.13	0.618	1.18	0.648	1.34
1454549_at	2900005I04Rik	RIKEN cDNA 2900005I04 gene	1.85	0.039	1.11	0.88	1.23	0.762	1.87	0.282	1.51
1430394_a_at	Abcb9	ATP-binding cassette, sub-family B (MDR/TAP), member 9	1.14	0.795	1.35	0.726	1.69	0.433	1.36	0.534	1.39
1420274_at	Tap1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	1.07	0.931	2.03	0.384	1.08	0.889	1.55	0.39	1.43
1423021_s_at	Insl3 /// Jak3	insulin-like 3 /// Janus kinase 3	1.3	0.046	1.19	0.303	1.69	0.089	1.42	0.203	1.4
1450404_at	Slc23a1	solute carrier family 23 (nucleobase transporters), member 1	1.47	0.195	1.08	0.766	1.63	0.159	1.55	0.23	1.43
1436123_at	Bsn	bassoon	1.57	0.281	1.56	0.452	1.06	0.774	1.07	0.905	1.31
1420856_a_at	Lancl2	LanC (bacterial lantibiotic synthetase component C)-like 2	1.15	0.729	1.24	0.787	1.8	0.203	2.05	0.37	1.56
1453204_at	4933431K14Rik	RIKEN cDNA 4933431K14 gene	1.87	0.284	1.27	0.703	1.05	0.921	1.44	0.332	1.41
1458022_at	D830039M14Rik	RIKEN cDNA D830039M14 gene	1.55	0.54	1.55	0.414	1.09	0.603	1	0.999	1.3
1447660_at	Tbl3	transducin (beta)-like 3	1.26	0.545	1.42	0.543	1.51	0.279	1.01	0.988	1.3
1432295_a_at	2310035K24Rik	RIKEN cDNA 2310035K24 gene	1.13	0.593	1.23	0.274	1.83	0.123	1.55	0.311	1.44
1450142_a_at	Card14	caspase recruitment domain family, member 14	1.69	0.228	1.07	0.632	1.44	0.483	1.04	0.919	1.31
1427165_at	Il13ra1	interleukin 13 receptor, alpha 1	1.04	0.675	1.88	0.152	1.28	0.524	1.1	0.585	1.32
1448534_at	Sirpa	signal-regulatory protein alpha	1.03	0.93	1.39	0.274	1.77	0.13	1.58	0.048	1.44
1424278_a_at	Birc5	baculoviral IAP repeat-containing 5	1.36	0.69	1.22	0.505	1.62	0.137	4.85	0.148	2.26
1427679_at	Lats1	large tumor suppressor	1.29	0.319	1.35	0.329	1.55	0.315	1.41	0.53	1.4
1459858_x_at	Crtac1	cartilage acidic protein 1	1.03	0.965	1.52	0.209	1.64	0.378	2.09	0.236	1.57

1458444_at	AI195381	Expressed sequence AI195381	1.06	0.825	2.01	0.037	1.13	0.451	1.45	0.255	1.41
1420001_at	D7Ertd1e	DNA segment, Chr 7, ERATO Doi 1, expressed	1.51	0.631	1.34	0.539	1.35	0.436	2.05	0.005	1.56
1417699_at	Gtf2f1	general transcription factor IIF, polypeptide 1	1.33	0.3	1.22	0.249	1.65	0.088	1.58	0.246	1.44
1426673_at	Cdh3	cadherin 3	1.95	0.493	1.19	0.773	1.06	0.885	2.31	0.138	1.63
1425322_at	Ifnz /// LOC435791	interferon zeta /// similar to interferon zeta /// similar to interferon zeta /// similar to	1.12	0.662	1.62	0.259	1.46	0.118	1.38	0.353	1.4
1417337_at	Epb4.2	erythrocyte protein band 4.2	1.03	0.918	1.25	0.691	1.92	0.287	7.8	0.188	3
1458521_at	Jmjd1c	Jumonji domain containing 1C	1.89	0.003	1.3	0.497	1.01	0.976	1.02	0.757	1.31
1451811_at	Cacng6	calcium channel, voltage-dependent, gamma subunit 6	1.28	0.444	1.68	0.209	1.25	0.319	1.83	0.334	1.51
1449293_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	1.35	0.066	1.65	0.467	1.2	0.681	3.52	0.117	1.93
1424007_at	Gdf10	growth differentiation factor 10	1.82	0.071	1.32	0.199	1.07	0.845	1.05	0.632	1.31
1449517_at	Qpctl	glutaminyl-peptide cyclotransferase-like	1.26	0.313	1.43	0.061	1.52	0.01	1.29	0.053	1.38
1450203_at	Smyd1	SET and MYND domain containing 1	1.11	0.384	1.51	0.268	1.59	0.141	1.28	0.297	1.37
1425447_at	Dkk4	dickkopf homolog 4 (Xenopus laevis)	1.64	0.619	1.13	0.809	1.44	0.19	1.3	0.679	1.38
1448757_at	Pml	promyelocytic leukemia	1.09	0.506	1.03	0.863	2.09	0.074	1.16	0.351	1.34
1446140_at	Pcm1	Pericentriolar material 1	1.44	0.228	1.15	0.603	1.62	0.006	1.36	0.512	1.39
1460267_at	Dmrt3	doublesex and mab-3 related transcription factor 3	1.24	0.222	1.74	0.392	1.23	0.431	2	0.077	1.55
1444367_at	Fndc7	fibronectin type III domain containing 7	1.35	0.645	1.23	0.41	1.64	0.149	1.93	0.412	1.53
1456003_a_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.1	0.622	1.91	0.15	1.2	0.422	1.71	0.04	1.48
1459429_at	Ktn1	kinectin 1	1.14	0.751	2.04	0.199	1.03	0.936	1.4	0.368	1.4
1429642_at	Anubl1	AN1, ubiquitin-like, homolog (Xenopus laevis)	1.24	0.161	1.32	0.054	1.66	0.286	2.15	0.06	1.59
1426331_a_at	Frmd4b	FERM domain containing 4B	1.34	0.33	1.51	0.101	1.37	0.492	1.35	0.467	1.39
1457448_at	Pnpla1	patatin-like phospholipase domain containing 1	1.61	0.342	1.24	0.655	1.37	0.603	1.97	0.218	1.55
1441808_at	2410002I01Rik	RIKEN cDNA 2410002I01 gene	1.7	0.283	1.26	0.374	1.26	0.525	1.32	0.531	1.38
1434498_at	Gm1673	gene model 1673, (NCBI)	1.04	0.937	1.89	0.33	1.3	0.195	1.34	0.607	1.39
1419665_a_at	Nupr1	nuclear protein 1	1.46	0.446	1.75	0.14	1.02	0.942	1.04	0.866	1.32
1449319_at	Rspo1	R-spondin homolog (Xenopus laevis)	1.73	0.253	1.27	0.148	1.23	0.57	1.5	0.324	1.43
1448402_at	Tln1	talin 1	1.42	0.29	1.15	0.227	1.66	0.025	1.2	0.439	1.36
1443805_at	Dact3	dact 3	1.19	0.647	1.41	0.292	1.63	0.277	1.01	0.979	1.31
1417926_at	Luzp5	leucine zipper protein 5	1.41	0.303	1.69	0.026	1.14	0.472	2.6	0.193	1.71
1432767_at	E130112B07Rik	RIKEN cDNA E130112B07 gene	1.19	0.201	1.42	0.481	1.63	0.39	2.22	0.316	1.61
1428643_at	Mgat5	mannoside acetylglucosaminyltransferase 5	1.04	0.693	1.86	0.131	1.33	0.002	1.11	0.453	1.34
1450269_a_at	Pfkl	phosphofructokinase, liver, B-type	1.05	0.563	1.41	0.143	1.78	0.001	1.08	0.516	1.33
1443780_at	---	Transcribed locus	1.57	0.045	1.56	0.105	1.11	0.829	1.55	0.52	1.45
1449906_at	Selp	selectin, platelet	1.32	0.77	1.76	0.038	1.17	0.536	1.97	0.371	1.55
1450364_a_at	Havcr1	hepatitis A virus cellular receptor 1	1.47	0.003	1.5	0.129	1.27	0.637	1.01	0.984	1.31
1435083_at	Ctxn1	cortexin 1	1.44	0.147	1.24	0.557	1.58	0.146	1.32	0.431	1.39
1423231_at	Nrgn	neurogranin	1.27	0.144	1.62	0.118	1.36	0.354	1.4	0.351	1.41
1430799_at	5830432E09Rik	RIKEN cDNA 5830432E09 gene	1.63	0.507	1.55	0.478	1.07	0.812	1.28	0.723	1.38
1453148_at	Sema3d	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	2.01	0.001	1.12	0.771	1.12	0.506	1.07	0.827	1.33
1435703_at	---	Transcribed locus	1.63	0.278	1.3	0.661	1.32	0.231	1.04	0.542	1.32
1418914_s_at	Bhmt2	betaine-homocysteine methyltransferase 2	1.03	0.844	1.14	0.218	2.09	0.045	2.63	0.071	1.72
1435587_at	Pcid2	PCI domain containing 2	1.36	0.25	1.28	0.352	1.62	0.069	1.16	0.424	1.36
1417101_at	Hspa2	heat shock protein 2	1.05	0.702	1.5	0.118	1.71	0.019	1.13	0.589	1.35
1457702_at	Gpr12	G-protein coupled receptor 12	1.11	0.739	2.13	0.337	1.02	0.902	1.87	0.381	1.53
1417602_at	Per2	period homolog 2 (Drosophila)	1.4	0.721	1.27	0.611	1.59	0.355	1.13	0.079	1.35
1449018_at	Pfn1	profilin 1	1.43	0.13	1.13	0.58	1.7	0.178	1.25	0.377	1.38
1432163_at	4930567K12Rik	RIKEN cDNA 4930567K12 gene	1.45	0.1	1.73	0.044	1.08	0.852	1.06	0.925	1.33
1426332_a_at	Cldn3	claudin 3	2.01	0.116	1	0.992	1.25	0.58	1.2	0.593	1.37
1446019_at	---	Transcribed locus	1.62	0.52	1.56	0.347	1.07	0.855	1.01	0.986	1.32
1457993_at	---	---	1.78	0.387	1.05	0.915	1.44	0.186	4.06	0.021	2.08
1418847_at	Arg2	arginase type II	1.57	0.149	1.56	0.336	1.13	0.778	1.39	0.524	1.41
1450399_at	Psen1	presenilin 1	1.09	0.732	1.17	0.418	2.01	0.074	1.24	0.285	1.38
1451127_at	AW146242	expressed sequence AW146242	1.26	0.24	1.76	0.009	1.24	0.155	4.14	0.091	2.1

1439860_at	Eef2k	eukaryotic elongation factor-2 kinase	1.31	0.681	1.56	0.13	1.4	0.105	1.76	0.273	1.51
1423761_at	5630401D24Rik	RIKEN cDNA 5630401D24 gene	1.17	0.52	1.41	0.12	1.69	0.224	1.07	0.671	1.34
1427221_at	Xtrp3s1	X transporter protein 3 similar 1 gene	1.61	0.221	1.03	0.957	1.63	0.022	3.27	0.228	1.89
1425285_a_at	Rab27a	RAB27A, member RAS oncogene family	1.21	0.791	1.07	0.913	2	0.298	1.37	0.381	1.41
1426975_at	4632413K17Rik	RIKEN cDNA 4632413K17 gene	1.56	0.364	1.04	0.92	1.68	0.424	1.17	0.777	1.36
1441916_s_at	Odf3	outer dense fiber of sperm tails 3	1.33	0.639	1.04	0.805	1.9	0.015	1.92	0.164	1.55
1426604_at	Rnasel	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	1.08	0.392	2.11	0	1.09	0.61	1.87	0.132	1.54
1425810_a_at	Csrp1	cysteine and glycine-rich protein 1	1.44	0.414	1.4	0.389	1.43	0.525	1.02	0.947	1.33
1420133_at	RP23-289L21.1	hypothetical protein LOC433719	1.58	0.443	1.51	0.644	1.19	0.692	1.19	0.761	1.37
1417502_at	Tspan7	tetraspanin 7	1.05	0.899	1.2	0.518	2.03	0.197	1.41	0.005	1.42
1417228_at	Capn1	calpain 1	1.44	0.343	1.41	0.001	1.44	0.145	2.3	0.057	1.65
1418206_at	Sdf2l1	stromal cell-derived factor 2-like 1	1.11	0.487	1.51	0.358	1.66	0.087	1.9	0.033	1.55
1450653_at	Spz1	spermatogenic Zip 1	1.17	0.807	1.88	0.388	1.23	0.628	1.59	0.546	1.47
1422745_at	Bicd2	bicaudal D homolog 2 (Drosophila)	1.25	0.606	1.46	0.489	1.58	0.152	3.09	0.006	1.84
1423775_s_at	Prc1	protein regulator of cytokinesis 1	1.16	0.726	1.7	0.268	1.43	0.266	5.37	0.167	2.41
1420081_s_at	D2Ertd750e	DNA segment, Chr 2, ERATO Doi 750, expressed	1.92	0.233	1.09	0.821	1.29	0.239	1.83	0.229	1.53
1441757_at	1190002F15Rik	RIKEN cDNA 1190002F15 gene	1.65	0.357	1.15	0.84	1.49	0.21	4.43	0.175	2.18
1449882_a_at	Casr	calcium-sensing receptor	1.1	0.888	2.1	0.114	1.09	0.863	1	0.994	1.32
1451921_a_at	Nfat5	nuclear factor of activated T-cells 5	1.28	0.618	1.41	0.566	1.6	0.343	1.11	0.863	1.35
1426165_a_at	Casp3	caspase 3	1.39	0.556	1.14	0.734	1.76	0.379	1.55	0.476	1.46
1432476_at	1700040F17Rik	RIKEN cDNA 1700040F17 gene	1.71	0.57	1.19	0.554	1.39	0.577	1.46	0.383	1.44
1436000_a_at	Skp2	S-phase kinase-associated protein 2 (p45)	1.66	0.37	1.51	0.388	1.13	0.532	1.78	0.002	1.52
1417271_a_at	Eng	endoglin	1.52	0.214	1.32	0.219	1.45	0.097	1.08	0.658	1.34
1445674_at	Nos3as	Nitric oxide synthase 3 antisense	1.4	0.512	1.09	0.805	1.81	0.376	2.08	0.142	1.59
1427013_at	Car9	carbonic anhydrase 9	1.61	0.315	1.52	0.214	1.17	0.511	1.16	0.605	1.36
1459554_at	---	---	1.19	0.259	2.03	0.407	1.08	0.641	1.37	0.607	1.42
1423549_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.31	0.066	1.17	0.774	1.83	0.166	1.38	0.387	1.42
1439417_at	Qscn6	Quiescin Q6	2	0.401	1.23	0.787	1.07	0.859	1.36	0.393	1.42
1418020_s_at	Cpd	carboxypeptidase D	1.67	0.181	1.33	0.559	1.3	0.589	3.7	0.223	2
1421265_a_at	Rbm38	RNA binding motif protein 38	1.01	0.926	1.03	0.847	2.26	0.101	2.16	0.223	1.62
1439617_s_at	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	1	0.994	1.07	0.811	2.23	0.317	1	0.991	1.33
1457708_at	Mbd4	methyl-CpG binding domain protein 4	1.09	0.732	1.98	0.369	1.24	0.229	1.18	0.391	1.37
1426897_at	Rcc2	regulator of chromosome condensation 2	1.25	0.005	1.01	0.955	2.05	0.029	1.12	0.336	1.36
1452423_at	Pclo	piccolo (presynaptic cytomatrix protein)	1.29	0.801	1.44	0.654	1.59	0.238	1.87	0.081	1.55
1433728_at	BC038479	cDNA sequence BC038479	1.38	0.104	1.38	0.485	1.56	0.117	1.02	0.935	1.33
1441150_x_at	---	Transcribed locus	1.36	0.267	1.19	0.09	1.77	0.441	1.65	0.134	1.49
1455779_at	---	Transcribed locus	1.06	0.885	1.58	0.397	1.68	0.089	1.14	0.753	1.36
1419970_at	Slc35a5	solute carrier family 35, member A5	1.79	0.541	1.22	0.671	1.3	0.07	1.28	0.541	1.4
1419240_at	Tex14	testis expressed gene 14	1.94	0.247	1.36	0.364	1.02	0.946	3.23	0.018	1.89
1439436_x_at	Incenp	inner centromere protein	1.17	0.758	1.38	0.018	1.78	0.055	2.58	0.163	1.72
1417423_at	Grina	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1 (glutam	1.23	0.51	1.46	0.077	1.63	0.16	3.51	0.106	1.96
1456080_a_at	Serinc3	serine incorporator 3	1.3	0.613	1.43	0.412	1.6	0.246	1.3	0.412	1.41
1448550_at	Lbp	lipopolysaccharide binding protein	1.37	0.329	1.76	0.204	1.2	0.231	2.6	0.338	1.73
1448276_at	Tspan4	tetraspanin 4	1.51	0.331	1.81	0.049	1.01	0.99	1.24	0.236	1.39
1421411_at	Pstpip2	proline-serine-threonine phosphatase-interacting protein 2	1.48	0.583	1.1	0.805	1.75	0.379	1.51	0.486	1.46
1450166_at	Ids	iduronate 2-sulfatase	1.55	0.167	1.02	0.962	1.77	0.091	1.25	0.638	1.4
1455266_at	Kif5c	kinesin family member 5C	1.13	0.528	2.11	0.294	1.09	0.826	1.77	0.192	1.53
1424600_at	Abp1	amiloride binding protein 1 (amine oxidase, copper-containing)	2.04	0.113	1.14	0.758	1.15	0.589	1.81	0.128	1.54
1430399_at	2810458H16Rik	RIKEN cDNA 2810458H16 gene	1.86	0.547	1.13	0.76	1.34	0.295	1.06	0.9	1.35
1419962_at	---	Transcribed locus	2.06	0.068	1.13	0.906	1.14	0.71	1.14	0.777	1.37
1422182_at	Hnf4g	hepatocyte nuclear factor 4, gamma	1.43	0.739	1.51	0.038	1.39	0.207	1.65	0.435	1.5
1434137_x_at	1810010M01Rik	RIKEN cDNA 1810010M01 gene	1.96	0.037	1.07	0.883	1.3	0.269	1.29	0.629	1.41
1449833_at	Sprr2f	small proline-rich protein 2F	1.79	0.376	1.04	0.798	1.51	0.227	1.1	0.738	1.36

1439148_a_at	Pfkl	phosphofructokinase, liver, B-type	1.12	0.053	1.34	0.168	1.88	0.009	1.06	0.627	1.35
1430044_at	4930415F15Rik	RIKEN cDNA 4930415F15 gene	1.7	0.051	1.12	0.864	1.52	0.21	1.65	0.232	1.5
1447392_s_at	Cpd	carboxypeptidase D	1.03	0.972	2.16	0.196	1.15	0.822	1.5	0.438	1.46
1420918_at	Sgk3	serum/glucocorticoid regulated kinase 3	1.08	0.543	1.05	0.886	2.21	0.076	1.42	0.494	1.44
1454630_at	Samd14	sterile alpha motif domain containing 14	1.45	0.202	1.28	0.479	1.61	0.081	4.04	0.189	2.1
1459740_s_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	1.19	0.416	1.23	0.363	1.93	0.013	1.52	0.187	1.47
1437824_at	Grid2	glutamate receptor, ionotropic, delta 2	1.59	0.336	1.13	0.21	1.63	0.392	2.46	0.167	1.7
1444040_at	Lair1	leukocyte-associated Ig-like receptor 1	1.19	0.14	1.92	0.079	1.24	0.249	1.05	0.799	1.35
1439525_at	1700066D14Rik	RIKEN cDNA 1700066D14 gene	1.83	0.31	1.44	0.104	1.08	0.354	1.09	0.537	1.36
1423746_at	Txndc5	thioredoxin domain containing 5	1.36	0.353	1.07	0.746	1.93	0.065	2.04	0.22	1.6
1432184_a_at	2610204M08Rik	RIKEN cDNA 2610204M08 gene	1.61	0.117	1.58	0.026	1.16	0.321	1.08	0.655	1.36
1416101_a_at	Hist1h1c	histone 1, H1c	1.21	0.278	1.59	0.211	1.55	0.146	1.21	0.688	1.39
1429203_at	2410076I21Rik	RIKEN cDNA 2410076I21 gene	1.44	0.629	1.75	0.197	1.16	0.752	2.05	0.118	1.6
1450771_at	Fut9	fucosyltransferase 9	1.04	0.927	2.29	0.111	1.02	0.974	1.02	0.974	1.34
1441879_x_at	Mkrn1	makorin, ring finger protein, 1	1.45	0.338	1.51	0.289	1.4	0.226	2.7	0.204	1.76
1434635_at	Rph3a	rabphilin 3A	1.04	0.864	1.39	0.51	1.94	0.095	1.31	0.569	1.42
1419890_at	---	---	1.27	0.641	1.75	0.375	1.35	0.458	1.15	0.754	1.38
1417153_at	Btbd14a	BTB (POZ) domain containing 14A	1.35	0.549	1.04	0.934	1.97	0.145	1.72	0.025	1.52
1448650_a_at	Pole	polymerase (DNA directed), epsilon	1.25	0.489	1.29	0.724	1.83	0.102	2.99	0.141	1.84
1428661_at	Nfkbil2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 2	1.51	0.666	1.34	0.519	1.51	0.311	1.33	0.402	1.42
1433862_at	Espl1	extra spindle poles-like 1 (S. cerevisiae)	1.2	0.274	1.92	0.167	1.24	0.042	2.75	0.221	1.78
1445763_at	1700013F07Rik	RIKEN cDNA 1700013F07 gene	1.42	0.372	1.75	0.069	1.2	0.298	1.19	0.652	1.39
1432737_at	2810026P18Rik	RIKEN cDNA 2810026P18 gene	1.51	0.255	1.21	0.509	1.65	0.233	1.5	0.492	1.47
1420028_s_at	Mcm3 /// LOC6719(	minichromosome maintenance deficient 3 (S. cerevisiae) /// similar to DNA replica	1.39	0.073	1.27	0.085	1.71	0.104	1.72	0.231	1.52
1419280_at	Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	1.15	0.669	1.86	0.141	1.36	0.354	1.35	0.312	1.43
1439621_at	---	17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920178F	1.03	0.965	1.97	0.109	1.37	0.272	1.43	0.622	1.45
1438518_at	9930021J03Rik	RIKEN cDNA 9930021J03 gene	1.4	0.469	1.52	0.502	1.45	0.275	5.79	0.189	2.54
1441120_at	Ceacam16	CEA-related cell adhesion molecule 16	1.31	0.513	1.4	0.228	1.66	0.136	1.42	0.523	1.45
1420867_at	Tmed2	transmembrane emp24 domain trafficking protein 2	1.69	0.354	1.12	0.739	1.56	0.558	1.79	0.153	1.54
1425620_at	Tgfbr3	transforming growth factor, beta receptor III	1.29	0.625	1.55	0.35	1.54	0.545	1.31	0.509	1.42
1458447_at	Cenpf	centromere protein F	1.95	0.012	1.24	0.593	1.19	0.404	5.61	0.147	2.5
1440191_s_at	Leng9	leukocyte receptor cluster (LRC) member 9	1.66	0.402	1.04	0.933	1.69	0.113	1.36	0.112	1.43
1421071_at	Vhlh	von Hippel-Lindau syndrome homolog	1.43	0.3	1.84	0.022	1.11	0.668	1.1	0.781	1.37
1447418_at	Kcnq1	Potassium voltage-gated channel, subfamily Q, member 1	1.73	0.458	1.52	0.558	1.13	0.855	1.52	0.471	1.48
1451798_at	Il1rn	interleukin 1 receptor antagonist	1.03	0.821	1.87	0.067	1.49	0.218	1.13	0.069	1.38
1447678_at	Dhrs10	Dehydrogenase/reductase (SDR family) member 10	1.72	0.005	1.37	0.192	1.29	0.564	1.06	0.892	1.36
1421026_at	Gna12	guanine nucleotide binding protein, alpha 12	1.72	0.502	1	0.995	1.66	0.366	1.69	0.195	1.52
1459807_x_at	4933406E20Rik	RIKEN cDNA 4933406E20 gene	1.41	0.366	1.2	0.492	1.78	0.055	1.34	0.154	1.43
1448626_at	Cdk5rap1	CDK5 regulatory subunit associated protein 1	1.54	0.323	1.26	0.197	1.59	0.026	1.78	0.173	1.54
1459519_at	---	---	1.29	0.675	1.81	0.355	1.28	0.587	1.65	0.092	1.51
1438855_x_at	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	1.08	0.766	1.74	0.034	1.57	0.098	2.01	0.175	1.6
1436148_at	---	Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:643053	1.04	0.967	1.73	0.257	1.62	0.192	1.46	0.467	1.46
1434357_a_at	Kpnb1	karyopherin (importin) beta 1	1.13	0.502	1.73	0.046	1.53	0.094	1.84	0.198	1.56
1457986_at	---	Transcribed locus	1.81	0.293	1.23	0.783	1.35	0.444	1.83	0.368	1.56
1439523_at	D330027G24Rik	RIKEN cDNA D330027G24 gene	1.35	0.308	1.09	0.671	1.96	0.384	1.23	0.289	1.41
1418714_at	Dusp8	dual specificity phosphatase 8	1.09	0.441	2.3	0.067	1.01	0.982	3.69	0.134	2.02
1422965_at	Agtrap	angiotensin II, type I receptor-associated protein	1.05	0.824	1.59	0.421	1.75	0.105	1.67	0.181	1.52
1460309_at	Tal2	T-cell acute lymphocytic leukemia 2	1.45	0.701	1.65	0.489	1.3	0.394	1.21	0.673	1.4
1419943_s_at	Ccnb1	cyclin B1	1.27	0.453	1.3	0.501	1.84	0.46	6.14	0.209	2.63
1453138_at	Rpusd2	RNA pseudouridylate synthase domain containing 2	1.13	0.843	1.42	0.35	1.85	0.181	1.57	0.536	1.49
1425825_at	C230094A16Rik	RIKEN cDNA C230094A16 gene	1.15	0.678	1.97	0.152	1.28	0.031	1.41	0.159	1.45
1421721_a_at	Arnt	aryl hydrocarbon receptor nuclear translocator	1.54	0.169	1.31	0.458	1.54	0.271	1.24	0.505	1.41
1421832_at	Twsg1	twisted gastrulation homolog 1 (Drosophila)	1.54	0.451	1.05	0.913	1.81	0.424	1.74	0.202	1.53

1434278_at	Mtm1	X-linked myotubular myopathy gene 1	1.07	0.609	1.41	0.129	1.93	0.349	2.06	0.121	1.61
1460266_at	1700094J05Rik	RIKEN cDNA 1700094J05 gene	1.38	0.259	1.28	0.52	1.75	0.087	1.13	0.706	1.38
1433661_at	BC034204	cDNA sequence BC034204	1.06	0.859	1.05	0.765	2.3	0.02	1.5	0.214	1.48
1431430_s_at	Trim59 /// LOC630	tripartite motif-containing 59 /// similar to mouse RING finger 1	1.01	0.988	1.54	0.095	1.86	0.173	5.47	0.289	2.47
1419027_s_at	Gltp	glycolipid transfer protein	1.23	0.153	2.11	0.014	1.07	0.527	1.15	0.62	1.39
1443405_at	---	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030	1.07	0.889	1.77	0.384	1.57	0.346	1.04	0.958	1.36
1448158_at	Sdc1	syndecan 1	1.27	0.772	1.42	0.407	1.72	0.302	3.16	0.077	1.89
1453067_at	2610040C18Rik	RIKEN cDNA 2610040C18 gene	1.09	0.913	1.72	0.454	1.61	0.342	1.22	0.506	1.41
1458701_at	Prei4	preimplantation protein 4	1.85	0.245	1.1	0.851	1.47	0.31	1.71	0.364	1.53
1448148_at	Grn	granulin	1	0.995	1.52	0.057	1.9	0.015	1.26	0.469	1.42
1450615_at	Ear4	eosinophil-associated, ribonuclease A family, member 4	1.19	0.853	1.07	0.887	2.16	0.088	1.47	0.443	1.47
1425548_a_at	Lst1	leukocyte specific transcript 1	1.4	0.176	1.5	0.009	1.52	0.276	1.08	0.818	1.38
1449382_at	Slc6a12	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12	2.17	0.083	1.05	0.755	1.2	0.598	1.21	0.312	1.41
1428902_at	Chst11	carbohydrate sulfotransferase 11	1.17	0.423	2.18	0.273	1.08	0.345	1.46	0.107	1.47
1436994_a_at	Hist1h1c	histone 1, H1c	1.09	0.71	1.71	0.205	1.63	0.139	1.13	0.799	1.39
1422180_a_at	Mcpt6	mast cell protease 6	1.18	0.794	1.23	0.727	2.02	0.301	1.47	0.471	1.47
1422649_at	Cntn6	contactin 6	1.54	0.475	1.25	0.747	1.63	0.261	1.69	0.204	1.53
1424757_at	BC018242	cDNA sequence BC018242	1.01	0.953	1.63	0.268	1.8	0.123	1.73	0.371	1.54
1418541_at	Cenpo	centromere protein O	1.26	0.585	1.95	0.036	1.23	0.388	1.46	0.165	1.47
1421188_at	Ccr2	chemokine (C-C motif) receptor 2	1.54	0.017	1.85	0.066	1.04	0.901	1.67	0.002	1.53
1424356_a_at	Metrnl	meteorin, glial cell differentiation regulator-like	1.05	0.6	1.78	0.112	1.62	0.003	1.68	0.149	1.53
1459820_at	A630082K20Rik	RIKEN cDNA A630082K20 gene	1.13	0.603	1.95	0.359	1.36	0.437	1.17	0.217	1.4
1416802_a_at	Cdca5	cell division cycle associated 5	1.02	0.921	1.48	0.336	1.94	0.279	2.86	0.203	1.83
1454164_at	4921523L03Rik	RIKEN cDNA 4921523L03 gene	2.18	0.547	1.08	0.852	1.18	0.623	1.19	0.861	1.41
1422016_a_at	Cenph	centromere protein H	1.22	0.738	1.81	0.382	1.42	0.366	3.01	0.275	1.86
1450378_at	Tapbp	TAP binding protein	1.49	0.408	1.24	0.57	1.72	0.267	1.36	0.363	1.45
1448520_at	Dclre1b	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	1.14	0.766	1.3	0.365	2.01	0.001	1.59	0.261	1.51
1430865_s_at	Ttll9	tubulin tyrosine ligase like family 9	1.3	0.788	1.47	0.236	1.68	0.324	1.21	0.721	1.42
1436508_at	2410014A08Rik	RIKEN cDNA 2410014A08 gene	1.64	0.095	1.19	0.655	1.63	0.419	1.13	0.727	1.4
1446149_at	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	2.2	0.02	1.12	0.53	1.14	0.551	1.1	0.827	1.39
1430692_a_at	Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	1.15	0.453	1.14	0.752	2.17	0.227	1.72	0.038	1.55
1417752_at	Coro1c	coronin, actin binding protein 1C	1.24	0.556	1.5	0.391	1.72	0.334	1.13	0.823	1.4
1427344_s_at	Rasd2	RASD family, member 2	1.15	0.59	2.18	0.291	1.14	0.636	1.2	0.715	1.42
1440291_at	---	Transcribed locus	1.09	0.737	1.78	0.176	1.6	0.368	1.07	0.8	1.38
1450097_s_at	Gna12	guanine nucleotide binding protein, alpha 12	1.89	0.303	1.06	0.874	1.51	0.395	2.03	0.102	1.62
1456893_at	---	Adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730013D	1.02	0.973	1.43	0.067	2.02	0.043	1.12	0.53	1.4
1416388_at	Pip5k2c	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	1.45	0.459	1.25	0.202	1.77	0.296	2.25	0.297	1.68
1448966_a_at	Nfat5	nuclear factor of activated T-cells 5	1.38	0.696	2.02	0.376	1.08	0.773	1.68	0.192	1.54
1421016_at	Ighmbp2	immunoglobulin mu binding protein 2	2.12	0.411	1.1	0.667	1.25	0.771	1.19	0.718	1.41
1443887_at	Ankrd13c	ankyrin repeat domain 13c	1.26	0.58	1.87	0.007	1.35	0.12	2.15	0.006	1.65
1454162_at	4930518P08Rik	RIKEN cDNA 4930518P08 gene	1.28	0.431	1.39	0.611	1.81	0.421	1.39	0.556	1.47
1439112_at	2810442I21Rik	RIKEN cDNA 2810442I21 gene	1.19	0.708	2.23	0.003	1.06	0.906	1.42	0.284	1.47
1450200_s_at	Csf2rb1 /// Csf2rb2	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage	1.3	0.493	1.29	0.428	1.9	0.047	1.51	0.089	1.5
1419153_at	2810417H13Rik	RIKEN cDNA 2810417H13 gene	1.34	0.356	1.61	0.154	1.54	0.213	2.02	0.186	1.62
1451546_s_at	Tmem40	transmembrane protein 40	1.5	0.315	1.11	0.87	1.87	0.215	1.99	0.433	1.62
1434366_x_at	C1qb	complement component 1, q subcomponent, beta polypeptide	1.42	0.24	1.8	0.001	1.27	0.462	1.17	0.576	1.41
1454193_at	5430401H09Rik	RIKEN cDNA 5430401H09 gene	1.84	0.001	1.17	0.686	1.47	0.307	7.97	0.18	3.11
1448602_at	Pygm	muscle glycogen phosphorylase	1.25	0.197	1.47	0.522	1.77	0.257	1.12	0.644	1.4
1448380_at	Lgals3bp	lectin, galactoside-binding, soluble, 3 binding protein	1.19	0.574	1.23	0.253	2.07	0.024	1.05	0.88	1.39
1419422_at	Pkd2l2	polycystic kidney disease 2-like 2	2.3	0.191	1.08	0.785	1.11	0.679	1.44	0.391	1.48
1418698_a_at	Fech	ferrochelatase	1.08	0.297	1.05	0.498	2.36	0.287	3.92	0.188	2.1
1417911_at	Ccna2	cyclin A2	1.16	0.504	1.58	0.074	1.76	0.11	4.7	0.177	2.3
1456043_at	Usp22	ubiquitin specific peptidase 22	1.23	0.687	1.72	0.07	1.55	0.206	1.01	0.97	1.38

1417963_at	Pltp	phospholipid transfer protein	1.68	0.012	1.55	0.011	1.27	0.135	1.52	0.114	1.51
1454597_at	4930423O20Rik	RIKEN cDNA 4930423O20 gene	1.11	0.867	1.35	0.604	2.04	0.016	1.23	0.599	1.43
1452818_at	Ttf2	transcription termination factor, RNA polymerase II	1.65	0.097	1.23	0.725	1.62	0.196	1.49	0.237	1.5
1454260_at	Uhmk1	U2AF homology motif (UHM) kinase 1	1.53	0.622	1.41	0.555	1.57	0.263	2.01	0.263	1.63
1418932_at	Nfil3	nuclear factor, interleukin 3, regulated	1.11	0.726	1.83	0.138	1.57	0.322	1.22	0.614	1.43
1420408_a_at	Abcc9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	1.48	0.014	1.85	0.166	1.19	0.577	1.18	0.505	1.42
1420382_at	Apob48r	apolipoprotein B48 receptor	1.5	0.246	1.31	0.309	1.71	0.144	1.25	0.28	1.44
1449941_at	Myo1e	myosin IE	1.74	0.43	1.23	0.765	1.56	0.306	1.35	0.708	1.47
1416253_at	Cdkn2d	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	1.1	0.593	1.66	0.136	1.77	0.248	2.31	0.164	1.71
1452181_at	Ckap4	cytoskeleton-associated protein 4	1.13	0.104	2.12	0.038	1.28	0.147	1.54	0.031	1.52
1417545_at	Trpv4	transient receptor potential cation channel, subfamily V, member 4	1.05	0.792	1.53	0.112	1.95	0.18	1.2	0.823	1.43
1432273_a_at	Darc	Duffy blood group, chemokine receptor	2.03	0.288	1.14	0.645	1.36	0.167	4.86	0.205	2.35
1447813_x_at	Sla	src-like adaptor	1.06	0.719	1.81	0.029	1.66	0.063	1.04	0.756	1.39
1436399_s_at	Nrk	Nik related kinase	1.29	0.742	2.06	0.039	1.18	0.641	2.21	0.059	1.69
1451904_a_at	Adam33	a disintegrin and metallopeptidase domain 33	1.93	0.16	1.52	0.087	1.08	0.625	1.06	0.875	1.4
1454992_at	Slc7a1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	1.22	0.324	1.71	0.105	1.6	0.065	1.63	0.087	1.54
1415989_at	Vcam1	vascular cell adhesion molecule 1	1.45	0.065	2.09	0.007	1	0.992	1.29	0.422	1.46
1460386_a_at	Slc1a1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, syst	1.12	0.705	1.04	0.859	2.38	0.106	1.36	0.45	1.48
1439785_at	9630013A20Rik	RIKEN cDNA 9630013A20 gene	1.89	0.429	1.59	0.259	1.06	0.866	1.6	0.286	1.54
1448061_at	Msr1	macrophage scavenger receptor 1	1.86	0.424	1.66	0.013	1.02	0.931	1.74	0.368	1.57
1434590_at	B230209C24Rik	RIKEN cDNA B230209C24 gene	1.69	0.107	1.84	0.191	1.02	0.859	1.43	0.119	1.49
1442486_at	---	---	1.29	0.292	1.56	0.265	1.7	0.409	1.33	0.531	1.47
1415993_at	Sqle	squalene epoxidase	1.11	0.495	2.2	0.157	1.24	0.246	1.32	0.625	1.47
1450731_s_at	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	1.17	0.743	2.17	0.036	1.21	0.301	1.97	0.079	1.63
1434789_at	Depdc1b	DEP domain containing 1B	1.08	0.676	1.84	0.246	1.63	0.19	5.39	0.182	2.48
1438852_x_at	Mcm6	minichromosome maintenance deficient 6 (MIS5 homolog, S. pombe) (S. cerevisi	1.36	0.074	1.79	0.014	1.41	0.269	2.4	0.151	1.74
1449856_at	Rgs18	regulator of G-protein signaling 18	1.3	0.55	1.27	0.611	1.99	0.155	1.08	0.857	1.41
1435721_at	Kcnq4	potassium voltage-gated channel, subfamily Q, member 4	1.05	0.946	1.37	0.302	2.13	0.097	2.04	0.062	1.65
1452226_at	Rcc2	regulator of chromosome condensation 2	1.9	0.205	1	0.99	1.66	0.204	1.02	0.942	1.39
1456323_at	Pofut1	protein O-fucosyltransferase 1	1.35	0.496	1.45	0.603	1.77	0.144	1.25	0.645	1.46
1423426_at	1300012G16Rik	RIKEN cDNA 1300012G16 gene	1.73	0.302	1.47	0.213	1.37	0.116	1.17	0.367	1.43
1419152_at	2810417H13Rik	RIKEN cDNA 2810417H13 gene	1.63	0.495	1.41	0.407	1.53	0.165	2.45	0.093	1.76
1428427_at	Fbxl2	F-box and leucine-rich repeat protein 2	1.1	0.058	1.76	0.203	1.72	0.115	1.49	0.543	1.51
1424799_a_at	Gcc1	golgi coiled coil 1	1.71	0.485	1.19	0.725	1.67	0.364	2.02	0.404	1.65
1421307_at	Car13	carbonic anhydrase 13	1.2	0.752	2.08	0.106	1.28	0.266	2.58	0.244	1.79
1431352_s_at	Pvt1	plasmacytoma variant translocation 1	1.7	0.464	1.19	0.448	1.68	0.283	1.71	0.04	1.57
1441289_at	---	Transcribed locus	2.36	0.135	1.07	0.825	1.14	0.234	1.09	0.501	1.42
1421575_at	2310057N15Rik	RIKEN cDNA 2310057N15 gene	1.99	0.385	1.37	0.289	1.22	0.731	1.08	0.9	1.42
1447469_at	Ccdc66	coiled-coil domain containing 66	1.15	0.752	1.42	0.461	2	0.236	1.2	0.682	1.45
1424518_at	2310016F22Rik ///	RIKEN cDNA 2310016F22 gene /// cDNA sequence BC020489	1.51	0.16	1.05	0.718	2.02	0.315	1.7	0.234	1.57
1429220_at	Wdr85	WD40 repeat domain 85	1.61	0.439	1.5	0.141	1.47	0.084	1.32	0.415	1.48
1456486_at	Zfp574	zinc finger protein 574	1.97	0.058	1.07	0.8	1.55	0.239	1.14	0.701	1.43
1448741_at	Slc3a1	solute carrier family 3, member 1	1.09	0.286	2.48	0.176	1.01	0.961	1.53	0.421	1.53
1425461_at	Fbxw11	F-box and WD-40 domain protein 11	1.45	0.44	1.16	0.779	1.98	0.342	1.27	0.699	1.46
1426768_at	1700060H10Rik	RIKEN cDNA 1700060H10 gene	1.59	0.38	1.71	0.111	1.28	0.221	1.25	0.374	1.46
1421952_at	Capn6	calpain 6	1.25	0.683	2.34	0.452	1.01	0.942	1.19	0.691	1.45
1422514_at	Aebp1	AE binding protein 1	1.23	0.264	1.24	0.58	2.12	0.053	1.18	0.416	1.44
1441662_at	Cyp4x1	Cytochrome P450, family 4, subfamily x, polypeptide 1	1.3	0.527	2.21	0.197	1.08	0.875	1.98	0.377	1.64
1434466_at	Atcay	ataxia, cerebellar, Cayman type homolog (human)	1.33	0.695	1.1	0.843	2.17	0.088	1.06	0.821	1.42
1416022_at	Fabp5	fatty acid binding protein 5, epidermal	1.11	0.739	2.42	0.274	1.07	0.611	1.34	0.111	1.48
1422259_a_at	Ccr5	chemokine (C-C motif) receptor 5	1.42	0.277	1.78	0.139	1.39	0.106	1.19	0.205	1.45
1450218_at	Ccl28	chemokine (C-C motif) ligand 28	2.5	0.486	1.07	0.539	1.02	0.953	1.15	0.311	1.44
1441504_at	Gm817	gene model 817, (NCBI)	1.58	0.393	1.25	0.304	1.77	0.263	1.39	0.408	1.5

1417500_a_at	Tgm2	transglutaminase 2, C polypeptide	1.01	0.933	2.14	0.076	1.45	0.046	1.2	0.008	1.45
1448472_at	Vars2	valyl-tRNA synthetase 2	1.05	0.775	1.12	0.077	2.44	0.159	1.05	0.733	1.41
1448323_a_at	Bgn	biglycan	1.89	0.069	1.57	0.014	1.14	0.462	1.11	0.754	1.43
1423418_at	Fdps	farnesyl diphosphate synthetase	1.2	0.651	2.07	0.094	1.34	0.345	1.18	0.789	1.45
1421109_at	Cml2	camello-like 2	1.29	0.026	1.28	0.607	2.04	0.044	1.47	0.284	1.52
1433499_at	2010005J08Rik	RIKEN cDNA 2010005J08 gene	1.22	0.269	1.05	0.389	2.34	0.052	1.45	0.314	1.51
1439240_x_at	Lin7b	lin-7 homolog B (C. elegans)	1.57	0.334	1.77	0.169	1.27	0.398	1.06	0.832	1.42
1418194_at	Galnt10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransfe	1.32	0.063	1.97	0.09	1.32	0.389	1.57	0.251	1.54
1444944_at	---	---	1.19	0.702	1.29	0.415	2.13	0.091	1.26	0.288	1.47
1431970_at	Tm7sf4	transmembrane 7 superfamily member 4	1.47	0.666	1.86	0.037	1.28	0.729	1.02	0.924	1.41
1437412_at	Prdx6-rs1	peroxiredoxin 6, related sequence 1	1	0.995	2.17	0.1	1.44	0.231	3.06	0.067	1.92
1427170_at	Psma8	proteasome (prosome, macropain) subunit, alpha type, 8	1.4	0.595	1.75	0.125	1.46	0.174	1.47	0.087	1.52
1450676_at	Tceb3	transcription elongation factor B (SIII), polypeptide 3	1.71	0.263	1.19	0.702	1.72	0.173	1.79	0.362	1.6
1420163_at	AA511261	expressed sequence AA511261	1.45	0.522	1.57	0.453	1.6	0.114	1.29	0.583	1.48
1418345_at	Tnfsf13 /// Tnfsf12-t	tumor necrosis factor (ligand) superfamily, member 13 /// tumor necrosis factor (li	1.2	0.468	2.22	0.019	1.21	0.282	1.3	0.262	1.48
1426274_at	Slc9a8	solute carrier family 9 (sodium/hydrogen exchanger), member 8	1.67	0.082	1.36	0.446	1.6	0.461	3	0.249	1.91
1458194_at	---	---	1.12	0.886	1.38	0.567	2.12	0.445	2.47	0.08	1.77
1438767_at	Osm	oncostatin M	1.04	0.917	1.83	0.302	1.76	0.313	1.75	0.037	1.59
1453562_a_at	Nmral1	NmrA-like family domain containing 1	2.05	0.372	1.42	0.396	1.16	0.723	1.96	0.235	1.65
1418271_at	Bhlhb5	basic helix-loop-helix domain containing, class B5	1.09	0.516	1.64	0.424	1.9	0.025	1.91	0.223	1.63
1437325_x_at	Aldh18a1	aldehyde dehydrogenase 18 family, member A1	1.75	0.026	1.45	0.359	1.43	0.104	1.35	0.052	1.5
1441433_at	---	Transcribed locus	1.05	0.948	1.63	0.379	1.96	0.091	1.5	0.378	1.53
1436628_at	Ulk4	unc-51-like kinase 4 (C. elegans)	1.16	0.625	1.21	0.739	2.27	0.031	1.59	0.462	1.56
1444634_at	Nsun3	NOL1/NOP2/Sun domain family 3	1.39	0.067	1.18	0.577	2.06	0.102	1.18	0.591	1.46
1432513_a_at	1700001C02Rik	RIKEN cDNA 1700001C02 gene	1.6	0.271	1.8	0.28	1.25	0.392	1.33	0.484	1.49
1447326_s_at	Zmym3	zinc finger, MYM-type 3	1.24	0.683	2.4	0.006	1.01	0.985	1.37	0.426	1.5
1430618_at	2610020C07Rik	RIKEN cDNA 2610020C07 gene	2.04	0.047	1.04	0.914	1.56	0.333	1.79	0.461	1.61
1419442_at	Matn2	matrilin 2	1.41	0.039	1.98	0.025	1.26	0.104	1.32	0.169	1.49
1460054_at	Trappc6a	trafficking protein particle complex 6A	1.33	0.043	2.21	0.035	1.1	0.828	1.17	0.814	1.46
1438253_at	Ssh1	slingshot homolog 1 (Drosophila)	1.08	0.417	1	1	2.57	0.071	1.05	0.796	1.42
1434292_at	E130013N09Rik	RIKEN cDNA E130013N09 gene	1.26	0.345	2.12	0.038	1.27	0.638	2.78	0.13	1.86
1443394_at	Hmga2	High mobility group AT-hook 2	1.04	0.931	2.57	0.041	1.05	0.915	1.73	0.347	1.6
1416190_a_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	1.63	0.425	1.13	0.799	1.91	0.505	1.29	0.687	1.49
1441329_at	Galr1	galanin receptor 1	1.71	0.373	1.73	0.27	1.22	0.697	1.36	0.451	1.5
1421375_a_at	S100a6	S100 calcium binding protein A6 (calcyclin)	1.17	0.319	2.37	0.02	1.12	0.481	1.25	0.506	1.48
1454305_at	Cbx3	chromobox homolog 3 (Drosophila HP1 gamma)	1.69	0.072	1.02	0.936	1.96	0.057	1.4	0.369	1.52
1456881_at	Nbeal2	neurobeachin-like 2	1.73	0.052	1.14	0.715	1.79	0.326	1.01	0.977	1.42
1439814_at	Atp8b4	ATPase, class I, type 8B, member 4	1.3	0.345	1.72	0.022	1.66	0.163	1.25	0.183	1.48
1425213_at	6430514L14Rik	RIKEN cDNA 6430514L14 gene	1.5	0.191	2.14	0.213	1.03	0.937	1.07	0.632	1.44
1456887_at	Cmklr1	chemokine-like receptor 1	1.98	0.364	1.46	0.036	1.24	0.022	1.19	0.483	1.47
1415803_at	Cx3cl1	chemokine (C-X3-C motif) ligand 1	1.71	0.066	1.77	0.068	1.2	0.472	1.24	0.352	1.48
1419276_at	Enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1	1.33	0.187	1.39	0.111	1.96	0.019	1.36	0.28	1.51
1423048_a_at	Tollip	toll interacting protein	1.06	0.845	1.05	0.921	2.57	0.248	2.06	0.22	1.68
1443034_at	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	1.54	0.37	1.55	0.396	1.58	0.141	1.04	0.939	1.43
1417938_at	Rad51ap1	RAD51 associated protein 1	1.06	0.935	1.86	0.045	1.76	0.221	3.64	0.213	2.08
1454911_at	LOC382106	hypothetical protein LOC382106	1.27	0.55	2.32	0.159	1.09	0.778	1.59	0.176	1.57
1425252_a_at	Mad1l1	mitotic arrest deficient 1-like 1	1.87	0.174	1.71	0.025	1.1	0.2	1.29	0.432	1.49
1452595_at	Adamts4	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	2.1	0.244	1.49	0.554	1.1	0.829	1.96	0.183	1.66
1420545_a_at	Chn1	chimerin (chimaerin) 1	1.04	0.288	2.65	0.265	1	0.998	1.12	0.423	1.45
1433788_at	Nrxn3	neurexin III	1.93	0.221	1.64	0.302	1.13	0.844	2	0.276	1.67
1428794_at	Specc1	spectrin domain with coiled-coils 1	1.31	0.207	1.88	0.193	1.5	0.19	4.48	0.225	2.29
1452250_a_at	Col6a2	procollagen, type VI, alpha 2	1.87	0.312	1.79	0.126	1.04	0.866	1.55	0.148	1.56
1423557_at	Ifngr2	interferon gamma receptor 2	1.71	0.29	1.62	0.343	1.37	0.345	1.07	0.804	1.44

1453736_s_at	B230219D22Rik	RIKEN cDNA B230219D22 gene	1.4	0.249	1.09	0.83	2.22	0.132	1.11	0.738	1.45
1440173_x_at	Selp	selectin, platelet	1.84	0.21	1.39	0.651	1.47	0.411	1.89	0.507	1.65
1450116_at	D3Ertd300e	DNA segment, Chr 3, ERATO Doi 300, expressed	1.37	0.27	1.42	0.579	1.91	0.138	1.04	0.866	1.44
1422165_at	Pou3f4	POU domain, class 3, transcription factor 4	1.08	0.924	2.12	0.228	1.51	0.349	1.13	0.581	1.46
1440796_at	A330021E22Rik	RIKEN cDNA A330021E22 gene	1.6	0.26	1.55	0.294	1.57	0.422	1.41	0.575	1.53
1430255_at	Klf5	Kruppel-like factor 5	1.76	0.023	1.6	0.23	1.35	0.413	1.26	0.766	1.49
1438055_at	Rarres1	retinoic acid receptor responder (tazarotene induced) 1	1.64	0.154	1.06	0.784	2.01	0.029	1.07	0.897	1.44
1453392_at	1810054D07Rik	RIKEN cDNA 1810054D07 gene	2.13	0.058	1.43	0.245	1.15	0.432	1.24	0.51	1.49
1427574_s_at	Sh3d19	SH3 domain protein D19	1.62	0.313	1.17	0.812	1.92	0.43	1.09	0.664	1.45
1425985_s_at	Masp1	mannan-binding lectin serine peptidase 1	2.38	0.216	1.21	0.087	1.12	0.786	3.83	0.073	2.14
1453203_at	1700011K15Rik	RIKEN cDNA 1700011K15 gene	1.2	0.379	2.08	0.174	1.44	0.498	2.41	0	1.78
1446270_at	E030042O20Rik	RIKEN cDNA E030042O20 gene	1.3	0.165	1.73	0.348	1.68	0.21	1.28	0.225	1.5
1434365_a_at	BC055324	cDNA sequence BC055324	1.47	0.013	2.01	0.021	1.23	0.55	1.65	0.453	1.59
1430977_at	A930021C24Rik	RIKEN cDNA A930021C24 gene	1.34	0.634	1.71	0.077	1.68	0.08	1.82	0.095	1.64
1436265_at	6330405H19	hypothetical protein 6330405H19	1.95	0.299	1.25	0.591	1.52	0.13	1.68	0.17	1.6
1456640_at	Sh3rf2	SH3 domain containing ring finger 2	1.08	0.893	2.39	0.074	1.25	0.369	1	0.997	1.43
1450300_at	Gabrr1	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1	1.88	0.469	1.43	0.478	1.42	0.506	1.04	0.834	1.44
1441280_at	Kcnk12	potassium channel, subfamily K, member 12	1	0.989	1.97	0.144	1.75	0.149	2.49	0.295	1.8
1416303_at	Litaf	LPS-induced TN factor	1.04	0.806	2.21	0.115	1.47	0.075	1.18	0.087	1.48
1424143_a_at	Cdt1	chromatin licensing and DNA replication factor 1	1.39	0.16	1.38	0.066	1.96	0.087	2.04	0.152	1.69
1457536_at	Gpc5	glypican 5	1.51	0.434	2.07	0.05	1.16	0.807	1.6	0.323	1.58
1443934_at	9230110C19Rik	RIKEN cDNA 9230110C19 gene	1.15	0.572	2.39	0.073	1.2	0.622	1.52	0.418	1.56
1458252_at	---	Mus musculus, Similar to RIKEN cDNA B430319H21 gene, clone IMAGE:39911(	1.39	0.501	1.43	0.293	1.92	0.25	1.37	0.573	1.53
1443688_at	BC050092	cDNA sequence BC050092	2.35	0.471	1.24	0.745	1.14	0.837	1.42	0.368	1.54
1421644_at	Slfn3	schlafen 3	1.96	0.228	1.6	0.363	1.18	0.67	1.1	0.901	1.46
1451749_at	Irak4	interleukin-1 receptor-associated kinase 4	1.17	0.251	1.57	0.214	2	0.109	1.07	0.608	1.45
1452934_at	Tmc5	transmembrane channel-like gene family 5	2.04	0.079	1.06	0.897	1.64	0.107	2.37	0.107	1.78
1430786_at	1110002E22Rik	RIKEN cDNA 1110002E22 gene	2.29	0.201	1.11	0.875	1.33	0.391	1.83	0.06	1.64
1422831_at	Fbn2 /// LOC63904	fibrillin 2 /// similar to fibrillin 2	1.54	0.459	1.23	0.648	1.97	0.064	1.37	0.702	1.53
1443667_at	C79407	expressed sequence C79407	2.13	0.158	1.36	0.287	1.25	0.541	1.54	0.432	1.57
1426045_at	Kng1	kininogen 1	1.98	0.295	1.12	0.006	1.65	0.184	1.74	0.011	1.62
1421277_at	Spna1 /// LOC6309	spectrin alpha 1 /// similar to spectrin alpha 1	1.57	0.549	1.54	0.345	1.64	0.38	11.73	0.189	4.12
1431966_at	Agbl3	ATP/GTP binding protein-like 3	1.8	0.126	1.67	0.224	1.28	0.457	1.74	0.24	1.62
1420995_at	Plxna3	plexin A3	2.01	0.28	1.54	0.411	1.21	0.362	1.1	0.87	1.46
1438683_at	Wasf2	WAS protein family, member 2	1.62	0.325	1.47	0.158	1.66	0.085	1.18	0.678	1.48
1417546_at	Il2rb	interleukin 2 receptor, beta chain	1.22	0.846	1.75	0.197	1.78	0.019	1.06	0.894	1.45
1424511_at	Aurka	aurora kinase A	1.03	0.842	2.43	0.039	1.29	0.205	4.19	0.226	2.24
1434098_at	Glra2	glycine receptor, alpha 2 subunit	1.29	0.669	1.03	0.96	2.44	0.012	1.01	0.982	1.44
1421787_at	---	---	1.12	0.882	2.33	0.257	1.31	0.529	1.68	0.217	1.61
1445404_at	Kif27	kinesin family member 27	1.29	0.669	2.22	0.388	1.25	0.44	1.27	0.684	1.51
1417403_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	1.21	0.252	1.08	0.86	2.47	0.444	1.73	0.003	1.62
1431709_at	Mtl5	metallothionein-like 5, testis-specific (tesmin)	1.69	0.307	1.96	0.328	1.11	0.68	2.29	0.03	1.76
1440821_x_at	Odf1	outer dense fiber of sperm tails 1	2.34	0.164	1.03	0.96	1.4	0.578	1.12	0.744	1.47
1435069_at	BC064078	cDNA sequence BC064078	1.17	0.08	1.48	0.163	2.12	0.121	1.8	0.006	1.64
1436808_x_at	Mcm5	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	1.25	0.297	1.73	0.033	1.79	0.183	1.88	0.181	1.66
1439779_at	---	16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:963(	1.69	0.146	1.46	0.365	1.62	0.303	1.04	0.808	1.45
1433837_at	8430408G22Rik	RIKEN cDNA 8430408G22 gene	1.73	0.435	1.47	0.251	1.57	0.219	2.18	0.401	1.74
1457118_at	Shc4	SHC (Src homology 2 domain containing) family, member 4	1.05	0.73	2.07	0.373	1.66	0.33	3.25	0.066	2.01
1418500_at	Nap1l3	nucleosome assembly protein 1-like 3	1.72	0.307	1.81	0.012	1.24	0.176	1.56	0.037	1.58
1450104_at	Adam10	a disintegrin and metallopeptidase domain 10	1.25	0.427	1.19	0.672	2.33	0.147	3.18	0.318	1.99
1460537_at	9430085L16Rik	RIKEN cDNA 9430085L16 gene	1.79	0.268	1.58	0.372	1.41	0.485	1.18	0.828	1.49
1418870_at	4930579J09Rik	RIKEN cDNA 4930579J09 gene	1.55	0.533	1.19	0.712	2.05	0.069	1.09	0.881	1.47
1417821_at	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	1.81	0.112	1.59	0.247	1.39	0.326	1.56	0.174	1.59

1460314_s_at	Hist2h3c1 /// Hist2h	histone 2, H3c1 /// histone 2, H3c2 /// histone 1, H3g /// histone 1, H3f /// histone1	2.43	0.154	1.17	0.693	1.19	0.22	3.25	0.287	2.01
1450450_at	Dscr1l2	Down syndrome critical region gene 1-like 2	1.6	0.083	1.54	0.394	1.65	0.316	1.3	0.579	1.52
1438375_at	Fbln2	Fibulin 2	1.13	0.885	1.37	0.637	2.3	0.154	1.37	0.663	1.54
1437816_at	Pax6	paired box gene 6	1.34	0.698	1.92	0.15	1.54	0.108	1.73	0.168	1.63
1434990_at	Ppm1e	protein phosphatase 1E (PP2C domain containing)	1.26	0.186	2.31	0.031	1.22	0.24	1.76	0.468	1.64
1455274_at	a	Nonagouti	1.43	0.584	2.12	0.155	1.25	0.58	1.42	0.19	1.55
1449528_at	Figf	c-fos induced growth factor	2.57	0.001	1.08	0.862	1.15	0.518	1.55	0.115	1.59
1457987_at	6030458C11Rik	RIKEN cDNA 6030458C11 gene	1.47	0.183	1.78	0.31	1.56	0.241	1.59	0.072	1.6
1421206_at	Lif	leukemia inhibitory factor	1.29	0.412	1.9	0.316	1.61	0.075	2.12	0.144	1.73
1416774_at	Wee1	wee 1 homolog (S. pombe)	1.24	0.477	1.98	0.399	1.58	0.049	2.55	0.149	1.84
1449974_at	Gapdhs	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic	1.55	0.008	1.68	0.244	1.58	0.334	1.59	0.477	1.6
1452277_at	Arsg	arylsulfatase G	1.06	0.876	1.17	0.68	2.58	0.1	1.61	0.117	1.61
1442804_at	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	1.34	0.291	1.48	0.026	1.98	0.122	1.03	0.756	1.46
1449511_a_at	Ssbp4	single stranded DNA binding protein 4	1.38	0.115	2.34	0.018	1.09	0.622	1.36	0.252	1.54
1459796_at	1700061E18Rik	RIKEN cDNA 1700061E18 gene	2	0.023	1.41	0.008	1.41	0.462	1.32	0.098	1.53
1420558_at	Selp	selectin, platelet	1.52	0.404	1.59	0.156	1.71	0.061	2.8	0.288	1.9
1426116_at	Asb18	ankyrin repeat and SOCS box-containing 18	2.18	0.229	1.23	0.673	1.41	0.529	1.63	0.396	1.61
1452548_x_at	H2-T18 /// H2-T3 ///	histocompatibility 2, T region locus 18 /// histocompatibility 2, T region locus 3 /// s	2.37	0.113	1.16	0.777	1.29	0.452	1.89	0.135	1.68
1423586_at	Axl	AXL receptor tyrosine kinase	1.7	0.018	1.98	0.012	1.15	0.494	1.22	0.531	1.51
1436929_x_at	Adcy3	adenylate cyclase 3	1.96	0.012	1.82	0.451	1.04	0.825	1.37	0.588	1.55
1440922_at	9130208D14Rik	RIKEN cDNA 9130208D14 gene	1.68	0.663	2	0.091	1.14	0.288	1.4	0.072	1.56
1432931_at	Nrxn3	neurexin III	1.69	0.319	1.44	0.486	1.69	0.31	2.17	0.024	1.75
1452803_at	Glipr2	GLI pathogenesis-related 2	1.56	0.396	1.76	0.356	1.5	0.214	1.17	0.186	1.5
1442031_at	D130073L02Rik	RIKEN cDNA D130073L02 gene	2.2	0.457	1.19	0.404	1.44	0.61	1.17	0.81	1.5
1454209_at	1500016O10Rik	RIKEN cDNA 1500016O10 gene	2.58	0.071	1.05	0.907	1.19	0.722	1.15	0.558	1.49
1422635_at	Ache	acetylcholinesterase	1.46	0.401	1.39	0.199	1.97	0.096	4.94	0.146	2.44
1432113_at	Ccdc18	coiled-coil domain containing 18	1.67	0.343	2.06	0.286	1.1	0.871	2.35	0.401	1.79
1452542_x_at	Tcfe2a	transcription factor E2a	1.16	0.743	1.75	0.349	1.92	0.077	1.28	0.259	1.53
1429794_a_at	P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	1.03	0.967	1.85	0.234	1.96	0.108	1.83	0.447	1.67
1435903_at	Cd300a	CD300A antigen	1.33	0.294	1.74	0.008	1.77	0.149	1.34	0.413	1.55
1434748_at	Ckap2	cytoskeleton associated protein 2	1.94	0.011	1.15	0.58	1.75	0.26	4.69	0.184	2.38
1432542_at	2810474C18Rik	RIKEN cDNA 2810474C18 gene	1	0.992	2.82	0.206	1.02	0.966	1.03	0.965	1.47
1416414_at	Emilin1	elastin microfibril interfacer 1	2.21	0.084	1.63	0.022	1	0.995	1.23	0.297	1.52
1430282_at	5730437N04Rik	RIKEN cDNA 5730437N04 gene	1.63	0.635	1.44	0.622	1.77	0.226	1.38	0.615	1.56
1417300_at	Smpdl3b	sphingomyelin phosphodiesterase, acid-like 3B	2.22	0.049	1.13	0.878	1.5	0.02	1.16	0.715	1.5
1419569_a_at	Isg20	interferon-stimulated protein	2.33	0.198	1.38	0.118	1.14	0.685	3.29	0.2	2.04
1431747_at	Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	1.79	0.299	1.59	0.458	1.48	0.172	1.78	0.395	1.66
1439727_at	Clca6 /// AI747448	chloride channel calcium activated 6 /// expressed sequence AI747448	1.17	0.544	2.05	0.205	1.64	0.029	1.1	0.703	1.49
1417215_at	Rab27b	RAB27b, member RAS oncogene family	2.63	0.053	1.17	0.707	1.06	0.872	3.68	0.308	2.14
1431993_a_at	Rnf38	ring finger protein 38	1.22	0.373	2.55	0.299	1.09	0.8	1.62	0.233	1.62
1451664_x_at	Klra1 /// Klra12 /// K	killer cell lectin-like receptor, subfamily A, member 1 /// killer cell lectin-like recept	2.02	0.38	1.66	0.272	1.19	0.797	1.03	0.944	1.47
1416076_at	Ccnb1-rs1 /// Ccnb1	cyclin B1, related sequence 1 /// cyclin B1 /// similar to G2/mitotic-specific cyclin-E	1.49	0.221	1.99	0.316	1.39	0.398	5.27	0.198	2.53
1425437_a_at	Kcnk7	potassium channel, subfamily K, member 7	2.46	0.007	1.16	0.656	1.25	0.665	4.06	0.265	2.23
1435490_at	Hk3	hexokinase 3	1.11	0.559	1.98	0.004	1.79	0.285	1.49	0.373	1.59
1441723_at	Dusp22	dual specificity phosphatase 22	1.27	0.251	1.22	0.741	2.38	0.02	1.3	0.677	1.54
1417586_at	Timeless	timeless homolog (Drosophila)	1.42	0.007	2.34	0.055	1.12	0.505	1.85	0.24	1.68
1432639_at	4633401L03Rik	RIKEN cDNA 4633401L03 gene	2.08	0.282	1.12	0.841	1.67	0.188	1.08	0.822	1.49
1434638_at	---	Adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone	1.72	0.463	1.9	0.223	1.27	0.552	1.17	0.516	1.51
1421346_a_at	Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	1.85	0.196	1.1	0.737	1.93	0.086	1.45	0.115	1.58
1424128_x_at	Aurkb	aurora kinase B	1.34	0.376	1.87	0.489	1.68	0.251	3.79	0.176	2.17
1426858_at	Inhbb	inhibin beta-B	1.72	0.035	1.48	0.188	1.7	0.022	1.07	0.614	1.49
1419524_at	Tph1	tryptophan hydroxylase 1	2.33	0.514	1.27	0.686	1.3	0.645	3.52	0.12	2.1
1447839_x_at	Adm	adrenomedullin	1.1	0.558	2.13	0.07	1.67	0.48	1.29	0.249	1.55

1428572_at	Basp1	brain abundant, membrane attached signal protein 1	1.3	0.228	2.02	0.081	1.57	0.017	1.33	0.542	1.56
1456458_at	---	---	1.84	0.421	1.66	0.425	1.39	0.507	1.77	0.377	1.67
1426509_s_at	Gfap	glial fibrillary acidic protein	2.05	0.324	1.67	0.336	1.19	0.708	3.53	0.247	2.11
1417837_at	Phlda2	pleckstrin homology-like domain, family A, member 2	1.12	0.401	2.74	0.269	1.04	0.815	3.31	0.084	2.05
1430715_at	2310014L17Rik	RIKEN cDNA 2310014L17 gene	1.94	0.359	1.49	0.271	1.48	0.205	1.11	0.769	1.5
1418588_at	Nrsn1	neurensin 1	1	0.992	2.58	0.067	1.32	0.414	1.14	0.823	1.51
1421571_a_at	Ly6c	lymphocyte antigen 6 complex, locus C	1.09	0.477	2.79	0.026	1.03	0.885	1.63	0.179	1.63
1421731_a_at	Fen1	flap structure specific endonuclease 1	1.52	0.193	1.47	0.412	1.92	0.05	3.31	0.221	2.06
1416299_at	Shcbp1	Shc SH2-domain binding protein 1	1.02	0.958	1.19	0.571	2.72	0.076	2.81	0.208	1.93
1452829_at	Cad	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorot	1.18	0.39	1.66	0.14	2.08	0.159	1.77	0.234	1.67
1417404_at	Elovl6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	1.1	0.61	1.12	0.753	2.71	0.419	1.04	0.66	1.49
1439396_x_at	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)	1.68	0.229	1.43	0.131	1.82	0.249	1.41	0.261	1.59
1419088_at	Timp3	tissue inhibitor of metalloproteinase 3	1.03	0.941	1.21	0.629	2.69	0.331	1.51	0.307	1.61
1416309_at	Nusap1	nucleolar and spindle associated protein 1	1.19	0.601	1.93	0.581	1.82	0.312	3.23	0.195	2.04
1424832_at	4732429D16Rik	RIKEN cDNA 4732429D16 gene	1.44	0.143	1.71	0.06	1.79	0.049	2.07	0.257	1.75
1445904_at	---	---	1.02	0.899	2.78	0.031	1.15	0.852	1.8	0.128	1.68
1424854_at	Hist1h4i	histone 1, H4i	1.45	0.075	1.95	0.136	1.54	0.278	2.4	0.309	1.84
1457878_at	C430042M11Rik	RIKEN cDNA C430042M11 gene	1.37	0.688	1.37	0.505	2.21	0.165	1.45	0.047	1.6
1415810_at	Uhrf1	ubiquitin-like, containing PHD and RING finger domains, 1	1.11	0.562	1.41	0.142	2.44	0.178	3.26	0.257	2.05
1453829_at	2310007J06Rik	RIKEN cDNA 2310007J06 gene	1.79	0.103	1.47	0.205	1.7	0.421	1.51	0.394	1.62
1429979_a_at	1810073N04Rik	RIKEN cDNA 1810073N04 gene	1.2	0.413	1.34	0.625	2.41	0.288	1.18	0.751	1.53
1459508_at	C85600	expressed sequence C85600	1.25	0.803	2.62	0.185	1.1	0.825	2.23	0.007	1.8
1426004_a_at	Tgm2	transglutaminase 2, C polypeptide	1.04	0.899	2.08	0.135	1.85	0.181	1.63	0.248	1.65
1429950_at	Unc5cl	unc-5 homolog C (C. elegans)-like	1.7	0.13	1.33	0.307	1.94	0.062	1.36	0.107	1.58
1450402_at	Pparbp	peroxisome proliferator activated receptor binding protein	1.58	0.46	1	0.997	2.4	0.149	1.15	0.834	1.53
1431977_at	4933402J15Rik	RIKEN cDNA 4933402J15 gene	1.77	0.425	1.18	0.775	2.02	0.265	2.1	0.366	1.77
1452598_at	Gins1	GINS complex subunit 1 (Psf1 homolog)	2.83	0.072	1.03	0.603	1.12	0.488	3.55	0.222	2.13
1422041_at	Pilrb1	paired immunoglobin-like type 2 receptor beta 1	1	0.964	2.05	0.004	1.93	0.152	1.43	0.439	1.6
1426330_at	Cacng5	calcium channel, voltage-dependent, gamma subunit 5	1.55	0.327	1.72	0.235	1.71	0.063	1.22	0.777	1.55
1421854_at	Fgl2	fibrinogen-like protein 2	1.75	0.384	1.85	0.02	1.38	0.4	2.63	0.001	1.9
1442280_at	D2Ertd750e	DNA segment, Chr 2, ERATO Doi 750, expressed	1.35	0.1	1.43	0.595	2.21	0.194	2.31	0.364	1.82
1445930_at	Fndc7	fibronectin type III domain containing 7	2.53	0.008	1.41	0.548	1.05	0.731	1.28	0.182	1.57
1443473_at	C79562	expressed sequence C79562	2.53	0.396	1.04	0.772	1.41	0.486	1.02	0.98	1.5
1426935_at	6330590E21Rik	RIKEN cDNA 6330590E21 gene	1.46	0.6	1.97	0.356	1.56	0.413	1.08	0.792	1.52
1421511_at	Itgb3	integrin beta 3	1.2	0.759	1.03	0.895	2.76	0.291	1.37	0.708	1.59
1431030_a_at	Rnf14	ring finger protein 14	1.78	0.436	1.04	0.947	2.17	0.448	1.6	0.542	1.65
1450080_at	Cxx1c	CAAX box 1 homolog C (human)	1.37	0.47	2.33	0.065	1.3	0.503	1.11	0.804	1.53
1437889_x_at	Bgn	biglycan	1.87	0.085	2.02	0.003	1.12	0.582	1.09	0.804	1.52
1450439_at	Hcfc1	host cell factor C1	1.8	0.421	1.41	0.586	1.79	0.129	2.99	0.244	2
1417944_at	Gng4	guanine nucleotide binding protein (G protein), gamma 4 subunit	2.36	0.196	1.49	0.32	1.15	0.735	1.03	0.94	1.51
1431321_at	4930513E20Rik	RIKEN cDNA 4930513E20 gene	1.42	0.523	2.16	0.346	1.42	0.567	1.45	0.468	1.61
1427704_a_at	Galr1	galanin receptor 1	1.23	0.663	1.87	0.134	1.91	0.023	3.07	0.263	2.02
1421226_at	Trem2	triggering receptor expressed on myeloid cells 2	1.9	0.129	2.07	0.364	1.04	0.933	2.07	0.25	1.77
1423550_at	Slc1a4	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	1.22	0.037	1.97	0.211	1.82	0.279	3	0.287	2
1417462_at	Cap1	CAP, adenylate cyclase-associated protein 1 (yeast)	1.26	0.115	1.47	0.042	2.28	0.097	1.08	0.834	1.52
1451707_s_at	Slc41a3	solute carrier family 41, member 3	1.56	0.128	2.1	0.005	1.37	0.115	2.44	0.044	1.87
1415843_at	Gbl	G protein beta subunit-like	1.61	0.359	1.57	0.688	1.84	0.249	1.3	0.613	1.58
1421842_a_at	Scamp4	secretory carrier membrane protein 4	1.14	0.67	1.24	0.69	2.65	0.068	1.07	0.858	1.52
1454276_at	1700021O21Rik	RIKEN cDNA 1700021O21 gene	1.4	0.619	1.72	0.392	1.91	0.197	1.26	0.454	1.57
1429956_at	1700021K02Rik	RIKEN cDNA 1700021K02 gene	1.56	0.063	1.31	0.653	2.16	0.194	1.4	0.389	1.61
1416704_at	Mapk14	mitogen activated protein kinase 14	1.36	0.4	1.11	0.78	2.56	0.273	1.12	0.822	1.54
1453228_at	Stx11	syntaxin 11	1.62	0.089	1.87	0.053	1.55	0.255	1.26	0.267	1.58
1422632_at	Ctsw	cathepsin W	2.3	0.21	1.47	0.324	1.28	0.105	1.08	0.908	1.53

1451771_at	Tpcn1	two pore channel 1	2.23	0.247	1.5	0.193	1.33	0.726	1.9	0.017	1.74
1444853_at	---	---	1.18	0.781	1.83	0.454	2.05	0.267	1.76	0.36	1.71
AFFX-PyruCarbMur	Pcx	pyruvate carboxylase	1.25	0.479	1.16	0.69	2.64	0.108	2.48	0.292	1.88
1457555_at	Gpr151	G protein-coupled receptor 151	1.17	0.298	2.68	0.233	1.2	0.601	1.61	0.282	1.67
1418809_at	Pira2	paired-Ig-like receptor A2	1.28	0.649	1.72	0.298	2.06	0.069	1.11	0.86	1.54
1427327_at	Pilra	paired immunoglobin-like type 2 receptor alpha	1.67	0.252	1.57	0.001	1.83	0.213	1.33	0.29	1.6
1452656_at	Zdhhc2	zinc finger, DHHC domain containing 2	1.49	0.671	1.88	0.19	1.7	0.327	1.38	0.247	1.61
1439012_a_at	Dck	deoxycytidine kinase	1.54	0.193	1.63	0.034	1.9	0.12	1.79	0.176	1.72
1450344_a_at	Ptger3	prostaglandin E receptor 3 (subtype EP3)	1.27	0.439	1.11	0.772	2.69	0.223	4.35	0.235	2.36
1440661_at	A430010J10Rik	RIKEN cDNA A430010J10 gene	1.51	0.358	1.98	0.131	1.58	0.378	2.68	0.021	1.94
1451951_at	LOC625794	Hypothetical protein LOC625794	1.46	0.651	1.37	0.635	2.25	0.09	2.54	0.455	1.9
1419254_at	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydr	1.13	0.744	2.32	0.047	1.63	0.367	2.38	0.277	1.86
1452406_x_at	Erdr1	erythroid differentiation regulator 1	2.16	0.164	1.44	0.315	1.48	0.343	1.09	0.893	1.54
1456136_at	Kifc1	Kinesin family member C1	2.87	0.341	1.09	0.861	1.11	0.866	2.21	0.309	1.82
1449264_at	Syt11	synaptotagmin XI	1.41	0.187	1.36	0.32	2.31	0.054	1.04	0.877	1.53
1450803_at	Ntf3	neurotrophin 3	2.11	0.096	1.87	0.318	1.1	0.646	1.25	0.139	1.58
1458802_at	Hivep3	human immunodeficiency virus type I enhancer binding protein 3	1.51	0.042	1.91	0.012	1.66	0.345	1.02	0.936	1.52
1421860_at	Clstn1	calsyntenin 1	2.04	0.207	1.44	0.414	1.61	0.352	3.06	0.097	2.04
1422757_at	Slc5a4b	solute carrier family 5 (neutral amino acid transporters, system A), member 4b	2.09	0.12	1.93	0.315	1.06	0.697	2.22	0.035	1.83
1422013_at	Clec4a2	C-type lectin domain family 4, member a2	1.51	0.488	2.24	0.032	1.34	0.493	1.81	0.09	1.72
1451891_a_at	Dysf	dysferlin	1.09	0.776	2.82	0.002	1.18	0.429	1.27	0.332	1.59
1449260_at	Rab3d	RAB3D, member RAS oncogene family	2.64	0.033	1.21	0.771	1.24	0.124	1.05	0.855	1.54
1422571_at	Thbs2	thrombospondin 2	2.4	0.075	1.09	0.825	1.61	0.401	1.48	0.222	1.65
1453458_at	9430019C24Rik	RIKEN cDNA 9430019C24 gene	2.59	0.059	1.21	0.665	1.31	0.606	1.09	0.361	1.55
1433112_at	4933424L07Rik	RIKEN cDNA 4933424L07 gene	1.15	0.63	1.53	0.367	2.44	0.124	1.09	0.799	1.55
1452881_at	4833427B12Rik	RIKEN cDNA 4833427B12 gene	1.92	0.172	1.72	0.475	1.48	0.304	2.62	0.22	1.93
1425470_at	---	---	1.83	0.394	1.21	0.744	2.08	0.027	1.02	0.974	1.53
1425435_at	Msr1	macrophage scavenger receptor 1	1.8	0.361	1.92	0.205	1.4	0.503	1.33	0.659	1.61
1444796_at	C76876	expressed sequence C76876	2.9	0.341	1.05	0.934	1.16	0.701	3.35	0.337	2.12
1440761_at	4833422C13Rik	RIKEN cDNA 4833422C13 gene	2.52	0	1.61	0.366	1	0.992	1.19	0.731	1.58
1420924_at	Timp2	tissue inhibitor of metalloproteinase 2	1.78	0.258	1.56	0.065	1.79	0.297	1.36	0.414	1.62
1434280_at	Wiz	Widely-interspaced zinc finger motifs	1.2	0.468	1.74	0.057	2.2	0.386	1.92	0.183	1.77
1418435_at	Mkrn1	makorin, ring finger protein, 1	1.39	0.443	1.06	0.663	2.69	0.177	2.4	0.307	1.88
1459730_at	---	Transcribed locus	1.27	0.703	2.8	0.172	1.06	0.913	1.41	0.124	1.64
1431681_at	Klk9	kallikrein 9	1.05	0.742	2.3	0.112	1.79	0.151	1.46	0.473	1.65
1447492_at	---	---	2.3	0.373	1.47	0.644	1.37	0.619	1.24	0.713	1.6
1419523_at	Cyp3a13	cytochrome P450, family 3, subfamily a, polypeptide 13	2.58	0.378	1.45	0.161	1.12	0.669	1.42	0.286	1.64
1447253_x_at	Nup54	nucleoporin 54	2.71	0.134	1.42	0.27	1.02	0.866	1.01	0.983	1.54
1456493_at	5031415C07Rik ///	RIKEN cDNA 5031415C07 gene /// RIKEN cDNA 5830484A20 gene /// similar to	1.59	0.433	1.4	0.051	2.16	0.191	1.74	0.04	1.72
1433802_at	Tmem151	transmembrane protein 151	2.62	0.279	1.08	0.668	1.46	0.516	1.47	0.539	1.66
1450317_at	Clec2g	C-type lectin domain family 2, member g	1.58	0.564	1.44	0.292	2.14	0.333	2.71	0.225	1.97
1455978_a_at	Matn2	matrilin 2	1.24	0.493	2.27	0.003	1.65	0.005	1.23	0.265	1.6
1459377_at	Palm2	paralemmin 2	2.07	0.411	2.04	0.191	1.05	0.911	1.01	0.968	1.54
1434911_s_at	Arhgap19	Rho GTPase activating protein 19	2.16	0.075	1.96	0.027	1.03	0.804	2.19	0.182	1.84
1441358_at	Pcdhb16	protocadherin beta 16	2.93	0.442	1.06	0.899	1.18	0.613	1.26	0.706	1.61
1434429_at	Syt16	synaptotagmin XVI	2.32	0.399	1.04	0.956	1.81	0.393	1.99	0.128	1.79
1430122_at	9430002A10Rik	RIKEN cDNA 9430002A10 gene	1.17	0.647	2.94	0.283	1.07	0.836	1.2	0.535	1.59
1452922_at	Ppp1r3d	protein phosphatase 1, regulatory subunit 3D	1.15	0.509	1.64	0.419	2.39	0.015	1.68	0.382	1.71
1452418_at	1200016E24Rik	RIKEN cDNA 1200016E24 gene	1.9	0.422	1.65	0.107	1.63	0.354	1.3	0.177	1.62
1440327_at	AI195470	expressed sequence AI195470	2.66	0.495	1.35	0.289	1.17	0.711	1.25	0.592	1.61
1426652_at	Mcm3 /// LOC6719(	minichromosome maintenance deficient 3 (S. cerevisiae) /// similar to DNA replica	1.93	0.15	1.03	0.931	2.23	0.033	1.98	0.258	1.79
1416191_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisiae)	1.61	0.479	1.13	0.838	2.45	0.351	1.32	0.526	1.63
1446435_at	---	0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130016A	2.36	0.247	1.2	0.309	1.62	0.361	1.39	0.18	1.64

1428492_at	Glipr2	GLI pathogenesis-related 2	1.78	0.401	1.55	0.386	1.86	0.43	1.17	0.725	1.59
AFFX-TransRecMur	Tfrc	transferrin receptor	1.31	0.744	2.65	0	1.24	0.706	3.55	0.272	2.19
1445874_at	Rorb	RAR-related orphan receptor beta	1.79	0.32	1.08	0.904	2.33	0.003	1.19	0.828	1.6
1417876_at	Fcgr1	Fc receptor, IgG, high affinity I	2.23	0.093	1.71	0.015	1.26	0.358	2.21	0.009	1.85
1419605_at	Mgl1	macrophage galactose N-acetyl-galactosamine specific lectin 1	1.94	0.153	1.96	0.389	1.3	0.418	1.22	0.768	1.61
1418909_at	Ermap	erythroblast membrane-associated protein	1.63	0.176	2.39	0.17	1.19	0.522	6.69	0.107	2.97
1436365_at	Zbtb7c	zinc finger and BTB domain containing 7C	2.03	0.137	1.53	0.515	1.64	0.283	1.04	0.962	1.56
1419014_at	Rhag	Rhesus blood group-associated A glycoprotein	1.31	0.677	2.58	0.292	1.32	0.615	6.11	0.131	2.83
1431807_at	Fbxw8	F-box and WD-40 domain protein 8	1.8	0.579	1.09	0.849	2.34	0.318	1.39	0.233	1.65
1452324_at	Pvt1	plasmacytoma variant translocation 1	1.4	0.619	2.12	0.111	1.71	0.387	1.84	0.011	1.77
1418246_at	Rbm9	RNA binding motif protein 9	2.75	0.031	1.36	0.451	1.12	0.769	1.21	0.649	1.61
1417587_at	Timeless	timeless homolog (Drosophila)	3.01	0.031	1	0.989	1.22	0.523	2.33	0.198	1.89
1454904_at	Mtm1	X-linked myotubular myopathy gene 1	1.61	0.048	1.95	0.006	1.69	0.455	2.96	0.199	2.05
1420686_at	Cryba4	crystallin, beta A4	2.01	0.471	2.01	0.207	1.23	0.687	1.22	0.625	1.62
1444836_at	Dek	DEK oncogene (DNA binding)	2.04	0.536	1.37	0.681	1.85	0.309	2.02	0.077	1.82
1422740_at	Tnfrsf21	tumor necrosis factor receptor superfamily, member 21	1.48	0.25	1.75	0.039	2.03	0.119	2.18	0.084	1.86
1421117_at	Dst	dystonin	1.93	0.432	1.98	0.432	1.35	0.366	1.08	0.492	1.59
1427141_at	2700099C18Rik	RIKEN cDNA 2700099C18 gene	2.18	0.443	1.76	0.068	1.32	0.621	1.34	0.491	1.65
1455436_at	Diras2	DIRAS family, GTP-binding RAS-like 2	1.59	0.47	1.65	0.517	2.02	0.1	2.78	0.018	2.01
1459702_at	---	---	1.94	0.233	1.75	0.453	1.57	0.458	1.2	0.543	1.62
1437938_x_at	Dnm2	dynamin 2	1.59	0.301	1.54	0.41	2.14	0.28	1.08	0.922	1.59
1436296_x_at	LOC432611	Similar to dynein, axonemal, intermediate polypeptide 2	1.42	0.519	1.44	0.656	2.42	0.12	1.24	0.599	1.63
1460129_at	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	1.55	0.474	2.19	0.116	1.55	0.063	1.12	0.153	1.6
1458531_at	D6Ertd588e	DNA segment, Chr 6, ERATO Doi 588, expressed	2.84	0.128	1.35	0.071	1.1	0.704	1.31	0.583	1.65
1448776_at	Gadd45gip1	growth arrest and DNA-damage-inducible, gamma interacting protein 1	1.81	0.185	2.43	0.092	1.06	0.906	1.24	0.48	1.63
1430802_at	H2-Q8	histocompatibility 2, Q region locus 8	2.25	0.03	1.1	0.701	1.94	0.155	1.14	0.648	1.61
1431364_a_at	2810047C21Rik	RIKEN cDNA 2810047C21 gene	1.8	0.019	1.4	0.467	2.1	0.048	1.06	0.938	1.59
1445882_at	Cd300lb	CD300 antigen like family member B	1.24	0.422	2.03	0.001	2.04	0.13	1.88	0.035	1.8
1451417_at	Brca1	breast cancer 1	1.06	0.941	2	0.375	2.25	0.058	3.57	0.226	2.22
1425714_a_at	Nfam1	Nfat activating molecule with ITAM motif 1	1.03	0.854	1.03	0.925	3.24	0.27	1.05	0.942	1.59
1436237_at	Ttc9	tetratricopeptide repeat domain 9	2.86	0.275	1.04	0.935	1.41	0.336	1.25	0.591	1.64
1420603_s_at	Raet1a /// Raet1b //	retinoic acid early transcript 1, alpha /// retinoic acid early transcript beta /// retinoi	2.2	0.494	1.81	0.102	1.31	0.588	1.12	0.841	1.61
1442000_at	Gm1964	gene model 1964, (NCBI)	1.26	0.423	1.1	0.78	2.96	0.052	6.01	0.148	2.83
1416658_at	Frzb	frizzled-related protein	1.42	0.198	2.76	0.102	1.15	0.767	1.16	0.556	1.62
1422313_a_at	Igfbp5	insulin-like growth factor binding protein 5	1.86	0.454	1.29	0.655	2.18	0.267	1.65	0.119	1.74
1420257_at	1700073E17Rik	RIKEN cDNA 1700073E17 gene	2.38	0.463	1.47	0.351	1.47	0.389	1.09	0.684	1.6
1450412_at	Tbl2	transducin (beta)-like 2	1.14	0.811	2.28	0.216	1.91	0.238	2.03	0.217	1.84
1456622_at	Camsap1	calmodulin regulated spectrin-associated protein 1	1.04	0.945	2.45	0.327	1.83	0.143	2.52	0.104	1.96
1460606_at	Hsd17b13	hydroxysteroid (17-beta) dehydrogenase 13	2.81	0.438	1	0.982	1.53	0.408	1.25	0.703	1.65
1420361_at	Slc11a1	solute carrier family 11 (proton-coupled divalent metal ion transporters), member	1.71	0.183	1.74	0.006	1.89	0.061	1.08	0.745	1.6
1453241_a_at	2810047C21Rik	RIKEN cDNA 2810047C21 gene	2.51	0.089	1.31	0.584	1.52	0.094	1.68	0.278	1.75
1448021_at	---	Transcribed locus	2.37	0.38	1.39	0.333	1.59	0.493	1.97	0.267	1.83
1450124_a_at	Atp2a3	ATPase, Ca++ transporting, ubiquitous	1.47	0.438	1.82	0.231	2.06	0.22	1.12	0.784	1.62
1459852_x_at	Trib2	tribbles homolog 2 (Drosophila)	1.02	0.917	2.94	0.198	1.4	0.511	1.81	0.285	1.79
1437147_at	Gabrg2	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 2	2.82	0.386	1.24	0.819	1.3	0.627	1.12	0.543	1.62
1446756_at	Ghsr	growth hormone secretagogue receptor	1.06	0.947	2.47	0.201	1.84	0.212	1.17	0.742	1.63
1454008_at	Prmt3	protein arginine N-methyltransferase 3	1.31	0.687	1.68	0.589	2.38	0.009	1.41	0.435	1.69
1436611_at	Slc39a12	solute carrier family 39 (zinc transporter), member 12	1.07	0.761	3.03	0.003	1.28	0.566	1.47	0.092	1.71
1450499_at	Atxn1	ataxin 1	2.55	0.383	1.67	0.316	1.17	0.723	1.81	0.428	1.8
1417576_a_at	Otub2	OTU domain, ubiquitin aldehyde binding 2	1.83	0.252	1.07	0.929	2.49	0.141	2.35	0.344	1.93
1418204_s_at	Aif1	allograft inflammatory factor 1	2.37	0.121	1.76	0.16	1.27	0.619	1.04	0.934	1.61
1431045_at	D12Ertd553e	DNA segment, Chr 12, ERATO Doi 553, expressed	1.08	0.259	2.32	0.03	2.02	0.493	1.05	0.925	1.62
1454392_at	9230112J17Rik	RIKEN cDNA 9230112J17 gene	2.01	0.201	2	0.124	1.42	0.105	2.37	0.36	1.95

1450753_at	Nkg7	natural killer cell group 7 sequence	2.21	0.077	1.81	0.017	1.4	0.176	1.91	0.305	1.83
1450267_at	Tlr8	toll-like receptor 8	1.32	0.511	2.36	0.013	1.76	0.245	1.09	0.794	1.63
1422341_s_at	Lypla3	lysophospholipase 3	1.36	0.371	1.94	0.186	2.15	0.271	1.12	0.842	1.64
1449850_at	Scube1	signal peptide, CUB domain, EGF-like 1	1.16	0.637	1.59	0.448	2.69	0.02	1.35	0.212	1.7
1435605_at	Actr3b	ARP3 actin-related protein 3 homolog B (yeast)	2.72	0.286	1.14	0.791	1.58	0.094	1.12	0.379	1.64
1459035_at	---	---	2.22	0.51	1.24	0.67	1.99	0.16	1.04	0.94	1.62
1420901_a_at	Hk1	hexokinase 1	1.53	0.396	1.25	0.429	2.67	0.05	3.98	0.236	2.36
1422966_a_at	Tfrc	transferrin receptor	2.06	0.497	1.58	0.498	1.81	0.532	15.96	0.242	5.35
1423598_at	Atp8a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	1.32	0.569	2.61	0.022	1.52	0.214	2.26	0.22	1.93
1448119_at	Bpgm	2,3-bisphosphoglycerate mutase	1.22	0.569	1.37	0.352	2.87	0.19	3.49	0.268	2.24
1419120_at	Lyl1	lymphoblastomic leukemia	1.94	0.082	1.68	0.023	1.84	0.11	1.03	0.696	1.62
1455019_x_at	Ckap4	cytoskeleton-associated protein 4	1.29	0.356	2.69	0.002	1.48	0.178	1.5	0.143	1.74
1422667_at	Krt15	keratin 15	2.89	0.409	1.12	0.107	1.46	0.264	1.19	0.713	1.66
1435313_at	Cd200r4	Cd200 receptor 4	1.95	0.411	2.08	0.069	1.43	0.01	1.54	0.194	1.75
1427017_at	Satb2	special AT-rich sequence binding protein 2	1.1	0.614	1.32	0.655	3.06	0.033	1.34	0.563	1.7
AFFX-TransRecMur	Tfrc	transferrin receptor	2.06	0.495	1.47	0.541	1.96	0.375	7.79	0.244	3.32
1421490_at	Prpmp5 /// BC0614	proline-rich protein MP5 /// cDNA sequence BC061494	1.38	0.551	3.08	0.223	1.03	0.945	1.14	0.579	1.66
1424599_at	Fgl1	fibrinogen-like protein 1	2.99	0.486	1.37	0.31	1.13	0.641	2.74	0.197	2.06
1431022_at	Snca	synuclein, alpha	1.83	0.463	1.53	0.043	2.14	0.225	4.21	0.205	2.43
1457167_at	Crsp2	cofactor required for Sp1 transcriptional activation, subunit 2	1.16	0.655	3.21	0.033	1.12	0.449	1.27	0.423	1.69
1435749_at	Gda	guanine deaminase	1.8	0.163	1.38	0.137	2.31	0.164	2.32	0.28	1.95
1456095_at	Tyr	tyrosinase	2.46	0.178	1.03	0.799	2	0.119	2.63	0.191	2.03
1427222_a_at	Svp2	seminal vesicle protein 2	1.41	0.647	2.67	0.064	1.42	0.192	1.24	0.509	1.69
1458565_at	---	---	1.86	0.327	1.13	0.818	2.52	0.011	2.09	0.411	1.9
1418556_at	Capza3	capping protein (actin filament) muscle Z-line, alpha 3	2.51	0.152	1.13	0.827	1.87	0.227	1.36	0.582	1.72
1439067_at	Lair1	leukocyte-associated Ig-like receptor 1	2.52	0.089	1.35	0.048	1.65	0.144	1.13	0.394	1.66
1452855_at	Ly6k	lymphocyte antigen 6 complex, locus K	1.02	0.93	3.45	0.234	1.05	0.868	1.36	0.657	1.72
1441579_at	Dmrta1	doublesex and mab-3 related transcription factor like family A1	1.91	0.446	2.32	0.034	1.31	0.638	1.88	0.159	1.85
1419647_a_at	Ier3	immediate early response 3	1.55	0.076	2.77	0.023	1.22	0.386	2.63	0.108	2.04
1457066_at	Abcc8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	1.53	0.588	2.5	0.161	1.52	0.297	1.67	0.477	1.8
1421525_a_at	Birc1e	baculoviral IAP repeat-containing 1e	2.76	0.084	1.28	0.073	1.52	0.173	1.09	0.846	1.66
1416077_at	Adm	adrenomedullin	1.19	0.108	2.6	0.095	1.77	0.432	1.35	0.105	1.73
1460304_a_at	Ubtf	upstream binding transcription factor, RNA polymerase I	2.5	0.022	1.22	0.57	1.85	0.058	1.64	0.378	1.8
1441968_at	Tspan9	tetraspanin 9	1.72	0.563	2.43	0.23	1.42	0.708	1.21	0.48	1.7
1423914_at	C630004H02Rik	RIKEN cDNA C630004H02 gene	1.14	0.502	3.13	0.081	1.29	0.149	1.26	0.635	1.71
1427994_at	Cd300lf	CD300 antigen like family member F	1.21	0.735	2.06	0.022	2.31	0.142	1.17	0.465	1.69
1439520_at	---	---	2.05	0.102	2.25	0.323	1.29	0.662	4.41	0.203	2.5
1426001_at	Eomes	eomesodermin homolog (Xenopus laevis)	2.55	0.329	1.27	0.639	1.77	0.295	1.61	0.465	1.8
1418368_at	Retnlb	resistin like beta	1.17	0.472	1.88	0.389	2.55	0.151	1.69	0.433	1.82
1416986_a_at	Sirpa	signal-regulatory protein alpha	1.14	0.847	1.56	0.605	2.9	0.173	1.57	0.278	1.79
1421291_at	Il18rap	interleukin 18 receptor accessory protein	2.51	0.3	1.19	0.729	1.9	0.246	1.26	0.251	1.72
1422163_at	Sh3pxd2a	SH3 and PX domains 2A	1.96	0.273	2.13	0.144	1.52	0.442	1.45	0.664	1.76
1441910_x_at	Ccne1	cyclin E1	1.32	0.742	2.41	0.224	1.88	0.202	3.37	0.108	2.25
1432379_at	4930590A17Rik	RIKEN cDNA 4930590A17 gene	2.23	0.529	1.67	0.309	1.72	0.374	1.06	0.946	1.67
1458499_at	Pde10a	phosphodiesterase 10A	1.84	0.018	2.34	0.042	1.43	0.457	1.26	0.472	1.72
1454555_at	4930472F24Rik	RIKEN cDNA 4930472F24 gene	2.07	0.542	2.24	0.319	1.31	0.582	1.04	0.875	1.66
1422062_at	Msr1	macrophage scavenger receptor 1	1.02	0.979	2.88	0.032	1.72	0.063	1.87	0.479	1.87
1434275_at	---	Transcribed locus	3.44	0.112	1.03	0.973	1.15	0.623	1.2	0.405	1.71
1451612_at	Mt1	metallothionein 1	1.11	0.847	3.37	0.164	1.14	0.796	3.73	0.299	2.34
1448719_at	Tada3l	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	1.87	0.454	2.39	0.406	1.36	0.55	1.43	0.384	1.76
1430104_at	Rspo2	R-spondin 2 homolog (Xenopus laevis)	1.99	0.359	1.46	0.519	2.19	0.283	1.37	0.646	1.75
1422377_at	V1rb4	vomeronasal 1 receptor, B4	2.11	0.07	2.16	0.012	1.36	0.009	1.27	0.543	1.73
1427764_a_at	Tcfe2a	transcription factor E2a	1.56	0.213	1.81	0.249	2.27	0.022	2.14	0.025	1.94

1436520_at	AI450948	expressed sequence AI450948	2.09	0.389	1.65	0.246	1.9	0.089	3.12	0.055	2.19
1418993_s_at	F10	coagulation factor X	2.15	0.572	1.26	0.179	2.24	0.11	3.36	0.179	2.25
1459639_at	Brsk2	BR serine/threonine kinase 2	1.25	0.41	2.45	0.171	1.95	0.093	1.04	0.948	1.67
1421714_at	Tmprss3	transmembrane protease, serine 3	1.19	0.418	3.26	0.045	1.2	0.718	1.79	0.08	1.86
1422145_at	Mgat3	mannoside acetylglucosaminyltransferase 3	1.25	0.789	2.08	0.427	2.33	0.222	1.09	0.865	1.69
1460513_a_at	Ednra	endothelin receptor type A	1.71	0.351	2.3	0.21	1.64	0.217	1.14	0.344	1.7
1426282_at	Hnt	neurotrimin	2.37	0.366	1.41	0.193	1.89	0.464	1.72	0.412	1.84
1452357_at	Gp1bb /// Sept5	glycoprotein Ib, beta polypeptide /// septin 5	1.28	0.2	2.89	0.057	1.5	0.186	1.57	0.53	1.81
1421510_at	Prss7	protease, serine, 7 (enterokinase)	1.23	0.771	3.29	0.107	1.15	0.783	2.22	0.378	1.97
1460011_at	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	1.63	0.345	1.25	0.441	2.8	0.001	1.04	0.943	1.68
1434240_at	4632434I11Rik	RIKEN cDNA 4632434I11 gene	2.72	0.124	1.51	0.431	1.45	0.615	3.26	0.268	2.24
1436863_at	1700010I14Rik	RIKEN cDNA 1700010I14 gene	2.64	0.05	1.59	0.467	1.46	0.271	1.09	0.793	1.69
1416034_at	Cd24a	CD24a antigen	1.19	0.326	3.06	0.303	1.44	0.211	1.81	0.165	1.88
1442134_at	Prr11	proline rich 11	2.32	0.445	1.73	0.143	1.64	0.47	2.37	0.124	2.02
1420941_at	Rgs5	regulator of G-protein signaling 5	2.43	0.301	2.17	0.171	1.09	0.818	1.02	0.949	1.68
1450764_at	Aoah	acyloxyacyl hydrolase	1.2	0.076	2.79	0.052	1.71	0.006	1.64	0.118	1.84
1422908_at	Atp1b4	ATPase, (Na+)/K+ transporting, beta 4 polypeptide	1.06	0.599	3.47	0.016	1.17	0.315	1.82	0.277	1.88
1422953_at	Fpr-rs2	formyl peptide receptor, related sequence 2	1.75	0.448	1.68	0.006	2.28	0.327	3.02	0.183	2.18
1419993_at	Rab3il1	RAB3A interacting protein (rabin3)-like 1	1.26	0.455	3.2	0.169	1.26	0.563	3.71	0.021	2.36
1420860_at	Itga9	integrin alpha 9	1.51	0.402	2.64	0.189	1.58	0.172	1.73	0.381	1.86
1444748_at	Pspc1	Paraspeckle protein 1	2.25	0.107	2.4	0.257	1.08	0.868	1.44	0.422	1.79
1444586_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	1.49	0.476	2.75	0.172	1.49	0.579	1.11	0.871	1.71
1434803_a_at	Sycn	syncollin	2.57	0.11	1.67	0.191	1.5	0.381	1.16	0.766	1.73
1447284_at	Trem1	triggering receptor expressed on myeloid cells 1	1.7	0.323	1.79	0.316	2.26	0.228	1.04	0.93	1.7
1435748_at	Gda	guanine deaminase	1.85	0.06	1.35	0.113	2.55	0.088	2.56	0.262	2.08
1418340_at	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide	1.83	0.258	2.06	0	1.87	0.14	1.5	0.101	1.81
1455504_a_at	Mkrn1	makorin, ring finger protein, 1	1.69	0.162	1.2	0.203	2.87	0.244	2.65	0.262	2.1
1452279_at	Cfp	complement factor properdin	1.81	0.291	1.84	0.015	2.11	0.047	1.43	0.605	1.8
1450179_at	Sost	sclerostin	2.59	0.164	2.05	0.428	1.13	0.643	1.03	0.927	1.7
1451626_x_at	---	Transcribed locus	1.25	0.061	2.42	0.002	2.11	0.251	1.88	0.094	1.91
1417172_at	Ube2l6	ubiquitin-conjugating enzyme E2L 6	2.77	0.05	1.31	0.017	1.69	0.452	3.06	0.228	2.21
1458623_at	---	Transcribed locus	1.74	0.307	2.39	0.332	1.64	0.129	2.19	0.057	1.99
1455257_at	Itgb3	integrin beta 3	1.15	0.892	1.78	0.35	2.85	0.112	1.61	0.537	1.85
1448377_at	Slpi	secretory leukocyte peptidase inhibitor	1.48	0.584	1.84	0.088	2.46	0.031	1.9	0.093	1.92
1436738_at	AI449441	expressed sequence AI449441	3.47	0.008	1.16	0.781	1.15	0.72	3.48	0.184	2.32
1418267_at	Mst1	macrophage stimulating 1 (hepatocyte growth factor-like)	2.46	0.44	1.17	0.035	2.16	0.061	2.17	0.313	1.99
1426501_a_at	T2bp	Traf2 binding protein	1.23	0.054	3.35	0.098	1.22	0.185	1.2	0.518	1.75
1415864_at	Bpgm	2,3-bisphosphoglycerate mutase	1.3	0.282	2.04	0.126	2.46	0.226	2.09	0.345	1.97
1417750_a_at	Slc25a37	solute carrier family 25, member 37	1.39	0.439	1.48	0.099	2.94	0.28	2.72	0.169	2.13
1416804_at	G430002G23Rik	RIKEN cDNA G430002G23 gene	1.69	0.046	2.24	0.005	1.89	0.016	2.26	0.145	2.02
1459955_at	5830484A20Rik	RIKEN cDNA 5830484A20 gene	3.38	0.109	1.22	0.527	1.21	0.594	1.1	0.853	1.73
1456714_at	Wwp2	WW domain containing E3 ubiquitin protein ligase 2	1.75	0.487	2.86	0.183	1.21	0.47	1.42	0.152	1.81
1417714_x_at	Hba-a1	hemoglobin alpha, adult chain 1	2.08	0.194	2.51	0.193	1.24	0.382	1.27	0.506	1.77
1424486_a_at	Txnrd1	thioredoxin reductase 1	1.5	0.475	1.1	0.888	3.23	0.251	1.62	0.164	1.86
1428377_at	Btbd11	BTB (POZ) domain containing 11	1.35	0.195	2.39	0.228	2.09	0.169	1.07	0.86	1.73
1436779_at	Cybb	cytochrome b-245, beta polypeptide	1.42	0.029	2.04	0.002	2.37	0.058	1.18	0.567	1.75
1417229_at	Capn1	calpain 1	2.4	0.22	1.22	0.656	2.22	0.43	1.97	0.214	1.95
1439902_at	C5ar1	complement component 5a receptor 1	1.38	0.642	2.34	0.051	2.12	0.009	1.04	0.92	1.72
1431439_at	5830487J09Rik	RIKEN cDNA 5830487J09 gene	1.13	0.815	3.64	0.101	1.08	0.884	1.04	0.827	1.72
1421182_at	Clec1b	C-type lectin domain family 1, member b	1.69	0.633	1.69	0.001	2.47	0.179	1.38	0.441	1.81
1442082_at	C3ar1	complement component 3a receptor 1	2.14	0.384	2.21	0.044	1.51	0.004	1.96	0.17	1.96
1425425_a_at	Wif1	Wnt inhibitory factor 1	2.06	0.295	1.32	0.6	2.49	0.162	1.07	0.905	1.73
1459994_x_at	Trfr2	transferrin receptor 2	2.83	0.41	1.1	0.264	1.95	0.001	6.35	0.189	3.06

1421244_at	Esr1	estrogen receptor 1 (alpha)	1.17	0.478	3.52	0.022	1.2	0.403	2.03	0.21	1.98
1417381_at	C1qa	complement component 1, q subcomponent, alpha polypeptide	2.51	0.14	1.78	0.02	1.59	0.326	1.17	0.596	1.76
1432253_at	4921523P09Rik	RIKEN cDNA 4921523P09 gene	3.54	0.232	1.1	0.839	1.26	0.121	1.34	0.508	1.81
1421278_s_at	LOC630963	similar to spectrin alpha 1	1.22	0.783	2.31	0.137	2.36	0.192	7.09	0.135	3.25
1419773_at	2010301N04Rik	RIKEN cDNA 2010301N04 gene	1.13	0.67	3.7	0.001	1.08	0.807	1.92	0.203	1.95
1418849_x_at	Aqp7	aquaporin 7	1.96	0.219	1.83	0.154	2.12	0.24	1.15	0.675	1.77
1448898_at	Ccl9	chemokine (C-C motif) ligand 9	1.89	0.179	1.16	0.295	2.88	0.183	1.09	0.546	1.76
1446575_at	C77583	expressed sequence C77583	2.64	0.006	2.03	0.132	1.26	0.58	1.05	0.881	1.75
1430911_at	D19Ertd652e	DNA segment, Chr 19, ERATO Doi 652, expressed	1.72	0.085	3.19	0.045	1.05	0.946	1.48	0.654	1.86
1422380_at	V1rb5	vomeronasal 1 receptor, B5	2.54	0.103	2.35	0.254	1.07	0.882	1.08	0.863	1.76
1416304_at	Litaf	LPS-induced TN factor	1.21	0.037	2.11	0.14	2.65	0.14	1.56	0.03	1.88
1448424_at	Frzb	frizzled-related protein	2.86	0.048	1.71	0.348	1.4	0.383	1.41	0.421	1.85
1459039_at	Heatr1	HEAT repeat containing 1	2.74	0.484	2.24	0.086	1.01	0.984	1.19	0.843	1.79
1425584_x_at	---	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched library,	1.76	0.074	2.27	0.014	1.96	0.051	1.18	0.143	1.79
1447846_x_at	Leng4	leukocyte receptor cluster (LRC) member 4	1.92	0.551	1.81	0.28	2.26	0.001	1.4	0.429	1.85
1425307_at	Dnahc1	dynein, axonemal, heavy chain 1	1.62	0.441	3.26	0.071	1.11	0.271	1	1	1.75
1439864_at	Ccdc40	coiled-coil domain containing 40	1.51	0.375	2.59	0.035	1.91	0.083	2.97	0.053	2.24
1457215_at	---	Adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C63002	1.08	0.506	3.29	0.087	1.65	0.228	1.65	0.531	1.92
1437272_at	4932443J21Rik	RIKEN cDNA 4932443J21 gene	3.67	0.005	1.32	0.673	1.04	0.928	1.45	0.417	1.87
1459059_at	2010308F09Rik	RIKEN cDNA 2010308F09 gene	2.56	0.488	1.16	0.815	2.32	0.233	1.88	0.285	1.98
1418346_at	Insl6	insulin-like 6	1.15	0.582	3.34	0.129	1.55	0.428	1.04	0.841	1.77
1424966_at	Tmem40	transmembrane protein 40	1.01	0.965	2.85	0.113	2.2	0.136	2.12	0.376	2.04
1437726_x_at	C1qb	complement component 1, q subcomponent, beta polypeptide	2.14	0.233	2.06	0.001	1.87	0.229	1.08	0.58	1.79
1421792_s_at	Trem2	triggering receptor expressed on myeloid cells 2	1.13	0.472	2.99	0.418	1.94	0.084	1.44	0.099	1.88
1422926_at	Mc2r	melanocortin 2 receptor	2.11	0.302	1.58	0.488	2.39	0.212	1.24	0.534	1.83
1442459_at	Adamts19	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type	2.56	0.333	1.77	0.249	1.75	0.347	1.54	0.275	1.9
1450245_at	Slc10a2	solute carrier family 10, member 2	1.11	0.809	2.22	0.316	2.74	0.034	1.82	0.398	1.97
1460057_at	Gdf3	growth differentiation factor 3	1.81	0.499	2.85	0.06	1.42	0.468	5.49	0.197	2.89
1428481_s_at	Cdca8	cell division cycle associated 8	1.86	0.03	1.25	0.577	2.97	0.219	4.12	0.207	2.55
1425750_a_at	Jak3	Janus kinase 3	1.09	0.267	2.34	0.026	2.67	0.026	1.08	0.741	1.79
1439289_s_at	0710005I19Rik	RIKEN cDNA 0710005I19 gene	1.21	0.669	2.16	0.078	2.75	0.049	1.66	0.226	1.94
1432377_x_at	Shroom3	shroom family member 3	1.03	0.948	3.73	0.006	1.37	0.051	1.41	0.55	1.89
1419756_at	Dgkg	diacylglycerol kinase, gamma	3.37	0.035	1.08	0.749	1.69	0.168	3.13	0.257	2.32
1450194_a_at	Myb	myeloblastosis oncogene	2.12	0.391	2.99	0.176	1.05	0.896	1.65	0.329	1.95
1420399_at	Gfi1b	growth factor independent 1B	2.14	0.335	2.31	0.183	1.71	0.399	7.69	0.203	3.46
1437549_at	2810408I11Rik	RIKEN cDNA 2810408I11 gene	2.32	0.142	1.78	0.214	2.06	0.156	2.52	0.157	2.17
1417729_at	Myh6	myosin, heavy polypeptide 6, cardiac muscle, alpha	1.53	0.192	1.07	0.929	3.57	0.188	1.05	0.904	1.81
1449365_at	Edg8	endothelial differentiation, sphingolipid G-protein-coupled receptor, 8	1.19	0.763	3.91	0.002	1.08	0.763	1.63	0.546	1.95
1419610_at	Ccr1	chemokine (C-C motif) receptor 1	1.62	0.513	1.18	0.693	3.38	0.151	1.18	0.443	1.84
1449305_at	F10	coagulation factor X	2.9	0.365	1.24	0.199	2.05	0.219	3.02	0.287	2.3
1418776_at	5830443L24Rik /// I	RIKEN cDNA 5830443L24 gene /// similar to macrophage activation 2 like	2.3	0.003	2.06	0.011	1.84	0.165	1.08	0.856	1.82
1433966_x_at	Asns	asparagine synthetase	1.07	0.461	4.07	0.085	1.07	0.763	5.89	0.162	3.03
1430487_at	Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	3.34	0.172	1.53	0.496	1.35	0.627	1.52	0.212	1.93
1421837_at	Rps18	ribosomal protein S18	2.4	0.034	2.03	0.358	1.8	0.154	1.09	0.565	1.83
1419182_at	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1	1.57	0.053	3.51	0.028	1.14	0.69	1.05	0.836	1.82
1451563_at	Emr4	EGF-like module containing, mucin-like, hormone receptor-like sequence 4	2.99	0.039	1.7	0.026	1.54	0.162	1.16	0.791	1.85
1419082_at	Serpinb2	serine (or cysteine) peptidase inhibitor, clade B, member 2	1.3	0.767	2.03	0.121	2.9	0.137	2.26	0.372	2.12
1421921_at	Serpina3m	serine (or cysteine) peptidase inhibitor, clade A, member 3M	2.96	0.557	1.37	0.071	1.91	0.315	1.05	0.909	1.82
1422868_s_at	Gda	guanine deaminase	1.66	0.145	1.6	0.122	3.01	0.064	3.49	0.265	2.44
1457753_at	Tlr13	toll-like receptor 13	1.17	0.556	2.69	0.004	2.41	0.171	1.4	0.394	1.92
1447347_at	App	Amyloid beta (A4) precursor protein	1.47	0.645	1.23	0.45	3.57	0.07	1.63	0.063	1.98
1419339_at	Neu3	neuraminidase 3	1.33	0.555	3.84	0.113	1.11	0.499	2.08	0.097	2.09
1425471_x_at	---	---	1.9	0.218	2.36	0.167	2.03	0.02	1.4	0.613	1.92

1438009_at	MGC73635	similar to histone 2a	1.8	0.208	2.35	0.136	2.15	0.377	1.41	0.273	1.93
1429607_at	Trak2	trafficking protein, kinesin binding 2	1.65	0.59	1.23	0.787	3.42	0.061	1.52	0.428	1.96
AFFX-PyruCarbMur	Pcx	pyruvate carboxylase	1.81	0.454	1.19	0.796	3.31	0.231	1.23	0.718	1.88
1437514_at	B430306N03Rik	RIKEN cDNA B430306N03 gene	1.28	0.711	1.95	0.006	3.08	0.091	1.04	0.843	1.84
1419762_at	Ubd	ubiquitin D	1.79	0.108	1.13	0.619	3.4	0.071	2.18	0.321	2.12
1426027_a_at	Arhgap10	Rho GTPase activating protein 10	1.28	0.496	3.34	0.138	1.69	0.072	5.6	0.003	2.98
1443357_at	Zfr	Zinc finger RNA binding protein	2.94	0.175	2.33	0.181	1.05	0.944	1.34	0.408	1.91
1432198_at	---	---	2.09	0.239	2.05	0.143	2.18	0.021	1.13	0.754	1.86
1438085_at	A230048G03Rik ///	RIKEN cDNA A230048G03 gene /// similar to CG2747-PB, isoform B	3.8	0.084	1.3	0.789	1.22	0.79	1.68	0.449	2
1452016_at	Alox5ap	arachidonate 5-lipoxygenase activating protein	2.02	0.162	2.32	0.001	2	0.227	1.39	0.1	1.93
1421454_at	Zfp108	zinc finger protein 108	1.32	0.239	3.42	0.098	1.62	0.271	1.72	0.206	2.02
1449401_at	C1qc	complement component 1, q subcomponent, C chain	2.9	0.135	1.89	0.001	1.58	0.255	1.32	0.341	1.92
1417063_at	C1qb	complement component 1, q subcomponent, beta polypeptide	2.6	0.167	2.1	0.004	1.66	0.227	1.47	0.126	1.96
1432300_at	1190003K10Rik	RIKEN cDNA 1190003K10 gene	2.32	0.448	2.73	0.003	1.32	0.491	2	0.375	2.09
1449164_at	Cd68	CD68 antigen	2.06	0.122	2.37	0.008	1.95	0.013	1.68	0.266	2.02
1417266_at	Ccl6	chemokine (C-C motif) ligand 6	1.57	0.053	3.5	0.008	1.33	0.103	1.31	0.422	1.93
1433314_at	4930486A15Rik	RIKEN cDNA 4930486A15 gene	1.65	0.26	3.23	0.017	1.51	0.401	1.59	0.31	2
1457824_at	---	Adult male bone cDNA, RIKEN full-length enriched library, clone:9830165G24 pr	1.77	0.086	3.31	0.074	1.34	0.38	2.45	0.057	2.22
1459971_at	Kcnt2	Potassium channel, subfamily T, member 2	1.1	0.575	3.46	0.217	1.86	0.352	1.56	0.417	2
1422699_at	Alox12	arachidonate 12-lipoxygenase	1.15	0.593	1.73	0.283	3.56	0.116	2.01	0.409	2.11
1435386_at	Vwf	Von Willebrand factor homolog	1.91	0.38	2.43	0.147	2.09	0.001	1.46	0.574	1.97
1426665_at	Katnb1	katanin p80 (WD40-containing) subunit B 1	1.18	0.619	2.68	0.053	2.58	0.033	1.35	0.253	1.95
1443423_at	Wnk2 /// LOC62467	WNK lysine deficient protein kinase 2 /// hypothetical LOC624678	3.22	0.442	1.37	0.462	1.86	0.419	1.36	0.695	1.95
1449172_a_at	Lin7b	lin-7 homolog B (C. elegans)	1.26	0.566	2.99	0.159	2.2	0.176	1.69	0.306	2.04
1418619_at	Icam5	intercellular adhesion molecule 5, telencephalin	3.91	0.031	1.05	0.923	1.5	0.265	1.32	0.74	1.95
1455104_at	Mxd1	MAX dimerization protein 1	1.09	0.832	1.16	0.201	4.21	0.13	2.54	0.292	2.25
1421038_a_at	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfamily	1.97	0.409	2.6	0.337	1.89	0.08	2.81	0.187	2.32
1428317_at	---	---	1.13	0.865	4.29	0.124	1.06	0.849	1.02	0.969	1.87
1424942_a_at	Myc	myelocytomatosis oncogene	1.58	0.316	1.36	0.601	3.57	0.219	1.14	0.511	1.91
1425337_at	Slc12a5	solute carrier family 12, member 5	3.48	0.241	1.98	0.268	1.05	0.871	1.22	0.32	1.93
1425225_at	Fcgr3a	Fc fragment of IgG, low affinity IIIa, receptor	1.75	0.084	1.76	0.015	3.03	0.054	2.38	0.088	2.23
1418326_at	Slc7a5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	2.08	0.282	1.96	0.427	2.52	0.119	4.87	0.13	2.86
1426817_at	Mki67 /// LOC6387	antigen identified by monoclonal antibody Ki 67 /// similar to Antigen KI-67	1.7	0.266	3.41	0.071	1.5	0.3	2.97	0.124	2.39
1424754_at	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	2.85	0.213	2.22	0.126	1.56	0.23	1.38	0.075	2
1417852_x_at	Clca1	chloride channel calcium activated 1	2.29	0.358	2.43	0.102	1.92	0.165	1.12	0.761	1.94
1448620_at	Fcgr3	Fc receptor, IgG, low affinity III	2.89	0.123	1.67	0	2.08	0.106	1.04	0.856	1.92
1426161_at	---	---	1.7	0.009	1.11	0.719	3.84	0.07	1.7	0.605	2.09
1417638_at	Lefty1	left right determination factor 1	3.15	0.24	2.35	0.353	1.18	0.238	1.69	0.158	2.09
1421410_a_at	Pstpip2	proline-serine-threonine phosphatase-interacting protein 2	1.61	0.487	1.33	0.038	3.73	0.173	1.6	0.057	2.07
1449826_a_at	Fgf2	fibroblast growth factor 2	3.79	0.008	1.18	0.648	1.72	0.054	1	0.993	1.92
1420249_s_at	Ccl6	chemokine (C-C motif) ligand 6	1.23	0.656	3.79	0.043	1.66	0.087	1.93	0.023	2.15
1421670_a_at	Irak4	interleukin-1 receptor-associated kinase 4	1.98	0.002	2.64	0.17	2.07	0.26	1.07	0.883	1.94
1426755_at	Ckap4	cytoskeleton-associated protein 4	1.39	0.31	3.85	0.068	1.47	0.188	1.63	0.082	2.08
1456980_at	9830134C10Rik	RIKEN cDNA 9830134C10 gene	1.3	0.711	4.17	0.028	1.25	0.333	2.17	0.441	2.22
1432459_a_at	Zbtb32	zinc finger and BTB domain containing 32	1.2	0.761	1.38	0.546	4.15	0.226	2.54	0.122	2.32
1416967_at	Sox2	SRY-box containing gene 2	3.52	0.041	1.79	0.268	1.44	0.125	1.4	0.486	2.04
1429954_at	Clec4a3	C-type lectin domain family 4, member a3	3.18	0.084	2	0	1.58	0.087	1.67	0.243	2.11
1453239_a_at	Ankrd22	ankyrin repeat domain 22	3.85	0.044	1.19	0.635	1.73	0.461	3.14	0.191	2.48
1441654_at	Gnal	Guanine nucleotide binding protein, alpha stimulating, olfactory type	1.49	0.633	2.16	0.141	3.15	0.028	2.07	0.069	2.21
1418946_at	St3gal1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	4.08	0.219	1.43	0.174	1.31	0.216	1.25	0.495	2.02
1447444_at	Ubxd5	UBX domain containing 5	3.63	0.341	2.04	0.296	1.18	0.681	1.1	0.847	1.99
1451927_a_at	Mapk14	mitogen activated protein kinase 14	2.74	0.161	1.06	0.927	3.07	0.301	1.01	0.995	1.97
1460197_a_at	Steap4	STEAP family member 4	1.7	0.634	3.09	0.121	2.09	0.072	1.07	0.864	1.99

1419532_at	Il1r2	interleukin 1 receptor, type II	1.59	0.264	1.4	0.501	3.89	0.299	1.51	0.54	2.1
1450813_a_at	Tnni1	troponin I, skeletal, slow 1	1.15	0.323	2.66	0.121	3.08	0.113	1.15	0.857	2.01
1454514_at	5730415C11Rik	RIKEN cDNA 5730415C11 gene	3.1	0.405	2.71	0.029	1.08	0.786	2.53	0.311	2.35
1446714_x_at	---	Transcribed locus	1.97	0.184	3.69	0.144	1.25	0.678	1.08	0.778	2
1427856_a_at	---	Immunoglobulin kappa chain complex	2.32	0.01	2.59	0.148	2	0.06	1.21	0.69	2.03
1448083_at	LOC675405	similar to voltage gated channel like 1	1.03	0.923	2.68	0.071	3.21	0.02	1.37	0.671	2.07
1417507_at	Cyb561	cytochrome b-561	1.14	0.133	4.63	0.123	1.21	0.029	1.21	0.397	2.05
1421186_at	Ccr2	chemokine (C-C motif) receptor 2	1.99	0.134	3.57	0.004	1.42	0.241	1.92	0.019	2.22
1449136_at	Epx	eosinophil peroxidase	2.49	0.382	3.13	0.147	1.37	0.541	3.64	0.222	2.66
1453943_a_at	Acpp	acid phosphatase, prostate	1.41	0.646	3.38	0.209	2.2	0.423	1.84	0.448	2.21
1460014_at	Treml4	triggering receptor expressed on myeloid cells-like 4	2.71	0.491	2.74	0.002	1.55	0.168	1.33	0.542	2.08
1422760_at	Padi4 /// LOC67054	peptidyl arginine deiminase, type IV /// similar to Protein-arginine deiminase type	2	0.267	1.49	0.513	3.5	0.193	1.67	0.434	2.17
1448995_at	Cxcl4	chemokine (C-X-C motif) ligand 4	1.2	0.626	4.09	0.028	1.75	0.219	1.67	0.519	2.18
1446678_at	D14Ertd16e	DNA segment, Chr 14, ERATO Doi 16, expressed	1.59	0.583	1.55	0.232	3.91	0	1.06	0.831	2.03
1424825_a_at	Glycam1	glycosylation dependent cell adhesion molecule 1	1.39	0.505	1.48	0.477	4.23	0.117	11.55	0.271	4.66
1450678_at	Itgb2	integrin beta 2	2	0.156	2.7	0.001	2.44	0.009	1.11	0.583	2.06
1439898_at	Ebna1bp2	EBNA1 binding protein 2	3.97	0.228	1.82	0.237	1.39	0.59	1.78	0.067	2.24
1449360_at	Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage	1.71	0.008	3.14	0.01	2.35	0.001	1.24	0.162	2.11
1434046_at	AA467197	expressed sequence AA467197	1.28	0.686	3.96	0.01	1.98	0.322	4.19	0.311	2.85
1437245_at	Tmem154	transmembrane protein 154	3.71	0.051	1.16	0.82	2.37	0.032	1.37	0.552	2.15
1427415_at	Fbxo43	F-box protein 43	2.26	0.418	3.88	0.025	1.11	0.863	1.48	0.591	2.18
1420394_s_at	Gp49a /// Lilrb4	glycoprotein 49 A /// leukocyte immunoglobulin-like receptor, subfamily B, membe	2.59	0.213	2.32	0.01	2.36	0.048	1.53	0.14	2.2
1422952_at	Ng23	Ng23 protein	1.68	0.403	1.28	0.166	4.31	0.139	1.55	0.212	2.21
1420398_at	Rgs18	regulator of G-protein signaling 18	1.86	0.253	2.91	0.077	2.53	0.195	1.43	0.513	2.18
1421326_at	Csf2rb1	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-macrophage	1.54	0.184	2.98	0.019	2.79	0.014	1.25	0.092	2.14
1451128_s_at	Kif22	kinesin family member 22	2.06	0.26	4.03	0.077	1.22	0.475	3.48	0.22	2.7
1418806_at	Csf3r	colony stimulating factor 3 receptor (granulocyte)	2.38	0.423	1.89	0.126	3.07	0.15	1.13	0.719	2.12
1435287_at	Add2	adducin 2 (beta)	2.81	0.276	2.03	0.411	2.51	0.271	7.69	0.207	3.76
1431010_a_at	Rdh12	retinol dehydrogenase 12	2.09	0.469	1.06	0.849	4.22	0.176	1.11	0.81	2.12
1448749_at	Plek	pleckstrin	2	0.257	2.54	0.035	2.84	0.068	1.12	0.622	2.13
1417325_at	Btrc	beta-transducin repeat containing protein	3.11	0.058	2.53	0.031	1.76	0.285	3.39	0.015	2.7
1424930_s_at	AW544981	expressed sequence AW544981	2.41	0.134	2.48	0.131	2.53	0.094	1.2	0.781	2.15
1418021_at	C4b /// LOC675521	complement component 4B (Childo blood group) /// similar to Complement C4 pre	3.88	0.337	1.14	0.291	2.4	0.038	1.21	0.461	2.16
1439862_at	---	Visual cortex cDNA, RIKEN full-length enriched library, clone:K530032J01 produc	1.57	0.661	1.11	0.814	4.74	0	2.29	0.319	2.43
1421162_a_at	Nfia	nuclear factor I/A	4.07	0.125	2.24	0.133	1.11	0.817	1.52	0.024	2.24
1434067_at	AI662270	expressed sequence AI662270	2.63	0.206	2.28	0.04	2.62	0.236	1.39	0.098	2.23
1422817_at	Gp5	glycoprotein 5 (platelet)	1.99	0.485	1.94	0.058	3.6	0.103	1.82	0.427	2.34
1444214_at	2810484G07Rik	RIKEN cDNA 2810484G07 gene	1.69	0.429	1.87	0.211	3.99	0.121	2	0.449	2.39
1419282_at	Ccl12	chemokine (C-C motif) ligand 12	3.93	0.093	1.19	0.784	2.48	0.104	2.41	0.025	2.5
1451651_at	Vsig4	V-set and immunoglobulin domain containing 4	2.07	0.408	2.37	0	3.16	0.15	2.6	0.004	2.55
1453047_at	Bzrpl1	benzodiazapine receptor, peripheral-like 1	1.37	0.148	4.04	0	2.21	0.345	5.44	0.229	3.27
1435264_at	Emilin2	elastin microfibril interfacer 2	1.05	0.864	2.33	0.023	4.26	0.076	6.2	0.201	3.46
1420442_at	Cacna1s	calcium channel, voltage-dependent, L type, alpha 1S subunit	3.76	0.153	1.26	0.466	2.63	0.09	2.17	0.042	2.45
1452954_at	Ube2c	ubiquitin-conjugating enzyme E2C	2.41	0.053	3.16	0.02	2.16	0.286	4.84	0.153	3.14
1444223_at	Hcrtr2	hypocretin (orexin) receptor 2	4.6	0.228	2.15	0.182	1.03	0.95	1.43	0.245	2.3
1422327_s_at	G6pd2 /// G6pdx	glucose-6-phosphate dehydrogenase 2 /// glucose-6-phosphate dehydrogenase X	1.4	0.542	3.89	0.029	2.55	0.255	1.82	0.307	2.42
1449222_at	Ebi3	Epstein-Barr virus induced gene 3	2.12	0.166	2.4	0.01	3.47	0.248	1.16	0.636	2.29
1435761_at	Stfa3	stefin A3	1.27	0.804	2.54	0.343	4.28	0.149	2.09	0.441	2.54
1440342_at	G530011O06Rik	RIKEN cDNA G530011O06 gene	2.37	0.014	3.27	0.04	2.46	0.077	1.69	0.459	2.45
1426178_at	---	Immunoglobulin kappa chain complex	1.52	0.156	3.3	0.039	3.29	0.153	1.19	0.73	2.33
1439119_a_at	BC010304	cDNA sequence BC010304	5.85	0.014	1.14	0.876	1.16	0.83	1.4	0.692	2.39
1424357_at	Tmem45b	transmembrane protein 45b	1.04	0.698	1.26	0.552	5.93	0.357	1.76	0.379	2.5
1456998_at	---	7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730	4.5	0.253	1.97	0.434	1.78	0.109	1.55	0.347	2.45

1418497_at	Fgf13	fibroblast growth factor 13	3.79	0.013	1.42	0.384	3.02	0.249	1.61	0.615	2.46
1451874_at	---	---	2.53	0.481	4.19	0.058	1.57	0.311	1.75	0.291	2.51
1429482_at	1700003H04Rik	RIKEN cDNA 1700003H04 gene	5.96	0.12	1	0.996	1.41	0.493	1.88	0.254	2.56
1448194_a_at	H19	H19 fetal liver mRNA	1.38	0.295	1.67	0.267	5.34	0.301	1.1	0.865	2.37
1451675_a_at	Alas2	aminolevulinic acid synthase 2, erythroid	4.37	0.311	1.31	0.52	2.74	0.251	2.38	0.244	2.7
1418069_at	Apoc2	apolipoprotein C-II	4.06	0.492	1.73	0.001	2.64	0.169	1.87	0.149	2.57
1437052_s_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	1.52	0.012	2.57	0.038	4.36	0.101	1.1	0.793	2.39
1427102_at	Slfn4	schlafen 4	1.02	0.983	3.15	0.115	4.29	0.19	2.03	0.493	2.62
1418480_at	Cxcl7	chemokine (C-X-C motif) ligand 7	1.98	0.401	3.65	0.127	2.89	0.166	1.5	0.55	2.5
1456212_x_at	Socs3	suppressor of cytokine signaling 3	2.92	0.151	4.03	0.104	1.57	0.237	1.26	0.142	2.45
1424155_at	Fabp4	fatty acid binding protein 4, adipocyte	1.39	0.082	1.9	0.475	5.24	0.368	5.21	0.167	3.44
1417853_at	Clca1	chloride channel calcium activated 1	2.69	0.345	3.92	0.112	1.92	0.303	1.36	0.353	2.47
1460259_s_at	Clca1 /// Clca2	chloride channel calcium activated 1 /// chloride channel calcium activated 2	3.17	0.346	2.34	0.104	3.06	0.095	1.04	0.901	2.4
1419311_at	Trim10	tripartite motif protein 10	2.82	0.335	2.59	0.212	3.42	0.266	5.19	0.154	3.51
1434068_s_at	AI662270	expressed sequence AI662270	3.69	0.15	2.13	0.018	3.02	0.179	1.46	0.14	2.57
1450322_s_at	Slfn3 /// Slfn4	schlafen 3 /// schlafen 4	1.18	0.45	2.21	0.429	5.51	0.312	2.04	0.534	2.73
1418493_a_at	Snca	synuclein, alpha	2.7	0.363	3.4	0.367	2.8	0.21	3.29	0.223	3.05
1427866_x_at	Hbb-b1	hemoglobin, beta adult major chain	3.91	0.125	2.08	0.214	2.96	0.306	4.09	0.26	3.26
1431049_at	Ica1l	islet cell autoantigen 1-like	4.23	0.013	1.1	0.892	3.63	0.028	1.28	0.654	2.56
1425829_a_at	Steap4	STEAP family member 4	1.62	0.692	4.09	0.175	3.3	0.25	1.07	0.898	2.52
1418675_at	Osmr	oncostatin M receptor	1.79	0.129	6.04	0.032	1.19	0.657	1.31	0.429	2.58
1448025_at	LOC668101	similar to SIRP beta 1 isoform 2	2.98	0.134	4.25	0.048	1.83	0.193	1.18	0.362	2.56
1422046_at	Itgam	integrin alpha M	2.29	0.049	2.47	0.059	4.47	0.139	2.4	0.133	2.91
1419684_at	Ccl8	chemokine (C-C motif) ligand 8	2.4	0.361	1.52	0.439	5.39	0.203	5.97	0.013	3.82
1445047_at	C79246	expressed sequence C79246	1.21	0.733	1.52	0.403	6.58	0.031	2.33	0.15	2.91
1422977_at	Gp1bb	glycoprotein Ib, beta polypeptide	1.14	0.717	2.46	0.222	5.75	0.129	2.45	0.386	2.95
1427577_x_at	Igk-V28 /// Igk-V8 //	immunoglobulin kappa chain variable 28 (V28) /// immunoglobulin kappa chain va	2.69	0.126	2.84	0.037	3.85	0.064	1.75	0.456	2.78
1423016_a_at	Gypa	glycophorin A	2.33	0.475	2.32	0.435	4.75	0.231	5.71	0.194	3.78
1422280_at	Gzmk	granzyme K	2.24	0.002	3.43	0.156	3.79	0.004	5.08	0.071	3.63
1427576_at	Igk-V28 /// Igk-V8 //	immunoglobulin kappa chain variable 28 (V28) /// immunoglobulin kappa chain va	3.41	0.26	2.93	0.03	3.15	0.085	2.18	0.336	2.92
1419609_at	Ccr1	chemokine (C-C motif) receptor 1	1.35	0.56	4.67	0.02	3.5	0.104	1.76	0.121	2.82
1425840_a_at	Sema3f	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semap	2.69	0.145	5.49	0.014	1.4	0.135	1.38	0.098	2.74
1418199_at	Hemgn	hemogen	1.02	0.969	6.59	0.33	2.11	0.081	5.47	0.099	3.8
1431362_a_at	Smoc2	SPARC related modular calcium binding 2	1.84	0.233	6.98	0.01	1.02	0.963	1.47	0.361	2.83
1449077_at	Eraf	erythroid associated factor	2.35	0.383	4.74	0.171	2.77	0.355	2.15	0.114	3
1424256_at	Rdh12	retinol dehydrogenase 12	1.73	0.579	1.45	0.64	6.76	0.1	1.22	0.318	2.79
1422140_at	Sp100-rs /// LOC62	similar to component of Sp100-rs /// similar to component of Sp100-rs /// similar to	2.76	0.082	3.25	0.014	3.98	0.002	1.6	0.257	2.9
1420496_at	F12	coagulation factor XII (Hageman factor)	7.89	0.385	1.01	0.902	1.12	0.508	1.19	0.55	2.8
1457354_at	Krt222	keratin 222	1.06	0.934	1.4	0.331	7.65	0.248	2.38	0.006	3.12
1449824_at	Prg4	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protei	3.09	0.426	2.75	0.128	4.39	0.153	1.24	0.363	2.87
1427857_x_at	---	Ig kappa chain V-region mRNA, partial cds, clone 2F2	3.59	0.239	1.24	0.267	5.45	0.017	1.74	0.367	3
1431834_a_at	Emilin1	elastin microfibril interfacer 1	3	0.034	5.7	0.087	1.66	0.415	1.75	0.225	3.03
1436649_at	Zfpn1a3	zinc finger protein, subfamily 1A, 3 (Aiolos)	2.71	0.448	1.14	0.761	6.54	0.237	1.07	0.866	2.86
1418126_at	Ccl5	chemokine (C-C motif) ligand 5	6.15	0.198	1.55	0.393	2.82	0.021	1.87	0.404	3.1
1458683_at	Sirpb1 /// LOC6731	signal-regulatory protein beta 1 /// similar to SIRP beta 1 isoform 1	1.49	0.693	7.45	0.003	1.78	0.154	1.57	0.086	3.07
1439893_at	---	CDNA clone IMAGE:3471071	1.24	0.751	2.1	0.164	7.6	0.205	1.41	0.237	3.09
1427393_at	F9	coagulation factor IX	8.44	0.397	1.1	0.556	1.68	0.112	1.24	0.308	3.11
1455898_x_at	Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	1.66	0.289	4.55	0.047	5.35	0.071	1.33	0.563	3.22
1430781_at	Ak7	adenylate kinase 7	1.29	0.16	9.36	0.167	1.1	0.666	1.17	0.723	3.23
1420330_at	Clec4e	C-type lectin domain family 4, member e	1.99	0.334	2.15	0.213	7.7	0.157	1.81	0.47	3.41
1426201_at	Gm1499	Gene model 1499, (NCBI)	4.27	0.022	1.81	0.415	5.78	0.057	2.63	0.027	3.62
1448929_at	F13a1	coagulation factor XIII, A1 subunit	1.5	0.675	8.53	0.068	1.95	0.187	2.15	0.408	3.53
1436853_a_at	Snca	synuclein, alpha	3.92	0.342	5.01	0.266	3.19	0.304	2.31	0.213	3.61

1417290_at	Lrg1	leucine-rich alpha-2-glycoprotein 1	7.27	0.36	1.77	0.227	3.16	0.012	3.61	0.171	3.95
1419598_at	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	4.9	0.297	3.86	0.001	3.48	0.074	2.72	0.009	3.74
1421187_at	Ccr2	chemokine (C-C motif) receptor 2	6.87	0.028	2.79	0.219	3.03	0.242	1.82	0.183	3.63
1449159_at	Gnb3	guanine nucleotide binding protein, beta 3	2.92	0.392	1.18	0.689	8.69	0.309	2.44	0.007	3.81
1449366_at	Mmp8	matrix metallopeptidase 8	1.86	0.453	4.67	0.189	6.52	0.3	3.55	0.344	4.15
1452001_at	Nfe2	nuclear factor, erythroid derived 2	1.01	0.988	6.36	0.027	5.77	0.107	6.71	0.197	4.96
1452732_at	2300003P22Rik	RIKEN cDNA 2300003P22 gene	2.31	0.058	1.45	0.52	9.47	0.229	1	0.99	3.56
1422815_at	C9	complement component 9	9.92	0.365	1.16	0.565	2.21	0.05	1.48	0.428	3.69
1448291_at	Mmp9	matrix metallopeptidase 9	1.59	0.27	2.22	0.08	9.84	0.2	2.13	0.395	3.94
1425451_s_at	Chi3l3 /// Chi3l4	chitinase 3-like 3 /// chitinase 3-like 4	1.67	0.625	10.58	0.114	1.71	0.083	2.64	0.467	4.15
1436530_at	---	CDNA clone MGC:107680 IMAGE:6766535	2.38	0.113	2.81	0.004	9.69	0.107	3.37	0.049	4.57
1425643_at	Gypa	glycophorin A	1.2	0.674	3.29	0.357	10.6	0.216	6.96	0.195	5.51
1451054_at	Orm1	orosomucoid 1	10.26	0.448	1.34	0.126	3.74	0.069	2.85	0.168	4.55
1444962_at	LOC665317	similar to component of Sp100-rs	6.68	0.043	5.17	0.012	4.11	0.132	3.14	0.207	4.78
1427381_at	Irg1	immunoresponsive gene 1	1.13	0.635	1.17	0.597	13.75	0.142	1.82	0.537	4.47
1422141_s_at	Csprs	component of Sp100-rs	2.37	0.153	2.87	0.004	10.91	0.002	1.65	0.212	4.45
1419594_at	Ctsg	cathepsin G	1.3	0.306	5.97	0.141	8.97	0.284	4.84	0.349	5.27
1448804_at	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1	1.74	0.138	1.43	0.125	13.43	0.274	5.52	0.177	5.53
1419599_s_at	Ms4a11	membrane-spanning 4-domains, subfamily A, member 11	11.96	0.042	2.55	0.006	2.21	0.079	2.58	0.003	4.82
1440865_at	Ifitm6	interferon induced transmembrane protein 6	1.34	0.555	4.67	0.067	11.09	0.227	3.01	0.335	5.03
1435660_at	C130026I21Rik /// A	RIKEN cNDA C130026I21 gene /// RIKEN cDNA A530032D15Rik gene /// similar	1.49	0.218	4.15	0.003	11.63	0.05	7.18	0.071	6.11
1460416_s_at	Csprs /// Sp100-rs /	component of Sp100-rs /// similar to component of Sp100-rs /// similar to compon	8.59	0.026	4.99	0.03	3.76	0.023	1.34	0.377	4.67
1419394_s_at	S100a8	S100 calcium binding protein A8 (calgranulin A)	4.03	0.445	11.87	0.112	2.09	0.266	1.35	0.666	4.83
1448756_at	S100a9	S100 calcium binding protein A9 (calgranulin B)	5.77	0.378	10.6	0.107	2.62	0.205	1.26	0.78	5.06
1451796_s_at	Hdc	histidine decarboxylase	15.52	0.067	2.39	0.292	1.33	0.516	2.53	0.385	5.44
1429916_at	9530077C05Rik	RIKEN cDNA 9530077C05 gene	1.26	0.147	16.67	0.127	1.33	0.604	2.33	0.201	5.4
1434484_at	1100001G20Rik	RIKEN cDNA 1100001G20 gene	14.64	0.422	1.08	0.435	4.14	0.231	2.16	0.456	5.51
1415977_at	Isyna1	myo-inositol 1-phosphate synthase A1	1.51	0.359	16.46	0.117	2.16	0.004	1.04	0.913	5.29
1440927_x_at	A330102K04Rik	RIKEN cDNA A330102K04 gene	7.62	0.379	3.83	0.389	9	0.268	8.01	0.136	7.11
1457307_at	A330102K04Rik	RIKEN cDNA A330102K04 gene	7.72	0.405	5.44	0.356	8.45	0.253	5.32	0.095	6.73
1449193_at	Cd5l	CD5 antigen-like	14.22	0.25	2.02	0.009	5.7	0.04	1.11	0.706	5.76
1424509_at	Cd177	CD177 antigen	2.96	0.147	7.78	0.159	11.43	0.163	3.9	0.355	6.52
1425078_x_at	LOC620078	similar to SP140 nuclear body protein (predicted)	3.09	0.279	4.54	0.011	15.21	0.122	14.57	0.033	9.35
1427747_a_at	Lcn2	lipocalin 2	13.68	0.302	9.7	0.106	1.75	0.228	2.63	0.449	6.94
1452463_x_at	---	Immunoglobulin kappa chain complex	11.75	0.035	7.1	0.002	7.06	0.015	1	0.98	6.73
1449123_at	Itih3	inter-alpha trypsin inhibitor, heavy chain 3	24.67	0.419	1.21	0.477	1.11	0.665	1.06	0.788	7.01
1450826_a_at	Saa3	serum amyloid A 3	5.07	0.434	2.94	0.039	19.74	0.239	8.95	0.27	9.17
1424631_a_at	Ighg	Immunoglobulin heavy chain (gamma polypeptide)	9.14	0.136	1.48	0.495	17.18	0.045	1.86	0.167	7.42
1419528_at	Sult2a2	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferring, member	5.48	0.384	2.94	0.119	19.78	0.142	5.42	0.082	8.4
1418722_at	Ngp	neutrophilic granule protein	1.34	0.536	10.69	0.11	16.43	0.249	1.8	0.61	7.57
1425385_a_at	Igh-1a	immunoglobulin heavy chain 1a (serum IgG2a)	17.4	0.046	1.59	0.274	10.52	0.001	1.19	0.839	7.67
1435792_at	Csprs /// LOC66533	component of Sp100-rs /// similar to component of Sp100-rs	16.51	0.007	5	0	9.69	0.021	1.76	0.357	8.24
1419691_at	Camp	cathelicidin antimicrobial peptide	3.86	0.002	16.3	0.083	13.76	0.307	1.61	0.707	8.88
1431808_a_at	Itih4	inter alpha-trypsin inhibitor, heavy chain 4	35.62	0.421	1	0.971	1.01	0.964	1.76	0.249	9.85
1453547_at	1810046K07Rik	RIKEN cDNA 1810046K07 gene	6.62	0.188	1.45	0.486	33.69	0.269	3.69	0.04	11.36
1426174_s_at	Ighg	Immunoglobulin heavy chain (gamma polypeptide)	13.97	0.198	5.81	0.271	23.03	0	2.69	0.058	11.37
1419764_at	Chi3l3	chitinase 3-like 3	5.59	0.477	42.11	0.112	1.18	0.225	1.98	0.586	12.71
1451962_at	LOC213481	immunoglobulin kappa light chain 17-1A	3.11	0.02	2.54	0.187	44.42	0.127	3.79	0.199	13.46
1419704_at	Cyp3a41	cytochrome P450, family 3, subfamily a, polypeptide 41	65.35	0.419	1.22	0.198	3.26	0.3	6.69	0.241	19.13
1419669_at	Prtn3	proteinase 3	1.79	0.595	72.86	0.109	9.85	0.207	2.49	0.484	21.75
1420447_at	Sult1e1	sulfotransferase family 1E, member 1	6.34	0.407	78.77	0.062	1.06	0.504	2.4	0.058	22.14
1419075_s_at	Saa1	serum amyloid A 1	81.62	0.407	7.3	0.035	1.15	0.385	1.63	0.085	22.93
1425738_at	Igk-V21-12 /// LOC6	immunoglobulin kappa chain variable 21 (V21)-12 /// similar to Ig kappa chain V-I	29.83	0.013	18.11	0.14	56.5	0.001	1.31	0.486	26.44