Supplementary table 1. List of significant expression profiles of wt cells irradiated with 0.6J/m2 of UV (gray color) as compared to non-irradiated wt controls

code	Gene Title	Symbol	WT_0.6J/m2	p	WT_4J/m2	p	XPA_0.6J/m2	p	CSB_0.6J/m2	p	DKO_0.6J/m2	p
1456774_at	protein phosphatase 1, regulatory (inhibitor) subunit 13 like	Ppp1r13l	6.79	0.026	6.29	0.202	2.21	0.379	2.14	0.178	1.03	0.879
1422745_at	bicaudal D homolog 2 (Drosophila)	Bicd2	5.75	0.050	8.26	0.071	1.32	0.251	-1.12	0.481	-1.34	0.131
1438210_at	G protein-coupled receptor 149	Gpr149	4.65	0.049	2.79	0.377	1.13	0.547	-1.27	0.134	1.03	0.916
1417000_at	ankyrin repeat and BTB (POZ) domain containing 1	Abtb1	4.61	0.036	3.54	0.007	-1.44	0.121	-1.23	0.140	1.4	0.215
1453058_at	WD repeat domain 5B	Wdr5b	4.53	0.030	2.81	0.166	-1.39	0.014	-1.03	0.419	-1.09	0.381
1452606_at	meiotic nuclear divisions 1 homolog (S. cerevisiae)	Mnd1	4.48	0.001	3.89	0.279	-1.22	0.305	1.18	0.567	1.8	0.793
1436832_at	RIKEN cDNA 1110067B18 gene	1110067B18Rik	4.46	0.035	1.98	0.794	-1.33	0.380	3.45	0.121	1.62	0.850
1443301_at	RIKEN cDNA C230086A09 gene	C230086A09Rik	4.38	0.004	1.87	0.201	-1.14	0.473	-1.17	0.491	1.29	0.830
1443537_at	RIKEN cDNA C130009A20 gene	C130009A20Rik	4.23	0.012	1.88	0.266	1.62	0.282	1.31	0.745	1.07	0.710
1440355_at	potassium channel tetramerisation domain containing 12b	Kctd12b	4.08	0.046	2	0.164	2.26	0.033	1.2	0.944	-1.19	0.560
1446261_at	DNA segment, Chr 1, ERATO Doi 507, expressed	D1Ertd507e	4.05	0.002	3.12	0.745	-1.21	0.473	1	0.815	-1.37	0.351
1457274_at	hypothetical protein E330017N17	E330017N17	4.03	0.032	4.89	0.299	-1.18	0.477	-1.69	0.131	1.16	0.844
1425990_a_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent	Nfatc2	3.95	0.018	4.4	0.033	-1.08	0.457	-1.05	0.590	-1.35	0.304
1421273_at	suppressor of cytokine signaling 4	Socs4	3.93	0.031	3.39	0.026	1.14	0.671	1.34	0.181	1.58	0.297
1444329_at	glutamine fructose-6-phosphate transaminase 1	Gfpt1	3.92	0.039	1.67	0.476	1.6	0.601	1.23	0.801	1.54	0.810
1430215_at	RIKEN cDNA 2610020H08 gene	2610020H08Rik	3.84	0.024	2.53	0.118	1	0.849	1.07	0.746	-1.05	0.568
1443920_at	coiled-coil domain containing 66	Ccdc66	3.76	0.041	1.32	0.628	1.61	0.633	2.13	0.402	1.45	0.993
1450329_a_at	arrestin 3, retinal	Arr3	3.75	0.018	2.32	0.023	1.24	0.454	1.06	0.689	1.26	0.695
1422177_at	interleukin 13 receptor, alpha 2	Il13ra2	3.7	0.046	3.68	0.027	1.37	0.724	2.26	0.526	2.07	0.052
1424245_at	carboxylesterase 2 /// similar to carboxylesterase 2	Ces2	3.68	0.029	1.06	0.845	1.07	0.501	-1.34	0.258	1.58	0.059
1433099_at	RIKEN cDNA 4933428L12 gene	4933428L12Rik	3.65	0.044	2.21	0.644	1.54	0.525	2.8	0.128	2.34	0.102
1453926_at	RAD54 like (S. cerevisiae)	Rad54l	3.64	0.017	-1.07	0.403	1.1	0.812	1.24	0.332	1	0.619
1422011_s_at	X-linked lymphocyte-regulated complex /// RIKEN cDNA 3830403N18	Xlr	3.62	0.021	3.3	0.064	1.07	0.860	1.01	0.377	-1.16	0.457
1453537_a_at	WD repeat domain 17	Wdr17	3.6	0.032	1.89	0.417	1.28	0.818	4.11	0.313	1.63	0.109
1419751_x_at	cDNA sequence AB056442	AB056442	3.57	0.005	2.81	0.150	1.83	0.843	2.45	0.663	1.51	0.782
1425942_a_at	glycoprotein m6b	Gpm6b	3.55	0.039	2.88	0.316	-1.2	0.376	-1.09	0.912	-1.37	0.025
1447675_x_at	myogenic differentiation 1	Myod1	3.47	0.014	1.37	0.534	1.99	0.199	1.11	0.533	-1.47	0.177
1443424_at	RIKEN cDNA 2210018M11 gene	2210018M11Rik	3.43	0.045	3.98	0.086	1.23	0.726	2.03	0.101	1.12	0.878
1445379_at	Atpase, class VI, type 11C	Atp11c	3.39	0.021	1.02	0.815	1.54	0.499	-1.12	0.192	1.77	0.443
1443044_at	hypothetical A830091E24	A830091E24	3.38	0.008	2.03	0.227	1.96	0.895	1.76	0.948	1.32	0.646
1431245_at	RIKEN cDNA 1700063H04 gene	1700063H04Rik	3.36	0.037	2.39	0.109	-2.54	0.069	2.29	0.241	-1.64	0.189
1432637_at	similar to Hippocalcin-like protein 1 (Visinin-like protein 3) (VILIP-3) (N	LOC675539	3.33	0.008	2.24	0.497	-1.9	0.236	-1.15	0.780	-1.65	0.240
1432012_a_at	NOL1/NOP2/Sun domain family 6	Nsun6	3.27	0.017	3.56	0.020	1.36	0.583	1.35	0.022	-1.24	0.038
1448873_at	occludin	Ocln	3.26	0.038	2.06	0.501	1.04	0.821	1.62	0.497	1.11	0.942
1439559_at	RIKEN cDNA 1700040D17 gene	1700040D17Rik	3.26	0.003	2.21	0.361	-1.09	0.895	1.97	0.218	-1.15	0.374
1440768_x_at	RIKEN cDNA 1700052I22 gene	1700052I22Rik	3.24	0.006	1.08	0.713	-1.23	0.619	1.52	0.877	2.17	0.293
1426509_s_at	glial fibrillary acidic protein	Gfap	3.2	0.022	1.07	0.639	1.08	0.833	-1.19	0.128	1.78	0.784

1428604_at	RIKEN cDNA 2610305D13 gene	2610305D13Rik	3.19	0.048	2.3	0.333	1.08	0.736	-1.36	0.056	2.31	0.643
1456333_a_at	Rho GTPase activating protein 6	Arhgap6	3.18	0.035	1.84	0.327	-1.64	0.245	1.5	0.588	1.93	0.308
1427868_x_at	myosin, heavy polypeptide 1, skeletal muscle, adult	Myh1	3.14	0.001	2.1	0.186	1.08	0.623	-1.23	0.314	-1.08	0.498
1435053_s_at	pleckstrin homology domain containing, family H (with MyTH4 domain)	Plekhh1	3.13	0.033	1.14	0.325	1.58	0.284	1.14	0.819	-1.41	0.053
1427180_at	solute carrier family 27 (fatty acid transporter), member 3	Slc27a3	3.12	0.001	1.71	0.509	1.56	0.846	1.57	0.467	-1.29	0.383
1421924_at	solute carrier family 2 (facilitated glucose transporter), member 3	Slc2a3	3.11	0.046	1.32	0.291	1.74	0.494	1.44	0.074	3.66	0.332
1447685_x_at	E26 avian leukemia oncogene 2, 3' domain	Ets2	3.1	0.036	1.44	0.160	3.25	0.538	-1.73	0.057	1.45	0.797
1421663_at	dehydrogenase/reductase member 2	Dhrs2	3.1	0.039	3.75	0.046	-1.12	0.384	-1.15	0.225	2.13	0.713
1451800_at	GRIP and coiled-coil domain containing 2	Gcc2	3.08	0.001	3.94	0.007	1.16	0.810	1.17	0.792	1.26	0.928
1456777_at	maltase-glucoamylase	Mgam	3.07	0.046	1.84	0.022	1.3	0.456	1.11	0.811	1.08	0.859
1442812_at	similar to Anapc5 protein	LOC433844	3.05	0.008	2.72	0.376	1.11	0.911	2	0.492	1.65	0.702
1440211_at	cytochrome P450, family 2, subfamily j, polypeptide 11	Cyp2j11	3.04	0.042	3.72	0.134	1.92	0.418	1.21	0.579	4.3	0.784
1436647_at	tau tubulin kinase 2	Ttbk2	3	0.021	3.74	0.601	1.02	0.416	-1.23	0.169	-1.12	0.415
1446105_at	exocyst complex component 1	Exoc1	3	0.002	-1.51	0.008	1.85	0.194	-1.3	0.382	2.42	0.019
1441577_at	RIKEN cDNA C530014P21 gene	C530014P21Rik	2.98	0.036	2.96	0.075	1.42	0.210	2.81	0.113	1.03	0.840
1455471_at	RIKEN cDNA 1500012D20 gene	1500012D20Rik	2.97	0.024	1.81	0.527	-1.31	0.355	1.3	0.892	2.1	0.591
1433310_at	RIKEN cDNA D530031A16 gene	D530031A16Rik	2.95	0.014	1.64	0.169	1.54	0.479	-1.11	0.386	-1.05	0.923
1448845_at	ribonuclease P 25 subunit (human)	Rpp25	2.94	0.029	1.29	0.177	1.91	0.363	-1.16	0.429	-1.31	0.312
1430642_at	RIKEN cDNA 2900001G08 gene	2900001G08Rik	2.94	0.030	1.51	0.715	1.83	0.090	1.52	0.544	2.84	0.606
1456770_at	zinc finger protein 14	Zfp14	2.93	0.029	3	0.096	1.63	0.959	1.11	0.562	1.95	0.046
1429314_at	synaptotagmin XI	Syt11	2.92	0.005	2.93	0.185	1.29	0.448	1.53	0.894	1.39	0.323
1430122_at	RIKEN cDNA 9430002A10 gene	9430002A10Rik	2.89	0.032	-1.04	0.614	1.32	0.759	1.52	0.230	1.32	0.412
1457307_at	RIKEN cDNA A330102K04 gene	A330102K04Rik	2.88	0.026	1.44	0.989	1.45	0.785	1.82	0.205	1.38	0.126
1457989_at	solute carrier family 4, sodium bicarbonate transporter-like, member 11	Slc4a11	2.86	0.007	3.87	0.068	1.86	0.056	1.11	0.700	1.92	0.439
1457308_at	Ubiquitin specific petidase 45	Usp45	2.83	0.036	2.14	0.451	1.13	0.880	2.62	0.043	-1.78	0.064
1422311_a_at	polymerase (RNA) II (DNA directed) polypeptide A	Polr2a	2.83	0.036	3.1	0.210	1.88	0.173	1.68	0.810	1.68	0.246
1416072_at	CD34 antigen	Cd34	2.83	0.021	1.33	0.680	1.77	0.715	1.14	0.722	1.88	0.032
1436564_at	Regulating synaptic membrane exocytosis 4	Rims4	2.81	0.045	2.9	0.288	-1.05	0.609	2.03	0.396	1.15	0.051
1459277_at	Nuclear receptor coactivator 1	Ncoa1	2.81	0.036	3	0.136	1.53	0.465	1.18	0.211	2.11	0.580
1427459_at	carboxypeptidase N, polypeptide 2	Cpn2	2.8	0.015	1.22	0.338	2.74	0.162	-1.22	0.252	3.66	0.010
1443613_x_at	Activating signal cointegrator 1 complex subunit 2	Ascc2	2.8	0.028	1.91	0.556	-1.72	0.171	-1.06	0.523	1.16	0.970
1435309_at	cDNA sequence BC019943	BC019943	2.77	0.031	1.43	0.390	1.68	0.836	1.96	0.297	1.11	0.560
1427836_at	stretch responsive protein 278	Sr278	2.76	0.029	1.28	0.971	1.72	0.952	1.27	0.662	1.01	0.834
1453701_at	RIKEN cDNA 4921515E04 gene	4921515E04Rik	2.75	0.009	1.37	0.807	-1.2	0.387	1.68	0.489	-1.03	0.523
1447489_at	RIKEN cDNA 1110039B18 gene	1110039B18Rik	2.75	0.021	1.4	0.988	-1.2	0.534	1.3	0.903	1.04	0.780
1433177_at	RIKEN cDNA 5830411G16 gene	5830411G16Rik	2.73	0.024	2.83	0.281	1.48	0.576	1.99	0.189	1.35	0.887
1443637_at	RIKEN cDNA 2900084M01 gene	2900084M01Rik	2.69	0.009	1.21	0.335	1.63	0.071	4	0.051	3.5	0.205
1451944_a_at	tumor necrosis factor (ligand) superfamily, member 11	Tnfsf11	2.63	0.023	2.72	0.012	1.17	0.885	1.63	0.615	-1.14	0.479
1436700_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48	Ddx48	2.63	0.002	1.79	0.274	1.46	0.967	1.66	0.220	1.16	0.826
1436227_at	Left-right determination factor 2	Lefty2	2.62	0.003	2.33	0.221	1.3	0.240	3.56	0.257	2.02	0.765
1430531_at	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-assoc	Bphl	2.61	0.004	2.95	0.117	1.46	0.846	1.28	0.232	-1.24	0.093

1452763_at	non imprinted in Prader-Willi/Angelman syndrome 1 homolog (human)	Nipa1	2.6	0.024	2.29	0.542	-1.06	0.505	1.29	0.055	-1.05	0.560
1445660_at	RIKEN cDNA 2700094F01 gene	2700094F01Rik	2.6	0.000	2.38	0.489	2.75	0.734	2.15	0.290	-1.23	0.246
1440696_at	RIKEN cDNA 2300002D11 gene	2300002D11Rik	2.59	0.015	1.83	0.685	-1.06	0.359	-1.4	0.140	-1.28	0.267
1433573_x_at	protease, serine, 2	Prss2	2.58	0.035	3.41	0.145	1.99	0.272	1.35	0.063	1.17	0.577
1457648_x_at	cDNA sequence BC004044	BC004044	2.58	0.029	2	0.498	1.09	0.847	-1	0.745	1.95	0.594
1458366_at	Additional sex combs like 2 (Drosophila)	Asxl2	2.57	0.006	1.45	0.369	-1.66	0.087	1.73	0.560	1.02	0.538
1431690_at	potassium voltage-gated channel, subfamily H (eag-related), member	Kcnh3	2.56	0.044	2.1	0.154	-1.35	0.268	1.69	0.283	1.48	0.634
1442603_at	Polybromo 1	Pb1	2.55	0.020	2.99	0.036	-1.33	0.259	-1.11	0.598	-1.53	0.028
1430943_at	RIKEN cDNA 6030498E09 gene	6030498E09Rik	2.55	0.009	1.77	0.235	-1.25	0.227	1.99	0.271	-1.12	0.388
1444229_at	nuclear receptor subfamily 2, group F, member 2	Nr2f2	2.54	0.046	1.9	0.083	1.17	0.997	1.06	0.733	1.02	0.912
1442136_at	ankyrin repeat and IBR domain containing 1	Ankib1	2.54	0.047	2.54	0.083	1.78	0.150	1.41	0.114	-1.03	0.842
1444765_at	RNA binding protein gene with multiple splicing	Rbpms	2.51	0.019	1.54	0.876	1.22	0.981	-1.69	0.080	-1.61	0.086
1451805_at	pleckstrin homology domain interacting protein	Phip	2.5	0.015	1.95	0.163	2.93	0.244	-1.14	0.358	2.01	0.661
1453393_a_at	carbohydrate (chondroitin 6/keratan) sulfotransferase 4	Chst4	2.49	0.040	2.35	0.050	-1.41	0.234	-1.21	0.191	2.98	0.258
1446088_at	RIKEN cDNA 9430081I23 gene	9430081I23Rik	2.49	0.035	2.38	0.762	-1.04	0.500	1.2	0.338	-1.53	0.077
1429928_at	RIKEN cDNA 1700030B21 gene	1700030B21Rik	2.49	0.009	1.23	0.681	-1.1	0.531	1.07	0.787	1.29	0.987
1443143_at	fibronectin leucine rich transmembrane protein 3	Flrt1	2.48	0.019	1.23	0.809	-1.28	0.283	1.66	0.653	1.32	0.616
1452339_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombosp	Adamts7	2.48	0.033	1.38	0.622	2.39	0.256	1.9	0.183	1.49	0.965
1432894_at	RIKEN cDNA 9130011L11 gene	9130011L11Rik	2.48	0.002	2.49	0.338	-1.89	0.079	-1.73	0.074	2.07	0.150
1421251_at	zinc finger protein 40	Zfp40	2.47	0.028	2.44	0.103	-1.21	0.143	1.67	0.790	-1.18	0.407
1456543_at	prokineticin receptor 1	Prokr1	2.46	0.011	2.45	0.014	2.2	0.016	1.66	0.659	1.22	0.724
1444545_at	Erythrocyte protein band 4.1	Epb4.1	2.45	0.034	1.02	0.811	1.43	0.139	1.62	0.150	-1.09	0.487
1450801_at	a disintegrin and metallopeptidase domain 21	Adam21	2.45	0.040	-1.42	0.110	1.51	0.291	-1.31	0.166	1.56	0.810
1431979_at	RIKEN cDNA 4930444M15 gene	4930444M15Rik	2.45	0.040	1.32	0.127	1.03	0.638	1.38	0.176	-1.15	0.369
1450753_at	natural killer cell group 7 sequence	Nkg7	2.44	0.049	3.86	0.385	-1.69	0.154	1.37	0.782	-1.47	0.192
1431981_at	hypoxia inducible factor 1, alpha subunit	Hif1a	2.43	0.003	1.72	0.555	1.42	0.470	2.62	0.154	2.15	0.093
1457756_at	zinc finger protein 192	Zfp192	2.42	0.016	2.06	0.007	1.04	0.697	1.27	0.765	1.01	0.933
1435467_at	FYVE, RhoGEF and PH domain containing 6	Fgd6	2.42	0.026	2.92	0.420	1.13	0.646	1.21	0.869	1.48	0.307
1427155_at	FCH and double SH3 domains 1	Fchsd1	2.42	0.025	2.81	0.218	2.49	0.585	1.03	0.924	2.91	0.325
1421120_at	myosin VI	Myo6	2.41	0.043	1.2	0.755	-1.51	0.192	2.37	0.118	1.71	0.999
1450829_at	tumor necrosis factor, alpha-induced protein 3	Tnfaip3	2.4	0.043	3.44	0.102	1.32	0.571	1.34	0.196	1.4	0.411
1447418_at	Potassium voltage-gated channel, subfamily Q, member 1	Kcnq1	2.4	0.005	1.26	0.376	1.74	0.101	1.5	0.329	1.25	0.391
1431871_at	thioredoxin domain containing 3 (spermatozoa)	Txndc3	2.39	0.040	1.8	0.249	-1.22	0.281	1.33	0.222	2.89	0.154
1425751_at	cDNA sequence BC014805	BC014805	2.39	0.045	1.82	0.223	1.14	0.956	1.11	0.497	-1.27	0.305
1425805_a_at	ubiquitin specific peptidase 12	Usp12	2.38	0.013	2.89	0.225	1.35	0.855	1.07	0.867	1.03	0.931
1428838_a_at	deoxycytidine kinase	Dck	2.38	0.032	2.79	0.006	1.43	0.032	1.29	0.301	1.24	0.325
1419985_s_at	coiled-coil domain containing 69	Ccdc69	2.38	0.049	2.08	0.860	1.19	0.527	1.58	0.540	3.18	0.174
1433004_at	RIKEN cDNA 4833446E11 gene	4833446E11Rik	2.38	0.026	1.08	0.584	1.03	0.779	-1.06	0.844	-1.16	0.499
1423064_at	DNA methyltransferase 3A	Dnmt3a	2.36	0.025	1.33	0.764	-1.63	0.080	-1.51	0.090	2.06	0.152
1454111_at	RIKEN cDNA 4930404A10 gene	4930404A10Rik	2.36	0.002	3.09	0.332	-1.2	0.250	1.31	0.318	2.72	0.443
1425604_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	Crkl	2.35	0.015	3.05	0.282	1.01	0.985	1.3	0.274	-1.16	0.391

1444772_at	SET and MYND domain containing 3	Smyd3	2.34	0.032	-1.23	0.124	-1.1	0.699	-1.37	0.100	-1.02	0.229
1442549_at	muscleblind-like 3 (Drosophila)	Mbnl3	2.34	0.015	2.16	0.173	-1.17	0.810	-1.05	0.718	1.8	0.044
1419016_at	RIKEN cDNA 1700034I23 gene	1700034I23Rik	2.33	0.044	1.47	0.672	2.91	0.010	1.68	0.404	1.73	0.132
1456983_at	Trichorhinophalangeal syndrome I (human)	Trps1	2.32	0.036	2.84	0.105	-1.08	0.244	1.16	0.304	-2.15	0.057
1421435_at	glutamate receptor, ionotropic, delta 2	Grid2	2.32	0.004	3.03	0.001	1.61	0.698	-1.11	0.636	-1.34	0.315
1448823_at	chemokine (C-X-C motif) ligand 12	Cxcl12	2.32	0.020	1.81	0.034	-1.26	0.094	-1.1	0.083	1.05	0.611
1433072_at	RIKEN cDNA 4933425E08 gene	4933425E08Rik	2.31	0.024	1.67	0.369	4.75	0.340	2.61	0.149	1.7	0.448
1460442_at	ribosomal protein S19	Rps19	2.3	0.015	1.16	0.824	1.73	0.826	-1.43	0.163	3.08	0.464
1440645_at	similar to deleted in malignant brain tumors 1 isoform c precursor	LOC546006	2.29	0.046	4.08	0.018	2.49	0.340	-1.05	0.328	-2.48	0.015
1441472_at	CDC-like kinase 3	Clk3	2.29	0.037	2.03	0.348	-1.04	0.591	1.48	0.882	1.29	0.503
1421242_at	ring finger protein 144	Rnf144	2.28	0.005	1.97	0.910	1.27	0.234	1.08	0.842	1.58	0.314
1444700_at	Neurexin III	Nrxn3	2.28	0.039	4.69	0.005	2.17	0.944	2.37	0.304	-1.01	0.438
1442019_at	RIKEN cDNA B230343A10 gene	B230343A10Rik	2.28	0.025	1.28	0.290	-2.66	0.046	-1.1	0.739	-1.96	0.038
1442388_at	RIKEN cDNA 2410137F16 gene	2410137F16Rik	2.28	0.019	1.3	0.088	1.58	0.647	1.63	0.613	-1.74	0.086
1455531_at	RIKEN cDNA A930031D07 gene	A930031D07Rik	2.27	0.047	1.77	0.243	-1.13	0.539	1.69	0.082	1.23	0.536
1421325_at	phospholipase A2, group IIF	Pla2g2f	2.26	0.033	1.1	0.862	-1.27	0.211	-1.28	0.259	1.49	0.315
1459186_at	expressed sequence C80165	C80165	2.26	0.005	1.98	0.196	1.44	0.965	-1.36	0.300	1.89	0.750
1456206_at	AlkB, alkylation repair homolog 3 (E. coli)	Alkbh3	2.26	0.031	-1.07	0.682	-1.23	0.452	-1.03	0.394	-1.35	0.225
1430659_at	RIKEN cDNA 4930548H24 gene	4930548H24Rik	2.26	0.026	2.55	0.135	1.23	0.536	1.29	0.746	1.78	0.203
1460292_a_at	SWI/SNF related, matrix associated, actin dependent regulator of chro	Smarca1	2.25	0.036	2.23	0.386	2.08	0.708	1.33	0.934	-1.35	0.257
1441365_at	forkhead box P2	Foxp2	2.24	0.034	1.94	0.330	1.15	0.826	-1.56	0.132	-1.17	0.104
1437559_at	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expressed	D13Bwg1146e	2.24	0.001	1.64	0.401	1.08	0.666	-1.35	0.320	1.61	0.839
1451914_a_at	adducin 2 (beta)	Add2	2.24	0.032	1.48	0.507	1.14	0.537	1.25	0.615	1.45	0.904
1447979_at	RUN and TBC1 domain containing 2	Rutbc2	2.23	0.040	1.45	0.901	-1.25	0.416	3.29	0.185	1.57	0.183
1443824_s_at	carbonic anhydrase 7	Car7	2.23	0.031	2.82	0.365	3.43	0.985	-1.15	0.183	1.1	0.998
1458553_at	plasminogen activator, tissue	Plat	2.22	0.034	-1.04	0.549	-1.25	0.362	-1.14	0.444	-1.04	0.751
1435465_at	kelch repeat and BTB (POZ) domain containing 11 /// similar to Protein	Kbtbd11 /// LOC632344	2.22	0.009	1.69	0.823	1.29	0.388	1.37	0.339	2.21	0.328
1456993_at	DNA segment, Chr 2, ERATO Doi 640, expressed	D2Ertd640e	2.22	0.047	1.38	0.263	-1.14	0.288	1.52	0.985	-1.05	0.656
1421925_at	mitogen-activated protein kinase 11	Mapk11	2.21	0.008	2.92	0.527	-1.05	0.550	-1.07	0.577	1.37	0.363
1457919_at	RIKEN cDNA D030054H15 gene	D030054H15Rik	2.21	0.035	2.15	0.154	-1.22	0.217	1.46	0.660	-1.43	0.250
1441141_at	RIKEN cDNA C730024G19 gene	C730024G19Rik	2.21	0.033	1.53	0.822	1.12	0.874	1.18	0.903	1.9	0.428
1425778_at	RIKEN cDNA C230043N17 gene	C230043N17Rik	2.21	0.003	2.22	0.058	-1.43	0.149	1.02	0.690	-1.06	0.861
1432941_at	RIKEN cDNA 5730408A14 gene	5730408A14Rik	2.21	0.025	-1.23	0.251	-1.14	0.315	1.27	0.561	-1.91	0.087
1429268_at	RIKEN cDNA 2610318N02 gene	2610318N02Rik	2.21	0.003	1.71	0.022	-1.18	0.469	1.97	0.024	1.27	0.089
1459011_at	Ubiquitin carboxyl-terminal esterase L5	Uchl5	2.2	0.032	1.84	0.894	1.04	0.760	1.16	0.338	-1.07	0.822
1437978_at	Slit homolog 2 (Drosophila)	Slit2	2.2	0.024	2.27	0.342	-1.11	0.416	1.16	0.639	2.81	0.321
1442125_at	KRIT1, ankyrin repeat containing	Krit1	2.2	0.047	2.25	0.149	1.17	0.638	1.21	0.609	-1.25	0.177
1441271_at	Isocitrate dehydrogenase 3 (NAD+) beta	Idh3b	2.2	0.014	1.33	0.459	1.21	0.862	1.63	0.038	1.51	0.143
1427461_at	cDNA sequence BC005561	BC005561	2.2	0.018	2.82	0.269	-1.14	0.631	-1.25	0.341	-1.55	0.027
1447713_at	tropomyosin 1, alpha	Tpm1	2.19	0.028	2.97	0.312	1.1	0.849	1.28	0.022	1.75	0.215
1449432_a_at	membrane metallo-endopeptidase-like 1	Mmel1	2.19	0.027	2.24	0.148	1.21	0.405	-1.15	0.290	1.99	0.088

1436560_at	expressed sequence AW124694	AW124694	2.19	0.008	1.89	0.017	1.18	0.119	1.33	0.263	1.33	0.066
1444913_at	Hedgehog acyltransferase	Hhat	2.18	0.041	3	0.160	1.15	0.716	3.26	0.107	1.34	0.530
1432947_at	RIKEN cDNA 4921519G19 gene	4921519G19Rik	2.17	0.044	1.51	0.384	1.49	0.424	1.48	0.129	1.34	0.809
1452408_at	G protein-coupled receptor 31, D17Leh66c region	Gpr31c	2.16	0.028	1.07	0.867	2.01	0.826	2.62	0.185	2.69	0.270
1444873_at	Huntingtin interacting protein 1	Hip1	2.15	0.027	1.55	0.175	1.09	0.912	1.08	0.816	1.83	0.624
1422287_at	per-hexamer repeat gene 2	Phxr2	2.14	0.010	1.74	0.227	1.17	0.726	1.19	0.691	3.44	0.396
1449234_at	carbonic anhydrase 15	Car15	2.14	0.050	2.15	0.328	-1.57	0.155	1.2	0.604	2.21	0.828
1457051_at	tripartite motif protein 27	Trim27	2.13	0.047	1.8	0.555	1.44	0.007	1.18	0.859	2.22	0.010
1440829_x_at	tubulin tyrosine ligase-like family, member 11	Ttll11	2.11	0.045	-1.05	0.488	-2.11	0.097	1.63	0.872	-1.01	0.560
1424952_at	OCIA domain containing 1	Ociad1	2.11	0.042	1.99	0.009	3.14	0.190	-1.13	0.404	1.66	0.444
1439795_at	G protein-coupled receptor 64	Gpr64	2.1	0.023	-1.21	0.409	1.47	0.950	1	0.808	1.26	0.238
1425167_a_at	guanine nucleotide binding protein (G protein), gamma transducing act	Gngt1	2.1	0.004	1.87	0.132	-1.11	0.313	2.11	0.426	1.57	0.050
1458325_x_at	Bcl2 modifying factor	Bmf	2.1	0.027	1.58	0.551	-1.22	0.225	1.39	0.378	-1.43	0.267
1431326_a_at	tropomodulin 2	Tmod2	2.09	0.004	1.1	0.575	1.63	0.614	3.93	0.066	-1.06	0.576
1458432_at	Non-catalytic region of tyrosine kinase adaptor protein 2	Nck2	2.09	0.038	3.01	0.090	2.05	0.082	1.31	0.378	1.26	0.640
1444284_at	RIKEN cDNA A130050O07 gene	A130050O07Rik	2.09	0.012	-1.04	0.399	1.44	0.664	-1.2	0.356	1.08	0.400
1443554_at	Single-stranded DNA binding protein 3	Ssbp3	2.08	0.034	1.37	0.443	-1.03	0.519	1.33	0.916	1.49	0.376
1460135_at	RIKEN cDNA A930005H10 gene	A930005H10Rik	2.08	0.010	1.06	0.823	-1.32	0.127	1.49	0.757	-1	0.348
1445230_at	Nuclear receptor co-repressor 1	Ncor1	2.07	0.049	-1.12	0.532	1.1	0.977	-1.49	0.017	-1.43	0.055
1432408_a_at	DNA segment, KIST 2	D0Kist2	2.07	0.015	1.49	0.661	1.2	0.564	-1.06	0.370	2.07	0.904
1438079_at	cDNA sequence BC050078	BC050078	2.07	0.006	1.61	0.434	1.36	0.478	2.12	0.200	1.68	0.321
1438620_x_at	secreted frizzled-related sequence protein 1	Sfrp1	2.06	0.023	1.53	0.932	2.23	0.055	-1.05	0.383	1.72	0.629
1439340_at	RIKEN cDNA D630036G22 gene	D630036G22Rik	2.05	0.002	2.51	0.456	-2.96	0.050	-1.13	0.280	1.56	0.338
1423366_at	stearoyl-coenzyme A desaturase 3	Scd3	2.04	0.050	2.85	0.258	-1.09	0.148	2.57	0.221	1.16	0.763
1427427_at	ryanodine receptor 3	Ryr3	2.04	0.039	2.53	0.139	1.14	0.476	1.02	0.442	1.24	0.704
1423578_at	procollagen, type XI, alpha 2	Col11a2	2.04	0.018	1.81	0.043	-2.01	0.119	1.06	0.949	2.92	0.763
1437949_x_at	zinc finger protein 313	Zfp313	2.02	0.039	1.93	0.009	1.52	0.738	1.21	0.340	-1.09	0.341
1436648_at	nanos homolog 1 (Drosophila)	Nanos1	2.01	0.042	2.82	0.165	2.48	0.098	1.46	0.042	1.84	0.044
1421220_at	ankyrin repeat domain 17	Ankrd17	2.01	0.015	3.7	0.047	1.31	0.156	-1.17	0.308	-1.13	0.602
1422878_at	synaptotagmin XII	Syt12	2	0.043	1.56	0.389	-1.06	0.881	1.21	0.209	-1.18	0.460
1455302_at	vacuolar protein sorting 29 (S. pombe)	Vps29	1.99	0.014	2.46	0.140	1	0.863	-1.21	0.398	1.83	0.386
1419236_at	helicase (DNA) B	Helb	1.99	0.028	2.18	0.060	1.56	0.792	2.56	0.102	-1.15	0.391
1435765_at	RIKEN cDNA E130114P18 gene	E130114P18Rik	1.97	0.044	-1	0.903	1.95	0.418	3	0.310	1.16	0.593
1458427_at	BRCA1 interacting protein C-terminal helicase 1	Brip1	1.97	0.012	1.7	0.226	1.2	0.423	1.44	0.542	1.32	0.896
1458479_at	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	Smc2l1	1.96	0.037	-1.32	0.447	1.22	0.864	1.66	0.199	1.08	0.604
1425509_at	MAP/microtubule affinity-regulating kinase 1	Mark1	1.96	0.023	1.41	0.387	-1.08	0.543	-1.02	0.502	-1.09	0.253
1422105_at	CD3 antigen, epsilon polypeptide	Cd3e	1.96	0.048	1.52	0.331	-1.14	0.253	-1.18	0.335	1.35	0.310
1419187_at	RIKEN cDNA 1700012L04 gene /// similar to Histone H2A.x (H2a/x)	1700012L04Rik /// LOC5	1.96	0.005	1.23	0.679	-1.02	0.777	-1.28	0.158	1.66	0.735
1454903_at	nerve growth factor receptor (TNFR superfamily, member 16)	Ngfr	1.95	0.002	2.21	0.070	1.16	0.981	1.03	0.352	2.46	0.142
1426202_at	Histocompatibility 2, class II antigen E alpha /// MHC class II E-sub-alpl	H2-Ea	1.95	0.017	1.53	0.063	-1.81	0.079	4.07	0.142	1.48	0.649
1458879_at	expressed sequence C76798	C76798	1.95	0.004	1.95	0.334	1.09	0.739	1.49	0.482	2.17	0.151

1426093_at	tripartite motif protein 34	Trim34	1.94	0.019	2.65	0.443	1.73	0.310	1.36	0.542	2.45	0.585
1441122_at	expressed sequence AU024342	AU024342	1.94	0.031	3.04	0.037	2.2	0.289	1.85	0.133	-1.01	0.486
1432390_at	RIKEN cDNA 4933400F21 gene	4933400F21Rik	1.94	0.024	1.83	0.218	2.22	0.972	-1.07	0.360	1.09	0.782
1432046_at	RIKEN cDNA 4930404K06 gene	4930404K06Rik	1.94	0.040	1.44	0.385	-1.23	0.370	1.32	0.494	2.72	0.200
1458729_at	FK506 binding protein 4	Fkbp4	1.93	0.006	1.78	0.024	1.43	0.532	1.13	0.236	1.83	0.320
1434752_at	zinc finger protein 207	Zfp207	1.91	0.016	1.74	0.005	1.45	0.244	1.23	0.481	-1.09	0.269
1449969_at	tropomodulin 4	Tmod4	1.91	0.036	1.68	0.663	1.98	0.320	1.31	0.407	-1.49	0.243
1445788_at	Insulin-like growth factor 2, binding protein 1	Igf2bp1	1.91	0.035	1.22	0.862	2.01	0.545	-1.37	0.064	1.86	0.679
1433577_at	RIKEN cDNA A730017C20 gene	A730017C20Rik	1.91	0.002	1.64	0.018	1.83	0.096	1.19	0.786	1.12	0.773
1454533_at	RIKEN cDNA 9430085L16 gene	9430085L16Rik	1.91	0.047	2.65	0.161	2.92	0.216	-1.45	0.187	1.79	0.385
1452530_a_at	runt related transcription factor 1	Runx1	1.9	0.033	2.22	0.199	-1.29	0.208	1.27	0.238	1.02	0.875
1438414_at	fukutin related protein	Fkrp	1.9	0.015	1.34	0.876	-1.11	0.332	2.57	0.078	-1.16	0.459
1425450_at	chitinase 3-like 4	Chi3l4	1.89	0.019	1.01	0.873	-1.63	0.104	-1.19	0.336	2.3	0.198
1454420_at	RIKEN cDNA 5730420F10 gene	5730420F10Rik	1.89	0.048	1.63	0.973	2.92	0.154	-1.01	0.387	1.08	0.829
1429666_at	potassium channel tetramerisation domain containing 16	Kctd16	1.88	0.009	1.39	0.309	1.33	0.201	2.47	0.159	2.02	0.039
1454229_a_at	exonuclease domain containing 1	Exod1	1.88	0.010	2.25	0.095	1.06	0.906	1.39	0.030	-1.06	0.818
1442661_at	expressed sequence C80113	C80113	1.88	0.045	1.61	0.393	1.19	0.771	1.23	0.763	1.29	0.460
1445758_at	CDNA sequence BC049816	BC049816	1.88	0.009	1.8	0.021	-1.03	0.688	1.12	0.933	1.04	0.769
1435351_at	RIKEN cDNA 2310026E23 gene	2310026E23Rik	1.88	0.005	-1.46	0.084	-1.52	0.066	1.67	0.405	1.16	0.554
1438911_at	Septin 7	7-Sep	1.88	0.044	1.19	0.402	-1.35	0.211	-1.12	0.461	-1.03	0.812
1419886_at	DNA segment, Chr X, ERATO Doi 223, expressed	DXErtd223e	1.87	0.038	2.5	0.193	1.06	0.973	-1.07	0.745	-1.19	0.210
1430884_at	RIKEN cDNA 4930568G15 gene	4930568G15Rik	1.86	0.041	1.77	0.096	1.13	0.537	1.2	0.739	-1.52	0.194
1458870_x_at	pam, highwire, rpm 1	Phr1	1.85	0.004	-1.35	0.299	-1.12	0.254	-1.03	0.828	-1.4	0.352
1417577_at	transient receptor potential cation channel, subfamily C, member 3	Trpc3	1.84	0.029	1.12	0.452	-1.16	0.501	-2.19	0.050	-1.14	0.444
1443418_at	Phosphoribosyl pyrophosphate synthetase 2	Prps2	1.84	0.030	2.27	0.114	1.41	0.575	1.83	0.701	1.34	0.064
1446557_at	RIKEN cDNA E130309F12 gene	E130309F12Rik	1.84	0.007	1.6	0.937	-1.28	0.300	-1.2	0.235	1.59	0.560
1439247_at	dedicator of cytokinesis 10 /// similar to Dedicator of cytokinesis protein	Dock10 /// LOC630691	1.84	0.029	2.47	0.564	1.19	0.775	1.19	0.862	-1.09	0.605
1443714_at	RIKEN cDNA C530044N13 gene	C530044N13Rik	1.84	0.044	2.26	0.194	-1.19	0.290	1.83	0.555	-1.34	0.229
1435109_at	RIKEN cDNA 0710007G10 gene /// RIKEN cDNA 3010001K23 gene	0710007G10Rik /// 3010	1.84	0.040	1.72	0.193	1.09	0.423	-1.23	0.153	1.04	0.959
1416463_at	GPI-anchored membrane protein 1	Gpiap1	1.83	0.047	1.98	0.135	-1.19	0.255	-1.21	0.081	-1.13	0.285
1456480_at	furry homolog (Drosophila)	Fry	1.83	0.036	2.06	0.336	1.26	0.475	-1.05	0.418	-1.04	0.476
1429937_at	RIKEN cDNA D530033C11 gene	D530033C11Rik	1.83	0.046	2.41	0.011	1.24	0.081	1.03	0.874	1.11	0.302
1443356_at	Cyclic AMP-regulated phosphoprotein, 21	Arpp21	1.83	0.029	1.42	0.583	1.31	0.886	1.06	0.976	1.71	0.125
1450936_a_at	deoxyribonuclease 1-like 2	Dnase1l2	1.82	0.044	3.41	0.149	1.34	0.700	-1.46	0.189	1.52	0.791
1441117_at	Ash1 (absent, small, or homeotic)-like (Drosophila)	Ash1l	1.82	0.019	1.32	0.554	-1.03	0.688	1.02	0.803	-1.97	0.120
1444472_at	SNF1-like kinase 2	Snf1lk2	1.81	0.028	2.28	0.093	-1.05	0.559	1.01	0.828	1.42	0.103
1432608_at	nicotinamide nucleotide transhydrogenase	Nnt	1.81	0.049	2.09	0.652	-1.11	0.278	1.24	0.193	1.31	0.797
1457398_at	Guanosine diphosphate (GDP) dissociation inhibitor 2	Gdi2	1.81	0.047	1.74	0.206	1.11	0.236	1.18	0.322	-1.15	0.179
1459567_at	expressed sequence C77905	C77905	1.81	0.021	1.15	0.967	-1.22	0.260	-1.28	0.251	2.67	0.225
1436361_at	vestigial like 2 homolog (Drosophila)	Vgll2	1.8	0.044	1.77	0.932	1.72	0.253	3.03	0.069	2.47	0.024
1458502_at	Kinectin 1	Ktn1	1.8	0.032	1.74	0.551	2.04	0.454	2.85	0.092	-1.56	0.178

1429600_at	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofolat	C630010D07Rik /// LOC	1.8	0.037	1.4	0.578	-1.34	0.001	-1.12	0.351	-1.17	0.188
1456643_at	RIKEN cDNA 9230114K14 gene	9230114K14Rik	1.79	0.015	3.25	0.006	1.22	0.409	1.12	0.323	1.34	0.003
1454572_at	RIKEN cDNA 2810414N06 gene	2810414N06Rik	1.79	0.035	1.31	0.305	-1.64	0.164	1.29	0.601	1.13	0.986
1445922_at	X-ray repair complementing defective repair in Chinese hamster cells 4	Xrcc4	1.78	0.033	-1.1	0.465	-1.12	0.349	2.95	0.204	1.06	0.496
1421196_at	protein tyrosine phosphatase, non-receptor type 11	Ptpn11	1.78	0.002	1.75	0.006	-1.03	0.751	1.09	0.547	1.05	0.614
1419895_at	expressed sequence AA536748	AA536748	1.78	0.007	2.6	0.067	-1.77	0.066	3.26	0.280	-1.08	0.899
1416552_at	developmental pluripotency associated 5	Dppa5	1.77	0.026	1.53	0.180	1.03	0.785	1.17	0.396	1.49	0.368
1416062_at	TBC1 domain family, member 15	Tbc1d15	1.76	0.037	1.47	0.447	-1.06	0.536	1.09	0.157	-1.06	0.599
1434878_at	SLIT and NTRK-like family, member 4	Slitrk4	1.76	0.036	-1.88	0.025	2.16	0.897	1.87	0.331	-2.58	0.033
1424414_at	opioid growth factor receptor-like 1 /// similar to opioid growth factor rec	Ogfrl1 /// LOC673882	1.76	0.042	2.03	0.277	2.01	0.398	2.47	0.110	1.21	0.767
1423886_at	laminin, gamma 1	Lamc1	1.75	0.005	1.21	0.595	-1.37	0.235	1.09	0.701	1.44	0.972
1422986_at	estrogen related receptor, beta	Esrrb	1.75	0.036	1.34	0.221	1.23	0.889	-1.39	0.126	1.21	0.779
1427973_s_at	Vcell division cycle 73, Paf1/RNA polymerase II complex component, h	Cdc73	1.75	0.011	1.46	0.127	-1.3	0.097	-1.31	0.023	-1.2	0.210
1449873_at	bone morphogenetic protein 8a	Bmp8a	1.75	0.004	1.11	0.663	-1.09	0.554	-1.29	0.540	1.21	0.986
1454521_at	RIKEN cDNA 2810421E14 gene	2810421E14Rik	1.75	0.019	2.06	0.105	-1.06	0.548	1.84	0.181	-1.51	0.340
1455219_at	RIKEN cDNA 1110030E23 gene	1110030E23Rik	1.75	0.025	1.88	0.187	-1.24	0.059	1.49	0.210	1.07	0.844
1425741_at	SLIT-ROBO Rho GTPase activating protein 3	Srgap3	1.74	0.047	1.02	0.936	-1.98	0.010	1.23	0.324	-1.6	0.146
1455416_at	Riken cDNA C130021I20 gene	C130021I20Rik	1.74	0.044	1.06	0.709	-2.08	0.017	1.51	0.407	1.54	0.168
1422292_at	RIKEN cDNA A030005K14 gene	A030005K14Rik	1.74	0.011	5.95	0.044	1.37	0.757	1.52	0.808	1.73	0.258
1453252_at	dihydrouridine synthase 4-like (S. cerevisiae)	Dus4l	1.73	0.033	2.08	0.005	1.44	0.627	2.72	0.013	1.27	0.260
1420993_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	B3gnt5	1.73	0.047	2.52	0.048	1.08	0.627	-1.13	0.430	-1.48	0.075
1429793_at	RIKEN cDNA 1600014K23 gene	1600014K23Rik	1.73	0.003	1.08	0.787	1.45	0.491	1.05	0.221	1.41	0.592
1457195_at	pleckstrin homology domain containing, family M (with RUN domain) m	Plekhm1	1.72	0.017	-1.06	0.342	1.93	0.976	2.57	0.404	2.34	0.620
1421615_at	myosin XV	Myo15	1.72	0.014	2.03	0.055	-1.66	0.007	1.15	0.349	1.1	0.928
1439332_at	DNA-damage-inducible transcript 4-like	Ddit4l	1.72	0.024	3.45	0.004	2.23	0.002	1.61	0.014	2.04	0.169
1427497_at	RIKEN cDNA 2610015P09 gene	2610015P09Rik	1.72	0.023	1.74	0.671	1.66	0.724	1.86	0.685	-1.45	0.298
1453477_at	zinc finger CCCH type containing 6	Zc3h6	1.71	0.038	1.34	0.013	1.24	0.952	-1.04	0.789	2.06	0.285
1460380_at	desmoglein 2	Dsg2	1.71	0.033	2.23	0.046	1.48	0.510	-1	0.717	1.19	0.354
1435600_s_at	cDNA sequence BC020535	BC020535	1.71	0.004	1.29	0.730	-1.38	0.017	1.69	0.332	-1.45	0.092
1430427_a_at	protocadherin 18	Pcdh18	1.7	0.016	2.49	0.021	2.08	0.133	1.7	0.129	1.75	0.029
1427214_at	agmatine ureohydrolase (agmatinase)	Agmat	1.7	0.024	2.82	0.120	-1.1	0.570	1.24	0.906	-1.18	0.592
1456554_at	RIKEN cDNA 7530414M10 gene	7530414M10Rik	1.7	0.009	1.53	0.279	1.51	0.075	-1.18	0.248	1.45	0.070
1457915_at	RIKEN cDNA 4833442J19 gene	4833442J19Rik	1.7	0.004	2.68	0.074	1.56	0.117	2.49	0.559	1.31	0.340
1437888_at	WNK lysine deficient protein kinase 1	Wnk1	1.69	0.040	-1.02	0.279	-1.46	0.080	-1.25	0.286	-1.16	0.615
1459604_at	SNRPN upstream reading frame	Snurf	1.69	0.023	-1.3	0.256	1.34	0.140	1.89	0.821	1.02	0.981
1430707_s_at	RIKEN cDNA 1700081D17 gene	1700081D17Rik	1.69	0.048	-1.01	0.759	1.03	0.915	-2.66	0.002	1.88	0.264
1449867_at	homeo box C9	Hoxc9	1.68	0.023	1.62	0.155	2.37	0.079	-1.37	0.129	2.2	0.419
1450677_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	1.68	0.027	2.07	0.039	1.17	0.018	1.05	0.626	1.19	0.150
1435605_at	ARP3 actin-related protein 3 homolog B (yeast)	Actr3b	1.68	0.011	-1.24	0.261	1	0.918	1.04	0.824	1.31	0.143
1438293_at	trichoplein, keratin filament binding	Tchp	1.67	0.049	2.77	0.036	1.33	0.199	1.28	0.292	1.27	0.300
1438934_x_at	sema domain, immunoglobulin domain (Ig), transmembrane domain (T	Sema4a	1.67	0.004	1.17	0.249	1.59	0.776	-1.03	0.992	1.58	0.851

1421144_at	retinitis pigmentosa GTPase regulator interacting protein 1	Rpgrip1	1.67	0.038	1.72	0.036	-1.02	0.571	1.17	0.016	1.03	0.995
1457176_at	GTPase activating RANGAP domain-like 1	Garnl1	1.67	0.040	1.42	0.244	-1.2	0.001	-1.21	0.063	-1.78	0.029
1441340_at	centrosomal protein 68	Cep68	1.67	0.017	3.27	0.251	1.62	0.970	1.74	0.076	-1.64	0.126
1429728_at	RIKEN cDNA 4930429M06Rik	4930429M06Rik	1.67	0.022	1.6	0.023	1.38	0.212	1.06	0.653	1.09	0.260
1432756_at	RIKEN cDNA 2210409O19 gene	2210409O19Rik	1.67	0.001	1.48	0.398	-1.05	0.463	1.9	0.133	1.69	0.298
1436952_at	Kruppel-like factor 9	Klf9	1.65	0.033	1.16	0.589	1.02	0.983	1.34	0.826	1.44	0.910
1423597_at	ATPase, aminophospholipid transporter (APLT), class I, type 8A, mem	Atp8a1	1.65	0.000	1.03	0.979	1.14	0.890	1.13	0.481	1.87	0.377
1437397_at	prolactin receptor	Prlr	1.64	0.004	1.43	0.313	1.5	0.952	-1.05	0.296	-1.6	0.048
1444405_at	RIKEN cDNA E430029J22 gene	E430029J22Rik	1.64	0.015	1.53	0.106	1.29	0.587	1.53	0.951	1.42	0.915
1419559_at	cytochrome P450, family 4, subfamily f, polypeptide 14	Cyp4f14	1.63	0.040	1.25	0.202	1.06	0.830	1.02	0.899	-1.1	0.437
1423352_at	cysteine-rich secretory protein LCCL domain containing 1	Crispld1	1.63	0.014	1.62	0.542	1.58	0.345	1.78	0.491	-1.16	0.182
1417940_s_at	RAD51 associated protein 1	Rad51ap1	1.61	0.030	1.77	0.053	1.28	0.298	1.37	0.856	1.11	0.780
1444525_at	EGF, latrophilin seven transmembrane domain containing 1	Eltd1	1.61	0.040	1.61	0.439	1.39	0.487	1.05	0.887	2.08	0.596
1441084_at	expressed sequence BE686333	BE686333	1.61	0.032	2.53	0.021	2.19	0.257	-1.17	0.116	1.31	0.455
1441128_at	Renal tumor antigen	Rage	1.6	0.024	1.43	0.018	1.15	0.092	-1.23	0.160	1.16	0.803
1448355_at	protease, serine, 16 (thymus)	Prss16	1.6	0.044	1.75	0.923	1.23	0.633	-1.08	0.651	-1.17	0.559
1423172_at	N-ethylmaleimide sensitive fusion protein attachment protein beta	Napb	1.6	0.042	2.83	0.043	1.02	0.872	1.16	0.184	-1.07	0.886
1441698_at	RIKEN cDNA 2410025L10 gene	2410025L10Rik	1.6	0.014	1.77	0.048	1.11	0.929	1.37	0.442	-1.16	0.597
1459759_s_at	RIKEN cDNA 1700065I17 gene	1700065I17Rik	1.6	0.022	1.25	0.750	-3.43	0.015	-1.16	0.387	-1.84	0.157
1431800_at	RIKEN cDNA 1300010F03 gene	1300010F03Rik	1.6	0.040	-1.09	0.660	2	0.050	1	0.564	-1.58	0.010
1434737_at	oligonucleotide/oligosaccharide-binding fold containing 1	Obfc1	1.59	0.023	1.85	0.060	1.2	0.371	1.42	0.013	1.3	0.073
1417256_at	matrix metallopeptidase 13	Mmp13	1.59	0.049	-1.2	0.595	1.01	0.551	-1.02	0.641	1.33	0.381
1444055_at	Heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Hs3st3b1	1.59	0.025	2.01	0.732	2.54	0.507	-1.15	0.250	2.17	0.614
1444992_at	expressed sequence AI120166	AI120166	1.59	0.042	1.41	0.017	1.06	0.212	-1.06	0.591	-1.33	0.074
1454799_at	RIKEN cDNA A230097K15 gene	A230097K15Rik	1.59	0.003	1.33	0.165	1.39	0.016	-1.03	0.656	1.14	0.445
1439876_at	vesicle transport through interaction with t-SNAREs homolog 1A (yeas	Vti1a	1.58	0.018	2.79	0.054	1.13	0.954	1.02	0.846	1.07	0.812
1460601_at	myosin VIIA and Rab interacting protein	Myrip	1.58	0.031	1.45	0.975	-1.09	0.423	-1.24	0.349	1.22	0.978
1429698_at	mitochondrial transcription termination factor	Mterf	1.58	0.031	1.51	0.162	1	0.960	1.16	0.465	1.2	0.437
1439039_at	transmembrane protein 104	Tmem104	1.57	0.030	1.38	0.066	1.46	0.547	1.33	0.269	1.35	0.592
1443378_s_at	MAP kinase-activated protein kinase 5 /// a disintegrin and metallopept	Mapkapk5 /// Adam1a	1.57	0.019	1.12	0.259	1.29	0.054	-1.03	0.753	1.2	0.773
1425347_a_at	zinc finger protein 318	Zfp318	1.56	0.016	1.18	0.345	-1.49	0.159	-1.05	0.602	1.35	0.898
1445064_at	developmentally regulated repeat element-containing transcript 1	Drr1	1.56	0.047	1.58	0.271	1.19	0.653	-1.08	0.422	1.21	0.154
1437689_x_at	clusterin	Clu	1.56	0.001	1.09	0.888	1.31	0.524	1.14	0.761	1.65	0.559
1444449_at	Ubiquitin specific peptidase 18	Usp18	1.55	0.047	2.77	0.044	-1.4	0.192	1.42	0.838	2.21	0.261
1458164_at	hypothetical LOC552913	LOC552913	1.55	0.032	1.41	0.050	1.08	0.766	1.31	0.102	-1.16	0.481
1438128_at	Guanine nucleotide binding protein, alpha transducing 2	Gnat2	1.55	0.044	2.18	0.201	1.29	0.821	1.94	0.918	3.07	0.202
1446246_at	gene model 438, (NCBI)	Gm438	1.55	0.042	1.1	0.892	1	0.956	1.26	0.858	-1.49	0.217
1424549_at	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	Degs2	1.55	0.030	1.14	0.628	-1.22	0.284	2.79	0.306	1.01	0.675
1419698_at	chemokine (C-X-C motif) ligand 11	Cxcl11	1.55	0.011	1.65	0.896	2.31	0.130	1.56	0.322	2.38	0.460
1435892_at	additional sex combs like 3 (Drosophila)	Asxl3	1.55	0.011	1.48	0.632	3.59	0.198	1.44	0.640	1.08	0.675
1442126_at	RIKEN cDNA 5830417C01 gene	5830417C01Rik	1.55	0.013	-1.05	0.758	1.03	0.723	-1.08	0.627	-1.12	0.426

1453116_at	zinc finger protein 689	Zfp689	1.54	0.040	1.33	0.254	-1.27	0.404	1.14	0.773	-2.21	0.031
1441685_at	proline synthetase co-transcribed	Prosc	1.54	0.036	1.63	0.327	-1.14	0.302	-1.01	0.816	2.36	0.206
1455925_at	PR domain containing 8	Prdm8	1.54	0.003	2.48	0.416	1.37	0.538	1.41	0.777	1.38	0.707
1439930_at	SWI/SNF related, matrix associated, actin dependent regulator of chro	Smarca2	1.53	0.001	1.28	0.791	-1.39	0.083	1.12	0.817	1.2	0.398
1440924_at	M-phase phosphoprotein 1	Mphosph1	1.53	0.025	1.08	0.780	-1.4	0.282	1.32	0.066	1.09	0.465
1452411_at	leucine rich repeat containing 1	Lrrc1	1.53	0.049	1.68	0.727	-1.09	0.523	-1.21	0.133	1.11	0.840
1441493_at	ELKS/RAB6-interacting/CAST family member 1	Erc1	1.53	0.047	1.24	0.935	1.13	0.545	-1	0.617	-1.38	0.159
1435215_at	AP1 gamma subunit binding protein 1	Ap1gbp1	1.53	0.027	2.07	0.887	1.85	0.738	-2.04	0.121	-1.32	0.344
1436649_at	zinc finger protein, subfamily 1A, 3 (Aiolos)	Zfpn1a3	1.52	0.021	1.27	0.538	1.6	0.285	2.69	0.106	-1.28	0.514
1449669_at	RAB interacting factor	Rabif	1.52	0.006	1.44	0.100	1.63	0.339	1.25	0.507	1.95	0.123
1425071_s_at	neurotrophic tyrosine kinase, receptor, type 3	Ntrk3	1.52	0.045	1.62	0.158	1.32	0.506	1.72	0.681	1.54	0.960
1422839_at	neurogenin 2	Neurog2	1.52	0.039	1.18	0.684	1.46	0.473	-1.11	0.628	-1.18	0.361
1443212_at	Like-glycosyltransferase	Large	1.52	0.019	1.9	0.144	1.28	0.932	1.17	0.476	1.01	0.849
1433260_at	RIKEN cDNA 4930500E03 gene	4930500E03Rik	1.52	0.002	1.29	0.537	-1.02	0.517	-1.12	0.927	1.28	0.966
1417620_at	RAS-related C3 botulinum substrate 2	Rac2	1.51	0.016	1.34	0.956	-1.01	0.615	-1.12	0.897	1.35	0.914
1423524_at	microtubule associated serine/threonine kinase-like	Mastl	1.51	0.047	1.72	0.025	1.06	0.586	1.26	0.101	1.01	0.824
1448015_at	RIKEN cDNA 2310047C04 gene	2310047C04Rik	1.51	0.009	1.45	0.474	1.44	0.855	-1.08	0.430	-2.19	0.072
1432097_a_at	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	Dclre1a	1.5	0.034	1.37	0.829	1.04	0.860	1.02	0.843	1.03	0.980
1456831_at	AT rich interactive domain 5B (Mrf1 like)	Arid5b	1.5	0.020	1.73	0.222	-1.06	0.564	-1.56	0.026	-1.41	0.091
1433241_at	RIKEN cDNA 9430013L17 gene	9430013L17Rik	1.5	0.002	1.39	0.718	-1.48	0.177	2.71	0.528	1.34	0.793
1420719_at	testis expressed gene 15	Tex15	1.49	0.024	1.49	0.261	-1.05	0.647	-1.13	0.692	1.42	0.883
1440633_at	nei like 3 (E. coli)	Neil3	1.49	0.033	1.28	0.787	1.14	0.288	1.07	0.811	1.11	0.575
1452845_at	hypoxia-inducible factor 1, alpha subunit inhibitor	Hif1an	1.49	0.028	1.42	0.481	1.32	0.311	-1.39	0.119	1.07	0.626
1434675_at	RIKEN cDNA 1700065O13 gene	1700065O13Rik	1.49	0.029	1.76	0.090	1.05	0.879	1.22	0.157	1.11	0.321
1437563_at	PHD finger protein 20-like 1	Phf20l1	1.48	0.011	1.67	0.034	1.12	0.719	1.02	0.876	1.05	0.734
1449490_at	methyl-CpG binding domain protein 4	Mbd4	1.48	0.047	1.53	0.413	1.25	0.107	1.85	0.473	1.02	0.807
1432729_at	RIKEN cDNA 5830415G21 gene	5830415G21Rik	1.48	0.003	2.09	0.161	1.28	0.671	-1.04	0.451	1.1	0.409
1422970_at	Max dimerization protein 3	Mxd3	1.47	0.050	1.71	0.010	-1	0.697	1.19	0.350	1.23	0.366
1456103_at	promyelocytic leukemia	Pml	1.46	0.025	2.28	0.001	1.7	0.132	1.26	0.189	1.13	0.235
1420939_at	heparan sulfate 6-O-sulfotransferase 2	Hs6st2	1.46	0.026	1.24	0.651	-1.63	0.003	-1.1	0.424	1.23	0.263
1446858_at	expressed sequence AU022245	AU022245	1.46	0.041	1.74	0.289	-1.36	0.126	1.06	0.997	1.19	0.093
1459446_at	leucine rich repeat containing 41	Lrrc41	1.45	0.013	-1.15	0.286	1.16	0.996	-1.69	0.073	1.62	0.296
1450206_at	deleted in liver cancer 1	Dlc1	1.45	0.044	1.36	0.553	1.21	0.575	1.71	0.087	1.25	0.588
1444723_at	RIKEN cDNA 6530418L21 gene	6530418L21Rik	1.45	0.037	2.38	0.026	1.2	0.384	1.03	0.879	1.07	0.747
1429734_at	RIKEN cDNA 4632434I11 gene	4632434I11Rik	1.45	0.010	2.17	0.002	1.35	0.157	1.4	0.002	1.57	0.048
1426472_at	zinc finger protein 52	Zfp52	1.44	0.034	2.33	0.024	1.45	0.028	1.45	0.196	1.2	0.699
1454954_at	WD repeat domain 61	Wdr61	1.44	0.036	1.79	0.053	1.2	0.158	1.01	0.914	1.13	0.728
1423636_at	WD repeat domain 31	Wdr31	1.44	0.036	1.16	0.757	1.26	0.245	1.22	0.377	1.34	0.727
1419105_at	nuclear receptor subfamily 1, group H, member 4	Nr1h4	1.44	0.023	2.04	0.137	1.59	0.623	1.91	0.842	1.4	0.471
1450236_at	forkhead box O3a	Foxo3a	1.44	0.002	2.56	0.184	-1.53	0.140	1.53	0.909	1.57	0.908
1439176_at	RIKEN cDNA E130120F12 gene	E130120F12Rik	1.44	0.008	1.33	0.281	1.33	0.077	1.42	0.067	-1.01	0.941

1456764_at	solute carrier family 35, member F3	Slc35f3	1.43	0.003	1.24	0.591	2.18	0.152	1.09	0.811	1.02	0.688
1451319_at	SUMO1/sentrin specific peptidase 1	Senp1	1.43	0.035	1.61	0.088	-1.11	0.572	-1.07	0.404	1.07	0.658
1438891_at	Catenin (cadherin associated protein), delta 2	Ctnnd2	1.43	0.039	1.77	0.200	-1.26	0.386	1.19	0.511	-1.29	0.009
1425176_at	C1q-like 3	C1ql3	1.43	0.042	1.78	0.034	-1.28	0.240	1.15	0.315	1.34	0.288
1445430_at	Rho GTPase activating protein 28	Arhgap28	1.43	0.002	1.18	0.388	1.15	0.525	1.15	0.605	-1.24	0.354
1444175_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin	Arfgef1	1.43	0.018	1.43	0.601	1.06	0.470	1.08	0.921	-1.02	0.350
1456833_at	G protein-coupled receptor 17	Gpr17	1.42	0.005	1.43	0.634	1.24	0.561	-1.02	0.834	1.8	0.236
1439076_at	DEAH (Asp-Glu-Ala-His) box polypeptide 29	Dhx29	1.42	0.043	1.53	0.132	1.11	0.498	1.5	0.178	-1.08	0.676
1445543_at	RIKEN cDNA 9830124H08 gene	9830124H08Rik	1.42	0.036	1.5	0.454	1.2	0.408	1.14	0.700	-1.04	0.424
1457262_at	RIKEN cDNA 2610207I05 gene	2610207I05Rik	1.42	0.039	1.14	0.369	-1.32	0.061	-1.17	0.159	1.08	0.806
1439033_at	zinc finger, CCHC domain containing 7	Zcchc7	1.41	0.032	-1	0.703	-1.42	0.078	-1.14	0.134	-1.89	0.009
1455708_at	Tropomodulin 3	Tmod3	1.41	0.021	1.18	0.706	1.85	0.929	2.29	0.484	-1.17	0.484
1449169_at	hyaluronan synthase 2	Has2	1.41	0.023	1.81	0.113	1.36	0.005	1.39	0.003	1.38	0.023
1432492_a_at	3-hydroxyanthranilate 3,4-dioxygenase	Haao	1.41	0.003	1.12	0.534	-1.14	0.295	-1.07	0.528	-1.25	0.285
1427709_at	glutamate receptor, ionotropic, kainate 3	Grik3	1.41	0.008	1.35	0.150	1.15	0.455	-1.04	0.652	1.02	0.880
1459979_x_at	zinc finger protein 68	Zfp68	1.4	0.029	1.72	0.104	1.08	0.706	-1.05	0.453	1.67	0.179
1453607_at	microfibrillar-associated protein 3-like	Mfap3l	1.4	0.046	1.71	0.056	-1.53	0.073	1.02	0.832	1.22	0.380
1455489_at	leucine rich repeat transmembrane neuronal 2	Lrrtm2	1.4	0.016	2.63	0.018	1.71	0.103	2	0.012	2.11	0.055
1457033_at	gene model 397, (NCBI) /// Mus musculus sequence XM_486399 /// sir	Gm397 /// XM_486399 //	1.4	0.004	-1.07	0.626	1.36	0.767	-1.38	0.218	1.25	0.972
1456605_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	1.4	0.033	1.07	0.668	1.76	0.257	1.23	0.981	1.25	0.098
1436219_at	RIKEN cDNA 4933403F05 gene	4933403F05Rik	1.4	0.038	2.63	0.005	1.56	0.008	1.75	0.002	1.69	0.008
1437257_at	WD repeat domain 47	Wdr47	1.39	0.022	1.23	0.499	2	0.762	1.18	0.969	-1.25	0.292
1416571_at	Tnf receptor associated factor 4	Traf4	1.39	0.041	2.03	0.000	1.36	0.110	1.08	0.484	1.73	0.048
1429327_at	serologically defined colon cancer antigen 1	Sdccag1	1.39	0.043	1.43	0.349	-1.1	0.531	1.03	0.769	-1.43	0.003
1459247_at	ATP/GTP binding protein-like 3	Agbl3	1.39	0.039	1.18	0.811	1.13	0.997	-1.3	0.118	-1.13	0.526
1437818_at	RIKEN cDNA 9430016H08 gene	9430016H08Rik	1.39	0.031	1.09	0.938	-1.18	0.185	1.08	0.897	1.15	0.762
1429198_at	RIKEN cDNA 1810030O07 gene	1810030O07Rik	1.39	0.005	1.51	0.036	1.13	0.187	1.21	0.122	1.15	0.258
1432555_at	whirlin	Whrn	1.38	0.028	1.36	0.405	1.83	0.386	1.17	0.912	1.11	0.462
1451080_at	ubiquitin specific peptdiase 1	Usp1	1.38	0.036	1.7	0.011	1.28	0.022	1.17	0.029	1.25	0.042
1443178_at	ring finger protein 13	Rnf13	1.38	0.039	1.9	0.050	1.69	0.794	1.19	0.822	1.35	0.297
1424156_at	retinoblastoma-like 1 (p107)	Rbl1	1.38	0.021	1.43	0.000	1.22	0.035	1.08	0.197	1.29	0.032
1427771_x_at	integrin beta 1 (fibronectin receptor beta)	Itgb1	1.38	0.006	1.12	0.908	1.12	0.503	1.09	0.563	-1.19	0.236
1415988_at	high density lipoprotein (HDL) binding protein	Hdlbp	1.38	0.035	1.09	0.784	-1.05	0.501	1.19	0.581	1.22	0.590
1435299_at	hypothetical protein C230069N13	C230069N13	1.38	0.040	1.03	0.865	1.22	0.481	-1.23	0.130	-1.19	0.228
1419574_at	zinc finger protein 292	Zfp292	1.37	0.033	1.24	0.569	-1.04	0.621	-1.14	0.424	-1.03	0.663
1433899_x_at	TSC22 domain family, member 1	Tsc22d1	1.37	0.037	1.5	0.029	1.38	0.152	1.27	0.074	1.27	0.203
1440936_at	serine active site containing 1	Serac1	1.37	0.030	1.56	0.229	1.92	0.279	1.12	0.099	1.36	0.112
1426421_s_at	RNA binding motif protein 26	Rbm26	1.37	0.007	1.14	0.612	1.16	0.232	-1.06	0.550	-1.13	0.129
1453405_at	phospholipase A2, group IVD	Pla2g4d	1.37	0.037	1.34	0.268	2.01	0.063	-1.01	0.657	1.24	0.078
1436281_at	Similar to hypothetical protein FLJ38281	LOC245305	1.37	0.039	1.57	0.039	1.04	0.951	1.1	0.159	-1.02	0.868
1427081_at	RIKEN cDNA A630072M18 gene	A630072M18Rik	1.37	0.028	1.72	0.008	1.41	0.185	1.17	0.040	1.4	0.031

1434689_at	zinc finger protein 637	Zfp637	1.36	0.042	1.48	0.006	1.26	0.027	1.11	0.310	1.31	0.020
1450090_at	zinc finger protein 101	Zfp101	1.36	0.002	1.19	0.136	1.12	0.507	1.42	0.037	-1.08	0.374
1454977_at	expressed sequence AU020772	AU020772	1.36	0.045	-1.02	0.546	1.09	0.592	-1.11	0.341	1.05	0.500
1458868_at	ATPase, Na+/K+ transporting, alpha 1 polypeptide	Atp1a1	1.36	0.042	1.17	0.304	2.31	0.844	2.49	0.567	1.29	0.954
1430097_at	RIKEN cDNA 8430436C05 gene	8430436C05Rik	1.36	0.007	1.77	0.472	1.48	0.386	1.41	0.321	-1.24	0.257
1446949_at	RIKEN cDNA 4930431P19 gene	4930431P19Rik	1.36	0.039	1.02	0.779	1.12	0.798	1.13	0.576	1.39	0.807
1450417_a_at	ribosomal protein S20 /// similar to 40S ribosomal protein S20 /// simila	Rps20 /// LOC245676 ///	1.35	0.045	1.55	0.049	1.9	0.449	1.25	0.412	1.59	0.016
1422207_at	5-hydroxytryptamine (serotonin) receptor 5A	Htr5a	1.35	0.030	4.12	0.309	1.22	0.724	1.95	0.056	-1.01	0.996
1417541_at	helicase, lymphoid specific	Hells	1.35	0.006	1.58	0.003	1.17	0.184	1.06	0.635	1.1	0.290
1422160_at	histocompatibility 2, T region locus 24	H2-T24	1.35	0.027	1.54	0.105	-1.1	0.237	-1.03	0.698	1.37	0.635
1455004_at	DNA segment, Chr 2, Wayne State University 81, expressed	D2Wsu81e	1.35	0.045	3.11	0.404	1.24	0.942	-1.16	0.345	1.18	0.466
1458873_at	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	Aspm	1.35	0.019	1.52	0.006	1.03	0.789	1.09	0.061	-1.01	0.934
1427832_at	tubulin alpha, related sequence 1	Tuba-rs1	1.34	0.037	1.11	0.984	1.01	0.774	-1.05	0.505	1.02	0.942
1417342_at	protein phosphatase 1, regulatory (inhibitor) subunit 2	Ppp1r2	1.34	0.031	1.22	0.065	-1	0.814	-1.03	0.682	1.32	0.092
1416505_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	1.34	0.031	2.01	0.033	1.48	0.004	1.38	0.001	1.56	0.010
1427083_a_at	mitogen-activated protein kinase kinase kinase kinase 5	Map4k5	1.34	0.048	1.25	0.413	-1.04	0.532	-1.19	0.061	-1.31	0.248
1431284_a_at	RIKEN cDNA 2210013K02 gene	2210013K02Rik	1.34	0.010	1.24	0.400	1.06	0.780	1.04	0.430	-1	0.820
1429131_at	ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	1.33	0.015	1.46	0.251	-1.09	0.229	1.02	0.681	-1.13	0.544
1434695_at	denticleless homolog (Drosophila)	Dtl	1.33	0.004	1.55	0.013	1.12	0.272	1.05	0.294	1.25	0.031
1455411_at	aquaporin 11	Aqp11	1.33	0.044	1.09	0.836	1.61	0.329	1.27	0.415	-1.16	0.564
1457566_at	RIKEN cDNA A830058L05 gene	A830058L05Rik	1.33	0.012	1.09	0.048	-1.12	0.368	1.07	0.465	1.24	0.056
1431955_at	RIKEN cDNA 4930453H23 gene	4930453H23Rik	1.33	0.000	1.55	0.644	-2.16	0.008	-1.31	0.258	1.71	0.262
1447973_at	thyroid hormone receptor interactor 11	Trip11	1.32	0.036	1.07	0.998	-1.26	0.273	-1.07	0.503	-1.09	0.323
1427253_s_at	suppressor of zeste 12 homolog (Drosophila)	Suz12	1.32	0.040	1.39	0.164	1.08	0.284	1.01	0.878	-1.08	0.048
1448506_at	serine (or cysteine) peptidase inhibitor, clade A, member 6	Serpina6	1.32	0.036	1.23	0.131	2.63	0.144	1.5	0.995	2.2	0.225
1443708_at	cDNA sequence BC068281	BC068281	1.32	0.020	1.84	0.232	2.47	0.359	2.11	0.062	1.99	0.082
1425483_at	thymocyte selection-associated HMG box gene	Tox	1.31	0.038	1.12	0.722	-1.1	0.508	-1.22	0.286	1.78	0.865
1438424_at	TBC1 domain family, member 24	Tbc1d24	1.31	0.009	1.3	0.164	1.06	0.753	1.16	0.773	1.4	0.421
1452179_at	PHD finger protein 17	Phf17	1.31	0.049	1.51	0.177	1.2	0.063	1	0.881	-1.01	0.706
1423218_a_at	mitochondrial ribosomal protein L49	Mrpl49	1.31	0.017	1.85	0.007	1.24	0.006	1.36	0.009	1.29	0.096
1419196_at	hepcidin antimicrobial peptide 1	Hamp1	1.31	0.025	1.64	0.215	-1.09	0.589	-1.05	0.545	-1.05	0.650
1426612_at	timeless interacting protein	Tipin	1.3	0.029	1.52	0.010	1.06	0.072	1.11	0.072	1.07	0.099
1447827_x_at	speckle-type POZ protein	Spop	1.3	0.006	1.03	0.285	-1.05	0.654	-1.28	0.083	-1.06	0.173
1449272_at	immunoglobulin superfamily, member 4B	Igsf4b	1.3	0.023	1.2	0.587	1.05	0.823	1.62	0.519	-1.23	0.100
1449116_a_at	deoxythymidylate kinase	Dtymk	1.3	0.011	1.24	0.006	1.06	0.517	-1	0.982	1.15	0.124
1417458_s_at	CDC28 protein kinase regulatory subunit 2	Cks2	1.3	0.041	1.24	0.058	1.04	0.521	1.07	0.033	1.15	0.005
1442429_at	Adaptor protein complex AP-2, mu1	Ap2m1	1.3	0.002	1.11	0.863	1.3	0.006	1.37	0.792	-1.57	0.117
1429665_at	RIKEN cDNA 6230416J20 gene	6230416J20Rik	1.3	0.031	1.24	0.021	1.26	0.022	1.26	0.408	1.03	0.621
1429660_s_at	structural maintenance of chromosomes 2	Smc2	1.29	0.026	1.06	0.546	-1.11	0.103	-1.1	0.312	-1.06	0.591
1425498_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	1.29	0.033	1.63	0.020	1.08	0.075	-1.04	0.498	-1.07	0.078
1450244_a_at	mitogen activated protein kinase kinase kinase kinase 2	Map4k2	1.29	0.012	1.13	0.481	-1.04	0.627	-1.11	0.149	1.1	0.548

1448984_at	excision repair cross-complementing rodent repair deficiency, complem	Ercc4	1.29	0.043	1.45	0.060	1.11	0.662	1.14	0.323	1.38	0.439
1442579_at	RIKEN cDNA 9330111N05 gene	9330111N05Rik	1.29	0.049	2.39	0.516	1.24	0.831	1.64	0.209	1.82	0.121
1453968_at	RIKEN cDNA 4833439F03 gene	4833439F03Rik	1.29	0.039	-1.06	0.478	-1.05	0.378	-1.11	0.398	-1	0.806
1418251_at	tubby-like protein 3	Tulp3	1.28	0.049	1.26	0.365	-1.13	0.563	1.05	0.774	2.39	0.179
1436184_at	gene model 632, (NCBI)	Gm632	1.28	0.004	1.38	0.068	1.15	0.234	-1.18	0.157	1.13	0.073
1418027_at	exonuclease 1	Exo1	1.28	0.025	1.73	0.002	1.24	0.305	1.42	0.078	-1	0.859
1434981_at	RIKEN cDNA E130303B06 gene	E130303B06Rik	1.28	0.005	1.42	0.029	1.23	0.277	1.02	0.574	1.32	0.160
1418585_at	cyclin H	Ccnh	1.28	0.019	1.26	0.143	1.24	0.037	1.16	0.189	1.4	0.048
1439020_at	expressed sequence AW146020	AW146020	1.28	0.039	1.44	0.042	1.01	0.832	-1.03	0.657	1.13	0.057
1434791_at	ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	1.28	0.049	1.28	0.035	1.03	0.606	1.25	0.138	1.08	0.490
1439038_at	RIKEN cDNA 9130227C08Rik gene	9130227C08Rik	1.28	0.032	1.31	0.386	-1.22	0.160	-1.11	0.355	1.01	0.971
1453183_at	RIKEN cDNA 1110034A24 gene	1110034A24Rik	1.28	0.043	1.56	0.001	1.21	0.066	1.08	0.496	1.18	0.193
1423440_at	RIKEN cDNA 1110001A07 gene	1110001A07Rik	1.28	0.020	1.32	0.226	1.16	0.313	1.24	0.004	1.14	0.516
1425410_at	Tp53rk binding protein	Tprkb	1.27	0.032	1.48	0.312	1.1	0.505	-1.02	0.607	1.1	0.842
1439358_a_at	neurexin I	Nrxn1	1.27	0.045	1.6	0.124	1.48	0.615	-1.04	0.607	-1.14	0.024
1460200_s_at	leucine zipper transcription factor-like 1	Lztfl1	1.27	0.007	1.1	0.256	1.25	0.347	1.02	0.942	1.19	0.467
1452315_at	kinesin family member 11	Kif11	1.27	0.015	1.01	0.763	-1.13	0.629	1.1	0.399	-1.02	0.793
1448719_at	transcriptional adaptor 3 (NGG1 homolog, yeast)-like	Tada3l	1.26	0.031	1.04	0.813	-1.04	0.648	-1.52	0.212	1.85	0.240
1452115_a_at	polo-like kinase 4 (Drosophila)	Plk4	1.26	0.010	1.19	0.074	1	0.682	1.07	0.147	1.06	0.959
1456748_a_at	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like prot	Nipsnap1	1.26	0.041	1.2	0.727	2.93	0.134	1.11	0.782	1.35	0.002
1421362_a_at	fyn-related kinase	Frk	1.26	0.002	1.1	0.742	-1.05	0.562	-1.07	0.512	1.1	0.264
1416333_at	docking protein 2	Dok2	1.26	0.031	1.62	0.495	1.04	0.520	1.14	0.466	-1.06	0.565
1434030_at	cDNA sequence BC034507	BC034507	1.26	0.014	1.67	0.016	1.31	0.165	1.07	0.711	1.16	0.342
1439758_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidat	Als2cr12	1.26	0.022	1.3	0.138	1.61	0.003	1.36	0.065	1.25	0.310
1449105_at	SH2 domain protein 2A	Sh2d2a	1.25	0.037	1.12	0.283	-1.04	0.638	1.45	0.361	1.18	0.102
1426075_at	klotho beta	Klb	1.25	0.042	1.37	0.084	-1.08	0.511	-1.12	0.354	1.1	0.494
1456280_at	claspin homolog (Xenopus laevis)	Clspn	1.25	0.013	1.58	0.007	1.11	0.244	1.08	0.420	1.16	0.119
1452128_a_at	BRCA1/BRCA2-containing complex, subunit 3	Brcc3	1.25	0.036	1.15	0.012	1.17	0.060	1.15	0.171	1.04	0.704
1436049_at	RIKEN cDNA 5730589K01 gene	5730589K01Rik	1.25	0.021	1.37	0.012	1.33	0.016	1.1	0.100	1.12	0.699
1420661_a_at	RIKEN cDNA 4933439F18 gene	4933439F18Rik	1.25	0.002	1.27	0.090	-1.08	0.320	1.13	0.355	-1.14	0.080
1432252_a_at	RIKEN cDNA 4933406K04 gene	4933406K04Rik	1.25	0.034	1.09	0.533	1.85	0.206	1.04	0.865	1.85	0.459
1456731_x_at	Polymerase (RNA) III (DNA directed) polypeptide K	Polr3k	1.24	0.025	1.18	0.165	3.14	0.204	1.11	0.015	1.28	0.066
1428615_at	purinergic receptor P2Y, G-protein coupled, 5	P2ry5	1.24	0.018	1.7	0.043	1.44	0.019	1.35	0.009	1.52	0.011
1457739_at	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratu	Fscn1	1.24	0.017	1.12	0.649	-1.05	0.428	-1.16	0.472	1.97	0.303
1457213_a_at	diacylglycerol kinase, eta	Dgkh	1.24	0.016	-1.04	0.806	-1.01	0.656	-1.26	0.092	-1.26	0.071
1442424_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) sm	Ctdspl2	1.24	0.019	1.22	0.638	1.98	0.801	1.14	0.929	1.19	0.810
1417175_at	casein kinase 1, epsilon	Csnk1e	1.24	0.008	1.21	0.163	1.21	0.172	-1	0.846	1.04	0.924
1420908_at	CD2-associated protein	Cd2ap	1.24	0.046	1.22	0.668	1.01	0.846	-1.13	0.294	-1.26	0.204
1436229_at	CDNA sequence BC049806	BC049806	1.24	0.005	1.07	0.644	-1.11	0.371	-1.12	0.312	-1.2	0.076
1425907_s_at	angiomotin	Amot	1.24	0.039	1.08	0.683	1.05	0.969	1.17	0.991	-1.07	0.549
1436574_at	RIKEN cDNA 1700029I01 gene /// similar to zinc finger protein 665 /// s	1700029I01Rik /// LOC6	1.24	0.039	1.14	0.610	1.04	0.800	-1.03	0.619	-1.15	0.128

1426993_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	1.23	0.032	1.12	0.417	-1.15	0.176	1.07	0.792	-1.11	0.486
1436012_s_at	secernin 2	Scrn2	1.23	0.013	2.39	0.397	-1.15	0.392	1.74	0.053	1.16	0.500
1458193_at	peripheral myelin protein 2	Pmp2	1.23	0.001	1.14	0.297	-1.03	0.361	1.01	0.914	1	0.838
1430617_at	Opa interacting protein 5	Oip5	1.23	0.007	1.1	0.549	1.27	0.155	1.3	0.328	1.04	0.438
1430442_at	nitric oxide synthase 1 (neuronal) adaptor protein	Nos1ap	1.23	0.045	1.55	0.278	-1.25	0.216	-1.03	0.669	1.41	0.054
1431066_at	fucosyltransferase 11	Fut11	1.23	0.034	1.28	0.018	-1.04	0.828	1.43	0.059	1.37	0.263
1422033_a_at	ciliary neurotrophic factor /// zinc finger protein 91	Cntf /// Zfp91	1.23	0.011	1.55	0.048	1.2	0.202	1.21	0.056	1.26	0.103
1434767_at	expressed sequence C79407	C79407	1.23	0.014	1.09	0.545	1.1	0.681	1.02	0.866	-1.13	0.057
1425531_at	zinc finger, HIT domain containing 1	Znhit1	1.22	0.043	1.18	0.058	1.03	0.451	1.02	0.695	1.08	0.212
1421718_at	striamin	Strm	1.22	0.036	1.71	0.332	1.11	0.505	-1.3	0.100	1.08	0.381
1423318_at	RAD18 homolog (S. cerevisiae)	Rad18	1.22	0.019	1.03	0.950	1.06	0.365	-1.07	0.380	1.04	0.498
1415679_at	presenilin enhancer 2 homolog (C. elegans)	Psenen	1.22	0.039	1.15	0.181	1.13	0.153	1.09	0.096	1.03	0.856
1448527_at	programmed cell death 10	Pdcd10	1.22	0.004	1.2	0.155	1.03	0.307	-1.09	0.348	-1.09	0.275
1455901_at	choline phosphotransferase 1	Chpt1	1.22	0.047	1.35	0.077	1.4	0.130	-1.05	0.495	-1.01	0.995
1441529_at	RIKEN cDNA 9130230N09 gene	9130230N09Rik	1.22	0.046	-1.62	0.176	1.02	0.517	1.57	0.973	-1.16	0.580
1435615_at	zinc finger protein 365	Zfp365	1.21	0.024	1.41	0.429	2.06	0.049	1.03	0.924	1.04	0.557
1456041_at	sorting nexin 16	Snx16	1.21	0.016	1.43	0.047	1.08	0.253	1.02	0.370	1.15	0.123
1417037_at	origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	1.21	0.006	1.51	0.035	1.16	0.047	1.18	0.018	1.2	0.052
1416298_at	matrix metallopeptidase 9	Mmp9	1.21	0.019	1.05	0.846	-1.24	0.160	1	0.991	2.04	0.501
1451922_at	lectin, mannose-binding 1 like	Lman1l	1.21	0.008	1.17	0.195	1.3	0.313	1.01	0.926	1.11	0.537
1426284_at	keratin 20	Krt20	1.21	0.030	1.3	0.005	1.25	0.035	1.07	0.145	1.23	0.123
1447495_at	fibronectin type 3 and ankyrin repeat domains 1	Fank1	1.21	0.018	1.85	0.013	-1.58	0.192	1.66	0.640	2.7	0.556
1416143_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	Atp5j	1.21	0.028	1.22	0.020	1.07	0.141	1.08	0.033	1.03	0.304
1415680_at	anaphase promoting complex subunit 1	Anapc1	1.21	0.048	1.01	0.864	1.05	0.974	-1.03	0.606	-1.12	0.118
1419262_at	acyl-Coenzyme A dehydrogenase family, member 8	Acad8	1.21	0.047	1.43	0.010	1.19	0.021	1.12	0.062	1.07	0.320
1455538_at	RIKEN cDNA 6330403M23 gene	6330403M23Rik	1.21	0.020	1.05	0.885	1.16	0.178	1.27	0.085	-1.01	0.517
1417830_at	structural maintenance of chromosomes 1A	Smc1a	1.2	0.031	1.12	0.153	1.06	0.170	1.01	0.947	-1.03	0.144
1422108_at	protein phosphatase 1, regulatory (inhibitor) subunit 3A	Ppp1r3a	1.2	0.007	1.09	0.958	1.23	0.781	1.52	0.416	-1.01	0.863
1428985_at	integrator complex subunit 12	Ints12	1.2	0.026	1.36	0.029	1.29	0.080	1.2	0.218	1.28	0.027
1445380_at	RIKEN cDNA A230072C01 gene	A230072C01Rik	1.2	0.019	-1.34	0.299	-1.07	0.262	-1.02	0.800	-1.19	0.257
1420548_a_at	RIKEN cDNA 2310008H09 gene	2310008H09Rik	1.2	0.028	1.37	0.004	1.12	0.140	1.15	0.264	1.07	0.666
1429111_at	talin 2 /// similar to talin 2	Tln2 /// LOC639214	-1.2	0.033	-1.68	0.002	-1.46	0.005	-1.41	0.006	-1.5	0.005
1416207_at	tafazzin	Taz	-1.2	0.043	-1.2	0.081	1.03	0.452	-1.06	0.090	1.03	0.500
1449815_a_at	single-stranded DNA binding protein 2	Ssbp2	-1.2	0.017	-2.62	0.010	-1.42	0.033	-1.2	0.086	-1.4	0.001
1436272_at	RAB3 GTPase activating protein subunit 2	Rab3gap2	-1.2	0.011	-1.51	0.003	1.01	0.889	-1.08	0.551	-1.27	0.030
1426755_at	cytoskeleton-associated protein 4	Ckap4	-1.2	0.015	-1.22	0.045	-1.26	0.045	1.03	0.775	1.05	0.553
1456930_at	calmodulin regulated spectrin-associated protein 1	Camsap1	-1.2	0.039	-1.24	0.224	1.01	0.950	1.04	0.810	-1.09	0.384
1427349_x_at	RIKEN cDNA 2810021G02 gene	2810021G02Rik	-1.2	0.029	1.12	0.292	1.04	0.960	-1.15	0.143	1.13	0.506
1429661_at	Rho-related BTB domain containing 3	Rhobtb3	-1.21	0.010	-1.43	0.042	-1.06	0.584	-1.06	0.082	-1.03	0.769
1452056_s_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	-1.21	0.023	-2.15	0.008	-1.25	0.127	-1.46	0.006	-1.37	0.001
1441617_at	positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated	Pcqap	-1.21	0.032	-1.23	0.007	-1.04	0.501	1.03	0.913	-1.35	0.071

1446087_at	Golgi autoantigen, golgin subfamily a, 1	Golga1	-1.21	0.042	-1.37	0.058	-2.81	0.116	2.14	0.738	4.01	0.087
1437547_s_at	DnaJ (Hsp40) homolog, subfamily C, member 14	Dnajc14	-1.21	0.028	1.08	0.339	-1.06	0.535	-1.05	0.003	1.12	0.131
1448761_a_at	coatomer protein complex, subunit gamma 2	Copg2	-1.21	0.012	-1.13	0.009	1.03	0.919	1.54	0.163	-1.16	0.320
1425812_a_at	calcium channel, voltage-dependent, N type, alpha 1B subunit	Cacna1b	-1.21	0.032	-1.08	0.642	1.06	0.953	1.32	0.099	1.01	0.858
1452704_at	RIKEN cDNA 1200015F23 gene	1200015F23Rik	-1.21	0.005	-1.04	0.388	1.12	0.588	1.03	0.671	1.12	0.008
1425747_at	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	1110060D06Rik /// Dock	-1.21	0.015	-1.53	0.002	-1.48	0.065	-1.52	0.003	-1.75	0.001
1452256_at	RIKEN cDNA 1110002N22 gene	1110002N22Rik	-1.21	0.044	1.04	0.832	1.16	0.154	1.16	0.264	1.18	0.205
1417542_at	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	-1.22	0.011	-1.66	0.014	-1.05	0.435	-1.09	0.009	-1.22	0.048
1443299_at	PDZ and LIM domain 3	Pdlim3	-1.22	0.022	-1.29	0.083	1.06	0.920	-1.03	0.983	1.05	0.833
1445475_at	p21 (CDKN1A)-activated kinase 6	Pak6	-1.22	0.018	1.12	0.625	1.28	0.798	1.23	0.786	-1.35	0.053
1456495_s_at	oxysterol binding protein-like 6	Osbpl6	-1.22	0.036	-2.72	0.017	1.15	0.868	1.03	0.681	1.29	0.652
1425784_a_at	olfactomedin 1	Olfm1	-1.22	0.025	-1.18	0.259	1.19	0.287	-1.03	0.527	1.24	0.047
1434418_at	longevity assurance homolog 6 (S. cerevisiae)	Lass6	-1.22	0.024	-2.06	0.010	-1.58	0.020	-1.66	0.006	-1.87	0.015
1451382_at	ChaC, cation transport regulator-like 1 (E. coli)	Chac1	-1.22	0.007	-2.44	0.001	-1.18	0.052	-1.24	0.002	-1.32	0.001
1441238_at	RIKEN cDNA 9030416H16 gene	9030416H16Rik	-1.22	0.039	1.1	0.928	1.25	0.387	1.12	0.134	1.27	0.774
1427187_at	RIKEN cDNA 6030413G23 gene	6030413G23Rik	-1.22	0.040	-1.52	0.042	1.03	0.879	1.1	0.479	1.82	0.032
1440318_at	WD repeat domain 35	Wdr35	-1.23	0.006	-1.08	0.419	1.35	0.519	1.04	0.913	1.16	0.481
1456488_at	WD repeat domain 33	Wdr33	-1.23	0.019	-1.02	0.693	-1.25	0.292	-1.14	0.031	-1.34	0.071
1427894_at	vasorin	Vasn	-1.23	0.033	-1.29	0.091	-1.19	0.031	-1.1	0.118	-1.33	0.034
1436542_at	Prostaglandin E receptor 1 (subtype EP1)	Ptger1	-1.23	0.035	-1.03	0.853	1.02	0.927	1.1	0.282	-1	0.925
1435432_at	centaurin, gamma 2	Centg2	-1.23	0.014	-2.53	0.001	-1.91	0.009	-1.57	0.005	-1.97	0.018
1426249_at	adrenergic receptor kinase, beta 1	Adrbk1	-1.23	0.030	-1.02	0.813	1.02	0.833	-1.03	0.049	1.06	0.348
1443005_at	zinc finger homeobox 1a	Zfhx1a	-1.24	0.029	-1.51	0.031	-1.29	0.041	-1.33	0.117	1.04	0.912
1454741_s_at	transmembrane protein 164	Tmem164	-1.24	0.029	-1.56	0.001	-1.06	0.263	-1.15	0.032	-1.22	0.039
1420696_at	sema domain, immunoglobulin domain (Ig), short basic domain, secret	Sema3c	-1.24	0.048	-1.05	0.701	-1.38	0.196	1.01	0.893	-1.17	0.247
1418895_at	src family associated phosphoprotein 2	Scap2	-1.24	0.042	-1.74	0.022	1.09	0.727	-1.11	0.114	-1.1	0.290
1418869_a_at	pseudouridine synthase 1	Pus1	-1.24	0.042	1.1	0.471	1.19	0.033	1.25	0.140	1.15	0.233
1427288_at	amyloid beta (A4) precursor protein-binding, family A, member 2	Apba2	-1.24	0.017	-1.16	0.316	1.05	0.737	-1.25	0.378	1.07	0.848
1460222_at	SH3-domain binding protein 1	Sh3bp1	-1.25	0.024	1.05	0.972	-1.11	0.316	-1.05	0.566	1.26	0.075
1436784_x_at	splicing factor 3b, subunit 4 /// similar to splicing factor 3b, subunit 4 (p	Sf3b4 /// LOC634414 ///	-1.25	0.042	-1.02	0.627	1.05	0.841	1.04	0.938	1.2	0.080
1417255_at	intraflagellar transport 140 homolog (Chlamydomonas)	Ift140	-1.25	0.042	-1.3	0.247	-1.01	0.871	-1.03	0.568	-1.1	0.435
1423966_at	Cd99 antigen-like 2	Cd99l2	-1.25	0.003	-1.41	0.010	-1.1	0.541	1.03	0.844	-1.17	0.065
1436503_at	cDNA sequence BC048546	BC048546	-1.25	0.021	2.06	0.426	1.33	0.247	-1.27	0.271	1	0.595
1457900_at	activating signal cointegrator 1 complex subunit 3	Ascc3	-1.25	0.050	-1.13	0.369	-1.14	0.406	1.11	0.552	1.5	0.234
1437466_at	activated leukocyte cell adhesion molecule	Alcam	-1.25	0.019	-1.44	0.216	-1.1	0.691	1.03	0.441	-1.12	0.342
1426937_at	RIKEN cDNA 6330406I15 gene	6330406I15Rik	-1.25	0.008	-1.51	0.148	-1.29	0.140	-1.48	0.031	-1.33	0.025
1452727_at	R3H domain containing 2	R3hdm2	-1.26	0.044	-1.37	0.008	-1.06	0.456	-1.11	0.225	-1.2	0.156
1449785_at	expressed sequence AA414993	AA414993	-1.26	0.048	-1.56	0.125	1.53	0.905	1.41	0.401	1.8	0.341
1441850_x_at	transcobalamin 2	Tcn2	-1.27	0.037	1.13	0.563	1.09	0.954	1.14	0.733	1.13	0.561
1443238_at	PHD finger protein 14	Phf14	-1.27	0.045	-1.22	0.097	-1.07	0.625	1.16	0.850	-1.09	0.458
1452320_at	low density lipoprotein receptor-related protein 2	Lrp2	-1.27	0.022	-1.36	0.144	-1.41	0.027	-1.31	0.000	-1.13	0.148

1452844_at	POU domain, class 6, transcription factor 1	Pou6f1	-1.28	0.010	-1.09	0.491	1.11	0.562	1.16	0.027	1.1	0.297
1438551_at	neurogenin 1	Neurog1	-1.28	0.006	1.27	0.256	-1.16	0.090	1.27	0.269	-1.07	0.616
1436143_at	RIKEN cDNA 4933425L03 gene	4933425L03Rik	-1.28	0.050	-1.93	0.063	-1.57	0.004	-1.42	0.024	-1.67	0.025
1421929_at	Eph receptor A4	Epha4	-1.29	0.021	-1.25	0.028	-1.65	0.142	-1.33	0.019	-1.33	0.166
1429987_at	RIKEN cDNA 9930013L23 gene	9930013L23Rik	-1.29	0.007	-3.17	0.004	-2.03	0.006	-1.74	0.000	-2.44	0.008
1452418_at	RIKEN cDNA 1200016E24 gene	1200016E24Rik	-1.29	0.020	1.03	0.472	-1.08	0.608	1.05	0.925	1.34	0.035
1443905_at	Splicing factor, arginine/serine-rich 8	Sfrs8	-1.3	0.010	-1.12	0.438	-1.11	0.090	-1.26	0.030	-1.15	0.317
1444379_at	PWWP domain containing 2	Pwwp2	-1.3	0.014	-1.49	0.104	1.28	0.215	-1.28	0.116	1.16	0.429
1430180_at	mitogen activated protein kinase kinase 5	Map2k5	-1.3	0.040	-1.41	0.196	-1.03	0.657	-1.13	0.312	-1.45	0.077
1441200_at	Kruppel-like factor 3 (basic)	Klf3	-1.3	0.047	1.01	0.772	-1.12	0.393	-1.22	0.183	-1.01	0.778
1420364_at	G protein-coupled receptor 87	Gpr87	-1.3	0.011	-1.02	0.783	-1.19	0.329	-1.26	0.347	1.05	0.826
1434158_at	GDP-mannose 4, 6-dehydratase	Gmds	-1.3	0.036	-1.34	0.039	-1.4	0.009	-1.13	0.033	-1.3	0.012
1438367_x_at	discoidin domain receptor family, member 1	Ddr1	-1.3	0.006	-1.19	0.473	1.75	0.111	-1.45	0.101	1.19	0.967
1436293_x_at	DNA segment, Chr 1, ERATO Doi 471, expressed	D1Ertd471e	-1.3	0.050	-1.13	0.404	1.42	0.321	-1.07	0.286	1.06	0.891
1429927_at	RIKEN cDNA 5830409B07 gene	5830409B07Rik	-1.3	0.044	-2.19	0.063	-1.13	0.444	1.5	0.032	1.21	0.408
1437246_x_at	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to	Rps6 /// LOC214738 /// L	-1.31	0.044	-1.06	0.527	1.17	0.162	-1.31	0.046	1.14	0.200
1431751_a_at	metallophosphoesterase domain containing 2	Mpped2	-1.31	0.013	-2.13	0.034	-1.39	0.141	1.2	0.467	-1.11	0.499
1459667_at	Rho GTPase activating protein 17	Arhgap17	-1.31	0.042	-1.43	0.128	1.03	0.812	1.11	0.535	-1.11	0.392
1431194_at	RIKEN cDNA 6030468B19 gene	6030468B19Rik	-1.31	0.006	-1.17	0.402	1.08	0.790	1.13	0.567	1.03	0.847
1443916_at	RIKEN cDNA 2900026A02 gene	2900026A02Rik	-1.31	0.007	-2.11	0.000	-1.07	0.428	-1.05	0.602	-1.52	0.015
1428439_at	negative regulator of ubiquitin-like proteins 1	Nub1	-1.32	0.011	-1.32	0.325	1.83	0.394	1.19	0.865	-1.07	0.635
1441928_x_at	elongation factor RNA polymerase II	Ell	-1.32	0.045	-1.04	0.928	1.45	0.929	-1.22	0.200	-1.08	0.656
1443889_at	RIKEN cDNA 9030619P08 gene	9030619P08Rik	-1.32	0.031	-1.18	0.421	1.01	0.759	2	0.268	1.89	0.213
1444059_at	RIKEN cDNA 6330415G19 gene	6330415G19Rik	-1.32	0.045	-1.37	0.095	1.32	0.116	1.24	0.497	-1.26	0.142
1454274_at	RIKEN cDNA 4930571C24 gene	4930571C24Rik	-1.32	0.022	-1.13	0.520	1.25	0.326	-1.07	0.362	-1.05	0.645
1440369_at	Prostaglandin E receptor 3 (subtype EP3)	Ptger3	-1.33	0.023	1.39	0.325	-1.21	0.301	-1.1	0.237	-1.17	0.092
1436311_at	gem (nuclear organelle) associated protein 5	Gemin5	-1.33	0.018	1.23	0.269	1.13	0.620	1.1	0.294	-1.06	0.984
1457042_at	EST AI256396	AI256396	-1.33	0.048	-1.47	0.094	1.03	0.927	1.16	0.894	1.13	0.574
1432861_at	RIKEN cDNA 2900046F13 gene	2900046F13Rik	-1.33	0.047	-1.09	0.519	1.67	0.038	1.74	0.362	-1.15	0.365
1429652_at	RIKEN cDNA 1190002C06 gene	1190002C06Rik	-1.33	0.047	-1.71	0.042	-1.09	0.416	1.05	0.666	-1.1	0.441
1427596_at	X (inactive)-specific transcript, antisense	Tsix	-1.34	0.049	1.48	0.760	-2.64	0.009	1.34	0.891	1.47	0.175
1435603_at	sushi, nidogen and EGF-like domains 1	Sned1	-1.34	0.008	-1.12	0.681	-1.28	0.345	-1.02	0.749	-1.13	0.385
1421672_at	interleukin 17A	Il17a	-1.34	0.036	-1.72	0.045	1.51	0.425	1.48	0.884	1.35	0.262
1442186_at	ataxin 7	Atxn7	-1.34	0.020	-1.03	0.515	1.22	0.548	-1.11	0.317	-1.41	0.066
1421563_at	ATPase, Cu++ transporting, beta polypeptide	Atp7b	-1.34	0.037	1.02	0.873	1.14	0.218	1.02	0.747	1.37	0.095
1453152_at	MAM domain containing 2	Mamdc2	-1.35	0.014	-1.32	0.236	-1.14	0.386	1.06	0.591	1.52	0.776
1422678_at	diacylglycerol O-acyltransferase 2	Dgat2	-1.35	0.049	-1.07	0.486	1.11	0.355	1.1	0.107	1.15	0.433
1442868_at	RIKEN cDNA C130026L21 gene	C130026L21Rik	-1.35	0.015	1.51	0.600	-1.34	0.210	1.22	0.486	-1.01	0.743
1455341_at	RIKEN cDNA 2010003J03 gene	2010003J03Rik	-1.35	0.032	-1.09	0.556	1.05	0.770	1.25	0.268	-1.24	0.128
1421245_at	sclerostin	Sost	-1.36	0.030	-1.19	0.168	1.05	0.572	1.08	0.855	1.02	0.754
1428661_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhib	Nfkbil2	-1.36	0.003	1.12	0.293	-1.04	0.572	1.15	0.369	1.32	0.027

1434994_at	death effector domain-containing	Dedd	-1.36	0.040	-1.04	0.591	1.11	0.425	1.1	0.283	1.13	0.196
1447083_at	RIKEN cDNA 4933407I05 gene	4933407I05Rik	-1.36	0.014	-2.21	0.006	1.34	0.895	1.86	0.223	1.59	0.448
1440779_s_at	solute carrier family 5 (sodium/glucose cotransporter), member 9	Slc5a9	-1.37	0.031	-1.04	0.611	-1.03	0.694	-1.08	0.640	1.85	0.086
1422548_at	dehydrodolichyl diphosphate synthase	Dhdds	-1.37	0.003	-1.16	0.257	1.09	0.979	1.03	0.524	1.22	0.643
1429097_at	RIKEN cDNA C030044C12 gene	C030044C12Rik	-1.37	0.047	-2.1	0.001	-1.07	0.655	-1.28	0.175	-1.24	0.196
1432832_at	RIKEN cDNA 4933435G04 gene	4933435G04Rik	-1.37	0.020	-1.29	0.255	1.45	0.983	1.89	0.354	1.12	0.612
1431712_a_at	RIKEN cDNA 2310022A10 gene	2310022A10Rik	-1.37	0.037	1.18	0.082	1.09	0.937	1.13	0.224	1.45	0.109
1419521_at	zinc finger protein 94	Zfp94	-1.38	0.030	-1.18	0.219	-1.09	0.513	1.25	0.246	-1	0.999
1437012_x_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	-1.38	0.049	-1.35	0.115	1.71	0.045	1.64	0.177	1.67	0.304
1437982_x_at	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	Cox15	-1.38	0.023	-1.16	0.285	1.22	0.821	-1.09	0.216	1.33	0.125
1456380_x_at	calponin 3, acidic	Cnn3	-1.38	0.026	1.02	0.545	-1.01	0.840	-1.07	0.508	1.1	0.903
1443497_at	Ankyrin repeat and BTB (POZ) domain containing 2	Abtb2	-1.38	0.027	-1.06	0.895	1.5	0.772	1.32	0.443	3.96	0.004
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	-1.38	0.031	-2.43	0.034	-1.39	0.004	-1.25	0.012	-1.34	0.049
1438033_at	thyrotroph embryonic factor	Tef	-1.39	0.046	1.15	0.751	-1.05	0.584	1.01	0.904	1.02	0.762
1444276_at	immature colon carcinoma transcript 1	Ict1	-1.39	0.002	-1.7	0.005	-1.35	0.182	-1.16	0.428	1.14	0.423
1440840_at	RIKEN cDNA D630004K10 gene	D630004K10Rik	-1.39	0.004	-1.77	0.052	-1.1	0.611	-1.13	0.421	-1.11	0.389
1442504_at	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ertd653e	-1.39	0.037	-1.74	0.053	-1.22	0.255	-1.3	0.044	-1.01	0.566
1455851_at	bone morphogenetic protein 5	Bmp5	-1.39	0.021	1.04	0.957	1.51	0.167	1.86	0.875	1.15	0.563
1452928_at	ABI gene family, member 3	Abi3	-1.39	0.038	-1.14	0.561	-1.19	0.266	1.56	0.101	-1.22	0.419
1429543_at	RIKEN cDNA 6230424C14 gene	6230424C14Rik	-1.39	0.010	-1.6	0.154	-1.06	0.407	-1.39	0.123	-1.22	0.281
1432313_at	RIKEN cDNA 4933433F19 gene	4933433F19Rik	-1.39	0.023	1.14	0.906	-1.09	0.387	-1.02	0.702	1.57	0.335
1419032_at	RIKEN cDNA 2610018G03 gene	2610018G03Rik	-1.39	0.007	-1.29	0.477	1.04	0.941	1.21	0.824	2.42	0.202
1455933_at	transformer 2 alpha homolog (Drosophila)	Tra2a	-1.4	0.029	-1.09	0.582	1.2	0.604	1.1	0.981	1.31	0.566
1459612_at	PH domain and leucine rich repeat protein phosphatase	Phlpp	-1.4	0.040	1.66	0.618	1.67	0.335	1.39	0.715	-1.11	0.367
1431844_at	potassium large conductance calcium-activated channel, subfamily M,	Kcnmb2	-1.4	0.025	1.03	0.845	4.12	0.152	1.01	0.936	1.03	0.924
1424856_at	ATPase, Na+/K+ transporting, alpha 3 polypeptide	Atp1a3	-1.4	0.006	-1.11	0.632	1.69	0.954	-1.16	0.741	1.21	0.679
1432570_at	RIKEN cDNA 6030458E02 gene	6030458E02Rik	-1.4	0.000	-1.56	0.013	-1.26	0.178	-1.06	0.521	1.1	0.986
1456906_at	RIKEN cDNA 4833432P19 gene	4833432P19Rik	-1.4	0.031	-1.17	0.226	1.25	0.267	1.16	0.448	-1.45	0.016
1449639_at	RIKEN cDNA 0610040J01 gene	0610040J01Rik	-1.4	0.041	-1.1	0.902	-1.29	0.238	-1.01	0.595	2.01	0.387
1458897_at	uronyl-2-sulfotransferase	Ust	-1.41	0.010	-2.9	0.007	-1.2	0.102	-1.41	0.087	-1.25	0.086
1427043_s_at	cytosolic ovarian carcinoma antigen 1	Cova1	-1.41	0.049	-2.99	0.005	-1.37	0.065	-1.69	0.008	-1.63	0.041
1422872_at	bone morphogenetic protein receptor, type 1B	Bmpr1b	-1.41	0.020	-1.71	0.089	-1.46	0.103	-1.65	0.092	1.23	0.516
1451407_at	junction adhesion molecule 4	Jam4	-1.42	0.038	-1.01	0.823	1.18	0.679	1.25	0.767	1.2	0.389
1441335_at	RIKEN cDNA 4930474N05 gene	4930474N05Rik	-1.42	0.010	1.16	0.997	1.3	0.234	-1.04	0.807	1.22	0.661
1449910_at	RIKEN cDNA 2210418O10 gene	2210418O10Rik	-1.42	0.016	1.15	0.461	1.06	0.934	1.11	0.473	1.02	0.790
1416997_a_at	huntingtin-associated protein 1	Hap1	-1.43	0.014	-1.05	0.675	1.32	0.557	-1.1	0.145	1.06	0.459
1428771_at	RIKEN cDNA 2410127E18 gene	2410127E18Rik	-1.43	0.036	-1.17	0.209	-1.26	0.066	1.06	0.655	-1.07	0.568
1457074_at	kinesin family member 24	Kif24	-1.44	0.029	-1.29	0.379	1.57	0.883	1.06	0.948	-1.24	0.312
1418668_at	acyl-CoA synthetase medium-chain family member 1	Acsm1	-1.44	0.031	-1.38	0.347	1.14	0.782	-1.37	0.217	-1.26	0.468
1439124_at	RIKEN cDNA 9530020G05 gene	9530020G05Rik	-1.44	0.023	-1.51	0.026	-1.48	0.118	1.12	0.660	1.38	0.231
1428284_at	RIKEN cDNA 8430427H17 gene	8430427H17Rik	-1.44	0.033	-1.22	0.121	-1.01	0.620	-1.08	0.492	-1.16	0.169

1455562_at	SRY-box containing gene 12	Sox12	-1.45	0.017	-1.17	0.147	1.07	0.488	-1.41	0.087	-1.09	0.136
1433930_at	Heparanase	Hpse	-1.45	0.045	-1.65	0.041	-1.54	0.157	2.33	0.506	2.9	0.101
1418508_a_at	growth factor receptor bound protein 2	Grb2	-1.45	0.044	-1.28	0.019	1.17	0.510	-1.3	0.026	1.12	0.447
1457020_at	GC-rich promoter binding protein 1-like 1	Gpbp1l1	-1.45	0.007	-1.41	0.243	2.7	0.173	1.05	0.682	1.74	0.067
1448744_at	galactosamine (N-acetyl)-6-sulfate sulfatase	Galns	-1.45	0.024	-1.42	0.084	1.12	0.160	1.04	0.315	1.09	0.353
1421280_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	Gabra1	-1.45	0.037	1.65	0.813	1.66	0.247	3.74	0.007	-1.16	0.395
1415994_at	cytochrome P450, family 2, subfamily e, polypeptide 1	Cyp2e1	-1.45	0.006	1.35	0.482	-1.46	0.116	-1.2	0.384	-1.32	0.182
1459054_at	cDNA sequence BC035954	BC035954	-1.45	0.034	-1.17	0.430	1.2	0.726	1	0.918	1.17	0.311
1460099_at	ATPas, class II, type 9B	Atp9b	-1.45	0.021	1.04	0.903	1.27	0.682	1.53	0.799	-1.28	0.272
1451116_at	acetoacetyl-CoA synthetase	Aacs	-1.45	0.028	-1.87	0.024	1.37	0.459	1.02	0.749	1.21	0.579
1431965_at	RIKEN cDNA 4933411E08 gene	4933411E08Rik	-1.45	0.003	-1.06	0.450	-1.31	0.195	-1.21	0.398	1.17	0.419
1438302_at	HCF-binding transcription factor Zhangfei	Zf	-1.46	0.012	-1.17	0.298	-1.07	0.580	1.01	0.967	1.63	0.652
1417362_at	Rhesus blood group-associated C glycoprotein	Rhcg	-1.46	0.015	1.46	0.267	1.32	0.560	1.11	0.767	1.34	0.413
1419498_at	transmembrane and immunoglobulin domain containing 1	Tmigd1	-1.47	0.034	-1.29	0.319	-1.16	0.111	-1.72	0.097	1.52	0.862
1420353_at	lymphotoxin A	Lta	-1.47	0.005	-1.63	0.035	1.05	0.931	-1.03	0.749	1.11	0.884
1448437_a_at	GTP binding protein 2	Gtpbp2	-1.47	0.036	-1.73	0.049	-1.27	0.328	2.04	0.092	1.03	0.485
1425101_a_at	FK506 binding protein 6	Fkbp6	-1.47	0.020	1.02	0.875	-1.21	0.091	-1	0.748	2.89	0.424
1419715_at	RIKEN cDNA 1700029F12 gene	1700029F12Rik	-1.47	0.042	1.12	0.508	-1.22	0.308	-1.44	0.341	1.14	0.576
1423515_at	sodium channel, voltage-gated, type VIII, alpha	Scn8a	-1.48	0.021	1.25	0.747	-1.01	0.420	1.51	0.519	1.98	0.788
1459485_at	Neogenin	Neo1	-1.48	0.040	-1	0.968	1.02	0.867	1.41	0.986	1.11	0.764
1449999_a_at	calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	-1.48	0.015	-2.16	0.018	-1.13	0.553	1	0.916	-1.3	0.076
1432293_at	RIKEN cDNA 4930579G18 gene	4930579G18Rik	-1.48	0.050	1.09	0.916	1.27	0.283	1.56	0.347	1.16	0.696
1428955_x_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulat	Slc9a3r2	-1.49	0.035	-1.29	0.222	1.85	0.366	1.06	0.956	1.41	0.261
1423278_at	protein tyrosine phosphatase, receptor type, K	Ptprk	-1.49	0.031	-2.67	0.015	-2.26	0.030	-2.01	0.007	-2.16	0.014
1442680_at	Neural cell adhesion molecule 1	Ncam1	-1.49	0.018	-1.61	0.114	-1.41	0.049	-1.97	0.043	-1.62	0.158
1444152_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	-1.49	0.015	-1.88	0.080	2.82	0.473	-1.23	0.294	1.21	0.995
1427016_at	RIKEN cDNA 4932438A13 gene /// similar to CG4841-PA	4932438A13Rik /// LOC6	-1.49	0.016	-1.91	0.029	-1.19	0.136	-1.22	0.270	-1.63	0.031
1417717_a_at	tyrosinase	Tyr	-1.5	0.012	-1.14	0.365	1.17	0.740	1.02	0.964	1.38	0.047
1456353_at	suppressor of Ty 4 homolog 1 (S. cerevisiae)	Supt4h1	-1.5	0.026	-1.35	0.327	1.52	0.319	1.53	0.062	1.72	0.193
1455030_at	protein tyrosine phosphatase, receptor type, J	Ptprj	-1.5	0.018	-2.07	0.027	-1.36	0.207	-1.54	0.024	-1.88	0.004
1431724_a_at	purinergic receptor P2Y, G-protein coupled 12	P2ry12	-1.5	0.007	-1.16	0.452	-1.11	0.383	-1.58	0.052	-1.01	0.692
1442334_at	PRAME family member LOC545693	MGC118150	-1.5	0.032	1.45	0.870	-1.14	0.226	-1.39	0.207	1.28	0.217
1458780_at	DNA segment, Chr 8, ERATO Doi 620, expressed	D8Ertd620e	-1.5	0.006	-1.04	0.660	-1.55	0.201	3.35	0.051	-1.09	0.489
1453793_at	RIKEN cDNA 1700026J12 gene	1700026J12Rik	-1.5	0.019	1.02	0.836	-1.2	0.257	-1.04	0.505	1.71	0.396
1432662_at	RIKEN cDNA 0610042E11 gene	0610042E11Rik	-1.5	0.016	1.23	0.804	1.31	0.699	2.08	0.257	-1.21	0.550
1446536_at	sema domain, transmembrane domain (TM), and cytoplasmic domain,	Sema6d	-1.51	0.033	1.09	0.596	-1.14	0.556	1.14	0.740	-1.02	0.653
1437877_at	coiled-coil domain containing 39 /// tetratricopeptide repeat domain 14	Ccdc39 /// Ttc14	-1.51	0.004	-1.13	0.511	1.24	0.238	1.45	0.109	1.08	0.638
1436117_at	RIKEN cDNA A830010M20 gene	A830010M20Rik	-1.51	0.049	-1.15	0.516	1.23	0.510	1.16	0.373	1.42	0.369
1432688_at	RIKEN cDNA 4631422I05 gene	4631422I05Rik	-1.51	0.036	1.35	0.388	1.05	0.724	1.58	0.836	1.18	0.834
1447353_at	G protein-coupled receptor 161	Gpr161	-1.52	0.028	-1.23	0.415	1.27	0.890	1.17	0.730	1.13	0.417
1437129_at	RIKEN cDNA E330018D03 gene	E330018D03Rik	-1.52	0.039	-1.4	0.126	-1.19	0.170	-1	0.745	1.03	0.956

1419756_at	diacylglycerol kinase, gamma	Dgkg	-1.52	0.046	-1.06	0.530	-1.12	0.361	-1.07	0.419	1.01	0.654
1416772_at	carnitine palmitoyltransferase 2	Cpt2	-1.52	0.019	-1.49	0.008	1.2	0.491	-1.12	0.245	1.33	0.519
1453417_at	RIKEN cDNA 4933407K13 gene	4933407K13Rik	-1.52	0.026	-1.15	0.089	1.92	0.004	1.41	0.376	1.46	0.633
1443303_at	RIKEN cDNA 4930521E07 gene	4930521E07Rik	-1.52	0.014	-1.22	0.338	-1.18	0.344	1.13	0.700	-1.25	0.143
1429524_at	myosin IF	Myo1f	-1.53	0.045	-1.08	0.649	1.49	0.669	1.4	0.903	-1.11	0.815
1418833_at	alanine-glyoxylate aminotransferase	Agxt	-1.53	0.033	1.05	0.912	1.46	0.906	1.25	0.511	-1.05	0.467
1422856_at	solute carrier family 12, member 3	Slc12a3	-1.54	0.036	-1.13	0.535	1.2	0.241	-1.25	0.315	-1.09	0.513
1441897_at	RIKEN cDNA B230120H23 gene	B230120H23Rik	-1.54	0.048	-1.76	0.101	1.36	0.316	-1.3	0.016	1	0.957
1448120_at	growth differentiation factor 9	Gdf9	-1.55	0.036	-1.02	0.912	1.23	0.869	1.34	0.727	1.17	0.442
1433435_at	expressed sequence AW551984	AW551984	-1.55	0.030	2.01	0.059	-1.36	0.112	1	0.541	-1.54	0.186
1455473_at	ubiquitin specific peptidase 13 (isopeptidase T-3)	Usp13	-1.56	0.039	-1.55	0.148	-1.54	0.034	-1.37	0.114	1.1	0.913
1458549_at	LOC436015	LOC436015	-1.56	0.050	-1.05	0.545	1.62	0.862	-1.04	0.491	1.64	0.148
1432949_at	RIKEN cDNA 5330421F21 gene	5330421F21Rik	-1.56	0.014	-1.09	0.361	1.17	0.474	1.16	0.803	1.02	0.891
1431458_at	RIKEN cDNA 4921507L20 gene	4921507L20Rik	-1.56	0.023	-1.11	0.487	1.3	0.406	-2.52	0.017	1.36	0.436
1457129_at	Zinc finger protein 458	Zfp458	-1.57	0.044	-1.09	0.546	1.13	0.959	1.26	0.474	1.03	0.783
1426430_at	jagged 2	Jag2	-1.57	0.008	-1.12	0.415	1.64	0.021	1.12	0.813	1.22	0.697
1450063_at	formin 2	Fmn2	-1.57	0.024	-2.47	0.003	-1.77	0.006	-1.48	0.012	-1.74	0.007
1446729_at	dispatched homolog 2 (Drosophila)	Disp2	-1.57	0.045	-1.15	0.229	1.64	0.974	1.42	0.405	2.01	0.040
1453750_x_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-1.58	0.042	-2.56	0.003	-1.32	0.190	-1.41	0.089	-1.71	0.038
1440702_at	expressed sequence AU022297	AU022297	-1.58	0.033	-1.37	0.056	-1.08	0.568	1.43	0.307	1.31	0.857
1420015_s_at	palmitoyl-protein thioesterase 1	Ppt1	-1.59	0.011	-1.36	0.011	1.11	0.920	-1.09	0.357	1.14	0.918
1427494_at	homeo box B7 /// homeo box B8	Hoxb7 /// Hoxb8	-1.59	0.007	-1.53	0.230	-1.04	0.394	-1.44	0.305	3.58	0.060
1436785_a_at	RIKEN cDNA 1110069O07 gene	1110069O07Rik	-1.59	0.006	1.09	0.989	-1.86	0.036	-1.1	0.382	1.56	0.189
1449683_x_at	tubulin, beta 2b	Tubb2b	-1.6	0.014	1.34	0.449	-1.46	0.171	-1.06	0.773	1.2	0.307
1438241_at	RGM domain family, member A	Rgma	-1.6	0.034	-1.22	0.248	1.02	0.992	1.54	0.337	1.63	0.430
1422278_at	dopamine receptor 3	Drd3	-1.6	0.017	-1.6	0.047	1.2	0.800	-1.49	0.266	-1.03	0.607
1450210_at	bone morphogenetic protein 15	Bmp15	-1.6	0.045	-1.4	0.240	1.01	0.905	1.54	0.437	2.27	0.477
1444897_at	expressed sequence AU017263	AU017263	-1.6	0.032	1.02	0.759	-1.1	0.530	1.13	0.448	-1.21	0.509
1431501_at	RIKEN cDNA 1700037C18 gene	1700037C18Rik	-1.6	0.000	-2.23	0.045	1.16	0.631	2.54	0.455	1.53	0.183
1419012_at	zinc finger protein, multitype 2	Zfpm2	-1.61	0.041	-2.55	0.051	-1.24	0.019	-1.63	0.175	-1.98	0.070
1444435_at	vacuolar protein sorting 13B (yeast) /// similar to vacuolar protein sortin	Vps13b	-1.61	0.045	1.04	0.940	1.8	0.945	2.1	0.403	-1.02	0.919
1429309_at	PR domain containing 16	Prdm16	-1.61	0.031	-1	0.897	-1.76	0.151	2.27	0.186	1.02	0.921
1457662_x_at	thiamine pyrophosphokinase	Tpk1	-1.62	0.031	-1.61	0.116	-1.2	0.264	-1.74	0.064	-1.44	0.039
1444232_at	protein kinase, cGMP-dependent, type I	Prkg1	-1.62	0.014	-2.34	0.001	-1.58	0.011	-1.35	0.096	-1.77	0.016
1451623_at	mitochondrial ribosomal protein L15	Mrpl15	-1.63	0.025	1.01	0.826	-1.39	0.188	-1.04	0.597	1.48	0.682
1444993_at	similar to mortality factor 4 like 1 (predicted) /// similar to mortality facto	LOC664949 /// LOC6710	-1.63	0.017	-1.48	0.234	1.76	0.775	1.96	0.568	1.73	0.908
1434572_at	histone deacetylase 9	Hdac9	-1.63	0.028	-2.01	0.147	-1.2	0.318	1.38	0.759	-1.39	0.406
1446053_at	G patch domain and KOW motifs	Gpkow	-1.64	0.014	-1.15	0.250	-1.4	0.056	-1.36	0.232	-1.81	0.005
1449912_at	synovial sarcoma, X member B, breakpoint 1 /// similar to SSXB1 prote	Ssxb1 /// LOC631002	-1.65	0.032	-1.12	0.840	1.51	0.631	1.01	0.882	1.64	0.613
1421752_a_at	serine (or cysteine) peptidase inhibitor, clade B, member 5	Serpinb5	-1.65	0.003	-2.52	0.004	1.76	0.862	2.43	0.761	1	0.732
1427843_at	expressed sequence AI840826	AI840826	-1.65	0.017	-1.08	0.293	1.67	0.199	1.33	0.415	-1.07	0.645

1444697_at	RIKEN cDNA 4732490B19 gene	4732490B19Rik	-1.65	0.037	1.7	0.643	1.4	0.806	2.44	0.126	1.3	0.574
1431674_at	RIKEN cDNA 2610303G11 gene	2610303G11Rik	-1.65	0.034	1.3	0.580	1.81	0.427	1.49	0.901	1.41	0.692
1421225_a_at	solute carrier family 4 (anion exchanger), member 4	Slc4a4	-1.66	0.043	-3.08	0.060	-1.79	0.062	-2.13	0.070	-1.82	0.131
1437944_at	Src homology 2 domain-containing transforming protein C2	Shc2	-1.66	0.039	1.05	0.969	1.04	0.980	1.99	0.319	-1.44	0.148
1422342_at	neuromedin B receptor	Nmbr	-1.66	0.028	1.27	0.688	1.14	0.763	1.2	0.721	1.07	0.477
1429841_at	multiple EGF-like-domains 10	Megf10	-1.66	0.022	-2.13	0.020	1.22	0.769	-1.87	0.023	-1.41	0.127
1422270_a_at	interleukin 6 receptor, alpha	Il6ra	-1.66	0.029	-1.32	0.226	1.09	0.425	-1.09	0.306	1.27	0.852
1418268_at	5-hydroxytryptamine (serotonin) receptor 3A	Htr3a	-1.67	0.013	1.23	0.807	-1.01	0.782	1.46	0.196	1.72	0.236
1421725_at	solute carrier family 26, member 5	Slc26a5	-1.68	0.018	1.71	0.342	1.31	0.516	2.93	0.175	2.81	0.065
1459829_x_at	CDNA sequence BC031781	BC031781	-1.68	0.024	-1.22	0.311	1.18	0.042	1.42	0.826	-1.1	0.589
1458116_at	RIKEN cDNA 9530079D04 gene	9530079D04Rik	-1.68	0.024	1.06	0.673	-1.51	0.076	2.99	0.039	-1.61	0.176
1430624_at	RIKEN cDNA 4921511M17 gene /// hypothetical LOC434874 /// hypoth	4921511M17Rik /// LOC4	-1.68	0.039	1.49	0.785	1.25	0.685	1.02	0.646	1.84	0.842
1426175_a_at	tryptase alpha/beta 1	Tpsab1	-1.69	0.000	1.23	0.448	-1.23	0.442	1.71	0.391	1.18	0.776
1457177_at	RAR-related orphan receptor alpha	Rora	-1.69	0.018	-1.47	0.240	1.46	0.864	-1.17	0.373	-1.9	0.051
1443907_at	leucyl/cystinyl aminopeptidase	Lnpep	-1.69	0.020	-1.31	0.228	1.05	0.975	-1.09	0.466	1.25	0.291
1447209_at	Forkhead box P1	Foxp1	-1.69	0.025	-1.8	0.103	-1.41	0.200	1.1	0.493	-1.48	0.169
1441255_at	cadherin 3	Cdh3	-1.69	0.014	-1.37	0.121	-1.19	0.169	-1.15	0.374	2.15	0.825
1421210_at	class II transactivator	C2ta	-1.69	0.042	-2.02	0.020	-1.31	0.202	1.08	0.485	-1	0.921
1432990_at	RIKEN cDNA 5830495A06 gene	5830495A06Rik	-1.69	0.024	-1.31	0.442	2.13	0.122	-1.46	0.292	2.42	0.566
1458158_at	WD repeat domain 67	Wdr67	-1.7	0.029	1.3	0.415	2.04	0.006	-1.02	0.650	1.79	0.504
1459641_at	Proteasome (prosome, macropain) subunit, beta type 2	Psmb2	-1.7	0.014	-1.38	0.228	1.89	0.135	1.48	0.243	1.3	0.364
1418989_at	cathepsin E	Ctse	-1.7	0.049	-1.15	0.557	-1.21	0.334	-1.15	0.452	1.13	0.034
1451029_at	Bcl2-like 2	Bcl2l2	-1.7	0.050	1.35	0.885	2.07	0.281	2.4	0.138	3.02	0.345
1442202_at	RIKEN cDNA 6430706D22 gene	6430706D22Rik	-1.7	0.033	-1.16	0.565	1.16	0.731	-1.03	0.560	-1.11	0.842
1432180_at	RIKEN cDNA 4933403G17 gene	4933403G17Rik	-1.7	0.042	-1.05	0.449	-1.23	0.362	2.5	0.159	1.05	0.811
1432813_at	RIKEN cDNA 2900064F13 gene	2900064F13Rik	-1.7	0.032	-1.49	0.289	-1.04	0.483	1.21	0.986	1.42	0.975
1429809_at	transmembrane and tetratricopeptide repeat containing 2	Tmtc2	-1.71	0.039	-3.89	0.037	-1.84	0.000	-1.63	0.044	-2	0.061
1430818_at	transmembrane channel-like gene family 1	Tmc1	-1.71	0.049	-1.43	0.212	3.33	0.106	1.17	0.720	1.73	0.175
1438616_x_at	seminal vesicle secretion 5	Svs5	-1.71	0.020	1.28	0.828	1.05	0.755	1.7	0.750	1.77	0.684
1438874_at	non-metastatic cells 7, protein expressed in	Nme7	-1.71	0.014	1.25	0.335	1.41	0.781	1.47	0.315	1.09	0.426
1433019_at	RIKEN cDNA 4833419G08 gene	4833419G08Rik	-1.71	0.043	-1.08	0.962	1.15	0.652	1.29	0.886	2.58	0.276
1419526_at	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	Fgr	-1.72	0.003	-1.31	0.300	-1.34	0.196	1.23	0.710	1.12	0.662
1432575_at	RIKEN cDNA 4930548F15 gene	4930548F15Rik	-1.72	0.026	1.18	0.811	-1.13	0.577	1.66	0.192	-1.29	0.194
1440409_at	RIKEN cDNA 2210401J11 gene	2210401J11Rik	-1.72	0.015	1.05	0.709	1.43	0.265	1.92	0.547	2.83	0.313
1448062_at	serine/threonine kinase 11	Stk11	-1.73	0.013	-1.53	0.272	1.33	0.661	1.21	0.701	-1.37	0.466
1422590_at	cyclin-dependent kinase 5	Cdk5	-1.73	0.020	-1.45	0.054	1.63	0.020	-1.09	0.370	-1.07	0.731
1456629_at	ankyrin repeat domain 47	Ankrd47	-1.73	0.025	1.14	0.879	1.43	0.870	1.52	0.407	1.81	0.124
1454063_at	RIKEN cDNA 4933412E24 gene	4933412E24Rik	-1.73	0.030	1.33	0.607	1.11	0.420	1.59	0.263	1.28	0.937
1432752_at	RIKEN cDNA 4930403O18 gene	4930403O18Rik	-1.73	0.038	-1.11	0.746	1.31	0.534	-1.3	0.197	1.54	0.006
1436094_at	VGF nerve growth factor inducible	Vgf	-1.74	0.008	-1.73	0.244	-1.27	0.601	1.44	0.790	-1.02	0.826
1426196_at	Immunoglobulin heavy chain 1a (serum IgG2a)	Igh-1a	-1.74	0.015	-1.5	0.175	1.56	0.716	3.44	0.159	1.74	0.208

1445117_at	Glycosyltransferase 28 domain containing 1	Glt28d1	-1.74	0.033	-1.65	0.088	1.55	0.716	-1.38	0.308	2.19	0.037
1445677_x_at	solute carrier family 35, member F2	Slc35f2	-1.75	0.036	-1.62	0.103	1.11	0.933	-1.56	0.233	-1.25	0.266
1452878_at	protein kinase C, epsilon	Prkce	-1.75	0.015	-5.11	0.011	-1.19	0.204	-1.78	0.034	-1.69	0.021
1439729_at	RIKEN cDNA A930038B10 gene	A930038B10Rik	-1.75	0.041	1.27	0.755	1.01	0.550	1.62	0.461	1.94	0.478
1454262_at	RIKEN cDNA 1700124P09 gene	1700124P09Rik	-1.75	0.025	1.67	0.891	1.19	0.536	1.13	0.493	1.98	0.531
1451699_at	similar to putative retrovirus-related gag protein /// hypothetical protein	LOC668468 /// LOC6686	-1.76	0.040	-1.6	0.033	-1.01	0.626	1.18	0.305	-1.05	0.521
1445751_at	Procollagen, type XII, alpha 1	Col12a1	-1.76	0.015	1.34	0.666	-1.59	0.229	1.19	0.302	2.06	0.502
1450168_at	ankyrin repeat domain 12	Ankrd12	-1.76	0.013	-1.32	0.428	-1.5	0.253	1.18	0.799	-1.19	0.364
1435510_at	protein phosphatase 1H (PP2C domain containing)	Ppm1h	-1.77	0.015	1.09	0.808	-1.65	0.113	-1.36	0.319	1.33	0.503
1442814_at	Glucocorticoid induced transcript 1	Glcci1	-1.77	0.031	-1.11	0.559	-1.06	0.514	2.44	0.205	1.97	0.617
1439002_s_at	chorionic somatomammotropin hormone 1	Csh1	-1.77	0.036	1.6	0.451	-1.58	0.098	1.94	0.435	1.52	0.994
1430200_at	RIKEN cDNA 4930579D07 gene	4930579D07Rik	-1.77	0.045	-1.27	0.177	-1.15	0.239	1.52	0.659	3.02	0.109
1454784_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	Hs3st2	-1.78	0.039	1	0.825	-1.06	0.866	1.02	0.603	1.54	0.281
1438801_at	dynamin 3	Dnm3	-1.78	0.031	-1.65	0.017	1.17	0.407	-1.73	0.065	-1.4	0.106
1436397_at	cDNA sequence BC027057	BC027057	-1.78	0.040	1.28	0.490	-1.33	0.282	1.26	0.951	1.83	0.151
1447663_at	A kinase (PRKA) anchor protein 13	Akap13	-1.78	0.047	-1.66	0.166	1.01	0.970	-1.18	0.457	1.82	0.445
1453076_at	RIKEN cDNA 9130211I03 gene	9130211I03Rik	-1.78	0.044	-1.45	0.291	1.76	0.981	1.3	0.802	-1.09	0.316
1429742_at	regulator of chromosome condensation (RCC1) and BTB (POZ) domai	Rcbtb2	-1.79	0.049	-1.37	0.169	1.07	0.789	-1.24	0.384	1.66	0.359
1444078_at	CD8 antigen, alpha chain /// similar to T-cell surface glycoprotein CD8	Cd8a /// LOC636147 /// L	-1.79	0.029	1.02	0.959	-1.11	0.387	1.12	0.139	1.24	0.248
1429197_s_at	RAB GTPase activating protein 1-like	Rabgap1l	-1.8	0.008	-2.32	0.006	-1.41	0.160	-1.5	0.005	-1.61	0.052
1421656_at	sprouty homolog 2 (Drosophila)	Spry2	-1.81	0.010	-1.04	0.881	1.44	0.364	2.76	0.103	1.25	0.435
1434308_at	solute carrier family 43, member 2	Slc43a2	-1.81	0.012	-1.04	0.532	1.25	0.819	1.38	0.119	1.34	0.360
1453354_at	NADH dehydrogenase (ubiquinone) Fe-S protein 1	Ndufs1	-1.81	0.048	-1.57	0.202	1.05	0.842	1.04	0.633	2.56	0.173
1437876_at	fibronectin type III domain containing 6	Fndc6	-1.81	0.047	1.11	0.993	2.42	0.384	1.57	0.935	1.42	0.298
1458716_at	dual specificity phosphatase 27 (putative)	Dusp27	-1.81	0.036	1.56	0.540	2.25	0.001	2.85	0.561	2.06	0.195
1418959_at	transmembrane protease, serine 5 (spinesin)	Tmprss5	-1.82	0.019	1.7	0.294	-1.13	0.410	1.37	0.879	1.64	0.214
1439318_at	microtubule associated serine/threonine kinase family member 4	Mast4	-1.82	0.036	-1.56	0.124	1.03	0.537	-1.07	0.770	1.14	0.979
1455540_at	carbamoyl-phosphate synthetase 1	Cps1	-1.82	0.026	-2.72	0.068	1.27	0.432	-2.13	0.029	1.46	0.460
1453691_at	RIKEN cDNA 4921528I07 gene	4921528I07Rik	-1.82	0.047	1.22	0.188	1.01	0.997	-1.64	0.136	-1.03	0.661
1426007_a_at	UBX domain containing 3	Ubxd3	-1.83	0.003	-1.53	0.152	-1.26	0.179	1.26	0.938	1.22	0.053
1458127_at	Cell adhesion molecule-related/down-regulated by oncogenes	Cdon	-1.83	0.033	-1.08	0.591	1.02	0.478	1.32	0.152	1.15	0.992
1452539_a_at	CD247 antigen	Cd247	-1.83	0.029	-1.46	0.162	1.07	0.445	-1.59	0.138	-1.14	0.298
1439759_x_at	RIKEN cDNA 2410078J06 gene	2410078J06Rik	-1.83	0.034	-1.42	0.230	1.24	0.931	-1.09	0.407	1.46	0.585
1453315_at	within bgcn homolog (Drosophila)	Wibg	-1.84	0.050	-1.42	0.266	1.99	0.152	1	0.493	-1.2	0.242
1418948_at	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus	Fscn3	-1.85	0.007	-1.07	0.540	1.14	0.612	-1.27	0.089	-1.97	0.040
1440754_at	Ankyrin repeat and KH domain containing 1	Ankhd1	-1.85	0.038	-1.56	0.227	1.75	0.878	-1.47	0.107	1.56	0.986
1447110_at	RIKEN cDNA 4921513D23 gene	4921513D23Rik	-1.85	0.015	-1.43	0.216	-1.32	0.363	1.38	0.264	1.53	0.065
1443515_at	RIKEN cDNA 1110032F04 gene	1110032F04Rik	-1.85	0.022	-1.37	0.212	-1.1	0.221	-1.08	0.271	1.14	0.614
1429577_at	IQ motif containing F4	Iqcf4	-1.86	0.030	-1.43	0.050	1.04	0.575	1.47	0.629	1.33	0.903
1459929_at	zinc finger protein 568	Zfp568	-1.87	0.030	-1.18	0.223	1.79	0.997	-1.71	0.077	1.19	0.795
1422081_at	kyphoscoliosis peptidase	Ky	-1.87	0.050	-1.42	0.245	2.02	0.636	-1.28	0.371	-1.03	0.550

1457579_at	DNA segment, Chr 11, ERATO Doi 717, expressed	D11Ertd717e	-1.87	0.031	-1.16	0.477	1.71	0.513	-1.79	0.103	1.42	0.436
1439642_at	RIKEN cDNA 5930403N24 gene	5930403N24Rik	-1.87	0.042	-1.06	0.672	-1.21	0.331	1.15	0.880	-1.2	0.442
1457239_at	Spleen tyrosine kinase	Syk	-1.88	0.022	-5.5	0.001	4.44	0.076	1.09	0.745	1.46	0.582
1437693_at	DNA segment, Chr 1, Pasteur Institute 1	D1Pas1	-1.88	0.020	-1.22	0.453	2.26	0.106	-1.41	0.265	-1.03	0.471
1432669_at	RIKEN cDNA 9030420N05 gene	9030420N05Rik	-1.88	0.020	1.12	0.915	1.58	0.318	1.18	0.736	-1.31	0.162
1447108_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	-1.89	0.000	-1.57	0.254	-1.06	0.784	2.3	0.295	1.87	0.718
1422276_at	pyrimidinergic receptor P2Y, G-protein coupled, 4	P2ry4	-1.89	0.046	1.19	0.302	1.14	0.904	1.92	0.075	2	0.179
1440586_at	RIKEN cDNA B430203I24 gene	B430203I24Rik	-1.89	0.031	-3.07	0.041	-1.74	0.111	3.59	0.832	-2.05	0.137
1456680_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (cor	B3gnt6	-1.89	0.025	-1.19	0.389	1.44	0.145	1	0.780	1.27	0.870
1456165_at	RIKEN cDNA 4921521F21 gene	4921521F21Rik	-1.89	0.028	-2.03	0.019	-1.12	0.448	-1.08	0.542	2.64	0.147
1427292_at	immunoglobulin lambda chain, variable 1	Igl-V1	-1.9	0.050	-3.15	0.016	1.08	0.664	2.86	0.435	2.85	0.005
1446542_at	acyl-CoA synthetase short-chain family member 2	Acss2	-1.9	0.045	-1.22	0.126	1.66	0.023	-1.13	0.256	1.76	0.498
1443592_at	expressed sequence AA617406	AA617406	-1.9	0.046	-1.31	0.273	2.12	0.602	1.05	0.883	1.11	0.942
1432933_at	RIKEN cDNA 4930429N05 gene	4930429N05Rik	-1.9	0.009	-1.54	0.274	1.02	0.997	1.15	0.896	2.08	0.108
1449887_at	RIKEN cDNA 2310010I16 gene	2310010I16Rik	-1.9	0.018	-1.15	0.400	1.31	0.472	1.6	0.750	1.99	0.880
1428751_at	Park2 co-regulated	Pacrg	-1.91	0.030	-1.66	0.072	-1.36	0.292	1.11	0.420	1.21	0.580
1458487_at	Kruppel-like factor 3 (basic) /// RIKEN cDNA C230096K16 gene	Klf3 /// C230096K16Rik	-1.91	0.042	1.26	0.535	1.27	0.874	-1.3	0.237	-1.01	0.703
1446513_at	A disintegrin-like and metallopeptidase (reprolysin type) with thrombos	Adamts19	-1.91	0.048	-1.01	0.735	1.93	0.532	-1.36	0.262	1.14	0.642
1427339_at	solute carrier family 30 (zinc transporter), member 2	Slc30a2	-1.93	0.038	-1.57	0.080	1.1	0.803	-1.04	0.479	-1.02	0.414
1428776_at	solute carrier family 10 (sodium/bile acid cotransporter family), membe	Slc10a6	-1.93	0.023	-1.21	0.459	1.1	0.889	-1.58	0.152	1.74	0.223
1439370_x_at	splicing factor 3b, subunit 5	Sf3b5	-1.93	0.025	-2.1	0.067	1.16	0.907	1.03	0.856	1.11	0.470
1457144_at	sodium channel, voltage-gated, type II, beta	Scn2b	-1.93	0.004	-1.37	0.383	1.63	0.884	-1.08	0.491	1.19	0.732
1438334_at	Dedicator of cyto-kinesis 2	Dock2	-1.93	0.036	-1.05	0.694	1.39	0.500	1.15	0.914	1.73	0.979
1446757_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	Sugt1	-1.94	0.041	-3.01	0.011	-1.02	0.863	1.95	0.129	-1.29	0.294
1440712_at	Poly(rC) binding protein 3	Pcbp3	-1.94	0.037	-1.14	0.345	1.16	0.920	1.7	0.842	-1.51	0.137
1445021_at	RIKEN cDNA 6030465E24 gene	6030465E24Rik	-1.94	0.022	-1.97	0.050	1.14	0.440	1.56	0.390	1.3	0.844
1451938_a_at	syntrophin, basic 1	Sntb1	-1.95	0.038	-1.01	0.700	1.09	0.606	-1.17	0.123	1.47	0.221
1440175_at	Epsin 2	Epn2	-1.95	0.049	-1.59	0.141	-1.42	0.224	1.69	0.879	-1.66	0.069
1444849_at	expressed sequence C76872	C76872	-1.95	0.032	-1.24	0.089	-1.06	0.545	1.05	0.957	1.15	0.626
1451614_a_at	amelogenin X chromosome	Amelx	-1.95	0.042	-1.51	0.167	-1.17	0.509	-2.41	0.014	1.6	0.954
1443274_at	RIKEN cDNA 4932435O22 gene	4932435O22Rik	-1.95	0.042	1.68	0.573	1.91	0.702	-1.02	0.585	1.1	0.566
1455737_at	RIKEN cDNA C030002B11 gene	C030002B11Rik	-1.96	0.021	1.25	0.825	3.02	0.085	1.2	0.876	2.13	0.011
1437833_at	latent transforming growth factor beta binding protein 3	Ltbp3	-1.97	0.039	-1.42	0.443	2.45	0.198	1.61	0.026	-1.29	0.472
1454152_a_at	G protein-coupled receptor kinase 2, groucho gene related (Drosophila	Gprk2l	-1.97	0.002	-1.53	0.139	2.03	0.812	1.23	0.118	1.99	0.540
1421244_at	estrogen receptor 1 (alpha)	Esr1	-1.97	0.015	1.18	0.875	1.19	0.672	1.41	0.968	1.73	0.498
1434755_at	coronin, actin binding protein, 2B	Coro2b	-1.97	0.038	-1.39	0.477	1.25	0.807	1.95	0.690	1.26	0.809
1432628_at	chromobox homolog 3 (Drosophila HP1 gamma)	Cbx3	-1.97	0.007	-1	0.770	1.25	0.563	1.28	0.554	1.35	0.094
1440770_at	B-cell leukemia/lymphoma 2	Bcl2	-1.97	0.018	-1.06	0.554	1.37	0.814	-1.03	0.428	2.29	0.758
1429358_at	RIKEN cDNA 4921533L14 gene	4921533L14Rik	-1.97	0.010	-1.55	0.201	2.26	0.145	1.53	0.768	1.44	0.798
1460611_at	expressed sequence C87499	C87499	-1.99	0.011	1.18	0.590	-1.67	0.201	1.02	0.636	2.94	0.635
1451261_s_at	expressed sequence AW049765	AW049765	-1.99	0.000	-1.28	0.335	1.68	0.875	1.28	0.831	3.51	0.297

1446230_at	Gene model 944, (NCBI)	Gm944	-2	0.031	1.28	0.316	1.69	0.768	1.17	0.580	2.6	0.260
1443552_at	RIKEN cDNA E230008N13 gene	E230008N13Rik	-2	0.001	1.11	0.887	1.21	0.844	3.18	0.279	-1.26	0.376
1443445_at	Diaphanous homolog 3 (Drosophila)	Diap3	-2	0.037	-1.25	0.420	1.03	0.517	1.32	0.215	1.08	0.971
1457766_at	WAP four-disulfide core domain 6A	Wfdc6a	-2.01	0.041	-1.68	0.086	1.32	0.596	1.73	0.684	-1.34	0.336
1437855_at	microtubule-associated protein 4	Mtap4	-2.01	0.011	-2.07	0.039	-1.06	0.748	-1.52	0.080	-1.48	0.144
1455833_at	expressed sequence AU041783	AU041783	-2.01	0.034	-1.58	0.059	-1.22	0.236	-1.03	0.848	1.1	0.831
1439355_at	Pleckstrin homology domain containing, family A member 5	Plekha5	-2.02	0.030	1.01	0.846	1.26	0.599	1.05	0.654	1.35	0.773
1457442_at	expressed sequence AW125324	AW125324	-2.02	0.009	-1.51	0.081	-1.12	0.438	-1.09	0.907	1.27	0.303
1449064_at	L-threonine dehydrogenase	Tdh	-2.03	0.047	-2.13	0.113	1.21	0.794	1.32	0.364	1.11	0.779
1417121_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 6	Gabra6	-2.03	0.012	-1.49	0.104	1.32	0.793	-1.21	0.109	1.15	0.653
1452135_at	glutathione peroxidase 6	Gpx6	-2.04	0.035	-1.49	0.384	-1.33	0.282	1.22	0.455	-1.02	0.512
1438160_x_at	solute carrier organic anion transporter family, member 4a1	Slco4a1	-2.05	0.030	1.19	0.909	1.65	0.792	2.27	0.007	-1.17	0.284
1459868_x_at	interleukin 11 receptor, alpha chain 1 /// interleukin 11 receptor, alpha c	Il11ra1 /// Il11ra2 /// LOC	-2.05	0.004	-1.58	0.160	1	0.522	1.51	0.068	-1.59	0.079
1420018_s_at	tetraspanin 8	Tspan8	-2.06	0.041	-1.26	0.378	-1.19	0.505	1.74	0.115	2.53	0.249
1444266_at	Homeobox only domain	Hod	-2.06	0.048	-1.66	0.153	-1.14	0.028	1.15	0.743	1.58	0.450
1440899_at	flavin containing monooxygenase 5	Fmo5	-2.06	0.044	-2.09	0.052	1.52	0.712	2.13	0.777	1.54	0.771
1430251_at	RIKEN cDNA D330022H12 gene	D330022H12Rik	-2.06	0.013	-1.29	0.352	1.28	0.429	-2.09	0.022	-1.61	0.192
1459491_at	DNA segment, Chr 12, ERATO Doi 673, expressed	D12Ertd673e	-2.06	0.019	1.02	0.944	-1.17	0.354	1.55	0.221	-2.28	0.038
1438364_x_at	angiogenin, ribonuclease A family, member 4	Ang4	-2.06	0.002	1.34	0.577	1.3	0.924	-1.45	0.232	2.04	0.492
1450810_at	follicle stimulating hormone receptor	Fshr	-2.07	0.022	1.21	0.865	2.06	0.757	1.4	0.758	1.13	0.937
1428118_at	leucine rich repeat neuronal 6A	Lrrn6a	-2.08	0.029	1.23	0.192	1.1	0.531	1.02	0.870	1.55	0.093
1430185_at	RIKEN cDNA 5830460E08 gene	5830460E08Rik	-2.08	0.019	-1.56	0.041	-1.01	0.985	1.47	0.843	-1.93	0.125
1448443_at	serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	-2.09	0.001	-3.42	0.005	2.14	0.536	2.54	0.667	1.23	0.611
1432981_at	mitogen-activated protein kinase kinase kinase 9	Map3k9	-2.09	0.045	-1.42	0.071	-1.23	0.420	1.02	0.743	-1.39	0.099
1449279_at	glutathione peroxidase 2	Gpx2	-2.09	0.031	1.02	0.900	1.23	0.493	1.39	0.500	-1.25	0.516
1426147_s_at	claudin 10	Cldn10	-2.09	0.017	-2.56	0.008	1.36	0.863	-1.32	0.279	1.11	0.898
1437590_at	RIKEN cDNA 4833409A17 gene	4833409A17Rik	-2.09	0.028	-1.24	0.497	1.97	0.321	1.42	0.766	-1.59	0.275
1458326_at	polymerase (RNA) II (DNA directed) polypeptide E	Polr2e	-2.1	0.031	-2.15	0.085	1.18	0.554	1.89	0.144	1.65	0.898
1424230_at	exocyst complex component 6	Exoc6	-2.1	0.003	-1.35	0.125	2.38	0.547	1.04	0.877	-1.04	0.790
1432771_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3	Slc9a3	-2.11	0.027	-1.44	0.157	-1.19	0.389	1.54	0.801	1.58	0.497
1442009_at	eukaryotic translation initiation factor 2C, 3	Eif2c3	-2.11	0.048	-1.49	0.065	1.01	0.771	-1.6	0.167	1.98	0.514
1459949_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	Atp5s	-2.11	0.032	-1.2	0.478	-1.26	0.187	-1.03	0.976	1.09	0.669
1453204_at	RIKEN cDNA 4933431K14 gene	4933431K14Rik	-2.12	0.036	1.12	0.447	1.1	0.996	-1.38	0.105	1.67	0.765
1431191_a_at	synaptotagmin I	Syt1	-2.13	0.048	1.01	0.919	-1.35	0.162	-1.17	0.489	1.89	0.521
1425111_at	sortilin-related VPS10 domain containing receptor 3	Sorcs3	-2.13	0.013	1.61	0.228	1.12	0.981	-1.37	0.248	1.14	0.884
1456334_s_at	RIKEN cDNA A230106D06 gene	A230106D06Rik	-2.13	0.004	-1.92	0.094	1.06	0.713	1.83	0.467	-1.12	0.528
1434616_at	RIKEN cDNA 1810073N04 gene	1810073N04Rik	-2.13	0.019	1.32	0.752	-1.3	0.336	1.42	0.943	-1.21	0.405
1438099_at	triple functional domain (PTPRF interacting)	Trio	-2.14	0.003	-2.44	0.075	-2.59	0.074	1.9	0.917	1.25	0.523
1435155_at	cingulin	Cgn	-2.14	0.001	-1.51	0.138	1.05	0.730	-1.11	0.619	-1.56	0.032
1452050_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-2.14	0.028	-5.47	0.022	-1.24	0.338	-2.13	0.093	-3.12	0.002
1435627_x_at	MARCKS-like 1 /// similar to MARCKS-related protein (MARCKS-like p	Marcksl1 /// LOC673071	-2.15	0.043	-1.04	0.646	-1.12	0.706	-1	0.980	1.22	0.059

1418642_at	lymphocyte cytosolic protein 2	Lcp2	-2.15	0.004	-1.31	0.325	1.44	0.350	1.7	0.772	1.13	0.099
1441310_at	A disintegrin-like and metallopeptidase (reprolysin type) with thrombos	Adamts15	-2.15	0.006	-1.07	0.478	1.17	0.568	1.35	0.132	-1.14	0.532
1453892_at	RIKEN cDNA A930007I19 gene	A930007I19Rik	-2.15	0.011	-1.34	0.230	-1.68	0.190	2.77	0.610	1.08	0.680
1445171_at	RIKEN cDNA 1700067C01 gene /// RIKEN cDNA A230107C01 gene	1700067C01Rik /// A230	-2.15	0.048	1.74	0.770	1.83	0.884	1.37	0.631	1.77	0.956
1444514_at	RIKEN cDNA B930096F20 gene	B930096F20Rik	-2.16	0.021	-2.19	0.013	1.95	0.144	-1.49	0.028	2.05	0.284
1458307_at	RIKEN cDNA B230334C09 gene	B230334C09Rik	-2.16	0.036	1.33	0.458	-1.46	0.157	-1.73	0.016	2.26	0.712
1431276_at	RIKEN cDNA 9130019P16 gene	9130019P16Rik	-2.16	0.020	-1.02	0.737	1.06	0.788	-1.23	0.553	2.9	0.543
1454446_at	RIKEN cDNA 4930564B12 gene	4930564B12Rik	-2.17	0.046	-2.46	0.097	1.33	0.883	-1.58	0.225	2.73	0.142
1428601_at	RIKEN cDNA 1700003E16 gene	1700003E16Rik	-2.17	0.046	-1.55	0.191	1.08	0.430	-1.24	0.328	1.53	0.364
1457768_at	prune homolog (Drosophila)	Prune	-2.18	0.021	-1.12	0.572	1.44	0.985	1.17	0.660	1.19	0.803
1442079_at	transmembrane protein 23	Tmem23	-2.19	0.004	-1.34	0.292	-1.21	0.555	-1.54	0.239	-1.3	0.225
1432956_at	RIKEN cDNA 4930444K16 gene	4930444K16Rik	-2.19	0.005	-1.45	0.228	1.79	0.585	1.96	0.417	1.83	0.255
1456369_at	protection of telomeres 1	Pot1	-2.2	0.048	-1.41	0.258	1.18	0.754	1.7	0.500	3.52	0.098
1434582_at	DNA segment, Chr 14, ERATO Doi 171, expressed	D14Ertd171e	-2.2	0.031	-3.44	0.041	-2.08	0.048	-1.68	0.048	-2.95	0.032
1439188_at	cleavage and polyadenylation specific factor 6	Cpsf6	-2.2	0.009	-2.19	0.021	-1.05	0.575	-1.32	0.358	-1.57	0.186
1432449_at	RIKEN cDNA 4930564B18 gene	4930564B18Rik	-2.2	0.045	-1.97	0.045	-1.07	0.423	1.9	0.090	1.26	0.382
1436903_at	ubiquilin 3	Ubqln3	-2.21	0.038	-1.75	0.153	1.18	0.647	-1.42	0.142	1.02	0.768
1451443_at	nuclear factor I/X	Nfix	-2.21	0.022	-2.23	0.006	1.17	0.766	-1.83	0.149	1.28	0.414
1432106_at	RIKEN cDNA 6530403M18 gene	6530403M18Rik	-2.21	0.014	-2.2	0.027	1.06	0.494	-1.03	0.626	2.01	0.162
1445120_at	expressed sequence AU021977	AU021977	-2.22	0.016	-1.31	0.336	-1.33	0.418	1.42	0.461	-1.08	0.624
1455140_at	RIKEN cDNA A330068P14 gene	A330068P14Rik	-2.22	0.036	-1.03	0.832	2.17	0.098	1.3	0.648	-1.78	0.033
1425386_at	RIKEN cDNA 4833422F24 gene	4833422F24Rik	-2.22	0.048	-2	0.079	1.41	0.430	-1.15	0.474	-1.12	0.199
1433337_at	RIKEN cDNA 6720460K10 gene	6720460K10Rik	-2.23	0.021	-1.2	0.277	-1.49	0.093	-1.03	0.877	1.58	0.097
1458000_at	desmoglein 1 alpha	Dsg1a	-2.26	0.039	1.16	0.964	1.01	0.521	1.81	0.027	2.01	0.750
1453232_at	calreticulin 3	Calr3	-2.26	0.016	-1.39	0.128	2.14	0.951	-2.49	0.033	1.06	0.946
1454091_at	pregnancy-specific glycoprotein 21	Psg21	-2.27	0.001	1.05	0.974	1.11	0.661	-1.03	0.866	-1.24	0.123
1432501_at	RIKEN cDNA 1700092E16 gene	1700092E16Rik	-2.27	0.010	-1.49	0.162	1.95	0.307	1.33	0.406	-1.3	0.090
1432210_at	RIKEN cDNA 4933401H06 gene	4933401H06Rik	-2.28	0.032	-1.32	0.341	1.25	0.287	-1.23	0.454	1.14	0.550
1456868_at	RIKEN cDNA 2900073G15 gene	2900073G15Rik	-2.28	0.031	-1.12	0.494	-1.09	0.671	-2.16	0.018	-1.34	0.157
1446663_at	Calcium/calmodulin-dependent protein kinase II, delta	Camk2d	-2.29	0.022	1.09	0.891	1.57	0.364	-1.88	0.037	1.58	0.985
1432237_at	RIKEN cDNA 5730522E02 gene	5730522E02Rik	-2.29	0.003	-2.19	0.061	1.05	0.555	-1.3	0.303	-1	0.917
1437139_at	glycine receptor, alpha 1 subunit	Glra1	-2.3	0.013	-1.04	0.938	1.73	0.199	1.13	0.973	1.95	0.388
1456047_at	phospholipase A2, group IVB (cytosolic)	Pla2g4b	-2.32	0.004	-1.72	0.108	-1.14	0.417	1.15	0.546	1.14	0.919
1456183_at	oogenesin 4	Oog4	-2.32	0.031	1.13	0.662	-1.06	0.625	-1.1	0.549	-1.13	0.459
1447632_at	Fanconi anemia, complementation group C	Fancc	-2.32	0.048	-2.45	0.029	2.92	0.347	2.93	0.090	-1.01	0.703
1420669_at	aryl hydrocarbon receptor nuclear translocator 2	Arnt2	-2.33	0.001	-1.68	0.102	2.41	0.037	1.63	0.329	1.02	0.946
1435367_at	mitogen-activated protein kinase 4	Mapk4	-2.34	0.024	-1.73	0.184	-1.22	0.272	2.69	0.504	-1.23	0.500
1425181_at	SH3-domain GRB2-like (endophilin) interacting protein 1	Sgip1	-2.35	0.022	1.02	0.959	1.63	0.778	1.42	0.675	1.4	0.927
1422657_at	prolactin-like protein L	Prlpl	-2.37	0.044	-1.25	0.275	2.43	0.089	1.27	0.893	1.17	0.696
1445628_at	Rho GTPase activating protein 21	Arhgap21	-2.37	0.048	1.71	0.527	2.79	0.091	1.89	0.410	-1.18	0.275
1431984_at	RIKEN cDNA 1700007F19 gene	1700007F19Rik	-2.37	0.013	-1.1	0.572	-1.04	0.925	-1.41	0.177	1.82	0.722

1454467_at	similar to Vinculin CG3299-PA /// similar to Vinculin CG3299-PA	LOC668894 /// LOC6714	-2.38	0.039	-1.46	0.211	-1.04	0.842	-1.04	0.641	1.16	0.930
1457478_at	Spermatid perinuclear RNA binding protein	Strbp	-2.41	0.039	-1.83	0.010	-1.19	0.358	-1.45	0.130	-1.18	0.311
1427346_at	ovary testis transcribed /// similar to ovary testis transcribed /// similar t	Ott /// LOC434863 /// LO	-2.41	0.020	1.55	0.545	1.06	0.538	-1.79	0.082	1.04	0.943
1450462_at	corticotropin releasing hormone receptor 2	Crhr2	-2.42	0.002	1.17	0.334	1.12	0.912	3.19	0.555	1.39	0.533
1423639_at	histamine receptor H 2	Hrh2	-2.43	0.026	-1.16	0.857	-1.99	0.047	-1.52	0.088	4.28	0.257
1449631_at	Enolase 3, beta muscle	Eno3	-2.43	0.007	-1.66	0.074	1.89	0.337	-1.73	0.233	1.26	0.695
1447595_x_at	RIKEN cDNA 1810012K16 gene	1810012K16Rik	-2.43	0.039	1.27	0.255	-1.34	0.197	1.74	0.575	1.67	0.403
1442728_at	Nuclear autoantigenic sperm protein (histone-binding)	Nasp	-2.44	0.049	-1.9	0.104	1.34	0.146	-1.27	0.283	1.07	0.829
1457650_x_at	autophagy-related 4A (yeast) /// similar to Cysteine protease ATG4A (A	Atg4a /// LOC666476 ///	-2.44	0.002	-1.63	0.127	1.51	0.406	-1.08	0.364	1	0.945
1439564_at	RIKEN cDNA 1700090G07 gene	1700090G07Rik	-2.45	0.018	-2.64	0.036	-1.31	0.417	1.54	0.993	-1.17	0.526
1440610_at	CAS1 domain containing 1	Casd1	-2.46	0.035	-1.31	0.392	1.42	0.276	1.58	0.108	1.9	0.725
1453910_at	RIKEN cDNA 4930500A05 gene	4930500A05Rik	-2.47	0.016	-1.99	0.053	-1.31	0.313	-1.18	0.407	-1.01	0.477
1438358_x_at	prefoldin 5 /// prefoldin 5 pseudogene	Pfdn5 /// LOC434860	-2.49	0.044	-1.63	0.069	-1.28	0.231	1.85	0.143	1.67	0.556
1417597_at	CD28 antigen	Cd28	-2.5	0.002	1.17	0.477	1.08	0.374	-1.59	0.213	2.43	0.369
1457495_at	RIKEN cDNA 2900052N01 gene	2900052N01Rik	-2.5	0.023	-1.01	0.972	2.59	0.198	1.47	0.896	1.29	0.273
1431809_at	RIKEN cDNA 4932442L08 gene	4932442L08Rik	-2.53	0.035	-1.27	0.285	-1.41	0.215	1.82	0.801	1.39	0.248
1459500_at	expressed sequence C85351	C85351	-2.54	0.049	-1.47	0.205	1.42	0.412	1.61	0.048	1.49	0.721
1420778_at	taste receptor, type 1, member 3	Tas1r3	-2.55	0.041	-2.34	0.045	-1.33	0.398	-1.53	0.323	1.52	0.875
1449166_at	S100 calcium binding protein A14	S100a14	-2.55	0.047	-1.26	0.388	1.3	0.654	-1.43	0.259	1.27	0.501
1454400_at	RIKEN cDNA 4632432E15 gene	4632432E15Rik	-2.55	0.009	1.38	0.867	2.02	0.593	1.84	0.891	2.29	0.176
1431168_at	Six3 opposite strand transcript 1	Six3os1	-2.56	0.026	-2.56	0.090	1.54	0.430	1.26	0.742	1.44	0.907
1445567_at	Growth associated protein 43	Gap43	-2.56	0.011	-1.2	0.565	1.2	0.929	1.16	0.753	-1.06	0.608
1455782_at	sterile alpha motif domain containing 7	Samd7	-2.57	0.003	-1.67	0.235	1.66	0.086	2.03	0.499	1.48	0.537
1447841_x_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	-2.58	0.029	-2.34	0.130	2.8	0.436	2.83	0.817	-1.31	0.213
1428964_at	solute carrier family 25 (mitochondrial carrier), member 18	Slc25a18	-2.61	0.032	-1.84	0.002	1.43	0.488	1.21	0.436	1.26	0.721
1441074_at	Ewing sarcoma breakpoint region 1	Ewsr1	-2.67	0.021	-1.07	0.591	-1.34	0.301	1.4	0.941	-1.17	0.316
1439333_at	potassium channel, subfamily V, member 1	Kcnv1	-2.68	0.007	-2.55	0.014	1.56	0.926	2.87	0.001	1.21	0.921
1443369_at	cDNA sequence BC052055	BC052055	-2.69	0.006	-1.14	0.340	1.74	0.763	1.29	0.864	1.07	0.349
1444404_at	RIKEN cDNA 330010C22 gene	D330010C22Rik	-2.71	0.007	-1.27	0.297	-1.21	0.050	1.71	0.833	-1.17	0.318
1446135_at	RIKEN cDNA D030051J21 gene	D030051J21Rik	-2.74	0.034	-1.42	0.266	-1.02	0.603	-1.13	0.362	-1.02	0.578
1430852_at	RIKEN cDNA 1600029I14 gene	1600029I14Rik	-2.76	0.044	-1.2	0.393	1.27	0.321	-1.1	0.392	1.01	0.968
1458800_at	Trinucleotide repeat containing 6C	Tnrc6c	-2.77	0.031	1.23	0.745	1.25	0.391	1.38	0.502	1.36	0.832
1422899_at	solute carrier family 6 (neurotransmitter transporter), member 20	Slc6a20	-2.77	0.014	-1.82	0.083	1.41	0.796	1.45	0.629	2.26	0.203
1456247_x_at	proteolipid protein 2 /// similar to Proteolipid protein 2 /// similar to Prote	Plp2 /// LOC620648 /// L	-2.78	0.035	-1.4	0.145	-1.01	0.323	1.79	0.408	2.5	0.976
1448094_at	hypothetical LOC546100	LOC546100	-2.79	0.026	1.26	0.981	2.13	0.480	2.37	0.840	1.03	0.685
1436901_at	Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enrich	Notch4	-2.81	0.041	-1.27	0.233	1.1	0.442	-1.14	0.672	1.6	0.414
1416098_at	synaptogyrin 3	Syngr3	-2.9	0.021	-1.6	0.120	2.06	0.806	2.92	0.132	2.51	0.305
1454207_at	RIKEN cDNA C430039J16 gene	C430039J16Rik	-2.91	0.017	-1.06	0.443	1.29	0.878	1.45	0.254	1.02	0.641
1442930_at	expressed sequence AW061147	AW061147	-2.91	0.012	1.38	0.492	3.03	0.119	2.78	0.237	1.34	0.600
1418990_at	membrane-spanning 4-domains, subfamily A, member 4D	Ms4a4d	-2.94	0.015	-1.06	0.706	2.24	0.125	1.81	0.192	-1.06	0.485
1454360_at	RIKEN cDNA 4930418C01 gene	4930418C01Rik	-2.94	0.006	-1.08	0.673	2.22	0.014	-1.37	0.153	1.13	0.579

1425880_x_at	zinc finger protein 352	Zfp352	-2.99	0.011	-2.2	0.018	-1.35	0.322	1.44	0.564	2.24	0.915
1430506_at	RIKEN cDNA 8430406P12 gene	8430406P12Rik	-2.99	0.014	-1.29	0.458	1.46	0.535	1.06	0.864	-1.13	0.414
1440094_at	cDNA sequence BC030870	BC030870	-3.07	0.021	-2.84	0.018	1.96	0.528	2.1	0.698	-1.54	0.151
1442950_at	Neuregulin 3	Nrg3	-3.11	0.004	-1.54	0.123	1.43	0.406	1.71	0.278	-1.29	0.396
1431534_at	protein kinase C and casein kinase substrate in neurons 3	Pacsin3	-3.16	0.037	-1.71	0.184	2.37	0.122	-1.27	0.352	-1.16	0.542
1435217_at	hypothetical protein LOC666185 /// hypothetical protein LOC666222 ///	LOC666185 /// LOC6662	-3.21	0.048	-1.03	0.717	1.03	0.338	2.6	0.103	2.16	0.392
1453408_s_at	RIKEN cDNA 4930519G04 gene	4930519G04Rik	-3.26	0.037	-1.79	0.161	1.35	0.778	-1.32	0.173	1.17	0.955
1457912_at	RIKEN cDNA E130317F20 gene	E130317F20Rik	-3.29	0.002	-1.3	0.240	1.09	0.574	1.02	0.757	2.48	0.294
1427761_at	prion protein interacting protein 1	Prnpip1	-3.31	0.031	-1.5	0.241	1.92	0.516	2.06	0.287	1.41	0.804
1459971_at	Potassium channel, subfamily T, member 2	Kcnt2	-3.31	0.007	-3.11	0.014	1.36	0.980	1.02	0.837	1.6	0.953
1434553_at	transmembrane protein 56	Tmem56	-3.32	0.042	-1.96	0.147	1.19	0.873	2.05	0.667	2.02	0.145
1419724_at	ectodysplasin-A receptor /// similar to Tumor necrosis factor receptor su	Edar /// LOC669001	-3.33	0.021	-2.56	0.045	1.54	0.985	2.9	0.360	-1.47	0.251
1439395_at	RIKEN cDNA 9630025I21 gene	9630025I21Rik	-3.35	0.013	-2.25	0.122	-1.05	0.916	1.94	0.502	-1.11	0.359
1438103_at	protocadherin gamma subfamily C, 4	Pcdhgc4	-3.53	0.031	-2.22	0.114	-1.13	0.661	2.19	0.360	1.32	0.648
1431544_at	RIKEN cDNA 4930524B17 gene	4930524B17Rik	-3.59	0.004	-1.41	0.128	-2.78	0.047	1.33	0.410	2.67	0.231
1443754_x_at	Limbic system-associated membrane protein	Lsamp	-3.62	0.020	-2.48	0.073	4.05	0.563	1.76	0.612	3.77	0.528
1438122_at	RIKEN cDNA 2900006K08 gene	2900006K08Rik	-3.67	0.011	-1.16	0.571	1.31	0.574	1.2	0.757	1.75	0.897
1437418_at	---	---	-4.73	0.004	-2.04	0.090	1.42	0.659	1.97	0.442	-1.72	0.196

Supplementary table 2. List of significant expression profiles of wt cells irradiated with 4J/m2 of UV (gray color) as compared to non-irradiated wt controls

code	Gene Title	Symbol	WT_0.6J/m2	p	WT_4J/m2	p	XPA_0.6J/m2	p	CSB_0.6J/m2	p	DKO_0.6J/m2	p
1452552_at	neoplastic progression 2	Npn2	2.01	0.566	11.69	0.000	3.34	0.102	7.33	0.002	3.96	0.024
1425416_s_at	proline/serine-rich coiled-coil 1	Psrc1	10.17	0.325	11.29	0.047	1.12	0.074	1.29	0.085	1.28	0.110
1452688_at	PRP39 pre-mRNA processing factor 39 homolog (yeast)	Prpf39	4.65	0.318	9.19	0.047	-1.09	0.631	1.17	0.132	1.06	0.796
1453760_at	mesoderm induction early response 1 homolog (Xenopus lae	Mier1	6.25	0.141	6.63	0.049	-1	0.929	1.01	0.868	1.09	0.830
1434959_at	desert hedgehog	Dhh	4.8	0.197	6.62	0.001	1.18	0.743	2.39	0.578	1.49	0.546
1432538_a_at	replication factor C (activator 1) 3	Rfc3	4.97	0.204	6.5	0.028	1.34	0.099	1.32	0.025	1.24	0.015
1424997_at	splicing factor, arginine/serine-rich 8	Sfrs8	6.48	0.122	6.27	0.045	1.32	0.410	1.11	0.562	1	0.767
1419234_at	helicase (DNA) B	Helb	4.19	0.085	6.26	0.025	1.47	0.031	1.31	0.058	1.28	0.386
1422292_at	RIKEN cDNA A030005K14 gene	A030005K14Rik	1.74	0.011	5.95	0.044	1.37	0.757	1.52	0.808	1.73	0.258
1429419_at	RIKEN cDNA 2310007A19 gene	2310007A19Rik	3.35	0.302	5.57	0.020	1.23	0.777	-1.02	0.501	2.7	0.504
1428784_at	Gem-interacting protein	Gmip	3.92	0.098	5.26	0.008	-1.04	0.741	1.58	0.163	1.2	0.180
1435373_at	casein kinase 1, epsilon	Csnk1e	5.06	0.217	5.22	0.045	-1.21	0.228	-1.25	0.082	1.11	0.680
1455241_at	cDNA sequence BC037703	BC037703	2.34	0.138	5.04	0.010	2.02	0.020	2.05	0.205	1.73	0.163
1454011_a_at	replication protein A2	Rpa2	4.17	0.273	4.99	0.007	1.09	0.455	1.3	0.013	1.13	0.222
1454857_at	ring finger protein 122	Rnf122	3	0.333	4.85	0.042	1.39	0.024	1.58	0.034	1.83	0.017
1426062_a_at	caspase 7	Casp7	5.88	0.227	4.83	0.026	4.19	0.126	1.03	0.898	1.25	0.543
1460007_at	thymocyte nuclear protein 1	Thyn1	5.82	0.231	4.81	0.037	1.5	0.207	2.84	0.077	1.59	0.434
1432294_at	RIKEN cDNA 9330177L23 gene	9330177L23Rik	3.04	0.193	4.75	0.035	2.39	0.858	1.59	0.719	1.45	0.662
1446979_at	Decapping enzyme, scavenger	Dcps	3.96	0.054	4.69	0.001	2.27	0.423	2.03	0.992	2.41	0.759
1444700_at	Neurexin III	Nrxn3	2.28	0.039	4.69	0.005	2.17	0.944	2.37	0.304	-1.01	0.438
1453567_s_at	RIKEN cDNA 2810441K11 gene	2810441K11Rik	4.22	0.295	4.68	0.037	1.25	0.059	1.1	0.400	1.12	0.625
1438448_at	otopetrin 1	Otop1	2.58	0.444	4.66	0.018	-1.24	0.230	-1.18	0.368	1.83	0.402
1418069_at	apolipoprotein C-II	Apoc2	4.9	0.162	4.54	0.041	-1.24	0.130	4.1	0.221	2.04	0.443
1424680_at	expressed sequence BB146404	BB146404	3.41	0.132	4.51	0.024	1.68	0.010	1.18	0.191	1.16	0.042
1447253_x_at	nucleoporin 54	Nup54	1.73	0.922	4.44	0.048	1.24	0.671	1.26	0.007	-1.14	0.709
1425990_a_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-de	Nfatc2	3.95	0.018	4.4	0.033	-1.08	0.457	-1.05	0.590	-1.35	0.304
1449293_a_at	S-phase kinase-associated protein 2 (p45)	Skp2	3.54	0.088	4.4	0.022	1.25	0.260	1.51	0.048	1.25	0.224
1433586_at	RGM domain family, member B	Rgmb	4.42	0.408	4.34	0.047	1.16	0.079	1.18	0.217	1.39	0.064
1451751_at	DNA-damage-inducible transcript 4-like	Ddit4l	1.6	0.390	4.33	0.002	1.72	0.231	1.33	0.161	1.31	0.326
1422979_at	suppressor of variegation 3-9 homolog 2 (Drosophila)	Suv39h2	3.4	0.061	4.32	0.003	1.2	0.422	1.43	0.354	1.13	0.972
1460521_a_at	RIKEN cDNA 5830411E10 gene	5830411E10Rik	3.24	0.308	4.28	0.012	1.06	0.258	1.26	0.060	1.27	0.353
1421706_at	matrix metallopeptidase 20 (enamelysin)	Mmp20	1.27	0.426	4.23	0.035	-1.6	0.181	3.41	0.079	1.3	0.457
1451949_at	immunoglobulin heavy chain 4 (serum IgG1) /// immunoglobu	Igh-4 /// Igh-6 /// Ig	2.02	0.640	4.22	0.039	-1.05	0.627	1.06	0.481	1.23	0.406
1422552_at	reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	1.6	0.294	4.18	0.007	1.31	0.022	1.36	0.042	2.34	0.011
1452990_at	metal response element binding transcription factor 1	Mtf1	2.21	0.125	4.16	0.050	-1.09	0.681	1.63	0.766	1.05	0.797
1427316_s_at	EST AA881470	AA881470	4.88	0.520	4.1	0.027	1.11	0.547	1.13	0.108	1.19	0.061
1440645_at	similar to deleted in malignant brain tumors 1 isoform c precu	LOC546006	2.29	0.046	4.08	0.018	2.49	0.340	-1.05	0.328	-2.48	0.015
1430026_at	stress 70 protein chaperone, microsome-associated, human I	Stch	5.91	0.067	4.06	0.044	-1.09	0.408	1.18	0.411	1.3	0.233
1416774_at	wee 1 homolog (S. pombe)	Wee1	3.75	0.208	4.03	0.037	-1.12	0.172	1.29	0.085	1.23	0.300
1446749_at	kinectin 1	Ktn1	2.15	0.529	4.02	0.027	-1.07	0.543	-1.63	0.186	-1.26	0.249
1431197_at	ADP-ribosylation factor-like 6 interacting protein 2	Arl6ip2	4.23	0.260	3.95	0.024	1.07	0.335	1.16	0.647	-1.12	0.431
1451635_at	RIKEN cDNA D630002G06 gene /// RIKEN cDNA C730048C	D630002G06Rik /	1.86	0.302	3.95	0.018	-1.55	0.137	1.17	0.303	-1.05	0.445
1451800_at	GRIP and coiled-coil domain containing 2	Gcc2	3.08	0.001	3.94	0.007	1.16	0.810	1.17	0.792	1.26	0.928
1453500_at	cytochrome P450, family 2, subfamily u, polypeptide 1	Cyp2u1	2.51	0.305	3.85	0.038	1.05	0.805	1.57	0.095	1.61	0.030
1455903_at	TBC1 domain family, member 4	Tbc1d4	1.12	0.792	3.84	0.010	1.05	0.682	1.64	0.295	-1.08	0.261
1423229_at	inositol polyphosphate-5-phosphatase E	Inpp5e	3.39	0.335	3.83	0.019	1.17	0.549	1.41	0.061	1.42	0.002
1424229_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase	Dyrk3	2.16	0.096	3.82	0.004	1.72	0.023	1.43	0.038	1.89	0.003
1449589_x_at	RIKEN cDNA 2610020O08 gene	2610020O08Rik	2.82	0.371	3.8	0.024	1.09	0.724	1.38	0.484	1.15	0.449
1426734_at	cDNA sequence BC022623	BC022623	3.84	0.469	3.79	0.002	1.24	0.172	1.47	0.066	1.7	0.024
1427401_at	cholinergic receptor, nicotinic, alpha polypeptide 5	Chrna5	1.12	0.300	3.75	0.025	1.73	0.932	1.04	0.679	1.1	0.802
1421663_at	dehydrogenase/reductase member 2	Dhrs2	3.1	0.039	3.75	0.046	-1.12	0.384	-1.15	0.225	2.13	0.713
1443264_at	membrane-spanning 4-domains, subfamily A, member 2	Ms4a2	1.47	0.535	3.75	0.045	1.43	0.514	1.32	0.601	1.59	0.068
1433452_at	RIKEN cDNA B630019K06 gene	B630019K06Rik	2.92	0.088	3.74	0.035	1.47	0.084	1.35	0.033	1.06	0.660

1433583_at	zinc finger protein 365 /// similar to zinc finger protein 365	Zfp365 /// LOC67	2.05	0.133	3.74	0.010	1.29	0.261	1.15	0.054	1.48	0.028
1431270_a_at	asteroid homolog 1 (Drosophila)	Aste1	3.42	0.452	3.72	0.023	1.3	0.203	1.32	0.158	1.31	0.108
1444226_at	forkhead box O3a	Foxo3a	1.43	0.216	3.71	0.037	1.6	0.802	1.18	0.355	2.25	0.253
1424772_at	H2A histone family, member J /// similar to H2A histone famil	H2afj /// LOC6324	2.52	0.510	3.71	0.037	1.71	0.057	1.47	0.045	1.52	0.113
1444341_at	RIKEN cDNA 8030451F13 gene	8030451F13Rik	1.26	0.983	3.69	0.022	-1.98	0.033	1.22	0.611	1.22	0.990
1422177_at	interleukin 13 receptor, alpha 2	Il13ra2	3.7	0.046	3.68	0.027	1.37	0.724	2.26	0.526	2.07	0.052
1443401_at	Astrotactin 2	Astn2	1.12	0.964	3.64	0.041	1.05	0.991	1.01	0.635	2.01	0.106
1453732_at	RIKEN cDNA 6230416A05 gene	6230416A05Rik	2.71	0.293	3.6	0.002	1.21	0.690	1.47	0.113	1.27	0.654
1422681_at	Ctr9, Paf1/RNA polymerase II complex component, homolog	Ctr9	2.47	0.514	3.56	0.050	1.06	0.743	1.27	0.161	1.11	0.299
1432012_a_at	NOL1/NOP2/Sun domain family 6	Nsun6	3.27	0.017	3.56	0.020	1.36	0.583	1.35	0.022	-1.24	0.038
1417000_at	ankyrin repeat and BTB (POZ) domain containing 1	Abtb1	4.61	0.036	3.54	0.007	-1.44	0.121	-1.23	0.140	1.4	0.215
1451417_at	breast cancer 1	Brca1	2.74	0.301	3.54	0.043	1.17	0.843	1.12	0.118	1.15	0.710
1421790_a_at	potassium voltage-gated channel, shaker-related subfamily,	Kcnab3	2.53	0.330	3.53	0.009	2.46	0.155	1.24	0.402	1.16	0.202
1438942_x_at	transglutaminase 2, C polypeptide	Tgm2	-1.58	0.136	3.53	0.033	-1.28	0.210	1.54	0.851	-1.37	0.301
1453422_a_at	RIKEN cDNA 1110020G09 gene	1110020G09Rik	4.08	0.191	3.49	0.014	1.48	0.033	1.23	0.166	1.16	0.244
1421487_a_at	non-catalytic region of tyrosine kinase adaptor protein 1	Nck1	3.33	0.259	3.47	0.047	-1	0.868	1.13	0.082	1	0.823
1416016_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP	Tap1	2.37	0.257	3.46	0.017	2.76	0.091	-1.03	0.629	1.32	0.260
1443770_x_at	Autism susceptibility candidate 2	Auts2	2.83	0.324	3.45	0.048	2.8	0.035	2.2	0.150	1.5	0.212
1458152_at	electron transferring flavoprotein, dehydrogenase	Etfdh	1.33	0.720	3.45	0.008	3.18	0.102	1.61	0.519	-1.2	0.369
1426988_at	kelch domain containing 5	Klhdc5	3.69	0.376	3.44	0.015	1.28	0.000	1.25	0.134	1.48	0.012
1417898_a_at	granzyme A	Gzma	2.12	0.288	3.43	0.037	1.66	0.652	1.84	0.511	-1.9	0.083
1435830_a_at	RIKEN cDNA 5430435G22 gene	5430435G22Rik	2.17	0.961	3.42	0.008	1.29	0.070	1.03	0.822	1.34	0.298
1456773_at	nucleoporin like 2	Nupl2	2.27	0.174	3.41	0.035	-1.03	0.628	1.25	0.256	1.23	0.540
1436593_at	RIKEN cDNA 1700016K19 gene	1700016K19Rik	1.67	0.544	3.4	0.034	2.4	0.177	1.26	0.129	1.74	0.042
1446870_at	DNA segment, Chr 4, ERATO Doi 510, expressed	D4Ertd510e	1.4	0.268	3.38	0.027	1.02	0.513	-1.58	0.101	1.07	0.645
1453713_s_at	RIKEN cDNA 4930546H06 gene	4930546H06Rik	1.45	0.362	3.37	0.048	1.38	0.441	1.61	0.271	2.74	0.449
1426412_at	neurogenic differentiation 1	Neurod1	2.23	0.471	3.34	0.006	-2.09	0.004	1.26	0.839	-2.11	0.049
1420584_at	phospholipase A2, group IIC	Pla2g2c	2.9	0.173	3.33	0.005	1.14	0.789	-1.29	0.249	-1.07	0.533
1459297_at	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	Cdc91l1	2.34	0.870	3.32	0.030	2.42	0.239	2.44	0.272	1.87	0.404
1436020_at	DNA segment, Chr 8, ERATO Doi 457, expressed	D8Ertd457e	2.6	0.272	3.31	0.034	1.11	0.204	1.21	0.056	1.12	0.306
1435404_at	dispatched homolog 2 (Drosophila)	Disp2	2.37	0.061	3.3	0.002	2.2	0.265	-1.7	0.033	1.21	0.473
1440946_at	Zinc finger protein 483	Zfp483	1.21	0.637	3.29	0.032	2.03	0.250	1.64	0.607	-1.36	0.184
1442032_at	cDNA sequence BC030500	BC030500	1.09	0.571	3.28	0.034	-1.14	0.312	1.05	0.321	1.18	0.530
1425220_x_at	cDNA sequence AF067061 /// hypothetical protein LOC6399	AF067061 /// LOC	2.15	0.275	3.27	0.031	1.23	0.478	1.75	0.204	1.19	0.402
1420730_a_at	t-complex protein 11	Tcp11	2.96	0.121	3.27	0.036	-1.07	0.844	-1.05	0.874	1.49	0.573
1447185_at	RIKEN cDNA 9330158H04 gene	9330158H04Rik	1.25	0.515	3.26	0.048	1.06	0.984	2.34	0.599	-1.06	0.214
1456643_at	RIKEN cDNA 9230114K14 gene	9230114K14Rik	1.79	0.015	3.25	0.006	1.22	0.409	1.12	0.323	1.34	0.003
1430572_at	RIKEN cDNA 1810042K04 gene	1810042K04Rik	-1.07	0.474	3.24	0.002	-1.65	0.100	-1.05	0.290	2.4	0.319
1439725_at	protein tyrosine phosphatase, receptor type, T	Ptprt	2.85	0.373	3.21	0.037	1.47	0.541	1.17	0.733	2.86	0.275
1440600_at	RIKEN cDNA 4930407I10 gene	4930407I10Rik	3.61	0.052	3.19	0.016	-1.16	0.394	2.28	0.512	-1.72	0.107
1454055_at	RIKEN cDNA 1600029O15 gene	1600029O15Rik	1.94	0.367	3.18	0.002	-1.36	0.026	-1.67	0.123	3.02	0.062
1443036_at	RIKEN cDNA C630007C17 gene	C630007C17Rik	1.38	0.782	3.18	0.009	1.12	0.548	1.09	0.886	1.19	0.878
1445523_at	Gap junction membrane channel protein epsilon 1	Gje1	3.17	0.086	3.18	0.015	1.57	0.805	1.11	0.759	-1.05	0.669
1457377_at	L(3)mbt-like 3 (Drosophila)	L3mbtl3	1.17	0.873	3.17	0.024	-1.36	0.204	-1.09	0.606	-1.36	0.040
1441963_at	ProSAPiP1 protein	Prosapip1	2.13	0.604	3.17	0.009	1.85	0.003	1.43	0.135	1.5	0.167
1430468_at	RIKEN cDNA 2810449G22 gene	2810449G22Rik	2.18	0.291	3.15	0.005	1.1	0.735	-1.17	0.310	1.44	0.599
1452407_at	sperm associated antigen 4	Spag4	1.67	0.201	3.15	0.046	2.05	0.220	-1.14	0.346	2.94	0.462
1421397_a_at	leucine-rich and death domain containing	Lrdd	1.6	0.518	3.14	0.006	1.22	0.500	1.46	0.059	1.45	0.405
1427565_a_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	4.46	0.236	3.13	0.041	1.31	0.545	-1.24	0.033	-1.04	0.748
1438837_at	Cholinergic receptor, nicotinic, alpha polypeptide 9	Chrna9	1.47	0.439	3.13	0.001	1.36	0.394	1.16	0.906	1.13	0.588
1447497_at	RAB21, member RAS oncogene family	Rab21	2.72	0.628	3.12	0.015	-1.02	0.656	1.79	0.575	-1.22	0.661
1428805_at	solute carrier family 35, member E3	Slc35e3	1.93	0.233	3.11	0.012	1.18	0.069	1.35	0.006	1.52	0.003
1438350_at	G protein-coupled receptor 64	Gpr64	3.38	0.167	3.1	0.025	1.68	0.224	-1.25	0.187	-2.88	0.031
1449894_at	leucine rich repeat containing 18	Lrrc18	2.15	0.199	3.1	0.000	1.16	0.694	1.59	0.344	1.73	0.968
1453380_a_at	XRCC6 binding protein 1	Xrcc6bp1	2.05	0.391	3.09	0.005	1.38	0.242	1.47	0.066	1.28	0.152
1445680_x_at	coagulation factor II (thrombin) receptor-like 2	F2rl2	1.84	0.495	3.08	0.042	1.58	0.526	1.28	0.620	3.74	0.068
1417876_at	Fc receptor, IgG, high affinity I	Fcgr1	2.38	0.067	3.06	0.032	-1.29	0.380	1.35	0.364	1.24	0.927
1423944_at	hemopexin	Hpxn	2.49	0.183	3.05	0.021	2.7	0.344	3.12	0.645	1.8	0.545

1438140_a_at	zinc finger protein 64	Zfp64	2.73	0.600	3.05	0.038	1.12	0.454	1.21	0.353	1.12	0.631
1441122_at	expressed sequence AU024342	AU024342	1.94	0.031	3.04	0.037	2.2	0.289	1.85	0.133	-1.01	0.486
1449654_s_at	expressed sequence C77545	C77545	1.59	0.225	3.03	0.001	2.04	0.430	1.27	0.616	1.6	0.382
1440729_at	epidermal growth factor receptor pathway substrate 15	Eps15	2.47	0.527	3.03	0.020	-1.45	0.179	1.16	0.937	1.1	0.720
1421435_at	glutamate receptor, ionotropic, delta 2	Grid2	2.32	0.004	3.03	0.001	1.61	0.698	-1.11	0.636	-1.34	0.315
1431624_a_at	RIKEN cDNA 2610206B13 gene	2610206B13Rik	1.58	0.292	3.02	0.018	2.2	0.036	1.83	0.547	-1.05	0.980
1434259_at	similar to H2A histone family, member J	LOC666811	1.04	0.794	3.02	0.030	-1.2	0.350	-1.91	0.095	2.88	0.950
1442603_at	Polybromo 1	Pb1	2.55	0.020	2.99	0.036	-1.33	0.259	-1.11	0.598	-1.53	0.028
1443994_at	RIKEN cDNA 6030407O03 gene	6030407O03Rik	2	0.409	2.98	0.003	1.27	0.325	-1.49	0.121	-1.42	0.182
1428994_s_at	RIKEN cDNA 1110017I16 gene	1110017I16Rik	1.2	0.921	2.97	0.012	1.33	0.460	-1.77	0.070	-1.45	0.158
1430204_at	RIKEN cDNA 5033425G24 gene	5033425G24Rik	1.66	0.248	2.97	0.011	-1.09	0.422	1.44	0.114	1.13	0.693
1446805_at	Gamma-aminobutyric acid (GABA-A) receptor, subunit alpha	Gabra2	3.15	0.113	2.97	0.046	1.13	0.828	1.25	0.578	-1.09	0.343
1433877_at	RIKEN cDNA 4732473B16 gene	4732473B16Rik	2.16	0.396	2.96	0.019	1.17	0.106	1.19	0.216	1.53	0.025
1416927_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.13	0.060	2.95	0.006	1.08	0.814	1.78	0.138	1.83	0.253
1460089_at	Period homolog 3 (Drosophila)	Per3	2.17	0.227	2.94	0.006	1.11	0.560	1.82	0.461	3.15	0.066
1449350_at	odd-skipped related 1 (Drosophila)	Osr1	2.84	0.116	2.92	0.005	1.01	0.909	1.21	0.500	-1.18	0.214
1449578_at	suppressor of Ty 16 homolog (S. cerevisiae)	Supt16h	3.86	0.130	2.9	0.006	1.56	0.243	1.27	0.354	1.15	0.321
1431000_at	RIKEN cDNA 2310002B06 gene	2310002B06Rik	1.13	0.999	2.89	0.047	-1.21	0.078	-1.27	0.198	1.11	0.762
1415843_at	G protein beta subunit-like	Gbl	3.13	0.164	2.89	0.034	-1.17	0.286	1.44	0.114	1.26	0.098
1446189_at	MYST histone acetyltransferase monocytic leukemia 4	Myst4	-1.23	0.350	2.89	0.027	1.5	0.687	1.15	0.536	1.45	0.874
1423231_at	neurogranin	Nrgn	2	0.527	2.88	0.009	1.52	0.006	2.04	0.850	-1.18	0.803
1432787_at	RIKEN cDNA 6720420G18 gene	6720420G18Rik	2	0.234	2.87	0.045	1.06	0.778	1.16	0.866	-1.27	0.278
1426117_a_at	solute carrier family 19 (thiamine transporter), member 2	Slc19a2	2.2	0.167	2.86	0.004	1.76	0.025	1.53	0.131	1.32	0.405
1418203_at	phorbol-12-myristate-13-acetate-induced protein 1	Pmaip1	1.33	0.093	2.85	0.020	1.42	0.015	1.22	0.008	1.68	0.090
1440546_at	RIKEN cDNA 9630002D21 gene	9630002D21Rik	2.64	0.111	2.84	0.033	2.98	0.940	1.94	0.206	1.04	0.897
1436472_at	schlafen 9	Slfn9	2.6	0.550	2.84	0.041	1.1	0.795	1.25	0.879	2.25	0.538
1423172_at	N-ethylmaleimide sensitive fusion protein attachment protein	Napb	1.6	0.042	2.83	0.043	1.02	0.872	1.16	0.184	-1.07	0.886
1453102_at	fibronectin leucine rich transmembrane protein 3	Flrt3	1.6	0.437	2.79	0.025	1.33	0.001	1.31	0.032	1.5	0.013
1432964_at	RIKEN cDNA 2410049M19 gene	2410049M19Rik	2	0.732	2.77	0.025	1.16	0.704	3.03	0.145	1.27	0.730
1439061_at	coiled-coil domain containing 84	Ccdc84	2.8	0.302	2.77	0.008	-1.46	0.173	1.29	0.220	-1.03	0.841
1455894_at	peptidyl-tRNA hydrolase 2	Ptrh2	1.57	0.223	2.77	0.009	1.65	0.003	1.8	0.019	1.56	0.012
1438293_at	trichoplein, keratin filament binding	Tchp	1.67	0.049	2.77	0.036	1.33	0.199	1.28	0.292	1.27	0.300
1444449_at	Ubiquitin specific peptidase 18	Usp18	1.55	0.047	2.77	0.044	-1.4	0.192	1.42	0.838	2.21	0.261
1433068_at	RIKEN cDNA 6330582A15 gene	6330582A15Rik	3.12	0.104	2.76	0.048	1.02	0.853	1.1	0.875	-1.17	0.530
1446990_at	nuclear factor I/A	Nfia	2.63	0.376	2.76	0.024	2.44	0.366	1.83	0.881	1.18	0.417
1430344_at	RIKEN cDNA 2900064P18 gene	2900064P18Rik	2.38	0.057	2.75	0.000	-1.25	0.147	-1.06	0.814	-1.68	0.055
1451773_s_at	polymerase (RNA) III (DNA directed) polypeptide F	Polr3f	2.42	0.270	2.74	0.048	-1.04	0.706	1.37	0.039	-1.03	0.810
1420020_at	suppressor of zeste 12 homolog (Drosophila)	Suz12	1.18	0.839	2.74	0.015	1.49	0.087	-2.29	0.023	1.84	0.416
1446010_at	similar to F-box only protein 34 /// similar to F-box only protei	LOC668019 /// LC	2.44	0.356	2.73	0.011	2.07	0.397	-1.11	0.522	1.72	0.213
1450303_at	ventral anterior homeobox containing gene 2	Vax2	1.87	0.317	2.73	0.040	1.28	0.746	1.15	0.640	1.89	0.787
1449128_at	coiled-coil domain containing 43	Ccdc43	2.28	0.750	2.72	0.017	-1.01	0.808	-1.03	0.643	1.38	0.096
1451944_a_at	tumor necrosis factor (ligand) superfamily, member 11	Tnfsf11	2.63	0.023	2.72	0.012	1.17	0.885	1.63	0.615	-1.14	0.479
1453234_at	RIKEN cDNA 1300002K09 gene	1300002K09Rik	2.51	0.166	2.71	0.038	1.21	0.805	1.25	0.929	1.01	0.861
1445997_at	ets variant gene 3	Etv3	2.02	0.306	2.71	0.041	1.65	0.430	1.94	0.960	2.17	0.349
1450241_a_at	ecotropic viral integration site 2a	Evi2a	1.95	0.080	2.71	0.015	1.58	0.010	1.72	0.000	1.79	0.077
1430067_at	RIKEN cDNA 5430401F13 gene /// hypothetical LOC625758	5430401F13Rik //.	1.39	0.879	2.7	0.015	1.03	0.964	1.83	0.141	1.2	0.666
1428077_at	transmembrane protein 163	Tmem163	1.67	0.329	2.7	0.003	2.2	0.596	1.58	0.739	1.14	0.790
1435497_at	RIKEN cDNA 5730590G19 gene	5730590G19Rik	2.57	0.108	2.69	0.011	1.14	0.437	1.09	0.390	1.23	0.037
1437856_at	inositol polyphosphate multikinase	Ipmk	3.26	0.218	2.68	0.021	-1.1	0.456	1.02	0.936	1.05	0.885
1433938_at	transformation related protein 53 binding protein 2	Trp53bp2	2.12	0.204	2.68	0.031	-1.04	0.753	1.13	0.284	1.09	0.344
1436285_at	coiled-coil domain containing 113	Ccdc113	2.51	0.311	2.67	0.021	1.6	0.352	1.16	0.748	2.32	0.786
1441723_at	dual specificity phosphatase 22	Dusp22	2.23	0.414	2.67	0.047	1.59	0.686	1.28	0.608	1.29	0.341
1416775_at	RIKEN cDNA 2310004L02 gene	2310004L02Rik	4.61	0.261	2.66	0.007	1.35	0.088	-1.1	0.436	1.24	0.244
1440000_at	RIKEN cDNA E330013P04 gene	E330013P04Rik	1.04	0.726	2.66	0.038	1.96	0.988	1.67	0.444	2.32	0.690
1454827_at	pogo transposable element with ZNF domain	Pogz	3.2	0.673	2.66	0.049	1.88	0.162	-1.03	0.749	1.9	0.052
1437183_at	leucine rich repeat containing 4B	Lrrc4b	1.87	0.082	2.65	0.049	-1.55	0.163	-1.04	0.543	1.27	0.616
1418685_at	toll-interleukin 1 receptor (TIR) domain-containing adaptor pr	Tirap	1.47	0.478	2.65	0.023	1.02	0.942	1.08	0.737	1.23	0.184
1459051_at	RIKEN cDNA 6530418L21 gene	6530418L21Rik	1.36	0.150	2.64	0.041	1.33	0.134	1.26	0.776	1.17	0.659

1443664_s_at	D164 sialomucin-like 2	Cd164l2	1.57	0.267	2.64	0.021	1.12	0.983	-1.45	0.167	2.01	0.057
1437255_at	Zinc finger and BTB domain containing 7a	Zbtb7a	1.29	0.386	2.64	0.040	2.7	0.103	1.27	0.049	-1.39	0.228
1436219_at	RIKEN cDNA 4933403F05 gene	4933403F05Rik	1.4	0.038	2.63	0.005	1.56	0.008	1.75	0.002	1.69	0.008
1449877_s_at	kinesin family member C1	Kifc1	2.19	0.447	2.63	0.046	1.5	0.298	1.94	0.055	1.42	0.683
1455489_at	leucine rich repeat transmembrane neuronal 2	Lrrtm2	1.4	0.016	2.63	0.018	1.71	0.103	2	0.012	2.11	0.055
1442846_at	Pre B-cell leukemia transcription factor 1	Pbx1	1.42	0.738	2.63	0.004	1.48	0.434	1.57	0.737	1.19	0.683
1448813_at	arylacetamide deacetylase (esterase)	Aadac	1.09	0.191	2.62	0.016	1.63	0.136	-1.34	0.116	2.76	0.534
1451562_at	cDNA sequence BC006662	BC006662	3.29	0.399	2.62	0.028	1.04	0.817	1.11	0.490	1.04	0.745
1434381_at	cDNA sequence BC060631	BC060631	2.84	0.424	2.62	0.042	1.14	0.534	1.22	0.210	1.14	0.189
1458826_at	expressed sequence C78809	C78809	1.72	0.900	2.62	0.004	1.78	0.056	1.52	0.720	-1.48	0.215
1437665_at	Interleukin 22 receptor, alpha 2	Il22ra2	1.53	0.575	2.61	0.004	-1.7	0.135	1.66	0.419	1.88	0.478
1424194_at	RCSD domain containing 1	Rcsd1	2.28	0.184	2.6	0.009	1.33	0.490	-1.11	0.663	1.48	0.326
1433406_at	hypothetical protein LOC668408 /// hypothetical protein LOC	LOC668408 /// LC	3.19	0.673	2.59	0.018	1.82	0.085	-1.33	0.233	1.23	0.776
1418105_at	stathmin-like 4	Stmn4	1.15	0.894	2.59	0.046	1.31	0.182	-2.01	0.071	2.69	0.734
1448966_a_at	nuclear factor of activated T-cells 5	Nfat5	3.6	0.283	2.58	0.020	-1.52	0.229	2.77	0.757	1.42	0.581
1458572_at	chromatin modifying protein 5	Chmp5	3.86	0.088	2.57	0.030	1.97	0.294	2.04	0.426	-1.03	0.525
1441391_at	Guanine nucleotide binding protein (G protein), beta polypept	Gnb1l	1.26	0.180	2.57	0.004	1.55	0.056	1.49	0.124	1.56	0.154
1455930_at	hypothetical protein LOC673503	LOC673503	1.64	0.223	2.57	0.046	1.02	0.999	1.74	0.114	1.43	0.297
1441595_at	Excision repair cross-complementing rodent repair deficiency	Csb	3.12	0.325	2.55	0.033	1.81	0.894	2.24	0.789	1.29	0.974
1431840_at	DENN/MADD domain containing 1C	Dennd1c	1.55	0.739	2.55	0.035	1.41	0.055	1.04	0.718	1.09	0.909
1438097_at	RAB20, member RAS oncogene family	Rab20	2.66	0.267	2.55	0.043	-1.05	0.634	1.25	0.440	1.2	0.728
1451755_a_at	apolipoprotein B editing complex 1	Apobec1	-1.08	0.962	2.54	0.007	2.02	0.456	2.17	0.140	3.17	0.039
1453211_at	coiled-coil domain containing 89	Ccdc89	2.04	0.109	2.54	0.009	1.08	0.877	1.19	0.729	1.1	0.995
1459215_at	Lysosomal-associated protein transmembrane 4B	Laptm4b	1.63	0.571	2.54	0.026	1.06	0.976	1.96	0.638	-1.05	0.878
1430797_at	exportin 4	Xpo4	2.2	0.140	2.54	0.014	1.4	0.823	-2.25	0.028	-1.59	0.048
1428803_at	RIKEN cDNA 4632408A20 gene	4632408A20Rik	2.11	0.278	2.53	0.038	-1.09	0.460	1.58	0.006	1.25	0.078
1441084_at	expressed sequence BE686333	BE686333	1.61	0.032	2.53	0.021	2.19	0.257	-1.17	0.116	1.31	0.455
1417479_at	RIKEN cDNA 4930511A21 gene	4930511A21Rik	3.38	0.288	2.52	0.032	1.34	0.127	1.14	0.456	1.27	0.042
1460499_at	RIKEN cDNA 9230110I02 gene	9230110I02Rik	1.86	0.176	2.52	0.010	-1.34	0.251	-1.19	0.336	1.4	0.098
1450926_at	ATPase, H+ transporting, lysosomal V1 subunit G1 /// similar	Atp6v1g1 /// LOC	3.74	0.263	2.52	0.019	3.48	0.187	-1.38	0.185	-1.19	0.245
1420993_at	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransfera	B3gnt5	1.73	0.047	2.52	0.048	1.08	0.627	-1.13	0.430	-1.48	0.075
1422016_a_at	centromere protein H	Cenph	2.13	0.105	2.51	0.029	1.12	0.481	1.05	0.557	1.1	0.094
1456010_x_at	hairy and enhancer of split 5 (Drosophila)	Hes5	3.31	0.100	2.51	0.020	1.1	0.679	2.87	0.015	1.21	0.883
1441933_x_at	phosphatidylinositol glycan anchor biosynthesis, class Z	Pigz	2.23	0.243	2.51	0.024	-1.27	0.319	1.8	0.397	1.37	0.899
1453996_a_at	cathepsin 3	Cts3	-1.07	0.505	2.5	0.038	2	0.155	1.27	0.629	2.27	0.753
1416296_at	interleukin 2 receptor, gamma chain	Il2rg	3.08	0.579	2.5	0.023	-1.1	0.589	-1.08	0.537	-1.44	0.378
1433423_at	RIKEN cDNA 2210008N01 gene	2210008N01Rik	1.68	0.751	2.49	0.015	3.22	0.181	1.79	0.781	1.57	0.783
1424518_at	RIKEN cDNA 2310016F22 gene /// cDNA sequence BC0204	2310016F22Rik //	1.81	0.247	2.49	0.042	1.43	0.134	1	0.848	1.2	0.158
1454139_at	RIKEN cDNA 4930405N21 gene	4930405N21Rik	2.21	0.199	2.49	0.049	1.5	0.271	-1.05	0.667	1.65	0.380
1456076_at	defensin beta 19	Defb19	1.15	0.426	2.49	0.009	-2.17	0.054	1.34	0.324	3.69	0.206
1422663_at	origin recognition complex, subunit 1-like (S.cereviaiae)	Orc1l	1.97	0.056	2.49	0.037	1.19	0.064	1.02	0.632	1.36	0.196
1430427_a_at	protocadherin 18	Pcdh18	1.7	0.016	2.49	0.021	2.08	0.133	1.7	0.129	1.75	0.029
1418181_at	protein tyrosine phosphatase 4a3	Ptp4a3	1.66	0.306	2.48	0.035	1.24	0.080	1.21	0.045	1.38	0.036
1428990_at	RIKEN cDNA 2310047K21 gene	2310047K21Rik	1.85	0.155	2.46	0.046	-1.1	0.584	-1.09	0.469	-1.06	0.615
1458159_at	Guanine nucleotide binding protein, alpha q polypeptide	Gnaq	1.15	0.312	2.46	0.009	1.21	0.658	2.26	0.432	1.5	0.309
1435860_at	solute carrier family 5 (sodium-dependent vitamin transporter	Slc5a6	1.23	0.599	2.46	0.033	1.17	0.729	1.28	0.289	1.94	0.028
1445271_at	RIKEN cDNA 9230105E10 gene	9230105E10Rik	2.34	0.116	2.45	0.043	3.17	0.261	1.61	0.513	-1.09	0.508
1430080_at	ficolin B	Fcnb	1.57	0.759	2.45	0.034	1.95	0.366	-1.1	0.705	1.5	0.279
1430780_a_at	phosphomannomutase 1	Pmm1	2.06	0.315	2.45	0.022	1.05	0.769	1.23	0.004	1.17	0.012
1456543_at	prokineticin receptor 1	Prokr1	2.46	0.011	2.45	0.014	2.2	0.016	1.66	0.659	1.22	0.724
1455852_at	RIKEN cDNA 4833432M17 gene	4833432M17Rik	1.92	0.197	2.44	0.010	1.12	0.593	1.3	0.030	1.04	0.997
1458121_at	RIKEN cDNA A430107O13 gene	A430107O13Rik	1.97	0.234	2.44	0.012	1.29	0.107	-1.93	0.033	-1.13	0.541
1436122_at	zinc finger protein 667	Zfp667	1.77	0.298	2.44	0.018	1.16	0.422	1.14	0.069	1.36	0.254
1454114_a_at	RIKEN cDNA 4933425K02 gene	4933425K02Rik	1.23	0.374	2.43	0.004	1.65	0.317	1.68	0.861	1.95	0.103
1455794_at	RIKEN cDNA D130058I21 gene	D130058I21Rik	-1.12	0.478	2.43	0.018	3.2	0.289	1.58	0.699	1.92	0.438
1419021_at	mcf.2 transforming sequence	Mcf2	2.3	0.630	2.43	0.016	-1.27	0.354	-1.33	0.343	-1.27	0.453
1442589_at	Transient receptor potential cation channel, subfamily C, mer	Trpc5	1.92	0.083	2.42	0.007	-1.06	0.534	1.38	0.392	-1.22	0.511
1454472_at	RIKEN cDNA 2900092N22 gene	2900092N22Rik	1.02	0.439	2.41	0.002	1.23	0.731	2.7	0.156	2.46	0.207

1456178_at	BMP and activin membrane-bound inhibitor, pseudogene (Xe	Bambi-ps1	2.55	0.349	2.41	0.014	3.5	0.008	1.67	0.965	2.08	0.379
1457083_at	PRP31 pre-mRNA processing factor 31 homolog (yeast)	Prpf31	1.59	0.196	2.41	0.030	1.35	0.032	1.41	0.043	1.74	0.020
1438532_at	hemicentin 1	Hmcn1	2.01	0.110	2.39	0.002	1.33	0.568	1.04	0.769	2.12	0.382
1460642_at	Tnf receptor associated factor 4	Traf4	1.67	0.344	2.39	0.029	1.21	0.005	1.43	0.079	1.48	0.090
1418865_at	zinc finger protein 385	Zfp385	1.84	0.386	2.39	0.035	1.22	0.203	1.15	0.529	1.11	0.495
1424232_a_at	cDNA sequence BC025546	BC025546	2.75	0.264	2.38	0.021	1.65	0.193	1.34	0.019	1.41	0.008
1417638_at	left right determination factor 1	Lefty1	1.45	0.294	2.38	0.003	1.11	0.775	1.14	0.097	1.26	0.213
1421112_at	NK2 transcription factor related, locus 2 (Drosophila)	Nkx2-2	2.71	0.344	2.38	0.008	2.19	0.424	1.99	0.240	1.99	0.435
1459343_at	RIKEN cDNA 2700008B19 gene	2700008B19Rik	1.73	0.202	2.37	0.029	1.61	0.340	1.17	0.435	1.32	0.139
1446478_at	RIKEN cDNA D130067I03 gene	D130067I03Rik	2.01	0.632	2.37	0.047	1.64	0.687	-2.28	0.069	1.8	0.666
1423093_at	inner centromere protein	Incenp	2.99	0.641	2.37	0.008	-1.01	0.844	1.03	0.622	-1.04	0.776
1425898_x_at	olfactomedin 3	Olfm3	5.03	0.097	2.37	0.044	1.23	0.586	1.84	0.257	1.17	0.948
1438893_at	RIKEN cDNA 5530601H04 gene	5530601H04Rik	1.54	0.209	2.36	0.030	2.13	0.758	2.22	0.035	-1.1	0.875
1454638_a_at	phenylalanine hydroxylase	Pah	2	0.616	2.36	0.001	-1.69	0.147	-1.23	0.497	1.15	0.332
1453393_a_at	carbohydrate (chondroitin 6/keratan) sulfotransferase 4	Chst4	2.49	0.040	2.35	0.050	-1.41	0.234	-1.21	0.191	2.98	0.258
1424676_s_at	SEC14-like 4 (S. cerevisiae)	Sec14l4	-1.08	0.444	2.35	0.045	-1.23	0.374	1.21	0.598	2.25	0.733
1422196_at	5-hydroxytryptamine (serotonin) receptor 5B	Htr5b	-1.42	0.076	2.34	0.027	-1.19	0.394	1.18	0.868	2.97	0.355
1457331_at	Retbindin	Rtbdn	1.05	0.618	2.34	0.005	1.7	0.329	1.76	0.053	1.3	0.760
1429350_at	RIKEN cDNA 1700027M21 gene	1700027M21Rik	2.19	0.423	2.33	0.032	2.8	0.163	1.17	0.751	1.78	0.165
1420588_at	serine protease inhibitor-like, with Kunitz and WAP domains 1	Spinlw1	1.9	0.175	2.33	0.035	2.85	0.058	1.12	0.788	1.92	0.447
1426472_at	zinc finger protein 52	Zfp52	1.44	0.034	2.33	0.024	1.45	0.028	1.45	0.196	1.2	0.699
1423494_at	RIKEN cDNA 2310042E22 gene	2310042E22Rik	1.16	0.650	2.32	0.001	1.29	0.733	-1.35	0.325	1.33	0.519
1460497_a_at	RIKEN cDNA 4933413B09 gene	4933413B09Rik	1.73	0.974	2.32	0.011	1.75	0.390	1.31	0.764	1.47	0.804
1439547_at	RIKEN cDNA A930007A09 gene	A930007A09Rik	1.43	0.231	2.32	0.007	4.39	0.167	1.21	0.139	1.44	0.160
1450329_a_at	arrestin 3, retinal	Arr3	3.75	0.018	2.32	0.023	1.24	0.454	1.06	0.689	1.26	0.695
1442400_at	Prickle like 1 (Drosophila)	Prickle1	1.36	0.440	2.31	0.011	-1.4	0.063	-1.09	0.377	2.42	0.680
1424974_at	zinc finger protein 418	Zfp418	2.02	0.158	2.31	0.021	-1.08	0.596	1.42	0.193	1.4	0.241
1421850_at	microtubule-associated protein 1 B	Mtap1b	4.5	0.089	2.29	0.043	2.04	0.941	-1.06	0.850	1.25	0.639
1435033_at	Rho guanine nucleotide exchange factor (GEF) 4	Arhgef4	1.46	0.144	2.28	0.026	-1.13	0.407	1.29	0.008	1.31	0.421
1418293_at	interferon-induced protein with tetratricopeptide repeats 2	Ifit2	1.48	0.508	2.28	0.039	1.33	0.466	1.11	0.539	-1.14	0.030
1436922_at	peptidylprolyl isomerase (cyclophilin) like 5	Ppil5	1.54	0.060	2.28	0.024	1.24	0.002	1.26	0.293	1.4	0.038
1434774_at	rhomboid 5 homolog 2 (Drosophila)	Rhbdf2	-1.6	0.092	2.28	0.036	3.36	0.456	1.85	0.534	-1.32	0.264
1454728_s_at	ATPase, aminophospholipid transporter (APLT), class I, type	Atp8a1	3.1	0.321	2.27	0.022	-1.23	0.096	-1.13	0.526	1.56	0.367
1458683_at	signal-regulatory protein beta 1 /// similar to SIRP beta 1 isof	Sirpb1 /// LOC673	1.28	0.118	2.27	0.050	1.44	0.773	1.32	0.274	-1.48	0.159
1423056_at	neuron specific gene family member 1	Nsg1	2.33	0.114	2.26	0.008	-1.25	0.455	-1.3	0.241	1.48	0.735
1454951_at	zinc finger protein 606	Zfp606	2.35	0.508	2.26	0.017	1.16	0.621	-1.1	0.189	1.15	0.596
1425083_at	otoraplin	Otor	2.51	0.488	2.25	0.039	3.43	0.020	1.02	0.261	1.19	0.957
1448414_at	RAD1 homolog (S. pombe)	Rad1	2.25	0.360	2.25	0.015	1.24	0.105	1.22	0.115	1.07	0.209
1427570_at	signal recognition particle receptor ('docking protein')	Srpr	3.12	0.330	2.25	0.032	-1.42	0.071	-1.2	0.391	-1.09	0.523
1443059_at	dehydrogenase/reductase (SDR family) member 8	Dhrs8	1.28	0.838	2.24	0.010	1.97	0.535	-1.06	0.674	-1.03	0.617
1453156_s_at	zinc binding alcohol dehydrogenase, domain containing 1	Zadh1	1.85	0.145	2.24	0.047	-1.03	0.677	1.47	0.120	1.09	0.833
1432513_a_at	RIKEN cDNA 1700001C02 gene	1700001C02Rik	1.33	0.725	2.23	0.015	1.04	0.614	2.81	0.205	3.01	0.068
1460333_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 59	Ddx59	1.73	0.241	2.23	0.031	1.07	0.293	1.07	0.594	1.34	0.161
1460380_at	desmoglein 2	Dsg2	1.71	0.033	2.23	0.046	1.48	0.510	-1	0.717	1.19	0.354
1455501_at	solute carrier family 2 (facilitated glucose transporter), membe	Slc2a12	1.82	0.284	2.23	0.035	1.18	0.541	-1.16	0.367	2.29	0.845
1416258_at	thymidine kinase 1	Tk1	2.05	0.153	2.23	0.014	1.25	0.061	1.18	0.115	1.22	0.082
1429702_at	RIKEN cDNA 2900072G11 gene	2900072G11Rik	1.46	0.794	2.22	0.048	2.25	0.544	-1.55	0.365	2.13	0.078
1458734_at	expressed sequence C78128	C78128	1.03	0.967	2.22	0.049	1.6	0.355	1.71	0.929	1.58	0.840
1433575_at	similar to Transcription factor SOX-4	LOC672274	1.53	0.189	2.22	0.048	1.45	0.012	1.39	0.011	1.56	0.000
1453739_at	transmembrane protein 126B	Tmem126b	1.8	0.254	2.22	0.048	1.41	0.038	1.44	0.298	1.45	0.035
1456652_at	denticleless homolog (Drosophila)	Dtl	1.66	0.013	2.21	0.006	1.13	0.802	1.82	0.366	-1.05	0.669
1431422_a_at	dual specificity phosphatase 14	Dusp14	1.88	0.299	2.21	0.031	1.32	0.019	1.37	0.006	1.27	0.039
1434734_at	RIKEN cDNA E130016E03 gene	E130016E03Rik	1.94	0.246	2.21	0.017	1.2	0.211	1.18	0.002	-1.14	0.345
1434762_at	transmembrane protein 142B	Tmem142b	2.36	0.588	2.21	0.031	1.32	0.346	1.19	0.264	1.19	0.067
1430481_at	RIKEN cDNA 4930545L23 gene	4930545L23Rik	1.46	0.554	2.19	0.049	1.38	0.005	1.45	0.673	1.29	0.489
1454812_at	RIKEN cDNA 5730601F06 gene	5730601F06Rik	1.11	0.226	2.19	0.003	1.12	0.340	1.43	0.032	1.41	0.064
1417885_at	microtubule-associated protein tau	Mapt	1.99	0.340	2.19	0.050	-1.37	0.258	1.79	0.073	-1.25	0.165
1447967_at	transmembrane protein 69	Tmem69	1.64	0.144	2.19	0.016	1.01	0.713	1.51	0.266	1.36	0.356

1421675_at	RIKEN cDNA 1700123K08 gene	1700123K08Rik	1.62	0.645	2.18	0.034	1.02	0.871	1.27	0.300	-1.34	0.233
1454291_at	RIKEN cDNA 4933428P19 gene	4933428P19Rik	1.37	0.916	2.18	0.025	3.5	0.068	1.59	0.463	1.55	0.190
1440085_at	ectodysplasin A2 isoform receptor	Eda2r	1.43	0.232	2.18	0.029	1.35	0.006	1.15	0.032	1.24	0.006
1429734_at	RIKEN cDNA 4632434I11 gene	4632434I11Rik	1.45	0.010	2.17	0.002	1.35	0.157	1.4	0.002	1.57	0.048
1415811_at	ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	2	0.415	2.17	0.021	1.17	0.133	1.03	0.629	1.24	0.285
1435802_at	zinc finger protein 499	Zfp499	1.8	0.430	2.17	0.021	1.03	0.889	1.07	0.485	1.21	0.291
1436837_at	maelstrom homolog (Drosophila)	Mael	2.1	0.280	2.16	0.034	1.25	0.530	-1.02	0.554	-1.79	0.098
1426176_a_at	prokineticin 2	Prok2	3.23	0.154	2.16	0.007	-1.53	0.257	1.68	0.929	1.13	0.531
1453027_at	discs, large (Drosophila) homolog-associated protein 1	Dlgap1	1.01	0.832	2.15	0.016	1.24	0.922	1.35	0.900	1.1	0.759
1450886_at	germ cell-specific gene 2	Gsg2	1.98	0.429	2.15	0.005	1.14	0.177	1.22	0.084	1.33	0.019
1416915_at	mutS homolog 6 (E. coli)	Msh6	1.1	0.060	2.15	0.000	1.51	0.047	1.47	0.029	1.4	0.023
1433582_at	RIKEN cDNA 1190002N15 gene	1190002N15Rik	1.6	0.203	2.14	0.039	1.45	0.015	1.24	0.030	1.13	0.156
1442406_at	RIKEN cDNA 9230104K21 gene	9230104K21Rik	1.61	0.696	2.14	0.020	1.87	0.121	1.19	0.035	1.65	0.291
1458544_at	cDNA sequence BC059841	BC059841	-1.04	0.361	2.14	0.028	-1.11	0.269	1.69	0.689	2.16	0.987
1418109_at	G1 to S phase transition 2	Gspt2	1.54	0.504	2.14	0.005	1.17	0.423	1.41	0.088	1.21	0.177
1448359_a_at	HIG1 domain family, member 1A	Higd1a	2.22	0.093	2.14	0.020	1.33	0.149	1.26	0.598	1.21	0.239
1423808_at	WD repeat domain 79	Wdr79	1.78	0.175	2.14	0.040	1.26	0.061	1.13	0.069	1.16	0.109
1435650_at	hyaluronan and proteoglycan link protein 4	Hapln4	2	0.408	2.13	0.049	1.14	0.744	1.42	0.775	1.71	0.473
1454197_a_at	coiled-coil domain containing 86	Ccdc86	1.61	0.509	2.12	0.035	1.04	0.332	1.14	0.094	1.24	0.010
1419209_at	chemokine (C-X-C motif) ligand 1	Cxcl1	1.36	0.074	2.12	0.010	1.44	0.142	1.23	0.300	1.68	0.117
1418140_at	doublecortin	Dcx	3.24	0.128	2.12	0.033	1.37	0.833	-1.5	0.235	2.12	0.085
1436496_at	RIKEN cDNA 1700012O15 gene	1700012O15Rik	-1.4	0.222	2.11	0.029	1.08	0.389	1.49	0.332	1.15	0.182
1433622_at	gem (nuclear organelle) associated protein 4	Gemin4	1.82	0.236	2.11	0.013	1.24	0.013	1.35	0.009	1.39	0.005
1453678_at	methyl-CpG binding domain protein 1	Mbd1	1.99	0.825	2.11	0.025	1.91	0.282	1.12	0.980	-1.23	0.427
1435213_at	NHL repeat containing 1	Nhlrc1	-1.04	0.561	2.11	0.038	-1.06	0.579	1.37	0.038	1.01	0.975
1453623_a_at	RAD23a homolog (S. cerevisiae)	Rad23a	2.58	0.265	2.11	0.046	1.24	0.028	1.08	0.550	1.16	0.173
1420710_at	reticuloendotheliosis oncogene	Rel	1.53	0.097	2.11	0.013	-1.44	0.111	1.43	0.035	1.14	0.696
1431934_at	RIKEN cDNA 4930505O20 gene	4930505O20Rik	3.97	0.092	2.09	0.034	-1.16	0.422	1.5	0.978	-1.16	0.486
1457403_at	RIKEN cDNA 9130409I23 gene	9130409I23Rik	1.9	0.947	2.09	0.034	1.84	0.596	1.22	0.976	-1.27	0.425
1458189_at	EMI domain containing 2	Emid2	2.81	0.131	2.09	0.016	-1.03	0.562	1.65	0.546	-1.07	0.399
1419061_at	ras homolog gene family, member D	Rhod	1.33	0.344	2.09	0.012	1.26	0.021	1.21	0.049	1.5	0.005
1449414_at	zinc finger protein 53	Zfp53	1.58	0.238	2.09	0.020	-1.07	0.388	1.16	0.231	1.16	0.108
1439087_a_at	RIKEN cDNA 1500004A08 gene	1500004A08Rik	1.48	0.114	2.08	0.017	1.13	0.476	1.34	0.024	-1.02	0.812
1453154_at	RIKEN cDNA 1700029M20 gene	1700029M20Rik	2.07	0.489	2.08	0.039	1.73	0.362	1.83	0.117	1.74	0.284
1430636_at	RIKEN cDNA C030010B13 gene	C030010B13Rik	1.92	0.183	2.08	0.041	1.59	0.486	1.54	0.720	-1.07	0.469
1453252_at	dihydrouridine synthase 4-like (S. cerevisiae)	Dus4l	1.73	0.033	2.08	0.005	1.44	0.627	2.72	0.013	1.27	0.260
1435390_at	exonuclease domain containing 1	Exod1	1.69	0.086	2.08	0.027	1.07	0.311	1.19	0.288	1.11	0.173
1440891_at	glutamate receptor, ionotropic, AMPA4 (alpha 4)	Gria4	1.39	0.755	2.08	0.041	-1.08	0.361	1.15	0.495	1.56	0.949
1452112_a_at	RNA binding motif protein 4B	Rbm4b	1.2	0.458	2.08	0.004	1.34	0.206	2.17	0.004	1.29	0.385
1424551_at	zinc finger, FYVE domain containing 27	Zfyve27	-1.16	0.618	2.08	0.041	1.49	0.241	1.23	0.104	1.72	0.221
1431250_at	RIKEN cDNA 9030624G23 gene /// similar to development- a	9030624G23Rik //	1.54	0.120	2.07	0.050	1.17	0.858	-1.2	0.257	1.27	0.069
1431142_s_at	apoptosis-inducing factor (AIF)-like mitochondrion-associatec	Amid	2.39	0.327	2.07	0.009	1.32	0.447	1.25	0.277	1.67	0.321
1450677_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	1.68	0.027	2.07	0.039	1.17	0.018	1.05	0.626	1.19	0.150
1425039_at	integrin, beta-like 1	Itgbl1	2.3	0.067	2.07	0.033	-1.08	0.672	1.41	0.308	1.22	0.151
1447961_s_at	mitochondrial ribosomal protein L38	Mrpl38	1.65	0.255	2.07	0.046	1.09	0.438	1.2	0.065	1.21	0.209
1422367_at	olfactory receptor 70	Olfr70	1.83	0.088	2.07	0.016	1.1	0.896	1.1	0.609	1.31	0.671
1427511_at	Beta-2 microglobulin	B2m	-1.29	0.230	2.06	0.044	1.44	0.385	1.23	0.473	1.4	0.162
1447116_at	Presenilin associated, rhomboid-like	Parl	-2.33	0.073	2.06	0.027	1.98	0.684	2.74	0.019	1.85	0.763
1457756_at	zinc finger protein 192	Zfp192	2.42	0.016	2.06	0.007	1.04	0.697	1.27	0.765	1.01	0.933
1428014_at	histone 1, H4h	Hist1h4h	1.88	0.081	2.05	0.044	1.17	0.339	1.03	0.856	1.53	0.018
1456891_at	DENN/MADD domain containing 2C	Dennd2c	1.56	0.475	2.04	0.021	1.04	0.921	1.09	0.374	1.26	0.023
1453050_at	GINS complex subunit 3 (Psf3 homolog)	Gins3	1.65	0.192	2.04	0.041	1.21	0.062	1.24	0.280	1.21	0.158
1456033_at	T-box 4	Tbx4	1.73	0.143	2.04	0.043	1.43	0.967	-1.05	0.442	1.34	0.795
1437770_at	expressed sequence AW557046	AW557046	1.9	0.302	2.03	0.024	1.07	0.642	-1.17	0.490	1.24	0.957
1458163_at	cDNA sequence BC066028	BC066028	1.74	0.642	2.03	0.027	1.8	0.031	1.37	0.126	1.19	0.446
1431353_at	RIKEN cDNA C330050A14 gene	C330050A14Rik	2.34	0.362	2.03	0.036	1.1	0.844	1.22	0.091	1.32	0.458
1441503_at	doublecortin domain containing 2a	Dcdc2a	2.07	0.104	2.03	0.041	-1.11	0.481	1.29	0.778	1.19	0.131
1459478_at	expressed sequence AA408396	AA408396	2.47	0.757	2.02	0.048	1.34	0.448	1.02	0.975	1.51	0.384

1428003_s_at	thiamine triphosphatase /// zinc finger homeobox 2, antisense	Thtpa /// Zfhx2as	1.67	0.117	2.02	0.004	1.32	0.656	-1.01	0.802	-1.18	0.258
1420248_at	tubulin, gamma 2	Tubg2	1.61	0.082	2.02	0.007	1.23	0.549	1.52	0.577	1.49	0.439
1432656_at	RIKEN cDNA 3222402N08 gene	3222402N08Rik	1.52	0.221	2.01	0.041	-1.22	0.047	1.16	0.656	2.11	0.036
1416505_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	1.34	0.031	2.01	0.033	1.48	0.004	1.38	0.001	1.56	0.010
1455034_at	Nuclear receptor subfamily 4, group A, member 2	Nr4a2	1.28	0.905	2.01	0.042	2.06	0.003	1.63	0.002	2.37	0.002
1454583_at	RIKEN cDNA 2810034D10 gene	2810034D10Rik	1.65	0.698	2	0.024	1.26	0.397	1.17	0.710	1.16	0.738
1433226_at	RIKEN cDNA 6330403N20 gene	6330403N20Rik	3.17	0.080	2	0.038	-1.35	0.227	-1.87	0.101	-1.66	0.191
1444024_at	excision repair cross-complementing rodent repair deficiency	Ercc6l	1.86	0.286	2	0.007	1.03	0.810	1.47	0.085	1.53	0.361
1434815_a_at	mitogen-activated protein kinase-activated protein kinase 3	Mapkapk3	1.31	0.221	2	0.037	-1.04	0.516	1.1	0.117	1.28	0.149
1451415_at	RIKEN cDNA 1810011O10 gene	1810011O10Rik	1.49	0.099	1.99	0.005	2.24	0.033	1.43	0.101	2.06	0.012
1452715_at	RIKEN cDNA 2310022K01 gene	2310022K01Rik	1.4	0.412	1.99	0.035	-1.06	0.636	1.16	0.179	-1.26	0.143
1440364_a_at	RIKEN cDNA A230062G08 gene	A230062G08Rik	1.57	0.404	1.99	0.038	1.34	0.686	1.07	0.688	-1.07	0.806
1434171_at	RIKEN cDNA C330011K17 gene	C330011K17Rik	1.31	0.509	1.99	0.022	1.15	0.357	1.28	0.110	1.37	0.026
1429067_at	calpain, small subunit 2	Capns2	1.6	0.205	1.99	0.048	-1.67	0.056	1.48	0.745	-1.19	0.389
1419456_at	dicarbonyl L-xylulose reductase	Dcxr	1.38	0.106	1.99	0.007	1.21	0.115	1.05	0.285	1.24	0.056
1421553_at	epilepsy, progressive myoclonic epilepsy, type 2 gene alpha	Epm2a	1.08	0.907	1.99	0.018	2.62	0.229	-1.76	0.076	-1.2	0.517
1424952_at	OCIA domain containing 1	Ociad1	2.11	0.042	1.99	0.009	3.14	0.190	-1.13	0.404	1.66	0.444
1450390_x_at	ribosomal protein S18	Rps18	2.47	0.066	1.99	0.012	-1.24	0.202	-1.09	0.650	1.37	0.089
1432272_a_at	excision repair cross-complementing rodent repair deficiency	Xpf	1.53	0.354	1.99	0.002	2.06	0.950	1.36	0.367	1.07	0.384
1449122_at	RIKEN cDNA 3110003A22 gene	3110003A22Rik	1.36	0.496	1.98	0.021	1.36	0.005	1.38	0.040	1.08	0.535
1440125_at	RIKEN cDNA A530054K11 gene	A530054K11Rik	1.55	0.065	1.98	0.030	1.69	0.029	-1.05	0.864	1.21	0.411
1448525_a_at	BCL2/adenovirus E1B interacting protein 3-like	Bnip3l	1.75	0.155	1.98	0.023	1.23	0.073	1.06	0.364	1.07	0.071
1444860_at	Laminin, alpha 3	Lama3	1.82	0.140	1.98	0.044	-1.07	0.518	-1.31	0.377	1.09	0.676
1459771_x_at	phytoceramidase, alkaline	Phca	1.94	0.126	1.98	0.030	1.29	0.928	1.47	0.235	1.05	0.607
1420559_a_at	short stature homeobox 2	Shox2	1.33	0.575	1.98	0.012	2.59	0.097	1.46	0.129	1.54	0.136
1436108_at	thioredoxin domain containing 9	Txndc9	1.33	0.432	1.98	0.006	1.36	0.025	1.18	0.000	1.13	0.531
1422810_at	zinc finger protein 191	Zfp191	1.47	0.293	1.97	0.002	1.13	0.144	1.38	0.050	1.19	0.369
1428361_x_at	hemoglobin alpha, adult chain 1	Hba-a1	1.4	0.123	1.96	0.008	2	0.069	1.08	0.858	-1.21	0.482
1417856_at	avian reticuloendotheliosis viral (v-rel) oncogene related B	Relb	1.23	0.340	1.96	0.027	1.25	0.322	1.11	0.160	1.78	0.508
1453945_at	RIKEN cDNA 2310005E17 gene	2310005E17Rik	2.46	0.587	1.95	0.037	-1.05	0.406	2.18	0.371	-1.06	0.547
1440405_at	Adenylate cyclase 3	Adcy3	1.39	0.450	1.95	0.032	-1.08	0.263	-1.12	0.506	1.24	0.260
1442218_at	mitogen-activated protein kinase kinase kinase 9	Map3k9	2.03	0.457	1.95	0.016	-1.16	0.510	1.36	0.611	-1.21	0.538
1438661_a_at	ADP-ribosylation factor 2	Arf2	1.98	0.417	1.94	0.028	-1.07	0.358	1.2	0.011	1.12	0.183
1437694_at	Expressed sequence BB114266	BB114266	1.41	0.094	1.94	0.036	1.11	0.498	1.04	0.740	1.09	0.637
1448272_at	B-cell translocation gene 2, anti-proliferative	Btg2	1.23	0.153	1.94	0.048	1.43	0.018	1.09	0.254	1.25	0.187
1418184_at	centromere protein M	Cenpm	2.4	0.205	1.94	0.030	1.15	0.148	1.15	0.345	-1.01	0.681
1426235_a_at	glutamate-ammonia ligase (glutamine synthetase)	Glul	1.53	0.402	1.94	0.027	1.2	0.964	1.03	0.688	1.16	0.021
1452224_at	microrchidia 3	Morc3	1.67	0.136	1.94	0.013	1.14	0.036	1.12	0.087	1.06	0.391
1437949_x_at	zinc finger protein 313	Zfp313	2.02	0.039	1.93	0.009	1.52	0.738	1.21	0.340	-1.09	0.341
1448924_at	RIKEN cDNA 4432406C05 gene	4432406C05Rik	1.73	0.733	1.92	0.031	-1.21	0.141	1.16	0.404	1.13	0.552
1449115_at	metal response element binding transcription factor 2	Mtf2	1.4	0.130	1.92	0.042	1.4	0.139	1.21	0.637	-1.17	0.168
1415975_at	calcium regulated heat stable protein 1	Carhsp1	1.61	0.152	1.91	0.034	1.22	0.024	1.17	0.056	1.29	0.008
1419070_at	cystin 1	Cys1	1.8	0.191	1.91	0.001	1.06	0.752	1.39	0.032	1.4	0.474
1442436_at	fructosamine 3 kinase	Fn3k	1.1	0.987	1.91	0.007	-1.34	0.184	-1.02	0.612	1.58	0.100
1456326_at	gene model 784, (NCBI)	Gm784	2.38	0.541	1.91	0.016	1.76	0.855	-1.36	0.388	2.28	0.486
1425868_at	Histone 2, H2bb	Hist2h2bb	1.96	0.132	1.91	0.034	1.36	0.078	1.01	0.632	1.06	0.654
1419455_at	interleukin 10 receptor, beta	Il10rb	1.67	0.199	1.91	0.049	1.28	0.128	1.2	0.002	1.31	0.001
1455636_at	limbic system-associated membrane protein	Lsamp	1.32	0.513	1.91	0.026	1.08	0.688	1.29	0.812	-1.06	0.435
1454946_at	myeloblastosis oncogene-like 2	Mybl2	1.4	0.747	1.91	0.031	1.43	0.268	1.52	0.571	1.61	0.058
1418640_at	sirtuin 1 ((silent mating type information regulation 2, homolo	Sirt1	1.68	0.228	1.91	0.026	1.33	0.090	1.22	0.088	1.38	0.023
1455098_a_at	vitronectin	Vtn	2.01	0.706	1.91	0.018	1.87	0.029	1.11	0.670	1.24	0.976
1430419_at	RIKEN cDNA 2310031A07 gene	2310031A07Rik	1.23	0.776	1.9	0.033	-1.69	0.154	-1.25	0.006	1.12	0.385
1454354_at	RIKEN cDNA 8030476L19 gene	8030476L19Rik	-1.03	0.459	1.9	0.027	1.34	0.100	1	0.977	1.35	0.602
1459525_at	Calcium binding atopy-related autoantigen 1	Cbara1	1.59	0.623	1.9	0.039	1.25	1.000	-1	0.723	2	0.143
1418982_at	CCAAT/enhancer binding protein (C/EBP), alpha	Cebpa	1.1	0.422	1.9	0.034	1.26	0.638	1.09	0.627	1.12	0.638
1452983_at	centrosomal protein 57	Cep57	1.46	0.253	1.9	0.036	1.23	0.197	1.41	0.186	1.17	0.356
1425289_a_at	complement receptor 2	Cr2	2.77	0.249	1.9	0.045	-1.08	0.448	1.44	0.522	1.93	0.413
1424724_a_at	DNA segment, Chr 16, ERATO Doi 472, expressed	D16Ertd472e	1.67	0.326	1.9	0.009	1.06	0.248	1.36	0.022	1.38	0.054

1422446_x_at	insulin II	Ins2	2.58	0.131	1.9	0.003	1.35	0.793	1.7	0.832	1.49	0.942
1419128_at	integrin alpha X	Itgax	1.3	0.882	1.9	0.009	-1.05	0.359	1.5	0.017	-1.79	0.190
1421265_a_at	RNA binding motif protein 38	Rbm38	1.33	0.594	1.9	0.045	1.36	0.540	1.1	0.323	1.52	0.044
1443178_at	ring finger protein 13	Rnf13	1.38	0.039	1.9	0.050	1.69	0.794	1.19	0.822	1.35	0.297
1446276_at	RIKEN cDNA 2310008H04 gene	2310008H04Rik	1.54	0.189	1.89	0.028	1.04	0.872	-1.16	0.545	-1.22	0.240
1444568_at	Actin related protein 2/3 complex, subunit 5	Arpc5	2.03	0.478	1.89	0.040	2.54	0.108	2.25	0.115	2.71	0.679
1436560_at	expressed sequence AW124694	AW124694	2.19	0.008	1.89	0.017	1.18	0.119	1.33	0.263	1.33	0.066
1426473_at	DnaJ (Hsp40) homolog, subfamily C, member 9	Dnajc9	1.24	0.075	1.89	0.007	1.12	0.448	1.23	0.082	1.2	0.008
1415945_at	minichromosome maintenance deficient 5, cell division cycle	Mcm5	1.86	0.277	1.89	0.024	1.03	0.327	1.13	0.064	1.09	0.276
1450087_a_at	nucleolar and coiled-body phosphoprotein 1	Nolc1	1.68	0.346	1.89	0.020	-1	0.959	1.32	0.022	1.11	0.357
1450185_a_at	potassium inwardly-rectifying channel, subfamily J, member 1	Kcnj15	1.34	0.210	1.88	0.006	1.87	0.279	1.45	0.085	2.1	0.272
1433407_at	minichromosome maintenance deficient 10 (S. cerevisiae)	Mcm10	1.91	0.373	1.88	0.031	1.51	0.546	-1.14	0.574	1.06	0.921
1459137_at	promyelocytic leukemia	Pml	1.22	0.245	1.88	0.004	1.32	0.160	-1.3	0.268	1.6	0.099
1432564_at	RIKEN cDNA 1700066C05 gene	1700066C05Rik	1.47	0.375	1.87	0.001	2.09	0.375	-1.08	0.474	-1.46	0.073
1446187_at	RIKEN cDNA 4831416G18 gene	4831416G18Rik	1.25	0.730	1.87	0.043	1.14	0.642	1.79	0.647	-1.18	0.406
1452796_at	differentially expressed in FDCP 6	Def6	1.45	0.151	1.87	0.024	1.22	0.002	1.24	0.012	1.4	0.012
1424679_at	mab-21-like 1 (C. elegans)	Mab21l1	1.28	0.980	1.87	0.020	2.39	0.150	3.17	0.033	-1.06	0.661
1450228_a_at	phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma	Pip5k1c	2.41	0.137	1.87	0.031	2.79	0.092	-1.41	0.263	1.19	0.820
1448370_at	Unc-51 like kinase 1 (C. elegans)	Ulk1	1.36	0.199	1.87	0.029	1.4	0.123	1.11	0.317	1.33	0.124
1453064_at	RIKEN cDNA 5730466H23 gene	5730466H23Rik	1.18	0.316	1.86	0.038	1.17	0.545	1.02	0.891	1.42	0.118
1455334_at	RIKEN cDNA 9830167H18 gene	9830167H18Rik	1.33	0.301	1.86	0.016	1.15	0.259	1.3	0.019	1.02	0.716
1448466_at	cell division cycle associated 5	Cdca5	1.66	0.380	1.86	0.026	1.19	0.167	1.18	0.206	1.19	0.042
1421827_at	delta-like 4 (Drosophila)	Dll4	1.54	0.467	1.86	0.025	1.12	0.908	1.24	0.453	1.18	0.816
1439323_a_at	mitogen activated protein kinase kinase kinase kinase 1 /// si	Map4k1 /// LOC67	2.37	0.250	1.86	0.018	1.36	0.901	1.3	0.751	-1.23	0.453
1444634_at	NOL1/NOP2/Sun domain family 3	Nsun3	2.49	0.396	1.86	0.029	1.03	0.708	1.45	0.005	1.1	0.724
1423481_at	RIO kinase 2 (yeast)	Riok2	1.49	0.271	1.86	0.017	-1.01	0.820	1.2	0.018	1.13	0.194
1431175_at	RIKEN cDNA 1810019D21 gene	1810019D21Rik	1.13	0.922	1.85	0.042	1.73	0.264	1.08	0.809	1.06	0.727
1430678_at	RIKEN cDNA 5730457N03 gene	5730457N03Rik	2.11	0.191	1.85	0.020	-1.28	0.235	1.28	0.365	1.55	0.766
1452301_at	aldehyde dehydrogenase 3 family, member B1	Aldh3b1	-1.04	0.893	1.85	0.029	-1.05	0.768	-1.1	0.475	1.14	0.875
1447495_at	fibronectin type 3 and ankyrin repeat domains 1	Fank1	1.21	0.018	1.85	0.013	-1.58	0.192	1.66	0.640	2.7	0.556
1422867_at	granzyme G	Gzmg	1.13	0.959	1.85	0.021	1.75	0.570	-1.07	0.483	-1.69	0.150
1423218_a_at	mitochondrial ribosomal protein L49	Mrpl49	1.31	0.017	1.85	0.007	1.24	0.006	1.36	0.009	1.29	0.096
1424985_a_at	SRY-box containing gene 10	Sox10	1.14	0.775	1.85	0.009	1.11	0.842	-1.33	0.170	1.04	0.718
1424777_at	WD repeat domain 21	Wdr21	1.17	0.585	1.85	0.024	1.07	0.557	1.33	0.270	1.42	0.078
1428469_a_at	DAZ interacting protein 1	Dzip1	1.44	0.295	1.84	0.014	1.51	0.126	1.34	0.133	-1.07	0.509
1423998_at	general transcription factor IIIC, polypeptide 5	Gtf3c5	1.55	0.208	1.84	0.026	1.33	0.040	1.13	0.090	1.33	0.050
1442671_at	Huntingtin interacting protein 2	Hip2	1.74	0.141	1.84	0.043	1.12	0.512	1.19	0.486	-1.23	0.400
1456777_at	maltase-glucoamylase	Mgam	3.07	0.046	1.84	0.022	1.3	0.456	1.11	0.811	1.08	0.859
1424692_at	RIKEN cDNA 2810055F11 gene	2810055F11Rik	1.53	0.251	1.83	0.018	1.25	0.007	1.3	0.039	1.47	0.008
1416969_at	G two S phase expressed protein 1	Gtse1	1.23	0.069	1.83	0.000	1.19	0.188	1.17	0.038	1.43	0.030
1429110_a_at	NOL1/NOP2/Sun domain family, member 4	Nsun4	1.51	0.097	1.83	0.026	1.47	0.012	1.46	0.012	1.38	0.086
1435632_at	nuclear fragile X mental retardation protein interacting protein	Nufip2	1.98	0.267	1.83	0.040	1.13	0.169	1.2	0.098	1.02	0.776
1450259_a_at	signal transducer and activator of transcription 5A	Stat5a	1.67	0.404	1.83	0.044	1.23	0.147	1.22	0.085	1.39	0.004
1442629_at	5'-nucleotidase, cytosolic II	Nt5c2	2.24	0.060	1.82	0.000	1.27	0.695	1.22	0.097	1.2	0.298
1425271_at	proteasome (prosome, macropain) 26S subunit, ATPase 3, ir	Psmc3ip	1.41	0.628	1.82	0.008	1.21	0.247	1.09	0.364	1.21	0.138
1425602_a_at	rabaptin, RAB GTPase binding effector protein 2	Rabep2	1.49	0.091	1.82	0.023	1.28	0.122	1.36	0.076	1.32	0.237
1441585_at	Spastic paraplegia 7 homolog (human)	Spg7	-1.31	0.176	1.82	0.002	-1.24	0.335	1.36	0.700	1.59	0.053
1447657_s_at	synaptopodin 2-like	Synpo2l	1.1	0.893	1.82	0.027	1.17	0.816	1.44	0.005	1.46	0.229
1444254_at	tensin 4	Tns4	1.4	0.487	1.82	0.011	-1.13	0.347	-1.07	0.554	2.37	0.303
1420891_at	wingless-related MMTV integration site 7B	Wnt7b	-1.06	0.447	1.82	0.043	-1.91	0.128	1.2	0.947	1.06	0.935
1428866_at	RIKEN cDNA 2810037O22 gene	2810037O22Rik	1.93	0.543	1.81	0.031	1.62	0.993	1.38	0.198	1.11	0.467
1423578_at	procollagen, type XI, alpha 2	Col11a2	2.04	0.018	1.81	0.043	-2.01	0.119	1.06	0.949	2.92	0.763
1448823_at	chemokine (C-X-C motif) ligand 12	Cxcl12	2.32	0.020	1.81	0.034	-1.26	0.094	-1.1	0.083	1.05	0.611
1444263_at	Enhancer of zeste homolog 2 (Drosophila)	Ezh2	1.56	0.482	1.81	0.031	1.36	0.639	1.64	0.299	-1.5	0.311
1436166_at	storkhead box 2	Stox2	1.51	0.061	1.81	0.008	1.01	0.667	-1.27	0.031	-1.78	0.007
1428821_at	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophospha	Agpat2	1.51	0.249	1.8	0.047	1.21	0.012	1.18	0.042	1.26	0.006
1445758_at	CDNA sequence BC049816	BC049816	1.88	0.009	1.8	0.021	-1.03	0.688	1.12	0.933	1.04	0.769
1448886_at	GATA binding protein 3	Gata3	1.33	0.086	1.8	0.017	6.7	0.196	1.21	0.857	-1.11	0.246

1449204_at	gap junction membrane channel protein beta 5	Gjb5	1.76	0.084	1.8	0.043	1.35	0.079	-1.14	0.279	1.74	0.195
1418825_at	immunity-related GTPase family, M	Irgm	1.22	0.160	1.8	0.032	1.22	0.061	1.17	0.044	1.34	0.116
1417838_at	spermiogenesis specific transcript on the Y 2 /// similar to RIK	Ssty2 /// LOC3821	1.65	0.511	1.8	0.048	1.24	0.129	-1.07	0.686	1.04	0.772
1432489_a_at	RIKEN cDNA 2410187C16 gene	2410187C16Rik	1.53	0.415	1.79	0.045	1.27	0.283	1.07	0.618	1.33	0.459
1457693_a_at	RIKEN cDNA 6430537H07 gene	6430537H07Rik	1.19	0.765	1.79	0.041	-1.1	0.374	1.69	0.339	-1.3	0.124
1436630_at	Aquaporin 11	Aqp11	1.52	0.761	1.79	0.029	1.36	0.451	-1.41	0.032	1.13	0.274
1427718_a_at	transformed mouse 3T3 cell double minute 2	Mdm2	1.1	0.296	1.79	0.000	1.17	0.109	1.14	0.025	1.25	0.199
1422055_at	midline 1	Mid1	1.21	0.615	1.79	0.002	-1.56	0.155	1.83	0.699	1.12	0.526
1443500_at	Myeloid/lymphoid or mixed lineage-leukemia translocation to	Mllt10	1.18	0.076	1.79	0.012	-1.01	0.837	1.17	0.603	1.06	0.684
1421131_a_at	zinc finger protein 111	Zfp111	1.07	0.795	1.79	0.002	1.13	0.235	1.08	0.939	1.48	0.035
1449607_at	RIKEN cDNA A230070E04 gene	A230070E04Rik	1.37	0.371	1.78	0.016	1.2	0.646	-1.09	0.235	1.35	0.654
1425176_at	C1q-like 3	C1ql3	1.43	0.042	1.78	0.034	-1.28	0.240	1.15	0.315	1.34	0.288
1454112_a_at	centrosomal protein 27	Cep27	1.33	0.301	1.78	0.045	1.09	0.276	1.23	0.045	1.13	0.567
1444673_at	RIKEN cDNA E030031F02 gene	E030031F02Rik	1.25	0.371	1.78	0.015	1.57	0.809	1.56	0.874	-1.09	0.565
1458729_at	FK506 binding protein 4	Fkbp4	1.93	0.006	1.78	0.024	1.43	0.532	1.13	0.236	1.83	0.320
1450448_at	stanniocalcin 1	Stc1	1.39	0.078	1.78	0.036	1.42	0.325	1.47	0.084	1.92	0.048
1441698_at	RIKEN cDNA 2410025L10 gene	2410025L10Rik	1.6	0.014	1.77	0.048	1.11	0.929	1.37	0.442	-1.16	0.597
1432220_at	RIKEN cDNA 4933430L12 gene	4933430L12Rik	1.41	0.062	1.77	0.039	-1.04	0.404	1.27	0.453	1.23	0.585
1449907_at	beta-carotene 15,15'-monooxygenase	Bcmo1	1.34	0.892	1.77	0.044	-1.32	0.345	1.1	0.784	1.3	0.427
1423711_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, ass	Ndufaf1	1.4	0.318	1.77	0.017	1.19	0.003	1.23	0.020	1.29	0.019
1456006_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	1.12	0.033	1.76	0.037	-1.12	0.348	1.28	0.092	1.45	0.081
1431843_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-	Nfkbie	1.9	0.195	1.76	0.033	1.19	0.970	1.14	0.485	1.49	0.056
1434333_a_at	protein kinase D2	Prkd2	1.14	0.337	1.76	0.021	1.28	0.116	1.09	0.604	1.41	0.188
1449127_at	selectin, platelet (p-selectin) ligand	Selpl	-1.05	0.616	1.76	0.019	1.1	0.900	1.34	0.197	1.72	0.218
1435452_at	transmembrane protein 20	Tmem20	1.9	0.073	1.76	0.005	-1.16	0.542	-1.15	0.356	1.31	0.277
1450231_a_at	baculoviral IAP repeat-containing 4	Birc4	-1.06	0.272	1.75	0.020	1.32	0.071	1.19	0.427	1.03	0.595
1429025_a_at	hexamthylene bis-acetamide inducible 2	Hexim2	1.87	0.233	1.75	0.025	-1.22	0.222	3.29	0.089	1.73	0.282
1421196_at	protein tyrosine phosphatase, non-receptor type 11	Ptpn11	1.78	0.002	1.75	0.006	-1.03	0.751	1.09	0.547	1.05	0.614
1425352_at	REST corepressor 3	Rcor3	3.09	0.165	1.75	0.031	-1.41	0.097	-1.05	0.631	1.11	0.123
1443158_at	Sex comb on midleg homolog 1	Scmh1	1.76	0.189	1.75	0.046	1.32	0.220	1.3	0.035	-1.01	0.908
1439385_x_at	Solute carrier family 13 (sodium-dependent dicarboxylate trar	Slc13a3	1.75	0.389	1.75	0.041	-1.01	0.982	5.04	0.075	1.04	0.511
1448940_at	tripartite motif protein 21	Trim21	2.57	0.753	1.75	0.004	2.97	0.013	1.14	0.363	1.81	0.015
1428932_at	tetratricopeptide repeat domain 21A	ttc21a	1.19	0.875	1.75	0.027	-1.08	0.470	-1.59	0.135	-1.07	0.939
1421320_a_at	queuine tRNA-ribosyltransferase domain containing 1	Qtrtd1	1.08	0.401	1.74	0.035	-1.08	0.961	2.26	0.105	1.11	0.867
1426604_at	ribonuclease L (2', 5'-oligoisoadenylate synthetase-depender	Rnasel	1.47	0.291	1.74	0.032	2.45	0.269	1.46	0.459	1.54	0.400
1426337_a_at	TEA domain family member 4	Tead4	1.49	0.173	1.74	0.016	-1.21	0.162	-1.01	0.696	1.35	0.316
1434752_at	zinc finger protein 207	Zfp207	1.91	0.016	1.74	0.005	1.45	0.244	1.23	0.481	-1.09	0.269
1418027_at	exonuclease 1	Exo1	1.28	0.025	1.73	0.002	1.24	0.305	1.42	0.078	-1	0.859
1426871_at	F-box only protein 33	Fbxo33	1.3	0.196	1.73	0.044	1.15	0.158	1.25	0.056	1.38	0.163
1431506_s_at	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomer	Ppih /// LOC43306	1.61	0.164	1.73	0.048	1.09	0.245	1.21	0.013	1.04	0.680
1460168_at	stem-loop binding protein	Slbp	1.2	0.071	1.73	0.002	1.27	0.009	1.23	0.002	1.28	0.092
1426415_a_at	tripartite motif protein 25	Trim25	1.15	0.791	1.73	0.023	1.3	0.964	1.1	0.329	1.16	0.012
1455674_at	WD repeat domain 76	Wdr76	1.16	0.409	1.73	0.003	1.59	0.144	1.05	0.869	1.41	0.618
1458863_at	RIKEN cDNA 6330415G19 gene	6330415G19Rik	1.51	0.144	1.72	0.010	1.45	0.007	1.34	0.123	2.68	0.024
1427081_at	RIKEN cDNA A630072M18 gene	A630072M18Rik	1.37	0.028	1.72	0.008	1.41	0.185	1.17	0.040	1.4	0.031
1426894_s_at	RIKEN cDNA C230093N12 gene	C230093N12Rik	1.27	0.315	1.72	0.038	1.43	0.108	1.71	0.000	1.61	0.089
1421688_a_at	chemokine (C-C motif) ligand 1	Ccl1	1.19	0.987	1.72	0.044	1.53	0.739	-1.14	0.498	-1.44	0.156
1454648_s_at	DNA segment, Chr 10, Wayne State University 102, expresse	D10Wsu102e	1.35	0.463	1.72	0.014	1.18	0.012	1.38	0.006	1.3	0.026
1449176_a_at	deoxycytidine kinase	Dck	1.24	0.631	1.72	0.018	1.3	0.234	-1.05	0.493	1.57	0.050
1426290_at	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	Dimt1	1.33	0.278	1.72	0.009	1.07	0.253	1.07	0.403	1.19	0.111
1432181_s_at	endothelial cell growth factor 1 (platelet-derived)	Ecgf1	1.17	0.185	1.72	0.003	1.5	0.155	1.5	0.006	1.67	0.016
1440742_at	Enhancer of polycomb homolog 1 (Drosophila)	Epc1	1.77	0.122	1.72	0.013	1.41	0.509	1.15	0.392	1.62	0.076
1430311_at	Myristoylated alanine rich protein kinase C substrate	Marcks	1.13	0.722	1.72	0.001	1.35	0.038	1.42	0.646	1.12	0.888
1423524_at	microtubule associated serine/threonine kinase-like	Mastl	1.51	0.047	1.72	0.025	1.06	0.586	1.26	0.101	1.01	0.824
1421144_at	retinitis pigmentosa GTPase regulator interacting protein 1	Rpgrip1	1.67	0.038	1.72	0.036	-1.02	0.571	1.17	0.016	1.03	0.995
1424399_at	uridine-cytidine kinase 1	Uck1	1.37	0.314	1.72	0.021	1.01	0.769	1.12	0.015	1.17	0.075
1429268_at	RIKEN cDNA 2610318N02 gene	2610318N02Rik	2.21	0.003	1.71	0.022	-1.18	0.469	1.97	0.024	1.27	0.089
1454421_at	RIKEN cDNA 4930423D22 gene	4930423D22Rik	1.23	0.518	1.71	0.036	-1.45	0.241	-2.56	0.001	-1.09	0.384

1451266_at	mitochondrial ribosomal protein L50	Mrpl50	1.3	0.341	1.71	0.015	1.19	0.109	1.23	0.125	1.04	0.917
1422970_at	Max dimerization protein 3	Mxd3	1.47	0.050	1.71	0.010	-1	0.697	1.19	0.350	1.23	0.366
1451767_at	neutrophil cytosolic factor 1	Ncf1	1.08	0.434	1.71	0.039	1.29	0.694	1.78	0.604	2.6	0.008
1423044_at	proline synthetase co-transcribed	Prosc	1.36	0.306	1.71	0.013	1.12	0.034	1.26	0.020	1.19	0.005
1429739_a_at	zinc finger protein 278	Zfp278	1.09	0.620	1.71	0.019	1.26	0.025	1.25	0.028	1.52	0.009
1454087_at	zinc fingerprotein 618	Zfp618	1.07	0.937	1.71	0.014	-1.19	0.490	1.17	0.973	-1.06	0.610
1450735_at	RIKEN cDNA 1810003N24 gene	1810003N24Rik	1.42	0.210	1.7	0.045	1.07	0.232	1.17	0.016	1.05	0.492
1459607_at	RIKEN cDNA 2900001O04 gene	2900001O04Rik	1.16	0.810	1.7	0.016	1.3	0.182	1.13	0.681	1.28	0.141
1424091_at	expressed sequence AI449175	AI449175	1.75	0.837	1.7	0.006	1.28	0.187	1.04	0.569	1.29	0.445
1446889_at	DNA segment, Chr 2, ERATO Doi 105, expressed	D2Ertd105e	1.78	0.193	1.7	0.032	1.1	0.854	2.34	0.360	-1.17	0.249
1442684_x_at	high mobility group 20A	Hmg20a	1.69	0.165	1.7	0.004	1.25	0.411	1.1	0.895	1.12	0.574
1451186_at	interferon stimulated exonuclease gene 20-like 1	Isg20l1	1.21	0.847	1.7	0.012	-1.17	0.308	1.37	0.053	-1.01	0.757
1427679_at	large tumor suppressor	Lats1	1.57	0.261	1.7	0.027	1.04	0.992	1.4	0.034	1.07	0.815
1453119_at	OTU domain containing 1	Otud1	1.36	0.140	1.7	0.002	1.6	0.116	1.1	0.400	1.33	0.088
1428615_at	purinergic receptor P2Y, G-protein coupled, 5	P2ry5	1.24	0.018	1.7	0.043	1.44	0.019	1.35	0.009	1.52	0.011
1420502_at	spermidine/spermine N1-acetyl transferase 1	Sat1	1.29	0.135	1.7	0.006	1.38	0.014	1.27	0.011	1.32	0.006
1456971_at	solute carrier family 1 (glutamate transporter), member 7	Slc1a7	1.08	0.636	1.7	0.034	1.78	0.542	1.97	0.798	1.22	0.863
1451080_at	ubiquitin specific peptdiase 1	Usp1	1.38	0.036	1.7	0.011	1.28	0.022	1.17	0.029	1.25	0.042
1439563_at	zinc finger protein 3	Zfp3	1.43	0.974	1.7	0.003	-1.24	0.186	1.14	0.376	1	0.994
1453610_at	RIKEN cDNA 4931406B18 gene	4931406B18Rik	1.1	0.502	1.69	0.022	1.68	0.353	-1.41	0.214	1.03	0.711
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	1.16	0.333	1.69	0.005	1.25	0.005	1.21	0.002	1.29	0.003
1446080_at	Cut-like 2 (Drosophila)	Cutl2	1.03	0.922	1.69	0.018	-1.13	0.354	1.33	0.089	1.03	0.890
1418898_at	lin-7 homolog C (C. elegans)	Lin7c	1.32	0.281	1.69	0.018	1.08	0.103	1.24	0.000	1.14	0.323
1426533_at	nucleolar protein 5A	Nol5a	1.43	0.428	1.69	0.040	1.27	0.001	1.43	0.008	1.2	0.087
1427518_at	cDNA sequence D10627	D10627	1.74	0.287	1.68	0.035	1.24	0.131	1.07	0.502	1.04	0.726
1452658_at	KRR1, small subunit (SSU) processome component, homolog	Krr1	1.21	0.670	1.68	0.043	1.12	0.534	1.26	0.065	1.07	0.709
1422009_at	ATPase, Na+/K+ transporting, beta 2 polypeptide	Atp1b2	1.37	0.097	1.67	0.038	1.12	0.676	1.42	0.114	1.29	0.269
1428069_at	cell division cycle associated 7	Cdca7	1.26	0.680	1.67	0.007	1.49	0.040	1.09	0.294	1.37	0.010
1424620_at	DNA segment, Chr 13, Wayne State University 177, express	D13Wsu177e	1.39	0.308	1.67	0.009	1.07	0.017	1.17	0.028	1.13	0.397
1415677_at	dehydrogenase/reductase (SDR family) member 1	Dhrs1	1.82	0.243	1.67	0.034	1.17	0.251	1.1	0.060	1.09	0.301
1426103_a_at	estrogen receptor 2 (beta)	Esr2	1.77	0.483	1.67	0.002	1.14	0.644	2.19	0.704	1.46	0.210
1449390_at	G patch domain containing 4	Gpatc4	1.28	0.223	1.67	0.025	1.23	0.362	1.08	0.788	1.11	0.620
1422527_at	histocompatibility 2, class II, locus DMa	H2-DMa	1.2	0.340	1.67	0.039	-1.09	0.620	1	0.924	1.37	0.284
1451552_at	Similar to lipoyltransferase	MGC28431	1.43	0.443	1.67	0.015	1.25	0.046	1.42	0.027	1.44	0.103
1423211_at	nucleolar protein family A, member 3	Nola3	1.51	0.167	1.67	0.043	1.22	0.191	1.12	0.059	1.25	0.119
1417273_at	pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	1.35	0.061	1.67	0.002	1.42	0.373	-1.06	0.748	1.51	0.100
1437563_at	PHD finger protein 20-like 1	Phf20l1	1.48	0.011	1.67	0.034	1.12	0.719	1.02	0.876	1.05	0.734
1422628_at	RIKEN cDNA 4632417K18 gene	4632417K18Rik	1.29	0.065	1.66	0.013	1.21	0.004	1.27	0.002	1.23	0.018
1430520_at	copine VIII	Cpne8	1.71	0.304	1.66	0.036	1.17	0.516	1.01	0.927	1.42	0.019
1450939_at	ectonucleoside triphosphate diphosphohydrolase 1	Entpd1	1.72	0.581	1.66	0.048	-1.26	0.273	-1.43	0.202	1.05	0.455
1460600_at	similar to ubiquitin-conjugating enzyme E2Q (putative) 2	LOC245350	1.13	0.686	1.66	0.009	1.07	0.103	1.12	0.089	1.18	0.155
1452132_at	TLC domain containing 1	Tlcd1	1.3	0.230	1.66	0.043	1.26	0.157	1.2	0.076	1.34	0.023
1439503_at	zinc finger protein 28	Zfp28	1.13	0.629	1.66	0.006	1.7	0.006	1.16	0.111	-1.03	0.707
1449391_at	zinc finger protein 37	Zfp37	1.6	0.298	1.66	0.042	1.51	0.276	1.34	0.002	1.41	0.024
1424548_at	zinc finger, CCCH-type with G patch domain	Zgpat	1.14	0.060	1.66	0.014	1.26	0.364	1.19	0.057	1.39	0.133
1451288_s_at	RIKEN cDNA 1810043G02 gene	1810043G02Rik	1.58	0.359	1.65	0.007	1.33	0.308	1.03	0.973	1.32	0.197
1435979_a_at	myosin XVB	Myo15b	1.17	0.253	1.65	0.042	1.28	0.796	1.11	0.886	-1.04	0.723
1455840_at	Rap guanine nucleotide exchange factor (GEF) 5	Rapgef5	1.17	0.784	1.65	0.042	1.69	0.633	2.27	0.023	-1.64	0.078
1421237_at	thymopoietin	Tmpo	4.59	0.386	1.65	0.006	-1.01	0.858	1.33	0.097	1.26	0.442
1430870_at	RIKEN cDNA 4930442P19 gene	4930442P19Rik	-1.28	0.390	1.64	0.033	-1.34	0.129	1.57	0.533	-2.05	0.061
1433577_at	RIKEN cDNA A730017C20 gene	A730017C20Rik	1.91	0.002	1.64	0.018	1.83	0.096	1.19	0.786	1.12	0.773
1422715_s_at	acid phosphatase 1, soluble /// similar to acid phosphatase 1,	Acp1 /// LOC6312	1.51	0.087	1.64	0.010	1.03	0.657	-1.02	0.399	1.1	0.336
1424528_at	cell growth regulator with EF hand domain 1	Cgref1	1.14	0.577	1.64	0.001	1.22	0.024	1.13	0.280	1.16	0.020
1455259_a_at	RIKEN cDNA D530033C11 gene	D530033C11Rik	1.46	0.530	1.64	0.025	1.07	0.645	1.23	0.101	1.13	0.801
1416716_at	embryonal Fyn-associated substrate	Efs	1.25	0.208	1.64	0.046	1.09	0.016	1.04	0.453	1.3	0.096
1416555_at	etoposide induced 2.4 mRNA	Ei24	1.18	0.276	1.64	0.007	1.11	0.125	1.12	0.007	1.17	0.021
1454835_at	EPM2A (laforin) interacting protein 1	Epm2aip1	1.21	0.167	1.64	0.030	1.1	0.375	1.34	0.102	1.5	0.123
1436601_at	F-box protein 46	Fbxo46	1.36	0.190	1.64	0.024	-1.07	0.675	-1.06	0.564	1.23	0.602

1460159_at	myb-like, SWIRM and MPN domains 1	Mysm1	2.26	0.055	1.64	0.050	1.76	0.721	1.53	0.056	-1.35	0.063
1419058_at	polymerase (RNA) I polypeptide E	Polr1e	1.3	0.129	1.64	0.012	1.13	0.472	1.13	0.212	1.41	0.115
1451301_at	tropomodulin 2	Tmod2	1	0.932	1.64	0.034	-1.01	0.645	1.1	0.700	1.94	0.568
1448821_at	tyrosinase	Tyr	1.15	0.890	1.64	0.008	1.57	0.059	1.02	0.584	1.34	0.460
1429586_at	RIKEN cDNA 4930558N01 gene	4930558N01Rik	1.32	0.065	1.63	0.033	-1.02	0.672	1.12	0.357	-1.02	0.628
1449513_at	a disintegrin and metallopeptidase domain 24 (testase 1)	Adam24	1.4	0.550	1.63	0.019	1.39	0.883	1.33	0.204	1.04	0.929
1435863_at	COMM domain containing 6	Commd6	1.44	0.059	1.63	0.012	1.12	0.038	1.2	0.044	1.26	0.012
1457806_at	dedicator of cyto-kinesis 1	Dock1	1.47	0.114	1.63	0.010	1.21	0.630	2.41	0.566	1.42	0.646
1451633_a_at	guanine nucleotide binding protein (G protein), gamma transc	Gngt1	-1.09	0.496	1.63	0.029	1.57	0.984	-1.11	0.371	1.13	0.774
1455238_at	melanoma associated antigen (mutated) 1-like 1	Mum1l1	1.36	0.100	1.63	0.045	1.46	0.009	1.4	0.011	1.1	0.240
1428040_at	one cut domain, family member 3	Onecut3	1.42	0.437	1.63	0.012	1.11	0.937	-1.09	0.449	-1.05	0.411
1429216_at	progestin and adipoQ receptor family member III	Paqr3	1.12	0.404	1.63	0.031	1.22	0.132	-1.1	0.274	1.15	0.373
1427094_at	polymerase (DNA directed), epsilon 2 (p59 subunit)	Pole2	1.28	0.196	1.63	0.037	1.23	0.052	1.16	0.061	1.32	0.087
1436300_at	receptor interacting protein kinase 5	Ripk5	1.48	0.152	1.63	0.042	1.11	0.108	1.1	0.008	1.03	0.852
1451803_a_at	vascular endothelial growth factor B	Vegfb	2.82	0.178	1.63	0.042	1.04	0.737	1.07	0.594	-1.35	0.114
1447401_at	WW domain binding protein 11	Wbp11	1.44	0.085	1.63	0.032	1.09	0.763	1.4	0.996	-1.87	0.165
1434697_at	RIKEN cDNA 1110001P04 gene	1110001P04Rik	1.22	0.127	1.62	0.013	1.13	0.241	1.07	0.108	1.22	0.004
1423100_at	FBJ osteosarcoma oncogene	Fos	-1.01	0.953	1.62	0.005	1.36	0.029	1.46	0.003	1.53	0.003
1441295_at	lectin, mannose-binding 2-like	Lman2l	1.07	0.807	1.62	0.040	-1.03	0.854	-1.08	0.300	-1.02	0.705
1416638_at	sal-like 2 (Drosophila)	Sall2	1.08	0.786	1.62	0.014	1.26	0.049	-1.01	0.778	1.33	0.393
1429260_at	RIKEN cDNA 1810014B01 gene	1810014B01Rik	1.55	0.306	1.61	0.020	1.22	0.567	1.44	0.568	1.19	0.718
1451144_at	brix domain containing 2	Bxdc2	1.31	0.240	1.61	0.046	1.09	0.147	1.19	0.000	1.07	0.226
1425846_a_at	calneuron 1	Caln1	1.38	0.754	1.61	0.009	2.41	0.402	1.18	0.850	1.12	0.443
1422969_s_at	inositol hexaphosphate kinase 1	Ihpk1	1.04	0.526	1.61	0.012	1.19	0.774	1.08	0.160	1.27	0.159
1429389_at	SET domain and mariner transposase fusion gene	Setmar	1.68	0.133	1.61	0.043	1.05	0.985	1.25	0.110	1.09	0.601
1443913_at	Vacuolar protein sorting 33A (yeast)	Vps33a	1.82	0.257	1.61	0.024	1.64	0.559	1.73	0.959	1.05	0.549
1429728_at	RIKEN cDNA 4930429M06Rik	4930429M06Rik	1.67	0.022	1.6	0.023	1.38	0.212	1.06	0.653	1.09	0.260
1434748_at	cytoskeleton associated protein 2	Ckap2	1.18	0.118	1.6	0.028	1.21	0.097	-1.02	0.644	1.29	0.075
1429888_a_at	heat shock protein 2	Hspb2	1.63	0.512	1.6	0.048	-1.04	0.721	1.23	0.299	1.1	0.668
1417922_at	kelch repeat and BTB (POZ) domain containing 4	Kbtbd4	1.23	0.136	1.6	0.008	1.27	0.027	-1	0.837	1.41	0.087
1417057_a_at	peptidylprolyl isomerase D (cyclophilin D) /// lysosomal-assoc	Ppid /// Lamp3 ///	1.1	0.617	1.6	0.030	1.12	0.381	1.24	0.030	1.19	0.227
1417139_at	RIKEN cDNA 1700022L09 gene	1700022L09Rik	1.06	0.416	1.59	0.038	1.02	0.555	1.03	0.492	1.21	0.399
1430280_at	RIKEN cDNA 1810062G17 gene	1810062G17Rik	2.24	0.257	1.59	0.027	2.09	0.217	2.45	0.014	2.15	0.982
1437780_at	Fanconi anemia, complementation group B	Fancb	1.22	0.213	1.59	0.008	1.16	0.290	1.14	0.096	1.16	0.177
1422250_at	mitogen activated protein kinase kinase kinase 2	Map3k2	1.29	0.201	1.59	0.012	-1.19	0.065	-1.01	0.742	-1.03	0.434
1433565_at	PRP38 pre-mRNA processing factor 38 (yeast) domain conta	Prpf38a	1.33	0.268	1.59	0.020	1.08	0.230	1.1	0.070	-1.04	0.480
1451560_at	proline rich 12	Prr12	1.2	0.299	1.59	0.028	1.01	0.889	1.5	0.622	1.51	0.194
1428983_at	scleraxis	Scx	1.09	0.499	1.59	0.001	-1.18	0.501	1.1	0.557	-1.02	0.908
1451302_at	RIKEN cDNA 1110012L19 gene	1110012L19Rik	1.24	0.261	1.58	0.011	1.24	0.028	1.19	0.013	1.2	0.054
1452273_at	expressed sequence AA409316	AA409316	1.23	0.209	1.58	0.035	1.42	0.014	1.3	0.012	1.55	0.033
1454814_s_at	expressed sequence AU021838	AU021838	1.26	0.123	1.58	0.015	1.17	0.023	1.28	0.052	1.29	0.007
1456280_at	claspin homolog (Xenopus laevis)	Clspn	1.25	0.013	1.58	0.007	1.11	0.244	1.08	0.420	1.16	0.119
1454737_at	dual specificity phosphatase 9	Dusp9	1.03	0.928	1.58	0.049	1.37	0.022	1.24	0.014	1.45	0.045
1436310_at	gem (nuclear organelle) associated protein 5	Gemin5	1.5	0.337	1.58	0.050	1.09	0.696	1.18	0.086	1.16	0.282
1417541_at	helicase, lymphoid specific	Hells	1.35	0.006	1.58	0.003	1.17	0.184	1.06	0.635	1.1	0.290
1424473_at	polymerase (RNA) II (DNA directed) polypeptide H	Polr2h	1.25	0.115	1.58	0.000	1.27	0.005	1.21	0.041	1.22	0.054
1417972_s_at	processing of precursor 5, ribonuclease P/MRP family (S. cer	Pop5	1.1	0.342	1.58	0.003	1.17	0.038	1.23	0.015	1.38	0.016
1418369_at	DNA primase, p49 subunit	Prim1	1.28	0.071	1.58	0.040	1.22	0.017	1.13	0.095	1.07	0.325
1428905_at	Ras-related GTP binding A	Rraga	1.41	0.300	1.58	0.012	1.12	0.009	1.58	0.002	1.23	0.012
1450461_at	transcription factor 7, T-cell specific	Tcf7	1.47	0.221	1.58	0.034	-1.01	0.720	-1.13	0.600	1.17	0.666
1423951_at	TM2 domain containing 3	Tm2d3	1.24	0.355	1.58	0.014	1.03	0.782	1.09	0.273	1.23	0.059
1449354_at	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1,	U2af1-rs1	1.26	0.055	1.58	0.016	1.17	0.083	1.05	0.826	1.15	0.354
1437979_at	Zinc finger, CCHC domain containing 2	Zcchc2	-1.29	0.266	1.58	0.001	-1.08	0.536	1.17	0.868	1.11	0.812
1416370_at	zinc finger proliferation 1	Zipro1	1.11	0.511	1.58	0.025	1.29	0.099	1.25	0.024	1.5	0.004
1453006_at	RIKEN cDNA 2610306H15 gene	2610306H15Rik	1.09	0.348	1.57	0.040	1.44	0.036	1.26	0.000	1.57	0.006
1450323_at	RIKEN cDNA 5730493B19 gene	5730493B19Rik	1.54	0.270	1.57	0.020	1.32	0.017	-1.35	0.138	-1.07	0.435
1428457_at	RIKEN cDNA 5830472M02 gene	5830472M02Rik	1.29	0.161	1.57	0.024	1.18	0.058	1.21	0.005	1.24	0.016
1451987_at	arrestin, beta 2	Arrb2	1.33	0.887	1.57	0.021	1.09	0.349	1.03	0.539	1.52	0.236

1447332_at	expressed sequence C86896	C86896	1.78	0.081	1.57	0.024	1.15	0.725	1.36	0.252	1.07	0.735
1425594_at	laminin gamma 3	Lamc3	1.17	0.913	1.57	0.037	1.46	0.882	-1.27	0.347	-1.4	0.265
1436281_at	Similar to hypothetical protein FLJ38281	LOC245305	1.37	0.039	1.57	0.039	1.04	0.951	1.1	0.159	-1.02	0.868
1417947_at	proliferating cell nuclear antigen	Pcna	1.36	0.148	1.57	0.047	1.15	0.007	1.16	0.058	1.13	0.150
1434229_a_at	polymerase (DNA directed), beta	Polb	1.43	0.113	1.57	0.033	-1.01	0.856	-1	0.935	1.11	0.198
1438421_at	poliovirus receptor-related 1	Pvrl1	1.39	0.195	1.57	0.028	1.14	0.922	-1.14	0.174	1.24	0.418
1440986_at	RNA polymerase II associated protein 1	Rpap1	1.86	0.163	1.57	0.025	2.5	0.587	1.35	0.042	1.61	0.522
1455335_at	X-ray repair complementing defective repair in Chinese hams	Xrcc2	1.14	0.145	1.57	0.000	1.46	0.141	1.01	0.965	1.2	0.261
1443985_at	zinc finger protein 719	Zfp719	1.55	0.079	1.57	0.003	-1.12	0.331	1.31	0.269	-1.04	0.435
1453183_at	RIKEN cDNA 1110034A24 gene	1110034A24Rik	1.28	0.043	1.56	0.001	1.21	0.066	1.08	0.496	1.18	0.193
1431903_at	RIKEN cDNA 4930524C18 gene	4930524C18Rik	1.37	0.802	1.56	0.035	-1.74	0.189	1.37	0.481	1.24	0.540
1422168_a_at	brain derived neurotrophic factor	Bdnf	1.23	0.273	1.56	0.011	1.1	0.089	1.18	0.033	1.3	0.043
1419547_at	fumarylacetoacetate hydrolase domain containing 1	Fahd1	1.39	0.200	1.56	0.041	1.1	0.372	1.11	0.054	-1.05	0.466
1421731_a_at	flap structure specific endonuclease 1	Fen1	1.18	0.546	1.56	0.001	1.28	0.003	1.25	0.030	1.27	0.001
1457230_at	glucosamine-6-phosphate deaminase 2	Gnpda2	1.58	0.344	1.56	0.047	1.32	0.126	1.25	0.318	1.19	0.191
1452906_at	GTL2, imprinted maternally expressed untranslated mRNA	Gtl2	2.02	0.351	1.56	0.029	1.01	0.927	1.15	0.775	-1.17	0.250
1425192_at	kelch-like 25 (Drosophila)	Klhl25	1.14	0.627	1.56	0.031	1.12	0.113	1.15	0.212	1.13	0.657
1450836_at	neurogenin 1	Neurog1	2.62	0.053	1.56	0.046	-1.25	0.336	1.79	0.610	-5.02	0.028
1449002_at	pleckstrin homology-like domain, family A, member 3	Phlda3	1.21	0.271	1.56	0.024	1.07	0.054	1.13	0.007	1.17	0.050
1434453_at	polymerase (RNA) III (DNA directed) polypeptide A	Polr3a	1.25	0.366	1.56	0.018	1.3	0.100	1.04	0.578	1.14	0.215
1451105_at	vasohibin 2	Vash2	1.11	0.368	1.56	0.006	1.11	0.359	1.19	0.049	1.26	0.360
1428127_at	RIKEN cDNA 4921506J03 gene	4921506J03Rik	1.14	0.404	1.55	0.026	1.06	0.914	1.31	0.003	1.24	0.145
1454405_at	RIKEN cDNA 4930453J04 gene	4930453J04Rik	1.19	0.758	1.55	0.031	1.27	0.574	-1.45	0.207	1.27	0.373
1424012_at	RIKEN cDNA 4930506L13 gene	4930506L13Rik	1.13	0.252	1.55	0.003	1.48	0.220	1.07	0.619	1.21	0.173
1448199_at	ankyrin repeat domain 10	Ankrd10	-1.06	0.126	1.55	0.005	1.45	0.019	1.24	0.040	1.39	0.049
1436543_at	cDNA sequence BC034507	BC034507	1.34	0.145	1.55	0.009	1.06	0.548	1.41	0.010	1.22	0.254
1422033_a_at	ciliary neurotrophic factor /// zinc finger protein 91	Cntf /// Zfp91	1.23	0.011	1.55	0.048	1.2	0.202	1.21	0.056	1.26	0.103
1457539_at	DNA segment, Chr 10, ERATO Doi 709, expressed	D10Ertd709e	1.79	0.143	1.55	0.008	-1.01	0.695	1.17	0.641	1.07	0.741
1452700_s_at	kelch repeat and BTB (POZ) domain containing 7	Kbtbd7	-1.03	0.673	1.55	0.008	1.52	0.005	1.29	0.083	1.58	0.025
1428255_at	Luc7 homolog (S. cerevisiae)-like	Luc7l	1.08	0.603	1.55	0.017	1.17	0.119	1.29	0.002	1.15	0.023
1419399_at	microsomal triglyceride transfer protein	Mttp	1.61	0.139	1.55	0.010	2.29	0.111	1.27	0.617	1.21	0.424
1442148_at	PC4 and SFRS1 interacting protein 1	Psip1	1.42	0.395	1.55	0.022	1.42	0.434	-1.04	0.547	1.26	0.050
1451106_at	RNA binding motif protein 21	Rbm21	1.18	0.165	1.55	0.028	1.17	0.242	1.35	0.014	1.44	0.023
1450417_a_at	ribosomal protein S20 /// similar to 40S ribosomal protein S2(	Rps20 /// LOC245	1.35	0.045	1.55	0.049	1.9	0.449	1.25	0.412	1.59	0.016
1450599_at	vomeronasal 1 receptor, B3	V1rb3	1.59	0.943	1.55	0.018	2.11	0.201	-1.51	0.126	1.22	0.700
1422070_at	alcohol dehydrogenase 4 (class II), pi polypeptide	Adh4	2.28	0.238	1.54	0.017	1.02	0.349	-1.16	0.427	2.29	0.428
1459952_at	Ankyrin repeat domain 17	Ankrd17	1.55	0.166	1.54	0.011	-1.17	0.246	1.04	0.523	-1.29	0.157
1439063_at	additional sex combs like 2 (Drosophila)	Asxl2	1.02	0.903	1.54	0.026	1.15	0.362	1.2	0.033	-1.03	0.558
1425488_at	DNA segment, Chr 11, ERATO Doi 730, expressed	D11Ertd730e	1.32	0.284	1.54	0.036	-1.11	0.356	1.15	0.040	1.08	0.752
1432207_a_at	target of EGR1, member 1 (nuclear)	Toe1	1.38	0.554	1.54	0.037	1.01	0.992	1.1	0.826	1.09	0.424
1434858_x_at	zinc finger protein 511	Zfp511	1.48	0.213	1.54	0.041	1.08	0.494	1.37	0.539	1.19	0.265
1428832_at	RIKEN cDNA 1600002H07 gene	1600002H07Rik	1.07	0.550	1.53	0.024	1.37	0.141	1.18	0.330	1.44	0.039
1454480_at	RIKEN cDNA 4933439N06 gene	4933439N06Rik	-1.31	0.275	1.53	0.039	1.28	0.581	-1.2	0.434	2.36	0.461
1448055_at	fibronectin type III domain containing 7	Fndc7	1.99	0.327	1.53	0.027	-1.1	0.397	1.24	0.131	2.5	0.284
1448417_at	ninjurin 1	Ninj1	1.36	0.314	1.53	0.044	1.25	0.180	1.14	0.001	1.82	0.089
1422913_at	protamine 3	Prm3	-1.01	0.903	1.53	0.040	-2.66	0.018	1.68	0.333	-1.15	0.230
1436573_at	secernin 3	Scrn3	1.04	0.771	1.53	0.041	1.14	0.187	1.19	0.264	1.25	0.237
1455297_at	spindlin family, member 2	Spin2	1.39	0.415	1.53	0.048	1.33	0.018	1.11	0.658	1.35	0.064
1443792_at	testis specific gene A14	Tsga14	1.43	0.354	1.53	0.009	1.02	0.925	1.07	1.000	1.25	0.404
1424892_at	zinc finger protein 95	Zfp95	1.17	0.399	1.53	0.031	1.25	0.032	1.2	0.031	1.47	0.023
1453775_at	RIKEN cDNA 4921505C17 gene	4921505C17Rik	1.47	0.111	1.52	0.010	-1.12	0.183	-1.02	0.869	1.11	0.427
1429921_at	RIKEN cDNA 9530068E07 gene	9530068E07Rik	2.05	0.080	1.52	0.003	1.1	0.697	-1.08	0.565	1.55	0.147
1424126_at	aminolevulinic acid synthase 1	Alas1	1.24	0.383	1.52	0.016	1.12	0.075	1.1	0.183	1.28	0.058
1458873_at	asp (abnormal spindle)-like, microcephaly associated (Droso|	Aspm	1.35	0.019	1.52	0.006	1.03	0.789	1.09	0.061	-1.01	0.934
1437909_at	RIKEN cDNA D030022P06 gene	D030022P06Rik	1.05	0.544	1.52	0.032	1.03	0.826	1.14	0.260	1.09	0.802
1436006_at	eukaryotic translation initiation factor 2 alpha kinase 1	Eif2ak1	1.42	0.124	1.52	0.022	1.03	0.867	1	0.955	1.16	0.501
1425937_a_at	hexamethylene bis-acetamide inducible 1	Hexim1	1.05	0.729	1.52	0.009	1.39	0.015	1.49	0.002	1.41	0.015
1457241_at	Leucine rich repeat containing 48	Lrrc48	1.77	0.316	1.52	0.049	1.25	0.302	1.66	0.512	-1.6	0.149

1449017_at	nuclear transport factor 2	Nutf2	1.22	0.263	1.52	0.011	1.16	0.093	1.23	0.004	1.24	0.002
1423856_at	popeye domain containing 3	Popdc3	1.23	0.956	1.52	0.046	-1.18	0.394	1.29	0.226	-1.21	0.426
1433947_at	RAB37, member of RAS oncogene family	Rab37	-1.37	0.270	1.52	0.023	1.39	0.883	1.5	0.139	1.24	0.925
1439548_at	RAP2B, member of RAS oncogene family	Rap2b	1.04	0.953	1.52	0.031	1.59	0.011	1.4	0.218	1.3	0.078
1426612_at	timeless interacting protein	Tipin	1.3	0.029	1.52	0.010	1.06	0.072	1.11	0.072	1.07	0.099
1451193_x_at	tetratricopeptide repeat domain 4	Ttc4	1.49	0.135	1.52	0.035	1.22	0.144	1.1	0.218	1.08	0.336
1423357_at	RIKEN cDNA 2610209A20 gene	2610209A20Rik	1.45	0.066	1.51	0.036	1.15	0.034	1.16	0.192	1.24	0.113
1429137_at	RIKEN cDNA 2810422O20 gene	2810422O20Rik	1.51	0.065	1.51	0.015	1.44	0.081	1.51	0.098	-1.07	0.439
1451688_s_at	calcium activated nucleotidase 1	Cant1	1.74	0.142	1.51	0.031	-1.06	0.895	1.36	0.311	1.01	0.772
1448455_at	ceroid-lipofuscinosis, neuronal 8	Cln8	1.13	0.409	1.51	0.026	1.09	0.500	1.17	0.021	1.17	0.072
1451058_at	malignant T cell amplified sequence 2	Mcts2	1.14	0.013	1.51	0.018	1.09	0.736	1.15	0.285	1.18	0.201
1450400_at	nuclear receptor coactivator 6 interacting protein	Ncoa6ip	1.16	0.134	1.51	0.035	1.07	0.636	1.19	0.002	1.15	0.116
1417037_at	origin recognition complex, subunit 6-like (S. cerevisiae)	Orc6l	1.21	0.006	1.51	0.035	1.16	0.047	1.18	0.018	1.2	0.052
1422994_at	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinas	Pip5k3	1.19	0.327	1.51	0.010	-1.24	0.160	-1.04	0.628	1.12	0.745
1448369_at	polymerase (DNA directed), alpha 2	Pola2	1.51	0.175	1.51	0.024	1.47	0.007	1.39	0.160	1.43	0.030
1450862_at	RAD54 like (S. cerevisiae)	Rad54l	1.49	0.138	1.51	0.036	1.04	0.678	1.28	0.002	-1.09	0.270
1441085_at	RAR-related orphan receptor alpha	Rora	-1	0.563	1.51	0.005	1.18	0.782	-1.13	0.163	2.14	0.405
1417548_at	squamous cell carcinoma antigen recognized by T-cells 3	Sart3	1.12	0.692	1.51	0.041	1.04	0.458	1.45	0.507	1.47	0.300
1423809_at	transcription factor 19	Tcf19	1.14	0.094	1.51	0.034	1.33	0.254	1.15	0.037	1.34	0.031
1428592_s_at	ubiquitin specific peptidase 38	Usp38	1.07	0.611	1.51	0.020	1.1	0.366	1.06	0.498	1.09	0.052
1427449_a_at	ADP-ribosylhydrolase like 2	Adprhl2	1.1	0.279	1.5	0.000	1.24	0.081	1.29	0.087	1.19	0.070
1450983_at	A kinase (PRKA) anchor protein 8	Akap8	1.08	0.413	1.5	0.002	1.23	0.084	1.2	0.066	1.09	0.266
1441067_at	Expressed sequence AL033314	AL033314	1.19	0.272	1.5	0.045	-1.04	0.703	1.05	0.365	3.02	0.125
1421635_at	cyclin M4	Cnnm4	1.21	0.096	1.5	0.042	2.02	0.315	1.04	0.792	1.68	0.398
1454963_at	RIKEN cDNA E430028B21 gene	E430028B21Rik	1.17	0.113	1.5	0.005	1.2	0.060	1.16	0.012	1.29	0.027
1448991_a_at	internexin neuronal intermediate filament protein, alpha	Ina	1.4	0.319	1.5	0.018	1.1	0.844	-1.2	0.140	1.12	0.518
1449092_at	protein phosphatase 1D magnesium-dependent, delta isoforn	Ppm1d	-1.03	0.558	1.5	0.007	1.16	0.026	1.23	0.015	1.29	0.024
1452789_at	stannin	Snn	1.05	0.805	1.5	0.010	1.2	0.229	1.28	0.002	1.42	0.012
1460164_at	spindlin	Spin	1.13	0.837	1.5	0.029	1.1	0.582	1.29	0.306	1.25	0.234
1419630_a_at	tripartite motif protein 11	Trim11	1.07	0.481	1.5	0.031	1.15	0.116	1.19	0.105	1.04	0.785
1424929_a_at	tripartite motif protein 26	Trim26	1.12	0.472	1.5	0.027	1.2	0.079	1.27	0.005	1.12	0.134
1433899_x_at	TSC22 domain family, member 1	Tsc22d1	1.37	0.037	1.5	0.029	1.38	0.152	1.27	0.074	1.27	0.203
1417031_at	RIKEN cDNA 2310028N02 gene	2310028N02Rik	1.28	0.220	1.49	0.027	1.08	0.500	1.15	0.401	1.08	0.641
1427209_at	bromodomain adjacent to zinc finger domain, 2A	Baz2a	1.3	0.200	1.49	0.044	1.08	0.602	1.12	0.379	1.15	0.508
1435969_at	BTB (POZ) domain containing 12	Btbd12	1.24	0.072	1.49	0.024	1.08	0.908	1.11	0.349	1.1	0.873
1456441_at	coiled-coil domain containing 87	Ccdc87	1.4	0.066	1.49	0.047	1.32	0.196	2.71	0.763	-1.11	0.409
1416332_at	cold inducible RNA binding protein	Cirbp	1.53	0.326	1.49	0.033	1.14	0.092	1	0.980	1.23	0.118
1421953_at	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	Crkl	1.32	0.116	1.49	0.028	1.06	0.687	1.26	0.496	1.12	0.825
1438765_at	DEAH (Asp-Glu-Ala-His) box polypeptide 33	Dhx33	1.54	0.187	1.49	0.016	-1.04	0.504	1.22	0.136	-1.08	0.398
1452797_at	FAST kinase domains 3	Fastkd3	1.14	0.345	1.49	0.007	1.21	0.005	1.2	0.009	1.02	0.430
1452316_at	integrator complex subunit 12	Ints12	1.15	0.111	1.49	0.002	1.25	0.012	1.18	0.058	1.28	0.111
1427999_at	small nuclear RNA activating complex, polypeptide 5	Snapc5	1.08	0.683	1.49	0.042	1.2	0.965	1.94	0.100	-1.01	0.682
1424967_x_at	troponin T2, cardiac	Tnnt2	1.31	0.137	1.49	0.047	1.06	0.671	1.24	0.049	-1.18	0.299
1449231_at	zinc finger protein 296	Zfp296	-1.01	0.813	1.49	0.041	1.21	0.105	1.47	0.019	1.81	0.019
1429671_at	RIKEN cDNA 2410018M08 gene	2410018M08Rik	1.01	0.990	1.48	0.044	1.38	0.434	1.33	0.065	1.26	0.175
1456181_at	RIKEN cDNA 9530020G05 gene	9530020G05Rik	-1.11	0.280	1.48	0.020	1.16	0.791	1.28	0.148	1.39	0.042
1417734_at	A kinase (PRKA) anchor protein 8-like	Akap8l	1.11	0.783	1.48	0.034	-1.03	0.487	1.31	0.044	1.11	0.365
1452902_at	dehydrogenase/reductase (SDR family) member 13	Dhrs13	1.04	0.700	1.48	0.008	1.21	0.043	1.31	0.137	1.26	0.201
1449859_at	golgi transport 1 homolog B (S. cerevisiae)	Golt1b	1.38	0.515	1.48	0.011	-1.2	0.917	-1	0.942	1.2	0.386
1416448_at	inosine triphosphatase (nucleoside triphosphate pyrophospha	Itpa	1.29	0.209	1.48	0.014	1.2	0.100	1.11	0.340	1.09	0.347
1417844_at	mediator of RNA polymerase II transcription, subunit 4 homol	Med4	1.26	0.249	1.48	0.047	1.15	0.174	1.16	0.013	1.13	0.116
1424081_at	polycomb group ring finger 6	Pcgf6	1.21	0.147	1.48	0.009	1.16	0.049	1.2	0.002	1.26	0.048
1450778_a_at	RNA U, small nuclear RNA export adaptor	Rnuxa	1.1	0.042	1.48	0.014	1.18	0.027	1.26	0.014	1.15	0.086
1427134_at	splicing factor, arginine/serine-rich 12	Sfrs12	1.06	0.652	1.48	0.026	1.15	0.256	1.19	0.015	1.08	0.890
1425682_a_at	Tp53rk binding protein	Tprkb	1.13	0.201	1.48	0.037	1.1	0.458	1.03	0.477	1.12	0.178
1417340_at	thioredoxin-like 2	Txnl2	1.22	0.513	1.48	0.024	1.06	0.667	1.03	0.742	1.03	0.513
1434689_at	zinc finger protein 637	Zfp637	1.36	0.042	1.48	0.006	1.26	0.027	1.11	0.310	1.31	0.020
1421031_a_at	RIKEN cDNA 2310016C08 gene	2310016C08Rik	1.12	0.597	1.47	0.003	1.29	0.067	1.31	0.002	1.21	0.066

1429619_a_at	RIKEN cDNA 8430406I07 gene	8430406I07Rik	1.28	0.868	1.47	0.029	1.28	0.217	1.37	0.119	1.1	0.449
1416569_at	actin-like 6A	Actl6a	1.12	0.840	1.47	0.011	1.15	0.362	-1.02	0.784	1.07	0.387
1418542_s_at	centromere protein O	Cenpo	1.56	0.188	1.47	0.002	1.05	0.756	1.26	0.026	1.14	0.779
1415713_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	1.19	0.333	1.47	0.035	1.1	0.027	1.14	0.004	1.14	0.016
1418409_at	jerky	Jrk	1.21	0.407	1.47	0.035	1.17	0.500	1.26	0.126	1.14	0.543
1422087_at	v-myc myelocytomatosis viral oncogene homolog 1, lung carc	Mycl1	1.57	0.190	1.47	0.047	1.33	0.890	1.02	0.939	-1.25	0.633
1422471_at	peroxisomal biogenesis factor 13	Pex13	1.07	0.714	1.47	0.013	1.17	0.012	1.24	0.000	1.21	0.008
1423234_at	proteasome (prosome, macropain) 26S subunit, non-ATPase	Psmd5	1.17	0.207	1.47	0.037	1.16	0.000	1.11	0.024	1.12	0.045
1441598_at	transmembrane protein with EGF-like and two follistatin-like c	Tmeff2	1.11	0.327	1.47	0.003	1.02	0.946	-1.3	0.182	-1.29	0.108
1422924_at	tumor necrosis factor (ligand) superfamily, member 9	Tnfsf9	-1.03	0.728	1.47	0.012	1.49	0.081	1.45	0.054	1.33	0.333
1430134_a_at	tyrosyl-tRNA synthetase 2 (mitochondrial)	Yars2	1.26	0.195	1.47	0.011	1.11	0.412	1.05	0.589	1.22	0.020
1425030_at	zinc finger protein 622	Zfp622	1.1	0.905	1.47	0.015	1.15	0.278	1.14	0.031	1.08	0.350
1433936_at	RIKEN cDNA 0610010E21 gene	0610010E21Rik	1.15	0.022	1.46	0.010	1.19	0.133	1.19	0.008	1.25	0.019
1434207_at	RIKEN cDNA 2900057K09 gene	2900057K09Rik	-1.06	0.522	1.46	0.027	1.25	0.081	1.02	0.968	1.11	0.153
1435024_at	RIKEN cDNA 4931428F04 gene	4931428F04Rik	-1.16	0.206	1.46	0.044	1.05	0.801	1.57	0.937	1.62	0.064
1439905_at	RIKEN cDNA A330062J17 gene	A330062J17Rik	1.1	0.624	1.46	0.008	-1.04	0.610	1.6	0.331	1.12	0.731
1455916_at	expressed sequence AI931714	AI931714	1.18	0.341	1.46	0.032	1.17	0.016	1.1	0.027	-1.02	0.537
1449019_at	A kinase (PRKA) anchor protein 1	Akap1	1.11	0.231	1.46	0.005	1.23	0.027	1.15	0.044	1.16	0.135
1417692_at	developmentally regulated GTP binding protein 2	Drg2	1.33	0.376	1.46	0.004	-1.02	0.936	1.06	0.478	-1.06	0.373
1424007_at	growth differentiation factor 10	Gdf10	1.38	0.727	1.46	0.048	1.35	0.433	-2.22	0.010	1.78	0.673
1421207_at	leukemia inhibitory factor	Lif	1.12	0.587	1.46	0.015	1.23	0.112	-1.12	0.215	1.13	0.566
1437226_x_at	MARCKS-like 1	Marcksl1	1.07	0.012	1.46	0.000	1.24	0.000	1.22	0.019	1.28	0.076
1424372_at	mitochondrial ribosomal protein L32	Mrpl32	1.17	0.156	1.46	0.034	1.21	0.146	1.24	0.053	1.23	0.021
1426447_at	nucleoporin 35	Nup35	1.29	0.066	1.46	0.014	1.02	0.947	1.08	0.242	1.08	0.303
1448419_at	processing of precursor 4, ribonuclease P/MRP family, (S. ce	Pop4	1.27	0.162	1.46	0.049	1.03	0.068	1.14	0.007	1.08	0.297
1449295_at	SAP30 binding protein	Sap30bp	1.29	0.313	1.46	0.030	1	0.840	1.07	0.574	1.15	0.012
1420935_a_at	serine/arginine repetitive matrix 1	Srrm1	1.09	0.670	1.46	0.023	-1.25	0.176	1.03	0.941	1.64	0.037
1428052_a_at	zinc finger, MYM domain containing 1	Zmym1	1.07	0.392	1.46	0.022	1.15	0.046	1.16	0.008	1.17	0.232
1432668_at	RIKEN cDNA 2210411G17 gene	2210411G17Rik	2.89	0.346	1.45	0.023	-1.35	0.257	1.12	0.862	-1.11	0.409
1455338_at	alpha 1,4-galactosyltransferase	A4galt	1.15	0.820	1.45	0.017	1.51	0.302	1.26	0.219	-1.01	0.815
1443692_at	cDNA sequence BC057022	BC057022	1.56	0.356	1.45	0.047	-1.21	0.169	-1.03	0.771	-1.67	0.127
1417207_at	dishevelled 2, dsh homolog (Drosophila)	Dvl2	1.23	0.139	1.45	0.045	1.46	0.060	1.11	0.290	1.25	0.112
1425857_at	F-box and WD-40 domain protein 9	Fbxw9	1.18	0.356	1.45	0.024	1.05	0.913	1.17	0.738	1.44	0.058
1450980_at	GTP binding protein 3	Gtpbp3	1.19	0.142	1.45	0.041	1.19	0.221	1.16	0.192	1.18	0.318
1447396_at	Hypothetical protein LOC545253	LOC545253	1.22	0.795	1.45	0.019	-1.35	0.121	-1	0.689	1.3	0.790
1426652_at	minichromosome maintenance deficient 3 (S. cerevisiae) /// s	Mcm3 /// LOC671	1.25	0.158	1.45	0.010	1.18	0.086	1.15	0.175	1.12	0.418
1449981_a_at	N-acetyltransferase 2 (arylamine N-acetyltransferase)	Nat2	1.31	0.202	1.45	0.043	1.1	0.282	1.03	0.629	1.02	0.850
1452062_at	phosphoribosyl pyrophosphate synthetase-associated protei	Prpsap2	1.04	0.966	1.45	0.043	1.06	0.724	1.23	0.032	-1.1	0.203
1416400_at	pyrroline-5-carboxylate reductase-like	Pycrl	1.14	0.225	1.45	0.008	1.47	0.015	1.22	0.062	1.4	0.071
1451189_at	zinc finger, SWIM domain containing 1	Zswim1	1.12	0.522	1.45	0.012	1.12	0.044	1.35	0.015	1.41	0.045
1435755_at	RIKEN cDNA 1110001A16 gene	1110001A16Rik	1.34	0.064	1.44	0.009	1.16	0.146	1.14	0.051	1.24	0.237
1456023_at	RIKEN cDNA 2210010B09 gene	2210010B09Rik	-1.13	0.226	1.44	0.011	1.34	0.106	1.37	0.190	1.17	0.434
1439020_at	expressed sequence AW146020	AW146020	1.28	0.039	1.44	0.042	1.01	0.832	-1.03	0.657	1.13	0.057
1438370_x_at	downstream of Stk11	Dos	1	0.958	1.44	0.010	1.41	0.022	1.12	0.078	1.64	0.070
1419267_at	nuclear transcription factor-Y beta	Nfyb	1.12	0.484	1.44	0.011	1.17	0.094	1.14	0.341	1.19	0.198
1448802_at	nuclear fragile X mental retardation protein interacting protei	Nufip1	1.11	0.096	1.44	0.009	1.04	0.731	1.1	0.250	1.11	0.113
1416530_a_at	purine-nucleoside phosphorylase	Pnp	1.1	0.233	1.44	0.035	1.21	0.003	1.17	0.006	1.26	0.058
1426637_a_at	sine oculis-related homeobox 3 homolog (Drosophila)	Six3	1.2	0.203	1.44	0.013	1.03	0.995	-1.25	0.031	1.29	0.331
1460667_at	cDNA sequence U90926	U90926	1.14	0.686	1.44	0.018	1.42	0.029	-1	0.945	1.06	0.874
1460357_at	YTH domain family 2	Ythdf2	1.18	0.074	1.44	0.010	1.1	0.430	1.09	0.169	1.15	0.033
1426654_at	zinc finger, C3HC type 1	Zc3hc1	1.23	0.632	1.44	0.029	1.07	0.587	1.01	0.955	1.1	0.055
1426679_at	zinc finger protein 706	Zfp706	1.25	0.165	1.44	0.040	1.11	0.181	1.16	0.002	1.12	0.102
1433946_at	zinc finger protein interacting with K protein 1	Zik1	1.13	0.031	1.44	0.041	1.36	0.002	1.22	0.041	1.23	0.015
1419661_at	RIKEN cDNA 1600012F09 gene /// hypothetical LOC624446	1600012F09Rik //	-1.04	0.628	1.43	0.028	1.02	0.973	1.09	0.787	-1	0.835
1443064_at	RIKEN cDNA 9130004C02 gene	9130004C02Rik	2.1	0.170	1.43	0.022	1.02	0.400	1.36	0.850	1.76	0.304
1419262_at	acyl-Coenzyme A dehydrogenase family, member 8	Acad8	1.21	0.047	1.43	0.010	1.19	0.021	1.12	0.062	1.07	0.320
1427472_a_at	complement component 8, beta subunit	C8b	2.47	0.181	1.43	0.047	-1.26	0.118	1.15	0.630	-1.57	0.221
1452529_a_at	cAMP responsive element binding protein 1	Creb1	1.17	0.532	1.43	0.029	1.21	0.051	1.09	0.263	1.17	0.048

1416106_at	KTI12 homolog, chromatin associated (S. cerevisiae)	Kti12	1.11	0.270	1.43	0.013	1.16	0.005	1.2	0.008	1.22	0.013
1416543_at	nuclear factor, erythroid derived 2, like 2	Nfe2l2	1.18	0.148	1.43	0.035	1.1	0.265	1.15	0.019	1.2	0.018
1422092_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	Pfkfb2	1.3	0.489	1.43	0.001	1.03	0.755	1.03	0.819	-1.28	0.147
1428543_at	phosphoribosyl pyrophosphate amidotransferase	Ppat	1.07	0.588	1.43	0.012	1.14	0.390	1.12	0.020	1.17	0.156
1454843_at	phosphoribosyl pyrophosphate synthetase 2	Prps2	1.25	0.260	1.43	0.040	1.07	0.255	1.07	0.432	1.1	0.151
1441128_at	Renal tumor antigen	Rage	1.6	0.024	1.43	0.018	1.15	0.092	-1.23	0.160	1.16	0.803
1424156_at	retinoblastoma-like 1 (p107)	Rbl1	1.38	0.021	1.43	0.000	1.22	0.035	1.08	0.197	1.29	0.032
1416928_at	RNA binding motif protein 12	Rbm12	1.08	0.306	1.43	0.026	1.13	0.235	1.12	0.315	1.17	0.210
1456041_at	sorting nexin 16	Snx16	1.21	0.016	1.43	0.047	1.08	0.253	1.02	0.370	1.15	0.123
1416849_at	zinc finger, CDGSH-type domain 1	Zcd1	1.28	0.090	1.43	0.047	1.17	0.175	1.04	0.477	1.11	0.255
1431252_a_at	zinc finger protein 655	Zfp655	1.21	0.383	1.43	0.044	1.06	0.799	1.28	0.015	1.23	0.120
1452880_at	zinc finger, HIT type 3	Znhit3	1.19	0.211	1.43	0.003	1.22	0.043	1.1	0.274	1.21	0.017
1428452_at	RIKEN cDNA 2810025M15 gene	2810025M15Rik	1.24	0.224	1.42	0.010	1.14	0.057	1.18	0.078	1.14	0.200
1430363_at	RIKEN cDNA 4933407O12 gene	4933407O12Rik	1.18	0.588	1.42	0.027	1.55	0.098	1.22	0.217	1.27	0.430
1456808_at	RIKEN cDNA 4933426M11 gene	4933426M11Rik	1.12	0.528	1.42	0.000	-1.12	0.368	1.06	0.746	1.22	0.563
1429048_at	biogenesis of lysosome-related organelles complex-1, subuni	Bloc1s2	1.08	0.502	1.42	0.048	1.11	0.415	1.11	0.051	1.19	0.013
1447420_at	bromodomain containing 1	Brd1	1.71	0.348	1.42	0.015	-1.2	0.235	1.28	0.474	1.22	0.257
1450467_at	bassoon	Bsn	1.55	0.375	1.42	0.025	-2.16	0.005	1.29	0.650	1.22	0.747
1450016_at	cyclin G1	Ccng1	1.14	0.019	1.42	0.008	1.14	0.124	1.28	0.051	1.22	0.180
1434981_at	RIKEN cDNA E130303B06 gene	E130303B06Rik	1.28	0.005	1.42	0.029	1.23	0.277	1.02	0.574	1.32	0.160
1454635_at	F-box and leucine-rich repeat protein 3	Fbxl3	1.35	0.136	1.42	0.024	1.14	0.232	1.07	0.409	1.32	0.073
1448767_s_at	gap junction membrane channel protein beta 1	Gjb1	-1.1	0.208	1.42	0.041	-1.11	0.518	1.38	0.439	1.12	0.695
1428532_at	integrator complex subunit 7	Ints7	1.37	0.386	1.42	0.049	1.49	0.045	1.11	0.424	1.41	0.030
1434770_at	IQ calmodulin-binding motif containing 1	Iqcb1	1.18	0.343	1.42	0.034	1.1	0.488	1.16	0.288	-1.08	0.420
1450722_at	nucleoporin 50	Nup50	1.09	0.047	1.42	0.002	1.08	0.441	1.07	0.256	1.09	0.430
1417890_at	pyridoxal (pyridoxine, vitamin B6) phosphatase	Pdxp	1.03	0.382	1.42	0.004	1.27	0.074	1.45	0.004	1.38	0.105
1424554_at	protein phosphatase 1, regulatory (inhibitor) subunit 8	Ppp1r8	1.05	0.486	1.42	0.001	1.17	0.134	1.16	0.053	1.26	0.017
1438481_at	PRP4 pre-mRNA processing factor 4 homolog (yeast)	Prpf4	1.3	0.058	1.42	0.002	1.59	0.023	1.09	0.362	1.3	0.187
1421528_a_at	surfeit gene 5	Surf5	1.03	0.625	1.42	0.007	1.34	0.007	1.3	0.009	1.48	0.025
1422532_at	xeroderma pigmentosum, complementation group C	Xpc	1.33	0.130	1.42	0.018	1.1	0.101	1.23	0.191	1.47	0.047
1434355_at	zinc finger protein 617	Zfp617	1.25	0.062	1.42	0.034	1.09	0.715	1.21	0.031	1.3	0.006
1453173_at	RIKEN cDNA 2310005E10 gene	2310005E10Rik	1.3	0.107	1.41	0.037	-1.05	0.426	1.07	0.405	1.01	0.968
1444992_at	expressed sequence AI120166	AI120166	1.59	0.042	1.41	0.017	1.06	0.212	-1.06	0.591	-1.33	0.074
1423620_at	centromere protein Q	Cenpq	1.45	0.070	1.41	0.005	1.13	0.100	1.16	0.039	-1.03	0.897
1457839_at	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	1.41	0.071	1.41	0.048	1.23	0.112	-1.45	0.012	1.18	0.345
1428185_at	potassium channel tetramerisation domain containing 18	Kctd18	1.12	0.398	1.41	0.012	1.26	0.014	1.26	0.026	1.12	0.294
1440341_at	similar to SMF protein	LOC629345	1.16	0.603	1.41	0.029	-1.01	0.624	1.24	0.051	1.13	0.713
1452289_a_at	ring finger protein 135	Rnf135	1.12	0.651	1.41	0.024	1.12	0.128	1.26	0.054	1.36	0.088
1433675_at	small nucleolar RNA, C/D box 22	Snord22	1.27	0.393	1.41	0.046	1.11	0.315	1.14	0.109	1.01	0.949
1418828_at	three prime histone mRNA exonuclease 1	Thex1	1.25	0.295	1.41	0.030	1.17	0.278	1.18	0.236	1.12	0.138
1424492_at	transient receptor potential cation channel, subfamily C, mem	Trpc2	-1.03	0.509	1.41	0.042	-1.1	0.290	1.28	0.693	1.73	0.354
1428218_a_at	RIKEN cDNA 1600012H06 gene	1600012H06Rik	1.18	0.230	1.4	0.041	1.12	0.365	1.32	0.011	1.17	0.159
1440381_at	RIKEN cDNA 2410085M17 gene	2410085M17Rik	1.23	0.090	1.4	0.035	1.28	0.060	1.17	0.138	1.16	0.121
1453040_at	RIKEN cDNA 2810402A17 gene	2810402A17Rik	1.27	0.062	1.4	0.007	-1.07	0.684	1.02	0.701	1.16	0.691
1430041_at	RIKEN cDNA 6330548G22 gene	6330548G22Rik	1.17	0.590	1.4	0.026	1.02	0.809	1.03	0.723	-1.11	0.252
1423884_at	cirrhosis, autosomal recessive 1A (human)	Cirh1a	1.11	0.342	1.4	0.024	1.13	0.059	1.09	0.026	1.05	0.536
1435320_at	CTD (carboxy-terminal domain, RNA polymerase II, polypept	Ctdspl2	1.22	0.087	1.4	0.029	1.09	0.344	1.28	0.014	1.04	0.889
1435926_at	RIKEN cDNA E030003F13 gene	E030003F13Rik	-1.03	0.574	1.4	0.017	1.23	0.022	1.27	0.028	1.29	0.047
1449559_at	homeo box, msh-like 2	Msx2	1.21	0.051	1.4	0.002	1.13	0.346	1.13	0.015	1.24	0.015
1452026_a_at	phospholipase A2, group XIIA	Pla2g12a	1.42	0.301	1.4	0.004	1.1	0.546	1.09	0.204	1.07	0.532
1449162_at	processing of precursor 7, ribonuclease P family, (S. cerevisia	Pop7	1.21	0.208	1.4	0.014	1.17	0.119	1.11	0.043	1.3	0.017
1455268_at	zinc finger, CSL domain containing 2	Zcsl2	1.11	0.191	1.4	0.003	1.22	0.046	1.17	0.168	1.32	0.018
1450644_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	-1.03	0.752	1.4	0.022	1.55	0.030	1.33	0.016	1.57	0.000
1424099_at	RIKEN cDNA 2310016C16 gene	2310016C16Rik	1.23	0.219	1.39	0.035	1.05	0.369	1.07	0.024	1.1	0.182
1419074_at	RIKEN cDNA 2510006C20 gene	2510006C20Rik	1.11	0.163	1.39	0.015	1.25	0.036	1.14	0.010	1.38	0.042
1434567_at	RIKEN cDNA 4732496O08 gene	4732496O08Rik	-1.02	0.654	1.39	0.009	1.22	0.043	1.12	0.085	1.19	0.043
1451232_at	CD151 antigen	Cd151	1.22	0.569	1.39	0.038	1.32	0.100	1.35	0.143	1.24	0.270
1433594_at	COMM domain containing 2	Commd2	1.28	0.194	1.39	0.048	1.15	0.442	1.14	0.029	1.13	0.417

1423880_at	DNA segment, Chr 10, Wayne State University 52, expresse	D10Wsu52e	1.29	0.348	1.39	0.039	1.02	0.740	1.05	0.174	1.04	0.517
1434606_at	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (a	Erbb3	-1.25	0.351	1.39	0.004	-1.98	0.082	1	0.719	1.03	0.791
1426607_at	similar to CG10866-PA	LOC633640	1.05	0.536	1.39	0.017	1.12	0.025	1.14	0.110	1.28	0.131
1460358_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 22	Nudt22	1.01	0.750	1.39	0.003	1.3	0.312	1.02	0.926	1.12	0.052
1455122_at	patched domain containing 2	Ptchd2	1.38	0.149	1.39	0.042	-1.48	0.037	2.27	0.042	1.44	0.918
1450630_at	queuine tRNA-ribosyltransferase 1	Qtrt1	1.31	0.241	1.39	0.014	1.11	0.759	1.2	0.024	1.26	0.106
1416721_s_at	splicing factor, arginine/serine-rich 6	Sfrs6	1.14	0.037	1.39	0.006	1.45	0.017	1.34	0.010	1.3	0.010
1424735_at	solute carrier family 25 (mitochondrial carrier, phosphate carr	Slc25a25	1.24	0.234	1.39	0.016	-1	0.889	1.14	0.145	1.11	0.266
1434317_s_at	testis expressed gene 10	Tex10	1.13	0.088	1.39	0.032	1.04	0.812	-1.07	0.180	1.02	0.620
1445235_at	YTH domain family 3	Ythdf3	1.15	0.531	1.39	0.015	-1.36	0.190	1.91	0.026	-1.02	0.857
1433705_at	zinc finger protein 213	Zfp213	1.04	0.972	1.39	0.007	1.3	0.020	1.31	0.007	1.52	0.023
1438460_at	zinc finger, MYM-type 4	Zmym4	1.07	0.382	1.39	0.018	1.03	0.905	-1.07	0.301	1.01	0.761
1429812_at	RIKEN cDNA 2610002D18 gene	2610002D18Rik	1.01	0.946	1.38	0.034	1.42	0.060	1.27	0.186	1.56	0.040
1457709_a_at	RIKEN cDNA A930005H10 gene	A930005H10Rik	1.03	0.821	1.38	0.014	-1.13	0.236	1.24	0.423	-1.13	0.232
1427959_at	abhydrolase domain containing 10	Abhd10	1.04	0.551	1.38	0.026	1.27	0.027	1.25	0.029	1.29	0.029
1416631_at	adaptor-related protein complex AP-4, beta 1	Ap4b1	1.22	0.516	1.38	0.031	1.28	0.009	1.08	0.246	1.2	0.002
1434065_at	CWF19-like 1, cell cycle control (S. pombe)	Cwf19l1	1.1	0.258	1.38	0.016	1.1	0.300	1.08	0.135	1.15	0.139
1423495_at	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	Decr2	1.09	0.528	1.38	0.050	1.01	0.781	1.02	0.889	-1	0.730
1420491_at	eukaryotic translation initiation factor 2, subunit 1 alpha	Eif2s1	1.41	0.180	1.38	0.029	1.04	0.758	1.18	0.293	1.04	0.772
1418839_at	glomulin, FKBP associated protein	Glmn	1.25	0.247	1.38	0.032	-1.08	0.490	1.27	0.345	-1.05	0.715
1442614_at	interleukin 1 receptor accessory protein	Il1rap	1.14	0.490	1.38	0.025	1.24	0.584	-1.43	0.199	1.39	0.012
1429833_at	lymphocyte antigen 6 complex, locus G6E	Ly6g6e	1.32	0.377	1.38	0.040	1.03	0.740	-1.47	0.194	1.23	0.456
1424001_at	Mki67 (FHA domain) interacting nucleolar phosphoprotein	Mki67ip	1.16	0.375	1.38	0.030	1.1	0.013	1.21	0.019	1.15	0.120
1424019_at	nucleolar protein 1	Nol1	1.04	0.555	1.38	0.009	1.06	0.631	1.23	0.025	1.19	0.092
1455002_at	protein tyrosine phosphatase 4a1	Ptp4a1	1.06	0.052	1.38	0.047	1.21	0.058	1.37	0.010	1.29	0.002
1448899_s_at	RAD51 associated protein 1	Rad51ap1	1.21	0.064	1.38	0.022	1.06	0.392	1.22	0.033	1.21	0.029
1422859_a_at	ribosomal protein L23	Rpl23	1.14	0.434	1.38	0.034	1.08	0.656	1.13	0.255	1.03	0.888
1418162_at	toll-like receptor 4	Tlr4	1.2	0.096	1.38	0.047	1.28	0.630	1.21	0.116	1.04	0.586
1448706_at	Traf and Tnf receptor associated protein	Ttrap	1.35	0.128	1.38	0.004	1.13	0.120	1.33	0.012	1.17	0.100
1456607_at	valosin containing protein (p97)/p47 complex interacting prot	Vcpip1	1.07	0.065	1.38	0.034	-1.01	0.870	-1.02	0.907	1	0.812
1436312_at	zinc finger protein, subfamily 1A, 1 (Ikaros)	Zfpn1a1	1.94	0.234	1.38	0.009	1.74	0.347	1.34	0.420	-1.58	0.174
1420548_a_at	RIKEN cDNA 2310008H09 gene	2310008H09Rik	1.2	0.028	1.37	0.004	1.12	0.140	1.15	0.264	1.07	0.666
1423838_s_at	RIKEN cDNA 2400003C14 gene	2400003C14Rik	1.06	0.358	1.37	0.011	1.07	0.264	1.14	0.005	1.08	0.169
1429371_at	RIKEN cDNA 2810426N06 gene	2810426N06Rik	-1.2	0.187	1.37	0.000	1.24	0.749	1.01	0.950	-1.07	0.663
1435724_at	RIKEN cDNA 4933400N17 gene	4933400N17Rik	1.46	0.076	1.37	0.034	1.55	0.339	-1.28	0.421	-1.05	0.662
1436049_at	RIKEN cDNA 5730589K01 gene	5730589K01Rik	1.25	0.021	1.37	0.012	1.33	0.016	1.1	0.100	1.12	0.699
1450717_at	angiogenin, ribonuclease A family, member 1	Ang1	1.39	0.202	1.37	0.023	-1.19	0.065	-1.21	0.038	-1.19	0.043
1431527_at	CD164 antigen	Cd164	-1.16	0.608	1.37	0.013	1.32	0.635	1.09	0.526	1.24	0.318
1428092_at	cell division cycle 5-like (S. pombe)	Cdc5l	1.17	0.426	1.37	0.021	1.01	0.869	1.03	0.623	1.05	0.726
1455734_at	cereblon	Crbn	1.36	0.414	1.37	0.035	1.1	0.103	-1.01	0.696	-1.01	0.858
1426837_at	methionyl aminopeptidase 1	Metap1	1.22	0.387	1.37	0.013	1.15	0.313	1.24	0.142	1.1	0.031
1442302_at	N-methylpurine-DNA glycosylase	Mpg	1.19	0.464	1.37	0.049	1.21	0.414	1.4	0.336	1.1	0.171
1418941_at	protocadherin beta 22	Pcdhb22	1.94	0.416	1.37	0.039	1.21	0.520	1.05	0.821	1.47	0.176
1415736_at	prefoldin 5	Pfdn5	1.26	0.212	1.37	0.030	1.04	0.403	1.05	0.329	1.11	0.267
1434076_at	WD repeat domain 37	Wdr37	1.14	0.382	1.37	0.046	1.09	0.349	-1.03	0.557	1.05	0.466
1420110_s_at	zinc finger protein 334	Zfp334	1.15	0.187	1.37	0.016	1.18	0.004	1.16	0.149	1.18	0.024
1456161_at	RIKEN cDNA 0610040B10 gene	0610040B10Rik	1.09	0.500	1.36	0.034	1.03	0.987	1.26	0.620	1.31	0.759
1419660_at	RIKEN cDNA 1600012F09 gene	1600012F09Rik	1.2	0.080	1.36	0.009	1.09	0.063	1.2	0.028	1.15	0.111
1416439_at	RIKEN cDNA 2410015N17 gene	2410015N17Rik	1.13	0.046	1.36	0.032	1.15	0.232	1.21	0.016	1.26	0.148
1456163_at	RIKEN cDNA 2700049P18 gene	2700049P18Rik	1.38	0.243	1.36	0.001	1.21	0.080	1.18	0.112	1.23	0.168
1427985_at	RIKEN cDNA 9630042H07 gene	9630042H07Rik	1.06	0.755	1.36	0.032	1.39	0.145	1.44	0.016	1.63	0.002
1448484_at	S-adenosylmethionine decarboxylase 1	Amd1	1.09	0.091	1.36	0.010	1.12	0.017	1.17	0.063	1.12	0.022
1451246_s_at	aurora kinase B	Aurkb	1.11	0.005	1.36	0.019	1.18	0.041	1.2	0.005	1.29	0.028
1435406_at	coiled-coil alpha-helical rod protein 1	Cchcr1	1.12	0.375	1.36	0.020	1.23	0.009	1.02	0.842	-1.05	0.464
1423701_at	Coenzyme A synthase	Coasy	1.14	0.627	1.36	0.010	1.01	0.948	1.13	0.088	1.24	0.066
1416023_at	fatty acid binding protein 3, muscle and heart	Fabp3	1.18	0.242	1.36	0.035	-1.06	0.427	1.04	0.171	1.03	0.918
1423348_at	frizzled homolog 8 (Drosophila)	Fzd8	1.24	0.138	1.36	0.016	1.11	0.163	1.31	0.119	1.07	0.649
1428608_at	myosin light chain, regulatory B	Mylc2b	1.04	0.566	1.36	0.015	1.15	0.117	1.14	0.119	1.29	0.004

1434384_at	nuclear receptor interacting protein 1	Nrip1	1.09	0.303	1.36	0.030	1.03	0.840	1.02	0.550	-1.09	0.161
1428277_at	OTU domain containing 6B	Otud6b	1.19	0.044	1.36	0.032	1.02	0.989	1.08	0.432	1.28	0.040
1417035_at	SAC3 domain containing 1	Sac3d1	1.04	0.715	1.36	0.026	1.23	0.034	1.23	0.023	1.28	0.048
1419656_at	solute carrier family 25, member 36	Slc25a36	1.07	0.070	1.36	0.026	1	0.862	1.13	0.048	1.09	0.461
1437500_at	Solute carrier family 39 (zinc transporter), member 12	Slc39a12	-1.01	0.784	1.36	0.028	1.16	0.366	1.02	0.223	1.13	0.214
1440303_at	Solute carrier family 7, member 6 opposite strand	Slc7a6os	1.09	0.679	1.36	0.018	1.2	0.432	1.16	0.023	1.04	0.538
1416346_at	translocase of inner mitochondrial membrane 8 homolog a1 (	Timm8a1	1.14	0.110	1.36	0.014	1.14	0.003	1.2	0.006	1.16	0.141
1441646_at	RIKEN cDNA 1110059P08 gene	1110059P08Rik	1.25	0.473	1.35	0.019	1.23	0.507	-1.19	0.238	-1.54	0.122
1426879_at	RIKEN cDNA 1190005F20 gene	1190005F20Rik	1.13	0.410	1.35	0.034	1.21	0.034	1.08	0.425	1.14	0.323
1419635_at	RIKEN cDNA 4833420G17 gene	4833420G17Rik	1.12	0.607	1.35	0.008	1.08	0.329	1.1	0.155	1.17	0.133
1421197_a_at	apoptotic chromatin condensation inducer 1	Acin1	1.07	0.254	1.35	0.027	1.14	0.115	1.14	0.056	1.14	0.000
1443291_at	Ankyrin 1, erythroid	Ank1	1.73	0.786	1.35	0.049	1.13	0.738	1	0.292	3.16	0.079
1451747_a_at	autophagy-related 12 (yeast)	Atg12	1.05	0.129	1.35	0.001	1.16	0.287	1.23	0.038	1.04	0.701
1426002_a_at	cell division cycle 7 (S. cerevisiae)	Cdc7	1.12	0.274	1.35	0.010	1.24	0.275	1.34	0.019	1.22	0.272
1435281_at	carnitine palmitoyltransferase 1c	Cpt1c	1.16	0.207	1.35	0.020	1.18	0.159	1.1	0.139	1.24	0.046
1416751_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	Ddx20	1.12	0.539	1.35	0.024	1.06	0.181	1.17	0.010	1.25	0.024
1452598_at	GINS complex subunit 1 (Psf1 homolog)	Gins1	1.14	0.153	1.35	0.035	1.16	0.013	1.04	0.603	1.08	0.169
1418367_x_at	histone 2, H3c1 /// histone 2, H2aa1 /// histone 1, H2ad /// his	Hist2h3c1 /// Hist2	1.36	0.291	1.35	0.026	1.04	0.402	1.14	0.100	1.05	0.629
1424639_a_at	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	Hmgcl	-1.05	0.112	1.35	0.005	-1	0.886	1.11	0.090	1.21	0.180
1424430_at	MTERF domain containing 2	Mterfd2	1.06	0.531	1.35	0.009	1.09	0.369	1.17	0.036	1.19	0.007
1422473_at	phosphodiesterase 4B, cAMP specific	Pde4b	1.06	0.396	1.35	0.020	1.1	0.216	1.27	0.084	1.33	0.020
1416172_at	pescadillo homolog 1, containing BRCT domain (zebrafish)	Pes1	1.11	0.788	1.35	0.044	-1	0.991	1.15	0.128	1.16	0.069
1448282_at	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	Plrg1	1.18	0.483	1.35	0.047	-1.02	0.655	1.15	0.035	1.05	0.032
1424258_at	polymerase (RNA) II (DNA directed) polypeptide D	Polr2d	1.19	0.122	1.35	0.023	1.17	0.023	1.12	0.018	1.11	0.111
1418491_a_at	pseudouridine synthase 3	Pus3	1.1	0.233	1.35	0.036	-1.12	0.283	1.01	0.950	-1.09	0.486
1452917_at	replication factor C (activator 1) 5	Rfc5	1.17	0.382	1.35	0.008	1.2	0.099	1.16	0.085	1.2	0.073
1415802_at	solute carrier family 16 (monocarboxylic acid transporters), m	Slc16a1	1.16	0.411	1.35	0.023	1.17	0.009	1.19	0.001	1.28	0.010
1421147_at	telomeric repeat binding factor 2	Terf2	1.1	0.233	1.35	0.006	-1	0.859	1.08	0.204	1.07	0.271
1458088_at	Ubiquitin-associated protein 2	Ubap2	-1.24	0.301	1.35	0.026	-1.01	0.677	1.26	0.366	1.46	0.360
1438669_at	WD repeat domain 40A	Wdr40a	1.02	0.775	1.35	0.004	1.1	0.537	1.28	0.010	1.03	0.917
1428294_at	zinc finger protein 259	Zfp259	1.04	0.988	1.35	0.031	1.08	0.352	1.22	0.191	1.25	0.072
1417055_at	RIKEN cDNA 0610009D07 gene	0610009D07Rik	1.22	0.189	1.34	0.010	1.13	0.438	1.09	0.714	1.16	0.087
1428908_at	RIKEN cDNA 2600011C06 gene	2600011C06Rik	1.09	0.238	1.34	0.009	1.07	0.369	1	0.879	-1.05	0.478
1439131_at	RIKEN cDNA 4932441K18 gene	4932441K18Rik	1.1	0.142	1.34	0.014	1.1	0.428	1.06	0.147	1.23	0.419
1451221_at	cDNA sequence BC018507	BC018507	1.4	0.165	1.34	0.029	-1.1	0.015	1.02	0.662	-1.23	0.099
1458541_at	dynactin 4	Dctn4	1.03	0.945	1.34	0.027	1.05	0.093	1.13	0.606	1.21	0.448
1459371_at	Eukaryotic translation initiation factor 4E	Eif4e	1.94	0.565	1.34	0.032	1.36	0.957	-1.64	0.093	-1.01	0.457
1432330_at	complement factor H-like	LOC381294	1.38	0.654	1.34	0.010	1.24	0.635	-1.5	0.182	2.39	0.050
1459592_a_at	similar to NFkB interacting protein 1	LOC669005	1.03	0.868	1.34	0.022	1.1	0.329	1.05	0.242	1.3	0.149
1455217_at	leucine-rich repeats and immunoglobulin-like domains 2	Lrig2	1.14	0.363	1.34	0.020	-1.24	0.018	-1.13	0.351	-1.17	0.285
1453725_a_at	mitchondrial ribosomal protein S7	Mrps7	1.17	0.227	1.34	0.038	1.06	0.343	1.09	0.089	1.16	0.080
1456104_at	proteasome (prosome, macropain) 26S subunit, non-ATPase	Psmd11	1.32	0.333	1.34	0.038	1.13	0.159	1.01	0.947	-1.08	0.528
1415674_a_at	trafficking protein particle complex 4	Trappc4	1.25	0.226	1.34	0.038	1.1	0.110	1.06	0.083	1.15	0.084
1448162_at	vascular cell adhesion molecule 1	Vcam1	1.22	0.191	1.34	0.014	1.38	0.091	1.17	0.071	1.2	0.016
1416890_at	WD repeat domain 74	Wdr74	1.11	0.298	1.34	0.005	1.11	0.547	1.19	0.102	1.2	0.139
1422844_a_at	WD repeat domain 77	Wdr77	1.11	0.573	1.34	0.030	1.11	0.048	1.08	0.051	1.17	0.001
1453477_at	zinc finger CCCH type containing 6	Zc3h6	1.71	0.038	1.34	0.013	1.24	0.952	-1.04	0.789	2.06	0.285
1424192_at	RIKEN cDNA 1500011H22 gene	1500011H22Rik	1.07	0.393	1.33	0.001	1.18	0.001	1.21	0.023	1.12	0.016
1433867_at	RIKEN cDNA 1810030O07 gene	1810030O07Rik	1.06	0.492	1.33	0.020	1.03	0.278	1.07	0.039	1.15	0.008
1417075_at	RIKEN cDNA 2010309E21 gene	2010309E21Rik	1.19	0.155	1.33	0.010	1.08	0.546	1.12	0.027	1.18	0.027
1450425_a_at	RIKEN cDNA 2700062C07 gene	2700062C07Rik	1.15	0.387	1.33	0.021	1.15	0.307	1.15	0.079	1.2	0.299
1424451_at	acetyl-Coenzyme A acyltransferase 1B	Acaa1b	-1.33	0.332	1.33	0.038	-2.06	0.024	1.07	0.807	1.92	0.641
1451439_at	cDNA sequence BC027231	BC027231	1.07	0.530	1.33	0.030	1.11	0.192	1.16	0.011	1.01	0.950
1424429_s_at	coiled-coil domain containing 95	Ccdc95	-1.04	0.555	1.33	0.001	1.17	0.385	1.25	0.003	1.23	0.023
1418579_at	centrin 2	Cetn2	1.28	0.050	1.33	0.038	1.1	0.074	1.13	0.006	1	0.849
1449820_at	cortistatin	Cort	1.26	0.338	1.33	0.046	1.15	0.457	1.11	0.945	-1.13	0.139
1419645_at	cleavage stimulation factor, 3' pre-RNA subunit 2	Cstf2	1.23	0.163	1.33	0.023	1.14	0.043	1.09	0.063	1.24	0.003
1422476_at	interferon gamma inducible protein 30	Ifi30	1.06	0.359	1.33	0.024	1.18	0.107	1.12	0.075	1.25	0.093

1416898_a_at	interferon regulatory factor 3	Irf3	1.68	0.315	1.33	0.015	1.16	0.056	1.16	0.164	1.16	0.096
1448531_at	lamin B2 /// similar to Lamin-B2	Lmnb2 /// LOC671	1.18	0.177	1.33	0.038	1.11	0.192	1.07	0.863	1.24	0.228
1429307_s_at	leucine zipper and CTNNBIP1 domain containing	Lzic	1.16	0.285	1.33	0.029	1.14	0.129	1.07	0.278	1.13	0.034
1416212_at	mago-nashi homolog, proliferation-associated (Drosophila)	Magoh	1.21	0.154	1.33	0.040	1.06	0.153	1.04	0.426	1.07	0.141
1426653_at	minichromosome maintenance deficient 3 (S. cerevisiae)	Mcm3	1.07	0.767	1.33	0.040	1.26	0.110	1.16	0.204	1.07	0.468
1424908_at	mitochondrial methionyl-tRNA formyltransferase	Mtfmt	1.15	0.059	1.33	0.033	1.17	0.061	1.29	0.004	1.19	0.010
1449550_at	myosin IC	Myo1c	1.05	0.348	1.33	0.019	1.3	0.048	1.25	0.012	1.32	0.020
1419753_at	nuclear transcription factor, X-box binding 1	Nfx1	1.14	0.468	1.33	0.034	1.22	0.245	1.29	0.007	1.21	0.101
1452294_at	protocadherin 1	Pcdh1	-1.45	0.202	1.33	0.032	1	0.582	-1.57	0.034	1.42	0.783
1415754_at	polymerase (RNA) II (DNA directed) polypeptide F	Polr2f	1.23	0.221	1.33	0.003	1.07	0.188	1.02	0.759	1.1	0.198
1416218_x_at	ribosomal protein L37a /// similar to 60S ribosomal protein L3	Rpl37a /// LOC62	1.17	0.342	1.33	0.026	1.17	0.006	1.12	0.016	1.09	0.137
1438900_at	SAC1 (suppressor of actin mutations 1, homolog)-like (S. cer	Sacm1l	1.73	0.234	1.33	0.030	1.19	0.872	-1.2	0.258	-1.26	0.163
1451596_a_at	sphingosine kinase 1	Sphk1	1.07	0.348	1.33	0.015	1.19	0.192	1.27	0.000	1.37	0.022
1415774_at	signal transducer and activator of transcription interacting pro	Statip1	1.38	0.361	1.33	0.046	-1.05	0.552	-1.18	0.069	1.04	0.864
1424938_at	six transmembrane epithelial antigen of the prostate 1	Steap1	1.13	0.760	1.33	0.020	1.11	0.301	1.09	0.175	1.16	0.039
1434708_at	von Hippel-Lindau syndrome homolog	Vhlh	1.01	0.876	1.33	0.001	1.25	0.030	1.17	0.031	1.15	0.071
1452581_at	RIKEN cDNA 2610304G08 gene	2610304G08Rik	1.19	0.166	1.32	0.025	1.28	0.287	-1.14	0.068	1.07	0.612
1424212_at	RIKEN cDNA 9430023L20 gene	9430023L20Rik	-1.03	0.712	1.32	0.024	1.16	0.016	1.07	0.091	1.2	0.027
1424020_at	ADP-ribosylation factor-like 6 interacting protein 6 /// similar t	Arl6ip6 /// LOC67	1.07	0.892	1.32	0.039	1.28	0.154	-1.09	0.471	1.06	0.319
1433611_s_at	BUD31 homolog (yeast)	Bud31	1.28	0.084	1.32	0.040	1.04	0.830	1.04	0.659	1.02	0.744
1418330_at	CCCTC-binding factor	Ctcf	1.19	0.003	1.32	0.022	1.1	0.212	1.06	0.270	-1.01	0.711
1416268_at	E26 avian leukemia oncogene 2, 3' domain	Ets2	1.03	0.898	1.32	0.027	1.26	0.064	1.3	0.047	1.2	0.020
1424685_at	exosome component 4	Exosc4	1.22	0.361	1.32	0.038	1.14	0.083	1.13	0.092	1.22	0.013
1424300_at	gem (nuclear organelle) associated protein 6	Gemin6	1.19	0.010	1.32	0.005	1.2	0.030	1.3	0.003	1.16	0.027
1452272_a_at	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver reg	Gfer	-1.04	0.433	1.32	0.021	1.08	0.652	1.05	0.507	1.06	0.523
1439686_at	Muscleblind-like 1 (Drosophila)	Mbnl1	1.43	0.272	1.32	0.032	-1.08	0.313	2.69	0.165	1.08	0.786
1448787_at	modulator of apoptosis 1	Moap1	1.09	0.018	1.32	0.014	1.15	0.130	1.12	0.076	1.18	0.057
1455330_at	nucleolar protein 9	Nol9	1.14	0.446	1.32	0.012	1.04	0.198	1.14	0.009	1.2	0.019
1451909_a_at	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	Prpf4b	1.06	0.716	1.32	0.046	1.2	0.288	1.12	0.268	-1.02	0.578
1449517_at	glutaminyl-peptide cyclotransferase-like	Qpctl	-1.1	0.301	1.32	0.050	1.1	0.771	1.09	0.053	-1.13	0.010
1419460_at	ribonuclease P 14 subunit (human)	Rpp14	1.15	0.014	1.32	0.020	1.11	0.024	1.15	0.014	1.2	0.067
1423176_at	transducer of ErbB-2.1	Tob1	1.01	0.995	1.32	0.013	1.56	0.016	1.22	0.039	1.63	0.000
1417754_at	topoisomerase I binding, arginine/serine-rich	Topors	1.12	0.043	1.32	0.006	1	0.983	1.15	0.147	1.23	0.141
1426971_at	ubiquitin-activating enzyme E1-like	Ube1l	-1.4	0.318	1.32	0.049	1.06	0.472	1.61	0.848	-1.07	0.544
1451244_a_at	zinc finger protein 422	Zfp422	1.15	0.006	1.32	0.020	1.18	0.114	1.04	0.258	1.28	0.007
1438742_at	zinc finger protein 629	Zfp629	1.01	0.617	1.32	0.049	1.68	0.910	1.59	0.341	1.64	0.361
1426495_at	RIKEN cDNA 2410042D21 gene	2410042D21Rik	1.1	0.410	1.31	0.011	1	0.749	1.01	0.807	-1.02	0.825
1455914_at	expressed sequence AI987944	AI987944	1.2	0.468	1.31	0.038	1.08	0.969	-1.08	0.558	-1.02	0.769
1415760_s_at	ATX1 (antioxidant protein 1) homolog 1 (yeast)	Atox1	1.19	0.056	1.31	0.023	1.08	0.358	1.07	0.042	1.12	0.244
1437203_at	Casitas B-lineage lymphoma-like 1	Cbll1	1.13	0.080	1.31	0.001	1.04	0.789	1.02	0.966	1.06	0.308
1416488_at	cyclin G2	Ccng2	-1	0.828	1.31	0.030	1.21	0.045	1.26	0.003	1.32	0.003
1419130_at	deaminase domain containing 1	Deadc1	1.1	0.701	1.31	0.003	1.05	0.410	1.17	0.232	1.27	0.169
1425062_at	Fc receptor-like 1	Fcrl1	1.72	0.262	1.31	0.049	1.73	0.249	1.12	0.099	1.72	0.005
1454634_at	fucokinase	Fuk	1.56	0.061	1.31	0.046	-1.24	0.116	1.33	0.346	1.11	0.964
1436270_at	gene model 740, (NCBI)	Gm740	1.12	0.105	1.31	0.024	1.22	0.188	1.13	0.018	1.46	0.004
1417948_s_at	interleukin enhancer binding factor 2	Ilf2	1.13	0.157	1.31	0.018	1.18	0.054	1.05	0.161	1.25	0.008
1421903_at	intersex-like (Drosophila)	Ixl	1.3	0.143	1.31	0.046	-1	0.950	1.1	0.417	1.28	0.041
1416503_at	latexin	Lxn	1.12	0.056	1.31	0.015	1.14	0.197	1.16	0.043	1.28	0.014
1435127_a_at	O-sialoglycoprotein endopeptidase-like 1	Osgepl1	1.15	0.126	1.31	0.028	1.08	0.204	1.08	0.338	1.19	0.123
1445137_at	PTK2 protein tyrosine kinase 2	Ptk2	1.16	0.792	1.31	0.035	1.17	0.393	-1.07	0.268	-1.36	0.045
1416861_at	signal transducing adaptor molecule (SH3 domain and ITAM	Stam	1.05	0.425	1.31	0.029	1.06	0.575	-1.03	0.266	1.02	0.704
1427915_s_at	transcription elongation factor B (SIII), polypeptide 1	Tceb1	1.52	0.316	1.31	0.037	1.08	0.480	1.21	0.065	-1.07	0.521
1448529_at	thrombomodulin	Thbd	1.11	0.415	1.31	0.047	1.29	0.101	1.24	0.010	1.15	0.222
1423112_at	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeas	Ube2d3	2.66	0.264	1.31	0.046	-1.06	0.100	-1.1	0.445	1	0.860
1422713_a_at	ubiquitin-conjugating enzyme E2I	Ube2i	1.16	0.262	1.31	0.029	1.07	0.763	1.01	0.890	1.26	0.204
1448260_at	ubiquitin carboxy-terminal hydrolase L1	Uchl1	1.29	0.106	1.31	0.005	1.15	0.218	1.06	0.012	1.19	0.150
1415689_s_at	zinc finger protein 306	Zfp306	1.19	0.211	1.31	0.022	1.15	0.029	1.07	0.403	1.1	0.104
1454774_at	zinc finger protein 445	Zfp445	1.11	0.212	1.31	0.024	1.15	0.080	1.17	0.009	1.09	0.293

1447403_a_at	Zinc finger, MYND domain containing 19	Zmynd19	-1.1	0.476	1.31	0.040	1.12	0.443	1.35	0.015	1.26	0.034
1454031_at	RIKEN cDNA 2310029O18 gene	2310029O18Rik	-1.02	0.741	1.3	0.033	-1.08	0.560	-1.08	0.126	1.1	0.722
1453534_at	RIKEN cDNA 2810004I08 gene	2810004I08Rik	1.17	0.507	1.3	0.028	1.39	0.038	1.42	0.567	1.15	0.843
1427334_s_at	RIKEN cDNA 2810474O19 gene	2810474O19Rik	-1.01	0.911	1.3	0.004	-1.01	0.856	1.17	0.158	1.37	0.102
1428540_at	RIKEN cDNA 3321401G04 gene	3321401G04Rik	1.09	0.047	1.3	0.049	-1.04	0.187	1.06	0.161	1.07	0.148
1432872_at	RIKEN cDNA 4932702M13 gene	4932702M13Rik	2.09	0.259	1.3	0.044	-1.15	0.331	1.18	0.510	1.19	0.113
1440478_at	DNA segment, Chr 10, ERATO Doi 438, expressed	D10Ertd438e	1.16	0.380	1.3	0.005	1.23	0.032	1.22	0.329	-1.06	0.623
1418258_s_at	dynein light chain LC8-type 2	Dynll2	1.03	0.583	1.3	0.011	1.14	0.335	1.19	0.133	1.18	0.028
1419805_s_at	geranylgeranyl diphosphate synthase 1	Ggps1	1.19	0.019	1.3	0.022	-1.04	0.231	-1.05	0.280	1.12	0.435
1426284_at	keratin 20	Krt20	1.21	0.030	1.3	0.005	1.25	0.035	1.07	0.145	1.23	0.123
1418435_at	makorin, ring finger protein, 1	Mkrn1	1.06	0.488	1.3	0.017	1.05	0.675	-1.01	0.788	1.25	0.090
1433517_at	myeloma overexpressed 2	Myeov2	1.56	0.120	1.3	0.016	1.3	0.517	1.09	0.317	-1.11	0.431
1448674_at	ring finger protein 25	Rnf25	1.08	0.939	1.3	0.041	1.15	0.083	1.17	0.081	1.22	0.031
1444221_at	TBC1D12: TBC1 domain family, member 12	Tbc1d12	1.16	0.356	1.3	0.015	1.06	0.151	-1.02	0.747	-1.09	0.444
1448230_at	ubiquitin specific peptidase 10	Usp10	1.18	0.386	1.3	0.035	1.03	0.845	1.02	0.125	1.07	0.206
1435099_at	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yea	Utp14a	-1.01	0.609	1.3	0.020	1.11	0.237	1.23	0.065	1.03	0.584
1455545_at	RIKEN cDNA 1110065P20 gene	1110065P20Rik	1.08	0.440	1.29	0.006	1.03	0.675	1.19	0.000	1.25	0.003
1434923_at	RIKEN cDNA 2810437L13 gene	2810437L13Rik	1.16	0.091	1.29	0.029	1.25	0.173	1.09	0.077	1.13	0.433
1441829_s_at	A kinase (PRKA) anchor protein 10	Akap10	1.13	0.356	1.29	0.016	-1.03	0.813	1.37	0.164	-1.47	0.087
1422461_at	ATPase family, AAA domain containing 3A	Atad3a	1.11	0.557	1.29	0.013	1.09	0.004	1.13	0.076	1.07	0.450
1439024_at	BCL2-associated athanogene 4	Bag4	1.15	0.183	1.29	0.026	1.06	0.509	1.36	0.090	1.26	0.548
1451702_at	CKLF-like MARVEL transmembrane domain containing 7	Cmtm7	-1.07	0.440	1.29	0.028	1	0.945	1.33	0.023	1.19	0.281
1452681_at	deoxythymidylate kinase	Dtymk	1.14	0.009	1.29	0.018	1.17	0.088	1.18	0.005	1.26	0.016
1452198_at	F-box and leucine-rich repeat protein 10	Fbxl10	1.03	0.877	1.29	0.033	1.07	0.181	1.03	0.281	1.17	0.029
1448273_at	glutathione synthetase	Gss	1.1	0.504	1.29	0.007	1.15	0.005	1.11	0.003	1.22	0.028
1416210_at	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp3	1.12	0.391	1.29	0.018	1.15	0.128	1.25	0.002	1.18	0.164
1417737_at	mitochondrial ribosomal protein S31	Mrps31	1.07	0.291	1.29	0.030	-1.01	0.634	1.08	0.079	-1.05	0.372
1448133_at	NMD3 homolog (S. cerevisiae)	Nmd3	1.06	0.561	1.29	0.006	1	0.983	1.11	0.015	1.09	0.490
1422488_at	NTF2-related export protein 1	Nxt1	1	0.969	1.29	0.020	1.11	0.019	1.2	0.042	1.1	0.390
1455394_at	protein inhibitor of activated STAT 4	Pias4	1.08	0.194	1.29	0.030	1.11	0.364	1.07	0.589	1.09	0.389
1417720_at	polymerase (RNA) II (DNA directed) polypeptide J	Polr2j	1.17	0.050	1.29	0.020	1.13	0.236	1.03	0.581	1.11	0.281
1424136_a_at	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomer	Ppih /// LOC43306	1.19	0.018	1.29	0.009	1.21	0.134	1.12	0.134	1.15	0.286
1426826_at	RNA binding motif protein 16	Rbm16	1.04	0.575	1.29	0.049	-1.2	0.155	-1.12	0.020	-1.25	0.057
1415908_at	testis-specific protein, Y-encoded-like 1	Tspyl1	-1.06	0.073	1.29	0.016	1.16	0.340	-1.05	0.352	1.31	0.017
1452189_at	WD repeat domain containing 82	Wdr82	1	0.763	1.29	0.007	1.12	0.162	1.1	0.030	1.13	0.074
1435628_x_at	RIKEN cDNA 2610305J24 gene /// cDNA sequence BC00551	2610305J24Rik ///	1.01	0.943	1.28	0.043	1.05	0.840	1.12	0.780	1.16	0.254
1455529_at	RIKEN cDNA 2700083E18 gene	2700083E18Rik	1.04	0.254	1.28	0.015	1.08	0.082	1.15	0.004	1.28	0.013
1430656_a_at	asparagine synthetase domain containing 1	Asnsd1	1.19	0.308	1.28	0.044	1.15	0.045	1.11	0.012	1.04	0.252
1434791_at	ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	1.28	0.049	1.28	0.035	1.03	0.606	1.25	0.138	1.08	0.490
1424940_s_at	cDNA sequence BC022687	BC022687	1.08	0.166	1.28	0.027	1.28	0.006	1.17	0.042	1.31	0.103
1449724_s_at	DNA segment, Chr 8, ERATO Doi 738, expressed	D8Ertd738e	1.32	0.231	1.28	0.035	-1.02	0.780	1.19	0.004	1.11	0.433
1431066_at	fucosyltransferase 11	Fut11	1.23	0.034	1.28	0.018	-1.04	0.828	1.43	0.059	1.37	0.263
1416522_a_at	gene rich cluster, C10 gene	Grcc10	1.16	0.444	1.28	0.024	-1	0.867	1.02	0.860	1.09	0.444
1426286_at	nucleolar complex associated 3 homolog (S. cerevisiae)	Noc3l	1.04	0.571	1.28	0.042	1.07	0.683	1.01	0.755	1.03	0.591
1416730_at	RNA terminal phosphate cyclase-like 1	Rcl1	1.03	0.684	1.28	0.010	1.06	0.844	1.06	0.376	1.08	0.171
1428227_at	RE1-silencing transcription factor	Rest	1.17	0.347	1.28	0.037	1.06	0.509	1.03	0.742	-1.01	0.722
1426494_at	RNA (guanine-9-) methyltransferase domain containing 3	Rg9mtd3	1.11	0.207	1.28	0.043	1.13	0.416	1.02	0.843	1.05	0.544
1455142_at	suppressor of cytokine signaling 4	Socs4	1.04	0.672	1.28	0.014	1.14	0.001	1.16	0.061	1.17	0.098
1428660_s_at	torsin family 3, member A	Tor3a	-1.04	0.634	1.28	0.003	1.13	0.294	1.24	0.013	1.17	0.419
1423962_at	WD repeat domain 26	Wdr26	1.23	0.054	1.28	0.041	1.01	0.828	1.1	0.375	-1.05	0.375
1424524_at	RIKEN cDNA 1200002N14 gene	1200002N14Rik	1.05	0.761	1.27	0.014	1.28	0.060	1.12	0.140	1.24	0.114
1428550_at	RIKEN cDNA 1810015A11 gene	1810015A11Rik	1.06	0.364	1.27	0.025	1.34	0.004	1.43	0.017	1.41	0.040
1423767_at	RIKEN cDNA 2810410M20 gene	2810410M20Rik	1.08	0.145	1.27	0.007	1.16	0.056	1.06	0.162	1.21	0.018
1456141_x_at	BRCA1/BRCA2-containing complex, subunit 3	Brcc3	-1.07	0.619	1.27	0.013	-1.24	0.196	1.32	0.209	-1.02	0.929
1416019_at	down-regulator of transcription 1	Dr1	1.01	0.987	1.27	0.015	1.24	0.259	1.27	0.012	1.12	0.393
1437284_at	frizzled homolog 1 (Drosophila)	Fzd1	1.03	0.393	1.27	0.017	1.34	0.060	1.23	0.012	1.39	0.042
1450135_at	frizzled homolog 3 (Drosophila)	Fzd3	1.05	0.975	1.27	0.038	1.22	0.267	-1.07	0.480	1.13	0.958
1438660_at	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	Gcnt2	-1	0.763	1.27	0.035	1.18	0.316	-1.02	0.554	1.08	0.314

1415800_at	gap junction membrane channel protein alpha 1	Gja1	1.08	0.202	1.27	0.042	1.22	0.297	1.04	0.154	1.16	0.046
1460495_s_at	HtrA serine peptidase 2	Htra2	1.39	0.215	1.27	0.046	1.02	0.939	1.08	0.202	1.13	0.200
1417079_s_at	lectin, galactose-binding, soluble 2	Lgals2	1.05	0.874	1.27	0.021	1.01	0.875	1.04	0.690	2.27	0.101
1424377_at	similar to ribosomal protein L24-like	LOC670726	1.11	0.150	1.27	0.009	1.11	0.534	1.14	0.013	1.23	0.082
1456118_at	methyltransferase like 2	Mettl2	-1.05	0.412	1.27	0.006	1.09	0.349	1.05	0.829	1.11	0.193
1450880_at	mitochondrial ribosomal protein L16	Mrpl16	1.09	0.531	1.27	0.046	-1	0.907	1.08	0.142	1.1	0.106
1415690_at	mitochondrial ribosomal protein L27	Mrpl27	1.21	0.183	1.27	0.039	1.04	0.631	1.06	0.146	1.07	0.186
1416931_at	Ngg1 interacting factor 3-like 1 (S. pombe)	Nif3l1	1.05	0.348	1.27	0.015	1.1	0.208	1.12	0.108	1.2	0.061
1448480_at	nuclear import 7 homolog (S. cerevisiae)	Nip7	1.04	0.912	1.27	0.003	1.08	0.279	1.1	0.077	1.08	0.076
1428892_at	peptidylprolyl isomerase (cyclophilin)-like 1	Ppil1	1.1	0.453	1.27	0.027	1.03	0.776	1.21	0.027	1.05	0.063
1416292_at	peroxiredoxin 3	Prdx3	1.24	0.240	1.27	0.045	1.05	0.744	1.1	0.035	1.04	0.179
1418859_at	regulatory factor X-associated protein	Rfxap	1.01	0.612	1.27	0.032	1.05	0.637	1.2	0.000	1.08	0.201
1419369_at	ring finger protein 138	Rnf138	1.17	0.247	1.27	0.021	1.18	0.325	1.15	0.076	1.21	0.110
1424873_at	ring finger protein 2	Rnf2	1.11	0.000	1.27	0.012	1.14	0.002	1.04	0.295	1.06	0.095
1423666_s_at	ribosomal protein L5 /// similar to 60S ribosomal protein L5 ///	Rpl5 /// LOC38274	-1.1	0.256	1.27	0.032	1.21	0.047	1.38	0.002	1.31	0.063
1455027_at	RUN and FYVE domain containing 3	Rufy3	1.01	0.830	1.27	0.037	-1.18	0.319	1.07	0.607	-1.09	0.554
1422676_at	SWI/SNF related, matrix associated, actin dependent regulat	Smarce1	1.04	0.501	1.27	0.002	1.18	0.048	1.14	0.035	1.21	0.013
1441435_at	Transducin (beta)-like 1 X-linked	Tbl1x	1.17	0.374	1.27	0.004	1.31	0.337	1.24	0.398	1.09	0.925
1449621_s_at	thrombospondin, type I, domain 1	Thsd1	-1.04	0.595	1.27	0.021	1.14	0.218	1.05	0.746	1.13	0.232
1427114_at	tetratricopeptide repeat domain 19	Ttc19	-1.02	0.597	1.27	0.016	1.01	0.901	1.1	0.033	1.04	0.557
1419179_at	thioredoxin-like 4	Txnl4	1.07	0.681	1.27	0.027	1.04	0.867	1.2	0.140	1.18	0.006
1417983_a_at	ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	1.18	0.124	1.27	0.024	1.04	0.532	1.05	0.692	1.01	0.882
1435114_at	WD repeat and HMG-box DNA binding protein 1	Wdhd1	1.06	0.573	1.27	0.001	1.04	0.376	1.29	0.105	1.03	0.496
1415941_s_at	zinc finger, AN1-type domain 2A	Zfand2a	1.09	0.339	1.27	0.009	1.07	0.309	1.01	0.769	1.19	0.049
1418048_at	RIKEN cDNA 1110059G10 gene	1110059G10Rik	1.04	0.651	1.26	0.030	1.12	0.060	1.17	0.153	1.12	0.091
1430872_at	RIKEN cDNA 4930412O13 gene	4930412O13Rik	1.18	0.435	1.26	0.045	1.42	0.678	1.78	0.141	1.07	0.834
1433649_at	amine oxidase, flavin containing 1	Aof1	1.05	0.807	1.26	0.009	1.49	0.071	1.1	0.288	1.18	0.224
1415719_s_at	armadillo repeat containing 1	Armc1	1.27	0.091	1.26	0.016	1	0.826	-1.01	0.883	1.01	0.898
1440881_at	bromodomain and WD repeat domain containing 3	Brwd3	1.45	0.176	1.26	0.014	-1.02	0.642	-1.12	0.348	-1.02	0.821
1417842_at	calcium modulating ligand	Caml	-1.03	0.572	1.26	0.043	1.16	0.066	1.19	0.002	1.17	0.014
1416873_a_at	cyclin-dependent kinase 2	Cdk2	1.13	0.194	1.26	0.002	1.16	0.221	1.24	0.041	1.13	0.214
1429101_at	gap junction membrane channel protein alpha 5	Gja5	-1.26	0.114	1.26	0.033	1.03	0.754	-1.27	0.120	1.02	0.790
1433528_at	general transcription factor II A, 2	Gtf2a2	1.25	0.093	1.26	0.008	1.12	0.260	1.08	0.299	1.05	0.788
1434936_at	HIRA interacting protein 3	Hirip3	1.11	0.166	1.26	0.025	1.26	0.113	1.18	0.126	1.16	0.214
1448871_at	mitogen activated protein kinase 13	Mapk13	1.28	0.309	1.26	0.033	1.09	0.530	-1.06	0.374	1.32	0.198
1448849_at	mitochondrial ribosomal protein L40	Mrpl40	1.17	0.203	1.26	0.030	-1.06	0.420	1.1	0.247	1.12	0.328
1422554_at	necdin-like 2	Ndnl2	1.05	0.432	1.26	0.027	1.13	0.238	1.15	0.043	1.14	0.177
1428080_at	phosphoglycerate mutase family member 5	Pgam5	1.08	0.783	1.26	0.023	1.07	0.384	1.13	0.033	1.23	0.037
1416174_at	retinoblastoma binding protein 9	Rbbp9	1.28	0.283	1.26	0.045	1.14	0.275	1.25	0.085	1.03	0.938
1416177_at	RNA binding motif protein, X chromosome retrogene	Rbmxrt	1.01	0.994	1.26	0.022	1.11	0.090	1.06	0.097	1.12	0.057
1422418_s_at	suppressor of Ty 4 homolog 1 (S. cerevisiae) /// suppressor o	Supt4h1 /// Supt4h	1.26	0.265	1.26	0.031	1.08	0.218	1.07	0.106	1.04	0.516
1428263_a_at	transcription elongation factor B (SIII), polypeptide 2	Tceb2	1.16	0.315	1.26	0.005	1.02	0.673	1.07	0.157	1.07	0.199
1448882_at	transmembrane protein 93	Tmem93	1.03	0.298	1.26	0.011	1.13	0.022	1.16	0.014	1.2	0.012
1428346_at	TRAF type zinc finger domain containing 1	Trafd1	-1.08	0.116	1.26	0.017	1.29	0.063	1.06	0.075	1.25	0.064
1448179_at	upregulated during skeletal muscle growth 5	Usmg5	1.02	0.986	1.26	0.003	1.17	0.353	1.15	0.088	-1.01	0.516
1436675_at	WD repeat domain 63	Wdr63	1.29	0.756	1.26	0.048	2.53	0.022	1.09	0.548	1.01	0.987
1420702_at	RIKEN cDNA 1700093K21 gene	1700093K21Rik	1.11	0.490	1.25	0.037	1.26	0.145	1.02	0.954	-1.09	0.329
1428966_at	RIKEN cDNA 2610204K14 gene	2610204K14Rik	1.08	0.332	1.25	0.035	1.07	0.044	1.15	0.051	1.06	0.327
1435018_at	RIKEN cDNA 5930434B04 gene	5930434B04Rik	1.06	0.501	1.25	0.040	1.18	0.140	1.13	0.087	1.09	0.223
1435584_at	expressed sequence AI662791	AI662791	1.29	0.255	1.25	0.001	1	0.964	-1.14	0.370	-1.07	0.738
1424026_s_at	cDNA sequence BC013529	BC013529	1.18	0.225	1.25	0.036	-1.01	0.840	1.04	0.611	1.12	0.010
1451400_at	cDNA sequence BC023488	BC023488	1.26	0.223	1.25	0.028	1.12	0.327	1.21	0.204	1.34	0.067
1416140_a_at	DEAH (Asp-Glu-Ala-His) box polypeptide 30	Dhx30	-1.03	0.387	1.25	0.008	1.13	0.218	1.1	0.031	1.17	0.026
1452012_a_at	exosome component 1	Exosc1	1.14	0.312	1.25	0.029	1.1	0.023	1.13	0.243	1.16	0.238
1433489_s_at	fibroblast growth factor receptor 2	Fgfr2	1.14	0.577	1.25	0.001	1.39	0.029	1.02	0.886	1.05	0.964
1430038_at	gephyrin	Gphn	1.02	0.888	1.25	0.024	1.11	0.465	1.23	0.406	1.54	0.046
1416323_at	potassium channel tetramerisation domain containing 20	Kctd20	1.08	0.460	1.25	0.001	1.08	0.452	1.14	0.085	1.12	0.063
1426913_at	lanosterol synthase	Lss	1.58	0.111	1.25	0.010	-1.04	0.613	1.1	0.026	-1.03	0.520

1418244_at	N-acetyltransferase 5 (ARD1 homolog, S. cerevisiae)	Nat5	1.08	0.175	1.25	0.021	1.04	0.306	1.02	0.587	1.06	0.189
1448896_at	phosphatidylinositol glycan anchor biosynthesis, class F	Pigf	1.11	0.051	1.25	0.002	1.13	0.007	1.07	0.162	1.14	0.025
1415695_at	proteasome (prosome, macropain) subunit, alpha type 1	Psma1	1.06	0.170	1.25	0.008	1.08	0.167	1.05	0.519	1.08	0.092
1424705_at	RNA binding motif protein, X-linked 2	Rbmx2	1.21	0.158	1.25	0.004	1.03	0.853	1.12	0.272	1.16	0.119
1426386_at	ribosomal protein L7-like 1	Rpl7l1	1.18	0.244	1.25	0.050	1	0.964	1.11	0.213	1.09	0.064
1417539_at	solute carrier family 35 (CMP-sialic acid transporter), membe	Slc35a1	1.05	0.917	1.25	0.048	1.05	0.277	1.05	0.098	1.26	0.062
1434712_at	Smith-Magenis syndrome chromosome region, candidate 7-li	Smcr7l	1.09	0.591	1.25	0.034	1.16	0.447	1.08	0.101	1.1	0.253
1418568_x_at	signal recognition particle 14	Srp14	1.13	0.350	1.25	0.031	1.12	0.052	1.08	0.062	1.07	0.290
1422469_at	TANK-binding kinase 1	Tbk1	1.23	0.073	1.25	0.042	1.13	0.366	1.1	0.170	-1.07	0.405
1454676_s_at	toll-like receptor adaptor molecule 1	Ticam1	-1.06	0.522	1.25	0.021	1.13	0.273	1.2	0.302	1.16	0.154
1448999_at	trafficking protein particle complex 5	Trappc5	1	0.895	1.25	0.041	1.1	0.470	1.11	0.091	1.24	0.059
1423575_a_at	Williams Beuren syndrome chromosome region 22	Wbscr22	1.2	0.142	1.25	0.029	-1.01	0.524	1.17	0.071	1.06	0.437
1428678_s_at	WD repeat domain 73	Wdr73	-1.01	0.808	1.25	0.047	1.24	0.016	1.2	0.055	1.22	0.024
1428843_at	membrane-associated ring finger (C3HC4) 5	5-Mar	1.03	0.418	1.24	0.010	-1.01	0.771	1.07	0.161	1.09	0.064
1428679_s_at	RIKEN cDNA 0610010K14 gene	0610010K14Rik	1.18	0.340	1.24	0.003	1.09	0.385	1.03	0.772	1.2	0.039
1451220_at	RIKEN cDNA 2310040A13 gene	2310040A13Rik	1.14	0.198	1.24	0.003	-1.07	0.060	-1.13	0.037	-1.16	0.045
1417062_at	RIKEN cDNA 2810037C14 gene	2810037C14Rik	1.16	0.188	1.24	0.045	1.18	0.074	1.15	0.006	1.13	0.180
1434625_at	RIKEN cDNA 4930432O21 gene	4930432O21Rik	1.26	0.173	1.24	0.027	1.06	0.520	-1.05	0.426	1.11	0.814
1449933_a_at	RIKEN cDNA 5730449L18 gene	5730449L18Rik	1.19	0.054	1.24	0.041	1.18	0.031	1.04	0.705	1.03	0.679
1429665_at	RIKEN cDNA 6230416J20 gene	6230416J20Rik	1.3	0.031	1.24	0.021	1.26	0.022	1.26	0.408	1.03	0.621
1424075_at	RIKEN cDNA 9430016H08 gene	9430016H08Rik	1.08	0.164	1.24	0.038	-1.01	0.763	1.04	0.474	1.17	0.087
1417112_at	ADP-ribosylation factor-like 2 binding protein	Arl2bp	1.11	0.281	1.24	0.023	1.15	0.061	1.09	0.289	1.16	0.003
1435488_at	RIKEN cDNA C630010D07 gene /// similar to methylenetetra	C630010D07Rik /	-1.03	0.730	1.24	0.024	1.26	0.091	1.21	0.136	1.35	0.019
1417233_at	coiled-coil-helix-coiled-coil-helix domain containing 4	Chchd4	-1.03	0.024	1.24	0.015	1.14	0.170	1.17	0.018	1.18	0.037
1435505_at	dystrophia myotonica-containing WD repeat motif	Dmwd	1.14	0.095	1.24	0.000	-1.04	0.555	1.02	0.427	1.06	0.567
1436070_at	glyoxalase 1	Glo1	1.17	0.100	1.24	0.002	1.11	0.212	1.12	0.272	1.29	0.171
1418260_at	hormonally upregulated Neu-associated kinase /// similar to h	Hunk /// LOC6305	-1.1	0.709	1.24	0.010	1.07	0.897	-1.02	0.789	-1.42	0.052
1423873_at	LSM1 homolog, U6 small nuclear RNA associated (S. cerevis	Lsm1	1.16	0.107	1.24	0.041	1.17	0.184	1.11	0.018	1.07	0.359
1431939_a_at	myc induced nuclear antigen	Mina	1.16	0.659	1.24	0.037	-1.03	0.751	1.03	0.978	1.04	0.804
1417371_at	pellino 1	Peli1	1.03	0.418	1.24	0.016	1.04	0.370	1.09	0.002	1.16	0.007
1448492_a_at	proteasome (prosome, macropain) 26S subunit, non-ATPase	Psmd12	1.06	0.387	1.24	0.027	-1	0.953	1.02	0.378	1.09	0.442
1436101_at	ring finger protein 24	Rnf24	1.05	0.215	1.24	0.032	1.16	0.172	1.12	0.210	1.1	0.121
1423654_a_at	ring finger protein 4	Rnf4	1.11	0.311	1.24	0.041	1.05	0.168	1	0.983	1.06	0.199
1434867_at	solute carrier family 4, sodium bicarbonate transporter-like, m	Slc4a11	1.06	0.470	1.24	0.009	-1.09	0.430	-1.08	0.414	-1	0.868
1424337_at	sorting nexin 15	Snx15	1.03	0.837	1.24	0.008	1.18	0.182	1.11	0.540	1.14	0.040
1448774_at	stomatin (Epb7.2)-like 2	Stoml2	1.22	0.322	1.24	0.026	1.05	0.511	1.02	0.498	1.09	0.055
1416889_at	troponin I, skeletal, fast 2	Tnni2	1.1	0.982	1.24	0.014	1.22	0.329	1.12	0.887	-1.12	0.380
1423360_at	YME1-like 1 (S. cerevisiae)	Yme1l1	1.11	0.394	1.24	0.018	1.01	0.947	1.14	0.899	-1.04	0.606
1428348_at	zinc finger protein 336	Zfp336	1.11	0.270	1.24	0.043	1.11	0.059	-1	0.892	1.18	0.033
1428256_at	RIKEN cDNA 2310047H23 gene	2310047H23Rik	1.17	0.079	1.23	0.049	1.05	0.664	1.07	0.300	1.14	0.196
1430515_s_at	aminoadipate-semialdehyde dehydrogenase-phosphopantet	Aasdhppt	1.09	0.362	1.23	0.024	1.13	0.007	1.12	0.005	1.2	0.083
1424804_at	cDNA sequence BC020002	BC020002	1.12	0.268	1.23	0.035	1.08	0.119	1.18	0.020	1.1	0.523
1428773_s_at	Bcl6 interacting corepressor	Bcor	-1.03	0.682	1.23	0.047	1.01	0.611	-1.02	0.050	1.02	0.871
1441989_at	BCL2/adenovirus E1B interacting protein 1, NIP2	Bnip2	-1.07	0.612	1.23	0.003	1.23	0.018	1.18	0.382	-1.09	0.704
1423447_at	caseinolytic peptidase X (E.coli)	Clpx	1.18	0.152	1.23	0.005	1.04	0.947	1.04	0.870	-1.03	0.602
1417103_at	D-dopachrome tautomerase	Ddt	1.15	0.189	1.23	0.016	1.12	0.487	1.09	0.111	1.01	0.792
1451076_s_at	dendritic cell protein GA17	Ga17	1.2	0.163	1.23	0.017	1.11	0.082	1.06	0.216	1.03	0.496
1442135_at	Gene model 237, (NCBI)	Gm237	1.05	0.510	1.23	0.036	1.18	0.176	1.3	0.059	1.35	0.027
1451135_at	general transcription factor IIB	Gtf2b	1.05	0.044	1.23	0.008	1.06	0.178	1.11	0.053	1.08	0.201
1428406_s_at	host cell factor C1 regulator 1 (XPO1-dependent)	Hcfc1r1	1.1	0.472	1.23	0.044	1.09	0.425	1.06	0.112	1.02	0.891
1438320_s_at	minichromosome maintenance deficient 7 (S. cerevisiae)	Mcm7	-1	0.899	1.23	0.022	1.17	0.002	1.09	0.033	1.15	0.010
1419290_at	methyltransferase like 6	Mettl6	1.05	0.403	1.23	0.018	1.06	0.292	1.07	0.258	1.15	0.030
1419471_a_at	nuclear distribution gene C homolog (Aspergillus)	Nudc	1.03	0.942	1.23	0.027	1.02	0.980	-1.01	0.651	1.03	0.542
1423460_at	PERQ amino acid rich, with GYF domain 1	Perq1	-1.13	0.354	1.23	0.045	1.06	0.563	-1.01	0.796	1.23	0.234
1426965_at	RAS related protein 2a	Rap2a	-1.03	0.529	1.23	0.019	1.22	0.040	1.17	0.048	1.38	0.008
1428766_at	RNA methyltransferase like 1	Rnmtl1	1.03	0.383	1.23	0.018	1.17	0.150	1.24	0.002	1.32	0.004
1453928_a_at	Sjogren syndrome antigen B	Ssb	1.14	0.216	1.23	0.050	1.14	0.214	1.16	0.124	-1.08	0.488
1448643_at	Sjogren's syndrome nuclear autoantigen 1	Ssna1	1.09	0.283	1.23	0.049	1.1	0.169	1.14	0.052	1.13	0.073

1422591_at	transcription elongation factor B (SIII), polypeptide 3	Tceb3	1.1	0.365	1.23	0.037	1.04	0.315	1.07	0.248	1.07	0.309
1424068_at	T-cell leukemia translocation altered gene	Tcta	1.1	0.224	1.23	0.018	1.09	0.546	1.2	0.181	1.17	0.041
1416628_at	RIKEN cDNA 0610006I08 gene	0610006I08Rik	1.07	0.381	1.22	0.002	1.11	0.444	1.16	0.109	1.16	0.016
1417886_at	RIKEN cDNA 1810009A15 gene	1810009A15Rik	1.16	0.095	1.22	0.044	1.11	0.017	1.11	0.140	1.16	0.128
1418662_at	RIKEN cDNA 2210012G02 gene	2210012G02Rik	1.31	0.419	1.22	0.001	-1.02	0.460	-1.03	0.643	-1.02	0.755
1423823_at	RIKEN cDNA 2610012O22 gene	2610012O22Rik	1.01	0.747	1.22	0.005	1.2	0.049	1.12	0.030	1.14	0.184
1426797_at	RIKEN cDNA 2700094F01 gene	2700094F01Rik	1.13	0.008	1.22	0.012	1.07	0.543	1.06	0.542	1.15	0.046
1457705_at	RIKEN cDNA 5330421C15 gene	5330421C15Rik	1.41	0.729	1.22	0.028	1.13	0.647	-1.98	0.064	-1.32	0.328
1423801_a_at	adenine phosphoribosyl transferase	Aprt	1.13	0.127	1.22	0.032	1.13	0.300	1.08	0.105	1.17	0.160
1416143_at	ATP synthase, H+ transporting, mitochondrial F0 complex, su	Atp5j	1.21	0.028	1.22	0.020	1.07	0.141	1.08	0.033	1.03	0.304
1426234_s_at	cDNA sequence BC002199	BC002199	-1.02	0.591	1.22	0.035	1.13	0.032	1.19	0.007	1.11	0.287
1425687_at	CASP8 and FADD-like apoptosis regulator	Cflar	1.09	0.405	1.22	0.044	-1.01	0.757	1.1	0.691	1.36	0.095
1425591_a_at	chromatin modifying protein 2A	Chmp2a	1.12	0.531	1.22	0.020	-1.02	0.783	1.04	0.243	-1	0.794
1417564_at	cofactor required for Sp1 transcriptional activation, subunit 9	Crsp9	-1	0.853	1.22	0.008	1.17	0.114	1.19	0.007	1.1	0.018
1427194_a_at	excision repaiross-complementing rodent repair deficiency, c	Csa	-1.01	0.873	1.22	0.041	-1.07	0.517	-1.06	0.577	-1.02	0.806
1452052_s_at	eukaryotic translation initiation factor 3, subunit 1 alpha	Eif3s1	1.12	0.016	1.22	0.037	1.03	0.336	1.09	0.102	1.06	0.175
1452262_at	GrpE-like 2, mitochondrial	Grpel2	1.02	0.399	1.22	0.003	1.1	0.043	1.07	0.016	1.08	0.031
1438019_at	inositol 1,3,4,5,6-pentakisphosphate 2-kinase	Ippk	1.01	0.976	1.22	0.005	1.08	0.227	1.03	0.848	1.15	0.239
1420585_a_at	nuclear RNA export factor 2	Nxf2	1.21	0.998	1.22	0.022	-1.02	0.815	-1.1	0.256	-1.01	0.979
1454888_at	prefoldin 4	Pfdn4	1.1	0.042	1.22	0.014	1.04	0.306	1.14	0.370	1.14	0.214
1436559_a_at	proteosome (prosome, macropain) 26S subunit, non-ATPase	Psmd10	1.11	0.181	1.22	0.000	1.06	0.269	1.1	0.264	-1.01	0.776
1448791_at	sorting nexin 5	Snx5	1.15	0.096	1.22	0.018	1.07	0.086	1.19	0.014	1.21	0.076
1443151_at	Synaptojanin 2 binding protein	Synj2bp	1.69	0.233	1.22	0.039	1.02	0.782	1.05	0.502	-1.14	0.392
1417820_at	torsin family 1, member B	Tor1b	-1	0.961	1.22	0.012	-1.06	0.547	1.21	0.078	1.17	0.198
1434508_at	ubiquitin-conjugating enzyme E2Q (putative)	Ube2q	1.04	0.565	1.22	0.039	1.15	0.043	1.11	0.004	1.22	0.080
1437414_at	zinc finger protein 217	Zfp217	1.06	0.126	1.22	0.005	1.01	0.888	1.17	0.006	1.29	0.005
1418801_at	zinc finger with KRAB and SCAN domains 1	Zkscan1	1	0.821	1.22	0.009	1.35	0.168	1.25	0.091	-1.12	0.068
1417158_at	ZXD family zinc finger C	Zxdc	-1.04	0.651	1.22	0.016	-1.01	0.927	-1.14	0.191	1.57	0.027
1450067_a_at	RIKEN cDNA 1810034K20 gene	1810034K20Rik	1.11	0.076	1.21	0.022	1.13	0.005	1.11	0.121	1.06	0.280
1429364_at	RIKEN cDNA 4930579G24 gene	4930579G24Rik	1.01	0.767	1.21	0.021	1.4	0.037	1.27	0.036	1.27	0.003
1419211_s_at	RIKEN cDNA 4933424B01 gene	4933424B01Rik	1.17	0.082	1.21	0.019	-1.02	0.829	1.11	0.049	-1.09	0.300
1457717_at	expressed sequence AI987986	AI987986	1.35	0.183	1.21	0.047	-1.01	0.675	1.12	0.965	1.17	0.408
1449523_at	B-cell CLL/lymphoma 7C	Bcl7c	1.01	0.154	1.21	0.042	1.14	0.179	1.05	0.437	1.17	0.183
1454779_s_at	RIKEN cDNA C230052I12 gene	C230052I12Rik	1	0.922	1.21	0.018	1.04	0.847	1.14	0.239	1.11	0.237
1452047_at	calcyclin binding protein	Cacybp	1.11	0.032	1.21	0.003	1.03	0.624	1.03	0.376	1.08	0.476
1454716_x_at	cytochrome c oxidase, subunit Vb	Cox5b	1.15	0.050	1.21	0.008	1.02	0.916	1.05	0.069	1.08	0.236
1455102_at	RIKEN cDNA D330037H05 gene /// similar to La-related prot	D330037H05Rik /	1.08	0.027	1.21	0.033	-1.01	0.405	-1.03	0.210	-1.12	0.245
1455108_at	eukaryotic translation initiation factor 4E member 2	Eif4e2	-1.01	0.966	1.21	0.033	1.15	0.118	1.31	0.044	1.12	0.256
1417913_at	GINS complex subunit 4 (Sld5 homolog)	Gins4	1.12	0.138	1.21	0.025	-1	0.852	1.15	0.018	-1.01	0.777
1435866_s_at	histone 3, H2a	Hist3h2a	-1.05	0.609	1.21	0.041	1.21	0.013	1.28	0.008	1.25	0.005
1427615_at	integrin alpha 4	Itga4	-1.77	0.103	1.21	0.033	1.36	0.914	-1	0.927	-1.36	0.094
1428589_at	mitochondrial ribosomal protein L41	Mrpl41	1.11	0.091	1.21	0.010	1.07	0.559	1	0.948	1.06	0.460
1449294_at	mitochondrial ribosomal protein S15	Mrps15	1.08	0.350	1.21	0.007	1.04	0.550	1.1	0.066	1.16	0.083
1424286_at	protein kinase, X-linked	Prkx	1.07	0.228	1.21	0.024	1.15	0.004	1.11	0.398	1.09	0.000
1416506_at	proteasome (prosome, macropain) subunit, alpha type 6	Psma6	1.11	0.055	1.21	0.008	1.03	0.422	1.01	0.992	1.08	0.088
1439635_at	regulator of G-protein signaling 9	Rgs9	1.33	0.886	1.21	0.017	2.39	0.248	-1.14	0.228	-1.69	0.019
1434361_at	SH3 and PX domain containing 3	Sh3px3	-1.05	0.111	1.21	0.003	1.1	0.152	1.05	0.631	1.13	0.059
1421733_a_at	protein-tyrosine sulfotransferase 1	Tpst1	1.23	0.129	1.21	0.043	1.23	0.200	1.14	0.176	1.28	0.055
1449096_at	RIKEN cDNA 0610011N22 gene	0610011N22Rik	1.05	0.205	1.2	0.010	1.06	0.394	1.18	0.114	1.1	0.261
1423705_at	RIKEN cDNA 2310057D15 gene	2310057D15Rik	1.14	0.078	1.2	0.048	-1.01	0.895	1.08	0.138	1.09	0.188
1460688_s_at	expressed sequence AA407659	AA407659	-1.04	0.390	1.2	0.002	1.06	0.244	1.12	0.079	1.17	0.055
1416135_at	apurinic/apyrimidinic endonuclease 1	Apex1	1.05	0.542	1.2	0.039	1.07	0.176	1.05	0.176	1.04	0.396
1452288_at	expressed sequence BB128963	BB128963	1.04	0.965	1.2	0.049	1.09	0.278	-1.03	0.427	1.05	0.268
1425646_at	cDNA sequence BC016495	BC016495	-1	0.799	1.2	0.039	1.29	0.164	1.24	0.155	1.2	0.111
1428865_at	BCL2-like 12 (proline rich)	Bcl2l12	1.11	0.560	1.2	0.036	1.09	0.334	1.16	0.109	1.31	0.102
1433970_at	bolA-like 3 (E. coli)	Bola3	1.08	0.033	1.2	0.015	1.01	0.449	1.14	0.025	1.11	0.028
1423877_at	chromatin assembly factor 1, subunit B (p60)	Chaf1b	1.17	0.101	1.2	0.006	1.15	0.027	1.21	0.112	1.07	0.397
1416971_at	cytochrome c oxidase, subunit VIIa 2	Cox7a2	1.13	0.090	1.2	0.025	1.13	0.074	1.13	0.013	1.03	0.468

1449406_at	cysteine and histidine rich 1	Cyhr1	1.22	0.219	1.2	0.004	-1.04	0.174	1.03	0.864	1.34	0.164
1451103_at	DNA segment, Chr 14, ERATO Doi 500, expressed	D14Ertd500e	1.26	0.364	1.2	0.026	1.09	0.493	1.08	0.276	1.1	0.007
1422627_a_at	McKusick-Kaufman syndrome protein	Mkks	1.22	0.095	1.2	0.041	1.02	0.896	1.05	0.222	1.08	0.321
1417252_at	5',3'-nucleotidase, cytosolic	Nt5c	1.04	0.472	1.2	0.013	1.16	0.006	1.07	0.339	1.1	0.049
1457716_at	OTU domain containing 7B	Otud7b	1.04	0.554	1.2	0.022	1.16	0.237	1.12	0.245	1.13	0.137
1448208_at	MAD homolog 1 (Drosophila)	Smad1	-1.03	0.601	1.2	0.042	1.06	0.619	-1.06	0.017	1.03	0.649
1416261_at	transmembrane protein 19	Tmem19	1.14	0.035	1.2	0.021	1.28	0.016	1.06	0.288	1.14	0.010
1433699_at	tumor necrosis factor, alpha-induced protein 3	Tnfaip3	1.12	0.165	1.2	0.006	1.24	0.054	1.2	0.202	1.1	0.710
1428747_at	tRNA selenocysteine associated protein 1	Trspap1	1.05	0.479	1.2	0.041	1.1	0.181	1.13	0.013	1.14	0.253
1417659_at	vacuolar protein sorting 29 (S. pombe)	Vps29	1.23	0.071	1.2	0.014	1.03	0.790	1.01	0.709	1.13	0.161
1437111_at	zinc finger CCCH type containing 12C	Zc3h12c	1.02	0.990	1.2	0.048	-1.22	0.058	1.04	0.948	-1.13	0.201
1427059_at	RIKEN cDNA 4732495E13 gene	4732495E13Rik	-1.1	0.226	-1.2	0.027	1.04	0.655	-1.12	0.032	-1.03	0.553
1448250_at	RIKEN cDNA 9030425E11 gene	9030425E11Rik	1.03	0.704	-1.2	0.030	1.02	0.732	-1.09	0.368	-1.06	0.400
1447926_at	ADP-ribosylation factor-like 5A	Arl5a	-1.04	0.491	-1.2	0.033	-1.14	0.097	1.03	0.947	-1.09	0.615
1455400_at	dimethylarginine dimethylaminohydrolase 1	Ddah1	1.07	0.580	-1.2	0.020	-1.09	0.105	-1.14	0.029	-1.15	0.106
1426759_at	mitogen-activated protein kinase kinase kinase kinase 3 /// si	Map4k3 /// LOC67	1.12	0.152	-1.2	0.049	-1.41	0.047	-1.51	0.007	-1.69	0.001
1419493_a_at	tumor protein D52	Tpd52	-1.01	0.675	-1.2	0.044	1.02	0.571	-1.05	0.182	-1.07	0.364
1450066_at	ubiquitin protein ligase E3 component n-recognin 1	Ubr1	1.01	0.915	-1.2	0.037	-1.09	0.151	-1.05	0.558	-1.11	0.082
1428949_at	exportin, tRNA (nuclear export receptor for tRNAs)	Xpot	-1.1	0.080	-1.2	0.013	-1.02	0.541	-1.06	0.290	-1.09	0.309
1451621_at	RIKEN cDNA 5830417C01 gene	5830417C01Rik	-1.04	0.629	-1.21	0.025	-1.11	0.302	-1.09	0.062	-1.06	0.144
1429383_at	casein kinase 1, gamma 3	Csnk1g3	-1.05	0.533	-1.21	0.046	-1.04	0.480	-1.3	0.016	-1.29	0.051
1417143_at	endothelial differentiation, lysophosphatidic acid G-protein-co	Edg2	1	0.991	-1.21	0.023	-1.05	0.464	-1.29	0.009	-1.15	0.086
1428011_a_at	Erbb2 interacting protein	Erbb2ip	-1.08	0.468	-1.21	0.010	-1.08	0.126	-1.24	0.085	-1.11	0.052
1417673_at	growth factor receptor bound protein 14	Grb14	1.1	0.479	-1.21	0.022	-1.18	0.005	-1.13	0.118	-1.12	0.046
1452030_a_at	heterogeneous nuclear ribonucleoprotein R	Hnrpr	-1.05	0.702	-1.21	0.031	-1.07	0.592	-1.01	0.820	-1.16	0.303
1428667_at	monoamine oxidase A	Maoa	-1.06	0.356	-1.21	0.045	1.04	0.679	-1.07	0.107	-1.11	0.049
1452740_at	myosin, heavy polypeptide 10, non-muscle	Myh10	-1.04	0.491	-1.21	0.045	-1.11	0.026	-1.11	0.133	-1.1	0.044
1417624_at	Ngfi-A binding protein 1	Nab1	1.01	0.959	-1.21	0.037	1.06	0.406	1.02	0.894	-1.21	0.041
1431375_s_at	parvin, alpha	Parva	-1.06	0.130	-1.21	0.035	-1.01	0.772	-1.1	0.138	-1.08	0.046
1423448_at	RAB11B, member RAS oncogene family	Rab11b	-1.14	0.004	-1.21	0.040	1.04	0.418	-1.04	0.410	-1.05	0.209
1426799_at	RAB8B, member RAS oncogene family	Rab8b	-1.05	0.308	-1.21	0.049	-1.08	0.322	-1.07	0.415	-1.22	0.010
1454962_at	spire homolog 1 (Drosophila)	Spire1	1.1	0.264	-1.21	0.048	-1.14	0.030	-1.23	0.038	-1.39	0.006
1433874_at	slingshot homolog 1 (Drosophila)	Ssh1	-1.15	0.367	-1.21	0.015	-1.04	0.831	-1.12	0.300	-1.19	0.070
1433807_at	RIKEN cDNA 6720463M24 gene	6720463M24Rik	-1.01	0.736	-1.22	0.012	1.13	0.463	-1	0.751	-1.06	0.523
1433897_at	expressed sequence AI597468	AI597468	-1.09	0.381	-1.22	0.031	1.03	0.706	-1.03	0.579	-1.08	0.386
1454863_at	ankyrin repeat domain 11	Ankrd11	-1.15	0.098	-1.22	0.033	-1.24	0.129	-1.27	0.068	-1.29	0.099
1426755_at	cytoskeleton-associated protein 4	Ckap4	-1.2	0.015	-1.22	0.045	-1.26	0.045	1.03	0.775	1.05	0.553
1448149_at	catenin (cadherin associated protein), alpha 1	Ctnna1	-1.06	0.189	-1.22	0.016	-1.03	0.453	-1.06	0.186	-1.21	0.004
1428354_at	forkhead box K2	Foxk2	-1.06	0.076	-1.22	0.003	-1.04	0.436	-1.1	0.055	-1.2	0.029
1453146_at	GTPase activating protein and VPS9 domains 1	Gapvd1	-1.17	0.214	-1.22	0.037	-1.1	0.291	-1.14	0.119	-1.04	0.474
1423144_at	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	-1.12	0.008	-1.22	0.032	-1.1	0.104	-1.08	0.407	-1.1	0.304
1418039_at	RAB, member of RAS oncogene family-like 3	Rabl3	-1.13	0.061	-1.22	0.009	-1.12	0.060	-1.17	0.019	-1.23	0.014
1460337_at	SH3-domain kinase binding protein 1	Sh3kbp1	1.04	0.176	-1.22	0.001	-1.19	0.008	-1.18	0.067	-1.26	0.018
1436137_at	solute carrier family 6 (neurotransmitter transporter), member	Slc6a17	-1.09	0.241	-1.22	0.014	1.01	0.987	1.03	0.598	-1.03	0.732
1460700_at	signal transducer and activator of transcription 3	Stat3	-1.02	0.776	-1.22	0.031	-1.14	0.059	-1.08	0.022	-1.09	0.154
1433740_at	RIKEN cDNA 2610301K12 gene	2610301K12Rik	-1.12	0.373	-1.23	0.028	1.07	0.391	-1.02	0.813	1.01	0.976
1426534_a_at	ADP-ribosylation factor GTPase activating protein 3	Arfgap3	1.04	0.590	-1.23	0.007	-1.19	0.007	-1.08	0.097	-1.24	0.027
1415711_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1	Arfgef1	-1.03	0.606	-1.23	0.017	-1.1	0.026	-1.16	0.176	-1.37	0.001
1438606_a_at	chloride intracellular channel 4 (mitochondrial)	Clic4	-1.01	0.253	-1.23	0.015	-1.1	0.027	-1.11	0.069	-1.13	0.069
1417563_at	eukaryotic translation initiation factor 4E binding protein 1	Eif4ebp1	-1.09	0.394	-1.23	0.016	-1.08	0.350	-1.08	0.544	-1.09	0.251
1428470_at	exocyst complex component 2	Exoc2	1.09	0.046	-1.23	0.027	-1.16	0.292	-1.24	0.004	-1.13	0.443
1437225_x_at	guanine nucleotide binding protein, alpha inhibiting 3	Gnai3	-1.2	0.289	-1.23	0.039	1.04	0.938	-1.28	0.121	1.11	0.394
1451629_at	limb-bud and heart	Lbh	-1.02	0.425	-1.23	0.001	-1.1	0.154	-1.04	0.507	-1.11	0.014
1456945_at	nudix (nucleoside diphosphate linked moiety X)-type motif 6	Nudt6	-1	0.934	-1.23	0.002	-1.13	0.046	-1.18	0.086	-1.18	0.005
1441617_at	positive cofactor 2, multiprotein complex, glutamine/Q-rich-as	Pcqap	-1.21	0.032	-1.23	0.007	-1.04	0.501	1.03	0.913	-1.35	0.071
1433761_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	-1.15	0.015	-1.23	0.041	-1.07	0.411	-1.15	0.018	-1.18	0.109
1432129_a_at	paired related homeobox 1	Prrx1	1.12	0.200	-1.23	0.008	-1.17	0.005	-1.2	0.025	-1.28	0.042
1420843_at	protein tyrosine phosphatase, receptor type, F	Ptprf	-1.06	0.479	-1.23	0.014	1.09	0.492	-1.05	0.527	1.04	0.696

1433871_at	R3H domain 1 (binds single-stranded nucleic acids)	R3hdm1	1.06	0.334	-1.23	0.014	-1.29	0.031	-1.17	0.004	-1.19	0.023
1422523_at	silver	Si	1.34	0.374	-1.23	0.046	-1.04	0.793	1.26	0.534	-1.3	0.304
1452445_at	solute carrier family 41, member 2	Slc41a2	1.17	0.245	-1.23	0.043	-1.15	0.024	-1.13	0.022	-1.27	0.002
1426531_at	zinc finger, MYND domain containing 11	Zmynd11	-1.13	0.227	-1.23	0.039	-1.09	0.203	-1.02	0.574	-1.2	0.040
1429353_a_at	RIKEN cDNA 4930511M11 gene	4930511M11Rik	1.55	0.566	-1.24	0.037	1.47	0.423	1.12	0.459	-1.04	0.577
1434376_at	CD44 antigen	Cd44	1.04	0.753	-1.24	0.040	-1.08	0.061	-1.12	0.038	-1.13	0.002
1452867_at	procollagen, type IV, alpha 3 (Goodpasture antigen) binding p	Col4a3bp	1.07	0.314	-1.24	0.022	-1.13	0.090	-1.22	0.095	-1.25	0.003
1423661_s_at	CTD (carboxy-terminal domain, RNA polymerase II, polypept	Ctdsp2	-1.23	0.142	-1.24	0.004	-1.04	0.598	-1	0.953	-1.06	0.265
1417567_at	catenin beta interacting protein 1	Ctnnbip1	-1.19	0.047	-1.24	0.045	1.07	0.510	1.12	0.201	1.09	0.463
1416125_at	FK506 binding protein 5	Fkbp5	-1.12	0.233	-1.24	0.022	1.2	0.133	-1.03	0.747	-1.11	0.386
1420980_at	p21 (CDKN1A)-activated kinase 1	Pak1	-1.13	0.258	-1.24	0.014	1.14	0.869	-1.05	0.426	1.03	0.956
1420611_at	protein kinase, cAMP dependent, catalytic, beta	Prkacb	-1.03	0.515	-1.24	0.002	-1.12	0.098	-1.07	0.171	-1.15	0.162
1422785_at	RAS p21 protein activator 2	Rasa2	-1.04	0.628	-1.24	0.033	-1.23	0.029	-1.32	0.047	-1.25	0.001
1420974_at	SET domain, bifurcated 1	Setdb1	-1.27	0.250	-1.24	0.028	1.03	0.953	-1.08	0.498	-1.57	0.183
1442237_at	Sequestosome 1	Sqstm1	-1.34	0.093	-1.24	0.044	-1.13	0.464	-1.05	0.499	1.49	0.029
1425011_x_at	syntaxin 18	Stx18	-1.04	0.406	-1.24	0.023	-1.15	0.067	-1.08	0.151	-1.1	0.167
1428586_at	transmembrane protein 41B	Tmem41b	-1.19	0.184	-1.24	0.035	1.08	0.780	1	0.963	1.09	0.467
1448670_at	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast	Ube2e3	-1.07	0.368	-1.24	0.014	-1.02	0.392	-1.18	0.019	-1.13	0.051
1428431_at	RIKEN cDNA 2310047A01 gene	2310047A01Rik	-1.03	0.665	-1.25	0.001	-1.08	0.048	1.03	0.592	-1.11	0.108
1455072_at	centrosomal protein 350	Cep350	1.06	0.133	-1.25	0.005	-1.13	0.185	-1.35	0.023	-1.46	0.008
1454654_at	disrupted in renal carcinoma 2 (human)	Dirc2	-1.1	0.147	-1.25	0.016	1.05	0.466	-1.1	0.057	1.07	0.644
1421929_at	Eph receptor A4	Epha4	-1.29	0.021	-1.25	0.028	-1.65	0.142	-1.33	0.019	-1.33	0.166
1459622_at	gene model 22, (NCBI)	Gm22	-1.04	0.244	-1.25	0.048	-1.06	0.346	-1.14	0.005	-1.23	0.014
1455048_at	immunoglobulin superfamily, member 3	Igsf3	-1.05	0.282	-1.25	0.039	-1.08	0.557	-1.06	0.459	-1	0.892
1437268_at	LanC lantibiotic synthetase component C-like 3 (bacterial)	Lancl3	-1.13	0.226	-1.25	0.031	1.21	0.312	-1.02	0.662	-1.01	0.871
1430365_at	nuclear transcription factor, X-box binding-like 1	Nfxl1	1.76	0.985	-1.25	0.036	2.76	0.816	1.31	0.779	-1.11	0.757
1449059_a_at	3-oxoacid CoA transferase 1	Oxct1	-1.07	0.126	-1.25	0.009	-1.1	0.131	-1.09	0.042	-1.14	0.130
1415729_at	3-phosphoinositide dependent protein kinase-1	Pdpk1	-1.11	0.214	-1.25	0.017	-1.02	0.513	-1.23	0.003	-1.16	0.047
1434924_at	PHD finger protein 2	Phf2	-1	0.883	-1.25	0.030	1.09	0.060	-1.37	0.015	-1.22	0.211
1419945_s_at	RAB2, member RAS oncogene family	Rab2	-1.03	0.303	-1.25	0.007	-1.13	0.068	-1.09	0.018	-1.21	0.049
1424134_at	ring finger and SPRY domain containing 1	Rspry1	1.02	0.817	-1.25	0.020	-1.2	0.102	-1.07	0.009	-1.14	0.085
1431204_at	RIKEN cDNA 4930578N16 gene	4930578N16Rik	1.21	0.792	-1.26	0.040	1.61	0.796	1.18	0.238	2	0.950
1454609_x_at	RIKEN cDNA 6430527G18 gene	6430527G18Rik	-1.1	0.267	-1.26	0.038	-1.02	0.570	-1.06	0.602	1.15	0.420
1434797_at	RIKEN cDNA 6720469N11 gene	6720469N11Rik	-1.03	0.586	-1.26	0.044	-1.28	0.066	-1.35	0.003	-1.32	0.010
1454918_at	alkylglycerone phosphate synthase	Agps	1.02	0.854	-1.26	0.007	-1.2	0.172	-1.29	0.072	-1.42	0.003
1442632_at	Centaurin, gamma 2	Centg2	-1.25	0.056	-1.26	0.010	-1.2	0.187	1.09	0.974	-1.05	0.295
1455440_at	chloride channel 6	Clcn6	1.02	0.952	-1.26	0.012	-1.29	0.025	-1.2	0.188	-1.37	0.013
1426407_at	CUG triplet repeat, RNA binding protein 1	Cugbp1	-1.12	0.288	-1.26	0.036	-1.05	0.284	-1.19	0.003	-1.11	0.094
1424981_at	neurolysin (metallopeptidase M3 family)	Nln	1.04	0.535	-1.26	0.012	-1.11	0.027	-1.04	0.419	-1.07	0.472
1429564_at	polycomb group ring finger 5	Pcgf5	1	0.961	-1.26	0.015	-1.02	0.613	-1.13	0.129	-1.09	0.278
1448568_a_at	solute carrier family 20, member 1	Slc20a1	-1.02	0.679	-1.26	0.001	-1.1	0.033	-1.11	0.000	-1.23	0.005
1436319_at	sulfatase 1	Sulf1	1.13	0.383	-1.26	0.006	1.21	0.333	1.02	0.702	-1.17	0.298
1452299_at	WW domain containing E3 ubiquitin protein ligase 1	Wwp1	1.01	0.947	-1.26	0.001	1.01	0.979	1.01	0.956	-1.01	0.664
1422032_a_at	zinc finger, AN1-type domain 6	Zfand6	1	0.981	-1.26	0.011	-1.04	0.413	-1.08	0.085	-1.23	0.008
1437208_at	septin 10	10-Sep	-1.08	0.240	-1.27	0.035	-1.03	0.559	-1.08	0.226	1.09	0.605
1460455_at	RIKEN cDNA 1110059H15 gene	1110059H15Rik	-1.06	0.452	-1.27	0.011	-1.02	0.546	-1.36	0.020	-1.39	0.084
1453392_at	RIKEN cDNA 1810054D07 gene	1810054D07Rik	-1.04	0.369	-1.27	0.037	-1.27	0.012	-1.09	0.433	-1.25	0.092
1430496_at	RIKEN cDNA 6720408I04 gene	6720408I04Rik	-1.19	0.253	-1.27	0.048	-1.49	0.313	1.16	0.310	1.2	0.928
1455032_at	RIKEN cDNA 9630037P07 gene	9630037P07Rik	1	0.958	-1.27	0.025	-1.19	0.007	-1.12	0.007	-1.16	0.003
1429083_at	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	Agl	-1.11	0.403	-1.27	0.004	-1.01	0.987	1.13	0.562	1.04	0.972
1460703_at	activating signal cointegrator 1 complex subunit 1	Ascc1	-1.1	0.254	-1.27	0.004	1.05	0.295	1.02	0.857	-1.04	0.395
1420652_at	arginine-tRNA-protein transferase 1	Ate1	1.18	0.204	-1.27	0.020	-1.71	0.036	-1.57	0.007	-1.84	0.029
1449595_at	expressed sequence C79490	C79490	-1.18	0.337	-1.27	0.037	-1.15	0.625	-1.11	0.522	1.5	0.918
1428537_at	casein kinase 1, alpha 1	Csnk1a1	-1.08	0.245	-1.27	0.032	-1.13	0.046	-1.16	0.095	-1.16	0.005
1436896_at	DNA segment, Chr 14, ERATO Doi 231, expressed	D14Ertd231e	-1.14	0.172	-1.27	0.024	1	0.988	-1.04	0.367	-1.05	0.560
1437974_a_at	hexokinase 1	Hk1	-1.15	0.059	-1.27	0.044	-1.12	0.078	-1.15	0.032	1.02	0.693
1433445_x_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	-1.02	0.232	-1.27	0.046	-1.09	0.260	-1.11	0.169	-1.11	0.130
1450730_at	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	1.03	0.695	-1.27	0.006	-1.2	0.003	-1.04	0.474	-1.27	0.007

1437103_at	insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	1.01	0.898	-1.27	0.042	-1.26	0.003	-1.25	0.001	-1.37	0.009
1424885_at	kelch domain containing 8A	Klhdc8a	-1.03	0.550	-1.27	0.011	1.08	0.293	-1.06	0.228	-1.11	0.054
1420728_at	keratin 32	Krt32	-1.14	0.099	-1.27	0.045	-1.15	0.364	1.05	0.842	-1.08	0.478
1421926_at	mitogen-activated protein kinase 11	Mapk11	1.02	0.933	-1.27	0.015	1.03	0.682	-1.22	0.108	-1.04	0.845
1419048_at	pecanex homolog (Drosophila)	Pcnx	1.04	0.011	-1.27	0.000	-1.12	0.256	-1.16	0.027	-1.18	0.147
1437953_at	preimplantation protein 4	Prei4	-1.02	0.688	-1.27	0.038	1.23	0.665	1.15	0.730	1.15	0.860
1427006_at	Rap guanine nucleotide exchange factor (GEF) 1	Rapgef1	-1.09	0.110	-1.27	0.032	-1.04	0.685	-1.23	0.021	-1.19	0.214
1451073_at	signal peptide peptidase 3	Sppl3	-1.09	0.291	-1.27	0.033	1.11	0.440	-1.22	0.051	-1.11	0.434
1460243_at	serine palmitoyltransferase, long chain base subunit 2	Sptlc2	1.01	0.892	-1.27	0.013	-1.18	0.169	-1.11	0.048	-1.24	0.022
1435841_s_at	succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	-1.04	0.295	-1.27	0.016	-1.08	0.020	-1.07	0.139	-1.01	0.724
1456623_at	tropomyosin 1, alpha	Tpm1	-1.04	0.504	-1.27	0.015	-1.28	0.212	-1.23	0.025	-1.15	0.141
1435608_at	zinc and ring finger 3 /// similar to Goliath homolog precursor	Znrf3 /// LOC6318	-1.05	0.634	-1.27	0.008	-1.05	0.584	-1.3	0.001	-1.21	0.040
1436638_at	RIKEN cDNA 6720401G13 gene	6720401G13Rik	1.05	0.907	-1.28	0.049	-1.2	0.345	1.39	0.096	1.19	0.690
1424214_at	RIKEN cDNA 9130213B05 gene	9130213B05Rik	-1.02	0.370	-1.28	0.028	-1	0.894	-1.13	0.136	-1.18	0.069
1435975_at	expressed sequence AI115600	AI115600	-1.14	0.090	-1.28	0.042	1.15	0.251	-1.45	0.015	-1.33	0.119
1434630_at	ankyrin repeat domain 28	Ankrd28	1.02	0.452	-1.28	0.044	-1.15	0.035	-1.25	0.025	-1.4	0.003
1434362_at	expressed sequence AW550831	AW550831	1.03	0.800	-1.28	0.009	1.03	0.587	-1.02	0.631	-1.13	0.209
1418659_at	circadian locomoter output cycles kaput	Clock	-1.01	0.769	-1.28	0.024	-1.2	0.137	-1.16	0.160	-1.53	0.032
1450625_at	procollagen, type V, alpha 2	Col5a2	-1	0.861	-1.28	0.009	-1.17	0.003	-1.18	0.026	-1.21	0.013
1418508_a_at	growth factor receptor bound protein 2	Grb2	-1.45	0.044	-1.28	0.019	1.17	0.510	-1.3	0.026	1.12	0.447
1434060_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus)	Herc1	1.18	0.045	-1.28	0.020	-1.23	0.065	-1.25	0.151	-1.28	0.082
1419647_a_at	immediate early response 3	Ier3	-1.16	0.103	-1.28	0.040	-1.07	0.168	-1.17	0.037	-1.05	0.226
1448925_at	twist homolog 2 (Drosophila)	Twist2	-1.06	0.022	-1.28	0.038	-1.14	0.162	-1.11	0.134	-1.22	0.015
1426909_at	uridine-cytidine kinase 2	Uck2	-1.06	0.436	-1.28	0.010	1.05	0.668	1.17	0.275	1.14	0.438
1456487_at	adenylate cyclase 1	Adcy1	-1.18	0.420	-1.29	0.043	-1.24	0.176	1.19	0.157	-1.1	0.365
1446965_at	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	-1.37	0.163	-1.29	0.042	-1.12	0.457	-1.02	0.695	-1.24	0.034
1416551_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	-1.03	0.298	-1.29	0.005	-1.09	0.361	-1.03	0.566	-1.07	0.220
1437244_at	growth arrest-specific 2 like 3	Gas2l3	1.05	0.519	-1.29	0.007	1.06	0.954	1.08	0.354	1.05	0.893
1417434_at	glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	1.05	0.273	-1.29	0.007	-1.13	0.220	-1.12	0.078	-1.2	0.097
1448890_at	Kruppel-like factor 2 (lung)	Klf2	-1.04	0.447	-1.29	0.022	-1.03	0.722	-1.04	0.087	-1.09	0.331
1454930_at	leucine rich repeat containing 35	Lrrc35	-1.12	0.192	-1.29	0.030	-1	0.908	-1.03	0.706	1.01	0.743
1426319_at	platelet-derived growth factor, D polypeptide	Pdgfd	-1.04	0.635	-1.29	0.023	-1.04	0.488	1.07	0.796	-1.06	0.682
1435251_at	sorting nexin 13	Snx13	1.05	0.862	-1.29	0.035	-1.06	0.375	-1.18	0.021	-1.48	0.000
1436805_at	RIKEN cDNA 2810457I06 gene	2810457I06Rik	-1.14	0.374	-1.3	0.012	-1.01	0.921	-1.63	0.004	-1.35	0.076
1426339_at	adenylate kinase 5	Ak5	-1.14	0.160	-1.3	0.023	-1.07	0.305	1.06	0.371	-1.17	0.273
1420618_at	cytoplasmic polyadenylation element binding protein 4	Cpeb4	-1.11	0.395	-1.3	0.013	1	0.893	-1.19	0.032	-1.16	0.113
1428737_s_at	GRAM domain containing 3	Gramd3	-1.12	0.182	-1.3	0.011	-1.05	0.472	1.03	0.786	-1.11	0.178
1425142_a_at	heterogeneous nuclear ribonucleoprotein D	Hnrpd	-1.11	0.036	-1.3	0.026	-1.29	0.008	-1.24	0.008	-1.19	0.103
1418628_at	KH domain containing, RNA binding, signal transduction ass	Khdrbs1	-1.08	0.443	-1.3	0.045	-1.03	0.649	-1.06	0.584	1.03	0.914
1448647_at	mannosidase 2, alpha 1	Man2a1	1.01	0.847	-1.3	0.008	-1.13	0.055	-1.09	0.114	-1.22	0.000
1417584_at	solute carrier family 11 (proton-coupled divalent metal ion tra	Slc11a2	1.04	0.980	-1.3	0.027	1.1	0.413	1.2	0.073	1.19	0.237
1424905_a_at	solute carrier family 39 (metal ion transporter), member 11	Slc39a11	-1.14	0.064	-1.3	0.045	-1.12	0.254	-1.12	0.012	-1.18	0.037
1459168_at	Zinc finger protein 521	Zfp521	1.08	0.421	-1.3	0.034	-1.02	0.684	-1.44	0.131	1.74	0.805
1438280_at	RIKEN cDNA 1700023L04 gene	1700023L04Rik	1.01	0.683	-1.31	0.029	-1.65	0.066	1.73	0.560	2.4	0.043
1450643_s_at	acyl-CoA synthetase long-chain family member 1	Acsl1	1.08	0.781	-1.31	0.049	1.17	0.503	1.04	0.893	1.06	0.767
1448712_at	choroidermia	Chm	1.02	0.964	-1.31	0.038	-1.13	0.095	1.01	0.873	-1.48	0.056
1456133_x_at	integrin beta 5	Itgb5	-1.14	0.148	-1.31	0.038	-1.07	0.236	-1.06	0.007	-1.06	0.428
1457449_at	Longevity assurance homolog 6 (S. cerevisiae)	Lass6	1.01	0.994	-1.31	0.012	-1.31	0.159	1.26	0.100	-1.65	0.058
1417827_at	N-glycanase 1	Ngly1	-1.06	0.190	-1.31	0.018	-1.05	0.241	-1.01	0.794	-1.07	0.289
1447408_at	Nipped-B homolog (Drosophila)	Nipbl	-1.01	0.418	-1.31	0.023	-1.24	0.370	1.38	0.829	-1.03	0.806
1440348_at	zinc finger, FYVE domain containing 9	Zfyve9	-1.13	0.144	-1.31	0.002	-1.17	0.011	-1.29	0.038	-1.1	0.006
1421949_a_at	RIKEN cDNA 2610507L03 gene	2610507L03Rik	1.07	0.802	-1.32	0.022	-1.03	0.630	1.25	0.055	-1.15	0.076
1435568_at	cDNA sequence AK129128	AK129128	-1.03	0.629	-1.32	0.024	-1.11	0.087	-1.12	0.154	-1.31	0.060
1450910_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	Cap2	1.09	0.566	-1.32	0.042	-1.28	0.064	-1.11	0.116	-1.19	0.016
1426491_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus)	Herc2	-1.13	0.065	-1.32	0.050	-1.25	0.001	-1.3	0.054	-1.4	0.006
1431160_x_at	similar to gonadotropin inducible ovarian transcription factor	LOC628850 /// LC	-1.09	0.338	-1.32	0.016	-1.01	0.836	-1.06	0.696	1.51	0.128
1439115_at	microcephaly, primary autosomal recessive 1	Mcph1	-1.12	0.592	-1.32	0.046	1.12	0.559	-1.03	0.546	-1.15	0.568
1423489_at	monocyte to macrophage differentiation-associated	Mmd	-1.08	0.012	-1.32	0.002	-1.03	0.412	-1.13	0.001	-1.01	0.700

1422456_at	N-ethylmaleimide sensitive fusion protein	Nsf	1.01	0.976	-1.32	0.014	-1.05	0.479	-1.08	0.056	-1.12	0.018
1422707_at	phosphoinositide-3-kinase, catalytic, gamma polypeptide	Pik3cg	-1.12	0.038	-1.32	0.028	1.12	0.437	1.16	0.057	1.32	0.031
1417667_a_at	phosphotriesterase related	Pter	-1.07	0.161	-1.32	0.013	-1.11	0.305	-1	0.937	-1.1	0.073
1416524_at	speckle-type POZ protein	Spop	-1.09	0.270	-1.32	0.040	-1.11	0.136	-1.13	0.145	-1.19	0.001
1460204_at	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	Tec	1.02	0.754	-1.32	0.003	-1.04	0.396	-1.3	0.027	-1.24	0.090
1449405_at	tensin 1	Tns1	-1.04	0.500	-1.32	0.040	-1.53	0.004	-1.42	0.008	-1.46	0.006
1425381_a_at	transferrin receptor 2	Trfr2	-1.25	0.172	-1.32	0.033	1.4	0.535	-1.13	0.197	1.06	0.941
1435133_at	UDP-glucose ceramide glucosyltransferase	Ugcg	1.12	0.406	-1.32	0.019	-1.19	0.087	-1.16	0.084	-1.24	0.006
1453343_s_at	vaccinia related kinase 2	Vrk2	-1	0.945	-1.32	0.031	-1.19	0.104	-1.3	0.007	-1.21	0.048
1455376_at	RIKEN cDNA 1300010F03 gene	1300010F03Rik	1.02	0.839	-1.33	0.005	-1.07	0.464	-1.08	0.370	1.02	0.975
1455299_at	RIKEN cDNA 1700110N18 gene	1700110N18Rik	-1.03	0.758	-1.33	0.011	-1.11	0.301	-1.09	0.114	-1.14	0.038
1449244_at	cadherin 2	Cdh2	1	0.807	-1.33	0.020	-1.37	0.040	-1.18	0.146	-1.5	0.002
1425423_at	GLIS family zinc finger 1	Glis1	-1.13	0.366	-1.33	0.017	-1.35	0.063	-1.42	0.061	-1.37	0.069
1455404_at	junctophilin 2	Jph2	-1.05	0.450	-1.33	0.003	-1.14	0.117	-1.27	0.006	-1.29	0.174
1434395_at	mannosidase, alpha, class 1A, member 2	Man1a2	1.16	0.136	-1.33	0.003	1.02	0.935	1.1	0.448	-1.05	0.818
1436660_at	ribosome binding protein 1	Rrbp1	-1.18	0.172	-1.33	0.030	-1.17	0.270	-1.21	0.004	-1.4	0.090
1455549_at	SEC14 and spectrin domains 1	Sestd1	-1.01	0.773	-1.33	0.021	-1.1	0.103	-1.27	0.012	-1.32	0.002
1418088_a_at	syntaxin 8	Stx8	1.03	0.787	-1.33	0.009	1.01	0.922	-1.04	0.175	-1.17	0.157
1430440_at	RIKEN cDNA 4930442J19 gene	4930442J19Rik	1.59	0.359	-1.34	0.041	-1.3	0.373	-1.15	0.511	1.34	0.887
1455083_at	Atpase, class VI, type 11C	Atp11c	1.06	0.562	-1.34	0.045	-1.23	0.045	-1.17	0.053	-1.19	0.008
1434749_at	cDNA sequence BC067068	BC067068	1.28	0.155	-1.34	0.000	-1.17	0.202	1.04	0.635	-1.06	0.526
1434718_at	cullin 3	Cul3	-1.06	0.442	-1.34	0.012	1.02	0.960	-1.19	0.178	-1.2	0.035
1433995_s_at	DNA segment, Chr 16, Brigham & Women's Genetics 1543 e	D16Bwg1543e	-1.04	0.162	-1.34	0.033	-1.04	0.234	-1.04	0.562	-1.14	0.057
1438997_at	Endoplasmic reticulum (ER) to nucleus signalling 1	Ern1	1.37	0.898	-1.34	0.010	1.22	0.957	-1.24	0.340	1.22	0.801
1416760_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga	Galntl1	-1.05	0.312	-1.34	0.048	1.05	0.625	-1.06	0.238	1.02	0.833
1428374_at	glucuronyl C5-epimerase	Glce	-1	0.800	-1.34	0.010	-1.07	0.316	-1.05	0.512	-1.21	0.045
1434158_at	GDP-mannose 4, 6-dehydratase	Gmds	-1.3	0.036	-1.34	0.039	-1.4	0.009	-1.13	0.033	-1.3	0.012
1433747_at	leucyl/cystinyl aminopeptidase	Lnpep	1.04	0.394	-1.34	0.036	-1.21	0.073	-1.12	0.105	-1.31	0.010
1427809_at	Latrophilin 3	Lphn3	1.71	0.105	-1.34	0.035	-1.3	0.028	1.67	0.859	1.05	0.651
1427572_at	Leucine rich repeat containing 51	Lrrc51	1.07	0.916	-1.34	0.028	1.56	0.854	1.22	0.491	-1.31	0.179
1445731_at	Phosphatidylinositol 3-kinase, catalytic, beta polypeptide	Pik3cb	-1.21	0.255	-1.34	0.046	1.01	0.954	-1.14	0.166	1.13	0.504
1443029_at	PTPRF interacting protein, binding protein 1 (liprin beta 1)	Ppfibp1	-1.36	0.314	-1.34	0.009	-1.25	0.168	1.1	0.651	-1.11	0.314
1416165_at	RAB31, member RAS oncogene family	Rab31	-1.06	0.276	-1.34	0.004	-1.09	0.019	-1.14	0.005	-1.19	0.055
1438404_at	ring finger protein 144	Rnf144	-1.03	0.790	-1.34	0.048	1.12	0.396	1.01	0.925	-1.01	0.841
1436774_at	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	Sel1h	-1.12	0.027	-1.34	0.031	-1.03	0.412	-1.01	0.762	-1.19	0.082
1453125_at	SRY-box containing gene 11	Sox11	-1.2	0.089	-1.34	0.012	-1.26	0.141	-1.05	0.410	-1.04	0.474
1436982_at	trinucleotide repeat containing 6b	Tnrc6b	1.03	0.876	-1.34	0.049	-1.09	0.190	-1.23	0.033	-1.29	0.015
1419577_at	RIKEN cDNA A530089I17 gene	A530089I17Rik	-1.11	0.081	-1.35	0.006	1	0.967	-1.03	0.571	1.03	0.765
1454708_at	actin-binding LIM protein 1	Ablim1	-1.24	0.308	-1.35	0.041	-1	0.806	1.12	0.117	1.22	0.119
1422573_at	AMP deaminase 3	Ampd3	-1.05	0.212	-1.35	0.001	-1.11	0.050	-1.17	0.022	-1.2	0.024
1449955_at	calcium channel, voltage-dependent, alpha 1F subunit	Cacna1f	-1.46	0.116	-1.35	0.026	1.59	0.261	1.05	0.771	1.09	0.827
1453372_at	DnaJ (Hsp40) homolog, subfamily C, member 1	Dnajc1	1.05	0.384	-1.35	0.013	-1.38	0.031	-1.2	0.010	-1.51	0.009
1437282_at	Dedicator of cyto-kinesis 2	Dock2	-1.52	0.119	-1.35	0.029	1.16	0.368	-1.56	0.298	1.51	0.224
1423702_at	H1 histone family, member 0	H1f0	-1.12	0.085	-1.35	0.022	1.01	0.770	-1.05	0.367	-1.08	0.094
1417379_at	IQ motif containing GTPase activating protein 1	Iqgap1	-1.09	0.324	-1.35	0.038	-1.23	0.038	-1.19	0.026	-1.17	0.002
1433776_at	lipoma HMGIC fusion partner	Lhfp	-1.01	0.728	-1.35	0.002	-1.23	0.000	-1.22	0.037	-1.29	0.005
1433842_at	leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	-1.04	0.280	-1.35	0.011	-1.26	0.097	-1.25	0.019	-1.34	0.009
1448870_at	latent transforming growth factor beta binding protein 1	Ltbp1	-1.13	0.155	-1.35	0.038	-1.28	0.009	-1.28	0.007	-1.41	0.018
1417110_at	mannosidase 1, alpha	Man1a	-1.09	0.078	-1.35	0.001	-1.33	0.095	-1.17	0.158	1.04	0.833
1426369_at	male sterility domain containing 2	Mlstd2	-1.01	0.808	-1.35	0.024	-1.09	0.270	-1.16	0.134	-1.29	0.037
1451140_s_at	protein kinase, AMP-activated, gamma 2 non-catalytic subun	Prkag2	-1.27	0.082	-1.35	0.045	-1.08	0.261	-1.09	0.038	-1.04	0.112
1438470_at	suppressor of cytokine signaling 2	Socs2	1.33	0.209	-1.35	0.004	1.05	0.394	-1.21	0.339	-1.37	0.119
1435878_at	serine/threonine kinase 38 like	Stk38l	-1.07	0.395	-1.35	0.024	-1.24	0.003	-1.29	0.006	-1.11	0.240
1452092_at	RIKEN cDNA 4631426J05 gene	4631426J05Rik	-1.1	0.767	-1.36	0.004	1.04	0.677	-1.04	0.373	1.13	0.661
1426392_a_at	ARP3 actin-related protein 3 homolog (yeast)	Actr3	-1.27	0.167	-1.36	0.037	-1.09	0.246	-1.12	0.097	-1.15	0.092
1450586_at	bradykinin receptor, beta 1	Bdkrb1	-1.24	0.115	-1.36	0.049	-1.07	0.448	-1.22	0.188	1.07	0.788
1449375_at	carboxylesterase 6	Ces6	-1.14	0.224	-1.36	0.045	1.51	0.575	2.98	0.175	-1.01	0.721
1444181_at	GTPase, IMAP family member 5	Gimap5	-1.27	0.091	-1.36	0.002	1.06	0.761	-1.01	0.862	-1.26	0.138

1454851_at	nuclear receptor subfamily 2, group C, member 2	Nr2c2	-1.13	0.161	-1.36	0.021	-1.22	0.096	-1.36	0.014	-1.3	0.001
1420015_s_at	palmitoyl-protein thioesterase 1	Ppt1	-1.59	0.011	-1.36	0.011	1.11	0.920	-1.09	0.357	1.14	0.918
1451179_a_at	quaking	Qk	-1.04	0.550	-1.36	0.003	-1.2	0.001	-1.27	0.004	-1.26	0.001
1431335_a_at	WAP four-disulfide core domain 1	Wfdc1	1.15	0.922	-1.36	0.034	1.52	0.619	1.61	0.690	1.73	0.184
1436161_at	androgen-induced proliferation inhibitor	Aprin	1.12	0.419	-1.37	0.011	-1.08	0.288	-1.19	0.214	-1.34	0.027
1418071_s_at	chromodomain protein, Y chromosome-like	Cdyl	-1.05	0.426	-1.37	0.034	-1.27	0.080	-1.39	0.004	-1.39	0.022
1423779_at	coiled-coil-helix-coiled-coil-helix domain containing 6	Chchd6	-1.11	0.273	-1.37	0.009	1.03	0.848	-1	0.868	1.08	0.524
1419353_at	dolichol-phosphate (beta-D) mannosyltransferase 1	Dpm1	-1.02	0.726	-1.37	0.018	1.32	0.009	1.09	0.629	-1.13	0.660
1435682_at	leucyl-tRNA synthetase, mitochondrial	Lars2	1.05	0.745	-1.37	0.008	-1.3	0.007	-1.15	0.106	-1.05	0.462
1453104_at	mitogen activated protein kinase 1	Mapk1	-1.18	0.242	-1.37	0.048	1.04	0.039	1.04	0.263	1.1	0.068
1426382_at	protein phosphatase 1B, magnesium dependent, beta isoforn	Ppm1b	-1.08	0.263	-1.37	0.011	-1.26	0.034	-1.31	0.005	-1.34	0.000
1452727_at	R3H domain containing 2	R3hdm2	-1.26	0.044	-1.37	0.008	-1.06	0.456	-1.11	0.225	-1.2	0.156
1417696_at	sterol O-acyltransferase 1	Soat1	-1.05	0.309	-1.37	0.014	-1.13	0.066	-1.18	0.016	-1.09	0.111
1452405_x_at	T-cell receptor alpha chain /// RIKEN cDNA A430107P09 ger	Tcra /// A430107P	-1.01	0.572	-1.37	0.014	-1.02	0.805	-1.23	0.105	-1.16	0.101
1452213_at	testis expressed gene 2	Tex2	1.14	0.850	-1.37	0.027	-1.05	0.572	-1.07	0.371	-1.07	0.274
1456981_at	transmembrane channel-like gene family 7	Tmc7	-1.26	0.107	-1.37	0.045	1.26	0.069	1.24	0.167	1.16	0.303
1447908_x_at	tetratricopeptide repeat domain 3	Ttc3	-1.57	0.058	-1.37	0.047	-1.05	0.602	-1.33	0.158	1.09	0.418
1450782_at	wingless-related MMTV integration site 4	Wnt4	-1.05	0.454	-1.37	0.001	-1.16	0.013	1.01	0.468	-1.07	0.591
1428663_at	RIKEN cDNA 5133401H06 gene	5133401H06Rik	-1.04	0.485	-1.38	0.025	1.02	0.848	-1.09	0.359	-1	0.884
1441007_at	RIKEN cDNA A330102I10 gene	A330102I10Rik	-1.76	0.079	-1.38	0.007	1.05	0.800	-1.57	0.101	1.34	0.821
1454916_s_at	ADP-ribosylation factor interacting protein 1	Arfip1	1.01	0.891	-1.38	0.004	-1.19	0.078	-1.22	0.002	-1.4	0.022
1452921_at	RIKEN cDNA B130050I23 gene	B130050I23Rik	-1.01	0.672	-1.38	0.025	-1.03	0.681	-1.05	0.417	-1.02	0.803
1427837_at	Immunoglobulin kappa chain variable 32 (V32)	Igk-V32	1.03	0.907	-1.38	0.010	-1.46	0.190	1.31	0.922	1.06	0.653
1446618_at	hypothetical gene supported by AK038224	LOC432971	-1.14	0.124	-1.38	0.049	1.11	0.770	1.15	0.012	-1.1	0.365
1426245_s_at	microtubule-associated protein, RP/EB family, member 2	Mapre2	-1.11	0.291	-1.38	0.016	1.08	0.394	-1.1	0.060	-1.04	0.430
1448943_at	neuropilin 1	Nrp1	1.02	0.673	-1.38	0.026	-1.42	0.013	-1.35	0.002	-1.34	0.031
1444943_at	SH3 domain containing ring finger 1	Sh3rf1	-1.19	0.503	-1.38	0.011	1.41	0.686	-1.28	0.317	-1.49	0.216
1434261_at	signal-induced proliferation-associated 1 like 2	Sipa1l2	1.02	0.688	-1.38	0.041	-1.2	0.014	-1.32	0.011	-1.47	0.002
1454992_at	solute carrier family 7 (cationic amino acid transporter, y+ sys	Slc7a1	-1.12	0.150	-1.38	0.022	-1.15	0.182	-1.17	0.052	-1.16	0.113
1454960_at	MAD homolog 3 (Drosophila)	Smad3	-1.12	0.305	-1.38	0.010	-1.2	0.031	-1.16	0.081	-1.22	0.092
1443354_at	Tripartite motif-containing 59	Trim59	1.04	0.793	-1.38	0.027	1.8	0.041	-1.18	0.332	1.07	0.556
1419954_s_at	zinc finger, AN1-type domain 3	Zfand3	1.09	0.693	-1.38	0.023	-1.42	0.001	-1.57	0.000	-1.56	0.003
1428500_at	RIKEN cDNA 2210419D22 gene	2210419D22Rik	-1.21	0.197	-1.39	0.011	-1.1	0.077	-1.22	0.127	-1.29	0.130
1433256_at	RIKEN cDNA A930011E06 gene	A930011E06Rik	1.15	0.460	-1.39	0.015	2.05	0.118	2.41	0.202	1.69	0.195
1456735_x_at	acid phosphatase-like 2	Acpl2	-1.22	0.202	-1.39	0.028	1	0.712	-1.18	0.007	1.02	0.702
1434052_at	expressed sequence AI593442	AI593442	1.54	0.426	-1.39	0.044	1.55	0.053	-1.2	0.343	-1.38	0.083
1419922_s_at	attractin like 1	Atrnl1	-1.14	0.030	-1.39	0.048	-1.18	0.109	-1.17	0.261	-1.32	0.013
1459416_at	B-cell CLL/lymphoma 7A	Bcl7a	1.44	0.623	-1.39	0.049	-1.14	0.409	-1.14	0.171	1.69	0.181
1419610_at	chemokine (C-C motif) receptor 1	Ccr1	1.02	0.839	-1.39	0.045	1.18	0.965	-1.69	0.134	2.85	0.544
1433808_at	RIKEN cDNA D330001F17 gene	D330001F17Rik	-1.18	0.272	-1.39	0.041	1.05	0.318	1.02	0.443	1.13	0.169
1426833_at	eukaryotic translation initiation factor 4 gamma, 3	Eif4g3	-1.14	0.128	-1.39	0.027	-1.19	0.063	-1.16	0.220	-1.28	0.048
1416891_at	numb gene homolog (Drosophila)	Numb	-1.01	0.740	-1.39	0.011	-1.2	0.050	-1.41	0.008	-1.4	0.002
1420429_at	protocadherin beta 3	Pcdhb3	-1.35	0.107	-1.39	0.030	2.03	0.961	1.3	0.367	1.23	0.534
1456389_at	zinc finger homeobox 1b	Zfhx1b	1.06	0.363	-1.39	0.029	-1.3	0.015	-1.31	0.075	-1.47	0.022
1434192_at	zinc finger, ZZ-type with EF hand domain 1	Zzef1	-1.05	0.236	-1.39	0.015	-1.2	0.111	-1.44	0.026	-1.48	0.007
1429189_at	RIKEN cDNA 1110007C02 gene	1110007C02Rik	-1.17	0.220	-1.4	0.021	-1.02	0.386	-1.02	0.644	1.04	0.780
1421422_at	cDNA sequence AF397014	AF397014	-1.01	0.803	-1.4	0.007	1.02	0.845	-1.03	0.550	1.66	0.688
1450913_at	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeı	B4galt6 /// LOC67	-1.02	0.638	-1.4	0.027	-1.23	0.007	1	0.836	-1.18	0.366
1425262_at	CCAAT/enhancer binding protein (C/EBP), gamma	Cebpg	-1.07	0.184	-1.4	0.021	-1.11	0.184	-1.05	0.342	-1.06	0.497
1418195_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga	Galnt10	-1.07	0.117	-1.4	0.001	-1.13	0.037	-1.07	0.255	-1.04	0.554
1418664_at	multiple PDZ domain protein	Mpdz	-1.08	0.341	-1.4	0.031	-1.15	0.168	-1.17	0.055	-1.29	0.046
1451405_at	propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	1.04	0.760	-1.4	0.031	-1.16	0.004	-1.15	0.073	-1.28	0.051
1433648_at	sperm associated antigen 9	Spag9	1.08	0.400	-1.4	0.049	-1.34	0.002	-1.22	0.021	-1.36	0.006
1459666_at	trafficking protein, kinesin binding 1	Trak1	-1.26	0.096	-1.4	0.005	-1.36	0.020	-1.22	0.046	-1.4	0.044
1416156_at	vinculin	Vcl	-1.05	0.137	-1.4	0.008	-1.17	0.015	-1.19	0.001	-1.2	0.001
1455588_at	cDNA sequence BC034664	BC034664	1.13	0.265	-1.41	0.004	-1.06	0.449	-1.18	0.070	-1.21	0.119
1423966_at	Cd99 antigen-like 2	Cd99l2	-1.25	0.003	-1.41	0.010	-1.1	0.541	1.03	0.844	-1.17	0.065
1451289_at	doublecortin and calcium/calmodulin-dependent protein kinas	Dcamkl1	1.04	0.721	-1.41	0.036	-1.1	0.218	-1.11	0.265	-1.07	0.283

1428622_at	DEP domain containing 6	Depdc6	1.06	0.539	-1.41	0.005	1	0.966	-1.26	0.191	1.04	0.999
1434754_at	GTPase activating RANGAP domain-like 4	Garnl4	-1.14	0.012	-1.41	0.009	-1.26	0.014	-1.29	0.011	-1.55	0.005
1435967_s_at	3-hydroxyisobutyrate dehydrogenase	Hibadh	-1.18	0.021	-1.41	0.008	-1.06	0.519	-1.06	0.107	1	0.904
1449071_at	myosin, light polypeptide 7, regulatory	Myl7	1.91	0.261	-1.41	0.035	1.02	0.709	1.26	0.484	-1.35	0.207
1423990_at	RAB28, member RAS oncogene family	Rab28	-1.02	0.506	-1.41	0.005	-1.1	0.045	-1.16	0.106	-1.21	0.003
1457097_at	src family associated phosphoprotein 2	Scap2	-1.37	0.216	-1.41	0.025	-1.06	0.618	-1.1	0.495	-1.51	0.044
1438087_at	thiopurine methyltransferase	Tpmt	1.11	0.934	-1.41	0.039	-1.11	0.323	-1.16	0.489	-1.09	0.576
1455180_at	expressed sequence AA407270	AA407270	-1.22	0.111	-1.42	0.041	-1.04	0.386	1.11	0.483	1.48	0.183
1453199_at	acyl-Coenzyme A binding domain containing 6	Acbd6	-1.02	0.710	-1.42	0.008	-1.14	0.318	-1.15	0.245	-1.07	0.412
1436633_at	BAH domain and coiled-coil containing 1	Bahcc1	-1.06	0.676	-1.42	0.003	-1.29	0.021	1.08	0.595	1.05	0.538
1423891_at	glutathione S-transferase, theta 3	Gstt3	-1.21	0.133	-1.42	0.012	1.08	0.993	-1.12	0.349	1.64	0.551
1451783_a_at	kinesin-associated protein 3	Kifap3	-1.13	0.263	-1.42	0.046	-1.1	0.078	-1.2	0.025	-1.11	0.033
1436766_at	LUC7-like 2 (S. cerevisiae)	Luc7l2	-1.05	0.595	-1.42	0.048	-1.21	0.209	-1.06	0.555	-1.39	0.093
1460202_at	myozenin 1	Myoz1	1.16	0.687	-1.42	0.037	1.03	0.991	-1.18	0.148	1.56	0.350
1427299_at	ribosomal protein S6 kinase polypeptide 3	Rps6ka3	-1.05	0.287	-1.42	0.011	-1.37	0.010	-1.29	0.039	-1.42	0.005
1431098_at	restin (Reed-Steinberg cell-expressed intermediate filament-a	Rsn	-1.08	0.529	-1.42	0.023	1.09	0.896	1.02	0.836	-1.17	0.481
1428929_s_at	solute carrier family 25 (mitochondrial carrier, phosphate carr	Slc25a26	-1.1	0.527	-1.42	0.018	-1.06	0.677	-1.22	0.045	-1.09	0.464
1428070_at	synovial apoptosis inhibitor 1, synoviolin	Syvn1	-1.23	0.082	-1.42	0.033	-1.05	0.467	-1.03	0.668	-1.01	0.843
1447070_at	Williams-Beuren syndrome chromosome region 1 homolog (h	Wbscr1	-1.18	0.213	-1.42	0.007	-1.02	0.862	1.06	0.518	1.02	0.973
1448611_at	WW, C2 and coiled-coil domain containing 2	Wwc2	-1	0.839	-1.42	0.007	-1.31	0.031	-1.63	0.031	-1.69	0.031
1448857_a_at	zinc finger, DHHC domain containing 12	Zdhhc12	-1	0.914	-1.42	0.009	1.01	0.976	-1.01	0.750	1.11	0.905
1441338_at	RIKEN cDNA 5930412G12 gene	5930412G12Rik	-1.11	0.587	-1.43	0.001	1.19	0.366	1.12	0.908	1.14	0.354
1433324_at	RIKEN cDNA 9330154F10 gene	9330154F10Rik	1.07	0.796	-1.43	0.046	1.66	0.121	1.2	0.882	-1.08	0.445
1455703_at	thymoma viral proto-oncogene 2	Akt2	-1.54	0.167	-1.43	0.045	1.75	0.305	1.18	0.336	1.94	0.817
1429535_at	armadillo repeat containing 8	Armc8	-1.01	0.839	-1.43	0.007	-1.03	0.705	-1.24	0.005	-1.19	0.083
1428774_at	glypican 6	Gpc6	-1.15	0.095	-1.43	0.036	-1.22	0.012	-1.27	0.054	-1.29	0.008
1433605_at	inositol polyphosphate-5-phosphatase A	Inpp5a	-1.08	0.409	-1.43	0.015	-1.23	0.000	-1.25	0.001	-1.31	0.021
1429661_at	Rho-related BTB domain containing 3	Rhobtb3	-1.21	0.010	-1.43	0.042	-1.06	0.584	-1.06	0.082	-1.03	0.769
1441926_x_at	transmembrane inner ear	Tmie	1.15	0.335	-1.43	0.021	2.32	0.448	1.4	0.785	1.22	0.021
1456992_at	ubiquitin protein ligase E3C	Ube3c	1.29	0.305	-1.43	0.008	1.14	0.489	2.17	0.280	1.37	0.439
1439025_at	zinc finger protein 446	Zfp446	-1.47	0.099	-1.43	0.010	1.11	0.693	-1.18	0.062	-1.06	0.715
1429185_at	RIKEN cDNA 4631416L12 gene	4631416L12Rik	1.13	0.720	-1.44	0.038	1.22	0.784	1.3	0.140	1.95	0.413
1449895_at	preproacrosin	Acr	-1.24	0.489	-1.44	0.030	1.65	0.247	-1.32	0.199	1.66	0.110
1429095_at	centromere protein P	Cenpp	-1.03	0.756	-1.44	0.030	-1.03	0.811	1.09	0.739	1.18	0.198
1419703_at	procollagen, type V, alpha 3	Col5a3	-1.02	0.716	-1.44	0.046	-1.15	0.054	-1.05	0.404	-1.12	0.050
1448892_at	dedicator of cytokinesis 7	Dock7	-1.05	0.118	-1.44	0.001	-1.08	0.068	-1.21	0.065	-1.24	0.002
1450861_at	Fanconi anemia, complementation group C	Fancc	-1.1	0.455	-1.44	0.002	-1.11	0.278	-1.21	0.160	-1.21	0.510
1437001_at	glycogen synthase kinase 3 beta	Gsk3b	-1.07	0.459	-1.44	0.005	-1.55	0.010	-1.66	0.003	-1.48	0.007
1418349_at	heparin-binding EGF-like growth factor	Hbegf	-1.05	0.581	-1.44	0.006	-1.22	0.029	-1.33	0.036	-1.22	0.025
1437406_x_at	insulin-like growth factor binding protein 4	Igfbp4	-1.26	0.104	-1.44	0.030	1.06	0.677	-1.12	0.195	1.06	0.942
1422706_at	similar to Nedd4 WW binding protein 4	LOC637870	-1.1	0.144	-1.44	0.004	-1.14	0.047	-1.23	0.004	-1.16	0.030
1438422_at	leucine rich repeat containing 20	Lrrc20	1.04	0.600	-1.44	0.008	-1.09	0.619	1.08	0.730	-1.19	0.111
1437722_x_at	Poly(rC) binding protein 3	Pcbp3	-1.27	0.326	-1.44	0.041	-1.17	0.311	1.14	0.431	-1.18	0.325
1430033_at	RIKEN cDNA 5330431K02 gene	5330431K02Rik	-1.25	0.086	-1.45	0.020	-1.23	0.185	1.9	0.120	-1.3	0.229
1446677_at	RIKEN cDNA A830029E22 gene	A830029E22Rik	-1.1	0.636	-1.45	0.012	1.06	0.887	-1	0.822	1.03	0.959
1458832_at	Growth hormone receptor	Ghr	-1.1	0.402	-1.45	0.008	-1.23	0.279	-1.74	0.016	-1.78	0.099
1449407_at	intraflagellar transport 81 homolog (Chlamydomonas)	Ift81	1.07	0.576	-1.45	0.033	1.01	0.949	-1.1	0.333	-1.1	0.254
1418932_at	nuclear factor, interleukin 3, regulated	Nfil3	-1.09	0.316	-1.45	0.021	-1.18	0.331	1.01	0.856	-1.18	0.379
1429514_at	phosphatidic acid phosphatase type 2B	Ppap2b	1.01	0.882	-1.45	0.010	-1.14	0.085	-1.27	0.023	-1.25	0.037
1415850_at	RAS p21 protein activator 3	Rasa3	1.04	0.391	-1.45	0.004	-1.09	0.244	-1.18	0.020	-1.28	0.015
1444089_at	spectrin beta 2	Spnb2	-1.11	0.265	-1.45	0.010	-1.37	0.101	-1.15	0.145	-1.45	0.005
1448939_at	ubiquitin specific peptidase 25	Usp25	-1.07	0.527	-1.45	0.024	-1.29	0.014	-1.29	0.095	-1.2	0.322
1436217_at	zinc finger protein 148	Zfp148	-1.1	0.300	-1.45	0.028	1.1	0.809	1.17	0.260	-1.4	0.051
1420681_at	RIKEN cDNA 1700120K04 gene	1700120K04Rik	-1.78	0.123	-1.46	0.013	1.08	0.606	1.07	0.910	1.25	0.516
1433173_at	RIKEN cDNA 5430440L12 gene	5430440L12Rik	1.13	0.888	-1.46	0.030	-1.06	0.370	-1.1	0.535	1.08	0.387
1434197_at	attractin	Atrn	1.14	0.239	-1.46	0.027	-1.17	0.004	-1.39	0.033	-1.26	0.179
1435480_at	Braf transforming gene	Braf	-1.02	0.889	-1.46	0.026	-1.22	0.163	-1.2	0.133	-1.65	0.031
1456116_at	catenin (cadherin associated protein), delta 2	Ctnnd2	-1.14	0.437	-1.46	0.036	-1.19	0.482	-1.06	0.597	-1.19	0.368

1418944_at	cysteinyl leukotriene receptor 1	Cysltr1	-1.59	0.055	-1.46	0.035	2.03	0.023	1.19	0.859	1.8	0.335
1450477_at	5-hydroxytryptamine (serotonin) receptor 2C	Htr2c	1	0.934	-1.46	0.046	1.73	0.163	1.43	0.249	1.39	0.692
1428005_at	MOCO sulphurase C-terminal domain containing 1	Mosc1	-1.1	0.504	-1.46	0.049	1.21	0.272	1.01	0.993	1.87	0.734
1418892_at	ras homolog gene family, member J	Rhoj	1.03	0.973	-1.46	0.025	-1.36	0.036	-1.23	0.018	-1.13	0.225
1456153_at	slingshot homolog 2 (Drosophila)	Ssh2	1.21	0.251	-1.46	0.012	-1.3	0.002	-1.26	0.087	-1.62	0.007
1459737_s_at	transthyretin	Ttr	-1.16	0.413	-1.46	0.001	-1.01	0.516	1.61	0.263	1.61	0.891
1437155_a_at	WW domain containing transcription regulator 1	Wwtr1	-1.05	0.470	-1.46	0.005	-1.38	0.007	-1.35	0.023	-1.25	0.001
1457173_at	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase ac	Ywhae	-1.02	0.626	-1.46	0.030	-1.12	0.391	1.26	0.774	-1.64	0.120
1429556_at	RIKEN cDNA 2610024B07 gene	2610024B07Rik	-1.01	0.892	-1.47	0.030	-1.46	0.030	-1.52	0.052	-1.71	0.012
1431496_at	RIKEN cDNA B230104F01 gene	B230104F01Rik	-1.03	0.697	-1.47	0.009	1.16	0.368	1.14	0.686	1.35	0.015
1417403_at	ELOVL family member 6, elongation of long chain fatty acids	Elovl6	-1.03	0.883	-1.47	0.038	1.05	0.455	1.09	0.317	1.08	0.608
1425891_a_at	GH regulated TBC protein 1	Grtp1	-1.18	0.409	-1.47	0.029	1.97	0.453	-1.46	0.165	3.21	0.242
1422465_a_at	nucleoredoxin	Nxn	-1.02	0.832	-1.47	0.016	-1.27	0.015	-1.25	0.001	-1.36	0.019
1456214_at	protocadherin 7	Pcdh7	1.03	0.603	-1.47	0.021	-1.81	0.015	-1.71	0.019	-2.25	0.150
1418036_at	DNA primase, p58 subunit	Prim2	1.02	0.738	-1.47	0.005	-1.1	0.249	-1.22	0.042	-1.37	0.005
1426775_s_at	secretory carrier membrane protein 1	Scamp1	-1.12	0.253	-1.47	0.010	-1.01	0.455	-1.12	0.118	-1.27	0.055
1436376_s_at	S1 RNA binding domain 1	Srbd1	1.06	0.777	-1.47	0.012	-1.08	0.310	-1.32	0.064	-1.14	0.352
1446771_at	Tubulin, alpha 8	Tuba8	-1.22	0.384	-1.47	0.010	1.02	0.853	1.2	0.111	1.1	0.317
1460626_at	septin 11	11-Sep	-1.02	1.000	-1.48	0.004	-1.1	0.466	-1.18	0.045	-1.18	0.052
1436921_at	ATPase, Cu++ transporting, alpha polypeptide	Atp7a	-1.25	0.114	-1.48	0.011	1.04	0.894	-1.11	0.033	-1.2	0.013
1458862_at	expressed sequence C78704	C78704	-1.27	0.262	-1.48	0.023	1.64	0.268	1.16	0.810	-1.1	0.683
1435342_at	potassium inwardly-rectifying channel, subfamily K, member	Kcnk6	-1.29	0.090	-1.48	0.037	1.03	0.536	1.34	0.082	1.4	0.105
1417324_at	microtubule associated serine/threonine kinase 2	Mast2	1.01	0.920	-1.48	0.002	-1.3	0.009	-1.21	0.003	-1.33	0.004
1427040_at	MyoD family inhibitor domain containing	Mdfic	-1.04	0.347	-1.48	0.026	-1.16	0.018	-1.15	0.003	-1.18	0.009
1423201_at	nuclear receptor co-repressor 1	Ncor1	-1.13	0.234	-1.48	0.004	-1.5	0.033	-1.47	0.001	-1.39	0.055
1416297_s_at	pancreatitis-associated protein	Pap	-1.6	0.154	-1.48	0.017	1.18	0.921	1.51	0.770	1.21	0.688
1455284_x_at	phosphatidylinositol glycan anchor biosynthesis, class X	Pigx	-1.46	0.058	-1.48	0.031	-1.13	0.246	-1.05	0.302	1.29	0.406
1435771_at	phospholipase C, beta 4	Plcb4	-1.02	0.735	-1.48	0.011	-1.22	0.075	-1.33	0.065	-1.38	0.063
1424810_at	taspase, threonine aspartase 1	Tasp1	-1.14	0.354	-1.48	0.049	-1.1	0.142	-1.03	0.698	-1.07	0.471
1428336_at	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophospha	Agpat4	-1.1	0.335	-1.49	0.009	-1.25	0.033	-1.17	0.010	-1.29	0.001
1434310_at	bone morphogenic protein receptor, type II (serine/threonine	Bmpr2	-1.04	0.375	-1.49	0.014	-1.25	0.013	-1.18	0.127	-1.44	0.005
1416772_at	carnitine palmitoyltransferase 2	Cpt2	-1.52	0.019	-1.49	0.008	1.2	0.491	-1.12	0.245	1.33	0.519
1448665_at	dystrophin, muscular dystrophy	Dmd	-1.02	0.519	-1.49	0.028	-1.33	0.015	-1.45	0.039	-1.39	0.019
1441409_at	Grp94 neighboring nucleotidase variant 4	Gnn	1.04	0.928	-1.49	0.015	-1.2	0.399	1.21	0.531	-1.28	0.226
1422742_at	human immunodeficiency virus type I enhancer binding prote	Hivep1	-1.14	0.273	-1.49	0.041	-1.08	0.395	-1.41	0.022	-1.22	0.205
1457809_at	p300/CBP-associated factor /// similar to p300/CBP-associate	Pcaf /// LOC33012	1.22	0.779	-1.49	0.028	1	0.984	1.31	0.689	1.8	0.693
1418390_at	PHD finger protein 21A	Phf21a	-1.08	0.374	-1.49	0.040	-1.16	0.245	-1.57	0.007	-1.42	0.046
1446057_at	rearranged L-myc fusion sequence	Rlf	-1.2	0.449	-1.49	0.046	1.13	0.915	1.38	0.375	-1.08	0.520
1424089_a_at	transcription factor 4	Tcf4	1.05	0.260	-1.49	0.036	-1.31	0.026	-1.3	0.023	-1.54	0.024
1434603_at	thyroid hormone receptor associated protein 2	Thrap2	1.03	0.170	-1.49	0.000	-1.55	0.024	-1.64	0.014	-2.04	0.025
1433404_at	RIKEN cDNA 4930423O20 gene	4930423O20Rik	-1.25	0.194	-1.5	0.030	1.31	0.720	-1.02	0.678	1.31	0.507
1429691_at	RIKEN cDNA 5430405N12 gene	5430405N12Rik	1.17	0.640	-1.5	0.027	-1.62	0.027	-1.25	0.000	-1.57	0.211
1454983_at	expressed sequence AI465301	AI465301	-1.1	0.559	-1.5	0.034	1.02	0.766	-1.03	0.772	1.18	0.161
1456021_at	activating transcription factor 6	Atf6	1.15	0.680	-1.5	0.046	-1.37	0.013	-1.28	0.133	-1.79	0.005
1438354_x_at	Calponin 3, acidic	Cnn3	-1.37	0.261	-1.5	0.025	-1.02	0.911	-1.12	0.162	-1.02	0.757
1455627_at	procollagen, type VIII, alpha 1	Col8a1	-1.1	0.228	-1.5	0.018	-1.2	0.084	-1.17	0.032	-1.24	0.036
1454965_at	RIKEN cDNA D430039N05 gene	D430039N05Rik	-1.11	0.321	-1.5	0.049	1.08	0.496	1.02	0.846	-1.02	0.596
1418285_at	ephrin B1	Efnb1	-1.33	0.061	-1.5	0.010	-1.42	0.019	-1.28	0.002	-1.11	0.115
1449439_at	Kruppel-like factor 7 (ubiquitous)	Klf7	-1.11	0.187	-1.5	0.041	-1.47	0.008	-1.51	0.026	-1.51	0.046
1449099_at	LPS-responsive beige-like anchor	Lrba	-1.14	0.097	-1.5	0.013	-1.21	0.075	-1.34	0.014	-1.32	0.065
1458182_at	RNA binding motif protein 18	Rbm18	-1.18	0.267	-1.5	0.037	1.15	0.342	-1.05	0.518	-1.26	0.037
1453174_at	RIKEN cDNA 2310076G13 gene	2310076G13Rik	-1	0.844	-1.51	0.000	-1.27	0.107	-1.27	0.057	-1.5	0.039
1434375_at	RIKEN cDNA B930006L02 gene	B930006L02Rik	-1.03	0.434	-1.51	0.008	-1.16	0.078	-1.21	0.122	-1.18	0.123
1436029_at	bicaudal C homolog 1 (Drosophila)	Bicc1	-1	0.945	-1.51	0.007	-1.16	0.330	-1.19	0.018	-1.24	0.005
1427974_s_at	calcium channel, voltage-dependent, L type, alpha 1D subuni	Cacna1d	-1.24	0.284	-1.51	0.049	1.21	0.983	-1.5	0.058	-1.33	0.358
1424770_at	caldesmon 1	Cald1	-1.18	0.327	-1.51	0.043	-1.42	0.036	-1.15	0.077	-1.31	0.001
1446105_at	exocyst complex component 1	Exoc1	3	0.002	-1.51	0.008	1.85	0.194	-1.3	0.382	2.42	0.019
1445534_at	Filamin, beta	Flnb	-1.11	0.277	-1.51	0.033	-2.03	0.045	-1.77	0.006	-2.31	0.001

1439030_at	GDP-mannose pyrophosphorylase B	Gmppb	-1.11	0.270	-1.51	0.019	-1.08	0.020	-1.11	0.116	-1.23	0.004
1443546_at	High density lipoprotein (HDL) binding protein	Hdlbp	-1.17	0.230	-1.51	0.004	-1.05	0.602	-1.21	0.080	1	0.607
1436218_at	similar to leucine-rich repeat-containing G protein-coupled re	LOC676300	-1.19	0.125	-1.51	0.035	-1.16	0.210	-1.16	0.138	-1.17	0.171
1436193_at	mannosidase, alpha, class 1C, member 1	Man1c1	-1.04	0.199	-1.51	0.001	-1.2	0.124	-1.08	0.180	-1.42	0.062
1435970_at	nemo like kinase	Nlk	-1.15	0.193	-1.51	0.017	-1.43	0.016	-1.49	0.009	-1.56	0.010
1429783_at	PDZ and LIM domain 5	Pdlim5	-1.3	0.170	-1.51	0.040	-1.84	0.005	-1.89	0.000	-1.95	0.046
1443408_at	Polo-like kinase 1 (Drosophila)	Plk1	-1.11	0.455	-1.51	0.023	1.2	0.875	-1.08	0.464	1.2	0.579
1436272_at	RAB3 GTPase activating protein subunit 2	Rab3gap2	-1.2	0.011	-1.51	0.003	1.01	0.889	-1.08	0.551	-1.27	0.030
1420919_at	serum/glucocorticoid regulated kinase 3	Sgk3	-1.01	0.763	-1.51	0.014	-1.03	0.545	1.13	0.724	-1	0.620
1443005_at	zinc finger homeobox 1a	Zfhx1a	-1.24	0.029	-1.51	0.031	-1.29	0.041	-1.33	0.117	1.04	0.912
1456108_x_at	zinc finger protein 179	Zfp179	-1.85	0.128	-1.51	0.048	1.03	0.915	1.48	0.403	1.35	0.192
1427187_at	RIKEN cDNA 6030413G23 gene	6030413G23Rik	-1.22	0.040	-1.52	0.042	1.03	0.879	1.1	0.479	1.82	0.032
1426733_at	inositol 1,3,4-triphosphate 5/6 kinase	Itpk1	-1.17	0.243	-1.52	0.012	-1	0.992	-1.06	0.554	1.07	0.544
1447084_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-de	Nfatc1	-1.41	0.222	-1.52	0.022	-1.25	0.165	1.07	0.952	-1.57	0.031
1423405_at	tissue inhibitor of metalloproteinase 4	Timp4	1.15	0.962	-1.52	0.029	1.66	0.343	1.82	0.160	2.06	0.364
1425747_at	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	1110060D06Rik //	-1.21	0.015	-1.53	0.002	-1.48	0.065	-1.52	0.003	-1.75	0.001
1458369_at	RIKEN cDNA 2310050B05 gene	2310050B05Rik	-1.11	0.570	-1.53	0.028	1.2	0.530	1.05	0.194	-1.02	0.601
1454599_at	RIKEN cDNA 4930425F17 gene	4930425F17Rik	-1.21	0.277	-1.53	0.028	2.08	0.179	1.27	0.836	1.46	0.293
1443665_at	Expressed sequence AI852444	AI852444	-1.07	0.549	-1.53	0.049	1.1	0.191	-1.27	0.131	-1.27	0.034
1436380_at	Cdc42 binding protein kinase alpha	Cdc42bpa	1.13	0.236	-1.53	0.039	-1.83	0.021	-1.74	0.005	-1.62	0.026
1445774_at	Potassium large conductance calcium-activated channel, sub	Kcnma1	-1.09	0.542	-1.53	0.020	1.24	0.928	-1.05	0.687	-1.27	0.327
1451336_at	lectin, galactose binding, soluble 4	Lgals4	-1.01	0.819	-1.53	0.004	2.06	0.436	-1.07	0.497	1.1	0.856
1417284_at	mitogen-activated protein kinase associated protein 1	Mapkap1	-1.03	0.679	-1.53	0.008	-1.27	0.137	-1.31	0.166	-1.33	0.016
1449975_a_at	parkin	Park2	-1.2	0.261	-1.53	0.022	2.55	0.119	-1.35	0.228	-1.43	0.227
1442060_at	prolyl endopeptidase-like	Prepl	-1.17	0.585	-1.53	0.023	1.59	0.702	1.06	0.708	1.08	0.284
1434005_at	RNA binding motif, single stranded interacting protein 1	Rbms1	-1.01	0.888	-1.53	0.001	-1.37	0.002	-1.49	0.003	-1.58	0.005
1434902_at	ring finger protein 157	Rnf157	1.08	0.702	-1.53	0.048	1.03	0.965	-1.01	0.909	1.17	0.235
1457689_at	SET binding factor 2	Sbf2	-1.18	0.469	-1.53	0.022	2.34	0.431	-1.22	0.459	1.76	0.921
1449865_at	sema domain, immunoglobulin domain (Ig), short basic doma	Sema3a	1.23	0.725	-1.53	0.043	-1.23	0.081	-1.17	0.076	-1.39	0.047
1418798_s_at	serine/arginine-rich protein specific kinase 3	Srpk3	-1.37	0.309	-1.53	0.038	-1.43	0.203	-1.69	0.180	2.47	0.566
1436499_at	transmembrane protein 23	Tmem23	-1.08	0.076	-1.53	0.023	-1.38	0.024	-1.61	0.001	-1.55	0.030
1448551_a_at	tripartite motif protein 2	Trim2	1.04	0.902	-1.53	0.014	1.03	0.934	-1.05	0.552	-1.21	0.043
1420339_at	RIKEN cDNA 0610016J10 gene	0610016J10Rik	-1.04	0.706	-1.54	0.003	-1.39	0.006	-1.18	0.024	-1.49	0.010
1430784_a_at	RIKEN cDNA 4932417H02 gene	4932417H02Rik	1.18	0.131	-1.54	0.028	-1.03	0.788	-1.26	0.118	-1.06	0.484
1425878_at	calcium binding protein 4	Cabp4	-1.75	0.143	-1.54	0.021	-1.08	0.534	1.14	0.929	-1	0.900
1444279_at	HECT, UBA and WWE domain containing 1	Huwe1	1.24	0.436	-1.54	0.030	1.27	0.870	-1.6	0.043	-1.83	0.072
1425625_at	interleukin 13 receptor, alpha 1	Il13ra1	1.63	0.574	-1.54	0.045	1.12	0.874	-1.26	0.183	2.01	0.283
1437716_x_at	kinesin family member 22	Kif22	-1.23	0.125	-1.54	0.028	1.04	0.813	-1.18	0.036	-1.18	0.127
1444285_at	Mortality factor 4 like 1	Morf4l1	-1.08	0.628	-1.54	0.003	-1.91	0.096	-2.37	0.016	-2.07	0.062
1433839_at	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	Nars2	1.03	0.912	-1.54	0.015	-1.19	0.239	-1.18	0.016	-1.04	0.566
1433835_at	protein phosphatase 3, catalytic subunit, beta isoform	Ppp3cb	-1.21	0.115	-1.54	0.016	1.02	0.826	-1.17	0.030	-1.11	0.282
1418845_at	protein C	Proc	-1.37	0.308	-1.54	0.021	1.17	0.821	1.62	0.505	-1.01	0.513
1428260_at	spastic paraplegia 3A homolog (human)	Spg3a	-1.01	0.734	-1.54	0.027	-1.09	0.398	-1.01	0.853	1.19	0.032
1455398_at	leucine rich repeat containing 8 family, member C	Lrrc8c	-1.14	0.225	-1.55	0.040	-1.04	0.452	-1.19	0.016	-1.22	0.026
1425132_at	neuropilin (NRP) and tolloid (TLL)-like 1	Neto1	1.48	0.360	-1.55	0.039	1.07	0.782	1.89	0.183	1.69	0.934
1426193_at	otospiralin	Otos	-1.54	0.099	-1.55	0.013	-1.08	0.493	1.27	0.280	1.67	0.638
1434392_at	ubiquitin specific peptidase 34	Usp34	-1.07	0.518	-1.55	0.049	-1.29	0.035	-1.46	0.018	-1.65	0.008
1430185_at	RIKEN cDNA 5830460E08 gene	5830460E08Rik	-2.08	0.019	-1.56	0.041	-1.01	0.985	1.47	0.843	-1.93	0.125
1432570_at	RIKEN cDNA 6030458E02 gene	6030458E02Rik	-1.4	0.000	-1.56	0.013	-1.26	0.178	-1.06	0.521	1.1	0.986
1442670_at	RIKEN cDNA 6430517E21 gene	6430517E21Rik	-1.09	0.463	-1.56	0.000	1.08	0.838	1.63	0.344	1.07	0.551
1425099_a_at	aryl hydrocarbon receptor nuclear translocator-like	Arntl	-1.08	0.412	-1.56	0.015	-1.38	0.020	-1.43	0.010	-1.77	0.007
1442595_at	Expressed sequence C77713	C77713	-1.05	0.611	-1.56	0.012	-1.25	0.005	-1.11	0.018	-1.23	0.018
1457339_at	Cerebral cavernous malformation 2 homolog (human)	Ccm2	1.04	0.974	-1.56	0.032	-1.2	0.211	-1.25	0.170	-1.24	0.133
1449419_at	dedicator of cytokinesis 8	Dock8	-1.18	0.231	-1.56	0.022	-1.28	0.123	-1.41	0.035	1.01	0.741
1426057_a_at	Eph receptor A3	Epha3	-1.19	0.232	-1.56	0.042	1.34	0.861	-1.09	0.574	1.01	0.646
1416236_a_at	epithelial V-like antigen 1	Eva1	-1.69	0.169	-1.56	0.040	1.6	0.820	1.54	0.797	1.69	0.241
1437363_at	homer homolog 1 (Drosophila)	Homer1	-1.04	0.442	-1.56	0.026	-1.13	0.089	-1.02	0.550	-1.28	0.012
1456784_at	hypothetical protein LOC623781	LOC623781	1.11	0.113	-1.56	0.042	1.56	0.919	1.24	0.797	1.15	0.603

1454741_s_at	transmembrane protein 164	Tmem164	-1.24	0.029	-1.56	0.001	-1.06	0.263	-1.15	0.032	-1.22	0.039
1454723_at	RIKEN cDNA 1110033M05 gene	1110033M05Rik	1.06	0.927	-1.57	0.007	-1.53	0.004	-1.38	0.011	-1.67	0.003
1452703_at	RIKEN cDNA 4631427C17 gene	4631427C17Rik	-1.18	0.032	-1.57	0.022	-1.05	0.464	-1.07	0.137	1.04	0.265
1457622_at	cDNA sequence BE983540	BE983540	1.18	0.733	-1.57	0.037	2.38	0.565	1.58	0.927	-1.59	0.087
1427873_at	defensin related cryptdin 15	Defcr15	1.02	0.688	-1.57	0.034	-1.18	0.553	-1.17	0.340	1.45	0.792
1424443_at	hepatoma-derived growth factor, related protein 3 /// transme	Hdgfrp3 /// Tm6sf1	1.24	0.082	-1.57	0.025	-1.03	0.369	1	0.584	1.67	0.192
1453712_a_at	mitogen activated protein kinase kinase 5	Map2k5	1.06	0.837	-1.57	0.032	-1.39	0.104	-1.46	0.064	-2.23	0.013
1434509_at	Rap guanine nucleotide exchange factor (GEF) 6	Rapgef6	-1.05	0.564	-1.57	0.000	-1.21	0.025	-1.35	0.011	-1.4	0.008
1439302_at	ubiquitin-activating enzyme E1-like 2	Ube1l2	-1.06	0.526	-1.57	0.038	-1.49	0.015	-1.32	0.003	-1.47	0.018
1425913_a_at	RIKEN cDNA 2810022L02 gene	2810022L02Rik	1.14	0.835	-1.58	0.032	-1.12	0.089	-1.25	0.024	-1.31	0.028
1454563_at	RIKEN cDNA 4930573C08 gene	4930573C08Rik	-1.35	0.215	-1.58	0.004	1.24	0.032	-1.37	0.313	2.13	0.008
1430268_at	RIKEN cDNA 9630005C17 gene	9630005C17Rik	-1.14	0.326	-1.58	0.024	1.03	0.875	2.08	0.589	1.38	0.033
1452996_a_at	apoptosis, caspase activation inhibitor	Aven	-1.06	0.201	-1.58	0.035	-1.08	0.213	-1.1	0.057	-1.13	0.129
1439903_at	cDNA sequence BC028663	BC028663	-1.36	0.189	-1.58	0.032	1.21	0.964	-1.05	0.610	3.38	0.314
1457425_at	RIKEN cDNA C130038G02 gene	C130038G02Rik	-1.82	0.090	-1.58	0.044	-1.16	0.421	-1.64	0.018	1.16	0.525
1439493_at	RIKEN cDNA D630040G17 gene /// similar to zinc finger prot	D630040G17Rik /	-1.16	0.298	-1.58	0.036	-1.24	0.041	-1.57	0.003	-1.31	0.047
1457316_at	microtubule-associated protein 6	Mtap6	-1.19	0.017	-1.58	0.001	-1.47	0.075	-1.37	0.007	-1.7	0.006
1419108_at	oligophrenin 1	Ophn1	-1.08	0.508	-1.58	0.032	-1.44	0.080	-1.14	0.238	-1.97	0.031
1434037_s_at	p300/CBP-associated factor	Pcaf	-1.15	0.237	-1.58	0.046	-1.07	0.064	-1.09	0.275	-1.1	0.213
1446954_at	Pyruvate dehydrogenase E1 alpha 1	Pdha1	-1.12	0.184	-1.58	0.021	1.05	0.970	-1.14	0.467	1.06	0.680
1437067_at	putative homeodomain transcription factor 2	Phtf2	-1.15	0.056	-1.58	0.015	1.07	0.450	-1.05	0.409	-1.03	0.717
1449334_at	tissue inhibitor of metalloproteinase 3	Timp3	-1.06	0.483	-1.58	0.001	-1.13	0.002	1.04	0.964	-1.24	0.070
1434997_at	cell division cycle 2-like 6 (CDK8-like)	Cdc2l6	1.14	0.156	-1.59	0.002	1.08	0.463	-1.08	0.426	-1.03	0.680
1436181_at	development and differentiation enhancing factor 2	Ddef2	1.02	0.911	-1.59	0.047	-1.07	0.354	-1.28	0.132	1.05	0.526
1442116_at	G protein-coupled receptor 176	Gpr176	-1.15	0.045	-1.59	0.001	-1.22	0.062	-1.18	0.068	-1.4	0.020
1428484_at	oxysterol binding protein-like 3	Osbpl3	-1.03	0.297	-1.59	0.026	-1.28	0.005	-1.25	0.078	-1.4	0.000
1419053_at	peroxisomal biogenesis factor 14	Pex14	-1	0.770	-1.59	0.035	-1.13	0.263	-1.4	0.001	-1.38	0.048
1437161_x_at	RNA binding protein gene with multiple splicing	Rbpms	-1.03	0.655	-1.59	0.019	-1.27	0.017	-1.33	0.007	-1.31	0.014
1423592_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	1.08	0.497	-1.59	0.012	-1.28	0.045	-1.31	0.032	-1.45	0.042
1446760_at	thyroid hormone receptor interactor 13	Trip13	1.05	0.926	-1.59	0.021	1.03	0.790	2	0.049	-1	0.914
1452368_at	breakpoint cluster region homolog	Bcr	-1.06	0.639	-1.6	0.000	-1.1	0.369	-1.24	0.125	-1.04	0.669
1425680_a_at	beta-transducin repeat containing protein	Btrc	1.07	0.829	-1.6	0.018	1.03	0.854	-1.12	0.417	-1.27	0.115
1422278_at	dopamine receptor 3	Drd3	-1.6	0.017	-1.6	0.047	1.2	0.800	-1.49	0.266	-1.03	0.607
1451699_at	similar to putative retrovirus-related gag protein /// hypothetica	LOC668468 /// LC	-1.76	0.040	-1.6	0.033	-1.01	0.626	1.18	0.305	-1.05	0.521
1435514_at	leucine zipper transcription factor-like 1	Lztfl1	-1.08	0.614	-1.6	0.002	1.06	0.185	1.01	0.896	-1.15	0.250
1428700_at	purinergic receptor P2Y, G-protein coupled 13	P2ry13	-1.09	0.452	-1.6	0.011	1.3	0.153	1.2	0.345	-1.32	0.172
1419279_at	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	Pip5k2a	1.07	0.574	-1.6	0.004	-1.4	0.012	-1.48	0.009	-1.46	0.002
1437092_at	restin-like 2	Rsnl2	-1.37	0.059	-1.6	0.024	-1.09	0.461	1.17	0.514	-1.09	0.412
1459846_x_at	transmembrane protein 4	Tmem4	-1.23	0.366	-1.6	0.035	-1.08	0.534	1.24	0.340	1.19	0.382
1436225_at	transient receptor potential cation channel, subfamily M, mem	Trpm2	-1.74	0.074	-1.6	0.024	1.12	0.677	-1.22	0.235	1.36	0.318
1459480_at	DNA segment, Chr 6, ERATO Doi 90, expressed	D6Ertd90e	1.28	0.537	-1.61	0.040	1.04	0.561	1.53	0.864	1.47	0.447
1456217_at	DNA segment, Chr 7, Wayne State University 128, expresse	D7Wsu128e	-1.15	0.506	-1.61	0.023	-1.07	0.482	1.19	0.053	-1.04	0.361
1435241_at	RIKEN cDNA D930036F22 gene	D930036F22Rik	-1.06	0.204	-1.61	0.003	-1.38	0.006	-1.26	0.013	-1.47	0.000
1429806_at	Era (G-protein)-like 1 (E. coli)	Eral1	-1.16	0.327	-1.61	0.008	1.34	0.685	1.02	0.855	1.06	0.991
1449269_at	coagulation factor V	F5	-1.65	0.091	-1.61	0.029	1.55	0.962	1.02	0.989	1.69	0.406
1455078_at	Heat shock protein 90kDa alpha (cytosolic), class A member	Hsp90aa1	1.04	0.800	-1.61	0.011	-1.37	0.008	-1.54	0.017	-1.38	0.016
1459109_at	sema domain, seven thrombospondin repeats (type 1 and typ	Sema5a	-2.04	0.080	-1.61	0.050	2.18	0.186	2.16	0.095	2.01	0.830
1425074_at	Werner syndrome homolog (human)	Wrn	-1.05	0.530	-1.61	0.006	-1.23	0.210	-1.22	0.021	-1.06	0.699
1431470_a_at	RIKEN cDNA 4933414I15 gene	4933414I15Rik	-1.91	0.071	-1.62	0.040	1.28	0.655	1.02	0.625	1.2	0.722
1436025_at	RIKEN cDNA A430106J12 gene	A430106J12Rik	-1.04	0.602	-1.62	0.017	-1.35	0.004	-1.33	0.107	-1.73	0.021
1448789_at	aldehyde dehydrogenase family 1, subfamily A3	Aldh1a3	-1.04	0.532	-1.62	0.005	-1.2	0.053	-1.27	0.001	-1.17	0.011
1432507_at	RIKEN cDNA B430319H21 gene	B430319H21Rik	1.21	0.736	-1.62	0.034	-1.87	0.033	1.07	0.441	1.05	0.865
1439104_at	RIKEN cDNA C230081A13 gene	C230081A13Rik	-1.06	0.339	-1.62	0.000	-1.7	0.002	-1.67	0.002	-1.68	0.009
1434311_at	CCR4-NOT transcription complex, subunit 6-like	Cnot6l	1.01	0.956	-1.62	0.017	-1.26	0.095	-1.18	0.260	-1.2	0.184
1455748_at	G protein-coupled receptor 178	Gpr178	1.17	0.680	-1.62	0.008	1.88	0.654	-1.07	0.411	-1.07	0.489
1446408_at	Homeo box A10	Hoxa10	-1.2	0.421	-1.62	0.022	1.53	0.846	-1.01	0.759	1.11	0.603
1418420_at	myogenic differentiation 1	Myod1	1.18	0.224	-1.62	0.010	1.21	0.936	-1.94	0.007	1.26	0.472
1432592_at	pregnancy-associated plasma protein A	Pappa	-1.12	0.352	-1.62	0.022	-1.72	0.052	-1.34	0.015	-1.58	0.006

1448852_at	regucalcin	Rgn	-1.57	0.053	-1.62	0.022	-1.16	0.499	1.09	0.638	-1.28	0.318
1442801_x_at	transmembrane 7 superfamily member 3	Tm7sf3	-1.34	0.351	-1.62	0.016	-1.12	0.521	-1.5	0.135	1.28	0.786
1428517_at	WD repeat and FYVE domain containing 3	Wdfy3	-1.13	0.058	-1.62	0.025	-1.23	0.120	-1.82	0.006	-1.91	0.002
1431381_at	RIKEN cDNA 3110005L24 gene	3110005L24Rik	-1.04	0.476	-1.63	0.028	1.36	0.396	-1.01	0.677	1.49	0.541
1420679_a_at	androgen-induced 1	Aig1	-1.03	0.730	-1.63	0.032	-1.14	0.180	-1.16	0.011	-1.26	0.000
1434260_at	FCH and double SH3 domains 2	Fchsd2	-1.03	0.511	-1.63	0.031	-1.32	0.011	-1.68	0.000	-1.35	0.005
1426148_at	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	Gbgt1	-1.66	0.186	-1.63	0.038	1.33	0.888	1.62	0.365	1.57	0.080
1420353_at	lymphotoxin A	Lta	-1.47	0.005	-1.63	0.035	1.05	0.931	-1.03	0.749	1.11	0.884
1450650_at	myosin X	Myo10	-1.13	0.229	-1.63	0.015	-1.7	0.022	-1.58	0.013	-1.49	0.017
1449481_at	solute carrier family 25 (mitochondrial carrier, adenine nucleo	Slc25a13	1.08	0.505	-1.63	0.032	-1.11	0.081	-1.21	0.059	-1.37	0.089
1450923_at	transforming growth factor, beta 2	Tgfb2	-1.01	0.934	-1.63	0.002	-1.18	0.125	-1.21	0.022	-1.27	0.025
1456705_at	Zinc finger protein 532	Zfp532	-1.48	0.096	-1.63	0.041	1.04	0.566	1.43	0.186	-1.33	0.032
1434335_at	expressed sequence AI317237	AI317237	-1.17	0.067	-1.64	0.024	-1.18	0.003	-1.5	0.018	-1.38	0.003
1457827_at	arylsulfatase J	Arsj	-1.08	0.299	-1.64	0.013	-1.01	0.675	-1.12	0.271	-1.2	0.078
1435297_at	gap junction membrane channel protein alpha 9	Gja9	-1.05	0.434	-1.64	0.046	-1.33	0.265	-1.95	0.183	-1.41	0.073
1455056_at	LIM domain only 7	Lmo7	-1.14	0.299	-1.64	0.020	-1.11	0.099	-1.56	0.093	-1.38	0.074
1443941_at	hypothetical gene supported by AK049058; BC025881	LOC433886	-1.09	0.429	-1.64	0.024	1.08	0.848	1.2	0.157	-1.29	0.154
1449494_at	RAB3C, member RAS oncogene family	Rab3c	-1.34	0.222	-1.64	0.028	-1.25	0.400	-1.77	0.079	-1.35	0.396
1453333_at	RIKEN cDNA 1700012P22 gene	1700012P22Rik	-1.07	0.559	-1.65	0.048	-1.32	0.037	-1.29	0.131	-1.18	0.251
1453166_at	RIKEN cDNA D130073L02 gene	D130073L02Rik	-1.16	0.361	-1.65	0.040	-1.05	0.499	-1.11	0.401	-1.2	0.206
1444814_at	DNA segment, Chr 15, ERATO Doi 180, expressed	D15Ertd180e	1.18	0.466	-1.65	0.032	-1.62	0.005	-1.15	0.503	1	0.517
1438801_at	dynamin 3	Dnm3	-1.78	0.031	-1.65	0.017	1.17	0.407	-1.73	0.065	-1.4	0.106
1442223_at	Enabled homolog (Drosophila)	Enah	1.03	0.462	-1.65	0.011	-1.65	0.111	-1.56	0.038	-2.05	0.035
1433930_at	Heparanase	Hpse	-1.45	0.045	-1.65	0.041	-1.54	0.157	2.33	0.506	2.9	0.101
1449270_at	plexin domain containing 2	Plxdc2	-1.29	0.125	-1.65	0.033	-1.27	0.207	-1.68	0.062	-1.69	0.046
1453269_at	unc-5 homolog B (C. elegans)	Unc5b	-1.24	0.135	-1.65	0.038	-1.28	0.156	-1.17	0.065	-1.23	0.032
1452150_at	expressed sequence AU040320	AU040320	-1.16	0.096	-1.66	0.035	-1.17	0.005	-1.06	0.318	-1.19	0.002
1460011_at	cytochrome P450, family 26, subfamily b, polypeptide 1	Cyp26b1	-1.14	0.450	-1.66	0.039	1.17	0.785	1.27	0.253	1	0.892
1458464_at	HECT, C2 and WW domain containing E3 ubiquitin protein lig	Hecw2	-1.37	0.279	-1.66	0.011	-1.04	0.501	1.17	0.602	1.76	0.254
1422851_at	high mobility group AT-hook 2	Hmga2	1.01	0.953	-1.66	0.016	-1.6	0.001	-1.7	0.000	-1.61	0.000
1454809_at	nuclear receptor coactivator 7	Ncoa7	1.11	0.489	-1.66	0.018	-1.09	0.454	-1.28	0.011	-1.19	0.365
1460615_at	5'-nucleotidase domain containing 1	Nt5dc1	1	0.918	-1.66	0.006	-1.19	0.023	-1.37	0.023	-1.66	0.014
1422363_at	olfactory receptor 65	Olfr64	-1.53	0.237	-1.66	0.020	1.16	0.614	1.24	0.278	1.35	0.711
1417542_at	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	-1.22	0.011	-1.66	0.014	-1.05	0.435	-1.09	0.009	-1.22	0.048
1444465_at	Ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	Ube4b	-1.01	0.838	-1.66	0.011	-1.19	0.168	1.61	0.558	1.18	0.190
1452008_at	RIKEN cDNA 9130422G05 gene	9130422G05Rik	-1.11	0.453	-1.67	0.039	-1.25	0.085	-1.25	0.041	-1.29	0.014
1440928_at	RIKEN cDNA D630037F22 gene	D630037F22Rik	-1.08	0.523	-1.67	0.006	1.27	0.017	-1.21	0.150	1.19	0.173
1422445_at	integrin alpha 6	Itga6	1.02	0.995	-1.67	0.034	-1.16	0.047	-1.41	0.002	-1.33	0.008
1424704_at	runt related transcription factor 2	Runx2	-1.11	0.370	-1.67	0.017	-1.44	0.001	-1.67	0.007	-1.65	0.016
1429428_at	transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	-1.03	0.449	-1.67	0.017	1.01	0.619	-1.33	0.005	-1.26	0.029
1458438_at	RIKEN cDNA 4933415L06 gene	4933415L06Rik	-1.37	0.235	-1.68	0.010	1.05	0.996	-1.4	0.008	1.01	0.904
1431517_at	RIKEN cDNA 4933417C20 gene	4933417C20Rik	-1.36	0.202	-1.68	0.018	1.14	0.670	-1.47	0.064	-1.27	0.236
1445125_at	DNA segment, Chr 8, ERATO Doi 107, expressed	D8Ertd107e	-1.59	0.250	-1.68	0.002	-1.36	0.401	1.39	0.169	3.52	0.784
1432296_a_at	integrin alpha V	Itgav	1.13	0.393	-1.68	0.034	-1.3	0.008	1.22	0.304	-1.02	0.349
1434129_s_at	lipoma HMGIC fusion partner-like 2	Lhfpl2	-1.04	0.817	-1.68	0.014	-1.29	0.008	-1.18	0.055	-1.5	0.019
1429111_at	talin 2 /// similar to talin 2	Tln2 /// LOC63921	-1.2	0.033	-1.68	0.002	-1.46	0.005	-1.41	0.006	-1.5	0.005
1455593_at	apolipoprotein B	Apob	-1.37	0.152	-1.69	0.035	1.36	0.909	1.11	0.797	-1.42	0.248
1455082_at	Casitas B-lineage lymphoma b	Cblb	-1.07	0.213	-1.69	0.007	-1.41	0.018	-1.48	0.044	-1.97	0.041
1426732_at	desmin	Des	-1.58	0.069	-1.69	0.028	1.23	0.849	2.6	0.178	3.21	0.254
1428321_at	echinoderm microtubule associated protein like 1 /// similar to	Eml1 /// LOC6341	-1.03	0.544	-1.69	0.009	-1.08	0.130	-1.01	0.918	-1.35	0.285
1425216_at	free fatty acid receptor 2	Ffar2	2.08	0.637	-1.69	0.038	-1.12	0.376	1.31	0.829	4.17	0.160
1437409_s_at	G protein-coupled receptor 126	Gpr126	1.13	0.354	-1.69	0.043	1.55	0.473	1.28	0.241	-1.02	0.574
1417400_at	retinoic acid induced 14	Rai14	-1.08	0.204	-1.69	0.008	-1.32	0.013	-1.36	0.016	-1.5	0.014
1427917_s_at	single-stranded DNA binding protein 3	Ssbp3	-1.21	0.148	-1.69	0.036	-1.13	0.096	-1.25	0.032	-1.07	0.397
1455109_at	transducin (beta)-like 1X-linked receptor 1	Tbl1xr1	-1.13	0.342	-1.69	0.002	1.14	0.502	-1.09	0.511	1.11	0.557
1458090_at	RIKEN cDNA 4930504E06 gene	4930504E06Rik	1.67	0.705	-1.7	0.023	1.38	0.789	-1.08	0.502	-1.39	0.376
1454080_at	RIKEN cDNA 4933428M03 gene	4933428M03Rik	-1.32	0.565	-1.7	0.028	2.05	0.416	1.47	0.820	2.05	0.503
1452013_at	ATPase, class V, type 10A	Atp10a	1.09	0.715	-1.7	0.008	1.39	0.240	-1.26	0.203	-1.4	0.073

1419490_at	expressed sequence AW049604	AW049604	1.06	0.982	-1.7	0.028	1.47	0.988	-1.22	0.089	-1.14	0.351
1456416_at	core-binding factor, runt domain, alpha subunit 2, translocate	Cbfa2t2h	-1.4	0.125	-1.7	0.034	-1.2	0.339	-1.47	0.132	1.65	0.547
1438255_at	checkpoint suppressor 1	Ches1	-1	0.861	-1.7	0.014	-1.35	0.012	-1.5	0.039	-1.3	0.060
1447233_at	RIKEN cDNA D330027H18 gene	D330027H18Rik	-1.25	0.321	-1.7	0.002	1.35	0.976	2.26	0.006	1.49	0.079
1415691_at	discs, large homolog 1 (Drosophila)	Dlgh1	1.04	0.898	-1.7	0.028	-1.68	0.001	-1.62	0.001	-1.95	0.004
1444276_at	immature colon carcinoma transcript 1	Ict1	-1.39	0.002	-1.7	0.005	-1.35	0.182	-1.16	0.428	1.14	0.423
1440621_at	Kit ligand	Kitl	-1.49	0.084	-1.7	0.040	-1.23	0.339	1.07	0.646	1.25	0.748
1425978_at	myocardin	Myocd	-1.34	0.095	-1.7	0.016	-1.27	0.079	-1.21	0.257	-1.24	0.234
1424659_at	slit homolog 2 (Drosophila)	Slit2	-1.27	0.100	-1.7	0.044	-1.22	0.043	-1.2	0.015	-1.22	0.025
1456645_at	WD repeat domain 25	Wdr25	1.12	0.660	-1.7	0.011	1.08	0.905	1.11	0.345	-1.37	0.146
1440703_at	RIKEN cDNA 2810429I04 gene	2810429I04Rik	1.34	0.427	-1.71	0.006	1.23	0.768	-1.6	0.173	-2.32	0.033
1453522_at	RIKEN cDNA 6530401N04 gene	6530401N04Rik	-1.42	0.069	-1.71	0.042	1.04	0.900	-1.2	0.214	1.19	0.767
1454984_at	expressed sequence AW061234	AW061234	-1.24	0.147	-1.71	0.050	-1.38	0.098	-1.09	0.480	1.23	0.430
1424361_at	cDNA sequence BC019943	BC019943	-1.71	0.113	-1.71	0.008	-1.22	0.117	-1.09	0.867	1.3	0.313
1427763_a_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	1.08	0.975	-1.71	0.043	-1.74	0.004	-1.51	0.005	-1.86	0.022
1452265_at	CLIP associating protein 1	Clasp1	-1.09	0.202	-1.71	0.006	-1.56	0.014	-1.73	0.001	-1.96	0.000
1420512_at	dickkopf homolog 2 (Xenopus laevis)	Dkk2	1.12	0.042	-1.71	0.019	-1.04	0.506	-1.2	0.212	-1.25	0.134
1422684_a_at	exocyst complex component 4	Exoc4	-1.15	0.021	-1.71	0.015	-1.39	0.013	-1.32	0.014	-1.51	0.082
1453771_at	GULP, engulfment adaptor PTB domain containing 1	Gulp1	1.03	0.785	-1.71	0.015	-1.19	0.027	-1.19	0.012	-1.22	0.110
1444620_at	Transcription factor 12	Tcf12	-1.11	0.498	-1.71	0.030	-1.14	0.330	1.02	0.486	-1.13	0.490
1437616_x_at	zinc finger, DHHC domain containing 14	Zdhhc14	1.03	0.886	-1.71	0.018	1.01	0.711	-1.21	0.382	-1.62	0.004
1438863_at	RIKEN cDNA A530079E22 gene	A530079E22Rik	-1.9	0.116	-1.72	0.024	1.04	0.790	1.64	0.063	1.47	0.711
1441650_at	Rho GTPase activating protein 15	Arhgap15	-1.32	0.065	-1.72	0.036	-1.25	0.414	1.26	0.837	-1.07	0.669
1421672_at	interleukin 17A	Il17a	-1.34	0.036	-1.72	0.045	1.51	0.425	1.48	0.884	1.35	0.262
1423140_at	lysosomal acid lipase 1	Lip1	-1.21	0.145	-1.72	0.010	1.07	0.846	1.07	0.539	1.05	0.947
1436746_at	WNK lysine deficient protein kinase 1	Wnk1	-1.29	0.169	-1.72	0.009	-1.62	0.046	-1.4	0.041	-1.23	0.085
1441688_at	RIKEN cDNA 6430537I21 gene	6430537I21Rik	-1.17	0.371	-1.73	0.022	1.24	0.059	1.07	0.909	-1.1	0.415
1435179_at	RIKEN cDNA C130071C03 gene	C130071C03Rik	-1.94	0.071	-1.73	0.046	1.22	0.429	1.58	0.900	1.33	0.842
1448437_a_at	GTP binding protein 2	Gtpbp2	-1.47	0.036	-1.73	0.049	-1.27	0.328	2.04	0.092	1.03	0.485
1453317_a_at	KH domain containing, RNA binding, signal transduction asso	Khdrbs3	-1.12	0.055	-1.73	0.007	-1.44	0.002	-1.28	0.011	-1.45	0.000
1444326_at	Prolyl 4-hydroxylase, beta polypeptide	P4hb	-1.01	0.746	-1.73	0.031	1.07	0.592	-1.12	0.140	-1.01	0.987
1428493_at	RIKEN cDNA 2610511M17 gene /// similar to signal-induced	2610511M17Rik ///	-1.17	0.275	-1.74	0.005	-1.4	0.047	-1.8	0.005	-1.63	0.000
1437704_at	RIKEN cDNA 2900024O10 gene	2900024O10Rik	-1.27	0.187	-1.74	0.012	1.03	0.937	-1	0.636	-1.12	0.519
1429909_at	RIKEN cDNA 4833411O04 gene	4833411O04Rik	-1.27	0.233	-1.74	0.015	1.34	0.733	1.11	0.592	1.27	0.780
1455720_at	a disintegrin-like and metallopeptidase (reprolysin type) with t	Adamts2	1.02	0.969	-1.74	0.023	-1.6	0.049	-1.05	0.842	-1.56	0.052
1448223_at	fatso	Fto	-1.12	0.224	-1.74	0.002	-1.23	0.030	-1.29	0.043	-1.29	0.041
1452232_at	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylg	Galnt7	1.04	0.812	-1.74	0.002	-1.08	0.276	-1.32	0.003	-1.19	0.069
1436356_at	lectin, galactose binding, soluble 7	Lgals7	1.06	0.633	-1.74	0.003	-1.83	0.004	-1.72	0.001	-2.08	0.013
1450786_x_at	similar to PDZ and LIM domain protein 5 (Enigma homolog) (	LOC669660	1.02	0.849	-1.74	0.031	-1.77	0.021	-1.76	0.004	-1.84	0.009
1443162_at	Protein tyrosine phosphatase, non-receptor type 3	Ptpn3	1.1	0.848	-1.74	0.037	-1.18	0.494	-1.08	0.623	1.23	0.790
1417622_at	solute carrier family 12, member 2	Slc12a2	-1.17	0.104	-1.74	0.032	1.03	0.414	1.06	0.820	-1.13	0.256
1432566_at	RIKEN cDNA 1700129I15 gene	1700129I15Rik	-1.19	0.374	-1.75	0.010	2.38	0.500	1.29	0.971	2.3	0.468
1418179_at	autophagy-related 3 (yeast)	Atg3	1.1	0.648	-1.75	0.038	-1.17	0.155	-1.13	0.346	1.13	0.479
1428638_at	EF-hand domain (C-terminal) containing 2	Efhc2	-1.06	0.769	-1.75	0.017	2.89	0.546	1.53	0.412	1.7	0.410
1456858_at	G protein-coupled receptor 149	Gpr149	1.24	0.264	-1.75	0.002	1.27	0.315	-1.08	0.552	1.17	0.333
1440582_at	itchy /// RIKEN cDNA 8030492O04 gene	Itch /// 8030492O0	-1.06	0.468	-1.75	0.015	-1.06	0.512	-1.04	0.753	-1.48	0.036
1453946_a_at	serologically defined colon cancer antigen 8	Sdccag8	-1.01	0.715	-1.75	0.023	-1.32	0.085	-1.1	0.372	-1.58	0.089
1444198_at	Dorso-medial telencephalon gene 2	Dmt2	-1.02	0.470	-1.76	0.040	1.02	0.610	1	0.922	1.28	0.776
1457713_at	Excision repair cross-complementing rodent repair deficiency	Ercc5	-1.62	0.094	-1.76	0.036	-1.7	0.065	1.05	0.560	1.32	0.891
1431296_at	G protein-coupled receptor 15	Gpr15	-1.68	0.068	-1.76	0.012	2.42	0.594	-1.17	0.294	1	0.787
1435293_at	RIKEN cDNA 2900022I03 gene	2900022I03Rik	-1.6	0.157	-1.77	0.040	1.11	0.969	1.07	0.780	-1.14	0.393
1455326_at	RIKEN cDNA 4932416N17 gene	4932416N17Rik	-1.17	0.243	-1.77	0.011	1.58	0.737	-1.67	0.078	-1.14	0.542
1435006_s_at	ATP-binding cassette, sub-family B (MDR/TAP), member 7	Abcb7	-1.02	0.624	-1.77	0.006	-1.02	0.669	-1.15	0.306	-1.24	0.019
1440097_at	miRNA containing gene	Mirg	-1.25	0.134	-1.77	0.021	1.23	0.621	-1.6	0.039	1.05	0.964
1434222_at	signal-induced proliferation-associated 1 like 1	Sipa1l1	1.05	0.438	-1.77	0.001	-1.76	0.006	-1.71	0.008	-1.87	0.001
1431449_at	solute carrier organic anion transporter family, member 6d1	Slco6d1	-1.13	0.544	-1.77	0.048	1.25	0.603	-1.14	0.686	1.92	0.030
1460118_at	Transcribed locus	---	-1.17	0.397	-1.78	0.010	-1	0.835	1.49	0.462	1.04	0.662
1434404_at	RIKEN cDNA C030011O14 gene	C030011O14Rik	-1.08	0.328	-1.78	0.027	1.08	0.114	1.01	0.820	1.06	0.950

1442242_at	expressed sequence C79127	C79127	1.07	0.981	-1.78	0.015	1.54	0.110	-1.33	0.264	1.19	0.442
1434957_at	cell adhesion molecule-related/down-regulated by oncogenes	Cdon	-1.31	0.028	-1.78	0.018	1.07	0.526	1.05	0.734	-1.16	0.173
1419983_at	zinc finger protein 644	Zfp644	1	0.708	-1.78	0.035	3.08	0.676	2.06	0.269	1.17	0.766
1433833_at	fibronectin type III domain containing 3B	Fndc3b	1.03	0.851	-1.79	0.021	-1.87	0.000	-2.01	0.000	-2.37	0.000
1446783_at	Growth arrest and DNA-damage-inducible, gamma interactin	Gadd45gip1	-1.26	0.171	-1.79	0.038	1.24	0.382	1.1	0.874	-1.07	0.646
1423271_at	gap junction membrane channel protein beta 2	Gjb2	-1.17	0.069	-1.79	0.017	-1.29	0.089	-1.35	0.003	-1.46	0.013
1452714_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil contai	Tanc1	1.07	0.602	-1.79	0.011	-1.62	0.004	-1.86	0.009	-1.89	0.001
1435888_at	epidermal growth factor receptor	Egfr	-1.14	0.236	-1.8	0.024	-1.44	0.025	-1.68	0.006	-1.68	0.015
1448024_at	natriuretic peptide receptor 3	Npr3	-1.12	0.331	-1.8	0.033	-1.44	0.035	-1.11	0.145	-1.29	0.116
1428083_at	RIKEN cDNA 2310043N10 gene	2310043N10Rik	-1.05	0.461	-1.81	0.049	-1.28	0.151	-1.42	0.178	-1.92	0.023
1416077_at	adrenomedullin	Adm	1.09	0.824	-1.81	0.029	-1.52	0.069	-1.6	0.003	-1.81	0.026
1456022_at	homeodomain interacting protein kinase 2	Hipk2	1.01	0.934	-1.81	0.048	-1.76	0.024	-1.99	0.001	-2.01	0.024
1419410_at	basic leucine zipper transcription factor, ATF-like	Batf	-2	0.120	-1.83	0.041	2.15	0.930	-1.34	0.193	-1.8	0.073
1459679_s_at	myosin IB	Myo1b	-1.1	0.068	-1.83	0.019	-1.36	0.018	-1.31	0.202	-1.86	0.076
1434653_at	PTK2 protein tyrosine kinase 2 beta	Ptk2b	-1.05	0.703	-1.83	0.010	-1.29	0.003	-1.41	0.026	-1.29	0.125
1457478_at	Spermatid perinuclear RNA binding protein	Strbp	-2.41	0.039	-1.83	0.010	-1.19	0.358	-1.45	0.130	-1.18	0.311
1433299_at	RIKEN cDNA 5830461L22 gene	5830461L22Rik	1.1	0.858	-1.84	0.034	-1.05	0.560	1.08	0.969	1.16	0.836
1447035_at	RIKEN cDNA A230091C14 gene	A230091C14Rik	-1.73	0.084	-1.84	0.025	-1.47	0.162	-1.27	0.212	1.48	0.865
1452253_at	cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	-1.29	0.150	-1.84	0.005	-1.44	0.102	-1.66	0.036	-1.07	0.751
1428964_at	solute carrier family 25 (mitochondrial carrier), member 18	Slc25a18	-2.61	0.032	-1.84	0.002	1.43	0.488	1.21	0.436	1.26	0.721
1433719_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform	Slc9a9	1.15	0.698	-1.84	0.023	-1.51	0.004	1.14	0.354	-1.19	0.471
1422256_at	somatostatin receptor 2	Sstr2	-1.06	0.497	-1.84	0.020	-1.21	0.033	1.13	0.799	-1.45	0.081
1453394_at	RIKEN cDNA 2410017I17 gene	2410017I17Rik	1.06	0.818	-1.85	0.001	1.4	0.854	1.07	0.176	1.49	0.996
1434645_at	RIKEN cDNA C530008M17 gene	C530008M17Rik	1.29	0.356	-1.85	0.032	-1.15	0.144	-1.47	0.007	-1.23	0.011
1430371_x_at	eukaryotic translation initiation factor 2 alpha kinase 3	Eif2ak3	1.21	0.937	-1.85	0.016	1.44	0.960	1.17	0.582	-1.17	0.567
1418217_at	non-metastatic cells 7, protein expressed in	Nme7	-1.18	0.093	-1.85	0.007	-1.06	0.096	-1.06	0.122	-1.24	0.126
1459903_at	sema domain, immunoglobulin domain (Ig), and GPI membra	Sema7a	-1.21	0.128	-1.85	0.049	-1.35	0.013	-1.38	0.018	-1.41	0.005
1428471_at	sorbin and SH3 domain containing 1	Sorbs1	-1.03	0.479	-1.85	0.015	-1.88	0.000	-1.93	0.000	-2.24	0.001
1419551_s_at	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	1.16	0.921	-1.85	0.012	-1.17	0.132	-1.49	0.027	-1.39	0.052
1445057_at	expressed sequence C81285	C81285	1.02	0.680	-1.86	0.008	1.63	0.821	1.49	0.458	1.56	0.544
1421381_a_at	procollagen, type IX, alpha 1	Col9a1	-1.28	0.173	-1.86	0.036	1.66	0.376	1.44	0.616	1.42	0.303
1455746_at	kinesin family member 13A	Kif13a	1.23	0.061	-1.86	0.020	-1.19	0.008	-1.4	0.003	-1.42	0.033
1415959_at	solute carrier family 2 (facilitated glucose transporter), membe	Slc2a4	-1.03	0.816	-1.86	0.028	1.81	0.625	-1.15	0.516	2.73	0.194
1418651_at	spermatogenesis associated 6	Spata6	-1.16	0.207	-1.86	0.032	1.03	0.894	-1.2	0.163	-1.42	0.042
1429053_at	RIKEN cDNA 1110012J17 gene	1110012J17Rik	-1.13	0.257	-1.87	0.002	-1.06	0.600	-1.13	0.071	1.17	0.056
1451116_at	acetoacetyl-CoA synthetase	Aacs	-1.45	0.028	-1.87	0.024	1.37	0.459	1.02	0.749	1.21	0.579
1442214_at	Nuclear factor I/B	Nfib	-1.31	0.269	-1.87	0.004	2.01	0.033	-1.04	0.521	1.01	0.529
1444422_at	protocadherin 19	Pcdh19	-1.21	0.242	-1.87	0.022	-1.34	0.002	-1.26	0.078	-1.41	0.006
1433608_at	sec1 family domain containing 2	Scfd2	-1.14	0.062	-1.87	0.029	-1.11	0.304	-1.21	0.093	-1.23	0.021
1453414_at	yippee-like 2 (Drosophila)	Ypel2	1.25	0.766	-1.87	0.000	1.48	0.308	2.01	0.839	-1.13	0.393
1431367_at	membrane-associated ring finger (C3HC4) 1	1-Mar	-1.11	0.433	-1.88	0.022	1.01	0.878	-1.58	0.172	-1.01	0.694
1437869_at	RIKEN cDNA 3222402P14 gene	3222402P14Rik	-1.12	0.021	-1.88	0.005	-1.29	0.159	-1.14	0.287	-1.72	0.040
1455660_at	colony stimulating factor 2 receptor, beta 1, low-affinity (granu	Csf2rb1	-1.42	0.156	-1.88	0.046	1.4	0.033	-1	0.635	-1.26	0.651
1434112_at	latrophilin 2	Lphn2	-1.15	0.327	-1.88	0.022	-1.34	0.002	-1.14	0.113	-1.43	0.019
1451141_at	methyltransferase like 8	Mettl8	-1.14	0.149	-1.88	0.019	1.03	0.793	1.03	0.868	-1.08	0.603
1434878_at	SLIT and NTRK-like family, member 4	Slitrk4	1.76	0.036	-1.88	0.025	2.16	0.897	1.87	0.331	-2.58	0.033
1456908_at	cDNA sequence BC023202	BC023202	1.03	0.965	-1.89	0.011	-1.39	0.282	-1.27	0.444	1.59	0.075
1441047_at	solute carrier family 45, member 4	Slc45a4	-1.64	0.068	-1.89	0.016	1.36	0.302	2.25	0.030	2.38	0.614
1431648_at	RIKEN cDNA 4930528F23 gene	4930528F23Rik	1.04	0.854	-1.9	0.019	1.24	0.692	1.16	0.715	-1.64	0.182
1444443_at	RIKEN cDNA A830039H10 gene	A830039H10Rik	-1.2	0.514	-1.9	0.035	-1.56	0.094	1.76	0.242	1.23	0.781
1460006_at	AT motif binding factor 1	Atbf1	-1.14	0.107	-1.9	0.002	-1.76	0.002	-1.99	0.000	-2.15	0.002
1457157_at	phospholipase C, eta 1	Plch1	-1.24	0.206	-1.9	0.027	-1.05	0.628	1.24	0.116	-1.32	0.257
1420910_at	phosphatidic acid phosphatase type 2c	Ppap2c	-1	0.943	-1.9	0.013	-1.13	0.321	1.66	0.306	2.49	0.232
1424602_s_at	X-ray repair complementing defective repair in Chinese hams	Xrcc4	-1.26	0.129	-1.9	0.030	-1.35	0.115	-1.22	0.050	-1.59	0.018
1439922_at	RIKEN cDNA 1190002C06 gene	1190002C06Rik	-1.11	0.594	-1.91	0.046	-1.4	0.025	-1.26	0.296	-1.46	0.067
1427016_at	RIKEN cDNA 4932438A13 gene /// similar to CG4841-PA	4932438A13Rik //	-1.49	0.016	-1.91	0.029	-1.19	0.136	-1.22	0.270	-1.63	0.031
1434265_s_at	ankyrin 2, brain	Ank2	-1.27	0.145	-1.91	0.049	-1.3	0.098	-1.28	0.041	-1.34	0.131
1460291_at	cyclin-dependent kinase 6	Cdk6	-1.22	0.314	-1.91	0.032	-1.01	0.375	-1.11	0.379	-1.15	0.823

1425016_at	Eph receptor B2	Ephb2	1.03	0.961	-1.91	0.017	-1.17	0.262	-1.14	0.298	-1.42	0.027
1416934_at	X-linked myotubular myopathy gene 1	Mtm1	-1.06	0.299	-1.91	0.012	-1.08	0.451	-1.18	0.212	-1.24	0.158
1453707_at	RIKEN cDNA 4930480G23 gene	4930480G23Rik	-1.05	0.667	-1.92	0.044	1.16	0.567	-1.94	0.047	2.04	0.291
1449763_at	Doublesex and mab-3 related transcription factor 3	Dmrt3	-1.01	0.670	-1.92	0.033	1.44	0.929	-1.82	0.126	-2.54	0.030
1446398_at	hypothetical gene supported by AK028463	LOC433197	-1.7	0.142	-1.92	0.022	-1.08	0.757	1.78	0.789	1.3	0.746
1450992_a_at	myeloid ecotropic viral integration site 1	Meis1	-1	0.849	-1.92	0.006	-1.43	0.029	-1.49	0.077	-1.28	0.049
1449351_s_at	platelet-derived growth factor, C polypeptide	Pdgfc	1.07	0.742	-1.92	0.015	-1.75	0.012	-1.91	0.007	-1.86	0.000
1449530_at	trichorhinophalangeal syndrome I (human)	Trps1	1.33	0.333	-1.92	0.043	-1.66	0.005	-1.63	0.004	-1.85	0.075
1434671_at	RIKEN cDNA B230337E12 gene	B230337E12Rik	-1.19	0.308	-1.93	0.024	-1.05	0.719	-1.38	0.097	-1.42	0.027
1435366_at	RIKEN cDNA D430042O09 gene	D430042O09Rik	1	0.797	-1.93	0.021	-1.18	0.062	-1.12	0.014	-1.07	0.585
1449431_at	transient receptor potential cation channel, subfamily C, mem	Trpc6	1.06	0.811	-1.93	0.045	1.69	0.913	-1.35	0.091	-1.51	0.006
1452964_at	tubulin tyrosine ligase-like family, member 11	Ttll11	-1.15	0.202	-1.93	0.021	-1.29	0.046	-1.32	0.017	-1.55	0.032
1446675_at	adenosine kinase	Adk	1.01	0.717	-1.94	0.012	-1.59	0.126	-1.07	0.471	2.43	0.326
1450509_at	carbohydrate sulfotransferase 11	Chst11	-1.11	0.224	-1.94	0.010	-1.76	0.003	-1.41	0.089	-1.45	0.092
1460324_at	DNA methyltransferase 3A	Dnmt3a	-1.44	0.074	-1.94	0.041	1.01	0.951	-1.27	0.026	-1.19	0.129
1455314_at	LIM domain containing preferred translocation partner in lipor	Lpp	-1.14	0.045	-1.94	0.001	-1.66	0.004	-1.55	0.000	-1.99	0.009
1453611_at	retinoblastoma binding protein 6	Rbbp6	1.63	0.990	-1.94	0.047	-1.34	0.128	1.75	0.383	-2.02	0.196
1454250_at	SEC15-like 2 (S. cerevisiae)	Sec15l2	-1.05	0.576	-1.94	0.031	-1.38	0.086	1.16	0.883	1.24	0.950
1460439_at	cDNA sequence BC033915	BC033915	-1.07	0.605	-1.95	0.001	-1.44	0.017	-1.34	0.010	-1.49	0.044
1450207_at	leukemia inhibitory factor receptor	Lifr	-1.31	0.245	-1.95	0.026	2.14	0.407	1.67	0.784	1.76	0.397
1417985_at	Notch-regulated ankyrin repeat protein	Nrarp	-1.09	0.329	-1.95	0.049	-1.35	0.074	-1.1	0.307	1.16	0.737
1417020_at	spermatogenesis associated 4	Spata4	-1.94	0.076	-1.95	0.006	1.07	0.844	1.78	0.672	-1.05	0.506
1454706_at	UV radiation resistance associated gene	Uvrag	-1.04	0.271	-1.95	0.005	-1.53	0.005	-1.98	0.004	-1.73	0.000
1435301_at	RIKEN cDNA 1110004E09 gene	1110004E09Rik	-1.18	0.258	-1.96	0.042	1.04	0.776	-1.26	0.220	1.61	0.226
1455331_at	RIKEN cDNA 9430067K14 gene	9430067K14Rik	-1.25	0.198	-1.96	0.021	-1.08	0.328	-1.05	0.576	-1.03	0.681
1419989_at	COMM domain containing 5	Commd5	-1.27	0.376	-1.96	0.006	2.14	0.243	3.97	0.716	-1.09	0.625
1430673_a_at	RIKEN cDNA 2210009G21 gene	2210009G21Rik	1.04	0.844	-1.97	0.045	-1.37	0.092	-1.14	0.348	1.87	0.067
1432449_at	RIKEN cDNA 4930564B18 gene	4930564B18Rik	-2.2	0.045	-1.97	0.045	-1.07	0.423	1.9	0.090	1.26	0.382
1445021_at	RIKEN cDNA 6030465E24 gene	6030465E24Rik	-1.94	0.022	-1.97	0.050	1.14	0.440	1.56	0.390	1.3	0.844
1459391_at	ATP-binding cassette, sub-family A (ABC1), member 5	Abca5	-1.25	0.324	-1.97	0.011	2.56	0.531	-1.11	0.331	-1.79	0.088
1418336_at	AFG3(ATPase family gene 3)-like 1 (yeast)	Afg3l1	-1.23	0.147	-1.97	0.007	1.05	0.482	1.1	0.527	1.25	0.222
1454780_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga	Galntl4	-1.13	0.099	-1.97	0.000	-1.73	0.000	-1.49	0.000	-1.89	0.000
1446096_at	RIKEN cDNA 2310001H17 gene	2310001H17Rik	-1.14	0.506	-1.98	0.045	1.46	0.784	3.12	0.020	-1.15	0.210
1431667_s_at	RIKEN cDNA 2610021K21 gene	2610021K21Rik	-1.13	0.138	-1.98	0.007	1.43	0.592	-1.26	0.143	-1.23	0.250
1430003_at	RIKEN cDNA 6330412A17 gene	6330412A17Rik	-1.13	0.577	-1.98	0.037	-1.96	0.093	1.86	0.678	1.24	0.054
1429166_s_at	calmin	Clmn	-1.22	0.399	-1.98	0.049	-1.74	0.173	-1.19	0.129	1.12	0.401
1417163_at	dual specificity phosphatase 10	Dusp10	1.12	0.919	-1.98	0.029	1.32	0.983	-1.37	0.361	-1.13	0.621
1428822_a_at	sorting nexing 24	Snx24	-1.09	0.370	-1.98	0.016	-1.53	0.043	-1.58	0.015	-1.83	0.000
1445654_at	RIKEN cDNA 4930422I07 gene	4930422I07Rik	1.1	0.745	-1.99	0.041	2.09	0.524	1.06	0.913	1.29	0.612
1432791_at	RIKEN cDNA 9030218A15 gene	9030218A15Rik	1.1	0.412	-1.99	0.002	-1.13	0.516	2.25	0.333	2.08	0.820
1424250_a_at	Rho guanine nucleotide exchange factor (GEF) 3	Arhgef3	-1.47	0.111	-1.99	0.004	-1.1	0.840	1.66	0.908	-1	0.490
1450468_at	myocilin	Myoc	-1.17	0.434	-1.99	0.015	5.22	0.192	-1.34	0.206	1.7	0.485
1439556_at	neural cell adhesion molecule 1	Ncam1	1.04	0.840	-1.99	0.037	-1.64	0.072	-1.27	0.211	-2.02	0.105
1444516_at	Protein tyrosine phosphatase, receptor-type, F interacting prc	Ppfibp2	-1.56	0.087	-1.99	0.005	-1.51	0.206	1.41	0.621	1.2	0.529
1450916_at	staufen (RNA binding protein) homolog 2 (Drosophila)	Stau2	1.04	0.892	-1.99	0.050	-1.28	0.043	-1.33	0.018	-1.35	0.016
1449009_at	T-cell specific GTPase	Tgtp	-1.36	0.082	-1.99	0.037	-1.16	0.426	-1.32	0.243	1.58	0.979
1459259_at	hypothetical protein A030007L22	A030007L22	-1.38	0.351	-2	0.003	1.99	0.335	1.31	0.717	2.18	0.250
1437082_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	1.05	0.597	-2	0.002	-1.47	0.142	-1.23	0.116	-1.16	0.168
1428610_at	autophagy-related 7 (yeast)	Atg7	-1.2	0.435	-2	0.022	-1.55	0.072	-1.05	0.493	1.29	0.648
1435994_at	potassium voltage-gated channel, subfamily H (eag-related),	Kcnh1	-1.14	0.178	-2	0.043	1.42	0.326	-1.04	0.719	-1.04	0.926
1436818_a_at	Musashi homolog 2 (Drosophila)	Msi2	1.28	0.999	-2	0.044	-1.17	0.473	-1.05	0.712	1.06	0.921
1433015_at	RIKEN cDNA 6330436F06 gene	6330436F06Rik	-1.32	0.216	-2.01	0.025	1.43	0.177	2.18	0.996	1.51	0.556
1447638_at	Arylformamidase	Afmid	-1.82	0.074	-2.01	0.009	2.69	0.387	1.08	0.982	1.73	0.044
1460090_at	Ariadne ubiquitin-conjugating enzyme E2 binding protein hom	Arih1	1.22	0.736	-2.01	0.022	2.09	0.210	-1.1	0.244	1.68	0.785
1442542_at	eyes absent 4 homolog (Drosophila)	Eya4	-1.13	0.431	-2.01	0.027	-1.24	0.084	-1.22	0.200	-1.14	0.268
1442283_at	Phosphoglycerate dehydrogenase like 1	Phgdhl1	-1.42	0.292	-2.01	0.049	1.31	0.737	2.24	0.131	1.55	0.768
1452209_at	plakophilin 4	Pkp4	-1.24	0.238	-2.01	0.027	-1.41	0.009	-1.6	0.000	-1.6	0.004
1438283_at	RIKEN cDNA 3110057O12 gene	3110057O12Rik	-1.3	0.075	-2.02	0.034	-1.09	0.674	-1.16	0.583	1.04	0.940

1430115_at	RIKEN cDNA 4833413E03 gene	4833413E03Rik	-1.86	0.074	-2.02	0.049	-1.49	0.041	-1.02	0.721	1.59	0.215
1421210_at	class II transactivator	C2ta	-1.69	0.042	-2.02	0.020	-1.31	0.202	1.08	0.485	-1	0.921
1427199_at	furry homolog-like (Drosophila)	Fryl	-1.07	0.138	-2.02	0.005	-1.61	0.012	-1.39	0.091	-1.43	0.008
1448185_at	homocysteine-inducible, endoplasmic reticulum stress-inducil	Herpud1	1.05	0.857	-2.02	0.023	-1.22	0.004	-1.05	0.109	-1.27	0.003
1421594_a_at	synaptotagmin-like 2	Sytl2	-1.09	0.141	-2.02	0.004	-1.33	0.004	-1.45	0.027	-1.43	0.026
1456165_at	RIKEN cDNA 4921521F21 gene	4921521F21Rik	-1.89	0.028	-2.03	0.019	-1.12	0.448	-1.08	0.542	2.64	0.147
1437031_at	Acyl-CoA synthetase long-chain family member 6	Acsl6	1.05	0.511	-2.03	0.050	1.72	0.353	1.09	0.754	2.85	0.248
1425092_at	cadherin 10	Cdh10	-1.22	0.716	-2.03	0.028	-1.24	0.352	1.08	0.837	-1.26	0.250
1460694_s_at	supervillin	Svil	-1.18	0.193	-2.03	0.003	-1.3	0.025	-1.54	0.001	-1.59	0.001
1422698_s_at	jumonji, AT rich interactive domain 2	Jarid2	1.11	0.755	-2.04	0.009	-1.58	0.007	-1.64	0.018	-1.7	0.034
1444466_at	Neurocalcin delta	Ncald	-1.02	0.626	-2.04	0.002	1.24	0.618	1.55	0.578	1.42	0.744
1421657_a_at	SRY-box containing gene 17	Sox17	-1.04	0.314	-2.04	0.022	1.53	0.848	-1.14	0.674	1.42	0.965
1456225_x_at	tribbles homolog 3 (Drosophila)	Trib3	-1.34	0.109	-2.04	0.020	1.16	0.317	-1.11	0.126	1.09	0.364
1433197_at	RIKEN cDNA 4930445B03 gene	4930445B03Rik	-1.03	0.684	-2.05	0.014	1.18	0.826	-1.58	0.193	1.24	0.694
1441867_x_at	RIKEN cDNA 4930534B04 gene	4930534B04Rik	-1.4	0.272	-2.05	0.048	-1.37	0.029	-1.26	0.164	-1.18	0.166
1435240_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	-1.06	0.442	-2.05	0.015	-1.06	0.385	-1.57	0.026	-1.82	0.028
1440427_at	expressed sequence BB124205	BB124205	1.02	0.892	-2.05	0.015	1.18	0.752	-1.64	0.051	1.14	0.510
1457687_at	B-cell leukemia/lymphoma 2	Bcl2	-1.03	0.798	-2.05	0.003	-1.18	0.054	-1.2	0.132	1.04	0.973
1425642_at	centrosomal protein 290	Cep290	1.04	0.726	-2.05	0.034	-1.11	0.306	-1.07	0.327	1.38	0.849
1427671_a_at	formin 1	Fmn1	-1.09	0.418	-2.05	0.013	-1.68	0.016	-1.72	0.034	-1.68	0.080
1449899_at	glutamate receptor, ionotropic, NMDA3B	Grin3b	1.2	0.751	-2.05	0.042	1.26	0.706	2.07	0.408	-1.37	0.100
1460203_at	inositol 1,4,5-triphosphate receptor 1	Itpr1	-1.24	0.068	-2.05	0.011	-1.32	0.029	-1.29	0.030	-1.46	0.037
1421650_at	matrix extracellular phosphoglycoprotein with ASARM motif (l	Mepe	-1.64	0.101	-2.05	0.039	1.36	0.918	-1.03	0.490	1.32	0.518
1425442_at	osteoclast associated receptor	Oscar	1.22	0.627	-2.05	0.037	1.21	0.881	-1.06	0.254	1.07	0.614
1437113_s_at	phospholipase D1	Pld1	-1.08	0.391	-2.05	0.025	-1.5	0.028	-1.11	0.320	1.22	0.282
1443065_at	Rhomboid domain containing 1	Rhbdd1	-1.62	0.129	-2.05	0.005	-1.17	0.095	-1.05	0.624	-1.16	0.313
1455214_at	microphthalmia-associated transcription factor	Mitf	-1.02	0.854	-2.06	0.043	-1.15	0.178	-1.1	0.261	-1.02	0.731
1426994_at	PH domain and leucine rich repeat protein phosphatase	Phlpp	1.01	0.795	-2.06	0.019	-1.62	0.001	-1.88	0.000	-2.1	0.001
1446000_at	Zinc finger protein 291	Zfp291	1.04	0.724	-2.06	0.047	1.54	0.617	1.34	0.551	-1.17	0.676
1437855_at	microtubule-associated protein 4	Mtap4	-2.01	0.011	-2.07	0.039	-1.06	0.748	-1.52	0.080	-1.48	0.144
1455030_at	protein tyrosine phosphatase, receptor type, J	Ptprj	-1.5	0.018	-2.07	0.027	-1.36	0.207	-1.54	0.024	-1.88	0.004
1418057_at	T-cell lymphoma invasion and metastasis 1	Tiam1	-1.28	0.188	-2.08	0.033	-1.3	0.024	-1.19	0.362	-1.51	0.048
1447735_x_at	ataxin 2 binding protein 1	A2bp1	-1.59	0.103	-2.09	0.036	1.67	0.791	-1.16	0.237	-1.11	0.519
1434683_at	Cut-like 1 (Drosophila)	Cutl1	-1.14	0.164	-2.09	0.007	-1.75	0.004	-1.96	0.003	-2.06	0.003
1450119_at	dystonin	Dst	-1.22	0.221	-2.09	0.013	-1.59	0.177	-1.59	0.072	-2.22	0.003
1446383_at	Ephrin A5	Efna5	-1.56	0.133	-2.09	0.044	-1.19	0.303	-1.26	0.353	-1.48	0.259
1424899_at	nicotinamide nucleotide adenylyltransferase 3	Nmnat3	1.13	0.676	-2.09	0.002	1.05	0.792	-1.17	0.098	1	0.766
1437181_at	pellino 2	Peli2	-1.11	0.129	-2.09	0.005	-1.46	0.002	-1.59	0.002	-1.7	0.006
1429097_at	RIKEN cDNA C030044C12 gene	C030044C12Rik	-1.37	0.047	-2.1	0.001	-1.07	0.655	-1.28	0.175	-1.24	0.196
1427181_at	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ertd653e	-1.16	0.512	-2.1	0.002	-2	0.067	-2.78	0.003	-1.92	0.031
1459950_at	Doublecortin and CaM kinase-like 2	Dcamkl2	1.31	0.698	-2.1	0.042	1.39	0.815	1.02	0.570	1.53	0.124
1436667_at	solute carrier family 6 (neurotransmitter transporter), member	Slc6a20	2.25	0.330	-2.1	0.036	1.05	0.891	2.38	0.407	1.2	0.827
1443916_at	RIKEN cDNA 2900026A02 gene	2900026A02Rik	-1.31	0.007	-2.11	0.000	-1.07	0.428	-1.05	0.602	-1.52	0.015
1438451_at	Rho GTPase-activating protein	Grit	-1.11	0.393	-2.11	0.035	-1.54	0.034	-1.78	0.004	-2.06	0.013
1436378_at	leucine rich repeat (in FLII) interacting protein 2	Lrrfip2	-1.19	0.145	-2.11	0.009	-1.17	0.202	-1.2	0.059	-1.24	0.143
1444068_at	thyroid hormone receptor associated protein 1	Thrap1	1.72	0.448	-2.11	0.043	1.74	0.741	1.9	0.448	2.2	0.199
1451577_at	zinc finger and BTB domain containing 20	Zbtb20	1.12	0.362	-2.11	0.005	-1.74	0.009	-1.59	0.040	-2.37	0.001
1456045_at	RIKEN cDNA 1700106N22 gene	1700106N22Rik	-1.65	0.139	-2.12	0.044	-1.64	0.004	-1.03	0.662	-1.49	0.044
1430820_a_at	bobby sox homolog (Drosophila)	Bbx	-1.27	0.136	-2.12	0.039	-1.43	0.155	-1.17	0.218	-1.46	0.032
1448748_at	pleckstrin	Plek	1.18	0.283	-2.12	0.032	1.1	0.776	-1.12	0.142	-1.77	0.097
1429841_at	multiple EGF-like-domains 10	Megf10	-1.66	0.022	-2.13	0.020	1.22	0.769	-1.87	0.023	-1.41	0.127
1438726_at	microtubule associated monoxygenase, calponin and LIM doi	Mical2	-1.15	0.012	-2.13	0.043	-1.82	0.009	-2.08	0.008	-1.58	0.078
1431751_a_at	metallophosphoesterase domain containing 2	Mpped2	-1.31	0.013	-2.13	0.034	-1.39	0.141	1.2	0.467	-1.11	0.499
1455970_at	Phosphodiesterase 5A, cGMP-specific	Pde5a	1.14	0.659	-2.13	0.043	-1.24	0.096	-1.28	0.083	-1.09	0.361
1448918_at	solute carrier organic anion transporter family, member 3a1	Slco3a1	1.29	0.754	-2.13	0.042	-1.37	0.092	-1.47	0.044	-1.54	0.078
1450029_s_at	integrin alpha 9	Itga9	-1.1	0.521	-2.14	0.035	-1.17	0.183	-1.28	0.200	-1.43	0.125
1456067_at	GLI-Kruppel family member GLI3	Gli3	-1.02	0.632	-2.15	0.005	-1.56	0.025	-1.77	0.019	-1.8	0.008
1417129_a_at	myeloid ecotropic viral integration site-related gene 1	Mrg1	-1	0.993	-2.15	0.001	-1.72	0.013	-1.72	0.003	-1.8	0.002

1435463_s_at	myosin ID	Myo1d	-1.18	0.000	-2.15	0.003	-1.29	0.000	-1.26	0.004	-1.31	0.014
1452056_s_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	-1.21	0.023	-2.15	0.008	-1.25	0.127	-1.46	0.006	-1.37	0.001
1415905_at	regenerating islet-derived 1	Reg1	-1.86	0.054	-2.15	0.031	-1.01	0.960	2.41	0.504	1.24	0.382
1434407_at	SLIT-ROBO Rho GTPase activating protein 2	Srgap2	-1	0.667	-2.15	0.050	-1.44	0.052	-1.22	0.192	-1.55	0.057
1449999_a_at	calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	-1.48	0.015	-2.16	0.018	-1.13	0.553	1	0.916	-1.3	0.076
1434290_at	glycosyltransferase-like domain containing 1	Gtdc1	-1.3	0.199	-2.16	0.048	-1.57	0.046	-1.58	0.107	-1.6	0.005
1440208_at	RAS-related C3 botulinum substrate 2	Rac2	-1.82	0.078	-2.16	0.022	1.01	0.645	1.65	0.477	1.01	0.627
1432291_at	RIKEN cDNA 0610033M10 gene	0610033M10Rik	-1.69	0.069	-2.17	0.012	-1.19	0.228	-1.04	0.596	-1.28	0.454
1428696_at	RIKEN cDNA 2310015N21 gene	2310015N21Rik	-1.2	0.056	-2.17	0.001	-1.14	0.075	-1.35	0.034	-1.45	0.021
1431525_at	RIKEN cDNA 9130002K18 gene	9130002K18Rik	-1.35	0.259	-2.17	0.031	1.97	0.963	1.73	0.050	-1.11	0.514
1452982_at	insulin-like growth factor I receptor	Igf1r	-1.05	0.553	-2.17	0.008	-1.54	0.002	-1.59	0.020	-1.84	0.022
1429796_at	kalirin, RhoGEF kinase	Kalrn	-1.29	0.066	-2.17	0.001	-1.4	0.047	-1.71	0.016	-1.54	0.003
1425449_at	phosphatidic acid phosphatase 2a	Ppap2a	1.11	0.936	-2.17	0.047	1.1	0.870	1.76	0.593	1.59	0.145
1418512_at	serine/threonine kinase 3 (Ste20, yeast homolog)	Stk3	-1.19	0.209	-2.17	0.011	-1.11	0.169	-1.28	0.015	-1.3	0.083
1456446_at	RIKEN cDNA 4930523C07 gene	4930523C07Rik	1.17	0.953	-2.18	0.043	-1.29	0.150	1.06	0.741	-1.86	0.084
1427231_at	roundabout homolog 1 (Drosophila)	Robo1	-1.33	0.075	-2.18	0.003	-1.25	0.068	-1.57	0.002	-1.37	0.018
1426435_at	transmembrane protein 135	Tmem135	1.05	0.836	-2.18	0.005	-1.16	0.031	-1.41	0.019	-1.92	0.001
1444514_at	RIKEN cDNA B930096F20 gene	B930096F20Rik	-2.16	0.021	-2.19	0.013	1.95	0.144	-1.49	0.028	2.05	0.284
1439188_at	cleavage and polyadenylation specific factor 6	Cpsf6	-2.2	0.009	-2.19	0.021	-1.05	0.575	-1.32	0.358	-1.57	0.186
1455732_at	RIKEN cDNA 1700025G04 gene	1700025G04Rik	-1.08	0.148	-2.2	0.012	-1.16	0.020	-1.3	0.045	-1.5	0.016
1432106_at	RIKEN cDNA 6530403M18 gene	6530403M18Rik	-2.21	0.014	-2.2	0.027	1.06	0.494	-1.03	0.626	2.01	0.162
1451154_a_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	-1.3	0.252	-2.2	0.047	-1.19	0.037	-1.3	0.003	-1.31	0.018
1444330_at	DNA segment, Chr 2, ERATO Doi 173, expressed	D2Ertd173e	-1.11	0.334	-2.2	0.045	1.07	0.827	2.13	0.596	1.95	0.285
1425782_at	phospholipase C, beta 1	Plcb1	-1.04	0.381	-2.2	0.030	1.54	0.891	1.48	0.449	1.78	0.285
1443924_at	WNK lysine deficient protein kinase 3	Wnk3	-1.21	0.252	-2.2	0.017	1.41	0.251	-1.33	0.042	-1	0.650
1425880_x_at	zinc finger protein 352	Zfp352	-2.99	0.011	-2.2	0.018	-1.35	0.322	1.44	0.564	2.24	0.915
1447083_at	RIKEN cDNA 4933407I05 gene	4933407I05Rik	-1.36	0.014	-2.21	0.006	1.34	0.895	1.86	0.223	1.59	0.448
1429205_at	myeloid/lymphoid or mixed lineage-leukemia translocation to	Mllt3	1.05	0.838	-2.21	0.043	1.09	0.767	-1.77	0.016	-1.1	0.497
1428509_at	myosin IE	Myo1e	1.14	0.661	-2.21	0.027	-1.76	0.006	-2.05	0.009	-2.04	0.005
1418749_at	pleckstrin and Sec7 domain containing 3	Psd3	-1.11	0.309	-2.21	0.043	-1.5	0.008	-1.4	0.051	-1.81	0.001
1448765_at	Fyn proto-oncogene	Fyn	-1.15	0.180	-2.22	0.004	-1.66	0.007	-1.92	0.000	-2.1	0.002
1436889_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha	Gabra1	-1.75	0.191	-2.22	0.037	-2.87	0.048	-1.87	0.133	-1.38	0.208
1444786_at	nucleolar protein 3 (apoptosis repressor with CARD domain)	Nol3	-1.28	0.494	-2.22	0.039	1.98	0.260	1.75	0.088	-1.02	0.882
1442443_at	Retinoblastoma binding protein 4	Rbbp4	1.92	0.264	-2.22	0.049	2.43	0.035	-1.11	0.596	1.32	0.788
1425162_at	RAR-related orphan receptor beta	Rorb	1.1	0.972	-2.22	0.018	-1.35	0.280	1.01	0.840	1.86	0.025
1431501_at	RIKEN cDNA 1700037C18 gene	1700037C18Rik	-1.6	0.000	-2.23	0.045	1.16	0.631	2.54	0.455	1.53	0.183
1436827_at	gene model 944, (NCBI)	Gm944	-1.06	0.498	-2.23	0.038	-1.31	0.053	-1.13	0.320	-1.6	0.007
1425252_a_at	mitotic arrest deficient 1-like 1	Mad1l1	1.48	0.971	-2.23	0.048	-1.28	0.088	-1.28	0.202	-1.75	0.011
1451443_at	nuclear factor I/X	Nfix	-2.21	0.022	-2.23	0.006	1.17	0.766	-1.83	0.149	1.28	0.414
1456829_at	paraneoplastic antigen MA3	Pnma3	-1.18	0.494	-2.23	0.011	1.69	0.666	-1.19	0.473	1.08	0.370
1440939_at	Septin 6	6-Sep	-2.03	0.084	-2.24	0.036	-1.14	0.423	-1.06	0.563	-1.37	0.188
1431949_at	RIKEN cDNA 4930544F09 gene	4930544F09Rik	-1.33	0.276	-2.25	0.004	1.86	0.775	2	0.522	1.7	0.467
1420210_at	Expressed sequence AV344025	AV344025	1.13	0.836	-2.25	0.021	1.83	0.690	-1.01	0.805	1.59	0.840
1458177_at	emopamil binding protein-like	Ebpl	-2.14	0.057	-2.25	0.019	-2.9	0.009	1.43	0.784	-1.09	0.660
1436302_at	RIKEN cDNA 2410193C02 gene	2410193C02Rik	-1.12	0.236	-2.26	0.003	-1.46	0.015	-1.52	0.001	-1.72	0.010
1456837_at	RIKEN cDNA A830007L07 gene	A830007L07Rik	1.06	0.479	-2.27	0.045	1.55	0.564	-2.69	0.121	1.74	0.715
1459433_at	RIKEN cDNA C130051F05 gene	C130051F05Rik	-1.28	0.408	-2.27	0.030	-1.75	0.086	-1.74	0.170	-1.9	0.182
1437699_at	RIKEN cDNA E430014B02 gene	E430014B02Rik	-1.3	0.059	-2.27	0.014	1.1	0.975	-1.1	0.454	1.78	0.146
1433885_at	IQ motif containing GTPase activating protein 2	Iqgap2	1.16	0.526	-2.27	0.038	-1.47	0.056	-1.07	0.420	1.03	0.902
1431921_a_at	stromal antigen 1	Stag1	-1.04	0.436	-2.27	0.016	-1.58	0.002	-1.59	0.002	-2.21	0.003
1434571_at	vacuolar protein sorting 13B (yeast) /// similar to vacuolar pro	Vps13b /// LOC66	-1.03	0.556	-2.27	0.040	-1.87	0.009	-2.07	0.001	-2.24	0.019
1427337_at	aldehyde dehydrogenase 8 family, member A1	Aldh8a1	-1.78	0.126	-2.28	0.038	2.01	0.080	1.49	0.153	-1.64	0.139
1431354_a_at	phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	1.04	0.699	-2.29	0.027	-1.51	0.022	-1.48	0.030	-2.01	0.002
1442364_at	Mitogen activated protein kinase 14	Mapk14	-1.02	0.950	-2.29	0.032	-1.12	0.410	1.91	0.694	1.51	0.840
1443884_at	thyroid adenoma associated	Thada	-1.03	0.742	-2.29	0.011	-1.37	0.134	-1.28	0.136	-1.33	0.114
1430434_at	transketolase-like 2	Tktl2	-1.03	0.876	-2.29	0.023	-1.09	0.700	1.34	0.768	1.44	0.949
1435028_at	WD repeat domain 7	Wdr7	-1.17	0.172	-2.29	0.008	-1.39	0.055	-1.49	0.014	-1.68	0.007
1429273_at	BMP-binding endothelial regulator	Bmper	-1.36	0.087	-2.3	0.047	-1.13	0.124	-1.14	0.297	-1.49	0.038

1435269_at	RIKEN cDNA 2510005D08 gene	2510005D08Rik	1.28	0.826	-2.31	0.028	-2.17	0.072	1.03	0.978	1.58	0.909
1431696_at	RIKEN cDNA 4632413K17 gene	4632413K17Rik	-1.75	0.100	-2.31	0.019	1.03	0.614	1.59	0.812	1.84	0.817
1438694_at	casein alpha s2-like A	Csn1s2a	-1.2	0.524	-2.31	0.030	1.34	0.601	-1.37	0.280	-1.14	0.448
1428303_at	RIKEN cDNA 1500005I02 gene	1500005I02Rik	-1.53	0.160	-2.32	0.029	2.23	0.218	-1.19	0.352	1.61	0.375
1426096_at	protein arginine N-methyltransferase 7	Prmt7	-1.89	0.096	-2.32	0.008	1.62	0.477	1.4	0.598	-1.17	0.255
1429197_s_at	RAB GTPase activating protein 1-like	Rabgap1l	-1.8	0.008	-2.32	0.006	-1.41	0.160	-1.5	0.005	-1.61	0.052
1425388_a_at	thiamine pyrophosphokinase	Tpk1	-1.26	0.057	-2.32	0.003	-1.05	0.558	-1.38	0.032	-1.32	0.042
1444035_at	mesoderm development candiate 2	Mesdc2	-1.05	0.648	-2.33	0.047	1.37	0.615	2.11	0.494	1.49	0.704
1431888_s_at	pregnancy-specific glycoprotein 21	Psg21	-1.76	0.073	-2.33	0.018	1.47	0.441	2.65	0.091	-1.15	0.340
1433118_at	RIKEN cDNA 2300004M11 gene	2300004M11Rik	-1.33	0.411	-2.34	0.022	2.33	0.339	1.84	0.271	2.38	0.098
1437429_at	RIKEN cDNA 5930437A14 gene	5930437A14Rik	-1.08	0.419	-2.34	0.004	-1.18	0.174	-1.1	0.536	-1.46	0.018
1420778_at	taste receptor, type 1, member 3	Tas1r3	-2.55	0.041	-2.34	0.045	-1.33	0.398	-1.53	0.323	1.52	0.875
1420080_a_at	glutamine fructose-6-phosphate transaminase 1	Gfpt1	1.03	0.954	-2.35	0.001	1.53	0.440	-1.07	0.598	-1.48	0.018
1435349_at	neuropilin 2	Nrp2	-1.16	0.184	-2.35	0.024	-1.34	0.119	-1.45	0.010	-1.58	0.001
1436907_at	neuron navigator 1	Nav1	-1.15	0.110	-2.36	0.006	-1.37	0.019	-1.58	0.000	-1.81	0.002
1425606_at	solute carrier family 5 (iodide transporter), member 8	Slc5a8	-1.43	0.146	-2.36	0.006	1.47	0.407	1.18	0.602	1.04	0.669
1432484_at	RIKEN cDNA 2310061C15 gene	2310061C15Rik	-1.46	0.146	-2.37	0.038	1.19	0.673	1.57	0.039	2.08	0.449
1431631_at	RIKEN cDNA 2900057B20 gene	2900057B20Rik	-1.7	0.158	-2.37	0.045	1.13	0.841	-1.1	0.384	-2.08	0.097
1454332_at	RIKEN cDNA 6030442H21 gene	6030442H21Rik	-1.14	0.658	-2.37	0.047	1.08	0.872	1.57	0.854	1.47	0.885
1443574_at	hypothetical protein 6530439I21	6530439I21	-1.59	0.153	-2.37	0.011	-1.02	0.528	-1.4	0.247	1.56	0.891
1433939_at	hypothetical protein A730046J16	A730046J16	-1.3	0.090	-2.39	0.020	-1.19	0.151	-1.53	0.014	-1.72	0.005
1420589_at	hyaluronan synthase 3	Has3	-1.71	0.201	-2.39	0.007	-1.42	0.121	1	0.684	1.16	0.359
1450945_at	protein kinase C, alpha	Prkca	1.16	0.926	-2.39	0.042	-2.09	0.001	-2.13	0.001	-2.58	0.005
1441964_at	RIKEN cDNA 1110003F05 gene	1110003F05Rik	1.23	0.566	-2.4	0.002	1.82	0.568	-1.5	0.166	-1.48	0.116
1437558_at	RIKEN cDNA B130021B11 gene	B130021B11Rik	1.1	0.468	-2.41	0.017	-1.48	0.070	-1.5	0.080	-1.75	0.017
1441256_at	Wdr45 like	Wdr45l	-1.25	0.411	-2.41	0.018	-1.41	0.280	-1.84	0.122	1.02	0.906
1450536_s_at	keratin associated protein 12-1	Krtap12-1	-1.22	0.261	-2.42	0.005	1.06	0.743	-1.11	0.299	-1.31	0.301
1451054_at	orosomucoid 1	Orm1	-2.8	0.054	-2.42	0.008	1.41	0.341	-1.49	0.137	1.55	0.255
1426455_at	serologically defined colon cancer antigen 10	Sdccag10	-1.26	0.198	-2.42	0.018	-1.52	0.077	-1.58	0.034	-1.51	0.059
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	-1.38	0.031	-2.43	0.034	-1.39	0.004	-1.25	0.012	-1.34	0.049
1449900_at	galactosylceramidase	Galc	1.18	0.041	-2.43	0.009	-1.47	0.091	1.56	0.338	-1.05	0.537
1451382_at	ChaC, cation transport regulator-like 1 (E. coli)	Chac1	-1.22	0.007	-2.44	0.001	-1.18	0.052	-1.24	0.002	-1.32	0.001
1442998_at	Cytidine 5'-triphosphate synthase 2	Ctps2	1.03	0.830	-2.45	0.037	2.53	0.509	1.62	0.025	2.34	0.076
1428579_at	formin-like 2	Fmnl2	1.26	0.449	-2.45	0.034	-1.45	0.031	-1.49	0.007	-1.81	0.018
1439618_at	phosphodiesterase 10A	Pde10a	-1.04	0.537	-2.45	0.032	-1.29	0.133	-1.68	0.068	-1.28	0.292
1445588_at	ankyrin repeat domain 44	Ankrd44	1.08	0.757	-2.46	0.018	-1.54	0.181	1.68	0.938	2.75	0.068
1426546_at	testis-specific kinase 2	Tesk2	-1.22	0.228	-2.46	0.000	-1.05	0.513	1	0.856	-1.03	0.725
1450063_at	formin 2	Fmn2	-1.57	0.024	-2.47	0.003	-1.77	0.006	-1.48	0.012	-1.74	0.007
1435234_at	nuclear receptor coactivator 2	Ncoa2	-1.13	0.235	-2.47	0.031	1.01	0.584	-1.73	0.014	-1.55	0.122
1460340_at	piwi-like homolog 1 (Drosophila)	Piwil1	-1.48	0.191	-2.47	0.042	-1.18	0.229	1	0.770	1	0.735
1443127_at	RIKEN cDNA 9630021D06 gene	9630021D06Rik	-1.26	0.290	-2.48	0.047	-1.35	0.237	-1.59	0.075	1.58	0.153
1454043_a_at	potassium voltage-gated channel, shaker-related subfamily, b	Kcnab1	-1.46	0.292	-2.48	0.033	-1.53	0.171	-1.05	0.541	-1.69	0.143
1457682_at	RIKEN cDNA 9030420J04 gene	9030420J04Rik	-1.07	0.466	-2.49	0.032	-1.49	0.127	-1.76	0.032	-1.55	0.064
1455962_at	hedgehog acyltransferase	Hhat	-1.07	0.379	-2.5	0.005	1.1	0.752	-1.41	0.059	-1.33	0.104
1437542_at	RIKEN cDNA A730095J18 gene	A730095J18Rik	-1.01	0.715	-2.51	0.023	-1.08	0.350	-1.52	0.008	-1.51	0.043
1421752_a_at	serine (or cysteine) peptidase inhibitor, clade B, member 5	Serpinb5	-1.65	0.003	-2.52	0.004	1.76	0.862	2.43	0.761	1	0.732
1452222_at	utrophin	Utrn	-1.22	0.149	-2.52	0.017	-1.94	0.006	-1.74	0.003	-2.28	0.007
1443896_at	TBC1 domain family, member 5	Tbc1d5	-1.07	0.568	-2.53	0.002	-1.67	0.015	-1.32	0.087	-1.8	0.003
1437556_at	zinc finger homeodomain 4	Zfhx4	1.16	0.224	-2.53	0.001	-1.04	0.694	-1.44	0.010	-1.57	0.007
1456636_at	RIKEN cDNA 4930414L22 gene	4930414L22Rik	-2.33	0.055	-2.54	0.044	1.03	0.623	1.48	0.804	1.17	0.653
1439333_at	potassium channel, subfamily V, member 1	Kcnv1	-2.68	0.007	-2.55	0.014	1.56	0.926	2.87	0.001	1.21	0.921
1419249_at	PFTAIRE protein kinase 1	Pftk1	1.03	0.439	-2.55	0.043	-1.68	0.003	-1.76	0.007	-2.17	0.015
1459056_at	RAS protein-specific guanine nucleotide-releasing factor 1	Rasgrf1	-1.29	0.201	-2.55	0.013	2.22	0.175	-1.58	0.152	1.02	0.896
1426147_s_at	claudin 10	Cldn10	-2.09	0.017	-2.56	0.008	1.36	0.863	-1.32	0.279	1.11	0.898
1456069_at	dystrobrevin alpha	Dtna	-1.02	0.741	-2.56	0.003	-1.07	0.487	-1.36	0.185	-1.58	0.123
1419724_at	ectodysplasin-A receptor /// similar to Tumor necrosis factor r	Edar /// LOC6690	-3.33	0.021	-2.56	0.045	1.54	0.985	2.9	0.360	-1.47	0.251
1424092_at	erythrocyte protein band 4.1	Epb4.1	-1.05	0.771	-2.56	0.003	-1.45	0.115	-1.05	0.441	-1.35	0.124
1438666_at	low density lipoprotein receptor class A domain containing 3	Ldlrad3	-1.09	0.260	-2.56	0.005	-1.18	0.421	-1.59	0.007	-1.84	0.013

1451236_at	RAS-like, estrogen-regulated, growth-inhibitor	Rerg	1.06	0.977	-2.56	0.017	-1.41	0.126	-1.96	0.008	-1.55	0.087
1429271_at	RIKEN cDNA 9130011E15 gene	9130011E15Rik	-1.08	0.727	-2.57	0.004	-1.29	0.205	-1.83	0.113	-1.19	0.403
1430921_at	RIKEN cDNA 9130015G15 gene	9130015G15Rik	-1.71	0.129	-2.59	0.035	-2.76	0.053	1.33	0.762	1.04	0.475
1456715_at	Pam, highwire, rpm 1	Phr1	1.36	0.291	-2.59	0.022	1.05	0.603	-1.61	0.028	-1.47	0.302
1429995_at	RIKEN cDNA 1700036D21 gene	1700036D21Rik	-2.28	0.071	-2.61	0.008	1.5	0.579	1.08	0.644	1.89	0.425
1424586_at	EH domain binding protein 1	Ehbp1	-1.19	0.028	-2.61	0.004	-1.37	0.008	-1.44	0.014	-1.71	0.031
1434179_at	myeloid/lymphoid or mixed-lineage leukemia 3	Mll3	-1.06	0.375	-2.61	0.014	-1.32	0.046	-1.36	0.017	-1.88	0.009
1449520_at	tetratricopeptide repeat domain 28	Ttc28	-1.28	0.065	-2.61	0.020	-1.74	0.010	-1.92	0.002	-2.11	0.036
1436764_at	par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	1.33	0.473	-2.62	0.028	-1.75	0.004	-1.7	0.000	-1.97	0.074
1449815_a_at	single-stranded DNA binding protein 2	Ssbp2	-1.2	0.017	-2.62	0.010	-1.42	0.033	-1.2	0.086	-1.4	0.001
1436031_at	cache domain containing 1	Cachd1	-1.26	0.126	-2.63	0.036	-1.18	0.118	-1.13	0.307	-1.37	0.035
1436047_at	gene model 672, (NCBI)	Gm672	-1.12	0.226	-2.63	0.015	-1.69	0.000	-2.21	0.001	-2.44	0.000
1455179_at	membrane protein, palmitoylated 7 (MAGUK p55 subfamily m	Mpp7	1.18	0.815	-2.63	0.004	-1.12	0.402	-1.29	0.110	-1.41	0.010
1449876_at	protein kinase, cGMP-dependent, type I	Prkg1	-1.69	0.071	-2.63	0.025	-1.89	0.006	-1.42	0.085	-1.45	0.112
1439564_at	RIKEN cDNA 1700090G07 gene	1700090G07Rik	-2.45	0.018	-2.64	0.036	-1.31	0.417	1.54	0.993	-1.17	0.526
1423147_at	methionine adenosyltransferase I, alpha	Mat1a	-1.19	0.475	-2.64	0.010	-1.1	0.592	-1.01	0.818	1.09	0.908
1444020_at	chondroitin sulfate proteoglycan 3	Cspg3	-1.99	0.073	-2.65	0.034	1.47	0.401	1.2	0.456	1.31	0.943
1419811_at	DNA segment, Chr 16, Wayne State University 65, expresse	D16Wsu65e	-1.22	0.313	-2.65	0.018	-1.06	0.708	1.06	0.474	1.51	0.369
1455879_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast	Gcn1l1	-1.34	0.445	-2.65	0.019	-1.13	0.486	1.88	0.423	3.17	0.729
1451764_at	MARVEL (membrane-associating) domain containing 3	Marveld3	-1.37	0.086	-2.65	0.003	2.16	0.040	1.11	0.861	1.76	0.085
1428900_s_at	methyltransferase 5 domain containing 1	Mett5d1	-1.36	0.125	-2.65	0.017	-1.2	0.142	-1.25	0.087	-1.26	0.049
1423953_at	CDK5 regulatory subunit associated protein 1-like 1	Cdkal1	-1.2	0.092	-2.66	0.005	-1.95	0.005	-1.74	0.017	-2.14	0.019
1422944_a_at	diaphanous homolog 3 (Drosophila)	Diap3	-1.46	0.136	-2.67	0.017	-1.86	0.010	-1.51	0.109	-1.53	0.041
1451279_at	ELKS/RAB6-interacting/CAST family member 1	Erc1	-1.21	0.161	-2.67	0.006	-1.54	0.012	-1.96	0.011	-2.03	0.004
1433638_s_at	homeo box D8	Hoxd8	-2.3	0.051	-2.67	0.007	1.41	0.483	-2.05	0.051	1.29	0.060
1435879_at	thymoma viral proto-oncogene 3	Akt3	-1.12	0.272	-2.7	0.030	-1.51	0.004	-1.37	0.010	-1.65	0.005
1444085_at	prenyl (solanesyl) diphosphate synthase, subunit 2	Pdss2	-1.39	0.111	-2.7	0.050	-1.5	0.038	-1.35	0.062	-1.18	0.171
1456495_s_at	oxysterol binding protein-like 6	Osbpl6	-1.22	0.036	-2.72	0.017	1.15	0.868	1.03	0.681	1.29	0.652
1422673_at	protein kinase C, mu	Prkcm	-1.38	0.174	-2.74	0.022	-1.27	0.036	-1.55	0.003	-1.53	0.045
1438149_at	Expressed sequence AI449441	AI449441	-1.41	0.269	-2.76	0.043	2.84	0.009	1.16	0.937	-1.25	0.493
1424358_at	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast	Ube2e2	-1.34	0.163	-2.76	0.034	-1.43	0.014	-1.63	0.000	-1.7	0.001
1439341_at	cDNA sequence AK220484	AK220484	-1.18	0.095	-2.77	0.003	1.15	0.007	-1.2	0.379	1.18	0.601
1452071_at	solute carrier family 4 (anion exchanger), member 4	Slc4a4	-1.49	0.187	-2.77	0.008	-1.31	0.104	-1.35	0.132	-1.28	0.055
1453331_at	RIKEN cDNA 1700013H16 gene	1700013H16Rik	-1.15	0.477	-2.78	0.039	2.02	0.725	1.08	0.694	2.1	0.608
1432243_a_at	RIKEN cDNA 4933433G15 gene	4933433G15Rik	-3.66	0.069	-2.78	0.003	1.04	0.618	2.05	0.480	-1.15	0.349
1445720_at	SAFB-like, transcription modulator	Sltm	-1.46	0.187	-2.78	0.030	1.22	0.761	2.96	0.148	1.04	0.967
1428643_at	mannoside acetylglucosaminyltransferase 5	Mgat5	-1.35	0.080	-2.8	0.007	-1.41	0.061	-1.57	0.005	-2.13	0.025
1452366_at	RIKEN cDNA 4732435N03 gene	4732435N03Rik	-1.29	0.286	-2.82	0.035	-1.64	0.017	-1.55	0.003	-1.94	0.000
1441277_s_at	protein tyrosine phosphatase, receptor type, K	Ptprk	-1.38	0.094	-2.82	0.009	1.03	0.833	-1.32	0.097	-1.33	0.329
1427484_at	echinoderm microtubule associated protein like 5	Eml5	-1.06	0.959	-2.83	0.007	1.36	0.100	-1.19	0.308	-1.01	0.205
1443738_at	Phosphatidylserine synthase 2	Ptdss2	-1.94	0.127	-2.83	0.025	2.76	0.225	-1.19	0.311	2.33	0.159
1440094_at	cDNA sequence BC030870	BC030870	-3.07	0.021	-2.84	0.018	1.96	0.528	2.1	0.698	-1.54	0.151
1459319_at	Polymerase (DNA directed), alpha 1	Pola1	-1.02	0.991	-2.84	0.020	1.35	0.632	-1.05	0.436	-1.53	0.251
1419300_at	FMS-like tyrosine kinase 1	Flt1	-1.01	0.942	-2.89	0.010	-1.83	0.031	-1.75	0.000	1.02	0.703
1458897_at	uronyl-2-sulfotransferase	Ust	-1.41	0.010	-2.9	0.007	-1.2	0.102	-1.41	0.087	-1.25	0.086
1436910_at	RAS protein activator like 2	Rasal2	1.04	0.327	-2.91	0.008	-1.78	0.017	-1.88	0.001	-1.98	0.002
1428603_at	glucocorticoid induced transcript 1	Glcci1	-1.22	0.234	-2.93	0.024	-1.02	0.658	-1.24	0.048	-1.33	0.121
1424625_a_at	DENN/MADD domain containing 1A	Dennd1a	-1.06	0.474	-2.94	0.002	-1.95	0.016	-2.58	0.012	-2.85	0.032
1438596_at	HECT domain containing 2	Hectd2	-1.74	0.193	-2.94	0.043	1.42	0.891	3.23	0.129	2.44	0.489
1432105_at	sirtuin 5	Sirt5	-1.26	0.407	-2.95	0.001	1.29	0.869	2.12	0.297	1.42	0.998
1434669_at	Ral GEF with PH domain and SH3 binding motif 1	Ralgps1	-1.03	0.654	-2.96	0.008	-1.05	0.660	-1.21	0.225	1.1	0.654
1427043_s_at	cytosolic ovarian carcinoma antigen 1	Cova1	-1.41	0.049	-2.99	0.005	-1.37	0.065	-1.69	0.008	-1.63	0.041
1440019_at	G protein-coupled receptor 22	Gpr22	-1.53	0.234	-2.99	0.004	1.16	0.848	1.78	0.206	-1.91	0.102
1428486_at	RIKEN cDNA 1700123L14 gene	1700123L14Rik	-2.26	0.081	-3.01	0.027	1.43	0.686	-1.4	0.184	1.06	0.992
1446757_at	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae)	Sugt1	-1.94	0.041	-3.01	0.011	-1.02	0.863	1.95	0.129	-1.29	0.294
1455979_at	AT rich interactive domain 1B (Swi1 like)	Arid1b	-1.36	0.229	-3.04	0.030	-1.49	0.017	-2.25	0.001	-2.03	0.009
1436294_at	ankyrin repeat domain 29	Ankrd29	-1.3	0.376	-3.06	0.010	-1.08	0.474	1.48	0.798	1.95	0.834
1437318_at	p21 (CDKN1A)-activated kinase 3	Pak3	-1.1	0.414	-3.06	0.036	-1.46	0.017	-1.68	0.009	-2.02	0.064

1440586_at	RIKEN cDNA B430203I24 gene	B430203I24Rik	-1.89	0.031	-3.07	0.041	-1.74	0.111	3.59	0.832	-2.05	0.137
1431243_at	RIKEN cDNA 1700120J03 gene	1700120J03Rik	1.18	0.150	-3.08	0.017	1.06	0.605	-1.18	0.409	-1.8	0.159
1459971_at	Potassium channel, subfamily T, member 2	Kcnt2	-3.31	0.007	-3.11	0.014	1.36	0.980	1.02	0.837	1.6	0.953
1429064_at	DIP2 disco-interacting protein 2 homolog C	Dip2c	-1.44	0.104	-3.12	0.032	-1.41	0.002	-1.55	0.004	-1.99	0.008
1459998_at	zinc finger protein 407	Zfp407	1.05	0.681	-3.13	0.001	-1.74	0.002	-2.18	0.004	-2.23	0.012
1427292_at	immunoglobulin lambda chain, variable 1	Igl-V1	-1.9	0.050	-3.15	0.016	1.08	0.664	2.86	0.435	2.85	0.005
1429987_at	RIKEN cDNA 9930013L23 gene	9930013L23Rik	-1.29	0.007	-3.17	0.004	-2.03	0.006	-1.74	0.000	-2.44	0.008
1440214_at	RIKEN cDNA A630001G21 gene	A630001G21Rik	-1.24	0.335	-3.17	0.008	1.55	0.934	1.77	0.683	1.34	0.939
1438730_at	cDNA sequence BC028801	BC028801	-1.18	0.257	-3.23	0.032	-1.51	0.152	-1.37	0.056	-1.66	0.040
1422541_at	protein tyrosine phosphatase, receptor type, M	Ptprm	-1.47	0.055	-3.24	0.022	-1.9	0.005	-1.86	0.004	-2.27	0.004
1424588_at	SLIT-ROBO Rho GTPase activating protein 3	Srgap3	-1.21	0.287	-3.26	0.022	-1.62	0.011	-1.92	0.002	-2.04	0.022
1435461_at	membrane associated guanylate kinase 3	Magi3	-1.16	0.207	-3.3	0.018	-1.37	0.020	-1.46	0.094	-1.68	0.004
1460508_at	mitochondrial ribosomal protein L1	Mrpl1	-1.29	0.282	-3.3	0.011	-1.93	0.035	1.91	0.083	-1.76	0.122
1439557_s_at	LIM domain binding 2	Ldb2	-1.68	0.129	-3.35	0.005	1.58	0.374	-1.26	0.321	1.55	0.603
1448443_at	serine (or cysteine) peptidase inhibitor 1	Serpini1	-2.09	0.001	-3.42	0.005	2.14	0.536	2.54	0.667	1.23	0.611
1434582_at	DNA segment, Chr 14, ERATO Doi 171, expressed	D14Ertd171e	-2.2	0.031	-3.44	0.041	-2.08	0.048	-1.68	0.048	-2.95	0.032
1457790_at	Ankyrin repeat and SOCS box-containing protein 3	Asb3	1.08	0.759	-3.48	0.023	-1.25	0.109	-1.87	0.024	1.11	0.627
1451804_a_at	leucine rich repeat containing 16	Lrrc16	1	0.759	-3.49	0.004	-1.37	0.018	-1.96	0.005	-1.71	0.014
1431682_at	RIKEN cDNA 4930594C11 gene	4930594C11Rik	-1.6	0.332	-3.55	0.031	2.21	0.977	-1.98	0.088	-1.04	0.622
1417318_at	deleted in bladder cancer 1 (human)	Dbc1	-1.37	0.141	-3.6	0.020	-1.99	0.004	-1.84	0.008	-2.43	0.006
1452761_a_at	RIKEN cDNA 8430436O14 gene	8430436O14Rik	-1.56	0.106	-3.62	0.026	-2.22	0.011	-1.72	0.001	-2.49	0.014
1440719_at	GLE1 RNA export mediator-like (yeast	Gle1l	-1.7	0.080	-3.65	0.003	-1.09	0.251	-1.23	0.265	-1.01	0.993
1447605_at	Zinc finger protein 457	Zfp457	-1.58	0.258	-3.68	0.039	-4.24	0.000	1.92	0.242	-1.21	0.525
1437201_at	leucine rich repeat containing 4C	Lrrc4c	-1.26	0.266	-3.7	0.014	-1.38	0.012	-1.53	0.005	-1.52	0.076
1455204_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-1.07	0.436	-3.71	0.010	-1.77	0.040	-2.02	0.012	-2.17	0.007
1435981_at	RIKEN cDNA E430014L09 gene	E430014L09Rik	-1.1	0.496	-3.72	0.001	-2.15	0.001	-3.24	0.000	-3.68	0.001
1443073_at	hypothetical protein LOC545681	LOC545681	1.18	0.948	-3.79	0.021	-1.3	0.218	1.47	0.205	1.69	0.992
1444168_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	-1.41	0.422	-3.86	0.040	2.37	0.231	1.22	0.881	-1.47	0.211
1434932_at	adenosine deaminase, RNA-specific, B1	Adarb1	1.56	0.599	-3.87	0.025	-2.05	0.044	-1.38	0.002	-1.34	0.323
1438473_at	ADP-ribosylation factor-like 15	Arl15	1.48	0.871	-3.88	0.021	-1.77	0.011	-1.64	0.059	-1.74	0.054
1429809_at	transme/ne and tetra/peptide repeat 2	Tmtc2	-1.71	0.039	-3.89	0.037	-1.84	0.000	-1.63	0.044	-2	0.061
1437393_at	expressed sequence AI875142	AI875142	-1.31	0.125	-3.91	0.004	-2.18	0.001	-2.12	0.006	-2.46	0.005
1450932_s_at	dedicator of cytokinesis 9	Dock9 /// LOC670	1.06	0.582	-3.95	0.010	-1.3	0.114	-1.47	0.005	-1.76	0.006
1438531_at	RIKEN cDNA A730054J21 gene	A730054J21Rik	-1.34	0.080	-3.96	0.006	-2.15	0.001	-2.14	0.003	-2.72	0.004
1436405_at	dedicator of cytokinesis 4	Dock4	-1.43	0.089	-3.97	0.026	-1.18	0.251	-1.83	0.053	-1.29	0.152
1458407_s_at	Expressed sequence AI429294	AI429294	-1.24	0.345	-4	0.046	-1.12	0.398	-1.99	0.067	-1.22	0.197
1453286_at	plexin A2	Plxna2	-1.08	0.544	-4.11	0.016	-1.17	0.129	-1.37	0.144	-1.65	0.002
1437667_a_at	BTB and CNC homology 2	Bach2	-1.18	0.294	-4.19	0.025	-2.06	0.006	-2.17	0.003	-2.31	0.063
1427564_at	diaphanous homolog 2 (Drosophila)	Diap2	-1.62	0.060	-4.29	0.032	-2.65	0.025	-1.57	0.072	-3.92	0.023
1431110_at	RIKEN cDNA 5430431D22 gene	5430431D22Rik	-1.28	0.197	-4.34	0.012	-1.93	0.004	-1.85	0.023	-1.89	0.015
1437312_at	bone morphogenetic protein receptor, type 1B	Bmpr1b	1.56	0.907	-4.36	0.038	-1.48	0.160	-2.17	0.001	-1.75	0.017
1429417_at	RIKEN cDNA 4833446K15 gene	4833446K15Rik	-1.34	0.062	-4.38	0.016	-1.62	0.080	-2.05	0.003	-2.67	0.001
1417435_at	like-glycosyltransferase	Large	-1.14	0.255	-4.38	0.003	-2.64	0.009	-2.16	0.002	-3.49	0.001
1434515_at	nuclear receptor coactivator 1	Ncoa1	-1.09	0.426	-4.38	0.008	-1.15	0.257	-1.61	0.057	-1.42	0.083
1452860_at	F-box and leucine-rich repeat protein 17	Fbxl17	-1.28	0.074	-4.57	0.011	-1.87	0.000	-2.24	0.002	-2.52	0.000
1442175_at	RIKEN cDNA C030027H14 gene	C030027H14Rik	-1.31	0.060	-4.62	0.014	-1.48	0.005	-1.6	0.022	-1.78	0.019
1436937_at	RNA binding motif, single stranded interacting protein	Rbms3	-1.53	0.158	-4.64	0.027	-2.33	0.002	-2	0.013	-2.53	0.015
1425819_at	zinc finger and BTB domain containing 7C	Zbtb7c	-1.61	0.120	-4.68	0.037	1.12	0.664	1.4	0.580	1.02	0.832
1430316_at	RIKEN cDNA 4930579E17 gene	4930579E17Rik	-1.23	0.145	-4.72	0.003	-1.17	0.251	-1.26	0.065	-1.93	0.001
1452342_at	amyloid beta (A4) precursor	Apbb2	-1.24	0.242	-4.81	0.045	-2.12	0.007	-2.59	0.000	-2.8	0.010
1452878_at	protein kinase C, epsilon	Prkce	-1.75	0.015	-5.11	0.011	-1.19	0.204	-1.78	0.034	-1.69	0.021
1438294_at	ataxin 1	Atxn1	1	0.863	-5.21	0.001	-2.99	0.004	-3.03	0.001	-3.85	0.010
1452050_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-2.14	0.028	-5.47	0.022	-1.24	0.338	-2.13	0.093	-3.12	0.002
1457239_at	Spleen tyrosine kinase	Syk	-1.88	0.022	-5.5	0.001	4.44	0.076	1.09	0.745	1.46	0.582
1436513_at	tetra/peptide repeat, ankyrin repeat coiled-coil 2	Tanc2	-1.2	0.128	-5.67	0.022	-1.44	0.082	-1.61	0.098	-2.06	0.005
1436515_at	RIKEN cDNA E030004N02 gene	E030004N02Rik	-1.01	0.682	-5.74	0.001	-1.46	0.218	-2.17	0.026	-2.54	0.032
1416301_a_at	early B-cell factor 1	Ebf1	-1.39	0.153	-5.85	0.015	-2.73	0.000	-2.68	0.008	-3.54	0.002
1456423_at	methyl-CpG binding domain protein 5	Mbd5	-1.34	0.162	-6.08	0.005	-2.29	0.026	-2.69	0.001	-2.88	0.005

1456220_at	F-box and leucine-rich repeat protein 7	Fbxl7	1	0.539	-6.34	0.021	-1.82	0.043	-2.23	0.000	-2.13	0.005
1434639_at	kelch repeat and BTB (POZ) domain containing 9	Kbtbd9	-1.15	0.176	-6.56	0.031	-1.84	0.006	-2.04	0.010	-1.98	0.107
1429063_s_at	kinesin family member 16B	Kif16b	-1.31	0.259	-6.74	0.022	-1.24	0.046	-1.72	0.000	-2.03	0.053
1449314_at	zinc finger protein, multitype 2	Zfpm2	-1.07	0.482	-8.16	0.005	-2.11	0.007	-2.19	0.002	-2.66	0.026
1453577_at	RIKEN cDNA 2610018I03 gene	2610018I03Rik	-1.16	0.248	-8.8	0.008	1.51	0.363	-1.19	0.395	-1.31	0.225
1438861_at	basonuclin 2	Bnc2	-1.43	0.148	-8.88	0.007	-2.42	0.029	-3.5	0.001	-4.02	0.002

Supplementary table 3. List of significant expression profiles of XPA cells irradiated with 0.6J/m2 of UV (gray color) as compared to non-irradiated XPA cotrols

code	Gene Title	Symbol	WT_0.6J/m2	p	WT_4J/m2	p	XPA_0.6J/m2	p	CSB_0.6J/m2	p	DKO_0.6J/m2	p
1447605_at	Zinc finger protein 457	Zfp457	-1.58	0.258	-3.68	0.039	-4.24	0.000	1.92	0.242	-1.21	0.525
1454097_at	zinc finger, CW type with PWWP domain 2	Zcwpw2	-1.08	0.546	-1.49	0.193	-4.05	0.040	-1.19	0.023	1.43	0.744
1450710_at	jumonji, AT rich interactive domain 2	Jarid2	2.48	0.625	-1.53	0.127	-3.92	0.029	-1.76	0.095	-1.63	0.155
1456224_x_at	cancer antigen 1	Cage1	1.89	0.167	1.71	0.197	-3.85	0.004	1.48	0.943	3.65	0.463
1446718_at	nuclear factor enhancer in B-cells inhibitor, beta	Nfkbib	1.09	0.870	1.03	0.728	-3.76	0.045	1.38	0.597	1.76	0.692
1445572_at	forkhead box Q1	Foxq1	1.01	0.368	-1.09	0.307	-3.51	0.043	2.18	0.612	-1.54	0.128
1454691_at	neurexin I	Nrxn1	-1.51	0.186	1.71	0.688	-3.49	0.004	-1.04	0.566	-1.38	0.184
1459759_s_at	RIKEN cDNA 1700065I17 gene	1700065I17Rik	1.6	0.022	1.25	0.750	-3.43	0.015	-1.16	0.387	-1.84	0.157
1458037_at	Neurocalcin delta	Ncald	-1.35	0.302	-1.59	0.070	-3.4	0.004	2.81	0.194	1.49	0.275
1429654_at	developmental pluripotency associated 2	Dppa2	1.85	0.518	2.56	0.359	-3.39	0.025	2.72	0.186	1.81	0.666
1433345_s_at	RIKEN cDNA 4930448K20 gene	4930448K20Rik	2.14	0.154	1.1	0.600	-3.26	0.024	-1.17	0.713	2.13	0.621
1443629_at	neuron navigator 1	Nav1	1.89	0.849	1.53	0.900	-3.25	0.022	-1.2	0.516	-2.02	0.104
1459230_at	RIKEN cDNA B430319G15 gene	D530025C14Rik	1.44	0.693	-1	0.590	-3.17	0.002	1.35	0.407	-1.31	0.302
1427645_a_at	interleukin 1 receptor accessory protein-like 2	Il1rapl2	1.33	0.781	2.95	0.372	-3.16	0.008	-1.5	0.229	2.77	0.399
1430249_at	RIKEN cDNA 4930473A02 gene	4930473A02Rik	-1.13	0.382	-1.06	0.556	-3.06	0.002	-1.47	0.229	-1.19	0.311
1426066_a_at	dystrobrevin alpha	Dtna	1.57	0.533	1.02	0.500	-3.04	0.003	-1.07	0.443	-1.41	0.282
1440148_at	G protein-coupled receptor 6	Gpr6	-1.21	0.380	-1.17	0.396	-3.04	0.019	1.81	0.200	-1.15	0.418
1430105_at	RIKEN cDNA 1700042O10 gene	1700042O10Rik	1.21	0.274	1.26	0.910	-3	0.002	-1.04	0.659	1.37	0.311
1443120_at	PDZ domain containing 4	Pdzd4	1.55	0.902	1.15	0.703	-3	0.002	2.32	0.652	-1.38	0.140
1438294_at	ataxin 1	Atxn1	1	0.863	-5.21	0.001	-2.99	0.004	-3.03	0.001	-3.85	0.010
1441826_x_at	Ubiquitin domain containing 1	Ubtd1	1.57	0.649	1.11	0.392	-2.96	0.010	2.47	0.008	1.94	0.261
1441215_at	TraB domain containing	Trabd	1.29	0.712	1.2	0.783	-2.93	0.009	1.94	0.043	1.42	0.855
1457224_at	RIKEN cDNA 4631422O05 gene	4631422O05Rik	1.08	0.679	1.44	0.711	-2.92	0.012	1.51	0.875	2.65	0.514
1458177_at	emopamil binding protein-like	Ebpl	-2.14	0.057	-2.25	0.019	-2.9	0.009	1.43	0.784	-1.09	0.660
1427444_at	ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	-1.12	0.504	1.81	0.939	-2.87	0.045	1.58	0.896	1.3	0.974
1436889_at	GABA-A receptor, subunit alpha 1	Gabra1	-1.75	0.191	-2.22	0.037	-2.87	0.048	-1.87	0.133	-1.38	0.208
1445318_at	Kelch-like 4 (Drosophila)	Klhl4	1.35	0.945	-1.15	0.358	-2.84	0.043	2.32	0.034	-1.52	0.186
1436602_x_at	calcium channel, voltage-dependent, N type, alpha 1B subunit	Cacna1b	1.82	0.732	-1.03	0.792	-2.82	0.048	-1.68	0.033	1.21	0.737
1423968_at	UDP glycosyltransferases 3 family, polypeptide A2	Ugt3a2	-1.32	0.501	-1.38	0.347	-2.82	0.033	1.41	0.913	1.06	0.860
1426876_at	RIKEN cDNA 4732466D17 gene	4732466D17Rik	2.16	0.174	1.46	0.147	-2.8	0.021	2.35	0.785	1.46	0.358
1450809_at	seminal vesicle antigen-like 2	Sval2	2.22	0.783	1.83	0.835	-2.8	0.028	2.6	0.382	2.04	0.435
1431544_at	RIKEN cDNA 4930524B17 gene	4930524B17Rik	-3.59	0.004	-1.41	0.128	-2.78	0.047	1.33	0.410	2.67	0.231
1446686_at	DnaJ (Hsp40) homolog, subfamily C, member 11	Dnajc11	-1.81	0.153	1.13	0.809	-2.78	0.021	-1.81	0.104	1.22	0.503
1421509_at	VPS10 domain receptor protein SORCS 1	Sorcs1	1.17	0.762	-1.5	0.226	-2.71	0.018	1.2	0.794	1.03	0.645
1420221_at	RIKEN cDNA 4930461P20 gene	4930461P20Rik	1.04	0.468	3.42	0.672	-2.69	0.030	1.31	0.701	1.18	0.623
1443183_at	HECT, UBA and WWE domain containing 1	Huwe1	2.61	0.155	1.18	0.492	-2.69	0.005	-1.44	0.141	1.64	0.546
1453835_at	RIKEN cDNA 4930505M18 gene	4930505M18Rik	-1.42	0.244	-1.32	0.299	-2.68	0.016	1.17	0.678	2.48	0.295
1441346_at	RIKEN cDNA 2810421E14 gene	2810421E14Rik	2.21	0.021	2.52	0.326	-2.66	0.026	2.34	0.039	1.12	0.632
1442019_at	RIKEN cDNA B230343A10 gene	B230343A10Rik	2.28	0.025	1.28	0.290	-2.66	0.046	-1.1	0.739	-1.96	0.038
1422913_at	protamine 3	Prm3	-1.01	0.903	1.53	0.040	-2.66	0.018	1.68	0.333	-1.15	0.230
1427564_at	diaphanous homolog 2 (Drosophila)	Diap2	-1.62	0.060	-4.29	0.032	-2.65	0.025	-1.57	0.072	-3.92	0.023
1446409_at	glycosyltransferase-like domain containing 1	Gtdc1	-1.16	0.632	1.03	0.861	-2.64	0.014	1.02	0.973	1.57	0.931
1458620_at	ubiquitin A-52 residue ribosomal protein fusion product 1	LOC332993	1.09	0.816	-1.37	0.405	-2.64	0.047	2.61	0.109	1.23	0.747
1427596_at	X (inactive)-specific transcript, antisense	Tsix	-1.34	0.049	1.48	0.760	-2.64	0.009	1.34	0.891	1.47	0.175
1422174_at	insulin promoter factor 1, homeodomain transcription factor	Ipf1	-1.27	0.394	1.13	0.495	-2.63	0.033	1.11	0.749	2.11	0.351
1459328_at	RIKEN cDNA 4930429A22 gene	4930429A22Rik	2.34	0.170	-1.2	0.401	-2.62	0.036	-1.14	0.477	-1.62	0.197
1430914_at	RIKEN cDNA 5330426L24 gene	5330426L24Rik	-1.07	0.657	1.43	0.868	-2.62	0.032	-1.24	0.534	1.15	0.965
1460097_at	Glutamate receptor, ionotropic, AMPA4 (alpha 4)	Gria4	1.77	0.484	1.31	0.280	-2.62	0.043	1.42	0.673	1.15	0.801
1429343_at	RIKEN cDNA 1700012H05 gene	1700012H05Rik	1.51	0.587	1.33	0.441	-2.6	0.023	1.96	0.614	1.27	0.947
1427455_x_at	immunoglobulin kappa chain variable 8 (V8)-16	Igk-C /// Igk-V28 ///	-1.61	0.071	1.13	0.777	-2.6	0.001	1.45	0.710	-1.2	0.471
1445984_at	PFTAIRE protein kinase 1	Pftk1	1.7	0.228	2.44	0.540	-2.56	0.029	-1.86	0.033	2.49	0.956
1457699_at	RIKEN cDNA E330009J07 gene	E330009J07Rik	2.85	0.303	1.94	0.443	-2.55	0.037	1.23	0.378	2.21	0.632
1439847_s_at	Kruppel-like factor 12	Klf12	2.49	0.136	2.76	0.668	-2.55	0.015	-1.1	0.379	2.42	0.964

1421238_a_at	protein tyrosine phosphatase, receptor type, T	Ptprt	1.9	0.520	1.36	0.913	-2.52	0.002	1.11	0.529	1.61	0.249
1458777_at	solute carrier family 18 (vesicular monoamine), member 1	Slc18a1	-1.84	0.122	-1.6	0.110	-2.52	0.043	1.08	0.654	1.62	0.362
1450305_at	RIKEN cDNA 4930591A17 gene	4930591A17Rik	-1.27	0.330	-1.24	0.219	-2.5	0.001	1.58	0.302	1.65	0.989
1444505_at	retinoic acid induced 17	Rai17	1.74	0.739	1.51	0.872	-2.5	0.040	1.42	0.886	1.17	0.866
1432750_at	RIKEN cDNA 2810409C01 gene	2810409C01Rik	2.71	0.697	1.39	0.121	-2.47	0.021	1.22	0.714	-1.44	0.313
1432412_at	RIKEN cDNA 9530004P13 gene	9530004P13Rik	-1.43	0.230	1.74	0.642	-2.47	0.025	1.96	0.966	2.77	0.439
1429693_at	disabled homolog 2 (Drosophila)	Dab2	1.94	0.280	3.16	0.295	-2.47	0.019	-1.25	0.315	1.25	0.689
1450823_at	OG9 homeobox gene	Og9x	-1.43	0.459	1.07	0.596	-2.45	0.000	1.71	0.919	-2.07	0.022
1430840_at	RIKEN cDNA 4930449C09 gene	4930449C09Rik	-1.07	0.271	-1.14	0.244	-2.43	0.023	2.25	0.330	1.09	0.216
1438861_at	basonuclin 2	Bnc2	-1.43	0.148	-8.88	0.007	-2.42	0.029	-3.5	0.001	-4.02	0.002
1432060_at	IQ motif containing with AAA domain	Iqca	1.14	0.325	-1.38	0.392	-2.42	0.031	1.16	0.894	1.96	0.604
1420445_at	solute carrier family 16_8	Slc16a8	2.14	0.981	1.03	0.448	-2.41	0.018	-1.24	0.347	-2.02	0.136
1440410_at	RIKEN cDNA A930011G23 gene	A930011G23Rik	2.39	0.207	2.59	0.159	-2.4	0.036	2.21	0.364	1.42	0.321
1422361_at	T lymphoma oncogene	Tlm	1.33	0.147	1.26	0.419	-2.39	0.018	1.1	0.924	1.64	0.790
1454325_at	RIKEN cDNA 4930487N04 gene	4930487N04Rik	-1.7	0.137	-1.43	0.056	-2.38	0.035	1.39	0.743	2.79	0.123
1433275_at	RIKEN cDNA 4933401B01 gene	4933401B01Rik	1.92	0.338	2.19	0.680	-2.38	0.038	1.41	0.888	1.54	0.764
1456560_at	gene model 93, (NCBI)	Gm93	1.83	0.516	2.07	0.474	-2.38	0.035	-2.01	0.032	3.14	0.379
1458396_at	purinergic receptor P2X, ligand-gated ion channel, 3	P2rx3	1.33	0.590	1.2	0.568	-2.38	0.006	1.27	0.548	1.33	0.481
1417730_at	exostoses (multiple) 1	Ext1	1.33	0.686	-1.75	0.098	-2.36	0.002	-2.41	0.001	-2.41	0.013
1453959_at	RIKEN cDNA 1700065O13 gene	1700065O13Rik	-1.79	0.194	1.45	0.897	-2.35	0.047	2.68	0.462	1.2	0.530
1427793_at	hypothetical protein, P4(21)n gene	AJ242955	1.73	0.716	1.05	0.679	-2.35	0.049	-1.27	0.349	-1.08	0.249
1425168_at	G protein, gamma transducing activity polypeptide 1	Gngt1	1.8	0.666	-1.08	0.647	-2.34	0.026	2.73	0.608	1.35	0.815
1459705_at	Olfactomedin 3	Olfm3	1.34	0.658	1.08	0.674	-2.34	0.030	1.46	0.812	1.21	0.915
1454000_s_at	RIKEN cDNA 4930578N16 gene	4930578N16Rik	1.94	0.803	1.01	0.474	-2.33	0.042	1.54	0.822	1.24	0.505
1446258_at	Syntrophin, basic 1	Sntb1	1.37	0.770	1.92	0.694	-2.32	0.020	1.63	0.272	1.22	0.290
1432762_at	RIKEN cDNA 9530025H10 gene	9530025H10Rik	-1.15	0.494	-1.84	0.132	-2.31	0.024	-1.12	0.666	2.31	0.719
1422384_at	olfactory receptor 1509	Olfr1509	1.81	0.294	1.83	0.578	-2.31	0.042	1.14	0.971	1.08	0.755
1438541_at	RIKEN cDNA 4933439F18 gene	4933439F18Rik	1.95	0.248	2.67	0.230	-2.3	0.008	1.74	0.049	3.69	0.227
1441820_at	cyclin-dependent kinase-like 2 (CDC2-related kinase)	Cdkl2	2.63	0.326	1.23	0.159	-2.3	0.042	2.01	0.376	1.53	0.183
1440675_at	Glucocorticoid receptor DNA binding factor 1	Grlf1	1.14	0.035	1.18	0.378	-2.3	0.008	-1.28	0.342	-1.11	0.699
1430486_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	2.58	0.694	2.67	0.963	-2.3	0.027	1.19	0.928	1.48	0.052
1436938_at	RNA binding motif, single stranded interacting protein	Rbms3	-1.51	0.261	-4.05	0.115	-2.3	0.013	-1.97	0.023	-2.67	0.026
1456423_at	methyl-CpG binding domain protein 5	Mbd5	-1.34	0.162	-6.08	0.005	-2.29	0.026	-2.69	0.001	-2.88	0.005
1457376_at	Integrin alpha 4	Itga4	2.92	0.140	1.32	0.609	-2.28	0.043	1.51	0.131	1.9	0.126
1454906_at	retinoic acid receptor, beta	Rarb	1.75	0.392	1.15	0.433	-2.27	0.030	1.15	0.569	-1.1	0.565
1460015_at	spermatogenesis and oogenesis specific basic helix-loop-helix 1	Sohlh1	-1.62	0.104	1.4	0.595	-2.27	0.024	1.98	0.206	1.09	0.724
1433274_at	RIKEN cDNA 2610200G18 gene	2610200G18Rik	1.18	0.572	1	0.952	-2.26	0.042	1.23	0.569	1.12	0.783
1423278_at	protein tyrosine phosphatase, receptor type, K	Ptprk	-1.49	0.031	-2.67	0.015	-2.26	0.030	-2.01	0.007	-2.16	0.014
1430209_at	RIKEN cDNA 4930404H21 gene	4930404H21Rik	1.91	0.663	1.05	0.801	-2.25	0.024	-1.22	0.200	2.42	0.020
1442912_at	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isc	Hsd3b7	2.21	0.222	2.34	0.528	-2.24	0.017	2.26	0.886	-1.28	0.268
1444546_at	cDNA sequence BC027057	BC027057	-1.64	0.036	-1.1	0.709	-2.23	0.036	-1.03	0.717	1.63	0.149
1431587_at	coiled-coil domain containing 7	Ccdc7	1.07	0.641	1	0.588	-2.23	0.005	1.19	0.575	1.32	0.109
1428987_at	dynein light chain roadblock-type 2	Dynlrb2	1.41	0.625	1.47	0.854	-2.23	0.035	-1.62	0.042	-1.04	0.592
1454493_at	RIKEN cDNA 5033425B01 gene	5033425B01Rik	-1.43	0.244	1.15	0.291	-2.21	0.006	1.24	0.978	-1.09	0.538
1447388_at	RIKEN cDNA 5830484A20 gene	5830484A20Rik	2.08	0.054	2.71	0.067	-2.21	0.011	2.81	0.562	1.95	0.164
1427237_at	RIKEN cDNA 2410015M20 gene	2410015M20Rik	-1.01	0.459	1.89	0.998	-2.2	0.028	1.61	0.653	2.08	0.197
1443425_at	A disintegrin-like and metallopeptidase (reprolysin type) with thromb	Adamts6	1.5	0.475	1.26	0.971	-2.2	0.027	-1.35	0.094	-1.65	0.098
1457297_at	LysM, putative peptidoglycan-binding, domain containing 4	Lysmd4	1.75	0.370	1.26	0.795	-2.2	0.015	1.15	0.758	-1.34	0.096
1446788_at	RIKEN cDNA A430091L06 gene	A430091L06Rik	1.61	0.268	1.25	0.986	-2.19	0.030	1.1	0.939	1.05	0.708
1443983_at	Sorbin and SH3 domain containing 1	Sorbs1	-1.14	0.407	-1.44	0.380	-2.19	0.014	-2.22	0.050	-2.67	0.065
1453510_s_at	RIKEN cDNA 4930589M24 gene	4930589M24Rik	2.15	0.507	1.03	0.878	-2.18	0.041	2.41	0.492	-1.13	0.529
1452762_at	RIKEN cDNA 8430436O14 gene	8430436O14Rik	-1.6	0.141	-3.44	0.061	-2.18	0.007	-1.79	0.002	-2.17	0.036
1437393_at	expressed sequence AI875142	AI875142	-1.31	0.125	-3.91	0.004	-2.18	0.001	-2.12	0.006	-2.46	0.005
1425842_at	EGF-like repeats and discoidin I-like domains 3	Edil3	1.64	0.505	1.2	0.201	-2.18	0.020	-1.04	0.689	-1.07	0.475
1446104_at	SLIT-ROBO Rho GTPase activating protein 3	Srgap3	1.05	0.730	2.09	0.967	-2.18	0.049	-1.22	0.355	1.01	0.893
1441681_at	exportin, tRNA (nuclear export receptor for tRNAs)	Xpot	1.52	0.489	1.33	0.944	-2.18	0.008	1.46	0.411	-1.22	0.161
1431955_at	RIKEN cDNA 4930453H23 gene	4930453H23Rik	1.33	0.000	1.55	0.644	-2.16	0.008	-1.31	0.258	1.71	0.262
1453909_at	RIKEN cDNA 4930505N22 gene	4930505N22Rik	1.34	0.882	2.76	0.279	-2.16	0.037	1.12	0.481	-1.24	0.060

1450467_at	bassoon	Bsn	1.55	0.375	1.42	0.025	-2.16	0.005	1.29	0.650	1.22	0.747
1427268_at	filaggrin /// similar to Filaggrin /// similar to Filaggrin	Flg /// LOC620355	1.17	0.341	1.39	0.866	-2.16	0.031	1.38	0.624	2.91	0.089
1452783_at	fibronectin type III domain containing 3B	Fndc3b	1.16	0.796	-1.44	0.119	-2.16	0.005	-2.1	0.000	-2.71	0.002
1417347_at	PYD and CARD domain containing	Pycard	1.89	0.790	1.64	0.611	-2.16	0.017	1.08	0.738	1.97	0.624
1431029_at	tubulin tyrosine ligase like family 9	Ttll9	-1.41	0.367	-1.4	0.235	-2.16	0.008	1.36	0.795	1.97	0.467
1438531_at	RIKEN cDNA A730054J21 gene	A730054J21Rik	-1.34	0.080	-3.96	0.006	-2.15	0.001	-2.14	0.003	-2.72	0.004
1435981_at	RIKEN cDNA E430014L09 gene	E430014L09Rik	-1.1	0.496	-3.72	0.001	-2.15	0.001	-3.24	0.000	-3.68	0.001
1451948_at	gene model 1409, (NCBI)	Gm1409	-1.07	0.834	1.62	0.277	-2.15	0.038	1.12	0.734	1.6	0.748
1432625_at	RIKEN cDNA 5830487K18 gene	5830487K18Rik	-1.01	0.497	2.05	0.102	-2.14	0.023	1.56	0.391	1.73	0.228
1440469_at	hypothetical protein LOC629141	LOC629141	-1.05	0.288	1.99	0.838	-2.14	0.005	1.68	0.467	1.47	0.907
1435059_at	development and differentiation enhancing	Ddef1	1.19	0.970	-1.45	0.158	-2.13	0.001	-2.06	0.003	-2.64	0.001
1442483_at	Fucosyltransferase 8	Fut8	1.81	0.995	1.1	0.443	-2.13	0.001	-1.05	0.379	1.35	0.571
1452342_at	amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	-1.24	0.242	-4.81	0.045	-2.12	0.007	-2.59	0.000	-2.8	0.010
1447132_at	CDK5 regulatory subunit associated protein 1-like 1	Cdkal1	1.2	0.550	1.41	0.349	-2.11	0.050	1.35	0.339	-1.08	0.544
1445442_at	microtubule-associated protein 9	Mtap9	2.02	0.329	3.45	0.325	-2.11	0.002	1.21	0.778	1.16	0.719
1440506_at	Solute carrier family 7 (cationic amino acid transporter, y+ system), r	Slc7a2	1.01	0.712	2.75	0.360	-2.11	0.022	1.39	0.713	1.91	0.954
1440695_at	Zinc finger protein 40	Zfp40	1.56	0.764	1.96	0.549	-2.11	0.048	1.76	0.548	-1.48	0.222
1449314_at	zinc finger protein, multitype 2	Zfpm2	-1.07	0.482	-8.16	0.005	-2.11	0.007	-2.19	0.002	-2.66	0.026
1432991_at	RIKEN cDNA 4930519E07 gene	4930519E07Rik	-1.22	0.567	-1.11	0.384	-2.1	0.010	1.42	0.828	1.69	0.918
1432927_at	RIKEN cDNA 4921507K24 gene	4921507K24Rik	-1.57	0.138	1.54	0.935	-2.09	0.019	1.56	0.855	1.63	0.215
1426412_at	neurogenic differentiation 1	Neurod1	2.23	0.471	3.34	0.006	-2.09	0.004	1.26	0.839	-2.11	0.049
1450945_at	protein kinase C, alpha	Prkca	1.16	0.926	-2.39	0.042	-2.09	0.001	-2.13	0.001	-2.58	0.005
1447570_s_at	A kinase (PRKA) anchor protein 10	Akap10	-1.48	0.321	-1.7	0.355	-2.08	0.047	-1.17	0.367	1.56	0.914
1455416_at	Riken cDNA C130021I20 gene	C130021I20Rik	1.74	0.044	1.06	0.709	-2.08	0.017	1.51	0.407	1.54	0.168
1434582_at	DNA segment, Chr 14, ERATO Doi 171, expressed	D14Ertd171e	-2.2	0.031	-3.44	0.041	-2.08	0.048	-1.68	0.048	-2.95	0.032
1419528_at	sulfotransferase family 2A, dehydroepiandrosterone (DHEA)-preferri	Sult2a2	-1.25	0.165	1.71	0.273	-2.08	0.043	1.58	0.993	-1.91	0.099
1459399_at	Solute carrier family 31, member 2	Slc31a2	-1.02	0.430	-1.91	0.187	-2.07	0.014	-1	0.871	1.31	0.690
1441808_at	RIKEN cDNA 2410002I01 gene	2410002I01Rik	1.05	0.767	-1.06	0.549	-2.06	0.031	2.31	0.454	1.68	0.983
1436406_at	RIKEN cDNA A930007I19 gene	A930007I19Rik	1.4	0.759	1.16	0.586	-2.06	0.039	2.47	0.256	1.48	0.723
1424451_at	acetyl-Coenzyme A acyltransferase 1B	Acaa1b	-1.33	0.332	1.33	0.038	-2.06	0.024	1.07	0.807	1.92	0.641
1437667_a_at	BTB and CNC homology 2	Bach2	-1.18	0.294	-4.19	0.025	-2.06	0.006	-2.17	0.003	-2.31	0.063
1436261_at	Dysferlin	Dysf	1.19	0.972	1.12	0.732	-2.06	0.018	1.05	0.949	-1.08	0.646
1423713_at	ATP-binding cassette, sub-family B (MDR/TAP), member 8	Abcb8	1.98	0.581	1.02	0.488	-2.05	0.018	1.86	0.545	1.2	0.423
1434932_at	adenosine deaminase, RNA-specific, B1	Adarb1	1.56	0.599	-3.87	0.025	-2.05	0.044	-1.38	0.002	-1.34	0.323
1444317_at	protocadherin 15	Pcdh15	1.79	0.736	1.55	0.752	-2.05	0.040	2.49	0.391	1.1	0.893
1456718_at	transmembrane protein 56	Tmem56	2.03	0.460	1.98	0.246	-2.05	0.043	1.4	0.929	1.27	0.393
1429987_at	RIKEN cDNA 9930013L23 gene	9930013L23Rik	-1.29	0.007	-3.17	0.004	-2.03	0.006	-1.74	0.000	-2.44	0.008
1430168_at	CSA-conditional, T cell activation-dependent protein	Cstad	1.76	0.206	2.15	0.150	-2.03	0.016	1.36	0.933	1.35	0.871
1445534_at	Filamin, beta	Flnb	-1.11	0.277	-1.51	0.033	-2.03	0.045	-1.77	0.006	-2.31	0.001
1447359_at	zinc finger protein 575	Zfp575	-1.21	0.341	1.66	0.775	-2.02	0.040	1.68	0.356	1.15	0.743
1425335_at	CD8 antigen, alpha chain /// similar to T-cell surface glycoprotein CD	Cd8a /// LOC63614	-1.08	0.448	1.63	0.737	-2.01	0.042	1.27	0.605	2.81	0.248
1431891_at	zinc finger, SWIM domain containing 5	Zswim5	-1.04	0.630	1.03	0.911	-2.01	0.000	1.29	0.661	2.27	0.043
1458036_at	Expressed sequence C77576	C77576	1.37	0.517	1.6	0.940	-2	0.031	1.61	0.137	1.3	0.926
1450263_at	protocadherin beta 5	Pcdhb5	2.3	0.491	1.56	0.390	-2	0.013	1.17	0.809	-1.23	0.405
1445133_at	Transcription factor 12	Tcf12	1.55	0.912	3.67	0.767	-2	0.049	1.29	0.795	1.47	0.637
1433195_at	RIKEN cDNA 9530006O14 gene	9530006O14Rik	1.2	0.871	1.08	0.370	-1.99	0.035	-1.13	0.336	1.12	0.970
1426951_at	cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	-1.11	0.025	-2.12	0.000	-1.99	0.027	-1.7	0.004	-1.64	0.011
1417318_at	deleted in bladder cancer 1 (human)	Dbc1	-1.37	0.141	-3.6	0.020	-1.99	0.004	-1.84	0.008	-2.43	0.006
1423639_at	histamine receptor H 2	Hrh2	-2.43	0.026	-1.16	0.857	-1.99	0.047	-1.52	0.088	4.28	0.257
1447858_x_at	interleukin 4 receptor, alpha	Il4ra	-1.04	0.394	-1.17	0.390	-1.99	0.027	1.08	0.748	1.59	0.620
1446589_at	Rhomboid domain containing 1	Rhbdd1	1.42	0.916	-1.49	0.362	-1.99	0.027	2	0.132	1.42	0.943
1425928_at	X Kell blood group precursor related family member 6 homolog	Xkr6	1.42	0.656	2.26	0.155	-1.99	0.033	1.75	0.593	2.29	0.064
1444341_at	RIKEN cDNA 8030451F13 gene	8030451F13Rik	1.26	0.983	3.69	0.022	-1.98	0.033	1.22	0.611	1.22	0.990
1422050_at	NK1 transcription factor related, locus 2 (Drosophila)	Nkx1-2	1.67	0.132	2.05	0.220	-1.98	0.029	1.24	0.674	2.25	0.641
1446587_at	RIKEN cDNA 2310042E16 gene	2310042E16Rik	-1.54	0.276	-1.28	0.363	-1.97	0.013	1.81	0.578	1.02	0.957
1430517_at	RIKEN cDNA 4930544O15 gene	4930544O15Rik	1.01	0.908	1.84	0.261	-1.97	0.020	1.26	0.556	2.02	0.003
1425339_at	phospholipase C, beta 4	Plcb4	1.5	0.370	1.22	0.486	-1.97	0.000	-1.37	0.003	-1.54	0.178
1447545_at	DNA segment, Chr 7, ERATO Doi 193, expressed	D7Ertd193e	-1.27	0.268	1.5	0.264	-1.96	0.028	2.08	0.211	2.11	0.601

1427387_a_at	integrin beta 4	Itgb4	1.14	0.469	-1.37	0.254	-1.96	0.019	1.12	0.707	1	0.529
1444310_at	polymerase (RNA) III (DNA directed) polypeptide A	Polr3a	-1.14	0.502	-1.16	0.626	-1.96	0.048	2.45	0.294	1.39	0.913
1426391_at	ADP-ribosylation factor 1 /// similar to ADP-ribosylation factor 1	Arf1 /// LOC545267	1.26	0.677	2.18	0.188	-1.95	0.010	1.12	0.536	3.03	0.145
1424625_a_at	DENN/MADD domain containing 1A	Dennd1a	-1.06	0.474	-2.94	0.002	-1.95	0.016	-2.58	0.012	-2.85	0.032
1430495_at	inositol (myo)-1(or 4)-monophosphatase 1	Impa1	1.62	0.479	-1.17	0.346	-1.95	0.038	1.25	0.341	1.58	0.959
1425640_at	AF4/FMR2 family, member 1	Aff1	1.4	0.353	1.09	0.857	-1.94	0.038	-1.25	0.037	-1.41	0.109
1440990_at	cDNA sequence BC056349	BC056349	-1.84	0.199	-4.12	0.094	-1.94	0.002	-2.52	0.009	-2.07	0.013
1446428_at	RIKEN cDNA D530005L17 gene	D530005L17Rik	1.64	0.145	-2.34	0.108	-1.94	0.012	-1.83	0.215	1.6	0.478
1458327_x_at	solute carrier family 26 (sulfate transporter), member 1	Slc26a1	2.06	0.404	2.26	0.686	-1.94	0.028	-1.49	0.335	-1.43	0.376
1452222_at	utrophin	Utrn	-1.22	0.149	-2.52	0.017	-1.94	0.006	-1.74	0.003	-2.28	0.007
1431635_at	RIKEN cDNA 4930412F09 gene	4930412F09Rik	1.47	0.719	-1.01	0.828	-1.93	0.019	1.52	0.412	-1.01	0.813
1431110_at	RIKEN cDNA 5430431D22 gene	5430431D22Rik	-1.28	0.197	-4.34	0.012	-1.93	0.004	-1.85	0.023	-1.89	0.015
1449825_at	actin-related protein T1	Actrt1	2.03	0.315	2.18	0.761	-1.93	0.034	1.41	0.258	1.35	0.949
1422012_at	corticotropin releasing hormone receptor 2	Crhr2	-1.17	0.295	1.05	0.848	-1.93	0.007	-1.07	0.751	1.17	0.575
1460508_at	mitochondrial ribosomal protein L1	Mrpl1	-1.29	0.282	-3.3	0.011	-1.93	0.035	1.91	0.083	-1.76	0.122
1422760_at	peptidyl arginine deiminase, type IV /// similar to Protein-arginine dei	Padi4 /// LOC67054	2.3	0.486	3.53	0.085	-1.93	0.018	1.44	0.255	-1.3	0.335
1423269_a_at	neural precursor cell expressed, developmentally down-regulated ge	Nedd4l	1.26	0.879	-2.06	0.051	-1.92	0.005	-2.03	0.000	-2.21	0.003
1435432_at	centaurin, gamma 2	Centg2	-1.23	0.014	-2.53	0.001	-1.91	0.009	-1.57	0.005	-1.97	0.018
1437880_at	ladybird homeobox 1 homolog (Drosophila) corepressor 1	Lbxcor1	1.89	0.859	1.29	0.650	-1.91	0.009	-1.33	0.278	3.61	0.020
1450669_at	mitogen activated protein kinase kinase kinase 11	Map3k11	1.65	0.180	1.21	0.309	-1.91	0.041	1.17	0.197	1.5	0.513
1436005_at	splicing factor, arginine/serine-rich 14	Sfrs14	1.09	0.739	1.14	0.736	-1.91	0.026	1.02	0.443	1.16	0.879
1438975_x_at	zinc finger, DHHC domain containing 14	Zdhhc14	-1.61	0.294	-5.72	0.178	-1.91	0.032	-2.53	0.001	-2.16	0.055
1446506_at	hypothetical protein B930041G04	B930041G04	1.35	0.810	-1.4	0.256	-1.9	0.007	1.9	0.933	-1.01	0.958
1443269_at	RIKEN cDNA D130009B15 gene	D130009B15Rik	2	0.636	1.36	0.899	-1.9	0.011	-1.16	0.766	1.43	0.750
1440071_at	membrane associated guanylate kinase, WW and PDZ domain conta	Magi1	1.57	0.292	-1.34	0.336	-1.9	0.046	-1.2	0.607	1.65	0.776
1421413_a_at	PDZ and LIM domain 5 /// similar to PDZ and LIM domain protein 5 (	Pdlim5 /// LOC6696	12.26	0.588	7	0.464	-1.9	0.034	-1.56	0.045	-1.95	0.040
1422541_at	protein tyrosine phosphatase, receptor type, M	Ptprm	-1.47	0.055	-3.24	0.022	-1.9	0.005	-1.86	0.004	-2.27	0.004
1449876_at	protein kinase, cGMP-dependent, type I	Prkg1	-1.69	0.071	-2.63	0.025	-1.89	0.006	-1.42	0.085	-1.45	0.112
1454385_at	RIKEN cDNA 1700018P08 gene	1700018P08Rik	1.51	0.930	1.65	0.778	-1.88	0.043	2.49	0.349	-1.24	0.387
1455522_at	Rho guanine nucleotide exchange factor (GEF) 15	Arhgef15	1.15	0.688	-1.32	0.330	-1.88	0.026	2.3	0.290	1.66	0.658
1419563_at	baculoviral IAP repeat-containing 6	Birc6	-1.1	0.444	1.02	0.519	-1.88	0.025	-1.08	0.507	1.55	0.407
1437886_at	kelch-like 6 (Drosophila)	Klhl6	3.34	0.304	3.1	0.214	-1.88	0.047	-1.03	0.636	1.81	0.897
1453448_at	RIKEN cDNA 2310067E19 gene	2310067E19Rik	2.05	0.314	-1.48	0.221	-1.87	0.038	-1.21	0.196	1.4	0.844
1430977_at	RIKEN cDNA A930021C24 gene	A930021C24Rik	1.47	0.912	2.52	0.335	-1.87	0.005	1.91	0.484	1.95	0.060
1432507_at	RIKEN cDNA B430319H21 gene	B430319H21Rik	1.21	0.736	-1.62	0.034	-1.87	0.033	1.07	0.441	1.05	0.865
1452860_at	F-box and leucine-rich repeat protein 17	Fbxl17	-1.28	0.074	-4.57	0.011	-1.87	0.000	-2.24	0.002	-2.52	0.000
1422868_s_at	guanine deaminase	Gda	2.12	0.656	1.58	0.949	-1.87	0.006	1.59	0.087	-1.09	0.644
1434571_at	vacuolar protein sorting 13B (yeast) /// similar to vacuolar protein sor	Vps13b /// LOC666	-1.03	0.556	-2.27	0.040	-1.87	0.009	-2.07	0.001	-2.24	0.019
1447647_at	wingless-related MMTV integration site 7A	Wnt7a	-1.23	0.284	1.61	0.806	-1.87	0.016	1.07	0.739	1.01	0.847
1419832_s_at	acid phosphatase, prostate	Acpp	1.66	0.585	1.36	0.724	-1.86	0.017	1.72	0.768	2.23	0.158
1451628_a_at	ankyrin 3, epithelial	Ank3	1.05	0.758	-1.36	0.208	-1.86	0.004	-1.84	0.016	-1.36	0.128
1422944_a_at	diaphanous homolog 3 (Drosophila)	Diap3	-1.46	0.136	-2.67	0.017	-1.86	0.010	-1.51	0.109	-1.53	0.041
1430749_at	RIKEN cDNA 2810040C05 gene	2810040C05Rik	-1.73	0.152	-1.53	0.193	-1.85	0.039	-1.06	0.591	-1.66	0.097
1454462_at	RIKEN cDNA 6430605C03 gene	6430605C03Rik	-1.5	0.140	-1.43	0.192	-1.85	0.030	-1.3	0.172	-1.51	0.231
1457104_at	RIKEN cDNA D930036F22 gene	D930036F22Rik	1.18	0.791	1.02	0.794	-1.85	0.005	-1.29	0.017	-1.43	0.139
1458023_at	DNA segment, Chr X, ERATO Doi 697, expressed	DXErtd697e	-1.66	0.157	-1.28	0.238	-1.85	0.017	1.11	0.211	-1.14	0.087
1450781_at	high mobility group AT-hook 2	Hmga2	1.1	0.952	-1.72	0.056	-1.85	0.000	-1.66	0.007	-1.99	0.003
1420542_at	open reading frame 28	ORF28	1.59	0.726	1.01	0.509	-1.85	0.029	1.57	0.327	1.76	0.193
1445025_at	expressed sequence AU015536	AU015536	2.16	0.386	2.65	0.173	-1.84	0.025	1.3	0.501	-1.28	0.396
1426463_at	gephyrin	Gphn	-1.17	0.284	-4.1	0.010	-1.84	0.001	-1.79	0.007	-1.9	0.012
1434639_at	kelch repeat and BTB (POZ) domain containing 9	Kbtbd9	-1.15	0.176	-6.56	0.031	-1.84	0.006	-2.04	0.010	-1.98	0.107
1457732_at	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain co	Pcmtd2	1.44	0.100	1.79	0.171	-1.84	0.011	-1.03	0.590	1.47	0.276
1459603_at	RIKEN cDNA C330008K14 gene	C330008K14Rik	-2.71	0.051	-1.18	0.349	-1.83	0.041	-1.28	0.184	-1.11	0.386
1442617_at	Core binding factor beta	Cbfb	1.05	0.699	-1.32	0.257	-1.83	0.001	2.13	0.471	1.31	0.299
1436380_at	Cdc42 binding protein kinase alpha	Cdc42bpa	1.13	0.236	-1.53	0.039	-1.83	0.021	-1.74	0.005	-1.62	0.026
1421449_at	CUB and Sushi multiple domains 1	Csmd1	1.32	0.663	1.26	0.656	-1.83	0.032	1.15	0.613	1.06	0.720
1436356_at	lectin, galactose binding, soluble 7	Lgals7	1.06	0.633	-1.74	0.003	-1.83	0.004	-1.72	0.001	-2.08	0.013
1438217_at	ataxin 2 binding protein 1	A2bp1	3.34	0.692	-1.61	0.076	-1.82	0.041	-1.43	0.015	-2.11	0.011

1456220_at	F-box and leucine-rich repeat protein 7	Fbxl7	1	0.539	-6.34	0.021	-1.82	0.043	-2.23	0.000	-2.13	0.005
1442305_at	GTP binding protein 2	Gtpbp2	-1.3	0.252	-1.6	0.068	-1.82	0.025	-1.14	0.324	1.25	0.148
1456344_at	Tenascin C	Tnc	1.17	0.774	-1.05	0.767	-1.82	0.023	-1.56	0.109	-2.42	0.052
1429347_at	Bcl2-like 14 (apoptosis facilitator)	Bcl2l14	-1.24	0.459	1.22	0.336	-1.81	0.038	-1.69	0.133	1.06	0.743
1453895_at	RIKEN cDNA C330026N13 gene	C330026N13Rik	-1.09	0.549	1.16	0.151	-1.81	0.047	2.57	0.929	-1.13	0.374
1439327_at	collagen and calcium binding EGF domains 1	Ccbe1	1.24	0.281	-1.6	0.239	-1.81	0.030	-1.54	0.200	-2.18	0.078
1448066_at	hypothetical LOC552909	LOC552909	1.43	0.235	-1.39	0.122	-1.81	0.050	-1.37	0.205	-1.15	0.260
1456927_at	microtubule associated serine/threonine kinase 2	Mast2	-1.51	0.227	-1.34	0.235	-1.81	0.004	-1.73	0.013	-1.47	0.131
1456214_at	protocadherin 7	Pcdh7	1.03	0.603	-1.47	0.021	-1.81	0.015	-1.71	0.019	-2.25	0.150
1450344_a_at	prostaglandin E receptor 3 (subtype EP3)	Ptger3	-1.13	0.778	-1.2	0.398	-1.81	0.023	1.04	0.842	1	0.825
1440931_at	scratch homolog 2, zinc finger protein (Drosophila)	Scrt2	2.34	0.515	1.68	0.788	-1.81	0.020	-1.14	0.422	1.93	0.494
1450286_at	natriuretic peptide receptor 3	Npr3	1.27	0.507	-1.23	0.377	-1.8	0.017	-1	0.938	-1.45	0.062
1434450_s_at	adrenergic receptor kinase, beta 2	Adrbk2	1.67	0.310	1.13	0.750	-1.79	0.012	1.16	0.783	-1.19	0.372
1418003_at	RIKEN cDNA 1190002H23 gene	1190002H23Rik	-1.29	0.114	1.07	0.763	-1.78	0.008	-1.33	0.201	1.33	0.437
1442072_at	RIKEN cDNA C230081A13 gene	C230081A13Rik	1.68	0.155	-1	0.448	-1.78	0.023	-1.18	0.240	-1.27	0.078
1442041_at	hypothetical LOC552876	LOC552876	-1.05	0.428	1.02	0.674	-1.78	0.042	1.01	0.820	-1.04	0.363
1436910_at	RAS protein activator like 2	Rasal2	1.04	0.327	-2.91	0.008	-1.78	0.017	-1.88	0.001	-1.98	0.002
1422689_at	RIKEN cDNA 4930547C10 gene	4930547C10Rik	1.19	0.899	1.47	0.674	-1.77	0.012	-1.93	0.082	1.37	0.696
1438473_at	ADP-ribosylation factor-like 15	Arl15	1.48	0.871	-3.88	0.021	-1.77	0.011	-1.64	0.059	-1.74	0.054
1422741_a_at	bobby sox homolog (Drosophila)	Bbx	3.72	0.186	-1.58	0.139	-1.77	0.049	1.05	0.924	-2.23	0.025
1437898_at	RIKEN cDNA C920009B18 gene	C920009B18Rik	1.6	0.793	1.17	0.712	-1.77	0.012	1.19	0.730	1.24	0.737
1450768_at	discs, large homolog 1 (Drosophila)	Dlgh1	1.22	0.982	-1.55	0.096	-1.77	0.007	-1.68	0.005	-2.35	0.001
1459242_at	ELOVL family member 5, elongation of long chain fatty acids (yeast)	Elovl5	1.17	0.775	-1.07	0.626	-1.77	0.010	-1.06	0.804	1.62	0.068
1450063_at	formin 2	Fmn2	-1.57	0.024	-2.47	0.003	-1.77	0.006	-1.48	0.012	-1.74	0.007
1417944_at	guanine nucleotide binding protein (G protein), gamma 4 subunit	Gng4	1.16	0.714	1.39	0.956	-1.77	0.038	-1.37	0.165	2.38	0.362
1450786_x_at	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma	LOC669660	1.02	0.849	-1.74	0.031	-1.77	0.021	-1.76	0.004	-1.84	0.009
1453982_at	transformed mouse 3T3 cell double minute 4	Mdm4	-1.61	0.084	1.02	0.557	-1.77	0.038	1.3	0.308	1.36	0.660
1455204_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-1.07	0.436	-3.71	0.010	-1.77	0.040	-2.02	0.012	-2.17	0.007
1449766_at	synaptotagmin VI	Syt6	1.49	0.253	1.7	0.305	-1.77	0.039	1.07	0.695	1.9	0.574
1440726_at	RIKEN cDNA A230062I15 gene	A230062I15Rik	-1.37	0.240	2.57	0.545	-1.76	0.049	1.73	0.346	-1.23	0.406
1460006_at	AT motif binding factor 1	Atbf1	-1.14	0.107	-1.9	0.002	-1.76	0.002	-1.99	0.000	-2.15	0.002
1450509_at	carbohydrate sulfotransferase 11	Chst11	-1.11	0.224	-1.94	0.010	-1.76	0.003	-1.41	0.089	-1.45	0.092
1456022_at	homeodomain interacting protein kinase 2	Hipk2	1.01	0.934	-1.81	0.048	-1.76	0.024	-1.99	0.001	-2.01	0.024
1444989_at	hypothetical protein LOC665914 /// hypothetical protein LOC671445	LOC665914 /// LOC	1.28	0.892	1.5	0.333	-1.76	0.017	-1.35	0.199	-1.69	0.170
1428509_at	myosin IE	Myo1e	1.14	0.661	-2.21	0.027	-1.76	0.006	-2.05	0.009	-2.04	0.005
1422324_a_at	parathyroid hormone-like peptide	Pthlh	1.35	0.896	1.45	0.139	-1.76	0.029	-1.17	0.434	3.63	0.053
1434804_at	SEC15-like 2 (S. cerevisiae)	Sec15l2	-1.23	0.223	-3.11	0.051	-1.76	0.009	-1.92	0.002	-2.06	0.002
1434222_at	signal-induced proliferation-associated 1 like 1	Sipa1l1	1.05	0.438	-1.77	0.001	-1.76	0.006	-1.71	0.008	-1.87	0.001
1457452_at	expressed sequence AA407782	AA407782	-1.08	0.393	-1.17	0.264	-1.75	0.033	2.09	0.860	1.09	0.981
1425955_at	caveolin 2	Cav2	1.35	0.968	1.72	0.796	-1.75	0.019	1.6	0.222	1.12	0.730
1434683_at	Cut-like 1 (Drosophila)	Cutl1	-1.14	0.164	-2.09	0.007	-1.75	0.004	-1.96	0.003	-2.06	0.003
1452343_at	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ertd653e	1.21	0.888	-1.57	0.124	-1.75	0.006	-2.07	0.045	-2.18	0.002
1460490_at	mitochondrial ribosomal protein L15	Mrpl15	1.93	0.420	1.72	0.186	-1.75	0.046	-1.94	0.025	-1.44	0.193
1436764_at	par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	1.33	0.473	-2.62	0.028	-1.75	0.004	-1.7	0.000	-1.97	0.074
1449351_s_at	platelet-derived growth factor, C polypeptide	Pdgfc	1.07	0.742	-1.92	0.015	-1.75	0.012	-1.91	0.007	-1.86	0.000
1431851_at	RIKEN cDNA 4930534P07 gene	4930534P07Rik	1.02	0.594	1.52	0.898	-1.74	0.043	2.13	0.040	1.22	0.377
1449520_at	tetratricopeptide repeat domain 28	Ttc28	-1.28	0.065	-2.61	0.020	-1.74	0.010	-1.92	0.002	-2.11	0.036
1445885_at	ubiquitin-conjugating enzyme E2D 2	Ube2d2	1.3	0.666	1.21	0.403	-1.74	0.018	1.31	0.770	1.51	0.982
1451577_at	zinc finger and BTB domain containing 20	Zbtb20	1.12	0.362	-2.11	0.005	-1.74	0.009	-1.59	0.040	-2.37	0.001
1459998_at	zinc finger protein 407	Zfp407	1.05	0.681	-3.13	0.001	-1.74	0.002	-2.18	0.004	-2.23	0.012
1431368_at	RIKEN cDNA 4930404N11 gene	4930404N11Rik	1.01	0.870	-1.21	0.380	-1.73	0.042	-1.72	0.079	1.12	0.449
1433894_at	expressed sequence AI591476	AI591476	2.21	0.333	1.1	0.303	-1.73	0.017	-1.49	0.026	-1.68	0.077
1453705_at	RIKEN cDNA B230110C06 gene	B230110C06Rik	-1.77	0.135	-1.57	0.298	-1.73	0.047	2.82	0.591	1.25	0.787
1454780_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	Galntl4	-1.13	0.099	-1.97	0.000	-1.73	0.000	-1.49	0.000	-1.89	0.000
1443201_at	Glypican 6	Gpc6	-1.08	0.354	1.11	0.610	-1.73	0.004	-1.01	0.724	-1.59	0.179
1418272_at	3-oxoacid CoA transferase 2A	Oxct2a	-1.49	0.099	-1.29	0.094	-1.73	0.034	1.52	0.310	1.49	0.864
1444738_at	RIKEN cDNA 5730419I09 gene	5730419I09Rik	-1.16	0.382	1.65	0.341	-1.72	0.038	-1.07	0.362	-1.09	0.413
1447104_at	AT rich interactive domain 1A (Swi1 like)	Arid1a	-1.04	0.543	-1.46	0.176	-1.72	0.042	1.35	0.867	1.31	0.028

1453280_at	melanoma antigen, family B, 5 /// similar to Melanoma-associated an	Mageb5 /// LOC629	-1.31	0.198	-1.18	0.288	-1.72	0.010	2.86	0.042	-1.03	0.804
1457753_at	toll-like receptor 13	Tlr13	-1.26	0.738	1.02	0.683	-1.72	0.044	-1.49	0.060	1.48	0.538
1448017_at	ubiquitin associated protein 2-like	Ubap2l	-1.22	0.271	-1.52	0.157	-1.72	0.041	-2.09	0.039	1.76	0.054
1430199_at	RIKEN cDNA 1700007E05 gene	1700007E05Rik	2.17	0.968	-1.19	0.262	-1.71	0.026	-1.4	0.187	2.31	0.065
1453828_at	RIKEN cDNA 4932422M17 gene	4932422M17Rik	1.62	0.156	1.07	0.902	-1.71	0.046	1.82	0.184	2.13	0.197
1433728_at	cDNA sequence BC038479	BC038479	1.33	0.831	2.12	0.745	-1.71	0.010	-1.22	0.248	1.41	0.382
1416846_a_at	PDZ domain containing RING finger 3	Pdzrn3	1.32	0.624	-1.43	0.178	-1.71	0.011	-1.86	0.006	-2.09	0.001
1429449_at	sterile alpha motif domain containing 4	Samd4	1.3	0.449	-1.28	0.218	-1.71	0.009	-1.48	0.013	-1.7	0.010
1424923_at	serine (or cysteine) peptidase inhibitor, clade A, member 3G	Serpina3g	2.88	0.500	1.01	0.347	-1.71	0.045	2.08	0.608	1.76	0.618
1446396_at	Angiopoietin-like 1	Angptl1	1.57	0.688	-1.02	0.777	-1.7	0.044	-1.14	0.353	-1.21	0.401
1437531_at	transient receptor potential cation channel, subfamily M, member 1	Trpm1	1.03	0.802	1.25	0.909	-1.7	0.043	-1.43	0.078	1.15	0.037
1436047_at	gene model 672, (NCBI)	Gm672	-1.12	0.226	-2.63	0.015	-1.69	0.000	-2.21	0.001	-2.44	0.000
1429902_at	RIKEN cDNA 5830443J22 gene	5830443J22Rik	1.17	0.341	1.03	0.632	-1.68	0.036	-1.89	0.072	-1.91	0.068
1458256_at	RIKEN cDNA 5830446M03 gene	5830446M03Rik	-1.05	0.989	1.77	0.466	-1.68	0.041	-1.26	0.131	-1.12	0.508
1445866_at	microtubule associated serine/threonine kinase family member 4	Mast4	1.02	0.901	-1.14	0.275	-1.68	0.046	-1.24	0.167	-2.24	0.007
1421515_at	nuclear receptor subfamily 6, group A, member 1	Nr6a1	1.1	0.635	-1.99	0.134	-1.68	0.021	1.02	0.930	1.03	0.621
1454711_at	triple functional domain (PTPRF interacting)	Trio	1.12	0.560	-1.51	0.126	-1.68	0.005	-2.53	0.002	-2.31	0.001
1446906_at	expressed sequence C81615	C81615	1.11	0.564	-1.2	0.410	-1.67	0.029	-1.42	0.178	-1.38	0.225
1417251_at	palmdelphin	Palmd	2.05	0.976	-1.12	0.390	-1.67	0.042	1.49	0.864	1.84	0.784
1418310_a_at	retinaldehyde binding protein 1	Rlbp1	1.93	0.641	1.43	0.808	-1.67	0.029	1.48	0.103	-1.03	0.566
1443896_at	TBC1 domain family, member 5	Tbc1d5	-1.07	0.568	-2.53	0.002	-1.67	0.015	-1.32	0.087	-1.8	0.003
1434880_at	ets variant gene 6 (TEL oncogene)	Etv6	1.08	0.579	-1.4	0.093	-1.66	0.003	-1.93	0.003	-2.34	0.001
1448765_at	Fyn proto-oncogene	Fyn	-1.15	0.180	-2.22	0.004	-1.66	0.007	-1.92	0.000	-2.1	0.002
1455314_at	LIM domain containing preferred translocation partner in lipoma	Lpp	-1.14	0.045	-1.94	0.001	-1.66	0.004	-1.55	0.000	-1.99	0.009
1421615_at	myosin XV	Myo15	1.72	0.014	2.03	0.055	-1.66	0.007	1.15	0.349	1.1	0.928
1423983_at	seizure related 6 homolog like 2	Sez6l2	2.17	0.148	1.5	0.439	-1.66	0.012	-1.53	0.123	1.43	0.190
1424531_a_at	transcription elongation factor A (SII), 3	Tcea3	-1.03	0.620	-1.41	0.118	-1.66	0.000	1.13	0.866	2.02	0.230
1449530_at	trichorhinophalangeal syndrome I (human)	Trps1	1.33	0.333	-1.92	0.043	-1.66	0.005	-1.63	0.004	-1.85	0.075
1454286_at	RIKEN cDNA 1110004M10 gene	1110004M10Rik	-1.04	0.962	-1.68	0.175	-1.65	0.027	-1	0.864	1.01	0.375
1430279_at	RIKEN cDNA 3110038A09 gene	3110038A09Rik	3.07	0.620	-1.64	0.129	-1.65	0.023	1.13	0.560	1.18	0.885
1453512_at	RIKEN cDNA 5830407P18 gene	5830407P18Rik	1.19	0.430	-1.14	0.529	-1.65	0.049	-1.33	0.247	-2.41	0.013
1430351_at	spermatogenesis associated 18	Spata18	1.43	0.487	1.52	0.552	-1.65	0.047	-2.02	0.028	1.21	0.771
1432460_at	RIKEN cDNA 1700125F08 gene	1700125F08Rik	-1.49	0.259	-1.42	0.282	-1.64	0.037	1.54	0.716	1.14	0.855
1452366_at	RIKEN cDNA 4732435N03 gene	4732435N03Rik	-1.29	0.286	-2.82	0.035	-1.64	0.017	-1.55	0.003	-1.94	0.000
1439274_at	RIKEN cDNA A230083H22 gene	A230083H22Rik	1.1	0.691	-1.07	0.485	-1.64	0.033	1.38	0.799	-1.27	0.250
1436440_at	RIKEN cDNA B230107K20 gene	B230107K20Rik	-1.38	0.223	-1.67	0.187	-1.64	0.011	-1.58	0.030	-1.69	0.130
1442972_at	Coronin, actin binding protein 1C	Coro1c	1.98	0.476	1.21	0.909	-1.64	0.001	-1.21	0.130	-1.39	0.139
1438018_at	hook homolog 1 (Drosophila)	Hook1	1.33	0.937	-1.18	0.318	-1.64	0.041	-1.13	0.333	-1.84	0.081
1453490_at	spindle assembly 6 homolog (C. elegans)	Sass6	1.47	0.794	1.91	0.344	-1.64	0.012	-1	0.900	1.09	0.276
1441711_at	unc-45 homolog B (C. elegans)	Unc45b	-1.35	0.337	1.35	0.952	-1.64	0.031	1.13	0.547	-1	0.579
1453262_at	RIKEN cDNA 2810032G03 gene	2810032G03Rik	2.65	0.747	-1.19	0.336	-1.63	0.043	1.91	0.244	1.18	0.775
1436264_at	cDNA sequence BC025920	BC025920	-1.31	0.284	-1.41	0.082	-1.63	0.043	-1.23	0.289	1.15	0.783
1433311_at	RIKEN cDNA D530031A16 gene	D530031A16Rik	-1.13	0.427	-1.55	0.303	-1.63	0.019	-1.13	0.148	-1.54	0.195
1451685_at	myeloid/lymphoid or mixed lineage-leukemia translocation to 6 homo	Mllt6 /// LOC63949	1.08	0.517	1.62	0.440	-1.63	0.004	1.21	0.957	1.13	0.618
1457864_at	RAB11 family interacting protein 3 (class II)	Rab11fip3	1.19	0.317	-1.3	0.481	-1.63	0.023	2.16	0.157	3.29	0.523
1441969_at	tripartite motif-containing 36	Trim36	1.32	0.879	1.38	0.436	-1.63	0.049	-1.08	0.699	1.84	0.024
1457793_a_at	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	Whsc1l1	1.62	0.488	1.23	0.751	-1.63	0.040	-1.33	0.089	-1.52	0.003
1433182_at	RIKEN cDNA 4930431N21 gene	4930431N21Rik	-1.33	0.314	-1.56	0.166	-1.62	0.008	-1.19	0.348	1.3	0.232
1429691_at	RIKEN cDNA 5430405N12 gene	5430405N12Rik	1.17	0.640	-1.5	0.027	-1.62	0.027	-1.25	0.000	-1.57	0.211
1444814_at	DNA segment, Chr 15, ERATO Doi 180, expressed	D15Ertd180e	1.18	0.466	-1.65	0.032	-1.62	0.005	-1.15	0.503	1	0.517
1458807_at	erythrocyte protein band 4.1	Epb4.1	1.42	0.633	1.54	0.593	-1.62	0.040	1.07	0.798	1.12	0.686
1455982_at	jumonji domain containing 4	Jmjd4	-1.06	0.527	1.3	0.986	-1.62	0.006	1.02	0.498	-1.33	0.143
1426994_at	PH domain and leucine rich repeat protein phosphatase	Phlpp	1.01	0.795	-2.06	0.019	-1.62	0.001	-1.88	0.000	-2.1	0.001
1438377_x_at	solute carrier family 13 (sodium-dependent dicarboxylate transporter	Slc13a3	2.06	0.327	1.74	0.352	-1.62	0.038	1.34	0.949	-1.41	0.166
1452714_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	Tanc1	1.07	0.602	-1.79	0.011	-1.62	0.004	-1.86	0.009	-1.89	0.001
1436746_at	WNK lysine deficient protein kinase 1	Wnk1	-1.29	0.169	-1.72	0.009	-1.62	0.046	-1.4	0.041	-1.23	0.085
1452025_a_at	zinc finger protein 2	Zfp2	2.47	0.221	1.92	0.307	-1.62	0.039	1.24	0.038	1.5	0.939
1451332_at	zinc finger protein 521	Zfp521	-1.06	0.376	-3.24	0.019	-1.62	0.003	-1.37	0.009	-1.77	0.001

1439485_at	zinc finger protein 608 /// RIKEN cDNA D430007A19 gene	Zfp608 /// D430007	-1.14	0.379	-1.05	0.732	-1.62	0.026	1.22	0.620	-1.06	0.523
1442897_at	RIKEN cDNA 2610024E20 gene	2610024E20Rik	-1.09	0.588	-1.08	0.518	-1.61	0.016	1.07	0.525	-1.39	0.178
1439394_x_at	cell division cycle 20 homolog (S. cerevisiae)	Cdc20	1.24	0.754	1.44	0.906	-1.61	0.016	1.15	0.349	1.71	0.405
1443611_at	DnaJ (Hsp40) homolog, subfamily B, member 4	Dnajb4	1.13	0.929	1.26	0.301	-1.61	0.040	1.07	0.875	1.04	0.705
1440926_at	FMS-like tyrosine kinase 1	Flt1	1.08	0.659	-1.44	0.149	-1.61	0.012	1.03	0.750	-1.41	0.207
1427199_at	furry homolog-like (Drosophila)	Fryl	-1.07	0.138	-2.02	0.005	-1.61	0.012	-1.39	0.091	-1.43	0.008
1456835_at	Hypothetical protein LOC624549	LOC624549	1.94	0.351	1.2	0.397	-1.61	0.014	1.09	0.630	1.31	0.550
1455720_at	a disintegrin-like and metallopeptidase (reprolysin type) with thromb	Adamts2	1.02	0.969	-1.74	0.023	-1.6	0.049	-1.05	0.842	-1.56	0.052
1420577_at	activation-induced cytidine deaminase	Aicda	-1.31	0.287	1.34	0.764	-1.6	0.015	1.16	0.542	1.36	0.088
1418028_at	dopachrome tautomerase	Dct	1.4	0.173	1.82	0.111	-1.6	0.037	1.04	0.729	1.41	0.435
1439397_at	formin 1	Fmn1	-1.32	0.348	-4.27	0.117	-1.6	0.001	-2.56	0.002	-2.54	0.000
1436743_at	immunoglobulin superfamily, member 4	Igsf4d	-1.4	0.197	-1.16	0.506	-1.6	0.045	-1.33	0.249	2.69	0.056
1432043_at	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	Smu1	-1.23	0.348	1.12	0.988	-1.6	0.036	3.06	0.330	-1.21	0.412
1437197_at	sorbin and SH3 domain containing 2	Sorbs2	1.18	0.863	-1.51	0.145	-1.6	0.006	-1.6	0.027	-1.55	0.007
1416434_at	Bcl2-like 10	Bcl2l10	-2.42	0.062	-1.01	0.807	-1.59	0.039	1.75	0.454	1.05	0.328
1440967_at	Brain protein I3 /// BAI1-associated protein 2-like 1	Bri3 /// Baiap2l1	1.03	0.795	-1.26	0.185	-1.59	0.014	1.55	0.513	1.03	0.975
1449581_at	EMI domain containing 1	Emid1	1.4	0.055	1.74	0.100	-1.59	0.005	1.08	0.892	3.3	0.015
1455685_at	microtubule associated monoxygenase, calponin and LIM domain co	Mical2	1.34	0.833	-1	0.305	-1.59	0.018	-1.61	0.029	-1.77	0.029
1459991_at	myosin IXa	Myo9a	-1.14	0.411	-1.6	0.142	-1.59	0.009	-1.19	0.495	-1.05	0.662
1439187_at	vacuolar protein sorting 13 D (yeast)	Vps13d	1.26	0.453	-1.27	0.211	-1.59	0.003	-1.59	0.001	-1.72	0.001
1444868_at	RIKEN cDNA 4921529O18 gene	4921529O18Rik	-1.09	0.550	1.17	0.951	-1.58	0.006	-1.36	0.167	1.58	0.957
1439331_at	RIKEN cDNA 4932439E07 gene	4932439E07Rik	2.62	0.355	1.12	0.644	-1.58	0.044	-1.41	0.268	2.09	0.020
1452641_at	cDNA sequence BC028663	BC028663	-1	0.882	1.34	0.680	-1.58	0.042	-1.25	0.331	1.54	0.476
1444855_at	B-cell CLL/lymphoma 9-like	Bcl9l	-1.69	0.164	-1.04	0.717	-1.58	0.036	1.2	0.470	-1.91	0.114
1442464_at	F-box and leucine-rich repeat protein 20	Fbxl20	1.18	0.834	1.03	0.691	-1.58	0.049	1.38	0.136	1.1	0.125
1451871_a_at	growth hormone receptor	Ghr	2.77	0.574	1.5	0.225	-1.58	0.012	-1.26	0.063	-1.76	0.024
1434418_at	longevity assurance homolog 6 (S. cerevisiae)	Lass6	-1.22	0.024	-2.06	0.010	-1.58	0.020	-1.66	0.006	-1.87	0.015
1443939_at	similar to C05G5.5 /// similar to C05G5.5 /// similar to C05G5.5	LOC230628 /// LOC	-1.29	0.188	-2.16	0.065	-1.58	0.014	-1.82	0.008	-1.21	0.201
1452274_at	zinc finger, AN1-type domain 3	Zfand3	-1.12	0.345	-1.63	0.103	-1.58	0.011	-1.42	0.002	-1.58	0.004
1447648_at	RIKEN cDNA 1700021N20 gene	1700021N20Rik	1.66	0.797	1.68	0.451	-1.57	0.032	1.97	0.255	1.38	0.688
1424739_at	RIKEN cDNA 4932432K03 gene	4932432K03Rik	1.16	0.644	-1.33	0.177	-1.57	0.001	2.52	0.235	1.07	0.992
1436143_at	RIKEN cDNA 4933425L03 gene	4933425L03Rik	-1.28	0.050	-1.93	0.063	-1.57	0.004	-1.42	0.024	-1.67	0.025
1430196_at	RIKEN cDNA 8430408J09 gene	8430408J09Rik	-1.18	0.405	1.02	0.766	-1.57	0.038	-1.14	0.201	-1.35	0.068
1447839_x_at	adrenomedullin	Adm	-1.45	0.226	-2.47	0.068	-1.57	0.012	-1.64	0.000	-1.95	0.008
1417950_a_at	apolipoprotein A-II	Apoa2	-1.13	0.446	1.09	0.579	-1.57	0.009	1.3	0.524	1.04	0.886
1452251_at	neurobeachin	Nbea	-1.44	0.152	-2.77	0.058	-1.57	0.024	-1.65	0.017	-2.22	0.014
1459372_at	neuronal PAS domain protein 4	Npas4	1.76	0.147	1.24	0.963	-1.57	0.038	-1.01	0.762	-2.81	0.016
1442430_at	cDNA sequence BC048562	BC048562	-1.33	0.223	-1.21	0.264	-1.56	0.010	-1.07	0.574	1.15	0.319
1421004_at	centrosomal protein 110	Cep110	-1.37	0.086	-1.39	0.064	-1.56	0.005	-1.27	0.148	1.42	0.164
1452265_at	CLIP associating protein 1	Clasp1	-1.09	0.202	-1.71	0.006	-1.56	0.014	-1.73	0.001	-1.96	0.000
1459005_at	RIKEN cDNA D030051N19 gene	D030051N19Rik	-1.14	0.377	-1.28	0.369	-1.56	0.029	-1.16	0.356	-1.39	0.010
1456067_at	GLI-Kruppel family member GLI3	Gli3	-1.02	0.632	-2.15	0.005	-1.56	0.025	-1.77	0.019	-1.8	0.008
1454132_at	RIKEN cDNA 7630402F16 gene	7630402F16Rik	1.72	0.654	1.8	0.571	-1.55	0.021	1.67	0.787	2.08	0.442
1444343_at	RIKEN cDNA A130064L14 gene	A130064L14Rik	-1.24	0.176	-1.18	0.481	-1.55	0.029	-1.09	0.305	-1.5	0.185
1433855_at	4-aminobutyrate aminotransferase	Abat	2.15	0.476	1.32	0.826	-1.55	0.024	1.09	0.351	-1.17	0.239
1460020_at	hypothetical protein LOC629623	LOC629623	-1.21	0.334	-1.02	0.677	-1.55	0.010	-1.46	0.143	-1.65	0.096
1451474_a_at	poly (ADP-ribose) polymerase family, member 8	Parp8	1.15	0.213	-1.22	0.210	-1.55	0.006	-1.53	0.001	-1.59	0.005
1434603_at	thyroid hormone receptor associated protein 2	Thrap2	1.03	0.170	-1.49	0.000	-1.55	0.024	-1.64	0.014	-2.04	0.025
1452074_at	transmembrane protein 135	Tmem135	-1.19	0.289	-1.21	0.383	-1.55	0.005	-1.76	0.074	1.15	0.829
1416157_at	vinculin	Vcl	17.94	0.717	9.94	0.341	-1.55	0.011	-1.09	0.299	-1.51	0.064
1432088_at	ventricular zone expressed PH domain homolog 1 (zebrafish)	Veph1	1.49	0.415	1.21	0.461	-1.55	0.043	1.71	0.208	-1.17	0.222
1453933_at	RIKEN cDNA 4933435E02 gene	4933435E02Rik	1.18	0.565	1.38	0.187	-1.54	0.029	-1.14	0.277	1.19	0.200
1454310_at	RIKEN cDNA 5830490A12 gene	5830490A12Rik	1.84	0.122	2.7	0.496	-1.54	0.005	1.69	0.195	1.14	0.310
1451438_s_at	C-type lectin domain family 2, member h	Clec2h	1.48	0.153	1.56	0.543	-1.54	0.017	1.06	0.796	-1.03	0.511
1451279_at	ELKS/RAB6-interacting/CAST family member 1	Erc1	-1.21	0.161	-2.67	0.006	-1.54	0.012	-1.96	0.011	-2.03	0.004
1449159_at	guanine nucleotide binding protein, beta 3	Gnb3	-1.48	0.212	-1.4	0.171	-1.54	0.030	1.37	0.344	1.16	0.995
1438451_at	Rho GTPase-activating protein	Grit	-1.11	0.393	-2.11	0.035	-1.54	0.034	-1.78	0.004	-2.06	0.013
1452982_at	insulin-like growth factor I receptor	Igf1r	-1.05	0.553	-2.17	0.008	-1.54	0.002	-1.59	0.020	-1.84	0.022

1438186_at	PDZ and LIM domain 5	Pdlim5	1.17	0.751	-1.4	0.193	-1.54	0.047	-1.49	0.174	-1.61	0.090
1437602_at	similar to Hypothetical protein MGC26988	RP23-273O7.4	-1.22	0.363	-1.39	0.387	-1.54	0.017	1.93	0.558	-2.19	0.028
1455473_at	ubiquitin specific peptidase 13 (isopeptidase T-3)	Usp13	-1.56	0.039	-1.55	0.148	-1.54	0.034	-1.37	0.114	1.1	0.913
1454723_at	RIKEN cDNA 1110033M05 gene	1110033M05Rik	1.06	0.927	-1.57	0.007	-1.53	0.004	-1.38	0.011	-1.67	0.003
1445843_at	chromodomain helicase DNA binding protein 2	Chd2	-1.25	0.315	-1.33	0.313	-1.53	0.022	-1.34	0.028	-1.17	0.454
1445044_at	Prostaglandin I2 (prostacyclin) synthase	Ptgis	2.5	0.368	-1.18	0.283	-1.53	0.040	-1.22	0.274	1.55	0.455
1428822_a_at	sorting nexing 24	Snx24	-1.09	0.370	-1.98	0.016	-1.53	0.043	-1.58	0.015	-1.83	0.000
1449405_at	tensin 1	Tns1	-1.04	0.500	-1.32	0.040	-1.53	0.004	-1.42	0.008	-1.46	0.006
1454706_at	UV radiation resistance associated gene	Uvrag	-1.04	0.271	-1.95	0.005	-1.53	0.005	-1.98	0.004	-1.73	0.000
1435930_at	zinc finger protein 291	Zfp291	-1.82	0.225	-3.26	0.140	-1.53	0.005	-1.9	0.019	-2.27	0.016
1420931_at	mitogen activated protein kinase 8	Mapk8	1.31	0.064	1.13	0.582	-1.52	0.047	-1.27	0.215	-1.49	0.172
1418650_at	spermatogenesis associated 6	Spata6	4.9	0.268	2.65	0.957	-1.52	0.003	-1.07	0.421	-1.18	0.252
1431831_at	RIKEN cDNA 2210009G21 gene	2210009G21Rik	1.8	0.871	1.38	0.385	-1.51	0.027	-1.28	0.029	-1.17	0.150
1430362_at	RIKEN cDNA 5730409N24 gene	5730409N24Rik	1.08	0.704	-1.05	0.886	-1.51	0.013	1.04	0.969	-1.68	0.096
1435879_at	thymoma viral proto-oncogene 3	Akt3	-1.12	0.272	-2.7	0.030	-1.51	0.004	-1.37	0.010	-1.65	0.005
1459457_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	1.01	0.580	-1.39	0.296	-1.51	0.027	-1.43	0.048	-2.13	0.014
1431354_a_at	phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	1.04	0.699	-2.29	0.027	-1.51	0.022	-1.48	0.030	-2.01	0.002
1427313_at	prostaglandin I receptor (IP)	Ptgir	-2	0.130	-1.68	0.132	-1.51	0.012	1.34	0.285	1.29	0.906
1445149_at	Poliovirus receptor	Pvr	1.33	0.458	-1.22	0.211	-1.51	0.020	1.78	0.214	3.13	0.150
1440428_at	sideroflexin 5	Sfxn5	1.38	0.966	1.17	0.944	-1.51	0.023	-1.16	0.234	1.09	0.678
1433719_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 9	Slc9a9	1.15	0.698	-1.84	0.023	-1.51	0.004	1.14	0.354	-1.19	0.471
1429705_at	sperm acrosome associated 4	Spaca4	1.54	0.391	-1.06	0.534	-1.51	0.011	1.31	0.583	-1.55	0.219
1456147_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	St8sia6	1.48	0.610	-1.2	0.492	-1.51	0.013	-1.43	0.092	-1.11	0.329
1448786_at	RIKEN cDNA 1100001H23 gene	1100001H23Rik	-1.21	0.447	1.11	0.469	-1.5	0.021	-1.14	0.709	1.53	0.846
1460475_at	RIKEN cDNA 3110056J03 gene	3110056J03Rik	1.08	0.742	1.19	0.942	-1.5	0.022	-1.09	0.281	-1.52	0.108
1454101_at	RIKEN cDNA 4933401P06 gene	4933401P06Rik	-1.07	0.458	1.43	0.582	-1.5	0.015	2.06	0.354	1.55	0.563
1455396_at	ATPase, class I, type 8B, member 1	Atp8b1	1.26	0.705	-1.8	0.073	-1.5	0.002	-1.57	0.012	-1.53	0.025
1431604_a_at	coiled-coil domain containing 97	Ccdc97	1.77	0.231	2.14	0.500	-1.5	0.049	-1.03	0.764	-1.14	0.283
1457672_at	chromodomain helicase DNA binding protein 9	Chd9	-1.09	0.413	-1.51	0.090	-1.5	0.003	-1.32	0.026	-1.71	0.031
1419781_at	RIKEN cDNA D630004N19 gene	D630004N19Rik	1.35	0.672	1.48	0.175	-1.5	0.031	-1.1	0.360	1.3	0.731
1424801_at	enabled homolog (Drosophila)	Enah	1.09	0.807	-1.52	0.114	-1.5	0.010	-1.24	0.138	-1.61	0.008
1439467_at	Microtubule-associated protein 4	Mtap4	1.05	0.612	-1.02	0.940	-1.5	0.021	-1.17	0.436	-1.75	0.045
1451637_a_at	mucin 10, submandibular gland salivary mucin	Muc10	1.46	0.652	1.08	0.415	-1.5	0.021	1.37	0.532	-1.15	0.426
1454731_at	myosin X	Myo10	1.13	0.553	-1.34	0.164	-1.5	0.018	-1.56	0.039	-1.56	0.015
1444085_at	prenyl (solanesyl) diphosphate synthase, subunit 2	Pdss2	-1.39	0.111	-2.7	0.050	-1.5	0.038	-1.35	0.062	-1.18	0.171
1437113_s_at	phospholipase D1	Pld1	-1.08	0.391	-2.05	0.025	-1.5	0.028	-1.11	0.320	1.22	0.282
1443406_at	phospholipid scramblase 4	Plscr4	1.07	0.999	1.06	0.931	-1.5	0.046	-1.56	0.129	1.48	0.285
1418749_at	pleckstrin and Sec7 domain containing 3	Psd3	-1.11	0.309	-2.21	0.043	-1.5	0.008	-1.4	0.051	-1.81	0.001
1451041_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	1.25	0.474	-1.39	0.145	-1.5	0.010	-1.27	0.009	-1.6	0.014
AFFX-r2-Bs-phe-3	---	---	-1.28	0.333	-1.46	0.293	-1.49	0.001	1.4	0.036	1.01	0.552
1432984_at	RIKEN cDNA 1700026H06 gene	1700026H06Rik	1.04	0.578	1.33	0.973	-1.49	0.006	-1.36	0.281	-1.21	0.325
1430115_at	RIKEN cDNA 4833413E03 gene	4833413E03Rik	-1.86	0.074	-2.02	0.049	-1.49	0.041	-1.02	0.721	1.59	0.215
1442062_at	RIKEN cDNA 7120426M23 gene	7120426M23Rik	-1.21	0.193	-1.28	0.141	-1.49	0.004	-1.19	0.144	-1.18	0.238
1455765_a_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	Abcc8	-1.73	0.207	-1.18	0.324	-1.49	0.013	1.09	0.854	1.91	0.757
1455979_at	AT rich interactive domain 1B (Swi1 like)	Arid1b	-1.36	0.229	-3.04	0.030	-1.49	0.017	-2.25	0.001	-2.03	0.009
1447623_s_at	RIKEN cDNA C130009A20 gene	C130009A20Rik	-1.64	0.226	-4.15	0.099	-1.49	0.029	-1.74	0.005	-1.69	0.008
1440510_at	RIKEN cDNA C430002N11 gene	C430002N11Rik	-1.48	0.172	-1.11	0.470	-1.49	0.039	-1.22	0.203	-1.28	0.159
1442471_at	Eph receptor B2	Ephb2	1.1	0.770	-1.19	0.313	-1.49	0.038	1.29	0.244	-1.12	0.524
1438169_a_at	FERM domain containing 4B	Frmd4b	1.22	0.733	1.01	0.367	-1.49	0.047	-1.41	0.169	-1.5	0.100
1430353_at	GLIS family zinc finger 3	Glis3	-1.28	0.287	-2.82	0.062	-1.49	0.008	-1.88	0.020	-1.83	0.000
1421902_at	intersex-like (Drosophila)	Ixl	-1.01	0.935	1.32	0.590	-1.49	0.016	2.04	0.420	1.91	0.740
1429911_at	microcephaly, primary autosomal recessive 1	Mcph1	-1.16	0.037	-2.34	0.006	-1.49	0.034	-1.5	0.032	-1.41	0.010
1425164_a_at	phosphorylase kinase gamma 1	Phkg1	-1.59	0.179	1.24	0.151	-1.49	0.021	1.21	0.567	1.05	0.697
1419614_at	phospholipase A2, group XIIB	Pla2g12b	-1.09	0.548	-1.2	0.396	-1.49	0.025	1.51	0.415	1	0.815
1445745_at	RNA binding motif protein 17 /// similar to RNA binding motif protein	Rbm17 /// LOC545	1.11	0.399	1.3	0.735	-1.49	0.036	1.62	0.559	1.86	0.157
1439302_at	ubiquitin-activating enzyme E1-like 2	Ube1l2	-1.06	0.526	-1.57	0.038	-1.49	0.015	-1.32	0.003	-1.47	0.018
1438691_at	zinc finger, ZZ-type with EF hand domain 1	Zzef1	-1.12	0.297	-1.56	0.107	-1.49	0.016	-1.47	0.001	-1.54	0.009
1443200_at	hypothetical protein A930011G24	A930011G24	1.36	0.867	1.31	0.687	-1.48	0.001	1.13	0.962	1.1	0.614

1442175_at	RIKEN cDNA C030027H14 gene	C030027H14Rik	-1.31	0.060	-4.62	0.014	-1.48	0.005	-1.6	0.022	-1.78	0.019
1426090_a_at	fer (fms/fps related) protein kinase, testis specific 2	Fert2	4.62	0.811	3.14	0.267	-1.48	0.035	-1.31	0.058	-1.84	0.053
1455122_at	patched domain containing 2	Ptchd2	1.38	0.149	1.39	0.042	-1.48	0.037	2.27	0.042	1.44	0.918
1417700_at	Rab38, member of RAS oncogene family	Rab38	-1.41	0.108	-1.19	0.409	-1.48	0.013	1.2	0.790	1.55	0.598
1429089_s_at	RIKEN cDNA 2900026A02 gene	2900026A02Rik	-1.14	0.108	-1.88	0.018	-1.47	0.007	-1.34	0.010	-1.52	0.001
1438738_at	CDNA sequence BC010584	BC010584	-1.62	0.167	1.09	0.929	-1.47	0.018	1.33	0.547	1.15	0.643
1437119_at	Endoplasmic reticulum (ER) to nucleus signalling 1	Ern1	-1.28	0.252	-1.68	0.148	-1.47	0.011	-1.1	0.276	-1.44	0.001
1455729_at	guanine nucleotide binding protein, alpha q polypeptide	Gnaq	-1.26	0.287	-2.02	0.098	-1.47	0.017	-1.76	0.008	-1.79	0.009
1423184_at	intersectin 2	Itsn2	-1.1	0.516	-1.24	0.195	-1.47	0.005	1.04	0.738	-1	0.874
1449439_at	Kruppel-like factor 7 (ubiquitous)	Klf7	-1.11	0.187	-1.5	0.041	-1.47	0.008	-1.51	0.026	-1.51	0.046
1455827_at	muscleblind-like 2	Mbnl2	1.45	0.445	-1.01	0.501	-1.47	0.012	-1.27	0.001	-1.63	0.019
1452464_a_at	methionine aminopeptidase-like 1	Metapl1	1.51	0.749	1.45	0.374	-1.47	0.020	1.07	0.432	1.03	0.840
1459665_s_at	MRV integration site 1	Mrvi1	-1.73	0.120	-1.91	0.138	-1.47	0.019	-1.43	0.035	-1.21	0.118
1434189_at	stromal antigen 1	Stag1	-1.27	0.169	-2.76	0.054	-1.47	0.010	-1.52	0.014	-2.02	0.033
1436302_at	RIKEN cDNA 2410193C02 gene	2410193C02Rik	-1.12	0.236	-2.26	0.003	-1.46	0.015	-1.52	0.001	-1.72	0.010
1429556_at	RIKEN cDNA 2610024B07 gene	2610024B07Rik	-1.01	0.892	-1.47	0.030	-1.46	0.030	-1.52	0.052	-1.71	0.012
1449588_at	ATP-binding cassette, sub-family A (ABC1), member 4	Abca4	-1.01	0.691	-1.02	0.695	-1.46	0.021	1.68	0.744	2.1	0.381
1457081_at	RIKEN cDNA D630038D15 gene	D630038D15Rik	-1.11	0.533	-1.24	0.257	-1.46	0.016	-1.23	0.313	-1.37	0.112
1429381_x_at	immunoglobulin heavy chain (J558 family) /// similar to immunoglobu	Igh-VJ558 /// LOC2	1.12	0.944	-1.25	0.350	-1.46	0.036	1.43	0.216	2.32	0.011
1423614_at	leucine rich repeat containing 8 family, member C	Lrrc8c	4.86	0.458	3.14	0.758	-1.46	0.033	-1.41	0.012	-1.37	0.041
1449156_at	lymphocyte antigen 9	Ly9	1.03	0.953	-1.01	0.824	-1.46	0.041	1.11	0.590	1.03	0.974
1437318_at	p21 (CDKN1A)-activated kinase 3	Pak3	-1.1	0.414	-3.06	0.036	-1.46	0.017	-1.68	0.009	-2.02	0.064
1437181_at	pellino 2	Peli2	-1.11	0.129	-2.09	0.005	-1.46	0.002	-1.59	0.002	-1.7	0.006
1416354_at	RNA binding motif protein, X chromosome	Rbmx	1.17	0.437	-1.36	0.076	-1.46	0.024	-1.12	0.343	1.03	0.872
1438665_at	sphingomyelin phosphodiesterase 3, neutral	Smpd3	-1.2	0.513	1.24	0.692	-1.46	0.036	1.65	0.222	1.2	0.031
1449201_at	steroidogenic acute regulatory protein	Star	-1.42	0.175	-1.01	0.635	-1.46	0.038	-1.23	0.390	1.16	0.610
1429111_at	talin 2 /// similar to talin 2	Tln2 /// LOC639214	-1.2	0.033	-1.68	0.002	-1.46	0.005	-1.41	0.006	-1.5	0.005
1427456_at	WD repeat and FYVE domain containing 3	Wdfy3	1.02	0.966	-1.46	0.071	-1.46	0.040	-1.53	0.016	-2.07	0.041
1419791_at	zinc fingers and homeoboxes 3	Zhx3	1.25	0.318	1.32	0.351	-1.46	0.044	1.18	0.853	-1.18	0.495
1458452_at	ankyrin repeat domain 11	Ankrd11	-1.08	0.604	-1.59	0.081	-1.45	0.022	-1.22	0.261	-2.25	0.012
1454015_a_at	cadherin 13	Cdh13	1.58	0.789	1.73	0.713	-1.45	0.024	1.93	0.668	-1.16	0.281
1428579_at	formin-like 2	Fmnl2	1.26	0.449	-2.45	0.034	-1.45	0.031	-1.49	0.007	-1.81	0.018
1426633_s_at	potassium channel tetramerisation domain containing 14	Kctd14	-1.06	0.457	1.67	0.890	-1.45	0.033	1.25	0.672	-1.01	0.475
1434627_at	Nuclear respiratory factor 1	Nrf1	-1.04	0.581	1.29	0.230	-1.45	0.018	-1.24	0.116	-1.26	0.089
1439034_at	sialophorin	Spn	1.01	0.592	1.17	0.722	-1.45	0.031	1.18	0.018	1.07	0.992
1435700_at	talin 2	Tln2	-1.04	0.562	-1.59	0.092	-1.45	0.017	-1.38	0.086	-1.6	0.024
1456029_a_at	tetratricopeptide repeat domain 7B	Ttc7b	1.22	0.581	-1.22	0.157	-1.45	0.037	-1.29	0.052	-1.38	0.069
1444638_at	titin	Ttn	1.04	0.592	1.42	0.865	-1.45	0.047	-1.33	0.237	-1.14	0.466
1422107_at	RIKEN cDNA 2410066E13 gene	2410066E13Rik	1.01	0.737	1.12	0.865	-1.44	0.032	-1.21	0.272	1.2	0.786
1431672_at	RIKEN cDNA 9430069I07 gene	9430069I07Rik	1.38	0.929	2.48	0.931	-1.44	0.034	2.63	0.494	1.79	0.997
1445701_at	ATPase, Ca++ transporting, plasma membrane 4	Atp2b4	1.1	0.458	1.35	0.557	-1.44	0.024	-1.07	0.595	1.13	0.828
1460439_at	cDNA sequence BC033915	BC033915	-1.07	0.605	-1.95	0.001	-1.44	0.017	-1.34	0.010	-1.49	0.044
1435428_at	cDNA sequence BC037112	BC037112	1	0.858	1.16	0.659	-1.44	0.037	-1.11	0.413	-1.33	0.022
1442695_at	RIKEN cDNA C030007I01 gene	C030007I01Rik	-2.74	0.059	-1.64	0.080	-1.44	0.039	1.86	0.773	-1.14	0.520
1423222_at	CAP, adenylate cyclase-associated protein, 2 (yeast)	Cap2	-1.2	0.187	-1.38	0.118	-1.44	0.037	-1.14	0.188	-1.34	0.102
1434705_at	C-terminal binding protein 2 /// zinc finger, RAN-binding domain cont	Ctbp2 /// Zranb1	1.12	0.159	-1.13	0.339	-1.44	0.006	-1.68	0.000	-1.43	0.005
1425315_at	dedicator of cytokinesis 7	Dock7	1.37	0.783	-1.15	0.410	-1.44	0.027	1.1	0.831	-2.01	0.038
1435888_at	epidermal growth factor receptor	Egfr	-1.14	0.236	-1.8	0.024	-1.44	0.025	-1.68	0.006	-1.68	0.015
1422686_s_at	exocyst complex component 4	Exoc4	-1.31	0.135	-1.62	0.082	-1.44	0.011	-1.35	0.006	-1.37	0.039
1453317_a_at	KH domain containing, RNA binding, signal transduction associated	Khdrbs3	-1.12	0.055	-1.73	0.007	-1.44	0.002	-1.28	0.011	-1.45	0.000
1445723_at	phospholipase C-like 1	Plcl1	-1.11	0.488	-2.54	0.052	-1.44	0.035	-1.41	0.169	-1.11	0.381
1441202_at	RAB GTPase activating protein 1-like	Rabgap1l	1.44	0.965	1.12	0.870	-1.44	0.010	1.01	0.513	2.93	0.421
1417401_at	retinoic acid induced 14	Rai14	1.34	0.362	-1.08	0.349	-1.44	0.028	-1.19	0.179	-1.33	0.047
1424704_at	runt related transcription factor 2	Runx2	-1.11	0.370	-1.67	0.017	-1.44	0.001	-1.67	0.007	-1.65	0.016
1429591_at	transforming, acidic coiled-coil containing protein 1	Tacc1	2.23	0.598	1.96	0.993	-1.44	0.041	1.01	0.818	1.15	0.776
1457342_at	zinc finger protein, subfamily 1A, 4 (Eos)	Zfpn1a4	-1.23	0.254	-2.18	0.057	-1.44	0.025	-1.19	0.448	1.17	0.501
1432536_at	RIKEN cDNA 1700055M20 gene	1700055M20Rik	1.06	0.737	1.12	0.870	-1.43	0.024	-1.15	0.395	-1.01	0.886
1445363_at	RIKEN cDNA 2810055G20 gene	2810055G20Rik	2.14	0.180	1.54	0.387	-1.43	0.013	-1.47	0.171	-1.25	0.433

1433114_at	RIKEN cDNA 4921504P20 gene	4921504P20Rik	1.61	0.710	-1.56	0.145	-1.43	0.027	1.28	0.992	1.86	0.128
1446632_at	Calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	-2.34	0.097	1.03	0.290	-1.43	0.043	1.01	0.909	1.21	0.514
1455164_at	Cdc42 GTPase-activating protein	Cdgap	1.07	0.324	-1.29	0.083	-1.43	0.014	-1.37	0.001	-1.61	0.001
1433731_at	insulin-like growth factor 2 mRNA binding protein 3	Igf2bp3	-1.3	0.181	-1.42	0.118	-1.43	0.006	-1.27	0.042	-1	0.963
1453576_at	Nipped-B homolog (Drosophila)	Nipbl	-1.14	0.425	-1.55	0.287	-1.43	0.009	-1.37	0.010	-1.35	0.108
1435970_at	nemo like kinase	Nlk	-1.15	0.193	-1.51	0.017	-1.43	0.016	-1.49	0.009	-1.56	0.010
1431352_s_at	plasmacytoma variant translocation 1	Pvt1	1.44	0.266	1.06	0.904	-1.43	0.005	-1.45	0.004	-1.61	0.012
1449292_at	RB1-inducible coiled-coil 1	Rb1cc1	-1.16	0.389	-1.19	0.272	-1.43	0.032	-1.23	0.160	-1.23	0.024
1419550_a_at	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	-1.1	0.297	-1.94	0.015	-1.43	0.034	-1.44	0.003	-1.6	0.014
1434869_at	tudor domain containing 3	Tdrd3	-1.24	0.353	-1.66	0.202	-1.43	0.006	-1.41	0.197	-1.35	0.053
1424358_at	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	-1.34	0.163	-2.76	0.034	-1.43	0.014	-1.63	0.000	-1.7	0.001
1439627_at	zinc finger protein of the cerebellum 1	Zic1	1.16	0.705	1.28	0.861	-1.43	0.038	1.53	0.331	-1.2	0.512
1434967_at	zinc finger, SWIM domain containing 6	Zswim6	1.03	0.057	-1.13	0.247	-1.43	0.015	-1.67	0.006	-1.73	0.001
1459839_x_at	BTB (POZ) domain containing 11	Btbd11	1.61	0.594	-1.97	0.116	-1.42	0.038	-1.16	0.090	-1.37	0.071
1456257_at	RIKEN cDNA C130065N10 gene	C130065N10Rik	1.14	0.362	1.12	0.661	-1.42	0.031	-1.06	0.299	-1.4	0.034
1424770_at	caldesmon 1	Cald1	-1.18	0.327	-1.51	0.043	-1.42	0.036	-1.15	0.077	-1.31	0.001
1431618_a_at	DNA segment, Chr 14, ERATO Doi 581, expressed	D14Ertd581e	4.82	0.443	3.57	0.925	-1.42	0.009	-1.24	0.037	-1.67	0.107
1456145_at	deleted in lymphocytic leukemia, 2	Dleu2	-1.02	0.610	-1.15	0.448	-1.42	0.042	1.14	0.492	1.12	0.829
1430532_at	dymeclin	Dym	1.2	0.669	1.53	0.622	-1.42	0.039	1.37	0.950	-1.2	0.343
1418285_at	ephrin B1	Efnb1	-1.33	0.061	-1.5	0.010	-1.42	0.019	-1.28	0.002	-1.11	0.115
1459749_s_at	FAT tumor suppressor homolog 4 (Drosophila)	Fat4	-1.29	0.307	-3.53	0.094	-1.42	0.024	-1.82	0.001	-1.35	0.087
1446794_at	G protein-coupled receptor 176	Gpr176	1.18	0.869	-1.39	0.243	-1.42	0.034	1.62	0.681	1.02	0.874
1436685_at	hypothetical LOC544888	LOC544888	-1.33	0.169	1.07	0.729	-1.42	0.043	1.63	0.433	1.88	0.017
1457632_s_at	myeloid ecotropic viral integration site-related gene 1	Mrg1	-1.46	0.281	-3.35	0.131	-1.42	0.028	-1.99	0.015	-1.54	0.006
1441055_at	paralemmin 2	Palm2	-1.3	0.362	-1.73	0.295	-1.42	0.015	-1.89	0.010	-1.87	0.004
1417626_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	-1.02	0.713	-1.72	0.005	-1.42	0.003	-1.48	0.000	-1.6	0.007
1416626_at	phospholipase A2, group IB, pancreas	Pla2g1b	1.09	0.967	1.59	0.311	-1.42	0.025	1.2	0.687	1.24	0.347
1437735_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	-1.16	0.388	-1.53	0.127	-1.42	0.038	-1.69	0.015	-1.68	0.006
1434406_at	SLIT-ROBO Rho GTPase activating protein 2	Srgap2	-1.24	0.295	-2.21	0.074	-1.42	0.003	-1.78	0.001	-1.67	0.008
1449815_a_at	single-stranded DNA binding protein 2	Ssbp2	-1.2	0.017	-2.62	0.010	-1.42	0.033	-1.2	0.086	-1.4	0.001
1418513_at	serine/threonine kinase 3 (Ste20, yeast homolog)	Stk3	6.86	0.489	3.77	0.372	-1.42	0.029	-1.11	0.011	-1.58	0.051
1434149_at	transcription factor 4	Tcf4	1.19	0.836	-1.54	0.066	-1.42	0.030	-1.51	0.040	-1.37	0.058
1444453_at	Trp53 regulating kinase	Trp53rk	-1.26	0.424	-1.29	0.145	-1.42	0.032	2.48	0.031	1.37	0.838
1416487_a_at	yes-associated protein 1	Yap1	1.29	0.502	1.03	0.746	-1.42	0.009	-1.26	0.028	-1.39	0.035
1447705_at	RIKEN cDNA 4833432M17 gene	4833432M17Rik	-1.73	0.092	-1.08	0.711	-1.41	0.025	1.44	0.630	-1.02	0.806
1430789_at	RIKEN cDNA 4930452B06 gene	4930452B06Rik	1.15	0.736	1.14	0.719	-1.41	0.049	1.78	0.324	1.01	0.822
1418403_at	a disintegrin and metallopeptidase domain 19 (meltrin beta)	Adam19	6.69	0.600	3.65	0.560	-1.41	0.006	-1.28	0.023	-1.54	0.010
1425223_at	baculoviral IAP repeat-containing 3	Birc3	1.5	0.973	-1.11	0.488	-1.41	0.029	1.29	0.932	-1.01	0.483
1427692_a_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family	Cask	2.84	0.743	1.5	0.203	-1.41	0.021	-1.35	0.045	-1.65	0.090
1455082_at	Casitas B-lineage lymphoma b	Cblb	-1.07	0.213	-1.69	0.007	-1.41	0.018	-1.48	0.044	-1.97	0.041
1450229_at	cofactor required for Sp1 transcriptional activation, subunit 2	Crsp2	1.22	0.193	-1.12	0.347	-1.41	0.015	1.03	0.939	1.21	0.824
1449339_at	DNA segment, Chr 10, ERATO Doi 641, expressed	D10Ertd641e	-1.03	0.657	1.07	0.792	-1.41	0.001	1	0.886	-1.04	0.666
1429064_at	DIP2 disco-interacting protein 2 homolog C (Drosophila)	Dip2c	-1.44	0.104	-3.12	0.032	-1.41	0.002	-1.55	0.004	-1.99	0.008
1419293_at	Down syndrome cell adhesion molecule	Dscam	-1.3	0.188	1.17	0.575	-1.41	0.040	-1.22	0.322	1.77	0.780
1418242_at	Fas-associated factor 1	Faf1	-1.27	0.202	-2.28	0.058	-1.41	0.002	-1.44	0.007	-1.69	0.002
1454958_at	glycogen synthase kinase 3 beta	Gsk3b	1.33	0.417	-1.09	0.447	-1.41	0.025	-1.62	0.001	-1.72	0.001
1454693_at	Histone deacetylase 4	Hdac4	1.19	0.393	-1.21	0.069	-1.41	0.049	-1.46	0.023	-1.77	0.053
1441642_at	Like-glycosyltransferase	Large	1.3	0.423	1.07	0.734	-1.41	0.041	-1.48	0.215	-1.58	0.163
1444625_at	Hypothetical LOC545822	LOC545822	-1.81	0.118	1.09	0.852	-1.41	0.031	2.5	0.665	2.24	0.298
1452320_at	low density lipoprotein receptor-related protein 2	Lrp2	-1.27	0.022	-1.36	0.144	-1.41	0.027	-1.31	0.000	-1.13	0.148
1426759_at	mitogen-activated protein kinase kinase kinase kinase 3 /// similar to	Map4k3 /// LOC675	1.12	0.152	-1.2	0.049	-1.41	0.047	-1.51	0.007	-1.69	0.001
1452209_at	plakophilin 4	Pkp4	-1.24	0.238	-2.01	0.027	-1.41	0.009	-1.6	0.000	-1.6	0.004
1446507_at	Prion protein	Prnp	1.57	0.187	2.24	0.183	-1.41	0.026	1.43	0.272	1.24	0.132
1426023_a_at	rabaptin, RAB GTPase binding effector protein 1	Rabep1	1.69	0.976	1.84	0.242	-1.41	0.037	-1.08	0.408	-1.19	0.262
1453631_at	syntaxin 8	Stx8	-1.19	0.085	1.13	0.567	-1.41	0.034	-1.78	0.025	-1.27	0.299
1457571_at	zinc finger protein 68	Zfp68	1.77	0.481	1.42	0.233	-1.41	0.027	1.48	0.344	-1.14	0.299
1439922_at	RIKEN cDNA 1190002C06 gene	1190002C06Rik	-1.11	0.594	-1.91	0.046	-1.4	0.025	-1.26	0.296	-1.46	0.067
1428493_at	RIKEN cDNA 2610511M17 gene /// similar to signal-induced prolifer	2610511M17Rik ///	-1.17	0.275	-1.74	0.005	-1.4	0.047	-1.8	0.005	-1.63	0.000

1430460_at	RIKEN cDNA 5830410F13 gene	5830410F13Rik	-1.08	0.501	1.25	0.768	-1.4	0.042	1.22	0.600	-1.8	0.164
1429579_at	RIKEN cDNA 6330407I18 gene	6330407I18Rik	1.37	0.889	-1.46	0.112	-1.4	0.047	-1.28	0.037	-1.76	0.015
1423199_at	bromodomain containing 3	Brd3	-1.06	0.492	1.06	0.738	-1.4	0.015	1.12	0.219	-1.04	0.535
1452483_a_at	CD44 antigen	Cd44	1.73	0.572	1.05	0.348	-1.4	0.006	-1.11	0.259	-1.41	0.069
1439040_at	centromere protein E	Cenpe	-1.19	0.477	-1.41	0.227	-1.4	0.022	-1.25	0.203	-1.01	0.803
1433491_at	erythrocyte protein band 4.1-like 2	Epb4.1l2	22.4	0.418	14.39	0.732	-1.4	0.005	-1.14	0.175	-1.48	0.027
1434158_at	GDP-mannose 4, 6-dehydratase	Gmds	-1.3	0.036	-1.34	0.039	-1.4	0.009	-1.13	0.033	-1.3	0.012
1429796_at	kalirin, RhoGEF kinase	Kalrn	-1.29	0.066	-2.17	0.001	-1.4	0.047	-1.71	0.016	-1.54	0.003
1439515_at	SET domain containing 5	Setd5	1.14	0.469	-1.3	0.053	-1.4	0.014	-1.35	0.025	-1.51	0.037
1419503_at	stanniocalcin 2	Stc2	1.46	0.198	1.37	0.354	-1.4	0.048	-1.11	0.412	1.2	0.483
1441842_s_at	zinc finger protein 707	Zfp707	1	0.921	1.31	0.227	-1.4	0.000	1.25	0.271	1.55	0.010
1420339_at	RIKEN cDNA 0610016J10 gene	0610016J10Rik	-1.04	0.706	-1.54	0.003	-1.39	0.006	-1.18	0.024	-1.49	0.010
1432720_at	RIKEN cDNA 4833412K13 gene	4833412K13Rik	1.27	0.113	1.06	0.911	-1.39	0.031	-1.07	0.553	1.23	0.392
1423244_at	RIKEN cDNA 9030012A22 gene	9030012A22Rik	-1.29	0.139	-1.52	0.167	-1.39	0.017	1.1	0.599	-1.05	0.763
1440430_at	RIKEN cDNA A130004G07 gene	A130004G07Rik	3.29	0.604	2.53	0.573	-1.39	0.003	2.47	0.577	-1.34	0.192
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	-1.38	0.031	-2.43	0.034	-1.39	0.004	-1.25	0.012	-1.34	0.049
1426300_at	activated leukocyte cell adhesion molecule	Alcam	-1.08	0.401	-1.12	0.050	-1.39	0.019	-1.17	0.167	-1.1	0.203
1447930_at	bromodomain adjacent to zinc finger domain 1A	Baz1a	1.07	0.137	1.12	0.233	-1.39	0.035	-1.07	0.032	-1.2	0.020
1422887_a_at	C-terminal binding protein 2	Ctbp2	1.03	0.459	-1.22	0.068	-1.39	0.009	-1.46	0.000	-1.37	0.012
1452220_at	dedicator of cyto-kinesis 1	Dock1	-1	0.781	-1.98	0.022	-1.39	0.024	-1.36	0.017	-1.61	0.008
1422018_at	human immunodeficiency virus type I enhancer binding protein 2	Hivep2	1.23	0.748	-1.12	0.303	-1.39	0.018	-1.44	0.025	-1.92	0.000
1444040_at	leukocyte-associated Ig-like receptor 1	Lair1	1.66	0.372	1.28	0.230	-1.39	0.025	1.31	0.897	1.93	0.754
1450437_a_at	neural cell adhesion molecule 1	Ncam1	1.76	0.774	1.54	0.358	-1.39	0.041	-1.12	0.296	-1.18	0.249
1440996_at	Neural precursor cell expressed, developmentally down-regulated ge	Nedd8	2.37	0.418	2.88	0.429	-1.39	0.050	1.2	0.296	1.27	0.275
1423117_at	pumilio 1 (Drosophila)	Pum1	1.49	0.629	1.73	0.371	-1.39	0.009	-1.36	0.011	-1.2	0.107
1452136_at	solute carrier family 5 (sodium/glucose cotransporter), member 9	Slc5a9	1.24	0.121	1.07	0.542	-1.39	0.046	1	0.778	1.56	0.331
1453058_at	WD repeat domain 5B	Wdr5b	4.53	0.030	2.81	0.166	-1.39	0.014	-1.03	0.419	-1.09	0.381
1441052_at	RIKEN cDNA 2310035C23 gene	2310035C23Rik	-1.11	0.453	1	0.684	-1.38	0.013	1	0.889	-1.47	0.085
1429595_at	RIKEN cDNA 2700049A03 gene	2700049A03Rik	-1.15	0.291	-1.54	0.174	-1.38	0.049	-1.03	0.658	-1.1	0.128
1430407_at	RIKEN cDNA 3110035C09 gene	3110035C09Rik	1.2	0.767	1.04	0.596	-1.38	0.039	-1.46	0.028	-1.27	0.204
1451568_at	RIKEN cDNA A630054L15 gene	A630054L15Rik	-1.23	0.296	-1.53	0.064	-1.38	0.034	1.03	0.988	1.4	0.025
1421172_at	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	Adam12	1.01	0.686	-1.48	0.109	-1.38	0.024	-1.23	0.050	-1.53	0.001
1425099_a_at	aryl hydrocarbon receptor nuclear translocator-like	Arntl	-1.08	0.412	-1.56	0.015	-1.38	0.020	-1.43	0.010	-1.77	0.007
1435600_s_at	cDNA sequence BC020535	BC020535	1.71	0.004	1.29	0.730	-1.38	0.017	1.69	0.332	-1.45	0.092
1443986_at	Vcell division cycle 73, Paf1/RNA polymerase II complex component	Cdc73	1.41	0.545	1.16	0.708	-1.38	0.035	-1.11	0.300	-1.61	0.003
1458534_at	DNA segment, Chr 13, Brigham & Women's Genetics 1146 expresse	D13Bwg1146e	1.26	0.923	1.42	0.603	-1.38	0.038	2.56	0.071	-1.22	0.339
1441631_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	Ddx24	2.29	0.613	4.56	0.453	-1.38	0.039	-1.03	0.674	1.21	0.747
1453372_at	DnaJ (Hsp40) homolog, subfamily C, member 1	Dnajc1	1.05	0.384	-1.35	0.013	-1.38	0.031	-1.2	0.010	-1.51	0.009
1450616_at	eosinophil-associated, ribonuclease A family, member 5	Ear5	1.16	0.805	-1.7	0.078	-1.38	0.044	-1.03	0.373	-1.37	0.264
1437201_at	leucine rich repeat containing 4C	Lrrc4c	-1.26	0.266	-3.7	0.014	-1.38	0.012	-1.53	0.005	-1.52	0.076
1426785_s_at	monoglyceride lipase	Mgll	-1.12	0.164	-1.47	0.063	-1.38	0.024	-1.17	0.028	-1.23	0.054
1432591_at	pregnancy-associated plasma protein A	Pappa	-1.06	0.413	-1.73	0.010	-1.38	0.021	-1.29	0.013	-1.61	0.003
1450406_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	1.09	0.508	-1.3	0.082	-1.38	0.012	-1.25	0.021	-1.26	0.094
1436499_at	transmembrane protein 23	Tmem23	-1.08	0.076	-1.53	0.023	-1.38	0.024	-1.61	0.001	-1.55	0.030
1437155_a_at	WW domain containing transcription regulator 1	Wwtr1	-1.05	0.470	-1.46	0.005	-1.38	0.007	-1.35	0.023	-1.25	0.001
1417848_at	zinc finger protein 704	Zfp704	-1.37	0.262	-3.26	0.102	-1.38	0.003	-1.36	0.109	-1.48	0.005
1441867_x_at	RIKEN cDNA 4930534B04 gene	4930534B04Rik	-1.4	0.272	-2.05	0.048	-1.37	0.029	-1.26	0.164	-1.18	0.166
1427980_at	RIKEN cDNA 4933407C03 gene	4933407C03Rik	1.3	0.240	-1.06	0.740	-1.37	0.002	-1.44	0.019	-1.4	0.001
1456011_x_at	acetyl-Coenzyme A acyltransferase 1A	Acaa1a	-1.19	0.412	1.02	0.514	-1.37	0.038	1.31	0.140	1.16	0.101
1456021_at	activating transcription factor 6	Atf6	1.15	0.680	-1.5	0.046	-1.37	0.013	-1.28	0.133	-1.79	0.005
1449244_at	cadherin 2	Cdh2	1	0.807	-1.33	0.020	-1.37	0.040	-1.18	0.146	-1.5	0.002
1452570_at	DNA segment, KIST 5	D0Kist5	1.3	0.671	1.31	0.914	-1.37	0.046	-1.08	0.838	1.23	0.863
1455244_at	dishevelled associated activator of morphogenesis 1	Daam1	1.25	0.378	-1.32	0.171	-1.37	0.015	-1.65	0.002	-1.65	0.000
1424586_at	EH domain binding protein 1	Ehbp1	-1.19	0.028	-2.61	0.004	-1.37	0.008	-1.44	0.014	-1.71	0.031
1429034_at	essential meiotic endonuclease 1 homolog 2 (S. pombe)	Eme2	-1.46	0.258	-1.72	0.230	-1.37	0.007	-1.21	0.171	1.36	0.501
1419829_a_at	Growth factor receptor bound protein 2-associated protein 2	Gab2	-1.33	0.264	-2.42	0.071	-1.37	0.022	-2.03	0.003	-1.69	0.007
1422154_at	G protein-coupled receptor 27	Gpr27	-1.06	0.561	-1.26	0.114	-1.37	0.028	1.52	0.358	1	0.986
1455078_at	Heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	1.04	0.800	-1.61	0.011	-1.37	0.008	-1.54	0.017	-1.38	0.016

1451804_a_at	leucine rich repeat containing 16	Lrrc16	1	0.759	-3.49	0.004	-1.37	0.018	-1.96	0.005	-1.71	0.014
1435461_at	membrane associated guanylate kinase, WW and PDZ domain conta	Magi3	-1.16	0.207	-3.3	0.018	-1.37	0.020	-1.46	0.094	-1.68	0.004
1435233_at	nuclear receptor coactivator 2	Ncoa2	-1.03	0.632	-2.98	0.003	-1.37	0.006	-1.79	0.001	-1.46	0.025
1459707_at	Phosphofurin acidic cluster sorting protein 1	Pacs1	-1.19	0.394	-1.51	0.296	-1.37	0.034	-1.21	0.360	1.11	0.880
1454900_s_at	pam, highwire, rpm 1	Phr1	-1.13	0.417	-1.97	0.055	-1.37	0.024	-1.64	0.005	-1.78	0.026
1460732_a_at	periplakin	Ppl	1.29	0.828	-1.32	0.250	-1.37	0.015	1.13	0.432	1.83	0.252
1434005_at	RNA binding motif, single stranded interacting protein 1	Rbms1	-1.01	0.888	-1.53	0.001	-1.37	0.002	-1.49	0.003	-1.58	0.005
1427299_at	ribosomal protein S6 kinase polypeptide 3	Rps6ka3	-1.05	0.287	-1.42	0.011	-1.37	0.010	-1.29	0.039	-1.42	0.005
1454699_at	sestrin 1	Sesn1	3.14	0.412	1.84	0.500	-1.37	0.033	1.22	0.404	-1.06	0.537
1454894_at	SMAD specific E3 ubiquitin protein ligase 2	Smurf2	1.12	0.422	-1.07	0.536	-1.37	0.000	-1.49	0.004	-1.44	0.002
1455042_at	Transducin (beta)-like 1 X-linked	Tbl1x	1.36	0.550	-1.02	0.467	-1.37	0.007	-1.38	0.003	-1.56	0.006
1444042_at	thyroid hormone receptor interactor 11	Trip11	1.48	0.242	1.38	0.473	-1.37	0.002	-1.12	0.507	1.06	0.365
1439129_at	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	1110060D06Rik ///	1.14	0.981	-1.62	0.077	-1.36	0.040	-1.61	0.013	-1.99	0.014
1454055_at	RIKEN cDNA 1600029O15 gene	1600029O15Rik	1.94	0.367	3.18	0.002	-1.36	0.026	-1.67	0.123	3.02	0.062
1429700_at	RIKEN cDNA 3110040M04 gene /// similar to U2-associated SR140	3110040M04Rik ///	1.08	0.650	1.14	0.435	-1.36	0.032	-1.15	0.126	-1.06	0.321
1430602_at	RIKEN cDNA 4930520K10 gene	4930520K10Rik	-1.23	0.358	-1.01	0.630	-1.36	0.011	1.96	0.380	1.23	0.192
1460560_at	BAH domain and coiled-coil containing 1	Bahcc1	1.21	0.944	-1.01	0.475	-1.36	0.002	-1.06	0.407	-1.08	0.483
1425123_at	cDNA sequence BC025816	BC025816	1.11	0.612	1.19	0.381	-1.36	0.021	1.35	0.117	-1.03	0.816
1423699_at	DNA segment, Chr 15, ERATO Doi 785, expressed	D15Ertd785e	-1.01	0.731	1.05	0.810	-1.36	0.018	1.01	0.971	-1.36	0.017
1449223_at	DnaJ (Hsp40) homolog, subfamily B, member 8	Dnajb8	2.1	0.465	1.76	0.820	-1.36	0.012	1.02	0.744	2.03	0.202
1455117_at	minichromosome maintenance deficient domain containing 1	Mcmdc1	1.07	0.923	-1.67	0.073	-1.36	0.015	-1.22	0.068	-1.03	0.767
1459679_s_at	myosin IB	Myo1b	-1.1	0.068	-1.83	0.019	-1.36	0.018	-1.31	0.202	-1.86	0.076
1418892_at	ras homolog gene family, member J	Rhoj	1.03	0.973	-1.46	0.025	-1.36	0.036	-1.23	0.018	-1.13	0.225
1459666_at	trafficking protein, kinesin binding 1	Trak1	-1.26	0.096	-1.4	0.005	-1.36	0.020	-1.22	0.046	-1.4	0.044
1432779_at	RIKEN cDNA 1700037N05 gene	1700037N05Rik	1.28	0.525	-1.01	0.666	-1.35	0.026	-1.02	0.700	1.06	0.896
1437216_at	RIKEN cDNA A430106J12 gene	A430106J12Rik	1.11	0.222	-1.3	0.181	-1.35	0.021	-1.32	0.037	-1.7	0.043
1436498_at	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1	Arih1	1.44	0.410	1.05	0.737	-1.35	0.007	-1.2	0.046	-1.51	0.018
1432900_at	cDNA sequence BC026657	BC026657	-1.2	0.291	-1.35	0.202	-1.35	0.049	-1.3	0.257	1.37	0.143
1435903_at	CD300A antigen	Cd300a	2.92	0.641	2.67	1.000	-1.35	0.048	1.21	0.138	1.48	0.423
1438255_at	checkpoint suppressor 1	Ches1	-1	0.861	-1.7	0.014	-1.35	0.012	-1.5	0.039	-1.3	0.060
1439090_at	RIKEN cDNA D030022P07 gene	D030022P07Rik	-1.22	0.122	-1.2	0.107	-1.35	0.004	-1.14	0.518	-1	0.592
1447631_at	MYST histone acetyltransferase 2	Myst2	-1.36	0.201	-1.84	0.111	-1.35	0.012	-1.07	0.357	1.63	0.075
1416818_at	parvin, alpha	Parva	1.97	0.421	1.61	0.661	-1.35	0.015	-1.04	0.380	-1.19	0.091
1449320_at	probasin	Pbsn	-1.04	0.498	-1.17	0.453	-1.35	0.024	1.26	0.846	1.31	0.876
1459903_at	sema domain, immunoglobulin domain (Ig), and GPI membrane anc	Sema7a	-1.21	0.128	-1.85	0.049	-1.35	0.013	-1.38	0.018	-1.41	0.005
1457528_at	solute carrier family 4, sodium bicarbonate cotransporter, member 7	Slc4a7	1.83	0.132	1.74	0.277	-1.35	0.003	1.08	0.173	-1.28	0.154
1421215_a_at	sarcolemma associated protein	Slmap	1.81	0.852	1.28	0.869	-1.35	0.017	-1.04	0.450	-1.07	0.398
1448639_a_at	spermatogenesis associated 5	Spata5	-1.23	0.262	-1.19	0.268	-1.35	0.013	-1.46	0.005	-1.58	0.001
1456634_at	RIKEN cDNA 9830001H06 gene	9830001H06Rik	1.22	0.912	1.28	0.954	-1.34	0.012	-1.32	0.042	-1.04	0.704
1437124_at	RIKEN cDNA A630052C17 gene	A630052C17Rik	-1.06	0.190	-1.07	0.414	-1.34	0.027	-1.19	0.070	1.12	0.561
1435769_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	-1.03	0.630	-1.71	0.022	-1.34	0.031	-1.31	0.030	-1.34	0.036
1429600_at	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofo	C630010D07Rik ///	1.8	0.037	1.4	0.578	-1.34	0.001	-1.12	0.351	-1.17	0.188
1420380_at	chemokine (C-C motif) ligand 2	Ccl2	1.21	0.920	1.13	0.461	-1.34	0.021	-1.14	0.131	-1.56	0.019
1439727_at	chloride channel calcium activated 6 /// expressed sequence AI7474	Clca6 /// AI747448	1.15	0.873	1.34	0.627	-1.34	0.017	-1.06	0.655	1.31	0.089
1434112_at	latrophilin 2	Lphn2	-1.15	0.327	-1.88	0.022	-1.34	0.002	-1.14	0.113	-1.43	0.019
1444422_at	protocadherin 19	Pcdh19	-1.21	0.242	-1.87	0.022	-1.34	0.002	-1.26	0.078	-1.41	0.006
1453164_a_at	phosphatidylserine synthase 2	Ptdss2	1.39	0.357	1.12	0.642	-1.34	0.013	1.12	0.957	-1.07	0.667
1448754_at	retinol binding protein 1, cellular	Rbp1	-1.08	0.489	1.11	0.183	-1.34	0.001	-1.04	0.692	1.27	0.702
1423129_at	soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	1.38	0.397	1.22	0.671	-1.34	0.008	-1.28	0.036	-1.45	0.025
1423077_at	sorting nexin 9	Snx9	1.87	0.466	1.3	0.660	-1.34	0.004	-1.18	0.007	-1.42	0.016
1433648_at	sperm associated antigen 9	Spag9	1.08	0.400	-1.4	0.049	-1.34	0.002	-1.22	0.021	-1.36	0.006
1419073_at	transmembrane protein with EGF-like and two follistatin-like domains	Tmeff2	-1.14	0.194	-2.11	0.017	-1.34	0.023	-1.21	0.080	-1.57	0.001
1422705_at	transmembrane, prostate androgen induced RNA	Tmepai	1.45	0.421	1.05	0.543	-1.34	0.014	-1.21	0.029	-1.18	0.012
1420725_at	trimethyllysine hydroxylase, epsilon	Tmlhe	-1.44	0.230	-1.59	0.167	-1.34	0.013	-1.43	0.069	-1.04	0.695
1451959_a_at	vascular endothelial growth factor A	Vegfa	6.67	0.537	4.92	0.934	-1.34	0.008	-1.01	0.654	-1.12	0.309
1446789_at	Zinc finger CCHC-type and RNA binding motif 1	Zcrb1	1.24	0.679	-1	0.589	-1.34	0.005	-1.02	0.524	-1.6	0.084
1436425_at	ankyrin repeat domain 38	Ankrd38	-1.31	0.375	-1.11	0.376	-1.33	0.034	-1.09	0.459	1.29	0.671
1450915_at	adaptor-related protein complex 3, beta 1 subunit	Ap3b1	1.11	0.514	-1.29	0.107	-1.33	0.032	-1.33	0.047	-1.35	0.012

1441980_at	RIKEN cDNA C030007I09 gene	C030007I09Rik	-1.15	0.394	-2.11	0.127	-1.33	0.031	-1.38	0.102	-1.76	0.003
1443417_at	expressed sequence C87122	C87122	1.54	0.506	1.29	0.605	-1.33	0.026	1.03	0.948	-1.22	0.104
1451811_at	calcium channel, voltage-dependent, gamma subunit 6	Cacng6	1.72	0.291	1.76	0.319	-1.33	0.002	-1.09	0.397	1.53	0.826
1450288_at	cadherin 6	Cdh6	1.08	0.578	-1.36	0.155	-1.33	0.007	-1.12	0.201	-1.77	0.083
1450756_s_at	cullin 3	Cul3	3.04	0.568	2.14	0.912	-1.33	0.021	-1.28	0.010	-1.55	0.000
1448665_at	dystrophin, muscular dystrophy	Dmd	-1.02	0.519	-1.49	0.028	-1.33	0.015	-1.45	0.039	-1.39	0.019
1428933_at	histone deacetylase 8	Hdac8	1.2	0.707	-1.5	0.082	-1.33	0.024	-1.24	0.221	-1.42	0.042
1418125_at	INO80 complex homolog 1 (S. cerevisiae)	Inoc1	-1.12	0.462	-1.27	0.298	-1.33	0.010	-1.52	0.007	-1.17	0.162
1427143_at	jumonji, AT rich interactive domain 1B (Rbp2 like)	Jarid1b	-1	0.695	1.03	0.948	-1.33	0.015	-1.2	0.053	-1.22	0.001
1428644_at	mannoside acetylglucosaminyltransferase 5	Mgat5	-1.45	0.195	-2.39	0.128	-1.33	0.047	-1.52	0.022	-1.31	0.100
1418391_at	PHD finger protein 21A	Phf21a	-1.02	0.647	-1.51	0.104	-1.33	0.043	-1.49	0.052	-1.75	0.018
1426401_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	-1.14	0.031	-2.45	0.013	-1.33	0.008	-1.44	0.010	-1.39	0.068
1432057_a_at	PR domain containing 5	Prdm5	1.02	0.684	-1.34	0.097	-1.33	0.003	-1.36	0.023	-1.27	0.031
1418245_a_at	RNA binding motif protein 9	Rbm9	1.18	0.522	1.1	0.840	-1.33	0.014	-1.16	0.253	-1.15	0.065
1422865_at	runt related transcription factor 1	Runx1	2.6	0.402	2.23	0.699	-1.33	0.038	-1.2	0.171	-1.46	0.020
1443762_s_at	SET binding factor 2	Sbf2	-1.32	0.225	-2.23	0.049	-1.33	0.004	-1.53	0.004	-1.55	0.007
1421594_a_at	synaptotagmin-like 2	Sytl2	-1.09	0.141	-2.02	0.004	-1.33	0.004	-1.45	0.027	-1.43	0.026
1443993_at	zinc finger CCCH type containing 12A	Zc3h12a	2.94	0.415	3.11	0.670	-1.33	0.050	-1.15	0.368	-1.28	0.086
1453333_at	RIKEN cDNA 1700012P22 gene	1700012P22Rik	-1.07	0.559	-1.65	0.048	-1.32	0.037	-1.29	0.131	-1.18	0.251
1435672_at	hypothetical protein 3830612M24	3830612M24	-1.16	0.404	-3.21	0.142	-1.32	0.001	-1.66	0.002	-1.43	0.104
1434949_at	armadillo repeat containing 8	Armc8	-1.07	0.545	-1.13	0.217	-1.32	0.005	-1.29	0.048	-1.43	0.034
1434409_at	armadillo repeat containing, X-linked 6	Armcx6	1.46	0.839	1.92	0.704	-1.32	0.040	1.88	0.539	1.16	0.776
1460597_at	Additional sex combs like 2 (Drosophila)	Asxl2	1.07	0.838	1.03	0.755	-1.32	0.019	-1.13	0.229	1.11	0.228
1434769_at	BTB (POZ) domain containing 9	Btbd9	-1.34	0.267	-2.53	0.139	-1.32	0.049	-1.95	0.022	-1.67	0.034
1450757_at	cadherin 11	Cdh11	1.18	0.506	-1.18	0.213	-1.32	0.004	-1.3	0.001	-1.35	0.007
1453409_at	cell growth regulator with ring finger domain 1	Cgrrf1	-1.01	0.691	1.02	0.796	-1.32	0.048	-1.14	0.211	1.15	0.196
1430161_at	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glut	Dlst	-1.23	0.233	1.39	0.678	-1.32	0.002	-1.01	0.420	-1.01	0.700
1434260_at	FCH and double SH3 domains 2	Fchsd2	-1.03	0.511	-1.63	0.031	-1.32	0.011	-1.68	0.000	-1.35	0.005
1460203_at	inositol 1,4,5-triphosphate receptor 1	Itpr1	-1.24	0.068	-2.05	0.011	-1.32	0.029	-1.29	0.030	-1.46	0.037
1434900_at	MKL (megakaryoblastic leukemia)/myocardin-like 1	Mkl1	1.31	0.483	1.25	0.647	-1.32	0.001	-1.44	0.018	-1.3	0.155
1434179_at	myeloid/lymphoid or mixed-lineage leukemia 3	Mll3	-1.06	0.375	-2.61	0.014	-1.32	0.046	-1.36	0.017	-1.88	0.009
1418912_at	plexin domain containing 2	Plxdc2	-1.04	0.549	-1.24	0.005	-1.32	0.006	-1.14	0.064	-1.34	0.023
1452788_at	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	Ppp2r5e	3.82	0.240	3.44	0.799	-1.32	0.049	-1.36	0.045	-1.61	0.012
1423025_a_at	schwannomin interacting protein 1	Schip1	1.22	0.673	-1.03	0.417	-1.32	0.034	-1.49	0.001	-1.44	0.012
1419255_at	spectrin beta 2	Spnb2	1.09	0.759	-1.25	0.125	-1.32	0.035	-1.26	0.017	-1.48	0.013
1455493_at	synaptic nuclear envelope 1	Syne1	-1.16	0.375	-2.54	0.079	-1.32	0.039	-1.19	0.136	-1.51	0.018
1427685_a_at	synaptojanin 2	Synj2	1.13	0.819	1.09	0.910	-1.32	0.018	-1.4	0.002	-1.25	0.000
1428703_at	RIKEN cDNA 1700012B07 gene	1700012B07Rik	-1.03	0.423	1.22	0.282	-1.31	0.003	1.02	0.737	1	0.926
1457982_at	RIKEN cDNA 1700052M18 gene	1700052M18Rik	1.17	0.648	2.78	0.586	-1.31	0.004	1.04	0.837	2.26	0.611
1454255_at	RIKEN cDNA 5430434F05 gene	5430434F05Rik	1.43	0.051	-1.09	0.530	-1.31	0.043	1.28	0.208	1.4	0.252
1453015_at	RIKEN cDNA 5830471E12 gene	5830471E12Rik	-1.23	0.336	-1.78	0.137	-1.31	0.008	-1.53	0.001	-1.64	0.020
1435280_at	expressed sequence AI452195	AI452195	-1.14	0.398	-1.32	0.249	-1.31	0.019	-1.13	0.031	-1.34	0.009
1427328_a_at	CLIP associating protein 2	Clasp2	-1.01	0.545	-1.42	0.122	-1.31	0.019	-1.24	0.288	-1.22	0.405
1445868_at	cytoplasmic polyadenylation element binding protein 3	Cpeb3	1.18	0.663	1.66	0.782	-1.31	0.013	1.04	0.669	1.37	0.365
1438658_a_at	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	Edg3	-1.43	0.285	-2	0.181	-1.31	0.006	-1.29	0.020	-1.37	0.015
1451264_at	FERM domain containing 6	Frmd6	1.16	0.580	-1.06	0.583	-1.31	0.016	-1.28	0.014	-1.37	0.002
1427746_x_at	histocompatibility 2, K1, K region	H2-K1	1.99	0.785	1.78	0.604	-1.31	0.007	-1.02	0.906	-1.05	0.473
1450692_at	kinesin family member 4	Kif4	1.03	0.388	-1.19	0.131	-1.31	0.009	-1.19	0.075	-1.24	0.041
1435139_at	NMDA receptor-regulated gene 1	Narg1	1	0.997	-1.16	0.062	-1.31	0.024	-1.15	0.275	-1.4	0.027
1457175_at	Numb gene homolog (Drosophila)	Numb	1.3	0.271	1.25	0.997	-1.31	0.047	1.63	0.636	-1.27	0.174
1438413_at	SUMO1/sentrin specific peptidase 7	Senp7	1.1	0.661	-1.19	0.177	-1.31	0.039	1.13	0.416	-1.04	0.581
1452296_at	slit homolog 3 (Drosophila)	Slit3	-1.25	0.272	-1.77	0.140	-1.31	0.020	-1.18	0.021	-1.28	0.090
1452604_at	serologically defined colon cancer antigen 13	Stard13	1.63	0.499	1.52	0.528	-1.31	0.030	-1.32	0.029	-1.52	0.014
1419447_s_at	TBC1 domain family, member 1	Tbc1d1	1.17	0.447	-1.26	0.126	-1.31	0.003	-1.5	0.001	-1.43	0.009
1455308_at	transmembrane protein 16F	Tmem16f	-1.2	0.296	-1.83	0.088	-1.31	0.008	-1.4	0.019	-1.5	0.007
1416231_at	Vac14 homolog (S. cerevisiae)	Vac14	-1.11	0.448	-1.45	0.279	-1.31	0.001	-1.24	0.279	1.16	0.698
1448611_at	WW, C2 and coiled-coil domain containing 2	Wwc2	-1	0.839	-1.42	0.007	-1.31	0.031	-1.63	0.031	-1.69	0.031
1419874_x_at	zinc finger and BTB domain containing 16	Zbtb16	-1.07	0.446	-1.11	0.403	-1.31	0.028	2.5	0.213	1.4	0.295

1429946_at	RIKEN cDNA 2610301F02 gene	2610301F02Rik	-1.18	0.382	-1.09	0.522	-1.3	0.014	1.62	0.153	1.22	0.723
1448460_at	activin A receptor, type 1	Acvr1	1.31	0.908	1.14	0.453	-1.3	0.043	-1.4	0.003	-1.55	0.001
1441228_at	apolipoprotein L domain containing 1	Apold1	1.1	0.658	1.25	0.142	-1.3	0.030	1.14	0.165	1.04	0.984
1427630_x_at	CEA-related cell adhesion molecule 1	Ceacam1	1.05	0.618	1.99	0.516	-1.3	0.029	1.88	0.979	-1.11	0.489
1453872_at	doublesex and mab-3 related transcription factor like family C2	Dmrtc2	-1.12	0.321	1.12	0.697	-1.3	0.029	1.41	0.609	1.22	0.519
1423065_at	DNA methyltransferase 3A	Dnmt3a	-1.33	0.330	-1.64	0.212	-1.3	0.017	-1.41	0.140	-1.33	0.171
1423626_at	dystonin	Dst	1.01	0.786	-1.21	0.059	-1.3	0.020	-1.18	0.079	-1.32	0.068
1451977_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	1.65	0.575	1.47	0.658	-1.3	0.009	-1.28	0.022	-1.29	0.035
1452280_at	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondroc	Farp1	1.44	0.705	-1.2	0.200	-1.3	0.019	-1.44	0.000	-1.65	0.000
1439662_at	homer homolog 1 (Drosophila)	Homer1	-1.03	0.569	-1.27	0.265	-1.3	0.048	-1.18	0.155	-1.14	0.307
1432296_a_at	integrin alpha V	Itgav	1.13	0.393	-1.68	0.034	-1.3	0.008	1.22	0.304	-1.02	0.349
1427809_at	Latrophilin 3	Lphn3	1.71	0.105	-1.34	0.035	-1.3	0.028	1.67	0.859	1.05	0.651
1427185_at	myocyte enhancer factor 2A	Mef2a	1.34	0.328	1.03	0.814	-1.3	0.009	-1.4	0.017	-1.51	0.012
1443498_at	methylmalonic aciduria (cobalamin deficiency) type B homolog (hum	Mmab	-1.38	0.061	-1.13	0.248	-1.3	0.010	-1.57	0.044	-1.05	0.694
1438684_at	NUAK family, SNF1-like kinase, 1	Nuak1	-1.22	0.248	-1.41	0.152	-1.3	0.006	-1.32	0.030	-1.4	0.010
1449120_a_at	pericentriolar material 1	Pcm1	1.26	0.462	1.17	0.659	-1.3	0.050	-1.25	0.124	-1.15	0.329
1442171_at	PRP40 pre-mRNA processing factor 40 homolog A (yeast)	Prpf40a	1.04	0.735	1.04	0.701	-1.3	0.042	-1.02	0.728	-1.14	0.432
1450122_at	protein tyrosine phosphatase, receptor type, G	Ptprg	3.12	0.668	2.32	0.778	-1.3	0.016	-1.16	0.195	-1.31	0.040
1456153_at	slingshot homolog 2 (Drosophila)	Ssh2	1.21	0.251	-1.46	0.012	-1.3	0.002	-1.26	0.087	-1.62	0.007
1450396_at	stromal antigen 2	Stag2	1.23	0.139	1.06	0.766	-1.3	0.013	-1.13	0.169	-1.37	0.059
1418057_at	T-cell lymphoma invasion and metastasis 1	Tiam1	-1.28	0.188	-2.08	0.033	-1.3	0.024	-1.19	0.362	-1.51	0.048
1447370_at	Transmembrane protein 16A	Tmem16a	-1.27	0.184	-2.23	0.051	-1.3	0.028	-1.05	0.616	1.02	0.744
1423036_at	thioredoxin-like 5	Txnl5	1.42	0.157	1.13	0.534	-1.3	0.013	-1.07	0.485	1.15	0.609
1456389_at	zinc finger homeobox 1b	Zfhx1b	1.06	0.363	-1.39	0.029	-1.3	0.015	-1.31	0.075	-1.47	0.022
1453384_at	RIKEN cDNA 4632404N19 gene	4632404N19Rik	1.06	0.951	-1.09	0.498	-1.29	0.041	-1.33	0.286	-1.66	0.051
1449709_s_at	arginine-tRNA-protein transferase 1	Ate1	1.07	0.569	-1.22	0.145	-1.29	0.031	-1.33	0.026	-1.51	0.004
1450457_at	Casitas B-lineage lymphoma	Cbl	1.5	0.729	1.77	0.683	-1.29	0.001	-1.09	0.130	1.05	0.959
1455440_at	chloride channel 6	Clcn6	1.02	0.952	-1.26	0.012	-1.29	0.025	-1.2	0.188	-1.37	0.013
1428806_at	casein kinase 1, gamma 1	Csnk1g1	1	0.927	-1.06	0.482	-1.29	0.001	-1.46	0.002	-1.41	0.005
1438045_at	early endosome antigen 1	Eea1	1.27	0.275	-1.34	0.109	-1.29	0.027	-1.24	0.012	-1.59	0.038
1425142_a_at	heterogeneous nuclear ribonucleoprotein D	Hnrpd	-1.11	0.036	-1.3	0.026	-1.29	0.008	-1.24	0.008	-1.19	0.103
1434129_s_at	lipoma HMGIC fusion partner-like 2	Lhfpl2	-1.04	0.817	-1.68	0.014	-1.29	0.008	-1.18	0.055	-1.5	0.019
1434674_at	lysosomal trafficking regulator	Lyst	1.54	0.537	-1.59	0.107	-1.29	0.034	-1.38	0.063	-1.59	0.012
1427212_at	mitogen-activated protein kinase associated protein 1	Mapkap1	1.39	0.788	-1.39	0.111	-1.29	0.016	-1.45	0.003	-1.48	0.007
1432177_a_at	menage a trois 1	Mnat1	1.11	0.613	-1.31	0.082	-1.29	0.024	-1.49	0.022	-1.61	0.003
1435463_s_at	myosin ID	Myo1d	-1.18	0.000	-2.15	0.003	-1.29	0.000	-1.26	0.004	-1.31	0.014
1423202_a_at	nuclear receptor co-repressor 1	Ncor1	1.09	0.341	-1.09	0.615	-1.29	0.041	-1.32	0.070	-1.57	0.056
1434653_at	PTK2 protein tyrosine kinase 2 beta	Ptk2b	-1.05	0.703	-1.83	0.010	-1.29	0.003	-1.41	0.026	-1.29	0.125
1433871_at	R3H domain 1 (binds single-stranded nucleic acids)	R3hdm1	1.06	0.334	-1.23	0.014	-1.29	0.031	-1.17	0.004	-1.19	0.023
1436923_at	RAB2B, member RAS oncogene family	Rab2b	1.07	0.371	1.1	0.386	-1.29	0.031	1.22	0.225	-1.05	0.481
1455181_at	RAS p21 protein activator 2	Rasa2	-1.01	0.704	-1.38	0.135	-1.29	0.032	-1.4	0.020	-1.5	0.020
1438932_at	RAS, guanyl releasing protein 2	Rasgrp2	1.06	0.703	1.13	0.896	-1.29	0.042	1.48	0.064	1.13	0.537
1455936_a_at	RNA binding protein gene with multiple splicing	Rbpms	-1.34	0.314	-1.88	0.150	-1.29	0.026	-1.44	0.001	-1.24	0.098
1452964_at	tubulin tyrosine ligase-like family, member 11	Ttll11	-1.15	0.202	-1.93	0.021	-1.29	0.046	-1.32	0.017	-1.55	0.032
1448939_at	ubiquitin specific peptidase 25	Usp25	-1.07	0.527	-1.45	0.024	-1.29	0.014	-1.29	0.095	-1.2	0.322
1434393_at	ubiquitin specific peptidase 34	Usp34	1.57	0.150	1.09	0.548	-1.29	0.011	-1.4	0.014	-1.83	0.015
1434517_at	WD repeat and FYVE domain containing 2	Wdfy2	-1.27	0.328	-1.84	0.174	-1.29	0.016	-1.28	0.003	-1.21	0.194
1438580_at	zinc finger, CCHC domain containing 7	Zcchc7	1.24	0.271	-1.23	0.228	-1.29	0.043	-1.18	0.237	-2	0.025
1443005_at	zinc finger homeobox 1a	Zfhx1a	-1.24	0.029	-1.51	0.031	-1.29	0.041	-1.33	0.117	1.04	0.912
1458439_a_at	RIKEN cDNA 2310047C04 gene	2310047C04Rik	1.02	0.647	-1.48	0.269	-1.28	0.002	1.02	0.848	-1.35	0.067
1453451_at	RIKEN cDNA 6820402I19 gene	6820402I19Rik	1.14	0.961	-1.39	0.203	-1.28	0.042	-1.12	0.239	-1.45	0.137
1439827_at	a disintegrin-like and metallopeptidase (reprolysin type) with thromb	Adamts12	1.22	0.304	-1.02	0.634	-1.28	0.003	-1.07	0.078	-1.3	0.019
1454763_at	ankyrin repeat domain 17	Ankrd17	1.59	0.304	1.63	0.542	-1.28	0.004	-1.36	0.005	-1.46	0.001
1427193_at	bromodomain containing 8	Brd8	1.47	0.113	-1.22	0.370	-1.28	0.008	-1.23	0.289	-1.19	0.394
1456523_at	expressed sequence C77713	C77713	1.61	0.624	1.13	0.488	-1.28	0.002	-1.25	0.032	-1.3	0.003
1439511_at	Cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activati	Cdk7	2.3	0.452	2.32	0.820	-1.28	0.044	-1.08	0.577	-1.07	0.649
1439820_at	Early B-cell factor 1	Ebf1	1.68	0.247	1.57	0.186	-1.28	0.008	-1.8	0.106	-1.68	0.140
1438405_at	fibroblast growth factor 7	Fgf7	1.25	0.173	1.09	0.571	-1.28	0.001	-1.26	0.003	-1.21	0.102

1433482_a_at	far upstream element (FUSE) binding protein 1	Fubp1	1.08	0.679	-1.15	0.179	-1.28	0.016	-1.16	0.030	-1.3	0.009
1434825_at	similar to CAGL79	LOC381742	-1.02	0.654	-1.06	0.510	-1.28	0.001	-1.3	0.026	-1.12	0.288
1448870_at	latent transforming growth factor beta binding protein 1	Ltbp1	-1.13	0.155	-1.35	0.038	-1.28	0.009	-1.28	0.007	-1.41	0.018
1430619_a_at	mevalonate kinase /// similar to mevalonate kinase	Mvk /// LOC637711	1.99	0.399	1.75	0.843	-1.28	0.007	1.02	0.816	-1.03	0.518
1425761_a_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-depende	Nfatc1	1.35	0.583	1.44	0.716	-1.28	0.031	-1.15	0.087	-1.17	0.239
1426464_at	nuclear receptor subfamily 1, group D, member 1	Nr1d1	-1.17	0.113	-1.01	0.783	-1.28	0.021	1.03	0.936	-1.16	0.206
1428484_at	oxysterol binding protein-like 3	Osbpl3	-1.03	0.297	-1.59	0.026	-1.28	0.005	-1.25	0.078	-1.4	0.000
1447640_s_at	pre B-cell leukemia transcription factor 3	Pbx3	-1.17	0.432	-2.01	0.182	-1.28	0.004	-1.48	0.009	-1.39	0.029
1456303_at	PHD finger protein 14	Phf14	-1	0.759	-1	0.954	-1.28	0.034	1.12	0.990	-1.65	0.043
1450916_at	staufen (RNA binding protein) homolog 2 (Drosophila)	Stau2	1.04	0.892	-1.99	0.050	-1.28	0.043	-1.33	0.018	-1.35	0.016
1455353_at	transmembrane and coiled coil domains 1	Tmcc1	1.28	0.054	1.03	0.682	-1.28	0.023	-1.02	0.713	-1.49	0.001
1426977_at	ubiquitin specific peptidase 47	Usp47	1.16	0.321	-1.06	0.572	-1.28	0.025	-1.18	0.026	-1.47	0.017
1430060_at	RIKEN cDNA 1700034G24 gene	1700034G24Rik	1.01	0.934	1.11	0.668	-1.27	0.022	-1.13	0.249	1.01	0.887
1451450_at	RIKEN cDNA 2010011I20 gene	2010011I20Rik	-1.18	0.028	-1.15	0.204	-1.27	0.039	1.14	0.247	1.39	0.003
1430831_at	RIKEN cDNA 4930404J24 gene	4930404J24Rik	1.3	0.796	1.56	0.514	-1.27	0.034	1.62	0.373	1.27	0.410
1435825_at	activin A receptor, type II-like 1	Acvrl1	2.59	0.366	4.55	0.166	-1.27	0.041	1.23	0.101	1.39	0.093
1439127_at	expressed sequence AI314180	AI314180	-1.29	0.339	-1.46	0.271	-1.27	0.029	-1.06	0.510	-1.13	0.371
1435768_at	AT rich interactive domain 4B (Rbp1 like)	Arid4b	1.05	0.973	-1.02	0.741	-1.27	0.015	-1.42	0.088	-1.52	0.014
1439120_at	cDNA sequence BC010304	BC010304	-1.16	0.392	-1.21	0.252	-1.27	0.002	-1.13	0.168	-1.07	0.486
1437857_at	dpy-19-like 3 (C. elegans)	Dpy19l3	-1.32	0.202	-1.73	0.115	-1.27	0.047	-1.04	0.650	-1.08	0.366
1419308_at	inversin	Invs	-1.14	0.426	-2.63	0.083	-1.27	0.038	-1.09	0.372	-1.31	0.021
1431922_at	intestine specific homeobox	Isx	1.19	0.602	-1.17	0.336	-1.27	0.042	1	0.841	1.25	0.259
1418232_s_at	LIM and senescent cell antigen-like domains 1	Lims1	1.55	0.387	1.08	0.804	-1.27	0.004	-1.27	0.009	-1.44	0.008
1419951_at	Lectin, mannose-binding, 1	Lman1	-1.11	0.467	1.05	0.725	-1.27	0.030	1.25	0.046	1.03	0.877
1418316_a_at	MAP/microtubule affinity-regulating kinase 3	Mark3	-1.03	0.547	-1	0.975	-1.27	0.043	-1.17	0.133	-1.21	0.091
1435649_at	nexilin	Nexn	1.1	0.471	-1.14	0.173	-1.27	0.010	-1.03	0.525	-1.03	0.437
1427705_a_at	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	Nfkb1	1.08	0.418	-1.06	0.673	-1.27	0.005	-1.25	0.007	-1.3	0.009
1417148_at	platelet derived growth factor receptor, beta polypeptide	Pdgfrb	1.19	0.743	1.01	0.722	-1.27	0.041	-1.14	0.230	-1.4	0.001
1437295_at	protein kinase N2	Pkn2	1.19	0.183	-1.04	0.510	-1.27	0.024	-1.33	0.016	-1.32	0.021
1422673_at	protein kinase C, mu	Prkcm	-1.38	0.174	-2.74	0.022	-1.27	0.036	-1.55	0.003	-1.53	0.045
1434360_s_at	protein tyrosine phosphatase, receptor type, G /// similar to protein ty	Ptprg /// LOC63266	1.42	0.865	-1.02	0.334	-1.27	0.045	-1.24	0.063	-1.31	0.007
1448584_at	arginine/serine-rich coiled-coil 1	Rsrc1	-1.09	0.255	-1.42	0.067	-1.27	0.010	-1.17	0.008	-1.36	0.015
1435516_x_at	regulator of telomere elongation helicase 1	Rtel1	1.74	0.475	2.2	0.169	-1.27	0.007	1.18	0.351	-1.14	0.573
1439161_at	SAPS domain family, member 3	Saps3	-1.01	0.993	-1.15	0.546	-1.27	0.024	-1.07	0.535	-1.01	0.935
1428396_at	SMAD specific E3 ubiquitin protein ligase 1 /// similar to Smad ubiqu	Smurf1 /// LOC640	2.4	0.944	2.7	0.838	-1.27	0.048	1.08	0.289	-1.26	0.010
1424652_at	transmembrane protein 166	Tmem166	1.15	0.276	1.24	0.147	-1.27	0.000	-1.25	0.004	-1.19	0.095
1423898_a_at	thyroid hormone receptor interactor 12	Trip12	-1.09	0.314	-1.28	0.051	-1.27	0.006	-1.35	0.002	-1.4	0.002
1422031_a_at	zinc finger, AN1-type domain 6	Zfand6	1.9	0.307	1.23	0.666	-1.27	0.011	1.01	0.832	-1.18	0.156
1455407_at	zinc finger protein 236	Zfp236	1.09	0.299	-1.36	0.102	-1.27	0.009	-1.3	0.067	-1.42	0.021
1457383_at	RIKEN cDNA 1500011J06 gene	1500011J06Rik	1.12	0.406	-1.13	0.408	-1.26	0.001	1.01	0.971	-1.35	0.107
1457759_at	RIKEN cDNA A630081D01 gene	A630081D01Rik	1.1	0.987	1.17	0.854	-1.26	0.030	1.07	0.817	1.24	0.112
1426755_at	cytoskeleton-associated protein 4	Ckap4	-1.2	0.015	-1.22	0.045	-1.26	0.045	1.03	0.775	1.05	0.553
1427563_at	distal-less homeobox 6, antisense	Dlx6as	1.98	0.272	1.4	0.444	-1.26	0.015	1.09	0.313	1.11	0.849
1429028_at	dedicator of cytokinesis 11	Dock11	-1.02	0.630	-1.9	0.083	-1.26	0.008	-1.39	0.028	-1.48	0.014
1452718_at	E3 ubiquitin protein ligase, HECT domain containing, 1	Edd1	-1.05	0.481	-1.13	0.125	-1.26	0.021	-1.29	0.021	-1.39	0.006
1434285_at	FERM domain containing 4A	Frmd4a	-1.07	0.386	-1.15	0.109	-1.26	0.017	-1.27	0.077	-1.31	0.042
1434754_at	GTPase activating RANGAP domain-like 4	Garnl4	-1.14	0.012	-1.41	0.009	-1.26	0.014	-1.29	0.011	-1.55	0.005
1418492_at	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	Grem2	1.13	0.632	-1.16	0.309	-1.26	0.031	-1.27	0.013	-1.33	0.004
1437103_at	insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	1.01	0.898	-1.27	0.042	-1.26	0.003	-1.25	0.001	-1.37	0.009
1418983_at	InaD-like (Drosophila)	Inadl	-1.25	0.263	-1.11	0.445	-1.26	0.016	-1.11	0.472	1.05	0.878
1415847_at	lactate dehydrogenase C	Ldhc	1.7	0.758	1.98	0.977	-1.26	0.035	1.88	0.910	2.25	0.226
1426528_at	neuropilin 2	Nrp2	-1.15	0.050	-1.71	0.001	-1.26	0.023	-1.4	0.001	-1.37	0.053
1449404_at	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	Pip5k2a	-1.2	0.260	-2.02	0.055	-1.26	0.008	-1.34	0.003	-1.37	0.006
1426382_at	protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	-1.08	0.263	-1.37	0.011	-1.26	0.034	-1.31	0.005	-1.34	0.000
1457200_at	serine (or cysteine) peptidase inhibitor, clade B, member 9d	Serpinb9d	-1.41	0.219	-1.46	0.122	-1.26	0.029	-1.07	0.412	1.17	0.806
1416944_a_at	tousled-like kinase 2 (Arabidopsis)	Tlk2	-1.03	0.622	-1.1	0.213	-1.26	0.027	-1.61	0.000	-1.33	0.006
1451378_at	UTP6, small subunit (SSU) processome component, homolog (yeast	Utp6	1.32	0.426	1.52	0.063	-1.26	0.045	-1.04	0.735	1.08	0.725
1458202_at	RIKEN cDNA 6330500D04 gene	6330500D04Rik	-1.25	0.362	-1.14	0.341	-1.25	0.025	-1.04	0.645	1.24	0.462

1440884_s_at	RIKEN cDNA A530047J11 gene	A530047J11Rik	-1.45	0.231	-1.73	0.197	-1.25	0.027	-1.2	0.172	-1.24	0.113
1428336_at	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic ac	Agpat4	-1.1	0.335	-1.49	0.009	-1.25	0.033	-1.17	0.010	-1.29	0.001
1434221_at	cDNA sequence BC030863	BC030863	1.68	0.351	1.02	0.505	-1.25	0.018	-1.47	0.003	-1.43	0.015
1450339_a_at	B-cell leukemia/lymphoma 11B	Bcl11b	-1.01	0.529	-1.05	0.383	-1.25	0.012	-1.05	0.398	-1.39	0.109
1434310_at	bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	-1.04	0.375	-1.49	0.014	-1.25	0.013	-1.18	0.127	-1.44	0.005
1453100_at	casein kinase 2, alpha prime polypeptide	Csnk2a2	2.63	0.428	1.93	0.332	-1.25	0.035	-1.02	0.705	-1.38	0.089
1428408_a_at	DNA segment, Chr 12, ERATO Doi 551, expressed	D12Ertd551e	1.34	0.475	-1.09	0.400	-1.25	0.001	-1.14	0.042	-1.32	0.018
1459906_at	Diacylglycerol kinase, eta	Dgkh	-1.1	0.496	-1.4	0.228	-1.25	0.036	-1.22	0.249	-1.4	0.113
1453746_at	formin binding protein 1	Fnbp1	-1.27	0.369	-1.42	0.298	-1.25	0.021	-1.29	0.023	-1.2	0.042
1415757_at	golgi-specific brefeldin A-resistance factor 1	Gbf1	1.48	0.816	1	0.364	-1.25	0.010	-1.21	0.002	-1.41	0.001
1426491_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain	Herc2	-1.13	0.065	-1.32	0.050	-1.25	0.001	-1.3	0.054	-1.4	0.006
1446674_at	Kinesin 2	Kns2	1.19	0.923	1.83	0.052	-1.25	0.021	1.16	0.987	-1.06	0.439
1451999_at	LIM domain binding 3	Ldb3	1.14	0.749	-1.25	0.321	-1.25	0.007	-1.14	0.395	-1.04	0.456
1450253_a_at	mitogen activated protein kinase kinase kinase 4	Map3k4	5	0.453	5.04	0.849	-1.25	0.037	-1.11	0.389	-1.26	0.018
1459512_at	Myeloid ecotropic viral integration site 1	Meis1	1.85	0.452	1.57	0.414	-1.25	0.019	1.12	0.701	1.08	0.329
1434181_at	pleckstrin homology domain containing, family C (with FERM domair	Plekhc1	1.19	0.374	-1.2	0.223	-1.25	0.008	-1.17	0.011	-1.31	0.039
1458171_at	solute carrier organic anion transporter family, member 2b1	Slco2b1	1.12	0.804	1.27	0.569	-1.25	0.023	-1.92	0.031	-1.07	0.562
1423658_at	signal peptide peptidase 3	Sppl3	-1.12	0.361	-1.29	0.084	-1.25	0.048	-1.41	0.050	-1.26	0.047
1460735_at	supervillin	Svil	1.1	0.774	-1.41	0.101	-1.25	0.026	-1.36	0.005	-1.43	0.003
1451795_at	target of myb1-like 2 (chicken)	Tom1l2	-1.24	0.393	-1.54	0.107	-1.25	0.030	1.14	0.826	1.15	0.625
1421096_at	transient receptor potential cation channel, subfamily C, member 1	Trpc1	1.07	0.843	-1.07	0.531	-1.25	0.012	-1.07	0.146	-1.08	0.379
1435235_at	thioredoxin-like 1	Txnl1	-1.11	0.492	-1.24	0.320	-1.25	0.002	-1.33	0.006	-1.21	0.107
1419575_s_at	zinc finger protein 292	Zfp292	1.26	0.741	1.09	0.929	-1.25	0.039	-1.16	0.201	-1.17	0.199
1417038_at	septin 9	9-Sep	1.09	0.765	-1.32	0.082	-1.24	0.028	-1.13	0.045	-1.11	0.226
1449923_at	RIKEN cDNA 1700018F24 gene	1700018F24Rik	1.2	0.410	-1.1	0.549	-1.24	0.023	-1.06	0.480	1.04	0.678
1448019_at	RIKEN cDNA 2900006A08 gene	2900006A08Rik	1.09	0.738	-1.05	0.635	-1.24	0.022	-1.29	0.209	-1.29	0.062
1454594_at	RIKEN cDNA 2900078I11 gene	2900078I11Rik	1.14	0.262	-1.03	0.738	-1.24	0.014	-1.02	0.750	-1.38	0.098
1433169_at	RIKEN cDNA 5830456J23 gene	5830456J23Rik	1.03	0.665	1.2	0.971	-1.24	0.045	-1.43	0.181	-1.38	0.219
1457389_at	RIKEN cDNA 9830166K06 gene	9830166K06Rik	-1.31	0.132	1.34	0.541	-1.24	0.029	1.67	0.677	-1.2	0.206
1437072_at	Rho GTPase activating protein 25	Arhgap25	1.85	0.942	1.29	0.381	-1.24	0.039	1.51	0.226	1.13	0.917
1435248_a_at	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (	Btaf1	1.09	0.044	1.07	0.348	-1.24	0.001	-1.24	0.009	-1.37	0.005
1427844_a_at	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	1.54	0.581	1.28	0.451	-1.24	0.008	1.23	0.034	1.13	0.042
1445017_at	CCR4-NOT transcription complex, subunit 2	Cnot2	-1.45	0.058	-1.24	0.208	-1.24	0.049	1.17	0.235	1.23	0.518
1426408_at	CUG triplet repeat, RNA binding protein 1	Cugbp1	-1.19	0.267	-1.43	0.190	-1.24	0.028	-1.17	0.114	-1.26	0.073
1428384_at	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	D4Bwg0951e	1.49	0.399	1.15	0.774	-1.24	0.015	-1.09	0.051	-1.32	0.002
1417321_at	DNA segment, Chr 4, Wayne State University 132, expressed	D4Wsu132e	-1.22	0.383	-1.41	0.301	-1.24	0.025	-1.68	0.012	-1.81	0.019
1439493_at	RIKEN cDNA D630040G17 gene /// similar to zinc finger protein 64 (	D630040G17Rik ///	-1.16	0.298	-1.58	0.036	-1.24	0.041	-1.57	0.003	-1.31	0.047
1424270_at	doublecortin and calcium/calmodulin-dependent protein kinase-like 1	Dcamkl1	-1.03	0.760	-1.31	0.308	-1.24	0.002	1.15	0.947	-1.21	0.259
1450522_a_at	H1 histone family, member 0	H1f0	1.11	0.933	1.05	0.576	-1.24	0.000	1.01	0.926	-1.04	0.457
1425969_a_at	Huntington disease gene homolog	Hdh	-1.27	0.254	-1.45	0.160	-1.24	0.029	-1.24	0.034	-1.41	0.002
1429063_s_at	kinesin family member 16B	Kif16b	-1.31	0.259	-6.74	0.022	-1.24	0.046	-1.72	0.000	-2.03	0.053
1455217_at	leucine-rich repeats and immunoglobulin-like domains 2	Lrig2	1.14	0.363	1.34	0.020	-1.24	0.018	-1.13	0.351	-1.17	0.285
1438284_at	oculocerebrorenal syndrome of Lowe	Ocrl	-1.42	0.057	1.1	0.757	-1.24	0.034	1.05	0.984	1.14	0.641
1435043_at	phospholipase C, beta 1	Plcb1	-1.48	0.109	-1.79	0.075	-1.24	0.003	-1.15	0.357	-1.25	0.121
1452833_at	Rap guanine nucleotide exchange factor (GEF) 2	Rapgef2	1.09	0.423	-1.19	0.211	-1.24	0.029	-1.62	0.000	-1.51	0.011
1448689_at	related RAS viral (r-ras) oncogene homolog 2	Rras2	1.06	0.308	-1.18	0.079	-1.24	0.005	-1.24	0.007	-1.4	0.002
1449221_a_at	ribosome binding protein 1	Rrbp1	-1.18	0.374	-1.25	0.248	-1.24	0.029	-1.06	0.407	-1.08	0.096
1418206_at	stromal cell-derived factor 2-like 1	Sdf2l1	1.21	0.929	1.11	0.833	-1.24	0.039	1.06	0.555	1.02	0.439
1421346_a_at	solute carrier family 6 (neurotransmitter transporter, taurine), membe	Slc6a6	1.93	0.772	1.52	0.652	-1.24	0.042	-1.2	0.028	-1.11	0.172
1431362_a_at	SPARC related modular calcium binding 2	Smoc2	1.41	0.597	1.11	0.633	-1.24	0.021	1.02	0.454	-1.12	0.136
1435878_at	serine/threonine kinase 38 like	Stk38l	-1.07	0.395	-1.35	0.024	-1.24	0.003	-1.29	0.006	-1.11	0.240
1426065_a_at	tribbles homolog 3 (Drosophila)	Trib3	-1.1	0.389	-1.9	0.069	-1.24	0.018	1	0.844	-1.03	0.432
1432569_at	RIKEN cDNA 1700121K02 gene	1700121K02Rik	2	0.907	1.78	0.759	-1.23	0.046	1.61	0.284	-1.23	0.397
1428195_at	RIKEN cDNA 4631427C17 gene	4631427C17Rik	1.23	0.545	-1.08	0.155	-1.23	0.049	-1.22	0.245	-1.03	0.689
1428691_at	RIKEN cDNA 5630401D06 gene	5630401D06Rik	-1	0.828	-1.14	0.200	-1.23	0.007	-1.07	0.168	-1.36	0.044
1428413_at	RIKEN cDNA 5730405I09 gene	5730405I09Rik	-1.18	0.391	-1.33	0.314	-1.23	0.006	-1.3	0.005	-1.15	0.118
1434184_s_at	RIKEN cDNA 9430080K19 gene	9430080K19Rik	1.1	0.319	-1.13	0.137	-1.23	0.048	-1.31	0.000	-1.35	0.007
1452233_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	-1.01	0.811	-1.22	0.119	-1.23	0.010	-1.16	0.035	-1.29	0.016

1446108_at	Ankyrin 2, brain	Ank2	1.14	0.891	1.09	0.971	-1.23	0.032	1.14	0.542	1.9	0.199
1455083_at	Atpase, class VI, type 11C	Atp11c	1.06	0.562	-1.34	0.045	-1.23	0.045	-1.17	0.053	-1.19	0.008
1450913_at	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	B4galt6 /// LOC675	-1.02	0.638	-1.4	0.027	-1.23	0.007	1	0.836	-1.18	0.366
1441137_at	bicaudal C homolog 1 (Drosophila)	Bicc1	1.08	0.730	-1.49	0.057	-1.23	0.003	-1.31	0.006	-1.35	0.043
1421001_a_at	carbonic anhydrase 6	Car6	-1.1	0.450	-1.13	0.318	-1.23	0.043	1.07	0.664	-1	0.689
1426928_at	coiled-coil domain containing 93	Ccdc93	-1.01	0.726	1.36	0.074	-1.23	0.005	-1.01	0.926	1	0.912
1429298_at	dimethylarginine dimethylaminohydrolase 1	Ddah1	1.2	0.521	-1.09	0.472	-1.23	0.002	-1.03	0.541	-1.25	0.060
1448223_at	fatso	Fto	-1.12	0.224	-1.74	0.002	-1.23	0.030	-1.29	0.043	-1.29	0.041
1433605_at	inositol polyphosphate-5-phosphatase A	Inpp5a	-1.08	0.409	-1.43	0.015	-1.23	0.000	-1.25	0.001	-1.31	0.021
1417379_at	IQ motif containing GTPase activating protein 1	Iqgap1	-1.09	0.324	-1.35	0.038	-1.23	0.038	-1.19	0.026	-1.17	0.002
1425342_a_at	potassium channel, subfamily K, member 3	Kcnk3	-1.12	0.409	1.07	0.955	-1.23	0.050	-1.2	0.055	-1	0.918
1455182_at	kinesin family member 1B	Kif1b	1.04	0.350	-1.04	0.774	-1.23	0.034	-1.21	0.083	-1.44	0.003
1433776_at	lipoma HMGIC fusion partner	Lhfp	-1.01	0.728	-1.35	0.002	-1.23	0.000	-1.22	0.037	-1.29	0.005
1451985_at	leucine-rich repeat kinase 1	Lrrk1	-1.11	0.205	-1.23	0.097	-1.23	0.033	-1.15	0.112	-1.29	0.027
1418594_a_at	nuclear receptor coactivator 1	Ncoa1	-1.11	0.410	-2.39	0.051	-1.23	0.026	-1.24	0.028	-1.63	0.009
1432603_at	nuclear receptor interacting protein 1	Nrip1	1.25	0.051	1.3	0.338	-1.23	0.039	-1.02	0.745	-1.1	0.489
1454862_at	pleckstrin homology-like domain, family B, member 2	Phldb2	-1.06	0.576	-1.35	0.115	-1.23	0.048	-1.37	0.008	-1.37	0.011
1429183_at	plakophilin 2	Pkp2	1.46	0.386	-1.03	0.478	-1.23	0.037	-1.26	0.029	-1.36	0.003
1416525_at	speckle-type POZ protein	Spop	3.11	0.528	2.55	0.855	-1.23	0.021	-1.08	0.179	-1.26	0.038
1423535_at	striatin, calmodulin binding protein 3	Strn3	1.07	0.353	-1.03	0.634	-1.23	0.015	-1.2	0.005	-1.24	0.071
1430535_at	TSC22 domain family 2	Tsc22d2	1.02	0.986	-1.31	0.060	-1.23	0.021	-1.32	0.000	-1.31	0.000
1457598_at	Thioredoxin-like 2	Txnl2	-1.04	0.688	1.38	0.081	-1.23	0.019	-1.04	0.705	1.1	0.297
1418479_at	vacuolar protein sorting 54 (yeast)	Vps54	1.05	0.658	-1.17	0.013	-1.23	0.003	-1.2	0.023	-1.35	0.019
1432656_at	RIKEN cDNA 3222402N08 gene	3222402N08Rik	1.52	0.221	2.01	0.041	-1.22	0.047	1.16	0.656	2.11	0.036
1428861_at	RIKEN cDNA 4631422O05 gene /// similar to downregulated in ovari	4631422O05Rik ///	1.5	0.614	1.18	0.626	-1.22	0.003	-1.11	0.039	-1.27	0.039
1453186_at	RIKEN cDNA 5730406M06 gene	5730406M06Rik	2.06	0.444	1.75	0.317	-1.22	0.030	-1.1	0.332	-1.2	0.043
1456658_at	actin, alpha 2, smooth muscle, aorta	Acta2	2.03	0.590	2.06	0.931	-1.22	0.014	-1.12	0.480	-1.75	0.014
1420621_a_at	amyloid beta (A4) precursor protein	App	1.72	0.469	1.52	0.849	-1.22	0.016	1.02	0.743	-1.21	0.023
1428369_s_at	Rho GTPase activating protein 21	Arhgap21	-1.03	0.670	-1.19	0.179	-1.22	0.000	-1.37	0.006	-1.3	0.002
1454745_at	Rho GTPase activating protein 29	Arhgap29	1.03	0.217	-1.1	0.074	-1.22	0.048	-1.21	0.009	-1.3	0.015
1426418_at	atonal homolog 8 (Drosophila)	Atoh8	1.88	0.509	1.2	0.568	-1.22	0.040	-1.17	0.099	-1.33	0.034
1452381_at	cAMP responsive element binding protein 3-like 2	Creb3l2	1.01	0.996	-1.42	0.052	-1.22	0.042	-1.2	0.046	-1.43	0.010
1424569_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Ddx46	1.5	0.243	1.34	0.188	-1.22	0.000	1.01	0.457	-1.09	0.560
1426010_a_at	erythrocyte protein band 4.1-like 3	Epb4.1l3	1.11	0.832	-1.2	0.146	-1.22	0.049	-1.12	0.097	-1.35	0.031
1425462_at	F-box and WD-40 domain protein 11	Fbxw11	1.09	0.436	1.08	0.678	-1.22	0.043	-1.3	0.004	-1.27	0.011
1416978_at	Fc receptor, IgG, alpha chain transporter	Fcgrt	1.24	0.667	1.24	0.571	-1.22	0.002	1.04	0.684	1.06	0.224
1455242_at	forkhead box P1	Foxp1	1.35	0.401	1.08	0.560	-1.22	0.027	-1.34	0.009	-1.36	0.003
1448185_at	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubi	Herpud1	1.05	0.857	-2.02	0.023	-1.22	0.004	-1.05	0.109	-1.27	0.003
1433864_at	low density lipoprotein-related protein 12	Lrp12	1.56	0.398	1.47	0.576	-1.22	0.032	-1.01	0.708	-1.11	0.027
1455941_s_at	mitogen activated protein kinase kinase 5	Map2k5	-1.32	0.257	-2.33	0.102	-1.22	0.016	-1.45	0.004	-1.31	0.030
1427920_at	PHD finger protein 19	Phf19	-1.03	0.670	-1.03	0.963	-1.22	0.006	1.03	0.901	1.05	0.817
1430640_a_at	protein kinase, cAMP dependent regulatory, type II beta	Prkar2b	1.08	0.737	-1.2	0.201	-1.22	0.017	-1.03	0.555	-1.26	0.153
1424659_at	slit homolog 2 (Drosophila)	Slit2	-1.27	0.100	-1.7	0.044	-1.22	0.043	-1.2	0.015	-1.22	0.025
1424452_at	SAFB-like, transcription modulator	Sltm	-1.04	0.126	-1.22	0.011	-1.22	0.040	-1.06	0.311	-1.39	0.091
1431345_a_at	TATA box binding protein (Tbp)-associated factor, RNA polymerase	Taf1b	1.89	0.508	1.5	0.727	-1.22	0.005	-1.05	0.552	-1.11	0.282
1452868_at	ubiquitin specific peptidase 24	Usp24	-1	0.854	-1.08	0.068	-1.22	0.000	-1.48	0.002	-1.33	0.005
1419984_s_at	zinc finger protein 644	Zfp644	1.01	0.879	1.02	0.735	-1.22	0.007	-1.17	0.263	-1.14	0.209
1436842_at	RIKEN cDNA B230380D07 gene	B230380D07Rik	-1.01	0.702	-1.33	0.096	-1.21	0.035	1	0.952	-1	0.950
1436387_at	RIKEN cDNA C330006P03 gene	C330006P03Rik	-1.14	0.434	-1.19	0.429	-1.21	0.000	-1.05	0.517	-1.03	0.588
1458536_at	Cyclin I	Ccni	1.19	0.633	1.18	0.684	-1.21	0.040	-1.18	0.463	-1.1	0.423
1420633_a_at	casein alpha s2-like A	Csn1s2a	-1.04	0.725	1.13	0.341	-1.21	0.037	-1.02	0.698	1.13	0.391
1426291_at	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	Dimt1	1.04	0.960	-1.16	0.312	-1.21	0.039	1.57	0.022	1.28	0.166
1434038_at	DnaJ (Hsp40) homolog, subfamily C, member 13	Dnajc13	1.02	0.591	-1.2	0.082	-1.21	0.009	-1.14	0.027	-1.27	0.000
1451276_at	RIKEN cDNA E030041M21 gene	E030041M21Rik	1.32	0.390	1.02	0.845	-1.21	0.006	-1.11	0.009	-1.21	0.103
1452753_at	forkhead box K2	Foxk2	1.32	0.641	1.24	0.571	-1.21	0.023	1.02	0.725	-1.01	0.839
1419372_at	golgi SNAP receptor complex member 2	Gosr2	-1.06	0.512	1.02	0.433	-1.21	0.011	-1.07	0.358	1.05	0.896
1418333_at	metal response element binding transcription factor 1	Mtf1	1.25	0.657	1.37	0.680	-1.21	0.029	1.05	0.883	1.05	0.737
1426040_a_at	outer dense fiber of sperm tails 2	Odf2	1.63	0.455	2.06	0.409	-1.21	0.015	1.14	0.593	1.14	0.686

1433768_at	palladin, cytoskeletal associated protein	Palld	1.23	0.688	-1.11	0.305	-1.21	0.037	-1.27	0.008	-1.28	0.000
1438012_at	protein phosphatase 1 (formerly 2C)-like	Ppm1l	1.05	0.891	-1.37	0.119	-1.21	0.028	-1.22	0.058	-1.23	0.010
1424347_at	protein phosphatase 6, catalytic subunit	Ppp6c	1.02	0.845	-1.11	0.212	-1.21	0.023	-1.18	0.102	-1.33	0.053
1453095_at	RAB10, member RAS oncogene family	Rab10	1.15	0.426	-1.06	0.693	-1.21	0.025	-1.18	0.122	-1.16	0.164
1454915_at	RAB3 GTPase activating protein subunit 2	Rab3gap2	1.09	0.494	-1.24	0.100	-1.21	0.020	-1.12	0.132	-1.22	0.015
1434509_at	Rap guanine nucleotide exchange factor (GEF) 6	Rapgef6	-1.05	0.564	-1.57	0.000	-1.21	0.025	-1.35	0.011	-1.4	0.008
1426478_at	RAS p21 protein activator 1	Rasa1	2.32	0.452	1.71	0.920	-1.21	0.018	-1.08	0.541	-1.1	0.195
1455310_at	RNA binding motif protein 16	Rbm16	-1.08	0.509	-1.24	0.324	-1.21	0.001	-1.26	0.000	-1.25	0.012
1415903_at	solute carrier family 38, member 1	Slc38a1	1.04	0.953	-1.16	0.256	-1.21	0.035	-1.15	0.063	-1.08	0.082
1422256_at	somatostatin receptor 2	Sstr2	-1.06	0.497	-1.84	0.020	-1.21	0.033	1.13	0.799	-1.45	0.081
1428546_at	synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	-1.1	0.384	-1.3	0.090	-1.21	0.031	-1.27	0.053	-1.4	0.004
1437358_at	WD repeat and FYVE domain containing 1	Wdfy1	1.07	0.506	-1.07	0.237	-1.21	0.036	-1.09	0.099	-1.2	0.010
1423961_at	WD repeat domain 26	Wdr26	1.67	0.572	1.97	0.600	-1.21	0.020	1.01	0.791	-1.05	0.557
1449821_a_at	RIKEN cDNA 0610016J10 gene /// hypothetical LOC619602	0610016J10Rik /// l	1.17	0.587	-1.14	0.284	-1.2	0.024	-1.19	0.021	-1.4	0.014
1424928_at	RIKEN cDNA 2210018M11 gene	2210018M11Rik	1.04	0.522	1.13	0.132	-1.2	0.010	-1.11	0.321	-1.23	0.021
1443722_at	RIKEN cDNA 6030419C18 gene	6030419C18Rik	-1.18	0.372	-1.14	0.465	-1.2	0.046	1.51	0.405	-1.02	0.831
1452009_at	RIKEN cDNA 9130422G05 gene	9130422G05Rik	1.1	0.566	-1.38	0.131	-1.2	0.022	-1.28	0.014	-1.33	0.005
1440447_at	abhydrolase domain containing 2	Abhd2	1.73	0.202	1.47	0.170	-1.2	0.027	-1.1	0.480	-1.44	0.066
1429012_at	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	Arhgef6	1.1	0.850	-1.13	0.439	-1.2	0.014	1.15	0.318	1.04	0.853
1434506_at	AT rich interactive domain 2 (Arid-rfx like)	Arid2	1.17	0.005	1.05	0.706	-1.2	0.009	-1.07	0.096	-1.18	0.292
1427516_a_at	biregional cell adhesion molecule-related/down-regulated by oncoge	Boc	1.19	0.092	1.07	0.493	-1.2	0.043	1.05	0.650	-1.01	0.650
1455287_at	cyclin-dependent kinase 6	Cdk6	-1.14	0.298	-1.85	0.073	-1.2	0.034	-1.26	0.053	-1.43	0.000
1429400_at	chloride channel 5	Clcn5	-1.15	0.289	-1.81	0.055	-1.2	0.040	-1.2	0.133	-1.17	0.030
1457176_at	GTPase activating RANGAP domain-like 1	Garnl1	1.67	0.040	1.42	0.244	-1.2	0.001	-1.21	0.063	-1.78	0.029
1450730_at	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	1.03	0.695	-1.27	0.006	-1.2	0.003	-1.04	0.474	-1.27	0.007
1436897_at	malignant fibrous histiocytoma amplified sequence 1	Mfhas1	-1.04	0.543	-1.09	0.321	-1.2	0.015	-1.09	0.172	-1.05	0.527
1422567_at	niban protein	Niban	1.18	0.643	-1.11	0.344	-1.2	0.023	-1.09	0.098	-1.22	0.046
1435088_at	nuclear receptor-binding SET-domain protein 1	Nsd1	1.06	0.489	-1.03	0.331	-1.2	0.000	-1.1	0.175	-1.22	0.152
1426456_a_at	protein inhibitor of activated STAT 2	Pias2	1.18	0.352	-1.01	0.695	-1.2	0.011	-1.19	0.021	-1.34	0.031
1451179_a_at	quaking	Qk	-1.04	0.550	-1.36	0.003	-1.2	0.001	-1.27	0.004	-1.26	0.001
1426912_at	ring finger and WD repeat domain 2 /// similar to constitutive photom	Rfwd2 /// LOC6212	1.22	0.333	1.05	0.966	-1.2	0.018	-1.17	0.014	-1.28	0.004
1417209_at	SERTA domain containing 2	Sertad2	1.23	0.151	1.13	0.672	-1.2	0.015	-1.02	0.517	-1.15	0.117
1422893_at	Scm-like with four mbt domains 1	Sfmbt1	-1.13	0.196	1.01	0.889	-1.2	0.038	-1.24	0.073	1.04	0.812
1434261_at	signal-induced proliferation-associated 1 like 2	Sipa1l2	1.02	0.688	-1.38	0.041	-1.2	0.014	-1.32	0.011	-1.47	0.002
1454960_at	MAD homolog 3 (Drosophila)	Smad3	-1.12	0.305	-1.38	0.010	-1.2	0.031	-1.16	0.081	-1.22	0.092
1433664_at	ubiquitin-conjugating enzyme E2Q (putative) 2	Ube2q2	1.98	0.594	1.58	0.921	-1.2	0.022	-1.02	0.561	1.02	0.829
1427163_at	ubiquitin protein ligase E3 component n-recognin 2	Ubr2	1.24	0.436	1.21	0.306	-1.2	0.049	-1.15	0.012	-1.31	0.011
1428194_at	ubiquitin specific peptidase 9, X chromosome	Usp9x	1.07	0.266	-1.27	0.111	-1.2	0.026	-1.15	0.024	-1.36	0.048
1457674_at	vacuolar protein sorting 13A (yeast)	Vps13a	-1.08	0.473	-1.24	0.186	-1.2	0.048	1.23	0.189	-1.02	0.923
1458255_at	WD repeat domain 33	Wdr33	-1.18	0.372	1.36	0.479	-1.2	0.002	1.85	0.848	1.05	0.775
1428370_at	RIKEN cDNA 1500011B03 gene	1500011B03Rik	1.81	0.975	1.92	0.947	1.2	0.023	1.45	0.005	1.26	0.196
1423823_at	RIKEN cDNA 2610012O22 gene	2610012O22Rik	1.01	0.747	1.22	0.005	1.2	0.049	1.12	0.030	1.14	0.184
1454702_at	RIKEN cDNA 4930503L19 gene	4930503L19Rik	1.61	0.371	1.79	0.164	1.2	0.037	1.27	0.082	1.08	0.839
1441960_x_at	RIKEN cDNA 5730494M16 gene	5730494M16Rik	-1.11	0.447	-1.09	0.467	1.2	0.001	1.01	0.758	1.21	0.000
1453062_at	RIKEN cDNA A930026I22 gene	A930026I22Rik	-1.19	0.371	1.03	0.917	1.2	0.017	1.32	0.758	-1.08	0.607
1448318_at	adipose differentiation related protein	Adfp	-1	0.917	1.22	0.056	1.2	0.034	1.14	0.108	1.23	0.002
1447903_x_at	adaptor-related protein complex 1, sigma 2 subunit	Ap1s2	-1.09	0.473	1.11	0.762	1.2	0.015	1.19	0.028	1.22	0.041
1434711_at	cDNA sequence BC030867	BC030867	1.07	0.755	1.2	0.142	1.2	0.003	1.19	0.038	1.25	0.015
1429561_at	BRF2, subunit of RNA polymerase III transcription initiation factor, B	Brf2	-1.07	0.448	1.24	0.642	1.2	0.039	1.16	0.023	1.25	0.004
1428490_at	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-gala	C1galt1	1.14	0.264	1.17	0.174	1.2	0.049	1.17	0.284	1.3	0.049
1426886_at	ceroid-lipofuscinosis, neuronal 5	Cln5	1.65	0.194	1.86	0.160	1.2	0.015	1.1	0.210	1.24	0.012
1460409_at	carnitine palmitoyltransferase 1a, liver	Cpt1a	1	0.977	-1.23	0.062	1.2	0.001	1	0.931	1.07	0.349
1428738_a_at	DNA segment, Chr 14, ERATO Doi 449, expressed	D14Ertd449e	2.23	0.396	2.54	0.557	1.2	0.025	1.02	0.560	1.06	0.385
1424697_at	DTW domain containing 1	Dtwd1	1.06	0.013	1.13	0.124	1.2	0.024	1.06	0.049	1.25	0.025
1422539_at	exotoses (multiple)-like 2	Extl2	1.18	0.167	1.17	0.157	1.2	0.014	1.13	0.073	1.12	0.123
1449528_at	c-fos induced growth factor	Figf	-1.1	0.272	1.04	0.822	1.2	0.008	-1.11	0.917	1.24	0.134
1424300_at	gem (nuclear organelle) associated protein 6	Gemin6	1.19	0.010	1.32	0.005	1.2	0.030	1.3	0.003	1.16	0.027
1429356_s_at	geranylgeranyl diphosphate synthase 1	Ggps1	1.34	0.206	1.61	0.127	1.2	0.001	1.16	0.053	1.07	0.447

1450881_s_at	G protein-coupled receptor 137B	Gpr137b	-1.03	0.641	-1.18	0.275	1.2	0.011	1.08	0.137	1.09	0.141
1456229_at	homeo box B3	Hoxb3	-1.04	0.117	1.2	0.053	1.2	0.014	-1.01	0.722	1.22	0.270
1458404_at	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	Ndufb8	-1.13	0.397	1.41	0.844	1.2	0.031	1.18	0.579	1.32	0.228
1420142_s_at	proliferation-associated 2G4	Pa2g4	-1.11	0.432	1.22	0.992	1.2	0.009	1.12	0.053	1.31	0.034
1418893_at	pre B-cell leukemia transcription factor 2	Pbx2	-1.3	0.104	-1.05	0.560	1.2	0.008	1.01	0.877	1.05	0.583
1424120_at	ring finger protein 8	Rnf8	-1.07	0.473	1.12	0.854	1.2	0.017	1.07	0.383	1.03	0.881
1415725_at	RRN3 RNA polymerase I transcription factor homolog (yeast)	Rrn3	1.1	0.373	1.19	0.107	1.2	0.013	-1.02	0.494	1.08	0.106
1448778_at	splicing factor, arginine/serine-rich 4 (SRp75)	Sfrs4	-1.11	0.262	1.1	0.461	1.2	0.028	1.15	0.067	1.1	0.320
1440598_at	syntrophin, gamma 1	Sntg1	1.26	0.949	-1.7	0.141	1.2	0.014	2.59	0.013	1.94	0.517
1429711_at	phosphoserine/threonine/tyrosine interaction protein	Styx	1.01	0.604	-1.16	0.383	1.2	0.050	1.11	0.201	1.09	0.241
1436826_at	transmembrane and tetratricopeptide repeat containing 3	Tmtc3	1.02	0.892	1.08	0.818	1.2	0.019	1.05	0.387	1.09	0.278
1442454_at	topoisomerase (DNA) II alpha	Top2a	1.11	0.774	1.02	0.805	1.2	0.009	1.2	0.294	-1.29	0.110
1448848_at	torsin family 1, member B	Tor1b	-1.04	0.601	1.12	0.832	1.2	0.000	1.06	0.142	1.14	0.177
1423395_at	translin-associated factor X	Tsnax	1.02	0.992	1.17	0.423	1.2	0.046	1.14	0.082	1.03	0.720
1451754_a_at	WD repeat domain 45	Wdr45	1.2	0.208	1.26	0.559	1.2	0.011	1.11	0.119	1.05	0.819
1426879_at	RIKEN cDNA 1190005F20 gene	1190005F20Rik	1.13	0.410	1.35	0.034	1.21	0.034	1.08	0.425	1.14	0.323
1423118_at	RIKEN cDNA 1200014J11 gene	1200014J11Rik	-1.1	0.069	1.22	0.105	1.21	0.032	1.08	0.163	-1	0.827
1454879_s_at	RIKEN cDNA 1700052N19 gene	1700052N19Rik	1.21	0.568	1.44	0.382	1.21	0.026	1.15	0.057	1.17	0.031
1428552_at	RIKEN cDNA 2610001J05 gene	2610001J05Rik	-1.06	0.521	1.04	0.972	1.21	0.017	-1.08	0.098	1.18	0.025
1430614_at	RIKEN cDNA 4632415K11 gene	4632415K11Rik	1.23	0.398	1.31	0.294	1.21	0.003	1	0.989	1.15	0.011
1422628_at	RIKEN cDNA 4632417K18 gene	4632417K18Rik	1.29	0.065	1.66	0.013	1.21	0.004	1.27	0.002	1.23	0.018
1428821_at	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic a	Agpat2	1.51	0.249	1.8	0.047	1.21	0.012	1.18	0.042	1.26	0.006
1425482_s_at	ankyrin repeat and MYND domain containing 2	Ankmy2	1.1	0.741	1.06	0.924	1.21	0.039	-1.07	0.387	-1.09	0.415
1417970_at	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s	Atp5s	-1.05	0.592	1.01	0.992	1.21	0.042	-1.06	0.236	1.09	0.316
1442005_at	expressed sequence AW987390	AW987390	1.61	0.534	1.56	0.834	1.21	0.025	1.07	0.912	1.19	0.000
1452902_at	dehydrogenase/reductase (SDR family) member 13	Dhrs13	1.04	0.700	1.48	0.008	1.21	0.043	1.31	0.137	1.26	0.201
1448877_at	distal-less homeobox 2	Dlx2	-1.03	0.505	-1.13	0.204	1.21	0.003	-1.09	0.349	-1.02	0.671
1452797_at	FAST kinase domains 3	Fastkd3	1.14	0.345	1.49	0.007	1.21	0.005	1.2	0.009	1.02	0.430
1435866_s_at	histone 3, H2a	Hist3h2a	-1.05	0.609	1.21	0.041	1.21	0.013	1.28	0.008	1.25	0.005
1457292_at	Josephin domain containing 3	Josd3	-1.18	0.399	-1.22	0.377	1.21	0.030	1.13	0.399	1.09	0.904
1439530_a_at	similar to NFkB interacting protein 1	LOC669005	-1.04	0.601	1.16	0.527	1.21	0.038	1.01	0.844	1.18	0.224
1451490_at	lysophospholipase-like 1	Lyplal1	-1.2	0.084	-1.57	0.071	1.21	0.023	1.05	0.456	1.19	0.356
1435447_at	major intrinsic protein of eye lens fiber	Mip	1.55	0.569	1.39	0.817	1.21	0.001	1.24	0.257	1.59	0.543
1430530_s_at	NmrA-like family domain containing 1	Nmral1	1.2	0.866	1.35	0.084	1.21	0.047	1.04	0.475	1.19	0.069
1460001_at	pyroglutamyl-peptidase I	Pgpep1	-1.25	0.251	1.09	0.975	1.21	0.033	-1.04	0.533	1.12	0.343
1416530_a_at	purine-nucleoside phosphorylase	Pnp	1.1	0.233	1.44	0.035	1.21	0.003	1.17	0.006	1.26	0.058
1451519_at	ring finger protein 2	Rnf2	1.1	0.539	1.23	0.228	1.21	0.037	1.09	0.368	-1.06	0.255
1423666_s_at	ribosomal protein L5 /// similar to 60S ribosomal protein L5 /// similar	Rpl5 /// LOC38274	-1.1	0.256	1.27	0.032	1.21	0.047	1.38	0.002	1.31	0.063
1459657_s_at	RNA polymerase 1-3	Rpo1-3	-1.13	0.293	-1.03	0.616	1.21	0.010	1	0.923	-1	0.837
1450129_a_at	suppressor of cytokine signaling 6	Socs6	1.3	0.397	1.43	0.089	1.21	0.021	1.09	0.170	1.06	0.109
1442590_at	tumor necrosis factor receptor superfamily, member 23	Tnfrsf23	1.43	0.672	1.47	0.352	1.21	0.015	1.05	0.121	1.16	0.076
1460642_at	Tnf receptor associated factor 4	Traf4	1.67	0.344	2.39	0.029	1.21	0.005	1.43	0.079	1.48	0.090
1437151_at	ubiquitin specific peptidase 22	Usp22	2.45	0.353	2.89	0.239	1.21	0.003	1.12	0.029	1.14	0.033
1427120_at	zinc finger protein 26	Zfp26	-1.03	0.657	-1.02	0.676	1.21	0.011	1.15	0.025	1.06	0.156
1452268_at	RIKEN cDNA 2810485I05 gene	2810485I05Rik	2.47	0.226	2.27	0.362	1.22	0.018	1.37	0.007	1.09	0.340
1434567_at	RIKEN cDNA 4732496O08 gene	4732496O08Rik	-1.02	0.654	1.39	0.009	1.22	0.043	1.12	0.085	1.19	0.043
1435745_at	RIKEN cDNA 5031439G07 gene	5031439G07Rik	-1.07	0.481	-1.01	0.643	1.22	0.021	1.11	0.064	1.23	0.128
1452203_at	RIKEN cDNA 5830411E10 gene	5830411E10Rik	1.21	0.393	1.62	0.053	1.22	0.043	1.05	0.412	1.1	0.262
1454644_at	RIKEN cDNA 6330569M22 gene	6330569M22Rik	1.01	0.893	1.05	0.589	1.22	0.028	1.18	0.013	1.14	0.058
1448431_at	ankyrin repeat and SOCS box-containing protein 6	Asb6	-1.02	0.430	1.32	0.669	1.22	0.026	1	0.956	1.17	0.272
1426883_at	expressed sequence AW491445	AW491445	1.1	0.877	1.06	0.959	1.22	0.014	1.24	0.232	-1.23	0.099
1452039_a_at	Brca1 associated protein 1	Bap1	-1.19	0.363	1.03	0.713	1.22	0.008	1.03	0.352	1.18	0.127
1415975_at	calcium regulated heat stable protein 1	Carhsp1	1.61	0.152	1.91	0.034	1.22	0.024	1.17	0.056	1.29	0.008
1448205_at	cyclin B1, related sequence 1 /// cyclin B1	Ccnb1-rs1 /// Ccnb	1.1	0.384	-1.12	0.073	1.22	0.003	1.07	0.246	-1	0.881
1424528_at	cell growth regulator with EF hand domain 1	Cgref1	1.14	0.577	1.64	0.001	1.22	0.024	1.13	0.280	1.16	0.020
1454679_at	DNA segment, Chr 8, ERATO Doi 457, expressed	D8Ertd457e	-1.06	0.440	1.22	0.092	1.22	0.022	1.19	0.013	1.13	0.092
1452796_at	differentially expressed in FDCP 6	Def6	1.45	0.151	1.87	0.024	1.22	0.002	1.24	0.012	1.4	0.012
1449940_a_at	eukaryotic translation initiation factor 2B, subunit 4 delta	Eif2b4	-1.01	0.692	1.13	0.480	1.22	0.018	1.14	0.329	1.16	0.011

1455904_at	growth arrest specific 5	Gas5	1.01	0.711	-1.03	0.544	1.22	0.002	1.23	0.038	1.1	0.140
1449746_s_at	GLI pathogenesis-related 1 (glioma)	Glipr1	-1.05	0.474	1.2	0.631	1.22	0.006	-1.12	0.559	1.7	0.065
1425201_a_at	hydroxypyruvate isomerase homolog (E. coli)	Hyi	1.1	0.913	1.1	0.958	1.22	0.013	1.05	0.852	1.1	0.242
1416324_s_at	potassium channel tetramerisation domain containing 20	Kctd20	-1.21	0.324	1.15	0.888	1.22	0.048	1.12	0.169	1.05	0.051
1418192_at	max binding protein	Mnt	-1.02	0.402	1.17	0.496	1.22	0.029	1.54	0.220	1.11	0.753
1417571_at	N-methylpurine-DNA glycosylase	Mpg	1.11	0.698	1.27	0.179	1.22	0.029	1.08	0.299	1.38	0.139
1437834_s_at	protein kinase C and casein kinase substrate in neurons 3	Pacsin3	-1.03	0.510	1.01	0.554	1.22	0.025	1.14	0.201	1.4	0.008
1451624_a_at	phosphatase, orphan 2	Phospho2	1.03	0.988	1.39	0.251	1.22	0.020	1.35	0.028	1.63	0.029
1418369_at	DNA primase, p49 subunit	Prim1	1.28	0.071	1.58	0.040	1.22	0.017	1.13	0.095	1.07	0.325
1417323_at	proline/serine-rich coiled-coil 1	Psrc1	1.09	0.506	1.46	0.007	1.22	0.004	1.16	0.006	1.24	0.009
1455438_at	peroxisomal membrane protein 4	Pxmp4	-1.05	0.513	-1.29	0.324	1.22	0.012	1.08	0.674	1.4	0.060
1426965_at	RAS related protein 2a	Rap2a	-1.03	0.529	1.23	0.019	1.22	0.040	1.17	0.048	1.38	0.008
1424156_at	retinoblastoma-like 1 (p107)	Rbl1	1.38	0.021	1.43	0.000	1.22	0.035	1.08	0.197	1.29	0.032
1428342_at	REST corepressor 3	Rcor3	1.16	0.335	1.26	0.137	1.22	0.038	1.11	0.124	1.12	0.333
1455265_a_at	regulator of G-protein signaling 16	Rgs16	-1.24	0.285	-1.28	0.160	1.22	0.029	-1.13	0.105	1.14	0.383
1423312_at	trophoblast glycoprotein	Tpbg	-1.08	0.469	1.01	0.869	1.22	0.015	-1.1	0.246	1.15	0.105
1455268_at	zinc finger, CSL domain containing 2	Zcsl2	1.11	0.191	1.4	0.003	1.22	0.046	1.17	0.168	1.32	0.018
1452880_at	zinc finger, HIT type 3	Znhit3	1.19	0.211	1.43	0.003	1.22	0.043	1.1	0.274	1.21	0.017
1455135_at	RIKEN cDNA 2610014I16 gene	2610014I16Rik	-1.12	0.317	-1.08	0.485	1.23	0.003	1.1	0.139	1.11	0.176
1429421_at	RIKEN cDNA 2610203E10 gene	2610203E10Rik	-1.19	0.377	-1.16	0.321	1.23	0.008	1.3	0.192	1.22	0.628
1453846_at	RIKEN cDNA 2810013C04 gene	2810013C04Rik	1.01	0.880	-1.06	0.654	1.23	0.004	1.04	0.739	1.59	0.336
1417218_at	RIKEN cDNA 2810048G17 gene	2810048G17Rik	1.1	0.459	1.22	0.180	1.23	0.047	1.2	0.004	1.12	0.000
1427167_at	expressed sequence AI448196	AI448196	1.22	0.321	1.32	0.185	1.23	0.022	1.47	0.043	1.44	0.057
1449019_at	A kinase (PRKA) anchor protein 1	Akap1	1.11	0.231	1.46	0.005	1.23	0.027	1.15	0.044	1.16	0.135
1449174_at	ADP-ribosyltransferase 4	Art4	2.01	0.517	1.45	0.821	1.23	0.007	1.56	0.201	1.47	0.211
1440831_at	BTB and CNC homology 1	Bach1	-1.05	0.574	1.13	0.939	1.23	0.042	1.12	0.099	1.27	0.014
1441989_at	BCL2/adenovirus E1B interacting protein 1, NIP2	Bnip2	-1.07	0.612	1.23	0.003	1.23	0.018	1.18	0.382	-1.09	0.704
1435406_at	coiled-coil alpha-helical rod protein 1	Cchcr1	1.12	0.375	1.36	0.020	1.23	0.009	1.02	0.842	-1.05	0.464
1436914_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) s	Ctdspl2	4.38	0.177	4.09	0.233	1.23	0.036	1.18	0.060	1.15	0.347
1418456_a_at	chemokine (C-X-C motif) ligand 14	Cxcl14	-1.05	0.601	1.01	0.965	1.23	0.042	1.11	0.107	1.34	0.105
1440478_at	DNA segment, Chr 10, ERATO Doi 438, expressed	D10Ertd438e	1.16	0.380	1.3	0.005	1.23	0.032	1.22	0.329	-1.06	0.623
1435926_at	RIKEN cDNA E030003F13 gene	E030003F13Rik	-1.03	0.574	1.4	0.017	1.23	0.022	1.27	0.028	1.29	0.047
1455514_at	potassium voltage-gated channel, Shal-related family, member 1	Kcnd1	1.31	0.947	1.11	0.652	1.23	0.029	1.26	0.280	1.25	0.478
1439261_x_at	MIT, microtubule interacting and transport, domain containing 1	Mitd1	-1.49	0.214	1.12	0.854	1.23	0.001	1.22	0.212	1.08	0.910
1436993_x_at	profilin 2	Pfn2	-1.14	0.421	1.08	0.918	1.23	0.022	1.06	0.220	1.16	0.050
1417166_at	PC4 and SFRS1 interacting protein 1	Psip1	1.04	0.933	1.06	0.731	1.23	0.014	1.26	0.035	1.27	0.027
1417035_at	SAC3 domain containing 1	Sac3d1	1.04	0.715	1.36	0.026	1.23	0.034	1.23	0.023	1.28	0.048
1417888_at	tripartite motif protein 13	Trim13	1.5	0.063	1.64	0.054	1.23	0.001	1.14	0.255	1.32	0.006
1429393_at	WD repeat domain 40A	Wdr40a	1.4	0.479	1.9	0.083	1.23	0.013	1.24	0.006	1.19	0.047
1451302_at	RIKEN cDNA 1110012L19 gene	1110012L19Rik	1.24	0.261	1.58	0.011	1.24	0.028	1.19	0.013	1.2	0.054
1428675_at	RIKEN cDNA 1110049F12 gene	1110049F12Rik	1.02	0.878	1.22	0.092	1.24	0.021	1.08	0.378	1.22	0.041
1438429_at	RIKEN cDNA 2610319H10 gene	2610319H10Rik	-1.14	0.349	1.13	0.456	1.24	0.040	1.35	0.113	1.23	0.159
1454563_at	RIKEN cDNA 4930573C08 gene	4930573C08Rik	-1.35	0.215	-1.58	0.004	1.24	0.032	-1.37	0.313	2.13	0.008
1432221_at	RIKEN cDNA 5330417H12 gene	5330417H12Rik	1.03	0.227	-1.45	0.375	1.24	0.033	1.4	0.453	1.24	0.757
1453210_at	RIKEN cDNA 5730507C01 gene	5730507C01Rik	-1.05	0.702	1.54	0.134	1.24	0.001	1.17	0.019	2.38	0.098
1434659_at	RIKEN cDNA 5830411G16 gene	5830411G16Rik	-1.15	0.270	1.18	0.084	1.24	0.030	-1.07	0.461	1.01	0.970
1426748_s_at	ATP-binding cassette, sub-family F (GCN20), member 3	Abcf3	-1.04	0.471	1.02	0.510	1.24	0.045	1.04	0.652	1.1	0.144
1416408_at	acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	-1.12	0.261	1	0.670	1.24	0.012	-1.03	0.707	1.13	0.136
1434729_at	cDNA sequence AK129302	AK129302	1.23	0.173	1.09	0.679	1.24	0.043	1.08	0.411	1.19	0.012
1418585_at	cyclin H	Ccnh	1.28	0.019	1.26	0.143	1.24	0.037	1.16	0.189	1.4	0.048
1448835_at	E2F transcription factor 6	E2f6	1.57	0.285	1.8	0.190	1.24	0.034	1.19	0.020	1.17	0.046
1433622_at	gem (nuclear organelle) associated protein 4	Gemin4	1.82	0.236	2.11	0.013	1.24	0.013	1.35	0.009	1.39	0.005
1433650_at	hydroxyacylglutathione hydrolase-like	Haghl	-1.43	0.148	-2.05	0.062	1.24	0.041	-1.03	0.546	-1.23	0.316
1437226_x_at	MARCKS-like 1	Marcksl1	1.07	0.012	1.46	0.000	1.24	0.000	1.22	0.019	1.28	0.076
1423218_a_at	mitochondrial ribosomal protein L49	Mrpl49	1.31	0.017	1.85	0.007	1.24	0.006	1.36	0.009	1.29	0.096
1417689_a_at	PDZK1 interacting protein 1	Pdzk1ip1	-1.47	0.301	-1.61	0.220	1.24	0.008	1.34	0.596	1.43	0.470
1440965_at	Phosphatidylinositol glycan, class L	Pigl	1.09	0.989	1.16	0.572	1.24	0.040	1.34	0.006	1.06	0.022
1453623_a_at	RAD23a homolog (S. cerevisiae)	Rad23a	2.58	0.265	2.11	0.046	1.24	0.028	1.08	0.550	1.16	0.173

1455584_at	stromal cell derived factor 4	Sdf4	-1.14	0.397	-1.17	0.414	1.24	0.010	-1.22	0.074	1.26	0.205
1459843_s_at	MAD homolog 1 (Drosophila)	Smad1	-1.15	0.391	1.1	0.946	1.24	0.001	1.02	0.724	1.11	0.195
1449629_s_at	Small nuclear ribonucleoprotein D3	Snrpd3	-1.22	0.375	-1.15	0.430	1.24	0.011	1.01	0.789	1.1	0.511
1424634_at	transcription elongation factor A (SII)-like 1	Tceal1	1.02	0.999	1.34	0.098	1.24	0.046	1.02	0.909	1.38	0.585
1427421_at	t-complex protein 10b	Tcp10b	1.04	0.961	-1.08	0.271	1.24	0.007	-1.32	0.182	-2.64	0.005
1419132_at	toll-like receptor 2	Tlr2	1.04	0.845	1.05	0.908	1.24	0.024	1.05	0.634	1.02	0.900
1425561_at	tRNA nucleotidyl transferase, CCA-adding, 1	Trnt1	10.01	0.198	8.94	0.140	1.24	0.041	1.17	0.033	1.12	0.482
1454846_at	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Utp15	-1.08	0.475	1.21	0.151	1.24	0.003	1.23	0.010	1.23	0.038
1434133_s_at	WD repeat domain 42A	Wdr42a	1.47	0.253	1.36	0.604	1.24	0.028	-1.06	0.725	1.24	0.392
1428678_s_at	WD repeat domain 73	Wdr73	-1.01	0.808	1.25	0.047	1.24	0.016	1.2	0.055	1.22	0.024
1434896_at	zinc finger protein 422, related sequence 1	Zfp422-rs1	1.03	0.952	1.12	0.542	1.24	0.036	1.18	0.127	1.04	0.221
1432322_at	RIKEN cDNA 2310016E02 gene	2310016E02Rik	1.32	0.898	1.47	0.318	1.25	0.035	-1.18	0.375	-1.45	0.159
1435076_at	RIKEN cDNA 2310047D13 gene	2310047D13Rik	1.2	0.442	1.31	0.162	1.25	0.025	1.21	0.009	1.05	0.487
1419074_at	RIKEN cDNA 2510006C20 gene	2510006C20Rik	1.11	0.163	1.39	0.015	1.25	0.036	1.14	0.010	1.38	0.042
1424692_at	RIKEN cDNA 2810055F11 gene	2810055F11Rik	1.53	0.251	1.83	0.018	1.25	0.007	1.3	0.039	1.47	0.008
1415717_at	RIKEN cDNA 4931406I20 gene	4931406I20Rik	-1.05	0.648	-1.05	0.561	1.25	0.042	1.1	0.557	1.04	0.561
1424496_at	RIKEN cDNA 5133401N09 gene	5133401N09Rik	1.47	0.477	1.62	0.199	1.25	0.035	1.09	0.105	1.27	0.106
1439259_x_at	abhydrolase domain containing 4	Abhd4	-1.04	0.586	1.36	0.323	1.25	0.009	1.11	0.005	1.25	0.093
1427912_at	carbonyl reductase 3	Cbr3	-1.03	0.630	1.43	0.160	1.25	0.019	1.16	0.073	1.34	0.004
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	1.16	0.333	1.69	0.005	1.25	0.005	1.21	0.002	1.29	0.003
1427822_a_at	coatomer protein complex, subunit gamma 2, antisense 2	Copg2as2	1.83	0.073	1.33	0.310	1.25	0.045	-1.61	0.212	-1.04	0.528
1417904_at	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	Dclre1a	-1.06	0.613	1.1	0.466	1.25	0.037	1.37	0.086	1.07	0.766
1425196_a_at	histidine triad nucleotide binding protein 2	Hint2	-1.19	0.410	1.05	0.558	1.25	0.026	1.25	0.004	1.21	0.011
1428329_a_at	intraflagellar transport 80 homolog (Chlamydomonas)	Ift80	1.02	0.684	-1.24	0.285	1.25	0.014	1.08	0.174	-1.15	0.462
1452316_at	integrator complex subunit 12	Ints12	1.15	0.111	1.49	0.002	1.25	0.012	1.18	0.058	1.28	0.111
1429351_at	kelch-like 24 (Drosophila)	Klhl24	1.35	0.202	1.74	0.063	1.25	0.004	1.1	0.198	1.03	0.762
1426284_at	keratin 20	Krt20	1.21	0.030	1.3	0.005	1.25	0.035	1.07	0.145	1.23	0.123
1436330_x_at	similar to reduced expression 2 /// similar to reduced expression 2	LOC278757 /// LOC	-1.06	0.436	1.11	0.689	1.25	0.035	1.04	0.882	1.34	0.250
1437481_at	hypothetical LOC623451	LOC623451	-1.24	0.255	1.24	0.604	1.25	0.047	1.14	0.103	1.22	0.023
1434956_at	similar to ring finger protein 170 /// similar to ring finger protein 170	LOC668047 /// LOC	-1.09	0.459	-1.25	0.290	1.25	0.026	1.12	0.304	1.04	0.971
1451552_at	Similar to lipoyltransferase	MGC28431	1.43	0.443	1.67	0.015	1.25	0.046	1.42	0.027	1.44	0.103
1416313_at	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Dro	Mllt11	-1.06	0.521	-1.04	0.736	1.25	0.001	1.15	0.023	1.18	0.005
1426963_at	phosphofurin acidic cluster sorting protein 2	Pacs2	1.78	0.307	1.3	0.952	1.25	0.023	1.13	0.188	1.08	0.726
1424793_a_at	phosphatidylethanolamine binding protein 2	Pbp2	1.01	0.733	1.25	0.156	1.25	0.006	1.26	0.243	1.36	0.011
1445203_at	PDZ domain containing 2	Pdzd2	1.05	0.885	1.16	0.405	1.25	0.027	-1.07	0.676	1.18	0.583
1426752_at	PHD finger protein 17	Phf17	-1.06	0.531	1.05	0.819	1.25	0.007	1.06	0.205	1.07	0.253
1422272_at	per-hexamer repeat gene 4	Phxr4	2.7	0.274	2.61	0.571	1.25	0.040	1.1	0.479	1.42	0.435
1449027_at	ras homolog gene family, member U	Rhou	-1.15	0.323	1.13	0.902	1.25	0.045	1.19	0.067	1.24	0.056
1437353_at	SET domain containing 1B	Setd1b	-1.07	0.513	-1.05	0.580	1.25	0.039	1.06	0.713	1.09	0.592
1434708_at	von Hippel-Lindau syndrome homolog	Vhlh	1.01	0.876	1.33	0.001	1.25	0.030	1.17	0.031	1.15	0.071
1458523_at	zinc finger, matrin-like	Zfml	2.03	0.703	1.21	0.444	1.25	0.033	1.6	0.325	1.53	0.945
1447432_s_at	zinc finger protein 263	Zfp263	-1.17	0.416	1.25	0.881	1.25	0.022	1.26	0.124	1.14	0.411
1424892_at	zinc finger protein 95	Zfp95	1.17	0.399	1.53	0.031	1.25	0.032	1.2	0.031	1.47	0.023
1422517_a_at	zinc ribbon domain containing, 1	Znrd1	-1.01	0.749	1.21	0.144	1.25	0.034	1.26	0.005	1.31	0.051
1431180_at	RIKEN cDNA 1700123A16 gene /// similar to zinc finger protein 709	1700123A16Rik ///	1.08	0.776	1.15	0.841	1.26	0.003	1.33	0.648	1.07	0.993
1447568_at	RIKEN cDNA 2010003O18 gene	2010003O18Rik	-1.23	0.306	-1.2	0.357	1.26	0.025	1.35	0.188	1.09	0.742
1456310_a_at	RIKEN cDNA 2610002J02 gene	2610002J02Rik	-1.21	0.402	-1.06	0.513	1.26	0.011	1.02	0.494	1.15	0.122
1429451_at	RIKEN cDNA 2610301B20 gene	2610301B20Rik	4.28	0.264	3.69	0.117	1.26	0.049	1.12	0.445	1.33	0.025
1424014_at	RIKEN cDNA 2900092E17 gene	2900092E17Rik	1.12	0.737	1.27	0.095	1.26	0.003	-1.03	0.714	1.17	0.023
1429665_at	RIKEN cDNA 6230416J20 gene	6230416J20Rik	1.3	0.031	1.24	0.021	1.26	0.022	1.26	0.408	1.03	0.621
1448539_a_at	aspartoacylase (aminoacylase) 3	Acy3	2.53	0.413	2.54	0.294	1.26	0.041	1.08	0.948	1.15	0.164
1419435_at	aldehyde oxidase 1	Aox1	-1.13	0.278	1.04	0.770	1.26	0.002	1.16	0.795	1.31	0.166
1440890_a_at	expressed sequence BB114266	BB114266	-1.07	0.496	1.24	0.985	1.26	0.035	1.19	0.098	1.25	0.100
1437455_a_at	B-cell translocation gene 1, anti-proliferative	Btg1	-1.21	0.180	1.1	0.674	1.26	0.042	1.03	0.948	1.54	0.005
1433781_a_at	claudin 12	Cldn12	-1.21	0.383	-1.02	0.609	1.26	0.012	1.09	0.326	1.19	0.010
1443869_at	RIKEN cDNA E430028B21 gene	E430028B21Rik	-1.05	0.144	1.13	0.294	1.26	0.013	1.12	0.014	1.35	0.109
1417969_at	F-box only protein 31	Fbxo31	-1.43	0.091	-1.21	0.125	1.26	0.041	1.08	0.451	1.13	0.037
1454996_at	hydroxysteroid dehydrogenase like 1	Hsdl1	-1.05	0.435	1.15	0.383	1.26	0.017	1.2	0.000	1.33	0.050

1428185_at	potassium channel tetramerisation domain containing 18	Kctd18	1.12	0.398	1.41	0.012	1.26	0.014	1.26	0.026	1.12	0.294
1452733_at	pantothenate kinase 2 (Hallervorden-Spatz syndrome)	Pank2	-1.17	0.327	1.13	0.979	1.26	0.001	1.34	0.070	1.17	0.321
1451516_at	Ras homolog enriched in brain like 1	Rhebl1	1.54	0.248	1.73	0.062	1.26	0.034	1.22	0.231	1.25	0.052
1419061_at	ras homolog gene family, member D	Rhod	1.33	0.344	2.09	0.012	1.26	0.021	1.21	0.049	1.5	0.005
1434626_at	RNA pseudouridylate synthase domain containing 3	Rpusd3	-1.04	0.452	1.09	0.853	1.26	0.046	1.16	0.140	1.28	0.220
1416638_at	sal-like 2 (Drosophila)	Sall2	1.08	0.786	1.62	0.014	1.26	0.049	-1.01	0.778	1.33	0.393
1418257_at	solute carrier family 12, member 7	Slc12a7	-1.05	0.648	-1.18	0.106	1.26	0.050	1.05	0.233	1.09	0.807
1455651_at	telomeric repeat binding factor 2	Terf2	-1.28	0.219	-1.11	0.476	1.26	0.038	1.04	0.569	1.12	0.741
1418123_at	unc-119 homolog (C. elegans)	Unc119	1.37	0.369	1.43	0.070	1.26	0.012	1.04	0.505	1.1	0.517
1415989_at	vascular cell adhesion molecule 1	Vcam1	1.77	0.526	2.37	0.419	1.26	0.029	1.19	0.079	1.2	0.209
1451277_at	zinc binding alcohol dehydrogenase, domain containing 2	Zadh2	-1.03	0.595	1.13	0.515	1.26	0.005	1.2	0.032	1.22	0.076
1434022_at	zinc finger and BTB domain containing 33	Zbtb33	-1.01	0.735	1.16	0.437	1.26	0.003	1.29	0.009	1.25	0.013
1429739_a_at	zinc finger protein 278	Zfp278	1.09	0.620	1.71	0.019	1.26	0.025	1.25	0.028	1.52	0.009
1424706_at	zinc finger protein 51	Zfp51	1.13	0.916	1.14	0.971	1.26	0.034	1.16	0.133	1.14	0.394
1434689_at	zinc finger protein 637	Zfp637	1.36	0.042	1.48	0.006	1.26	0.027	1.11	0.310	1.31	0.020
1435333_at	RIKEN cDNA 1110007M04 gene	1110007M04Rik	1.12	0.087	1.39	0.101	1.27	0.005	1.41	0.027	1.3	0.015
1424872_at	RIKEN cDNA 2310001H12 gene /// similar to zinc finger protein 709	2310001H12Rik ///	1.23	0.925	1.91	0.127	1.27	0.012	1.43	0.042	1.13	0.080
1436323_at	RIKEN cDNA 2810001A02 gene	2810001A02Rik	1.07	0.477	1.29	0.148	1.27	0.043	1.13	0.259	1.29	0.098
1427959_at	abhydrolase domain containing 10	Abhd10	1.04	0.551	1.38	0.026	1.27	0.027	1.25	0.029	1.29	0.029
1417326_a_at	anaphase promoting complex subunit 11 homolog (yeast)	Anapc11	1.01	0.647	1.12	0.118	1.27	0.007	1.04	0.289	1.07	0.278
1440928_at	RIKEN cDNA D630037F22 gene	D630037F22Rik	-1.08	0.523	-1.67	0.006	1.27	0.017	-1.21	0.150	1.19	0.173
1426870_at	F-box only protein 33	Fbxo33	-1.03	0.547	1.29	0.019	1.27	0.035	1.17	0.037	1.34	0.052
1417922_at	kelch repeat and BTB (POZ) domain containing 4	Kbtbd4	1.23	0.136	1.6	0.008	1.27	0.027	-1	0.837	1.41	0.087
1455155_at	LSM14 homolog B (SCD6, S. cerevisiae)	Lsm14b	-1.01	0.701	1.16	0.564	1.27	0.012	1.08	0.014	1.17	0.151
1434836_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-depender	Nfatc2ip	-1.06	0.550	1.11	0.821	1.27	0.023	1.12	0.145	1.31	0.015
1426533_at	nucleolar protein 5A	Nol5a	1.43	0.428	1.69	0.040	1.27	0.001	1.43	0.008	1.2	0.087
1429139_at	OTU domain containing 7B	Otud7b	1.01	0.705	1.19	0.305	1.27	0.032	-1.01	0.819	1.2	0.058
1453299_a_at	purine-nucleoside phosphorylase /// similar to purine-nucleoside pho	Pnp /// LOC545044	1.5	0.195	1.85	0.050	1.27	0.003	1.14	0.025	1.35	0.082
1433668_at	proline-rich nuclear receptor coactivator 1	Pnrc1	1	0.913	1.29	0.129	1.27	0.031	1.19	0.005	1.36	0.010
1424473_at	polymerase (RNA) II (DNA directed) polypeptide H	Polr2h	1.25	0.115	1.58	0.000	1.27	0.005	1.21	0.041	1.22	0.054
1460168_at	stem-loop binding protein	Slbp	1.2	0.071	1.73	0.002	1.27	0.009	1.23	0.002	1.28	0.092
1441315_s_at	solute carrier family 19 (thiamine transporter), member 2	Slc19a2	1.03	0.634	1.47	0.531	1.27	0.017	1.08	0.012	1.32	0.044
1448317_at	transmembrane protein 128	Tmem128	-1.01	0.844	1.13	0.313	1.27	0.018	1.04	0.509	1.05	0.607
1428779_at	zinc finger and BTB domain containing 41 homolog	Zbtb41	1.04	0.946	1.22	0.162	1.27	0.046	1.22	0.082	1.17	0.043
1452840_at	RIKEN cDNA 1500009L16 gene	1500009L16Rik	1.14	0.584	1.17	0.186	1.28	0.024	-1.29	0.009	1.16	0.365
1453332_at	RIKEN cDNA 2410002O22 gene	2410002O22Rik	-1.01	0.759	1.24	0.191	1.28	0.010	-1.01	0.681	1.13	0.163
1431865_a_at	RIKEN cDNA 4933405K07 gene	4933405K07Rik	1.23	0.229	2.47	0.492	1.28	0.004	-1.31	0.122	2.12	0.633
1437911_at	RIKEN cDNA 6330416L07 gene	6330416L07Rik	1.25	0.634	1.7	0.050	1.28	0.024	1.1	0.338	1.14	0.248
1437180_at	RIKEN cDNA 6530403A03 gene	6530403A03Rik	1.07	0.774	1.04	0.883	1.28	0.029	1.15	0.054	-1.12	0.156
1425354_a_at	angiogenic factor with G patch and FHA domains 1	Aggf1	-1.09	0.524	1.16	0.666	1.28	0.041	1.12	0.153	1.16	0.159
1433465_a_at	expressed sequence AI467606	AI467606	-1.27	0.253	1.11	0.641	1.28	0.028	1.09	0.778	2.35	0.079
1416631_at	adaptor-related protein complex AP-4, beta 1	Ap4b1	1.22	0.516	1.38	0.031	1.28	0.009	1.08	0.246	1.2	0.002
1435182_at	RIKEN cDNA C530028I08 gene	C530028I08Rik	-1.15	0.124	-1.09	0.468	1.28	0.022	1.02	0.877	-1.13	0.059
1420098_s_at	DNA segment, Chr 13, ERATO Doi 787, expressed	D13Ertd787e	-1.11	0.466	-1.38	0.135	1.28	0.028	1.54	0.064	1.22	0.711
1435348_at	RIKEN cDNA D930009K15 gene	D930009K15Rik	1.05	0.722	1.27	0.073	1.28	0.030	1.37	0.011	1.37	0.003
1421731_a_at	flap structure specific endonuclease 1	Fen1	1.18	0.546	1.56	0.001	1.28	0.003	1.25	0.030	1.27	0.001
1422977_at	glycoprotein Ib, beta polypeptide	Gp1bb	-1.15	0.403	-1.01	0.631	1.28	0.025	1.08	0.475	1.22	0.303
1416155_at	high mobility group box 3	Hmgb3	1.26	0.408	1.33	0.296	1.28	0.046	1.12	0.028	1.1	0.114
1422433_s_at	isocitrate dehydrogenase 1 (NADP+), soluble	Idh1	-1.14	0.426	-1.37	0.128	1.28	0.045	1.1	0.086	1.05	0.435
1449158_at	potassium channel, subfamily K, member 2	Kcnk2	1.28	0.180	1.36	0.162	1.28	0.038	1.25	0.006	1.04	0.314
1426988_at	kelch domain containing 5	Klhdc5	3.69	0.376	3.44	0.015	1.28	0.000	1.25	0.134	1.48	0.012
1423071_x_at	hypothetical gene supported by BC019681; BC027236 /// hypothetic	LOC270335 /// LOC	-1.06	0.518	1.02	0.874	1.28	0.001	1.26	0.008	1.2	0.023
1433644_at	protein-O-mannosyltransferase 2	Pomt2	1.31	0.856	1.35	0.409	1.28	0.041	1.06	0.424	1.34	0.186
1438753_at	Porcupine homolog (Drosophila)	Porcn	1.07	0.849	1.23	0.677	1.28	0.030	-1.2	0.322	-1.16	0.161
1451080_at	ubiquitin specific peptdiase 1	Usp1	1.38	0.036	1.7	0.011	1.28	0.022	1.17	0.029	1.25	0.042
1418928_a_at	RIKEN cDNA 2310038H17 gene	2310038H17Rik	-1.11	0.331	1.04	0.885	1.29	0.009	1.03	0.354	1.01	0.975
1448308_at	adaptor-related protein complex 3, mu 1 subunit	Ap3m1	1.1	0.037	1.23	0.073	1.29	0.018	1.22	0.002	1.14	0.090
1450877_at	cDNA sequence BC005537	BC005537	1.2	0.334	1.13	0.771	1.29	0.028	1.09	0.537	-1.01	0.699

1435175_at	cDNA sequence BC034090	BC034090	-1.04	0.573	1.19	0.496	1.29	0.012	-1	0.960	1.19	0.491
1453683_a_at	centrosomal protein 55	Cep55	7.88	0.278	4.93	0.608	1.29	0.017	1.15	0.424	-1.1	0.669
1419429_at	ciliary neurotrophic factor receptor	Cntfr	-1.09	0.673	1.56	0.071	1.29	0.011	2.1	0.036	1.68	0.835
1433809_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Ddx5	1.07	0.699	1.23	0.630	1.29	0.047	1.02	0.779	1.6	0.195
1427239_at	intraflagellar transport 122 homolog (Chlamydomonas)	Ift122	1.48	0.509	1.84	0.327	1.29	0.022	-1.04	0.738	-1.13	0.307
1422816_a_at	mutY homolog (E. coli)	Mutyh	1.05	0.627	1.36	0.883	1.29	0.036	1.19	0.238	1.16	0.780
1419967_at	SEH1-like (S. cerevisiae	Seh1l	-1.26	0.265	1.12	0.720	1.29	0.030	1.17	0.467	1.23	0.229
1452931_at	RIKEN cDNA 2810408M09 gene	2810408M09Rik	-1.1	0.472	-1.04	0.611	1.3	0.027	1.12	0.025	1.19	0.196
1427085_at	RIKEN cDNA 2810432D09 gene	2810432D09Rik	1.03	0.905	1.5	0.162	1.3	0.046	1.3	0.003	1.25	0.090
1429563_x_at	RIKEN cDNA 5031415C07 gene	5031415C07Rik	-1.2	0.401	-1	0.563	1.3	0.037	1.17	0.123	1.22	0.146
1446299_at	RIKEN cDNA 6720456B07 gene	6720456B07Rik	1.1	0.577	-1.01	0.922	1.3	0.014	1.46	0.097	-1.32	0.157
1436942_at	RIKEN cDNA A930035D04 gene	A930035D04Rik	-1.13	0.375	1.05	0.937	1.3	0.007	1.19	0.048	1.22	0.114
1423570_at	ATP-binding cassette, sub-family G (WHITE), member 1	Abcg1	-1.2	0.389	-1.58	0.098	1.3	0.046	-1.12	0.282	1.01	0.763
1442429_at	Adaptor protein complex AP-2, mu1	Ap2m1	1.3	0.002	1.11	0.863	1.3	0.006	1.37	0.792	-1.57	0.117
1450648_s_at	histocompatibility 2, class II antigen A, beta 1	H2-Ab1	1.13	0.676	1.16	0.164	1.3	0.006	1.1	0.228	-1.02	0.949
1453573_at	histone1, H3d	Hist1h3d	-1.28	0.284	-1.04	0.525	1.3	0.006	1.19	0.068	1.21	0.175
1441100_at	mbt domain containing 1	Mbtd1	1.12	0.820	-1.02	0.540	1.3	0.036	1.15	0.021	1.04	0.794
1449550_at	myosin IC	Myo1c	1.05	0.348	1.33	0.019	1.3	0.048	1.25	0.012	1.32	0.020
1448728_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inl	Nfkbiz	1.15	0.028	1.41	0.144	1.3	0.049	1.23	0.063	-1.03	0.732
1438951_x_at	nucleoporin 54	Nup54	-1.05	0.567	1.21	0.979	1.3	0.005	1.03	0.647	1.31	0.001
1424453_at	phosphate cytidylyltransferase 1, choline, alpha isoform	Pcyt1a	2.51	0.400	2.41	0.796	1.3	0.048	1.07	0.477	-1.03	0.658
1427929_a_at	pyridoxal (pyridoxine, vitamin B6) kinase	Pdxk	-1.26	0.343	-1.02	0.575	1.3	0.010	1.19	0.064	1.45	0.024
1451199_at	queuine tRNA-ribosyltransferase domain containing 1	Qtrtd1	-1.25	0.321	1.08	0.960	1.3	0.032	1.13	0.035	1.41	0.005
1417406_at	SERTA domain containing 1	Sertad1	-1.06	0.513	1.14	0.969	1.3	0.007	1.26	0.006	1.34	0.021
1423616_at	TAR (HIV) RNA binding protein 2	Tarbp2	1.05	0.469	1.1	0.176	1.3	0.004	1.12	0.688	1.2	0.230
1433705_at	zinc finger protein 213	Zfp213	1.04	0.972	1.39	0.007	1.3	0.020	1.31	0.007	1.52	0.023
1459383_at	Zinc finger protein 52	Zfp52	-1.04	0.691	-1.34	0.296	1.3	0.007	2.21	0.312	-1.07	0.730
1429099_at	RIKEN cDNA 1110051B16 gene	1110051B16Rik	1.24	0.768	1.11	0.369	1.31	0.014	-1.35	0.204	1.22	0.544
1429100_at	RIKEN cDNA 2010109K11 gene	2010109K11Rik	-1.04	0.700	1.11	0.506	1.31	0.012	1.08	0.073	1.23	0.107
1432447_a_at	RIKEN cDNA 2310005N01 gene	2310005N01Rik	1.08	0.919	1.44	0.267	1.31	0.045	1.11	0.092	1.27	0.126
1428873_a_at	RIKEN cDNA 4121402D02 gene	4121402D02Rik	1.98	0.440	1.95	0.300	1.31	0.049	1.03	0.901	1.11	0.487
1429422_at	RIKEN cDNA 4933412E12 gene	4933412E12Rik	2.4	0.131	3.35	0.237	1.31	0.042	1.03	0.224	1.11	0.326
1417655_a_at	arsenate resistance protein 2	Ars2	-1.11	0.397	1.14	0.341	1.31	0.009	1.24	0.048	1.25	0.020
1460360_at	asparaginase like 1	Asrgl1	1.09	0.694	-1.09	0.380	1.31	0.008	1.12	0.627	1.37	0.189
1434532_at	cDNA sequence BC035295	BC035295	-1.07	0.499	1.44	0.752	1.31	0.000	1.37	0.013	1.43	0.002
1451574_at	B-cell CLL/lymphoma 9	Bcl9	-1.38	0.134	-1.06	0.479	1.31	0.002	-1.1	0.337	1.08	0.572
1436917_s_at	G-protein signalling modulator 1 (AGS3-like, C. elegans)	Gpsm1	-1.19	0.425	-1.02	0.593	1.31	0.018	-1.07	0.130	1.29	0.123
1451660_a_at	homeo box B6	Hoxb6	-1.1	0.431	-1.09	0.471	1.31	0.001	1.01	0.922	1.43	0.262
1435950_at	hairless	Hr	-2.26	0.157	-1.13	0.466	1.31	0.026	1.2	0.167	1.18	0.417
1451016_at	interferon-related developmental regulator 2	Ifrd2	4.81	0.963	4.6	0.428	1.31	0.020	1.1	0.671	1.23	0.127
1452166_a_at	keratin 10	Krt10	1.07	0.957	1.32	0.247	1.31	0.018	1.22	0.099	1.37	0.012
1422552_at	reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	1.6	0.294	4.18	0.007	1.31	0.022	1.36	0.042	2.34	0.011
1449480_at	Sin3-associated polypeptide 18	Sap18	1.17	0.290	1.48	0.203	1.31	0.038	1.34	0.017	1.31	0.192
1418377_a_at	Cd27 binding protein (Hindu God of destruction)	Siva	1.05	0.327	1.41	0.067	1.31	0.021	1.15	0.101	1.31	0.068
1455212_at	WD repeat domain 24	Wdr24	1.07	0.989	1.26	0.260	1.31	0.000	1.11	0.376	1.19	0.039
1454790_at	WD repeat domain 35	Wdr35	-1.01	0.683	1.22	0.411	1.31	0.019	1	0.967	1.11	0.529
1428926_at	RIKEN cDNA 1110003O08 gene	1110003O08Rik	-1.17	0.300	-1	0.616	1.32	0.029	1.7	0.047	1.03	0.915
1450323_at	RIKEN cDNA 5730493B19 gene	5730493B19Rik	1.54	0.270	1.57	0.020	1.32	0.017	-1.35	0.138	-1.07	0.435
1428502_at	ARP6 actin-related protein 6 homolog (yeast)	Actr6	-1.09	0.550	1.1	0.528	1.32	0.040	1.18	0.100	1.35	0.012
1421603_a_at	CEA-related cell adhesion molecule 2	Ceacam2	1.27	0.192	1.5	0.163	1.32	0.041	2.45	0.469	1.24	0.431
1456795_at	RIKEN cDNA D330027G24 gene	D330027G24Rik	1.12	0.536	1.43	0.797	1.32	0.007	1	0.962	1.16	0.500
1419353_at	dolichol-phosphate (beta-D) mannosyltransferase 1	Dpm1	-1.02	0.726	-1.37	0.018	1.32	0.009	1.09	0.629	-1.13	0.660
1431422_a_at	dual specificity phosphatase 14	Dusp14	1.88	0.299	2.21	0.031	1.32	0.019	1.37	0.006	1.27	0.039
1450935_at	excision repair cross-complementing rodent repair deficiency, compl	Ercc5	-1.01	0.580	1.91	0.140	1.32	0.025	1.26	0.042	1.3	0.071
1455726_at	gene model 71, (NCBI)	Gm71	-1.11	0.406	1.04	0.799	1.32	0.016	1.13	0.097	1.19	0.031
1429180_at	guanosine monophosphate reductase 2	Gmpr2	1.06	0.987	-1.24	0.212	1.32	0.001	1.37	0.270	-1.05	0.405
1436459_at	G protein-coupled receptor 161	Gpr161	1.04	0.971	1.19	0.233	1.32	0.050	1.05	0.838	1.14	0.316
1417477_at	gene trap locus F3b	Gtlf3b	-1.11	0.340	1.19	0.500	1.32	0.004	1.17	0.001	1.37	0.016

1428856_at	Histocompatibility 13	H13	1.2	0.878	1.1	0.940	1.32	0.032	1.35	0.348	1.45	0.227
1417292_at	interferon gamma inducible protein 47	Ifi47	1.1	0.414	1.2	0.564	1.32	0.019	1.1	0.067	-1.06	0.207
1423104_at	insulin receptor substrate 1	Irs1	1.41	0.165	1.98	0.109	1.32	0.007	1.33	0.004	1.23	0.017
1457040_at	leucine-rich repeat LGI family, member 2	Lgi2	-1.23	0.294	1.13	0.727	1.32	0.042	1.11	0.159	1.5	0.069
1445330_at	protein disulfide isomerase associated 3	Pdia3	1.06	0.206	-1.19	0.123	1.32	0.005	1.08	0.658	-1.03	0.612
1428992_at	unc-13 homolog D (C. elegans)	Unc13d	1.97	0.250	2.01	0.219	1.32	0.033	1.09	0.827	1.19	0.542
1418284_at	vacuolar protein sorting 72 (yeast)	Vps72	2	0.548	2.34	0.313	1.32	0.018	1.2	0.121	1.16	0.340
1435565_at	RIKEN cDNA 1500011H22 gene	1500011H22Rik	1.08	0.642	1.64	0.699	1.33	0.008	1.47	0.009	1.35	0.066
1436049_at	RIKEN cDNA 5730589K01 gene	5730589K01Rik	1.25	0.021	1.37	0.012	1.33	0.016	1.1	0.100	1.12	0.699
1435913_at	beta-1,4-N-acetyl-galactosaminyl transferase 4	B4galnt4	1.18	0.253	-1.14	0.243	1.33	0.020	1.33	0.100	-1.05	0.838
1425095_at	cDNA sequence BC002059	BC002059	-1.06	0.618	1.25	0.622	1.33	0.037	1.02	0.919	1.09	0.447
1453102_at	fibronectin leucine rich transmembrane protein 3	Flrt3	1.6	0.437	2.79	0.025	1.33	0.001	1.31	0.032	1.5	0.013
1423998_at	general transcription factor IIIC, polypeptide 5	Gtf3c5	1.55	0.208	1.84	0.026	1.33	0.040	1.13	0.090	1.33	0.050
1456200_at	inositol polyphosphate multikinase	Ipmk	-1.06	0.495	1.1	0.830	1.33	0.039	1.28	0.008	1.1	0.255
1434354_at	monoamine oxidase B	Maob	1.06	0.542	1.02	0.750	1.33	0.036	-1.16	0.564	1.27	0.600
1424988_at	myosin regulatory light chain interacting protein	Mylip	1.01	0.556	1.05	0.498	1.33	0.015	1.45	0.007	1.33	0.038
1416853_at	neurochondrin	Ncdn	1.03	0.922	1.31	0.200	1.33	0.009	1.21	0.063	1.12	0.488
1457198_at	neuropilin 1	Nrp1	-1.02	0.526	1.1	0.642	1.33	0.010	1.38	0.098	1.08	0.029
1439348_at	S100 calcium binding protein A10 (calpactin)	S100a10	1.1	0.673	1.21	0.457	1.33	0.040	1.24	0.213	1.13	0.616
1453559_a_at	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	Sel1h	1.29	0.507	1.02	0.411	1.33	0.044	1.41	0.401	1.16	0.658
1455297_at	spindlin family, member 2	Spin2	1.39	0.415	1.53	0.048	1.33	0.018	1.11	0.658	1.35	0.064
1418261_at	spleen tyrosine kinase	Syk	-1.08	0.400	-1.14	0.129	1.33	0.010	-1.15	0.009	1.14	0.454
1449732_at	zinc finger proliferation 1	Zipro1	-1.25	0.396	1.16	0.543	1.33	0.011	1.42	0.083	1.61	0.143
1451321_a_at	RIKEN cDNA 0610033I05 gene	0610033I05Rik	-1.07	0.482	1.64	0.066	1.34	0.009	1.07	0.148	1.28	0.040
1428550_at	RIKEN cDNA 1810015A11 gene	1810015A11Rik	1.06	0.364	1.27	0.025	1.34	0.004	1.43	0.017	1.41	0.040
1455652_at	expressed sequence AW124694	AW124694	1.58	0.866	1.19	0.313	1.34	0.032	1.16	0.827	1.14	0.376
1441910_x_at	cyclin E1	Ccne1	-1.1	0.496	1.1	0.893	1.34	0.035	1.19	0.065	1.23	0.091
1436549_a_at	heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	-1.14	0.455	-1.16	0.433	1.34	0.013	1.21	0.055	1.25	0.110
1457907_at	NIMA (never in mitosis gene a)-related expressed kinase 7	Nek7	1.59	0.270	2.12	0.275	1.34	0.041	1.17	0.548	1.26	0.408
1442048_at	ring finger protein 11	Rnf11	-1.19	0.276	-1.19	0.331	1.34	0.012	1.12	0.332	1.09	0.013
1421528_a_at	surfeit gene 5	Surf5	1.03	0.625	1.42	0.007	1.34	0.007	1.3	0.009	1.48	0.025
1424175_at	thyrotroph embryonic factor	Tef	-1.08	0.438	1.21	0.225	1.34	0.043	1.09	0.288	1.11	0.188
1435350_at	Tnf receptor-associated factor 6	Traf6	-1.2	0.364	-1.1	0.445	1.34	0.020	-1.02	0.607	1.09	0.905
1426987_at	RIKEN cDNA 5430417L22 gene	5430417L22Rik	1.35	0.313	1.4	0.147	1.35	0.022	1.19	0.120	1.25	0.230
1455196_s_at	expressed sequence AA987161	AA987161	-1.05	0.520	1.1	0.861	1.35	0.050	1.2	0.472	-1.08	0.626
1450716_at	a disintegrin-like and metallopeptidase (reprolysin type) with thromb	Adamts1	1.09	0.215	1.27	0.083	1.35	0.001	1.35	0.039	1.49	0.059
1451533_at	cDNA sequence BC022687	BC022687	1.27	0.827	1.81	0.093	1.35	0.006	1.13	0.046	1.21	0.038
1436422_at	cDNA sequence BC026590	BC026590	1.33	0.507	1.82	0.058	1.35	0.019	1.29	0.003	1.48	0.005
1419046_at	brain protein 16	Brp16	-1.03	0.562	1.09	0.489	1.35	0.005	1.09	0.694	1.26	0.150
1449296_a_at	cyclic nucleotide phosphodiesterase 1	Cnp1	1.55	0.648	1.78	0.243	1.35	0.021	1.05	0.466	-1.09	0.843
1449037_at	cAMP responsive element modulator	Crem	1.25	0.126	1.6	0.053	1.35	0.001	1.24	0.053	1.52	0.005
1437187_at	E2F transcription factor 7	E2f7	-1.02	0.730	1.37	0.145	1.35	0.022	1.12	0.238	1.25	0.036
1440085_at	ectodysplasin A2 isoform receptor	Eda2r	1.43	0.232	2.18	0.029	1.35	0.006	1.15	0.032	1.24	0.006
1430311_at	Myristoylated alanine rich protein kinase C substrate	Marcks	1.13	0.722	1.72	0.001	1.35	0.038	1.42	0.646	1.12	0.888
1428339_at	nudix (nucleoside diphosphate linked moiety X)-type motif 21	Nudt21	1.3	0.259	1.38	0.091	1.35	0.003	1.27	0.003	1.3	0.007
1457480_at	Polycomb group ring finger 3	Pcgf3	1.01	0.650	1.01	0.684	1.35	0.033	1.14	0.607	1.17	0.965
1457083_at	PRP31 pre-mRNA processing factor 31 homolog (yeast)	Prpf31	1.59	0.196	2.41	0.030	1.35	0.032	1.41	0.043	1.74	0.020
1454639_x_at	ribosomal protein L41 /// RIKEN cDNA 2210411K19 gene	Rpl41 /// 2210411K	-1.26	0.353	-1.05	0.493	1.35	0.032	1.11	0.689	1.24	0.204
1424817_at	sperm flagellar 1	Spef1	-1.17	0.393	-1.01	0.642	1.35	0.010	1.47	0.110	1.18	0.237
1447159_at	Synaptic nuclear envelope 2	Syne2	1.44	0.440	1.05	0.897	1.35	0.050	1.23	0.023	-1.18	0.460
1418547_at	tissue factor pathway inhibitor 2	Tfpi2	-1.03	0.810	1.19	0.102	1.35	0.005	-1.02	0.943	1.17	0.240
1458511_at	RIKEN cDNA 2410025L10 gene	2410025L10Rik	1.58	0.375	1.74	0.324	1.36	0.008	-1.05	0.088	1.24	0.218
1449122_at	RIKEN cDNA 3110003A22 gene	3110003A22Rik	1.36	0.496	1.98	0.021	1.36	0.005	1.38	0.040	1.08	0.535
1453324_at	RIKEN cDNA 6330509M23 gene	6330509M23Rik	1.04	0.869	1.2	0.279	1.36	0.008	1.18	0.151	1.63	0.033
1459302_at	RIKEN cDNA A030007N12 gene	A030007N12Rik	1.32	0.530	1.33	0.222	1.36	0.046	2.74	0.348	1	0.736
1423100_at	FBJ osteosarcoma oncogene	Fos	-1.01	0.953	1.62	0.005	1.36	0.029	1.46	0.003	1.53	0.003
1449169_at	hyaluronan synthase 2	Has2	1.41	0.023	1.81	0.113	1.36	0.005	1.39	0.003	1.38	0.023
1449901_a_at	mitogen-activated protein kinase kinase kinase 6	Map3k6	-1.01	0.750	1.3	0.082	1.36	0.005	1.16	0.053	1.18	0.169

1423605_a_at	transformed mouse 3T3 cell double minute 2	Mdm2	1.14	0.055	1.86	0.013	1.36	0.008	1.08	0.245	1.12	0.282
1448722_s_at	phosphopantothenoylcysteine synthetase	Ppcs	-1.09	0.494	1.15	0.775	1.36	0.013	1.4	0.011	1.35	0.039
1426916_at	secernin 3	Scrn3	1.68	0.261	1.65	0.298	1.36	0.017	-1.01	0.811	1.05	0.680
1447901_x_at	Sfi1 homolog, spindle assembly associated (yeast) /// similar to spin	Sfi1 /// LOC673420	3.53	0.447	1.6	0.594	1.36	0.025	1.33	0.265	1.18	0.955
1419537_at	transcription factor EC	Tcfec	2.4	0.144	1.16	0.557	1.36	0.034	1.58	0.041	1.1	0.699
1436108_at	thioredoxin domain containing 9	Txndc9	1.33	0.432	1.98	0.006	1.36	0.025	1.18	0.000	1.13	0.531
1460589_at	zinc finger protein 597	Zfp597	1.37	0.912	1.21	0.870	1.36	0.021	-1.08	0.247	1.55	0.077
1435243_at	zinc finger protein 746	Zfp746	-1.12	0.391	1.1	0.197	1.36	0.011	1.1	0.304	1.26	0.331
1433946_at	zinc finger protein interacting with K protein 1	Zik1	1.13	0.031	1.44	0.041	1.36	0.002	1.22	0.041	1.23	0.015
1456929_at	CDNA sequence BC042782	BC042782	3.33	0.052	2.09	0.660	1.37	0.023	-1.13	0.111	-1.28	0.233
1419483_at	complement component 3a receptor 1	C3ar1	1.78	0.634	1.79	0.209	1.37	0.015	1.34	0.188	1.61	0.007
1448364_at	cyclin G2	Ccng2	4.9	0.271	5.52	0.140	1.37	0.002	1.38	0.035	1.18	0.306
1448182_a_at	CD24a antigen	Cd24a	-1.07	0.528	1.14	0.794	1.37	0.048	1.18	0.011	1.23	0.013
1454737_at	dual specificity phosphatase 9	Dusp9	1.03	0.928	1.58	0.049	1.37	0.022	1.24	0.014	1.45	0.045
1435044_at	early B-cell factor 4	Ebf4	-1.29	0.217	-1.18	0.314	1.37	0.002	1.73	0.101	-1.24	0.266
1447854_s_at	histone 2, H2be	Hist2h2be	-1.2	0.399	-1.21	0.397	1.37	0.018	1.03	0.971	1.2	0.605
1460462_at	mediator of RNA polymerase II transcription, subunit 18 homolog (ye	Med18	-1.29	0.232	-1.3	0.195	1.37	0.029	1.13	0.689	1.43	0.348
1435170_at	TSR2, 20S rRNA accumulation, homolog (S. cerevisiae)	Tsr2	1.19	0.633	1.48	0.260	1.37	0.033	1.07	0.397	1.36	0.269
1434552_at	WD repeat domain 77	Wdr77	-1.1	0.347	1.2	0.335	1.37	0.000	1.3	0.001	1.34	0.000
1449915_at	zinc finger protein 202	Zfp202	-1.06	0.560	-1.13	0.477	1.37	0.034	1.19	0.363	1.1	0.325
1459323_at	RIKEN cDNA 1700106N22 gene	1700106N22Rik	1.6	0.631	-1.22	0.412	1.38	0.028	-1.19	0.292	-1.18	0.224
1453025_at	RIKEN cDNA 2900006F19 gene	2900006F19Rik	-1.22	0.225	-1.28	0.258	1.38	0.036	-1.01	0.748	-1.09	0.415
1430481_at	RIKEN cDNA 4930545L23 gene	4930545L23Rik	1.46	0.554	2.19	0.049	1.38	0.005	1.45	0.673	1.29	0.489
1438760_x_at	a disintegrin and metallopeptidase domain 15 (metargidin)	Adam15	-1.24	0.176	-1.22	0.153	1.38	0.027	-1.07	0.519	-1.1	0.434
1456404_at	a disintegrin-like and metallopeptidase (reprolysin type) with thromb	Adamts5	-1	0.954	1.11	0.347	1.38	0.006	1.13	0.181	1.21	0.116
1427954_at	cDNA sequence BC048403	BC048403	1.42	0.651	1.57	0.291	1.38	0.047	-1.06	0.442	1.2	0.058
1418954_at	calcium/calmodulin-dependent protein kinase kinase 1, alpha	Camkk1	1.76	0.343	1.81	0.595	1.38	0.015	1	0.886	1.14	0.329
1450554_at	defensin beta 2	Defb2	-1.29	0.277	-1.02	0.584	1.38	0.016	-1.43	0.299	-1.09	0.459
1418434_at	makorin, ring finger protein, 1	Mkrn1	1.09	0.975	1.34	0.634	1.38	0.014	1.05	0.518	1.56	0.098
1417857_at	methylmalonic aciduria (cobalamin deficiency) type A	Mmaa	1.12	0.753	1.26	0.282	1.38	0.012	-1	0.950	1.17	0.295
1420502_at	spermidine/spermine N1-acetyl transferase 1	Sat1	1.29	0.135	1.7	0.006	1.38	0.014	1.27	0.011	1.32	0.006
1436871_at	splicing factor, arginine/serine-rich 7	Sfrs7	1.14	0.107	1.23	0.383	1.38	0.028	1.11	0.411	1.2	0.277
1439368_a_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regul	Slc9a3r2	-1.17	0.423	-1.03	0.526	1.38	0.010	1.1	0.063	1.18	0.017
1451339_at	sulfite oxidase	Suox	5.26	0.543	8.31	0.070	1.38	0.039	1.26	0.024	1.42	0.004
1451856_at	trinucleotide repeat containing 15	Tnrc15	1.02	0.580	-1.28	0.321	1.38	0.002	1.41	0.486	2.56	0.826
1451268_at	translocation associated membrane protein 1-like 1	Tram1l1	1.21	0.752	1.81	0.059	1.38	0.012	1.26	0.180	1.41	0.027
1434128_a_at	zinc finger protein 574	Zfp574	-1.26	0.281	-1.06	0.630	1.38	0.025	1.17	0.044	1.34	0.024
1453534_at	RIKEN cDNA 2810004I08 gene	2810004I08Rik	1.17	0.507	1.3	0.028	1.39	0.038	1.42	0.567	1.15	0.843
1454799_at	RIKEN cDNA A230097K15 gene	A230097K15Rik	1.59	0.003	1.33	0.165	1.39	0.016	-1.03	0.656	1.14	0.445
1449734_s_at	Bardet-Biedl syndrome 4 homolog (human)	Bbs4	1.48	0.225	1.28	0.721	1.39	0.003	-1.18	0.311	1.15	0.856
1435448_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	-1.2	0.336	1.26	0.236	1.39	0.020	1.28	0.007	1.54	0.001
1426281_at	cation channel of sperm 1	Catsper1	2.67	0.239	2.36	0.155	1.39	0.027	-1.06	0.903	1.62	0.443
1417581_at	dihydroorotate dehydrogenase	Dhodh	1.26	0.239	1.57	0.183	1.39	0.029	1.04	0.565	1.23	0.430
1429914_at	enhancer of polycomb homolog 1 (Drosophila)	Epc1	-1.1	0.492	1.07	0.879	1.39	0.023	1.2	0.154	1.32	0.026
1433489_s_at	fibroblast growth factor receptor 2	Fgfr2	1.14	0.577	1.25	0.001	1.39	0.029	1.02	0.886	1.05	0.964
1425937_a_at	hexamethylene bis-acetamide inducible 1	Hexim1	1.05	0.729	1.52	0.009	1.39	0.015	1.49	0.002	1.41	0.015
1437999_x_at	phosphatidylinositol glycan anchor biosynthesis, class Q	Pigq	-1.27	0.369	-1.19	0.393	1.39	0.012	-1.09	0.177	-1.03	0.680
1425245_a_at	regulator of G-protein signaling 11	Rgs11	1.56	0.790	-1.16	0.292	1.39	0.040	1.03	0.801	1.39	0.577
1454857_at	ring finger protein 122	Rnf122	3	0.333	4.85	0.042	1.39	0.024	1.58	0.034	1.83	0.017
1446687_at	splicing factor 3a, subunit 1	Sf3a1	1.1	0.856	1	0.686	1.39	0.031	1.67	0.016	1.03	0.980
1449579_at	Sh3 domain YSC-like 1	Sh3yl1	1.05	0.954	1	0.782	1.39	0.015	1.12	0.330	1.13	0.418
1439507_at	TRAF type zinc finger domain containing 1	Trafd1	1.87	0.443	-1.21	0.284	1.39	0.030	1.95	0.400	1.08	0.482
1434401_at	zinc finger, CCHC domain containing 2	Zcchc2	1.18	0.364	1.39	0.037	1.39	0.027	1.11	0.140	1.03	0.845
1456603_at	RIKEN cDNA 1500005K14 gene	1500005K14Rik	-1.12	0.460	1.31	0.753	1.4	0.024	1.2	0.067	1.25	0.199
1429364_at	RIKEN cDNA 4930579G24 gene	4930579G24Rik	1.01	0.767	1.21	0.021	1.4	0.037	1.27	0.036	1.27	0.003
1455660_at	colony stimulating factor 2 receptor, beta 1, low-affinity (granulocyte-	Csf2rb1	-1.42	0.156	-1.88	0.046	1.4	0.033	-1	0.635	-1.26	0.651
1439153_at	IBR domain containing 2	Ibrdc2	-1.1	0.337	-1.06	0.603	1.4	0.001	1.08	0.730	-1.55	0.008
1456909_at	similar to Glucose-6-phosphate isomerase (GPI) (Phosphoglucose is	LOC676974	-1.34	0.256	1.16	0.898	1.4	0.019	1.04	0.397	1.18	0.246

1460254_at	RIKEN cDNA 1810049H13 gene	1810049H13Rik	1.23	0.990	1.31	0.439	1.41	0.032	1.06	0.682	1.15	0.722
1426929_at	bruno-like 4, RNA binding protein (Drosophila)	Brunol4	-1.08	0.520	1.14	0.396	1.41	0.042	-1.06	0.558	1.1	0.570
1438370_x_at	downstream of Stk11	Dos	1	0.958	1.44	0.010	1.41	0.022	1.12	0.078	1.64	0.070
1439790_at	serine (or cysteine) peptidase inhibitor, clade B, member 9	Serpinb9	-1.01	0.624	1.46	0.592	1.41	0.010	1.1	0.547	1.22	0.536
1434588_x_at	tubulin cofactor a /// similar to Tubulin-specific chaperone A (Tubulin	Tbca /// LOC62031	-1.16	0.431	1.03	0.620	1.41	0.008	-1.1	0.570	-1.05	0.701
1453739_at	transmembrane protein 126B	Tmem126b	1.8	0.254	2.22	0.048	1.41	0.038	1.44	0.298	1.45	0.035
1424004_x_at	RIKEN cDNA 4930444A02 gene	4930444A02Rik	-1.11	0.257	1.29	0.442	1.42	0.021	1.29	0.123	1.41	0.127
1457461_at	RIKEN cDNA A630039O03 gene	A630039O03Rik	1.17	0.384	1.33	0.577	1.42	0.011	-1.01	0.830	1.29	0.464
1452273_at	expressed sequence AA409316	AA409316	1.23	0.209	1.58	0.035	1.42	0.014	1.3	0.012	1.55	0.033
1447974_s_at	aquaporin 6	Aqp6	1.31	0.591	1.23	0.724	1.42	0.041	1.51	0.510	1.95	0.239
1458436_at	AU RNA binding protein/enoyl-coenzyme A hydratase	Auh	-1.34	0.171	1.08	0.433	1.42	0.010	1.2	0.344	1.13	0.217
1417078_at	lectin, galactose-binding, soluble 2	Lgals2	1.83	0.918	-1.6	0.150	1.42	0.012	1.03	0.953	1.29	0.217
1434079_s_at	minichromosome maintenance deficient 2 mitotin (S. cerevisiae)	Mcm2	1.09	0.813	1.31	0.143	1.42	0.018	1.23	0.469	1.21	0.064
1418203_at	phorbol-12-myristate-13-acetate-induced protein 1	Pmaip1	1.33	0.093	2.85	0.020	1.42	0.015	1.22	0.008	1.68	0.090
1419245_at	RAB14, member RAS oncogene family	Rab14	1.03	0.970	1	0.857	1.42	0.023	-1.3	0.259	1.18	0.913
1460667_at	cDNA sequence U90926	U90926	1.14	0.686	1.44	0.018	1.42	0.029	-1	0.945	1.06	0.874
1419207_at	zinc finger protein 37	Zfp37	1.13	0.511	1.28	0.166	1.42	0.014	1.28	0.114	1.38	0.022
1441703_at	RIKEN cDNA 2210018M03 gene	2210018M03Rik	-1.26	0.293	1.22	0.713	1.43	0.020	1.7	0.479	1.07	0.740
1426217_at	RIKEN cDNA 2810441K11 gene	2810441K11Rik	1.53	0.201	1.72	0.047	1.43	0.026	1.29	0.096	1.2	0.169
1458667_at	RIKEN cDNA 4930519N13 gene	4930519N13Rik	-1.17	0.353	1.17	0.678	1.43	0.003	1.02	0.898	1.5	0.048
1454192_at	RIKEN cDNA 4930579C15 gene	4930579C15Rik	1.43	0.814	-1.34	0.067	1.43	0.025	1.04	0.856	1.46	0.809
1450855_at	armadillo repeat gene deleted in velo-cardio-facial syndrome	Arvcf	1.43	0.188	1.66	0.109	1.43	0.038	1.5	0.054	1.08	0.659
1427210_at	bromodomain adjacent to zinc finger domain, 2A	Baz2a	-1.42	0.273	-1.39	0.302	1.43	0.020	-1.27	0.209	1.29	0.763
1424074_at	basic transcription factor 3-like 4	Btf3l4	-1.01	0.894	1.17	0.209	1.43	0.005	1.4	0.036	1.4	0.328
1448272_at	B-cell translocation gene 2, anti-proliferative	Btg2	1.23	0.153	1.94	0.048	1.43	0.018	1.09	0.254	1.25	0.187
1428838_a_at	deoxycytidine kinase	Dck	2.38	0.032	2.79	0.006	1.43	0.032	1.29	0.301	1.24	0.325
1436487_x_at	F-box and WD-40 domain protein 2	Fbxw2	-1.13	0.427	1.49	0.674	1.43	0.042	-1	0.592	1.03	0.729
1425322_at	interferon zeta /// similar to interferon zeta /// similar to interferon zet	Ifnz /// LOC435791	-1.09	0.518	1.41	0.163	1.43	0.015	1.25	0.056	1.41	0.016
1422132_at	5,10-methylenetetrahydrofolate reductase	Mthfr	2.69	0.315	1.51	0.407	1.43	0.043	1.16	0.694	1.09	0.434
1424412_at	opioid growth factor receptor-like 1	Ogfrl1	-1.08	0.335	1.27	0.102	1.43	0.023	-1.09	0.264	1.4	0.630
1453006_at	RIKEN cDNA 2610306H15 gene	2610306H15Rik	1.09	0.348	1.57	0.040	1.44	0.036	1.26	0.000	1.57	0.006
1453642_at	RIKEN cDNA 6530411M01 gene	6530411M01Rik	1.92	0.234	1.65	0.197	1.44	0.042	-1.03	0.564	1.79	0.725
1457092_at	RIKEN cDNA C630007B19 gene	C630007B19Rik	1.36	0.739	1.81	0.920	1.44	0.005	-1.04	0.477	1.78	0.185
1459840_s_at	coiled coil domain containing 28B	Ccdc28b	1	0.482	1.27	0.549	1.44	0.040	-1.03	0.644	1.41	0.352
1417441_at	DnaJ (Hsp40) homolog, subfamily C, member 12	Dnajc12	-1.02	0.796	-1.01	0.994	1.44	0.047	-1.03	0.586	1.39	0.039
1434027_at	Down syndrome critical region gene 1-like 2	Dscr1l2	1.1	0.354	-1.01	0.798	1.44	0.037	1.19	0.006	1.26	0.027
1440741_at	5-hydroxytryptamine (serotonin) receptor 1D	Htr1d	-1.28	0.340	-1.16	0.534	1.44	0.004	1.15	0.495	1.05	0.990
1428615_at	purinergic receptor P2Y, G-protein coupled, 5	P2ry5	1.24	0.018	1.7	0.043	1.44	0.019	1.35	0.009	1.52	0.011
1453864_at	retinol dehydrogenase 14 (all-trans and 9-cis)	Rdh14	-1.06	0.457	1.15	0.585	1.44	0.022	1.02	0.824	1.06	0.769
1457051_at	tripartite motif protein 27	Trim27	2.13	0.047	1.8	0.555	1.44	0.007	1.18	0.859	2.22	0.010
1421465_at	wingless related MMTV integration site 2b	Wnt2b	1.85	0.140	1.21	0.980	1.44	0.025	-1.64	0.264	1.5	0.362
1437617_x_at	RIKEN cDNA 1110034G24 gene	1110034G24Rik	1.03	0.618	1.32	0.860	1.45	0.007	-1.67	0.016	1.36	0.019
1433582_at	RIKEN cDNA 1190002N15 gene	1190002N15Rik	1.6	0.203	2.14	0.039	1.45	0.015	1.24	0.030	1.13	0.156
1453431_at	RIKEN cDNA 2610206C17 gene	2610206C17Rik	6	0.265	3.32	0.217	1.45	0.050	-1.01	0.820	1.3	0.845
1419612_at	RIKEN cDNA 4632415L05 gene	4632415L05Rik	1.46	0.085	1.58	0.089	1.45	0.048	1.22	0.277	1.63	0.011
1458863_at	RIKEN cDNA 6330415G19 gene	6330415G19Rik	1.51	0.144	1.72	0.010	1.45	0.007	1.34	0.123	2.68	0.024
1460745_at	RIKEN cDNA A630098A13 gene	A630098A13Rik	1.11	0.746	1.52	0.418	1.45	0.029	1.13	0.435	1.32	0.251
1448199_at	ankyrin repeat domain 10	Ankrd10	-1.06	0.126	1.55	0.005	1.45	0.019	1.24	0.040	1.39	0.049
1433575_at	similar to Transcription factor SOX-4	LOC672274	1.53	0.189	2.22	0.048	1.45	0.012	1.39	0.011	1.56	0.000
1418540_a_at	protein tyrosine phosphatase, receptor type, E	Ptpre	1.13	0.198	1.2	0.504	1.45	0.016	1.15	0.220	1.18	0.500
1431740_at	solute carrier family 7, (cationic amino acid transporter, y+ system) n	Slc7a13	-1.15	0.516	-1.36	0.324	1.45	0.037	1.26	0.220	1.01	0.512
1444053_at	single-stranded DNA binding protein 1	Ssbp1	-1.82	0.239	-1.98	0.256	1.45	0.038	-2.12	0.068	1.03	0.560
1435464_at	RIKEN cDNA 1110003E01 gene	1110003E01Rik	-1.18	0.318	-1.4	0.153	1.46	0.000	1.07	0.376	1.21	0.100
1430992_s_at	RIKEN cDNA 1500009M05 gene	1500009M05Rik	1.29	0.072	1.31	0.107	1.46	0.034	1.1	0.182	1.57	0.073
1457260_at	RIKEN cDNA 7530403E16 gene	7530403E16Rik	-1.02	0.552	1.14	0.596	1.46	0.004	1.4	0.024	1.29	0.182
1441312_at	Cyclin M1	Cnnm1	1.26	0.192	1.33	0.434	1.46	0.003	-1.09	0.469	1.05	0.578
1423525_at	microtubule associated serine/threonine kinase-like	Mastl	2.66	0.377	3.91	0.514	1.46	0.007	1.02	0.910	1.34	0.021
1455238_at	melanoma associated antigen (mutated) 1-like 1	Mum1l1	1.36	0.100	1.63	0.045	1.46	0.009	1.4	0.011	1.1	0.240

1431993_a_at	ring finger protein 38	Rnf38	7.85	0.497	7.68	0.457	1.46	0.047	1.14	0.270	1.21	0.392
1421012_at	signal recognition particle receptor, B subunit	Srprb	-1.18	0.393	1.25	0.745	1.46	0.013	1.3	0.024	1.33	0.133
1437792_at	RIKEN cDNA 1700013D24 gene	1700013D24Rik	-1.25	0.323	1.7	0.969	1.47	0.023	1.92	0.342	1.39	0.982
1420482_at	cyclin M3	Cnnm3	-1.63	0.096	-1.02	0.831	1.47	0.001	1.1	0.418	1.9	0.096
1419234_at	helicase (DNA) B	Helb	4.19	0.085	6.26	0.025	1.47	0.031	1.31	0.058	1.28	0.386
1429110_a_at	NOL1/NOP2/Sun domain family, member 4	Nsun4	1.51	0.097	1.83	0.026	1.47	0.012	1.46	0.012	1.38	0.086
1448369_at	polymerase (DNA directed), alpha 2	Pola2	1.51	0.175	1.51	0.024	1.47	0.007	1.39	0.160	1.43	0.030
1448923_at	protein kinase, interferon inducible double stranded RNA dependent	Prkra	-1	0.872	-1.05	0.551	1.47	0.048	1.14	0.028	1.02	0.984
1416400_at	pyrroline-5-carboxylate reductase-like	Pycrl	1.14	0.225	1.45	0.008	1.47	0.015	1.22	0.062	1.4	0.071
1418545_at	WASP family 1	Wasf1	-1.36	0.270	-1.19	0.355	1.47	0.003	1.15	0.086	1.34	0.046
1453422_a_at	RIKEN cDNA 1110020G09 gene	1110020G09Rik	4.08	0.191	3.49	0.014	1.48	0.033	1.23	0.166	1.16	0.244
1449197_at	RIKEN cDNA 2310040A13 gene	2310040A13Rik	1.19	0.530	1.08	0.947	1.48	0.008	1.04	0.739	1.31	0.078
1431989_at	RIKEN cDNA 4930433E13 gene	4930433E13Rik	-1.49	0.200	-1.04	0.940	1.48	0.029	1.01	0.910	1.25	0.233
1455346_at	mannan-binding lectin serine peptidase 1	Masp1	1.38	0.728	-1.01	0.665	1.48	0.004	1.01	0.803	1.89	0.840
1455877_a_at	nanos homolog 1 (Drosophila)	Nanos1	-1.09	0.434	1.42	0.682	1.48	0.048	1.25	0.163	1.45	0.043
1416505_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	1.34	0.031	2.01	0.033	1.48	0.004	1.38	0.001	1.56	0.010
1429399_at	ring finger protein 125	Rnf125	-1.36	0.067	-1.21	0.181	1.48	0.050	1.37	0.008	1.49	0.054
1441756_at	Transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	-1.31	0.356	-1.25	0.383	1.48	0.046	-1.19	0.351	1.12	0.962
1429320_at	RIKEN cDNA 4921511I16 gene	4921511I16Rik	1.33	0.259	1.56	0.077	1.49	0.046	1.02	0.933	1.15	0.384
1429642_at	AN1, ubiquitin-like, homolog (Xenopus laevis)	Anubl1	1.15	0.857	-1	0.751	1.49	0.020	1.26	0.605	1.52	0.089
1428069_at	cell division cycle associated 7	Cdca7	1.26	0.680	1.67	0.007	1.49	0.040	1.09	0.294	1.37	0.010
1436011_at	engulfment and cell motility 2, ced-12 homolog (C. elegans)	Elmo2	-1.2	0.238	1.07	0.972	1.49	0.004	1.24	0.038	1.16	0.406
1428532_at	integrator complex subunit 7	Ints7	1.37	0.386	1.42	0.049	1.49	0.045	1.11	0.424	1.41	0.030
1454844_at	melanin-concentrating hormone receptor 1	Mchr1	1.36	0.974	1.87	0.672	1.49	0.041	1.19	0.611	1.47	0.171
1416159_at	nuclear receptor subfamily 2, group F, member 2	Nr2f2	1.19	0.206	1.17	0.853	1.49	0.011	-1.03	0.622	1.19	0.083
1438138_a_at	peroxisomal biogenesis factor 6	Pex6	-1.53	0.178	-1.12	0.399	1.49	0.007	-1.02	0.566	-1.03	0.781
1439934_at	solute carrier family 30, member 10	Slc30a10	2.59	0.236	2.01	0.761	1.49	0.017	-1.75	0.093	1.54	0.097
1422933_at	X-linked lymphocyte-regulated 5D /// similar to X-linked lymphocyte-r	Xlr5d /// LOC62708	-1.42	0.225	-1.22	0.498	1.49	0.021	2.07	0.867	1.45	0.078
1423594_a_at	endothelin receptor type B	Ednrb	1.16	0.826	1.06	0.995	1.5	0.012	1.44	0.680	1.31	0.966
1417602_at	period homolog 2 (Drosophila)	Per2	1.14	0.813	2.35	0.056	1.5	0.009	-1.01	0.821	1.11	0.496
1450653_at	spermatogenic Zip 1	Spz1	2.15	0.934	1.53	0.656	1.5	0.050	1.26	0.590	1.27	0.988
1439407_x_at	transgelin 2 /// similar to transgelin 2	Tagln2 /// LOC672	1.11	0.089	1	0.979	1.5	0.043	-1.05	0.613	1.01	0.648
1421707_at	transmembrane channel-like gene family 2	Tmc2	-2.2	0.107	1.38	0.931	1.5	0.032	2.59	0.229	1.86	0.692
1452006_x_at	zinc finger and BTB domain containing 8 opposite strand	Zbtb8os	1.26	0.820	1.36	0.654	1.5	0.001	-1.11	0.489	2.71	0.118
1432013_a_at	RIKEN cDNA 2610016C23 gene	2610016C23Rik	1.34	0.050	1.75	0.165	1.51	0.023	1.29	0.043	1.18	0.241
1433354_at	RIKEN cDNA D530015H24 gene	D530015H24Rik	-1.16	0.519	-1.18	0.513	1.51	0.033	2.59	0.233	2.18	0.358
1424897_at	G protein-coupled receptor 85	Gpr85	-1.01	0.484	1.74	0.682	1.51	0.003	1.16	0.390	1.62	0.927
1435977_at	hepatoma-derived growth factor, related protein 3	Hdgfrp3	1.13	0.295	1.13	0.595	1.51	0.027	2	0.205	1.05	0.747
1415977_at	myo-inositol 1-phosphate synthase A1	Isyna1	2.14	0.309	2.13	0.350	1.51	0.001	1.22	0.052	1.24	0.160
1416915_at	mutS homolog 6 (E. coli)	Msh6	1.1	0.060	2.15	0.000	1.51	0.047	1.47	0.029	1.4	0.023
1421328_at	microtubule-associated protein 2 /// hypothetical protein A730034C0	Mtap2 /// A730034	1.17	0.792	1.82	0.349	1.51	0.028	3.01	0.066	1.13	0.368
1419929_at	DNA segment, Chr 15, ERATO Doi 55, expressed	D15Ertd55e	1.08	0.673	1.06	0.929	1.52	0.018	1.03	0.627	1.18	0.771
1442182_at	DnaJ (Hsp40) homolog, subfamily C, member 19	Dnajc19	1.1	0.937	1.45	0.662	1.52	0.026	1.8	0.049	1.63	0.118
1452700_s_at	kelch repeat and BTB (POZ) domain containing 7	Kbtbd7	-1.03	0.673	1.55	0.008	1.52	0.005	1.29	0.083	1.58	0.025
1423231_at	neurogranin	Nrgn	2	0.527	2.88	0.009	1.52	0.006	2.04	0.850	-1.18	0.803
1457468_at	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	Tnks2	1.79	0.319	-1.2	0.311	1.52	0.011	1.31	0.382	-1.03	0.276
1451323_at	zinc finger protein 7	Zfp7	1.25	0.645	1.71	0.062	1.52	0.002	1.49	0.006	1.61	0.046
1433163_at	RIKEN cDNA 6230414M07 gene	6230414M07Rik	1.71	0.694	1.29	0.660	1.53	0.024	1.12	0.725	1.11	0.856
1454858_x_at	methyltransferase like 7A	Mettl7a	1.08	0.681	1.44	0.227	1.53	0.026	1.11	0.862	-1.02	0.778
1441412_s_at	tripartite motif-containing 45	Trim45	-1.05	0.493	-1.07	0.532	1.53	0.014	1.39	0.015	1.17	0.189
1418100_at	RIKEN cDNA A030009H04 gene	A030009H04Rik	1.18	0.496	2.52	0.059	1.54	0.003	1.76	0.031	1.88	0.110
1458930_at	alpha-1,4-N-acetylglucosaminyltransferase	A4gnt	1.08	0.306	-1.11	0.585	1.54	0.027	1.42	0.158	1.66	0.471
1449093_at	cardiotrophin 1	Ctf1	-1	0.945	1.37	0.353	1.54	0.026	1.09	0.119	1.26	0.131
1460206_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffol	Grasp	6.01	0.281	7.21	0.134	1.54	0.046	1.32	0.014	1.19	0.173
1452645_x_at	killer cell lectin-like receptor subfamily A, member 22	Klra22	1.54	0.311	-1.03	0.631	1.54	0.014	-1.04	0.894	-1.06	0.426
1430559_at	5'-nucleotidase, cytosolic III-like	Nt5c3l	4.27	0.531	2.47	0.501	1.54	0.034	1.01	0.812	-1.05	0.830
1435911_s_at	solute carrier family 2 (facilitated glucose transporter), member 12	Slc2a12	-1.14	0.526	-1.13	0.332	1.54	0.047	-1.18	0.519	-1.05	0.929
1453502_at	RIKEN cDNA 2210408I21 gene	2210408I21Rik	2.08	0.813	1.34	0.575	1.55	0.039	-1.28	0.042	-1.1	0.422

1428499_at	RIKEN cDNA 2810454L23 gene	2810454L23Rik	-1.01	0.572	1.03	0.690	1.55	0.029	1.02	0.978	-1.17	0.386
1437486_at	G protein-coupled receptor, family C, group 5, member A	Gprc5a	2.81	0.187	4.18	0.050	1.55	0.007	1.18	0.031	1.56	0.007
1455258_at	potassium voltage gated channel, Shaw-related subfamily, member	Kcnc2	1.85	0.505	-1.07	0.530	1.55	0.036	-1.15	0.301	-1.62	0.148
1436404_at	TLC domain containing 1	Tlcd1	-1.05	0.528	1.48	0.005	1.55	0.023	1.27	0.204	1.68	0.058
1450644_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	-1.03	0.752	1.4	0.022	1.55	0.030	1.33	0.016	1.57	0.000
1429286_at	RIKEN cDNA 1190003M12 gene	1190003M12Rik	1.18	0.844	1.45	1.000	1.56	0.050	1.21	0.328	2.22	0.464
1431412_at	RIKEN cDNA 2810455B08 gene	2810455B08Rik	-1.2	0.369	1.13	0.649	1.56	0.022	1.28	0.554	-1.04	0.622
1436219_at	RIKEN cDNA 4933403F05 gene	4933403F05Rik	1.4	0.038	2.63	0.005	1.56	0.008	1.75	0.002	1.69	0.008
1438442_at	expressed sequence AI450236	AI450236	-1.22	0.058	-1.04	0.365	1.56	0.032	1.1	0.635	1.4	0.296
1452458_s_at	peptidylprolyl isomerase (cyclophilin) like 5	Ppil5	-1.02	0.688	1.23	0.771	1.56	0.028	1.35	0.073	1.47	0.019
1423176_at	transducer of ErbB-2.1	Tob1	1.01	0.995	1.32	0.013	1.56	0.016	1.22	0.039	1.63	0.000
1439841_at	zinc finger, FYVE domain containing 27	Zfyve27	-1.12	0.457	1.51	0.634	1.56	0.012	1.95	0.076	1.24	0.443
1417216_at	proviral integration site 2	Pim2	-1.02	0.599	-1.04	0.620	1.57	0.008	1.08	0.564	-1.02	0.597
1459896_at	pogo transposable element with KRAB domain	Pogk	1.19	0.478	1.61	0.182	1.57	0.033	-1.11	0.304	1.01	0.939
1450343_at	vomeronasal 1 receptor, D1	V1rd1	1.12	0.533	1.56	0.195	1.57	0.024	-1.84	0.041	1.36	0.714
1424457_at	amyloid beta (A4) precursor protein-binding, family B, member 3	Apbb3	1.09	0.834	-1.42	0.083	1.58	0.026	1.48	0.368	1.47	0.238
1454617_at	arrestin domain containing 3	Arrdc3	-1.05	0.719	1.4	0.142	1.58	0.007	1.35	0.021	1.71	0.025
1438635_x_at	RIKEN cDNA B930041F14 gene	B930041F14Rik	-1.11	0.205	1.19	0.322	1.58	0.037	1.1	0.311	1.32	0.130
1426636_a_at	baculoviral IAP repeat-containing 4	Birc4	1.17	0.375	1.19	0.945	1.58	0.033	1.32	0.471	1.1	0.901
1444139_at	DNA-damage-inducible transcript 4-like	Ddit4l	1.47	0.166	4.02	0.001	1.58	0.015	1.51	0.165	1.84	0.062
1450241_a_at	ecotropic viral integration site 2a	Evi2a	1.95	0.080	2.71	0.015	1.58	0.010	1.72	0.000	1.79	0.077
1442713_at	Oxysterol binding protein-like 10	Osbpl10	2.51	0.543	2.75	0.308	1.58	0.004	1.24	0.438	-1.01	0.673
1441135_at	Zinc finger protein 672	Zfp672	1.15	0.853	-1.15	0.517	1.58	0.040	-1.68	0.103	1.35	0.263
1431898_at	RIKEN cDNA 4930403J07 gene	4930403J07Rik	1.37	0.567	1.17	0.083	1.59	0.042	1.97	0.742	-1.46	0.061
1431453_at	RIKEN cDNA 4933406K04 gene	4933406K04Rik	-1.43	0.330	-1.09	0.390	1.59	0.027	-1.12	0.608	1.14	0.643
1429272_a_at	RIKEN cDNA 9130022K13 gene /// RIKEN cDNA 2210421G13 gene	9130022K13Rik ///	1.19	0.556	1.39	0.678	1.59	0.040	2	0.281	2.33	0.134
1448049_at	jumonji domain containing 1C	Jmjd1c	1.35	0.514	1.73	0.766	1.59	0.013	1.54	0.721	-1.51	0.114
1438481_at	PRP4 pre-mRNA processing factor 4 homolog (yeast)	Prpf4	1.3	0.058	1.42	0.002	1.59	0.023	1.09	0.362	1.3	0.187
1439548_at	RAP2B, member of RAS oncogene family	Rap2b	1.04	0.953	1.52	0.031	1.59	0.011	1.4	0.218	1.3	0.078
1436786_at	RIKEN cDNA 1110069O07 gene	1110069O07Rik	1.02	0.477	-1.23	0.259	1.6	0.018	-1.06	0.632	-1.18	0.426
1439508_at	RIKEN cDNA A730055L17 gene	A730055L17Rik	-1.14	0.387	1.19	0.273	1.6	0.003	1.12	0.544	1.43	0.098
1452792_at	DAZ interacting protein 1	Dzip1	1.16	0.692	1.41	0.121	1.6	0.024	1.09	0.231	1.44	0.041
1454924_at	fucosyltransferase 10	Fut10	2	0.241	-1.04	0.362	1.6	0.003	-1.01	0.496	-1.06	0.399
1447701_x_at	isocitrate dehydrogenase 3 (NAD+) alpha	Idh3a	1.26	0.905	1.24	0.830	1.6	0.019	-1.2	0.467	1.23	0.971
1425239_at	SET domain containing 4	Setd4	-1.48	0.190	-1.05	0.556	1.6	0.031	1.29	0.206	1.36	0.051
1439758_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candic	Als2cr12	1.26	0.022	1.3	0.138	1.61	0.003	1.36	0.065	1.25	0.310
1437698_at	myosin Vb	Myo5b	1.99	0.844	2.65	0.994	1.61	0.040	-1.24	0.523	1.1	0.606
1447578_at	RIKEN cDNA 1700084J12 gene	1700084J12Rik	1.05	0.798	1.3	0.773	1.62	0.013	1.02	0.904	1.06	0.697
1431109_at	RIKEN cDNA 5430406M13 gene	5430406M13Rik	-1.01	0.341	-1.93	0.064	1.62	0.003	-1.5	0.289	2.28	0.967
1443502_at	baculoviral IAP repeat-containing 7 (livin)	Birc7	1.92	0.985	1.61	0.960	1.62	0.011	2.09	0.719	2.97	0.083
1426620_at	carbohydrate sulfotransferase 10	Chst10	-1.02	0.711	-1.2	0.279	1.62	0.025	1.02	0.996	-1	0.700
1434715_at	RIKEN cDNA 1600014C10 gene	1600014C10Rik	1.25	0.365	1.58	0.537	1.63	0.041	1.57	0.101	-1.06	0.763
1455646_at	RIKEN cDNA 2010004M13 gene	2010004M13Rik	-1.05	0.495	1.3	0.336	1.63	0.024	1.06	0.809	1.48	0.272
1432667_at	RIKEN cDNA 2210411G17 gene	2210411G17Rik	-1.2	0.409	-1.43	0.066	1.63	0.036	2.45	0.297	1.02	0.956
1453609_s_at	coiled-coil domain containing 9	Ccdc9	1.17	0.581	1.75	0.848	1.63	0.007	1.19	0.097	1.15	0.327
1422590_at	cyclin-dependent kinase 5	Cdk5	-1.73	0.020	-1.45	0.054	1.63	0.020	-1.09	0.370	-1.07	0.731
1425882_at	growth differentiation factor 2	Gdf2	-1.14	0.387	1	0.668	1.63	0.049	-1.29	0.172	1.05	0.826
1456008_at	leucine rich repeat containing 8 family, member E	Lrrc8e	-1.03	0.574	1.14	0.985	1.63	0.017	-1.05	0.675	1.23	0.369
1449103_at	testis expressed gene 101	Tex101	1.3	0.527	1.5	0.572	1.63	0.017	1.06	0.928	-1.04	0.553
1434240_at	RIKEN cDNA 4632434I11 gene	4632434I11Rik	1.32	0.450	2.03	0.140	1.64	0.019	1.45	0.051	1.48	0.005
1426430_at	jagged 2	Jag2	-1.57	0.008	-1.12	0.415	1.64	0.021	1.12	0.813	1.22	0.697
1457448_at	patatin-like phospholipase domain containing 1	Pnpla1	1.18	0.983	1.91	0.439	1.64	0.041	-1.1	0.365	2.04	0.698
1434909_at	Ras-related GTP binding D	Rragd	1.43	0.793	1.49	0.803	1.64	0.028	2.21	0.831	-1.37	0.372
1439659_at	Trf (TATA binding protein-related factor)-proximal protein homolog (	Trfp /// Usp49	-1.07	0.596	1.19	0.737	1.64	0.000	-1.08	0.544	1.15	0.529
1457312_at	NHL repeat containing 2	Nhlrc2	1.74	0.991	1.26	0.926	1.65	0.020	1.71	0.318	1.2	0.816
1436189_at	NAD(P)H dehydrogenase, quinone 2	Nqo2	1.42	0.175	1.6	0.242	1.65	0.006	1.21	0.001	1.34	0.790
1419365_at	peroxisomal biogenesis factor 11a	Pex11a	1.51	0.183	1.96	0.228	1.65	0.015	-1.06	0.676	1.69	0.083
1436962_at	PR domain containing 6	Prdm6	-1.19	0.450	1.97	0.778	1.65	0.002	1.24	0.814	-1.09	0.543

1455894_at	peptidyl-tRNA hydrolase 2	Ptrh2	1.57	0.223	2.77	0.009	1.65	0.003	1.8	0.019	1.56	0.012
1449509_at	small EDRK-rich factor 1	Serf1	1.09	0.433	1.31	0.189	1.65	0.012	1.35	0.047	1.09	0.681
1441033_at	transmembrane and tetratricopeptide repeat containing 2	Tmtc2	-1.09	0.482	-1.09	0.627	1.65	0.034	2.03	0.040	-1.03	0.561
1446542_at	acyl-CoA synthetase short-chain family member 2	Acss2	-1.9	0.045	-1.22	0.126	1.66	0.023	-1.13	0.256	1.76	0.498
1435354_at	potassium inwardly-rectifying channel, subfamily J, member 15	Kcnj15	1.16	0.327	1.77	0.028	1.66	0.032	1.22	0.284	1.16	0.976
1438351_at	homeo box, msh-like 2	Msx2	-1.62	0.071	-1.4	0.147	1.66	0.028	1.39	0.022	1.11	0.687
1454762_at	X Kell blood group precursor related X linked	Xkrx	-1.62	0.176	1.05	0.752	1.66	0.028	1.91	0.598	1.29	0.811
1432861_at	RIKEN cDNA 2900046F13 gene	2900046F13Rik	-1.33	0.047	-1.09	0.519	1.67	0.038	1.74	0.362	-1.15	0.365
1444564_at	apolipoprotein D	Apod	1.18	0.689	-2.06	0.052	1.67	0.021	-1.31	0.332	-1.6	0.177
1450297_at	interleukin 6	Il6	1.27	0.420	1.65	0.085	1.67	0.033	1.1	0.603	1.85	0.061
1425967_a_at	mast cell protease 4	Mcpt4	1.12	0.645	1.66	0.486	1.67	0.032	2.52	0.391	-1.26	0.256
1457887_at	SCO-spondin	Sspo	-1.1	0.439	1.11	0.605	1.67	0.003	1.08	0.797	1.26	0.291
1424680_at	expressed sequence BB146404	BB146404	3.41	0.132	4.51	0.024	1.68	0.010	1.18	0.191	1.16	0.042
1444878_at	Dedicator of cytokinesis 10	Dock10	1.09	0.451	1.27	0.496	1.68	0.020	1.82	0.391	2.09	0.343
1440125_at	RIKEN cDNA A530054K11 gene	A530054K11Rik	1.55	0.065	1.98	0.030	1.69	0.029	-1.05	0.864	1.21	0.411
1433619_at	expressed sequence AI894139	AI894139	-1.21	0.142	1.38	0.148	1.69	0.002	1.25	0.293	1.66	0.023
1437420_at	bromodomain adjacent to zinc finger domain, 1B	Baz1b	-1.01	0.947	1.71	0.401	1.69	0.018	-1.49	0.146	-1.07	0.449
1439617_s_at	phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	-1.18	0.416	-1.1	0.546	1.69	0.027	1.01	0.785	1.81	0.588
1444123_at	PR domain containing 2, with ZNF domain	Prdm2	-1.6	0.135	-1.68	0.170	1.69	0.017	1.31	0.106	1.18	0.577
1440886_at	cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	1.07	0.879	1.44	0.141	1.7	0.043	1.58	0.024	1.52	0.007
1422134_at	FBJ osteosarcoma oncogene B	Fosb	1.07	0.832	1.62	0.107	1.7	0.008	-1.09	0.250	1.46	0.118
1421668_x_at	spermatogenesis associated glutamate (E)-rich protein 3	Speer3	1.65	0.753	1.05	0.290	1.7	0.020	1.07	0.931	1.85	0.269
1444507_at	ubiquitin specific peptidase 53	Usp53	1.1	0.533	-1.41	0.336	1.7	0.022	-1.02	0.591	1.43	0.475
1439503_at	zinc finger protein 28	Zfp28	1.13	0.629	1.66	0.006	1.7	0.006	1.16	0.111	-1.03	0.707
1459953_at	Expressed sequence AW011752	AW011752	1.04	0.907	2.01	0.130	1.71	0.026	1.02	0.824	1.3	0.199
1418665_at	inositol (myo)-1(or 4)-monophosphatase 2	Impa2	-1.11	0.465	-1.47	0.266	1.71	0.011	1.1	0.753	2.47	0.193
1447361_at	Metaxin 1	Mtx1	-1.21	0.271	1.33	0.689	1.71	0.003	-1.04	0.812	1.35	0.047
1437012_x_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	-1.38	0.049	-1.35	0.115	1.71	0.045	1.64	0.177	1.67	0.304
1429069_at	STIP1 homology and U-Box containing protein 1	Stub1	-1.28	0.061	-1.07	0.603	1.71	0.015	1.24	0.084	1.08	0.785
1450496_a_at	RIKEN cDNA 2810433K01 gene	2810433K01Rik	1.57	0.917	2.09	0.562	1.72	0.040	1.21	0.669	1.19	0.373
1430566_at	RIKEN cDNA 4733401A01 gene	4733401A01Rik	1.72	0.355	2.09	0.140	1.72	0.019	1.65	0.106	-1.08	0.361
1456296_at	RIKEN cDNA 5830418K08 gene	5830418K08Rik	1.03	0.718	1.21	0.753	1.72	0.041	1.96	0.023	-1.47	0.169
1456894_at	RIKEN cDNA C130039O16 gene	C130039O16Rik	-1.18	0.227	1.89	0.521	1.72	0.018	1.51	0.660	1.51	0.632
1424229_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3	2.16	0.096	3.82	0.004	1.72	0.023	1.43	0.038	1.89	0.003
1457229_at	G-protein coupled receptor 173	Gpr173	1.87	0.410	1.65	0.420	1.72	0.018	-1.05	0.692	1.34	0.964
1434759_at	leucine rich repeat transmembrane neuronal 3	Lrrtm3	2.21	0.704	1.87	0.925	1.72	0.004	1.04	0.452	2.01	0.738
1449449_at	prostaglandin E synthase	Ptges	1.04	0.968	1.5	0.287	1.72	0.003	1.34	0.206	1.95	0.384
1431992_at	RIKEN cDNA 4930568K20 gene	4930568K20Rik	1.65	0.342	1.09	0.870	1.73	0.029	-1.68	0.067	1.17	0.310
1441172_at	AF4/FMR2 family, member 3	Aff3	-1.12	0.418	-1.25	0.336	1.73	0.000	1.35	0.036	1.32	0.712
1453410_at	angiopoietin-like 4	Angptl4	2.83	0.152	1.91	0.306	1.73	0.022	1.81	0.115	1.53	0.969
1419083_at	tumor necrosis factor (ligand) superfamily, member 11	Tnfsf11	2.87	0.270	1.67	0.427	1.73	0.016	1.68	0.187	1.6	0.030
1437127_at	RIKEN cDNA A630033E08 gene	A630033E08Rik	-1.25	0.390	-1.56	0.095	1.74	0.001	1.41	0.001	1.1	0.529
1444503_at	Glioblastoma amplified sequence	Gbas	-1.22	0.317	-1.31	0.340	1.74	0.013	-1.02	0.934	-1.11	0.309
1445003_at	phenylalanine-tRNA synthetase-like, alpha subunit	Farsla	1.67	0.535	2.82	0.159	1.75	0.015	1.03	0.818	1.2	0.837
1435560_at	integrin alpha L /// similar to Integrin alpha-L precursor (Leukocyte a	Itgal /// LOC671163	1.3	0.403	2.11	0.843	1.75	0.016	-1.22	0.302	-1.02	0.771
1458668_at	Tumor protein D52	Tpd52	1.63	0.967	-1.13	0.640	1.75	0.015	1.31	0.647	1.55	0.632
1431376_at	WD repeat domain 62	Wdr62	1.07	0.934	1.01	0.847	1.75	0.012	1.32	0.087	-1.52	0.270
1432797_at	RIKEN cDNA 2900060N12 gene	2900060N12Rik	1.61	0.142	-1.33	0.109	1.76	0.030	-1.51	0.008	1.41	0.808
1436661_at	dipeptidylpeptidase 10	Dpp10	1.25	0.495	1.06	0.454	1.76	0.032	2.56	0.271	-1.45	0.222
1457708_at	methyl-CpG binding domain protein 4	Mbd4	-1.11	0.547	1.21	0.367	1.76	0.034	1.12	0.815	-1.1	0.546
1437074_at	sorting nexin 5	Snx5	2.73	0.269	4.24	0.070	1.76	0.024	1.64	0.032	1.4	0.081
1432422_at	RIKEN cDNA 1700063K16 gene	1700063K16Rik	-1.21	0.441	1.18	0.728	1.77	0.006	2.38	0.219	1.42	0.652
1443934_at	RIKEN cDNA 9230110C19 gene	9230110C19Rik	1.22	0.174	1.5	0.065	1.77	0.014	1.22	0.288	1.45	0.065
1425653_at	activating transcription factor 7	Atf7	1.83	0.720	-1.21	0.231	1.78	0.046	1	0.645	1.97	0.907
1434631_at	DNA segment, Chr 3, ERATO Doi 751, expressed	D3Ertd751e	1.67	0.485	-1.43	0.215	1.78	0.009	1.16	0.739	1.13	0.939
1443672_at	leucyl-tRNA synthetase, mitochondrial	Lars2	-1.07	0.603	-1.19	0.306	1.78	0.040	-1.15	0.364	1.86	0.825
1452855_at	lymphocyte antigen 6 complex, locus K	Ly6k	1.48	0.366	1.33	0.795	1.78	0.039	1.11	0.837	-1.2	0.095
1444971_at	RNA binding motif protein 5	Rbm5	1.43	0.170	1.24	0.438	1.78	0.013	1.24	0.369	1.2	0.284

1449370_at	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	Sox4 /// LOC67227	1.04	0.137	1.63	0.065	1.78	0.033	1.5	0.022	1.78	0.018
1459828_at	Serine/arginine repetitive matrix 1	Srrm1	1.45	0.995	1.66	0.409	1.78	0.015	-1.64	0.022	-1.16	0.326
1458962_at	transmembrane emp24 protein transport domain containing 5	Tmed5	-1.2	0.070	1.5	0.318	1.78	0.047	1.03	0.744	1.01	0.971
1416869_x_at	Lck interacting transmembrane adaptor 1	Lime1	2.17	0.268	2.22	0.281	1.79	0.023	3.1	0.189	1.22	0.987
1422890_at	protocadherin 18	Pcdh18	-1.07	0.833	1.41	0.138	1.79	0.039	1.3	0.036	1.3	0.124
1460069_at	structural maintenance of chromosomes 6	Smc6	-1.12	0.399	-1.49	0.341	1.79	0.031	-1.12	0.435	1.16	0.637
1416926_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.12	0.621	2.52	0.002	1.79	0.000	1.45	0.047	1.69	0.003
1458163_at	cDNA sequence BC066028	BC066028	1.74	0.642	2.03	0.027	1.8	0.031	1.37	0.126	1.19	0.446
1421600_a_at	tripartite motif protein 26	Trim26	1.15	0.274	1.53	0.085	1.8	0.027	1.14	0.122	1.09	0.487
1443354_at	Tripartite motif-containing 59	Trim59	1.04	0.793	-1.38	0.027	1.8	0.041	-1.18	0.332	1.07	0.556
1445406_at	expressed sequence C77494	C77494	1.38	0.909	1.59	0.662	1.81	0.018	3.24	0.732	-1.58	0.066
1436617_at	centrin 4	Cetn4	1.08	0.945	1.19	0.720	1.81	0.029	-1.02	0.809	-1.15	0.329
1456599_at	nuclear transport factor 2-like export factor 2	Nxt2	1.18	0.300	1.2	0.568	1.81	0.010	1.17	0.103	-1.01	0.927
1448096_at	2-oxoglutarate and iron-dependent oxygenase domain containing 1	Ogfod1	1.2	0.455	1.15	0.799	1.81	0.049	1.49	0.358	1.04	0.806
1457072_at	RIKEN cDNA 2410127E16 gene /// B-cell CLL/lymphoma 11A (zinc	2410127E16Rik ///	1.33	0.593	1.02	0.383	1.82	0.012	-1.28	0.219	1.73	0.374
1432728_at	RIKEN cDNA 5830433D23 gene	5830433D23Rik	-2.61	0.112	-2.59	0.108	1.82	0.038	-1	0.974	2.39	0.323
1430100_at	mitochondrial ribosomal protein S15	Mrps15	1.55	0.639	1.82	0.288	1.82	0.048	1.6	0.552	-1.1	0.643
1460683_at	TEA domain family member 4	Tead4	-1.14	0.735	1.41	0.380	1.82	0.016	1.05	0.488	1.58	0.613
1457623_x_at	transformation related protein 53	Trp53	-1.06	0.547	1.21	0.769	1.82	0.014	1.12	0.134	1.15	0.066
1430544_at	RIKEN cDNA 5830404H04 gene	5830404H04Rik	1.46	0.961	1.51	0.590	1.83	0.019	1.17	0.882	1.12	0.640
1440206_at	RIKEN cDNA A930024E05 gene	A930024E05Rik	2.06	0.355	1.22	0.304	1.83	0.020	1.37	0.975	2.24	0.388
1456356_at	RIKEN cDNA B230217O12 gene	B230217O12Rik	1.69	0.785	1.61	0.796	1.83	0.026	1.09	0.295	-1.12	0.340
1419120_at	lymphoblastomic leukemia	Lyl1	1.5	0.444	1.81	0.467	1.83	0.032	1.87	0.724	1.66	0.981
1451785_at	retinitis pigmentosa GTPase regulator interacting protein 1	Rpgrip1	1.65	0.937	-1.8	0.169	1.83	0.027	2.05	0.109	1.26	0.274
1433007_at	RIKEN cDNA 5430430B14 gene	5430430B14Rik	1.62	0.620	1.6	0.942	1.84	0.041	1.86	0.413	1.47	0.824
1439081_at	meningioma expressed antigen 5 (hyaluronidase)	Mgea5	2.08	0.472	2.02	0.388	1.85	0.005	1.11	0.850	1.08	0.337
1441963_at	ProSAPiP1 protein	Prosapip1	2.13	0.604	3.17	0.009	1.85	0.003	1.43	0.135	1.5	0.167
1432376_at	RIKEN cDNA 3830403N18 gene	3830403N18Rik	2.58	0.314	2.22	0.675	1.86	0.001	-1.88	0.084	-1.48	0.156
1453685_at	nudix (nucleoside diphosphate linked moiety X)-type motif 7	Nudt7	-1.45	0.152	1.28	0.637	1.87	0.017	2.19	0.228	1.11	0.974
1455098_a_at	vitronectin	Vtn	2.01	0.706	1.91	0.018	1.87	0.029	1.11	0.670	1.24	0.976
1442528_at	exportin 4	Xpo4	-1.13	0.638	-1.17	0.065	1.87	0.026	1	0.792	-1.12	0.421
1436288_at	RIKEN cDNA 1700049M11 gene	1700049M11Rik	-1.21	0.408	1.21	0.317	1.88	0.013	1.09	0.971	-1.08	0.580
1432639_at	RIKEN cDNA 4633401L03 gene	4633401L03Rik	1.39	0.766	1.84	0.725	1.88	0.046	-1.24	0.347	2.13	0.026
1424989_at	transmembrane protein 142A	Tmem142a	1.07	0.572	1.05	0.571	1.89	0.001	-1.06	0.627	1.16	0.123
1439926_at	RIKEN cDNA 4632417D23 gene	4632417D23Rik	1.22	0.598	-1.35	0.239	1.9	0.042	1.32	0.569	1.58	0.452
1447076_at	NEL-like 1 (chicken)	Nell1	1.12	0.283	1.36	0.780	1.9	0.030	-1.11	0.290	2.71	0.426
1426663_s_at	solute carrier family 45, member 3	Slc45a3	2.82	0.391	2.66	0.278	1.9	0.026	1.46	0.161	1.58	0.404
1457570_at	RIKEN cDNA A230001M10 gene	A230001M10Rik	-1.14	0.299	-1.3	0.050	1.91	0.042	1.82	0.205	-1.3	0.458
1453003_at	sortilin-related receptor, LDLR class A repeats-containing	Sorl1	1.38	0.848	1.21	0.812	1.91	0.011	-1.58	0.115	3.51	0.198
1425080_at	zinc finger protein 286	Zfp286	-1.14	0.402	-1.21	0.333	1.91	0.021	-1.32	0.237	1.54	0.190
1453417_at	RIKEN cDNA 4933407K13 gene	4933407K13Rik	-1.52	0.026	-1.15	0.089	1.92	0.004	1.41	0.376	1.46	0.633
1421028_a_at	myocyte enhancer factor 2C	Mef2c	1.08	0.929	-1.23	0.288	1.92	0.033	2.18	0.550	2.01	0.545
1452015_at	RIKEN cDNA 6330416G13 gene	6330416G13Rik	1.16	0.885	1.09	0.888	1.93	0.024	1.01	0.986	1.02	0.366
1451528_at	cDNA sequence BC025833	BC025833	1.65	0.719	-1	0.401	1.93	0.018	1.11	0.958	-1.18	0.289
1457105_at	polycystic kidney disease 2-like 1	Pkd2l1	1.71	0.640	1.2	0.723	1.93	0.049	1.43	0.695	2.11	0.345
1451472_at	RIKEN cDNA 3230401I01 gene	3230401I01Rik	-1.53	0.265	-1.02	0.466	1.94	0.023	1.25	0.809	1.72	0.453
1441178_at	DTW domain containing 2	Dtwd2	1.03	0.988	1	0.962	1.94	0.022	-1.06	0.654	1.3	0.498
1456075_at	protein kinase D2	Prkd2	1.61	0.194	-1.25	0.361	1.94	0.011	1.65	0.611	-1.53	0.254
1453360_a_at	testis expressed gene 9	Tex9	1.28	0.356	1.08	0.283	1.94	0.010	1.04	0.981	1.13	0.583
1434735_at	hepatic leukemia factor	Hlf	2.15	0.992	1.74	0.609	1.95	0.034	1.17	0.587	1.2	0.852
1441035_at	potassium voltage-gated channel, Isk-related subfamily, member 1	Kcne1	-1.06	0.440	-1.01	0.480	1.95	0.048	1.07	0.424	-1.08	0.502
1424623_at	serine (or cysteine) peptidase inhibitor, clade B, member 5	Serpinb5	1.41	0.965	1.44	0.477	1.95	0.020	-1.1	0.460	-1.13	0.139
1441476_at	suppressor of cytokine signaling 2	Socs2	1.25	0.107	-1.22	0.346	1.95	0.007	-2.48	0.037	-1.08	0.661
1425191_at	RIKEN cDNA 9430098E02 gene	9430098E02Rik	1.53	0.402	2.28	0.354	1.96	0.031	-1.12	0.468	1.61	0.058
1447866_x_at	RIKEN cDNA 2300009A05 gene	2300009A05Rik	2.35	0.862	1.58	0.885	1.97	0.002	1.87	0.243	1.63	0.944
1447689_at	G protein-coupled receptor associated sorting protein 1	Gprasp1	1.24	0.857	1.93	0.494	1.97	0.001	1.38	0.444	1.8	0.777
1429071_at	malic enzyme 3, NADP(+)-dependent, mitochondrial	Me3	-1.01	0.672	-1.27	0.426	1.97	0.028	1.28	0.547	1.26	0.922
1429929_at	meiosis defective 1	Mei1	-1.09	0.288	-1.52	0.181	1.97	0.008	2.17	0.002	-1.36	0.255

1435968_at	Protein tyrosine phosphatase, receptor type, N polypeptide 2	Ptprn2	1.79	0.183	1.56	0.397	1.97	0.031	1.58	0.661	1.53	0.913
1449561_at	RIKEN cDNA 4921504I05 gene	4921504I05Rik	2.27	0.123	2.13	0.112	1.98	0.047	1.87	0.122	1.32	0.382
1427684_at	zinc finger protein 264	Zfp264	1.42	0.923	1.01	0.916	1.99	0.027	-1.98	0.104	1.23	0.561
1417337_at	erythrocyte protein band 4.2	Epb4.2	1.26	0.808	1.55	0.747	2	0.049	1.49	0.566	1.06	0.809
1457812_at	transformation related protein 53 binding protein 1	Trp53bp1	1.17	0.889	-1.09	0.434	2	0.014	-1.1	0.459	-1.45	0.301
1449457_at	acyl-CoA thioesterase 12	Acot12	1.11	0.980	-1.21	0.592	2.01	0.039	-1.18	0.342	1.37	0.753
1457038_at	Fras1 related extracellular matrix protein 2	Frem2	1.57	0.740	1.42	0.465	2.01	0.042	2.38	0.084	1.41	0.248
1442214_at	Nuclear factor I/B	Nfib	-1.31	0.269	-1.87	0.004	2.01	0.033	-1.04	0.521	1.01	0.529
1434345_at	transmembrane protein 12	Tmem12	1.27	0.628	-1.26	0.395	2.01	0.016	-1.88	0.055	2.51	0.655
1455241_at	cDNA sequence BC037703	BC037703	2.34	0.138	5.04	0.010	2.02	0.020	2.05	0.205	1.73	0.163
1429167_at	coiled-coil domain containing 112	Ccdc112	-1.07	0.483	-1.05	0.562	2.02	0.042	-1.09	0.786	1.38	0.439
1431599_at	RIKEN cDNA 2310069B03 gene	2310069B03Rik	1.89	0.675	1.6	0.901	2.03	0.006	1.16	0.453	-1.57	0.178
1418944_at	cysteinyl leukotriene receptor 1	Cysltr1	-1.59	0.055	-1.46	0.035	2.03	0.023	1.19	0.859	1.8	0.335
1451515_s_at	glycine-N-acyltransferase	Glyat	2.28	0.159	2.1	0.300	2.03	0.038	-1.19	0.189	-1.06	0.512
1443709_at	Yippee-like 2 (Drosophila)	Ypel2	-1.58	0.126	1.55	0.538	2.03	0.024	3.46	0.080	-1.15	0.385
1437137_at	RIKEN cDNA 6430550H21 gene	6430550H21Rik	2.75	0.457	-1.02	0.979	2.04	0.048	1.24	0.698	2.34	0.099
1449971_a_at	CD209f antigen	Cd209f	-2.15	0.217	1.13	0.460	2.04	0.042	1.98	0.035	-1.36	0.231
1458158_at	WD repeat domain 67	Wdr67	-1.7	0.029	1.3	0.415	2.04	0.006	-1.02	0.650	1.79	0.504
1440390_at	cDNA sequence BC025575	BC025575	-1.28	0.071	1.63	0.785	2.05	0.032	-1.04	0.734	1.65	0.051
1434414_at	FAD-dependent oxidoreductase domain containing 2	Foxred2	2.24	0.461	3.46	0.245	2.06	0.007	1.99	0.125	2.85	0.052
1442561_at	MAM domain containing 1	Mamdc1	1.46	0.836	1.08	0.544	2.06	0.001	-2.06	0.073	1.18	0.529
1416839_at	methylmalonyl-Coenzyme A mutase	Mut	2.03	0.904	1.65	0.760	2.06	0.033	-1.1	0.907	1.42	0.775
1455034_at	Nuclear receptor subfamily 4, group A, member 2	Nr4a2	1.28	0.905	2.01	0.042	2.06	0.003	1.63	0.002	2.37	0.002
1422723_at	stimulated by retinoic acid gene 6	Stra6	1.95	0.689	1.56	0.423	2.06	0.028	1.14	0.679	1.12	0.785
1435615_at	zinc finger protein 365	Zfp365	1.21	0.024	1.41	0.429	2.06	0.049	1.03	0.924	1.04	0.557
1458268_s_at	insulin-like growth factor binding protein 3	Igfbp3	1.13	0.864	1.03	0.482	2.07	0.012	2.8	0.390	1.26	0.238
1423523_at	aminoadipate-semialdehyde synthase	Aass	-1.25	0.147	1.23	0.533	2.08	0.034	1.33	0.952	2	0.242
1440333_at	MAM domain containing 4	Mamdc4	2.14	0.157	2	0.153	2.08	0.009	2.4	0.578	1.4	0.271
1432362_at	centromere protein P	Cenpp	1.28	0.442	1.47	0.484	2.09	0.049	1.19	0.479	-1.11	0.519
1425077_at	DnaJ (Hsp40) homolog, subfamily C, member 18	Dnajc18	1.82	0.711	1.5	0.731	2.09	0.047	-1.06	0.500	-1.08	0.669
1445404_at	kinesin family member 27	Kif27	1.73	0.530	3.32	0.167	2.1	0.028	2.47	0.598	1.78	0.867
1431805_a_at	rhophilin, Rho GTPase binding protein 2	Rhpn2	1.5	0.732	-1.42	0.195	2.1	0.003	-1.7	0.066	1.26	0.945
1433426_at	RIKEN cDNA 1700111A04 gene	1700111A04Rik	1.38	0.559	-1.03	0.499	2.11	0.040	-1.14	0.402	2.37	0.371
1459606_at	expressed sequence C79130	C79130	1.42	0.216	1.34	0.952	2.11	0.048	2.67	0.842	1.08	0.675
1458174_at	coiled-coil domain containing 52	Ccdc52	2.78	0.191	2.53	0.234	2.11	0.021	2.11	0.962	1.49	0.046
1426224_x_at	CKLF-like MARVEL transmembrane domain containing 2A	Cmtm2a	-1.25	0.291	1.24	0.855	2.11	0.035	1.76	0.977	1.25	0.968
1446864_at	S100P binding protein	S100pbp	1.54	0.739	1.38	0.625	2.11	0.024	1.73	0.568	1.96	0.039
1419186_a_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	St8sia4	1.92	0.427	1.8	0.974	2.11	0.002	-1.11	0.657	-1.15	0.309
1417906_at	RIKEN cDNA 1700001F09 gene	1700001F09Rik	1.2	0.871	-1.11	0.407	2.12	0.017	1.19	0.562	1.27	0.903
1445713_at	RIKEN cDNA 9630041G16 gene	9630041G16Rik	1.85	0.161	1.58	0.608	2.12	0.037	1.25	0.366	-1.32	0.232
1426183_a_at	CD209d antigen	Cd209d	1.71	0.627	1.31	0.971	2.12	0.016	-1.3	0.261	2.37	0.337
1425298_a_at	baculoviral IAP repeat-containing 1a	Birc1a	1.02	0.939	-2.06	0.081	2.13	0.025	1.79	0.017	1.32	0.458
1424958_at	carbonic anhydrase 8	Car8	-1.05	0.875	-1.06	0.575	2.13	0.031	-1.13	0.384	2.4	0.264
1421696_at	polycystic kidney and hepatic disease 1-like 1	Pkhd1l1	1.46	0.533	-1.86	0.074	2.13	0.013	2.67	0.150	1.51	0.025
1423003_at	SET domain containing (lysine methyltransferase) 7	Setd7	2.24	0.433	1.39	0.405	2.13	0.039	1.28	0.677	-1.39	0.272
1445777_at	UPF2 regulator of nonsense transcripts homolog (yeast)	Upf2	2.86	0.465	2.69	0.201	2.13	0.044	-1.37	0.241	-1.48	0.019
1435856_x_at	SWI/SNF related, matrix associated, actin dependent regulator of ch	Smarcb1	1.09	0.816	1.13	0.870	2.14	0.045	-1.04	0.769	1.08	0.541
1454336_at	Cyclin C	Ccnc	1.84	0.574	-1.14	0.317	2.15	0.029	1.38	0.932	1.32	0.939
1425038_at	solute carrier family 22 (organic anion transporter), member 19	Slc22a19	-1.16	0.368	-1.07	0.316	2.15	0.045	2.98	0.134	1.36	0.510
1451764_at	MARVEL (membrane-associating) domain containing 3	Marveld3	-1.37	0.086	-2.65	0.003	2.16	0.040	1.11	0.861	1.76	0.085
1436807_x_at	tripartite motif-containing 62	Trim62	-1.26	0.343	-1.63	0.249	2.16	0.017	1.24	0.627	1.5	0.699
1441750_x_at	RIKEN cDNA 4930447F24 gene	4930447F24Rik	1.78	0.554	2.12	0.225	2.18	0.044	1.27	0.458	1.01	0.998
1436870_s_at	expressed sequence AU041783	AU041783	2.5	0.658	1.78	0.815	2.18	0.026	1.11	0.911	1.16	0.958
1458839_at	exocyst complex component 8	Exoc8	1.06	0.649	1.34	0.819	2.18	0.035	1.51	0.998	-1.23	0.285
1458342_at	transmembrane protein 90a	Tmem90a	1.13	0.983	1.37	0.752	2.18	0.027	-1.66	0.081	1.01	0.917
1442841_at	Tetraspanin 3	Tspan3	-1.57	0.121	1.58	0.373	2.19	0.030	1.45	0.902	1.32	0.884
1431624_a_at	RIKEN cDNA 2610206B13 gene	2610206B13Rik	1.58	0.292	3.02	0.018	2.2	0.036	1.83	0.547	-1.05	0.980
1433240_at	RIKEN cDNA 9430013L17 gene	9430013L17Rik	3.17	0.147	2.11	0.283	2.2	0.032	-1.4	0.354	1.52	0.920

1438189_s_at	erythrocyte protein band 4.9	Epb4.9	1.25	0.158	1.14	0.268	2.2	0.018	1.4	0.686	1.27	0.775
1456543_at	prokineticin receptor 1	Prokr1	2.46	0.011	2.45	0.014	2.2	0.016	1.66	0.659	1.22	0.724
1449782_at	expressed sequence AA517650	AA517650	-1.61	0.125	-1.48	0.092	2.21	0.033	1.57	0.667	-1.18	0.386
1456619_at	Lipase, member H	Liph	1.1	0.897	1.11	0.329	2.21	0.043	1.74	0.562	1.67	0.203
1454360_at	RIKEN cDNA 4930418C01 gene	4930418C01Rik	-2.94	0.006	-1.08	0.673	2.22	0.014	-1.37	0.153	1.13	0.579
1422911_at	cerebellin 3 precursor protein	Cbln3	1.32	0.616	1.63	0.511	2.22	0.010	1.32	0.961	1.36	0.954
1427634_at	potassium voltage-gated channel, subfamily H (eag-related), membe	Kcnh7	1.23	0.535	1.92	0.709	2.22	0.004	-1.33	0.109	-1.58	0.211
1429263_at	RIKEN cDNA 4933425D22 gene	4933425D22Rik	-1.17	0.323	1.17	0.810	2.23	0.005	1.14	0.511	1.6	0.635
1451415_at	RIKEN cDNA 1810011O10 gene	1810011O10Rik	1.49	0.099	1.99	0.005	2.24	0.033	1.43	0.101	2.06	0.012
1421188_at	chemokine (C-C motif) receptor 2	Ccr2	1.01	0.803	1.23	0.906	2.24	0.038	-1.13	0.675	-1.76	0.071
1436625_at	Fc receptor, IgG, high affinity I	Fcgr1	-1.02	0.567	1.01	0.585	2.24	0.018	1.8	0.163	-1.02	0.972
1419908_at	Fc receptor-like A	Fcrla	1.36	0.620	2.45	0.172	2.24	0.024	2.19	0.445	1.48	0.378
1458850_at	Myosin, heavy polypeptide 6, cardiac muscle, alpha	Myh6	-1.14	0.440	-1.17	0.370	2.24	0.017	-1.2	0.132	-1.03	0.631
1425867_at	pleckstrin homology domain containing, family A (phosphoinositide b	Plekha4	-1.57	0.151	-1.33	0.362	2.24	0.006	-1.05	0.406	1.06	0.986
1455405_at	proline-serine-threonine phosphatase-interacting protein 2	Pstpip2	1.25	0.184	-1.28	0.353	2.24	0.006	-1.01	0.959	-1.38	0.122
1458716_at	dual specificity phosphatase 27 (putative)	Dusp27	-1.81	0.036	1.56	0.540	2.25	0.001	2.85	0.561	2.06	0.195
1420529_at	neuronal d4 domain family member	Neud4	1.23	0.872	1.82	0.834	2.25	0.047	1.44	0.241	-1.79	0.150
1440355_at	potassium channel tetramerisation domain containing 12b	Kctd12b	4.08	0.046	2	0.164	2.26	0.033	1.2	0.944	-1.19	0.560
1438878_at	RIKEN cDNA 6430537K16 gene	6430537K16Rik	1.1	0.475	1.15	0.650	2.28	0.000	-1.53	0.279	-1.09	0.399
1422283_at	CD40 ligand	Cd40lg	1.35	0.569	1.34	0.964	2.29	0.046	-1.48	0.163	1.24	0.904
1418287_a_at	deleted in malignant brain tumors 1	Dmbt1	-1.09	0.365	1.1	0.582	2.29	0.036	-1.57	0.087	1.09	0.587
1417600_at	solute carrier family 15 (H+/peptide transporter), member 2	Slc15a2	1.57	0.985	1.24	0.988	2.29	0.010	-1.57	0.119	-1.19	0.353
1453870_at	RIKEN cDNA 1810018F18 gene	1810018F18Rik	2.53	0.661	1.71	0.898	2.3	0.040	2.67	0.465	1.21	0.745
1459309_at	RUN and FYVE domain containing 3	Rufy3	1.7	0.544	1.89	0.833	2.3	0.037	1.01	0.847	1.25	0.766
1428837_at	kelch-like 14 (Drosophila)	Klhl14	1.02	0.807	-1.43	0.123	2.32	0.027	-1.59	0.117	1.21	0.579
1423979_a_at	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine trans	Slc25a29	-1.62	0.167	-1.32	0.415	2.32	0.005	1.23	0.197	2.13	0.176
1451960_a_at	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S.	Rev3l	-1.03	0.233	1.27	0.586	2.33	0.032	2.22	0.955	1.33	0.841
1449856_at	regulator of G-protein signaling 18	Rgs18	1.28	0.062	1.05	0.555	2.33	0.023	-1.1	0.743	-1.08	0.705
1429997_at	RIKEN cDNA 4832441B07 gene	4832441B07Rik	1.63	0.055	1.33	0.645	2.34	0.022	1.44	0.581	1.12	0.976
1458903_at	RIKEN cDNA A230057G18 gene	A230057G18Rik	2.18	0.152	2.13	0.184	2.34	0.035	1.58	0.158	1.4	0.827
1425313_at	calcium response factor	Carf	1.98	0.378	1.67	0.530	2.34	0.003	1.3	0.671	-1.79	0.120
1433052_at	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu anti	Elavl2	-1.2	0.425	1.51	0.647	2.34	0.030	-1.84	0.073	1.72	0.935
1432542_at	RIKEN cDNA 2810474C18 gene	2810474C18Rik	-1.43	0.369	1.52	0.061	2.35	0.004	1.58	0.893	1.39	0.636
1427818_at	B-cell leukemia/lymphoma 2	Bcl2	-1.16	0.235	-1.03	0.352	2.35	0.049	2.58	0.082	1.11	0.721
1433972_at	calmodulin binding transcription activator 1	Camta1	3.97	0.201	2.47	0.460	2.35	0.047	1.5	0.393	1.07	0.536
1457750_at	DNA segment, Chr 16, ERATO Doi 780, expressed	D16Ertd780e	-1.25	0.125	-1.48	0.188	2.36	0.032	-1.13	0.611	-1.38	0.224
1447791_s_at	guanine nucleotide binding protein, alpha 14	Gna14	1.68	0.918	1.52	0.645	2.36	0.048	1.1	0.660	-1.1	0.329
1445412_at	coiled-coil domain containing 73	Ccdc73	1.11	0.651	1.12	0.627	2.37	0.001	-1.03	0.643	1	0.815
1418013_at	camello-like 1	Cml1	-1.02	0.477	1.89	0.633	2.37	0.002	2.11	0.650	2.66	0.283
1432319_at	RIKEN cDNA 1700085C21 gene	1700085C21Rik	1.34	0.851	2	0.873	2.38	0.035	1.58	0.131	-1.23	0.205
1418812_a_at	BarH-like 1 (Drosophila)	Barhl1	-3.28	0.112	-2.42	0.149	2.39	0.029	1.31	0.723	1	0.591
1441146_at	expressed sequence C76132	C76132	-1.18	0.524	-1.77	0.094	2.39	0.017	-1.13	0.507	2.62	0.513
1447785_x_at	DNA segment, Chr 11, Wayne State University 99, expressed	D11Wsu99e	-1.2	0.563	1.18	0.614	2.4	0.039	1.95	0.262	-1.35	0.124
1460336_at	peroxisome proliferative activated receptor, gamma, coactivator 1 al	Ppargc1a	1.05	0.384	1.45	0.536	2.4	0.022	1.25	0.937	1.49	0.759
1420669_at	aryl hydrocarbon receptor nuclear translocator 2	Arnt2	-2.33	0.001	-1.68	0.102	2.41	0.037	1.63	0.329	1.02	0.946
1422197_at	potassium voltage-gated channel, shaker-related subfamily, membe	Kcna2	1.15	0.393	1.07	0.413	2.41	0.017	2.1	0.452	-1.14	0.812
1437075_at	FERM domain containing 3	Frmd3	-1.04	0.853	1.23	0.474	2.42	0.002	2.11	0.393	1.88	0.184
1449252_at	RIKEN cDNA 9030611O19 gene	9030611O19Rik	2.23	0.112	3.49	0.061	2.43	0.039	1.52	0.006	1.69	0.213
1446866_at	RIKEN cDNA A530089I17 gene	A530089I17Rik	-1.24	0.432	-1.48	0.185	2.43	0.028	1.06	0.340	1.5	0.682
1443631_at	Diacylglycerol kinase, beta	Dgkb	-1.21	0.231	-1.03	0.432	2.43	0.017	1.51	0.078	2.15	0.044
1442443_at	Retinoblastoma binding protein 4	Rbbp4	1.92	0.264	-2.22	0.049	2.43	0.035	-1.11	0.596	1.32	0.788
1425743_at	tripartite motif protein 7	Trim7	-1.11	0.298	-1.56	0.210	2.43	0.046	-1.19	0.482	1.03	0.665
1437310_at	Bardet-Biedl syndrome 1 homolog (human)	Bbs1	1.74	0.323	1.23	0.403	2.44	0.036	4.06	0.034	1.35	0.575
1456062_at	natriuretic peptide precursor type A	Nppa	-1.07	0.477	-1.07	0.440	2.45	0.031	-1.21	0.388	-1.72	0.046
1435590_at	RIKEN cDNA D430047L21 gene	D430047L21Rik	1.53	0.916	1.33	0.882	2.46	0.050	1.68	0.084	-1.2	0.230
1442405_at	Cysteine and glycine-rich protein 2 binding protein	Csrp2bp	1.2	0.898	-1.54	0.129	2.47	0.041	-1.28	0.097	-1.74	0.189
1440875_a_at	radical S-adenosyl methionine domain containing 1	Rsad1	-1.07	0.717	1.18	0.617	2.47	0.027	-1.67	0.075	1.6	0.127
1418626_a_at	clusterin	Clu	2.27	0.926	1.93	0.966	2.48	0.028	1.49	0.637	-1.28	0.328

1459884_at	cytochrome c oxidase, subunit VIIc	Cox7c	1.49	0.981	1.75	0.836	2.48	0.020	1.05	0.749	1.29	0.621
1419408_at	sine oculis-related homeobox 6 homolog (Drosophila)	Six6	1.42	0.403	-1.2	0.305	2.48	0.004	1.77	0.786	-1.74	0.108
1455568_at	RIKEN cDNA 2310015A05 gene	2310015A05Rik	1.57	0.314	2.07	0.121	2.49	0.040	1.07	0.984	-1.04	0.677
1429912_at	sperm associated antigen 4-like	Spag4l	-1.35	0.370	-1.9	0.073	2.49	0.021	-1.16	0.198	-1.04	0.662
1459042_at	regulating synaptic membrane exocytosis 3	Rims3	-1.35	0.157	-1.66	0.097	2.5	0.034	-1.32	0.249	1.36	0.506
1458959_at	AF4/FMR2 family, member 4	Aff4	1.14	0.552	2.4	0.441	2.51	0.040	1.01	0.773	1.64	0.382
1457906_at	RNA binding motif protein 13	Rbm13	1.65	0.405	1.53	0.286	2.51	0.036	1.24	0.485	1.01	0.273
1454102_at	RIKEN cDNA 5031425E22 gene	5031425E22Rik	2.06	0.210	2.56	0.669	2.52	0.034	1.4	0.083	1.81	0.687
1425530_a_at	syntaxin 3	Stx3	1.79	0.392	2.36	0.232	2.53	0.021	-1.04	0.810	1.57	0.230
1436675_at	WD repeat domain 63	Wdr63	1.29	0.756	1.26	0.048	2.53	0.022	1.09	0.548	1.01	0.987
1458055_at	Desmocollin 3	Dsc3	1.77	0.135	1.29	0.783	2.54	0.028	2.07	0.116	1.3	0.689
1451677_at	nuclear prelamin A recognition factor	Narf	-1.06	0.424	1.06	0.477	2.54	0.027	-1.06	0.542	1.29	0.945
1430321_at	RIKEN cDNA A930040G15 gene	A930040G15Rik	1.76	0.773	1.22	0.792	2.55	0.040	-2.5	0.018	1.28	0.656
1459750_s_at	G protein-coupled receptor 123	Gpr123	1.11	0.626	1.91	0.760	2.55	0.012	2.99	0.102	1.29	0.889
1446782_at	lines homolog 2 (Drosophila)	Lins2	1.14	0.542	1.12	0.453	2.55	0.038	2.3	0.055	1.99	0.113
1436074_at	cDNA sequence AY078069	AY078069	-1.04	0.469	1.88	0.896	2.56	0.042	1.52	0.040	1.64	0.491
1431718_at	kinesin family member 15	Kif15	2.86	0.625	1.62	0.779	2.56	0.003	2.36	0.469	1.27	0.887
1425116_a_at	spectrin beta 4	Spnb4	1.18	0.906	1.05	0.768	2.56	0.040	-1.11	0.524	-1.19	0.205
1453847_at	RIKEN cDNA A930037O16 gene	A930037O16Rik	-1.18	0.375	2.68	0.587	2.57	0.010	-1.15	0.382	2.46	0.521
1424937_at	RIKEN cDNA 2310076L09 gene	2310076L09Rik	1	0.459	-1.71	0.121	2.58	0.017	-1.04	0.574	2.36	0.548
1427860_at	immunoglobulin kappa chain variable 6-23 /// immunoglobulin kappa	Igkv6-23 /// Igk-V19	1.45	0.864	1.01	0.738	2.58	0.023	1.7	0.226	1.51	0.903
1440790_x_at	RIKEN cDNA 5033414K04 gene	5033414K04Rik	-1.08	0.534	1.11	0.926	2.59	0.032	2.03	0.642	2.21	0.114
1441002_at	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae	Pop1	1.17	0.697	1.85	0.989	2.6	0.004	1.02	0.766	1.3	0.774
1455120_at	glyoxalase domain containing 1	Gloxd1	1.54	0.829	1.82	0.196	2.61	0.012	2.96	0.129	2	0.073
1427697_a_at	transformation related protein 73	Trp73	1.2	0.887	1.25	0.883	2.61	0.036	-1.15	0.297	-1.13	0.464
1457146_at	dedicator of cytokinesis 4	Dock4	1.22	0.578	1.13	0.773	2.62	0.003	2.28	0.376	-1.1	0.701
1438295_at	Glucocorticoid induced transcript 1	Glcci1	1.55	0.202	1.77	0.170	2.62	0.005	1.49	0.021	-1.06	0.754
1417302_at	REST corepressor 2	Rcor2	1.02	0.667	1.07	0.769	2.63	0.029	1.4	0.720	2.3	0.237
1423866_at	serine (or cysteine) peptidase inhibitor, clade A, member 3K	Serpina3k	1.71	0.331	3.17	0.068	2.64	0.001	1.78	0.838	1.91	0.231
1453976_at	RIKEN cDNA 4432414F05 gene	4432414F05Rik	-1.06	0.398	1.14	0.915	2.65	0.046	1.36	0.453	2.1	0.336
1422699_at	arachidonate 12-lipoxygenase	Alox12	-1.1	0.553	-1.23	0.183	2.65	0.044	1.21	0.996	2.11	0.340
1449398_at	ribosomal protein L3-like	Rpl3l	-2.04	0.098	-1.61	0.102	2.67	0.032	1.96	0.742	1.62	0.355
1450287_at	neuronal PAS domain protein 3	Npas3	-1.09	0.262	1.57	0.687	2.71	0.030	1.09	0.812	3.13	0.232
1439064_at	cDNA sequence BC030046	BC030046	1.51	0.682	1.53	0.521	2.72	0.040	1.41	0.296	1.06	0.956
1427466_at	CDC91 cell division cycle 91-like 1 (S. cerevisiae)	Cdc91l1	1.01	0.988	1.15	0.623	2.73	0.000	1.05	0.801	1.09	0.924
1456494_a_at	tripartite motif protein 30 /// expressed sequence AI451617	Trim30 /// AI451617	-1.25	0.250	-1.27	0.560	2.74	0.020	-1.08	0.534	1.18	0.783
1431869_at	RIKEN cDNA 5730419F03 gene	5730419F03Rik	1.2	0.529	1.76	0.937	2.75	0.009	-1.26	0.164	-1.55	0.011
1417795_at	cell adhesion molecule with homology to L1CAM	Chl1	1.76	0.387	1.44	0.867	2.75	0.006	-2.3	0.044	1.14	0.846
1427436_at	sine oculis-related homeobox 2 homolog (Drosophila)	Six2	-1.04	0.493	-1.19	0.405	2.75	0.015	-1.71	0.109	1.14	0.870
1435049_s_at	expressed sequence AI854703	AI854703	1.1	0.940	-1.18	0.403	2.76	0.021	1.76	0.803	-1.35	0.344
1454685_at	G protein-coupled receptor 146	Gpr146	-1.38	0.121	1.1	0.951	2.77	0.015	1.24	0.541	-1.15	0.524
1419578_at	mannose binding lectin (A)	Mbl1	1.09	0.689	-1.15	0.386	2.78	0.004	1.26	0.966	2.06	0.095
1450261_a_at	solute carrier family 10 (sodium/bile acid cotransporter family), meml	Slc10a1	1.6	0.818	1.24	0.420	2.79	0.007	1.05	0.727	1.63	0.041
1443770_x_at	Autism susceptibility candidate 2	Auts2	2.83	0.324	3.45	0.048	2.8	0.035	2.2	0.150	1.5	0.212
1449259_at	RAB3D, member RAS oncogene family	Rab3d	2.05	0.298	1.3	0.821	2.8	0.023	2.06	0.313	1.7	0.783
1453009_at	carboxypeptidase M	Cpm	-1.09	0.161	2.04	0.829	2.81	0.031	1.79	0.155	1.24	0.747
1451964_at	melanoma inhibitory activity 2	Mia2	1.82	0.527	-1.23	0.376	2.82	0.001	1.9	0.137	-1.36	0.163
1445883_at	RAN binding protein 2	Ranbp2	1.15	0.556	-1.05	0.473	2.83	0.040	-1.12	0.541	1.19	0.501
1438149_at	Expressed sequence AI449441	AI449441	-1.41	0.269	-2.76	0.043	2.84	0.009	1.16	0.937	-1.25	0.493
1444719_at	DNA Segment, Chr 7, Mouse Genome Informatics 29	D7Mgi29	2.8	0.996	2.13	0.962	2.84	0.015	1.41	0.397	2.05	0.367
1453084_s_at	collagen, type XXII, alpha 1	Col22a1	1.05	0.691	1.02	0.373	2.85	0.047	1.13	0.985	1.41	0.473
1422392_at	vomeronasal 1 receptor, C6	V1rc6	1.22	0.694	1.34	0.694	2.87	0.039	1.91	0.512	-2.59	0.003
1421807_at	defensin beta 6	Defb6	1.02	0.858	1.48	0.516	2.88	0.003	1.6	0.132	2.19	0.751
1445419_at	GTP-binding protein 8 (putative)	Gtpbp8	1.57	0.774	1.91	0.449	2.88	0.048	2.08	0.948	2.87	0.724
1449937_at	placental protein 11 related	Pp11r	-1.18	0.300	1.7	0.893	2.88	0.012	1.85	0.453	2.64	0.374
1419016_at	RIKEN cDNA 1700034I23 gene	1700034I23Rik	2.33	0.044	1.47	0.672	2.91	0.010	1.68	0.404	1.73	0.132
1430730_at	RIKEN cDNA 9430024F10 gene	9430024F10Rik	-1.69	0.188	-1.27	0.242	2.91	0.025	-1.09	0.796	2.63	0.050
1420363_at	Bcl2-interacting killer	Bik	1.02	0.728	1.11	0.770	2.91	0.036	-1.2	0.281	1.51	0.395

1422921_at	pre-B lymphocyte gene 3	Vpreb3	-1.04	0.973	-1	0.919	2.91	0.026	-1.23	0.312	-1.13	0.691
1450318_a_at	purinergic receptor P2Y, G-protein coupled 2	P2ry2	4.17	0.635	3.51	0.798	2.92	0.038	1.37	0.484	1.53	0.389
1438279_at	Dipeptidylpeptidase 4	Dpp4	-1.36	0.263	-1.32	0.207	2.93	0.011	-1.12	0.485	-1.06	0.671
1457796_at	Ubiquitin protein ligase E3 component n-recognin 1	Ubr1	1.11	0.918	1.13	0.833	2.94	0.048	2.18	0.215	1.01	0.812
1442507_at	whirlin	Whrn	-1.15	0.226	-1.25	0.245	2.94	0.034	2.08	0.353	2	0.087
1417411_at	nucleosome assembly protein 1-like 5	Nap1l5	-1.02	0.584	1.28	0.057	2.95	0.014	1.55	0.213	1.56	0.121
1442235_at	Pleiomorphic adenoma gene-like 2	Plagl2	1.52	0.943	1.73	0.688	2.95	0.010	1.52	0.750	-1.03	0.706
1438475_at	cDNA sequence AB124611	AB124611	1.1	0.845	-1.19	0.849	2.96	0.004	1.6	0.795	1.23	0.960
1458649_at	expressed sequence AI662245	AI662245	1.67	0.209	2.08	0.485	2.96	0.046	-1.21	0.214	-1.1	0.542
1442974_at	DNA segment, Chr 6, ERATO Doi 160, expressed	D6Ertd160e	-1.21	0.643	-1.14	0.482	2.96	0.013	2.19	0.140	1.8	0.590
1456562_x_at	KIAA0415 protein	KIAA0415	1.27	0.534	1.66	0.808	2.96	0.003	-1.64	0.149	1.21	0.779
1448940_at	tripartite motif protein 21	Trim21	2.57	0.753	1.75	0.004	2.97	0.013	1.14	0.363	1.81	0.015
1430239_at	RIKEN cDNA 5430421F17 gene	5430421F17Rik	1.8	0.110	1.64	0.743	2.98	0.033	2.89	0.425	-1.01	0.951
1430181_at	H1 histone family, member N, testis-specific	H1fnt	1.52	0.653	1.12	0.943	3	0.008	-1	0.596	-1.04	0.769
1445557_at	RIKEN cDNA 0610040B10 gene	0610040B10Rik	1.32	0.830	1.25	0.580	3.02	0.032	1.2	0.910	1.98	0.545
1439728_at	RIKEN cDNA D330027H18 gene	D330027H18Rik	1.31	0.766	1.35	0.685	3.02	0.017	-1	0.997	2.26	0.800
1422773_at	myelin transcription factor 1	Myt1	-1.22	0.339	1.63	0.481	3.03	0.029	-1.22	0.406	1.85	0.438
1430988_at	RIKEN cDNA 2810407C02 gene	2810407C02Rik	1.8	0.676	2.49	0.121	3.04	0.000	1.58	0.792	2.16	0.161
1436566_at	Rab40b, member RAS oncogene family	Rab40b	1.59	0.160	-1.18	0.092	3.04	0.043	-1.06	0.643	1.14	0.321
1447144_at	RIKEN cDNA 9130011E15 gene	9130011E15Rik	-1.1	0.411	-1.12	0.368	3.05	0.045	3.61	0.061	1.74	0.774
1452993_at	RIKEN cDNA 5430416O09 gene	5430416O09Rik	1.27	0.727	1.63	0.748	3.06	0.002	-1.48	0.136	1.55	0.917
1444470_x_at	Bone morphogenetic protein 5	Bmp5	1.12	0.683	-1.14	0.374	3.1	0.041	1.39	0.949	-1.41	0.182
1453528_at	leukotriene A4 hydrolase	Lta4h	1.2	0.588	1.15	0.585	3.11	0.038	1.04	0.475	1.21	0.928
1422708_at	phosphoinositide-3-kinase, catalytic, gamma polypeptide	Pik3cg	-1.54	0.162	-1.64	0.148	3.13	0.011	2.36	0.049	1.7	0.483
1427554_at	helicase, mus308-like (Drosophila)	Hel308	3.24	0.105	2.46	0.183	3.15	0.033	1.34	0.044	-1.03	0.610
1421390_at	solute carrier family 12, member 1	Slc12a1	1.35	0.935	1.3	0.873	3.15	0.037	-1.07	0.433	1.51	0.354
1419014_at	Rhesus blood group-associated A glycoprotein	Rhag	1.41	0.770	3.34	0.133	3.17	0.001	1.51	0.787	3.28	0.341
1443541_at	Hypothetical gene supported by AK039231; AK039519; AK039710;	LOC381438	2.69	0.170	2.04	0.876	3.18	0.049	1.97	0.721	2.32	0.066
1452475_at	proprotein convertase subtilisin/kexin type 5	Pcsk5	-1.23	0.499	1.15	0.807	3.2	0.022	1.46	0.436	1.48	0.973
1438437_a_at	RIKEN cDNA 4933439C10 gene	4933439C10Rik	1.21	0.681	1.58	0.270	3.21	0.016	2.54	0.118	1.4	0.899
1423619_at	RAS, dexamethasone-induced 1	Rasd1	-1.01	0.706	1.35	0.403	3.22	0.025	1.95	0.288	1.27	0.542
1455632_at	Guanine nucleotide binding protein, beta 5	Gnb5	2.65	0.795	1.32	0.953	3.24	0.048	1.42	0.439	1.35	0.205
1448982_at	kallikrein 6	Klk6	1.57	0.863	1.05	0.674	3.28	0.003	1.81	0.201	3.12	0.269
1456265_at	hypothetical protein LOC624866	LOC624866	1	0.585	-1.18	0.396	3.28	0.046	-1.02	0.882	1.64	0.300
1449881_a_at	calcium-sensing receptor	Casr	-1.14	0.464	1.06	0.752	3.29	0.009	1.6	0.143	-1.18	0.237
1424553_at	Gup1, glycerol uptake/transporter homolog (yeast)	Gup1	1.1	0.731	-1.65	0.292	3.29	0.039	-1.45	0.263	1.5	0.832
1454396_at	RIKEN cDNA 4632409D06 gene	4632409D06Rik	1.14	0.996	1.85	0.194	3.3	0.043	1.93	0.164	1.26	0.783
1444770_at	RIKEN cDNA 1700095A13 gene	1700095A13Rik	-1.43	0.289	1.43	0.697	3.31	0.025	-1.92	0.144	1.35	0.455
1433791_at	RAB9B, member RAS oncogene family	Rab9b	-1.01	0.373	1.82	0.620	3.31	0.023	1.72	0.502	1.67	0.824
1457158_at	RIKEN cDNA 0610039J04 gene	0610039J04Rik	1.54	0.632	-1.33	0.276	3.35	0.025	2.8	0.075	1.58	0.003
1431260_at	RIKEN cDNA 4833417C18 gene	4833417C18Rik	1.25	0.979	1.63	0.671	3.36	0.045	-1.76	0.123	-1.14	0.385
1424354_at	RIKEN cDNA 1110007F12 gene	1110007F12Rik	3.47	0.083	4.84	0.191	3.42	0.001	1.34	0.865	1.63	0.144
1424303_at	DEP domain containing 7	Depdc7	1.07	0.576	1.07	0.288	3.42	0.033	1.98	0.020	2.96	0.026
1435061_at	nudix (nucleoside diphosphate linked moiety X)-type motif 10	Nudt10	2.11	0.491	1.46	0.480	3.42	0.011	-1.5	0.173	1.14	0.383
1452815_at	purinergic receptor P2Y, G-protein coupled 10	P2ry10	1.19	0.796	1.19	0.787	3.42	0.002	1.85	0.262	-1.07	0.598
1422300_at	noggin	Nog	2.78	0.120	3.18	0.178	3.43	0.002	1.25	0.103	1	0.950
1425083_at	otoraplin	Otor	2.51	0.488	2.25	0.039	3.43	0.020	1.02	0.261	1.19	0.957
1440005_at	hypothetical protein C730009D12	C730009D12	1.17	0.603	1.69	0.797	3.44	0.016	1.37	0.393	-1.22	0.346
1456178_at	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus	Bambi-ps1	2.55	0.349	2.41	0.014	3.5	0.008	1.67	0.965	2.08	0.379
1453884_at	RIKEN cDNA 4930402K13 gene	4930402K13Rik	1.17	0.515	1.97	0.332	3.51	0.032	2.34	0.276	1.46	0.114
1424450_at	G protein-coupled receptor, family C, group 5, member C	Gprc5c	1.62	0.362	1.23	0.449	3.53	0.010	-1.25	0.288	1.34	0.919
1444029_at	poly (ADP-ribose) polymerase family, member 11	Parp11	1.97	0.095	1.09	0.831	3.54	0.018	-2.2	0.035	-1.28	0.355
1460139_at	expressed sequence C79256	C79256	1.83	0.703	1.93	0.636	3.56	0.027	1.72	0.650	1.58	0.961
1459272_at	Pellino 1	Peli1	1.8	0.258	2.11	0.076	3.56	0.041	1.72	0.319	1.55	0.618
1440828_x_at	PHD finger protein 7	Phf7	1.39	0.797	2.52	0.409	3.58	0.012	1.65	0.771	1.99	0.836
1420590_at	hyaluronan synthase1	Has1	1.1	0.655	1.57	0.642	3.64	0.033	1.48	0.498	-1.46	0.235
1416097_at	leucine rich repeat containing 4	Lrrc4	1.17	0.856	2.74	0.439	3.68	0.041	2.06	0.863	1.3	0.834
1423469_at	RIKEN cDNA 1700129C05 gene	1700129C05Rik	2.23	0.301	2.03	0.403	3.69	0.009	1.04	0.965	1.13	0.779

1454098_at	olfactory receptor 112	Olfr112	1.26	0.692	-1.12	0.581	3.71	0.044	1.78	0.938	-1.47	0.172
1449424_at	pleckstrin 2	Plek2	1.02	0.927	1.07	0.968	3.73	0.042	-1.71	0.063	-1.24	0.267
1418619_at	intercellular adhesion molecule 5, telencephalin	Icam5	1.55	0.730	2.6	0.144	3.75	0.034	1.61	0.517	4.1	0.014
1433172_at	RIKEN cDNA 3110049I03 gene	3110049I03Rik	2.27	0.656	2.19	0.701	3.78	0.014	1.49	0.811	-1.35	0.149
1440475_at	expressed sequence AW011738	AW011738	-1.18	0.229	1.84	0.898	3.79	0.015	2.46	0.164	1.02	0.511
1451260_at	aldehyde dehydrogenase 1 family, member B1	Aldh1b1	3.62	0.095	2.65	0.198	3.83	0.006	1.27	0.380	1.39	0.743
1454660_at	RIKEN cDNA 1100001E04 gene	1100001E04Rik	2.3	0.239	-1.29	0.247	3.89	0.049	1.36	0.242	-1.16	0.451
1444207_at	Camello-like 3	Cml3	1.54	0.662	1.44	0.561	3.94	0.033	1.15	0.861	1.87	0.283
1447811_s_at	adhesion molecule with Ig like domain 1	Amigo1	2.2	0.480	2.38	0.618	4.11	0.046	2.06	0.468	1.08	0.310
1432166_at	RIKEN cDNA E130018N17 gene	E130018N17Rik	1.05	0.735	1.43	0.675	4.17	0.019	2.57	0.218	1.47	0.493
1442325_at	TBC1 domain family, member 24	Tbc1d24	1.62	0.397	2.13	0.708	4.71	0.015	1.19	0.715	2.69	0.111
1423497_at	kelch-like 10 (Drosophila)	Klhl10	-1.1	0.373	2.59	0.157	5.64	0.034	1.73	0.280	1.37	0.343

Supplementary table 4. List of significant expression profiles of CSB cells irradiated with 0.6J/m2 of UV (gray color) as compared to non-irradiated CSB cells

code	Gene Title	Symbol	WT_0.6J/m2	p	WT_4J/m2	p	XPA_0.6J/m2	p	CSB_0.6J/m2	p	DKO_0.6J/m2	p
1430941_at	Bardet-Biedl syndrome 7	Bbs7	1.06	0.539	1.51	0.318	1.64	0.346	-3.92	0.005	2.44	0.162
1459256_at	Neuropilin 2	Nrp2	1.13	0.470	-1.16	0.289	-1.45	0.098	-3.73	0.039	1.01	0.523
1442703_at	cDNA sequence AK220484	AK220484	1.83	0.466	1.17	0.247	1.24	0.887	-3.66	0.016	2.04	0.144
1425992_at	solute carrier family 6, member 5	Slc6a5	1.72	0.805	1.81	0.944	1.78	0.100	-3.66	0.002	2.25	0.515
1449794_x_at	Cathepsin F	Ctsf	-1.28	0.336	-1.03	0.445	1.16	0.295	-3.58	0.050	-3.13	0.036
1431156_at	RIKEN cDNA 9430040K09 gene	9430040K09Rik	2.53	0.597	1.23	0.360	-2.37	0.058	-3.51	0.003	-2.28	0.069
1438861_at	basonuclin 2	Bnc2	-1.43	0.148	-8.88	0.007	-2.42	0.029	-3.5	0.001	-4.02	0.002
1432170_at	Ts translation elongation factor, mitochondrial	Tsfm	1.04	0.471	1.46	0.593	-1.03	0.352	-3.46	0.021	1.36	0.903
1416302_at	early B-cell factor 1	Ebf1	2.21	0.743	-1.95	0.072	-3.29	0.002	-3.45	0.000	-3.44	0.006
1448600_s_at	vav 3 oncogene	Vav3	1.42	0.896	1.86	0.969	1.31	0.501	-3.4	0.003	-1.03	0.498
1441416_at	inositol polyphosphate-4-phosphatase, type II	Inpp4b	1.38	0.500	1.4	0.535	1.5	0.762	-3.39	0.022	-1.06	0.622
1432711_at	RIKEN cDNA 4933425M03 gene	4933425M03Rik	3.56	0.169	2.69	0.328	1.06	0.347	-3.36	0.012	-1.58	0.058
1417498_at	serine (or cysteine) peptidase inhibitor, clade F, member 2	Serpinf2	1.39	0.735	-1.19	0.411	3.35	0.629	-3.28	0.003	1.23	0.476
1423530_at	serine/threonine kinase 32C	Stk32c	2.77	0.742	1.84	0.884	1.1	0.751	-3.17	0.000	1.72	0.693
1431785_at	ribonuclease T2	Rnaset2	-1.16	0.622	1.03	0.850	1.24	0.718	-3.13	0.021	1.86	0.979
1444646_at	RIKEN cDNA 8430420F16 gene	8430420F16Rik	-1.05	0.484	-2.32	0.067	-2.75	0.064	-3.12	0.008	-2.07	0.132
1460535_at	golgi autoantigen, golgin subfamily b, macrogolgin 1	Golgb1	1.58	0.405	1.64	0.116	1.47	0.675	-3.09	0.004	-1.14	0.331
1438294_at	ataxin 1	Atxn1	1	0.863	-5.21	0.001	-2.99	0.004	-3.03	0.001	-3.85	0.010
1455256_at	TRAF2 and NCK interacting kinase	Tnik	-1.48	0.160	-3.74	0.050	-1.76	0.160	-3.01	0.002	-2.29	0.029
1458983_at	expressed sequence AU015559	AU015559	1.38	0.736	2.16	0.742	1.76	0.258	-2.99	0.029	-1.61	0.105
1442373_at	RIKEN cDNA 2610203C20 gene	2610203C20Rik	1.13	0.980	1.44	0.736	1.4	0.654	-2.98	0.031	-1.04	0.246
1425538_x_at	CEA-related cell adhesion molecule 1	Ceacam1	1.67	0.315	1.54	0.249	-1.09	0.424	-2.97	0.002	2.14	0.923
1450696_at	proteosome subunit, beta type 9	Psmb9	-1.35	0.401	-1.25	0.112	1.42	0.670	-2.97	0.001	-1.76	0.207
1447405_at	Expressed sequence AI449023	AI449023	-1.34	0.290	1.31	0.969	1.4	0.857	-2.94	0.012	2.18	0.423
1422306_at	lipocalin 3	Lcn3	1.1	0.670	-1.37	0.356	1.94	0.862	-2.92	0.042	2.39	0.372
1451893_s_at	membrane associated guanylate kinase	Magi1	-1.72	0.219	-4.1	0.103	-1.16	0.197	-2.92	0.005	-2.04	0.005
1441545_at	RIKEN cDNA 9230115F04 gene	9230115F04Rik	2.44	0.537	2.58	0.302	-1.05	0.655	-2.91	0.014	1.11	0.452
1430142_at	transglutaminase 5	Tgm5	-1.31	0.154	1.81	0.487	1.31	0.969	-2.88	0.019	1.02	0.630
1436799_at	RIKEN cDNA D230005D02 gene	D230005D02Rik	-1.63	0.145	-1.5	0.240	-1.83	0.143	-2.81	0.020	-1.49	0.120
1417436_at	like-glycosyltransferase	Large	1.72	0.830	1.09	0.853	1.31	0.532	-2.81	0.026	-1.2	0.408
1438337_x_at	RIKEN cDNA 9930032O22 gene	9930032O22Rik	-1.24	0.147	-1.13	0.362	1.62	0.686	-2.76	0.032	-1.02	0.485
1440265_at	Jun proto-oncogene related gene d1	Jund1	1.4	0.694	2.01	0.555	1.14	0.316	-2.76	0.018	-1.07	0.830
1434102_at	nuclear factor I/B	Nfib	-1.04	0.524	-1.38	0.300	-1.03	0.807	-2.75	0.013	1.66	0.702
1458995_at	Expressed sequence AA408296	AA408296	1.04	0.875	1.37	0.282	1.5	0.707	-2.72	0.021	2.73	0.200
1426150_at	GIPC PDZ domain containing family, member 3	Gipc3	1.89	0.919	1.11	0.548	-1	0.984	-2.71	0.031	-1.86	0.112
1456423_at	methyl-CpG binding domain protein 5	Mbd5	-1.34	0.162	-6.08	0.005	-2.29	0.026	-2.69	0.001	-2.88	0.005
1430707_s_at	RIKEN cDNA 1700081D17 gene	1700081D17Rik	1.69	0.048	-1.01	0.759	1.03	0.915	-2.66	0.002	1.88	0.264
1442782_at	Kelch-like 8 (Drosophila)	Klhl8	1.05	0.917	1.39	0.098	1.22	0.610	-2.64	0.006	2.12	0.349
1431867_a_at	RIKEN cDNA 1700007B13 gene	1700007B13Rik	1.18	0.569	1.11	0.389	1.16	0.706	-2.63	0.038	-1.2	0.420
1440161_at	Matrix metallopeptidase 16	Mmp16	1.53	0.953	1.14	0.638	1.55	0.660	-2.63	0.023	1.14	0.850
1448312_at	proprotein convertase subtilisin/kexin type 2	Pcsk2	1.1	0.431	-1.8	0.167	-1.23	0.483	-2.63	0.003	1.51	0.286
1459304_at	RIKEN cDNA A730054J21 gene	A730054J21Rik	1.03	0.545	-1.34	0.232	-1.67	0.053	-2.61	0.009	-1.15	0.485
1452342_at	amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	-1.24	0.242	-4.81	0.045	-2.12	0.007	-2.59	0.000	-2.8	0.010
1450094_at	RAN binding protein 17	Ranbp17	-1.28	0.388	-3.11	0.070	1.65	0.947	-2.59	0.026	1.78	0.476
1429969_at	RIKEN cDNA 4833403J16 gene	4833403J16Rik	1.77	0.764	1.71	0.204	1.41	0.692	-2.58	0.050	1.47	0.594
1424625_a_at	DENN/MADD domain containing 1A	Dennd1a	-1.06	0.474	-2.94	0.002	-1.95	0.016	-2.58	0.012	-2.85	0.032
1447523_at	Zinc finger protein 294	Zfp294	1.68	0.705	-2.41	0.175	2.96	0.472	-2.57	0.004	2.33	0.318
1454421_at	RIKEN cDNA 4930423D22 gene	4930423D22Rik	1.23	0.518	1.71	0.036	-1.45	0.241	-2.56	0.001	-1.09	0.384
1439397_at	formin 1	Fmn1	-1.32	0.348	-4.27	0.117	-1.6	0.001	-2.56	0.002	-2.54	0.000
1441254_at	RIKEN cDNA 1810008K04 gene	1810008K04Rik	-2.45	0.202	-2.13	0.271	-2.14	0.070	-2.54	0.031	-1.82	0.066
1433335_at	RIKEN cDNA 4930405G09 gene	4930405G09Rik	1.26	0.768	1.7	0.568	2.47	0.348	-2.54	0.006	1.8	0.020
1457924_at	muscleblind-like 1 (Drosophila)	Mbnl1	1.46	0.565	2.23	0.989	1.1	0.562	-2.53	0.006	-1.3	0.319
1438975_x_at	zinc finger, DHHC domain containing 14	Zdhhc14	-1.61	0.294	-5.72	0.178	-1.91	0.032	-2.53	0.001	-2.16	0.055

1431458_at	RIKEN cDNA 4921507L20 gene	4921507L20Rik	-1.56	0.023	-1.11	0.487	1.3	0.406	-2.52	0.017	1.36	0.436
1440990_at	cDNA sequence BC056349	BC056349	-1.84	0.199	-4.12	0.094	-1.94	0.002	-2.52	0.009	-2.07	0.013
1449926_at	tumor necrosis factor (ligand) superfamily, member 7	Tnfsf7	1.18	0.939	1.32	0.158	-1.32	0.300	-2.51	0.019	1.46	0.194
1430321_at	RIKEN cDNA A930040G15 gene	A930040G15Rik	1.76	0.773	1.22	0.792	2.55	0.040	-2.5	0.018	1.28	0.656
1426116_at	ankyrin repeat and SOCS box-containing 18	Asb18	-1.21	0.360	-1.1	0.439	1.03	0.948	-2.5	0.030	-1.22	0.097
1453232_at	calreticulin 3	Calr3	-2.26	0.016	-1.39	0.128	2.14	0.951	-2.49	0.033	1.06	0.946
1443076_at	RIKEN cDNA D030041N04 gene	D030041N04Rik	1.31	0.563	1.5	0.748	-1.08	0.451	-2.49	0.035	1.3	0.857
1457275_at	desmuslin	Dmn	1.34	0.816	1.82	0.307	-1.66	0.327	-2.49	0.047	2.33	0.382
1447828_x_at	RIKEN cDNA 2310005P05 gene	2310005P05Rik	1.04	0.702	1.46	0.615	1.7	0.342	-2.48	0.033	1.73	0.849
1420166_at	Deoxynucleotidyltransferase, terminal	Dntt	-1.32	0.183	-1.51	0.241	1.37	0.178	-2.48	0.016	1.05	0.993
1455472_at	RIKEN cDNA A630071D13 gene	A630071D13Rik	-1.32	0.140	-1.42	0.183	1.74	0.201	-2.47	0.026	-1.36	0.302
1435286_at	expressed sequence AW125296	AW125296	1.6	0.438	2.57	0.351	1.77	0.912	-2.47	0.049	-1.07	0.347
1452819_at	latrophilin 3	Lphn3	1.12	0.926	1.83	0.169	1.21	0.779	-2.46	0.004	-1.33	0.281
1440619_at	mitogen activated protein kinase 8 interacting protein 1	Mapk8ip1	2.14	0.611	1.91	0.718	1.21	0.971	-2.46	0.038	1.8	0.691
1456572_x_at	chaperonin subunit 4 (delta)	Cct4	-1.25	0.311	-1.37	0.297	-1.27	0.107	-2.45	0.013	2.36	0.290
1459318_at	semaphorin 6D	Sema6d	-1.11	0.120	-1.31	0.277	-1.15	0.579	-2.45	0.006	-1.04	0.999
1432528_at	RIKEN cDNA 1700021P04 gene	1700021P04Rik	2.31	0.569	3.66	0.449	-1.33	0.206	-2.44	0.030	1.43	0.782
1457920_at	RIKEN cDNA C130026L21 gene	C130026L21Rik	1.52	0.923	-1.04	0.507	-1.34	0.349	-2.44	0.041	-1.01	0.488
1419060_at	granzyme B	Gzmb	-1.18	0.475	-1.87	0.084	-1.07	0.473	-2.44	0.018	-1.07	0.752
1421396_at	proprotein convertase subtilisin/kexin type 1	Pcsk1	1.79	0.729	1.38	0.475	-1.03	0.677	-2.44	0.019	1.08	0.981
1437751_at	peroxisome proliferative activated receptor, gamma, coactivator 1a	Ppargc1a	-1.11	0.383	-2.43	0.080	2.3	0.325	-2.44	0.019	2.12	0.327
1443014_at	RIKEN cDNA 4833403I15 gene	4833403I15Rik	2.34	0.353	1.19	0.913	-1.76	0.173	-2.43	0.034	1.36	0.858
1426033_at	regulator of G-protein signaling 9	Rgs9	2.22	0.774	3.22	0.526	-1.21	0.398	-2.42	0.003	1.03	0.907
1440519_at	trans-acting transcription factor 8	Sp8	1.39	0.575	1.21	0.591	1.13	0.384	-2.42	0.024	2.72	0.531
1431481_at	RIKEN cDNA 4930443O20 gene	4930443O20Rik	3.29	0.301	1.2	0.825	1.56	0.988	-2.41	0.045	1.5	0.467
1451614_a_at	amelogenin X chromosome	Amelx	-1.95	0.042	-1.51	0.167	-1.17	0.509	-2.41	0.014	1.6	0.954
1441739_at	Early B-cell factor 4	Ebf4	-1.02	0.770	1.45	0.399	1.08	0.685	-2.41	0.007	-1.1	0.660
1417730_at	exostoses (multiple) 1	Ext1	1.33	0.686	-1.75	0.098	-2.36	0.002	-2.41	0.001	-2.41	0.013
1428807_at	RIKEN cDNA 4932702K14 gene	4932702K14Rik	2.36	0.168	3.14	0.066	1.39	0.659	-2.39	0.032	1.15	0.942
1459114_at	Ankyrin repeat and SAM domain containing 1	Anks1	1.04	0.572	1.6	0.758	-1.58	0.238	-2.38	0.018	1.62	0.755
1433317_at	RIKEN cDNA 4930477O15 gene	4930477O15Rik	3.1	0.663	2.11	0.827	-1.91	0.069	-2.37	0.010	2.01	0.088
1444285_at	Mortality factor 4 like 1	Morf4l1	-1.08	0.628	-1.54	0.003	-1.91	0.096	-2.37	0.016	-2.07	0.062
1446701_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Abcb1b	2.11	0.134	1.59	0.255	1.98	0.137	-2.36	0.044	1.22	0.780
1447287_at	expressed sequence C77137	C77137	2.01	0.905	3.69	0.216	-1.27	0.290	-2.36	0.038	1.88	0.935
1420439_at	testis specific X-linked gene	Tsx	-1.02	0.911	-1.4	0.198	1.21	0.889	-2.36	0.014	-1.09	0.344
1460318_at	cysteine and glycine-rich protein 3	Csrp3	1.19	0.386	1.23	0.603	-1.12	0.349	-2.35	0.037	1.89	0.235
1419793_at	DNA segment, Chr 5, ERATO Doi 615, expressed	D5Ertd615e	-1.13	0.402	1.09	0.449	1.33	0.717	-2.35	0.047	1.53	0.759
1449992_at	protease, serine, 29	Prss29	2.27	0.741	1.78	0.660	1.56	0.482	-2.35	0.049	1.24	0.600
1432673_at	RIKEN cDNA 2300010F08 gene	2300010F08Rik	1.16	0.715	1.36	0.578	1.11	0.807	-2.34	0.048	1.57	0.598
1432401_a_at	RIKEN cDNA 4930511M11 gene	4930511M11Rik	2.31	0.338	1.47	0.545	1.86	0.820	-2.34	0.049	1.5	0.635
1417388_at	brain expressed X-linked 2	Bex2	1.24	0.736	1.1	0.557	2.3	0.233	-2.34	0.024	-1.25	0.334
1428459_at	PRAME family member 12	Pramef12	1.48	0.852	-1.37	0.207	1.73	0.973	-2.34	0.024	1.42	0.225
1421168_at	ATP-binding cassette, sub-family G (WHITE), member 3	Abcg3	-1.49	0.149	1.31	0.446	-1.02	0.874	-2.32	0.026	-1.19	0.370
1445224_at	Adaptor-related protein complex 3, beta 2 subunit	Ap3b2	2.25	0.320	3.09	0.066	1.27	0.887	-2.32	0.040	-1.3	0.367
1424234_s_at	mesenchyme homeobox 2	Meox2	-1.26	0.300	-2.02	0.059	2.18	0.331	-2.32	0.034	1.71	0.974
1446962_at	ATP-binding cassette, sub-family D (ALD), member 2	Abcd2	1.04	0.613	-1	0.448	1.02	0.683	-2.31	0.039	-1.65	0.190
1460313_at	olfactory receptor 2	Olfr2	1.04	0.649	-1.19	0.277	1.05	0.609	-2.31	0.003	2.53	0.037
1456074_at	orphan short chain dehydrogenase/reductase	Sdro	1.01	0.830	1.86	0.224	2.56	0.280	-2.31	0.032	1.87	0.612
1430567_at	serine peptidase inhibitor, Kazal type 5	Spink5	1.59	0.691	1.31	0.650	2.34	0.374	-2.31	0.005	1.17	0.647
1439086_at	RIKEN cDNA A930009L07 gene	A930009L07Rik	1.1	0.461	2.15	0.260	1.48	0.851	-2.3	0.029	1.35	0.786
1434785_at	calcium channel, voltage-dependent, gamma subunit 5	Cacng5	-1.05	0.484	-1.76	0.119	-1.24	0.250	-2.3	0.041	-1.17	0.470
1417795_at	cell adhesion molecule with homology to L1CAM	Chl1	1.76	0.387	1.44	0.867	2.75	0.006	-2.3	0.044	1.14	0.846
1452333_at	SWI/SNF related, matrix associated, actin dependent regulator of chrom	Smarca2	1.03	0.824	1.66	0.103	1.17	0.738	-2.3	0.002	1.05	0.850
1420020_at	suppressor of zeste 12 homolog (Drosophila)	Suz12	1.18	0.839	2.74	0.015	1.49	0.087	-2.29	0.023	1.84	0.416
1447604_at	cDNA sequence BC053393	BC053393	1.19	0.595	1.11	0.559	1.01	0.940	-2.28	0.045	-1.21	0.399
1457232_at	F-box and leucine-rich repeat protein 21	Fbxl21	1.38	0.744	1.08	0.565	1.35	0.849	-2.28	0.020	-1.41	0.313
1453975_a_at	RIKEN cDNA 1700029M20 gene	1700029M20Rik	1.76	0.447	1.57	0.938	-1.07	0.326	-2.26	0.003	1.55	0.538
1455979_at	AT rich interactive domain 1B (Swi1 like)	Arid1b	-1.36	0.229	-3.04	0.030	-1.49	0.017	-2.25	0.001	-2.03	0.009

1430797_at	exportin 4	Xpo4	2.2	0.140	2.54	0.014	1.4	0.823	-2.25	0.028	-1.59	0.048
1452860_at	F-box and leucine-rich repeat protein 17	Fbxl17	-1.28	0.074	-4.57	0.011	-1.87	0.000	-2.24	0.002	-2.52	0.000
1456220_at	F-box and leucine-rich repeat protein 7	Fbxl7	1	0.539	-6.34	0.021	-1.82	0.043	-2.23	0.000	-2.13	0.005
1438590_at	Rap guanine nucleotide exchange factor (GEF) 3	Rapgef3	-1.06	0.687	1.47	0.909	-1.47	0.078	-2.23	0.028	1.36	0.877
1424007_at	growth differentiation factor 10	Gdf10	1.38	0.727	1.46	0.048	1.35	0.433	-2.22	0.010	1.78	0.673
1432785_at	RIKEN cDNA A930028O11 gene	A930028O11Rik	1.78	0.812	1.44	0.731	1.16	0.960	-2.21	0.043	-2.3	0.054
1436047_at	gene model 672, (NCBI)	Gm672	-1.12	0.226	-2.63	0.015	-1.69	0.000	-2.21	0.001	-2.44	0.000
1423363_at	sortilin 1	Sort1	1.43	0.432	1.35	0.791	2.12	0.062	-2.21	0.032	1.05	0.830
1444029_at	poly (ADP-ribose) polymerase family, member 11	Parp11	1.97	0.095	1.09	0.831	3.54	0.018	-2.2	0.035	-1.28	0.355
1433076_at	RIKEN cDNA 5430402O13 gene	5430402O13Rik	-1.03	0.496	-1.39	0.279	2.58	0.090	-2.19	0.003	1.54	0.226
1455230_at	calcium channel, voltage-dependent, gamma subunit 4	Cacng4	1.15	0.852	-1.02	0.522	1.1	0.262	-2.19	0.011	1.22	0.469
1420437_at	indoleamine-pyrrole 2,3 dioxygenase	Indo	1.78	0.681	-1.02	0.518	-1.44	0.064	-2.19	0.030	1.6	0.630
1449314_at	zinc finger protein, multitype 2	Zfpm2	-1.07	0.482	-8.16	0.005	-2.11	0.007	-2.19	0.002	-2.66	0.026
1459998_at	zinc finger protein 407	Zfp407	1.05	0.681	-3.13	0.001	-1.74	0.002	-2.18	0.004	-2.23	0.012
1443624_at	CDNA sequence BC013481	BC013481	1.62	0.973	1.83	0.900	-1.08	0.292	-2.17	0.013	1.22	0.887
1437312_at	bone morphogenetic protein receptor, type 1B	Bmpr1b	1.56	0.907	-4.36	0.038	-1.48	0.160	-2.17	0.001	-1.75	0.017
1436515_at	RIKEN cDNA E030004N02 gene	E030004N02Rik	-1.01	0.682	-5.74	0.001	-1.46	0.218	-2.17	0.026	-2.54	0.032
1430341_at	nudix (nucleoside diphosphate linked moiety X)-type motif 5	Nudt5	2.53	0.057	1.9	0.625	2.65	0.926	-2.17	0.038	-1.22	0.553
1416702_at	serine (or cysteine) peptidase inhibitor, clade I, member 1	Serpini1	1.57	0.696	1.08	0.790	2.16	0.518	-2.17	0.014	-1.2	0.295
1456868_at	RIKEN cDNA 2900073G15 gene	2900073G15Rik	-2.28	0.031	-1.12	0.494	-1.09	0.671	-2.16	0.018	-1.34	0.157
1454353_at	RIKEN cDNA 4833420D23 gene	4833420D23Rik	1.03	0.744	1.75	0.296	1.29	0.927	-2.16	0.024	-1.47	0.215
1441014_at	Alpha thalassemia/mental retardation syndrome X-linked homolog (huma	Atrx	-1.39	0.284	-1.01	0.485	1.03	0.699	-2.16	0.010	-1.1	0.284
1456496_at	Death-associated kinase 3	Dapk3	1.43	0.813	-1.1	0.980	-1.08	0.425	-2.15	0.028	1.19	0.711
1454193_at	RIKEN cDNA 5430401H09 gene	5430401H09Rik	1.28	0.745	1.12	0.564	-1.1	0.517	-2.14	0.021	1.92	0.100
1459337_at	asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltra	Alg6	-2.01	0.091	-1.11	0.643	1.79	0.114	-2.13	0.016	1.94	0.270
1454372_at	CD80 antigen	Cd80	2.13	0.191	2.45	0.531	-1.02	0.945	-2.13	0.016	1.82	0.420
1455540_at	carbamoyl-phosphate synthetase 1	Cps1	-1.82	0.026	-2.72	0.068	1.27	0.432	-2.13	0.029	1.46	0.460
1450945_at	protein kinase C, alpha	Prkca	1.16	0.926	-2.39	0.042	-2.09	0.001	-2.13	0.001	-2.58	0.005
1420352_at	protease, serine, 22	Prss22	1.13	0.465	2.17	0.696	-1.05	0.726	-2.13	0.047	2.05	0.005
1437393_at	expressed sequence AI875142	AI875142	-1.31	0.125	-3.91	0.004	-2.18	0.001	-2.12	0.006	-2.46	0.005
1447114_x_at	RIKEN cDNA 4930414L22 gene	4930414L22Rik	1.22	0.516	1.9	0.241	2.91	0.724	-2.11	0.001	1.78	0.173
1444000_at	RIKEN cDNA B930059L03 gene	B930059L03Rik	1.24	0.662	-2.19	0.083	1.44	0.894	-2.11	0.005	1.57	0.744
1442279_at	Enhancer of polycomb homolog 1 (Drosophila)	Epc1	2.4	0.166	-1.07	0.402	1.4	0.980	-2.11	0.016	2.33	0.682
1444708_at	transmembrane protein 29	Tmem29	1.07	0.531	1.68	0.709	2.6	0.117	-2.11	0.020	-1.04	0.661
1452783_at	fibronectin type III domain containing 3B	Fndc3b	1.16	0.796	-1.44	0.119	-2.16	0.005	-2.1	0.000	-2.71	0.002
1432930_at	RIKEN cDNA 4930453O09 gene	4930453O09Rik	1.94	0.876	2.66	0.846	1.46	0.891	-2.09	0.020	2.4	0.039
1451147_x_at	cold shock domain containing C2, RNA binding	Csdc2	-1.37	0.258	1.64	0.706	1.36	0.816	-2.09	0.018	1.08	0.627
1430251_at	RIKEN cDNA D330022H12 gene	D330022H12Rik	-2.06	0.013	-1.29	0.352	1.28	0.429	-2.09	0.022	-1.61	0.192
1420785_at	growth factor receptor bound protein 2-associated protein 2	Gab2	1.41	0.237	1.13	0.899	-1.16	0.320	-2.09	0.017	1.28	0.506
1430484_at	RIKEN cDNA 8430428J23 gene	8430428J23Rik	2.75	0.137	1.54	0.467	3.01	0.559	-2.08	0.000	-1.09	0.327
1449290_at	dihydropyrimidinase-like 5	Dpysl5	2.63	0.239	2.49	0.404	1.62	0.421	-2.08	0.036	-1.52	0.135
1442919_at	SH3 and PX domains 2B	Sh3pxd2b	1.94	0.071	-1.18	0.365	1.55	0.613	-2.08	0.043	-1.36	0.361
1447931_at	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	Whsc1l1	1.1	0.135	-1.11	0.413	-1.74	0.016	-2.08	0.001	-1.91	0.002
1452343_at	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ertd653e	1.21	0.888	-1.57	0.124	-1.75	0.006	-2.07	0.045	-2.18	0.002
1435078_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	Tanc2	-1.36	0.114	-5.07	0.015	-1.43	0.071	-2.07	0.001	-2.12	0.002
1434571_at	vacuolar protein sorting 13B (yeast) /// similar to vacuolar protein sorting	Vps13b /// LOC6661	-1.03	0.556	-2.27	0.040	-1.87	0.009	-2.07	0.001	-2.24	0.019
1446313_at	zinc finger protein 30	Zfp30	1.53	0.692	1.96	0.897	-1.71	0.187	-2.07	0.039	1.17	0.971
1435059_at	development and differentiation enhancing	Ddef1	1.19	0.970	-1.45	0.158	-2.13	0.001	-2.06	0.003	-2.64	0.001
1419438_at	single-minded homolog 2 (Drosophila)	Sim2	-1.05	0.984	2.04	0.563	-1.79	0.065	-2.06	0.025	1.84	0.571
1429417_at	RIKEN cDNA 4833446K15 gene	4833446K15Rik	-1.34	0.062	-4.38	0.016	-1.62	0.080	-2.05	0.003	-2.67	0.001
1457690_at	kalirin, RhoGEF kinase	Kalrn	1	0.723	-1.57	0.241	-1.58	0.132	-2.05	0.025	1.1	0.327
1428509_at	myosin IE	Myo1e	1.14	0.661	-2.21	0.027	-1.76	0.006	-2.05	0.009	-2.04	0.005
1425288_at	sterile alpha motif domain containing 11	Samd11	-1.03	0.372	2.33	0.651	-1.04	0.536	-2.05	0.020	1.69	0.311
1440159_at	RIKEN cDNA 1700010B09 gene	1700010B09Rik	-1.03	0.972	-1.22	0.466	1.26	0.595	-2.04	0.007	-1.04	0.624
1434639_at	kelch repeat and BTB (POZ) domain containing 9	Kbtbd9	-1.15	0.176	-6.56	0.031	-1.84	0.006	-2.04	0.010	-1.98	0.107
1422974_at	5' nucleotidase, ecto	Nt5e	1.5	0.676	1.64	0.780	1.41	0.700	-2.04	0.035	1.17	0.774
1442451_at	Tetratricopeptide repeat domain 15	Ttc15	1.7	0.363	-1.52	0.090	-1.56	0.141	-2.04	0.036	1.24	0.709
1417798_at	RIKEN cDNA 1810019J16 gene	1810019J16Rik	-2.19	0.057	-1.19	0.457	-1.05	0.463	-2.03	0.001	-1.5	0.100

1423269_a_at	neural precursor cell expressed, developmentally down-regulated gene 4	Nedd4l	1.26	0.879	-2.06	0.051	-1.92	0.005	-2.03	0.000	-2.21	0.003
1455204_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-1.07	0.436	-3.71	0.010	-1.77	0.040	-2.02	0.012	-2.17	0.007
1422711_a_at	pregnancy upregulated non-ubiquitously expressed CaM kinase	Pnck	-1.17	0.413	-1.35	0.343	1.69	0.279	-2.02	0.012	1.33	0.585
1440065_at	Polymerase (RNA) II (DNA directed) polypeptide J	Polr2j	1.65	0.707	-1.13	0.328	1.96	0.711	-2.02	0.025	-1.06	0.838
1430351_at	spermatogenesis associated 18	Spata18	1.43	0.487	1.52	0.552	-1.65	0.047	-2.02	0.028	1.21	0.771
1457154_at	Membrane-associated ring finger (C3HC4) 6	6-Mar	-1.02	0.406	1.12	0.465	1	0.751	-2.01	0.007	1.15	0.229
1454500_at	RIKEN cDNA 6330419E04 gene	6330419E04Rik	-1.33	0.279	-1.27	0.313	1.12	0.407	-2.01	0.044	2.78	0.070
1442645_at	ATPase, Ca++ transporting, plasma membrane 3	Atp2b3	-1.33	0.248	1.07	0.810	-1.04	0.512	-2.01	0.004	1.1	0.675
1443157_at	GLIS family zinc finger 3	Glis3	1.67	0.344	1.32	0.410	1.03	0.940	-2.01	0.003	1.18	0.194
1456560_at	gene model 93, (NCBI)	Gm93	1.83	0.516	2.07	0.474	-2.38	0.035	-2.01	0.032	3.14	0.379
1437293_x_at	uronyl-2-sulfotransferase	Ust	2.3	0.302	1.22	0.866	-1.49	0.183	-2.01	0.048	-1.3	0.302
1433167_at	RIKEN cDNA 4930444E06 gene	4930444E06Rik	1.22	0.549	1.44	0.836	1.19	0.726	-2	0.015	1.29	0.997
1439670_at	RIKEN cDNA B020006M18 gene	B020006M18Rik	1.34	0.663	1.57	0.156	1.41	0.437	-2	0.031	-1.04	0.529
1428051_a_at	calcium channel, voltage-dependent, L type, alpha 1D subunit	Cacna1d	-1.05	0.543	1.01	0.757	-1.25	0.306	-2	0.011	1.27	0.173
1437989_at	phosphodiesterase 8B	Pde8b	2.05	0.471	1.65	0.485	-1.09	0.682	-2	0.041	-1.04	0.823
1432152_at	RIKEN cDNA 2610109H07 gene	2610109H07Rik	1.71	0.613	2.32	0.097	1.17	0.500	-1.99	0.037	-1.59	0.162
1460006_at	AT motif binding factor 1	Atbf1	-1.14	0.107	-1.9	0.002	-1.76	0.002	-1.99	0.000	-2.15	0.002
1440293_at	RIKEN cDNA C230081A13 gene	C230081A13Rik	1.77	0.841	1.54	0.866	-1.45	0.190	-1.99	0.030	-1.68	0.072
1456022_at	homeodomain interacting protein kinase 2	Hipk2	1.01	0.934	-1.81	0.048	-1.76	0.024	-1.99	0.001	-2.01	0.024
1457632_s_at	myeloid ecotropic viral integration site-related gene 1	Mrg1	-1.46	0.281	-3.35	0.131	-1.42	0.028	-1.99	0.015	-1.54	0.006
1453679_at	RIKEN cDNA 1700100I10 gene	1700100I10Rik	-1.28	0.255	1.48	0.902	1.82	0.789	-1.98	0.034	1.16	0.323
1432920_at	RIKEN cDNA 5330421C15 gene	5330421C15Rik	-1.58	0.145	-1.01	0.488	-1.13	0.424	-1.98	0.007	-1.91	0.076
1453580_at	RIKEN cDNA 5630401D24 gene	5630401D24Rik	-1.22	0.341	-1.1	0.456	1.28	0.611	-1.98	0.019	1.4	0.247
1440352_at	region containing RIKEN cDNA 1700028E10 gene; hypothetical protein	LOC625175	1.68	0.781	1.6	0.981	-1.3	0.243	-1.98	0.005	3.2	0.022
1454706_at	UV radiation resistance associated gene	Uvrag	-1.04	0.271	-1.95	0.005	-1.53	0.005	-1.98	0.004	-1.73	0.000
1430400_at	RIKEN cDNA 4930521A18 gene	4930521A18Rik	1.44	0.994	-2.51	0.128	1.03	0.497	-1.97	0.028	2.09	0.296
1449544_a_at	potassium voltage-gated channel, subfamily H (eag-related), member 2	Kcnh2	2.22	0.609	-1.02	0.744	-1.12	0.519	-1.97	0.044	-1.4	0.235
1436938_at	RNA binding motif, single stranded interacting protein	Rbms3	-1.51	0.261	-4.05	0.115	-2.3	0.013	-1.97	0.023	-2.67	0.026
1435389_at	RALBP1 associated Eps domain containing protein 2	Reps2	1.98	0.949	-1.22	0.400	-1.12	0.445	-1.97	0.045	1.16	0.879
1457156_at	TRH-degrading enzyme	Trhde	2.38	0.165	3.66	0.111	1.57	0.980	-1.97	0.049	-1.47	0.275
1445607_at	RIKEN cDNA 4833418A01 gene	4833418A01Rik	-1.34	0.174	1.62	0.443	-1.04	0.960	-1.96	0.011	1.44	0.941
1434683_at	Cut-like 1 (Drosophila)	Cutl1	-1.14	0.164	-2.09	0.007	-1.75	0.004	-1.96	0.003	-2.06	0.003
1451279_at	ELKS/RAB6-interacting/CAST family member 1	Erc1	-1.21	0.161	-2.67	0.006	-1.54	0.012	-1.96	0.011	-2.03	0.004
1441450_s_at	jumonji, AT rich interactive domain 1C (Rbp2 like)	Jarid1c	1.99	0.238	1.85	0.837	1.11	0.997	-1.96	0.040	1.41	0.895
1451804_a_at	leucine rich repeat containing 16	Lrrc16	1	0.759	-3.49	0.004	-1.37	0.018	-1.96	0.005	-1.71	0.014
1436765_at	par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	3.12	0.674	-1.6	0.101	-1.75	0.064	-1.96	0.006	-3.48	0.003
1438671_at	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), gamr	Ppp2r2c	1.11	0.844	-1.02	0.568	-1.38	0.089	-1.96	0.018	1.17	0.731
1451236_at	RAS-like, estrogen-regulated, growth-inhibitor	Rerg	1.06	0.977	-2.56	0.017	-1.41	0.126	-1.96	0.008	-1.55	0.087
1451998_at	taspase, threonine aspartase 1	Tasp1	-1.23	0.307	-2.72	0.119	-1.23	0.310	-1.96	0.007	-1.99	0.079
1456493_at	RIKEN cDNA 5031415C07 gene /// RIKEN cDNA 5830484A20 gene /// s	5031415C07Rik /// 5	-2.01	0.083	-1.17	0.327	1.32	0.950	-1.95	0.005	1.29	0.187
1453673_at	ATPase type 13A4	Atp13a4	1.54	0.582	1.53	0.249	-1.25	0.359	-1.95	0.020	-1.11	0.756
1445307_at	Autism susceptibility candidate 2	Auts2	1.66	0.531	1.91	0.467	1.12	0.715	-1.95	0.037	-1.95	0.058
1434769_at	BTB (POZ) domain containing 9	Btbd9	-1.34	0.267	-2.53	0.139	-1.32	0.049	-1.95	0.022	-1.67	0.034
1444706_at	RIKEN cDNA E430014L09 gene	E430014L09Rik	1.18	0.846	-1.03	0.542	-1.34	0.269	-1.95	0.047	-1.43	0.049
1449978_at	zinc finger protein 2, Y linked	Zfy2	1.67	0.996	-1.19	0.222	-1.31	0.330	-1.95	0.031	-1.21	0.141
1430106_at	RIKEN cDNA 1700126L10 gene	1700126L10Rik	1.72	0.744	1.23	0.514	2.16	0.632	-1.94	0.022	1.66	0.377
1453707_at	RIKEN cDNA 4930480G23 gene	4930480G23Rik	-1.05	0.667	-1.92	0.044	1.16	0.567	-1.94	0.047	2.04	0.291
1445111_at	Exocyst complex component 4	Exoc4	1.17	0.601	1.68	0.232	1.1	0.847	-1.94	0.045	-3.64	0.045
1460490_at	mitochondrial ribosomal protein L15	Mrpl15	1.93	0.420	1.72	0.186	-1.75	0.046	-1.94	0.025	-1.44	0.193
1418420_at	myogenic differentiation 1	Myod1	1.18	0.224	-1.62	0.010	1.21	0.936	-1.94	0.007	1.26	0.472
1458121_at	RIKEN cDNA A430107O13 gene	A430107O13Rik	1.97	0.234	2.44	0.012	1.29	0.107	-1.93	0.033	-1.13	0.541
1434880_at	ets variant gene 6 (TEL oncogene)	Etv6	1.08	0.579	-1.4	0.093	-1.66	0.003	-1.93	0.003	-2.34	0.001
1449199_at	mucin 1, transmembrane	Muc1	1.41	0.288	1.13	0.612	1.11	0.983	-1.93	0.012	1.03	0.806
1422592_at	catenin (cadherin associated protein), delta 2	Ctnnd2	-1.53	0.118	-1.97	0.134	-1.45	0.128	-1.92	0.004	-1.4	0.086
1448765_at	Fyn proto-oncogene	Fyn	-1.15	0.180	-2.22	0.004	-1.66	0.007	-1.92	0.000	-2.1	0.002
1422991_at	phosphatidylinositol 3-kinase catalytic delta polypeptide	Pik3cd	1.1	0.658	-1.02	0.517	1.08	0.588	-1.92	0.013	1.11	0.510
1434804_at	SEC15-like 2 (S. cerevisiae)	Sec15l2	-1.23	0.223	-3.11	0.051	-1.76	0.009	-1.92	0.002	-2.06	0.002
1458171_at	solute carrier organic anion transporter family, member 2b1	Slco2b1	1.12	0.804	1.27	0.569	-1.25	0.023	-1.92	0.031	-1.07	0.562

1424588_at	SLIT-ROBO Rho GTPase activating protein 3	Srgap3	-1.21	0.287	-3.26	0.022	-1.62	0.011	-1.92	0.002	-2.04	0.022
1448973_at	sulfotransferase family 1D, member 1	Sult1d1	1.64	0.332	1.36	0.397	1.84	0.087	-1.92	0.047	1.05	0.387
1449520_at	tetratricopeptide repeat domain 28	Ttc28	-1.28	0.065	-2.61	0.020	-1.74	0.010	-1.92	0.002	-2.11	0.036
1443783_x_at	Histocompatibility 2, class II antigen A, alpha	H2-Aa	-1.35	0.083	2.02	0.653	1.58	0.910	-1.91	0.000	1.56	0.501
1449351_s_at	platelet-derived growth factor, C polypeptide	Pdgfc	1.07	0.742	-1.92	0.015	-1.75	0.012	-1.91	0.007	-1.86	0.000
1458363_at	zinc finger, DHHC domain containing 17	Zdhhc17	1.93	0.290	1.1	0.952	1.4	0.363	-1.91	0.032	-1.99	0.111
1457879_at	RIKEN cDNA A230107O07 gene	A230107O07Rik	1.03	0.652	1.31	0.929	1.83	0.847	-1.9	0.022	1.34	0.686
1455358_at	Ataxin 2 binding protein 1	A2bp1	1.24	0.723	-1.44	0.255	-1.52	0.196	-1.9	0.030	-3.22	0.007
1426027_a_at	Rho GTPase activating protein 10	Arhgap10	4.61	0.736	1.98	0.336	-1.54	0.114	-1.9	0.000	-2.56	0.012
1457465_at	shroom family member 4	Shroom4	-1.04	0.665	-1.26	0.060	-1.34	0.060	-1.9	0.003	-1.52	0.012
1435930_at	zinc finger protein 291	Zfp291	-1.82	0.225	-3.26	0.140	-1.53	0.005	-1.9	0.019	-2.27	0.016
1455427_at	angiopoietin 4	Angpt4	-1.19	0.129	-1.35	0.406	1.31	0.883	-1.89	0.024	1.01	0.980
1429783_at	PDZ and LIM domain 5	Pdlim5	-1.3	0.170	-1.51	0.040	-1.84	0.005	-1.89	0.000	-1.95	0.046
1432505_at	RIKEN cDNA 1700009J07 gene	1700009J07Rik	-1.22	0.360	-1.18	0.380	-1.2	0.358	-1.88	0.016	1.05	0.708
1433193_at	RIKEN cDNA 4930433M22 gene	4930433M22Rik	-1.37	0.306	-1.32	0.333	1.76	0.866	-1.88	0.001	1.5	0.876
1439703_at	CD200 receptor 1	Cd200r1	1.26	0.802	1.2	0.739	1.36	0.975	-1.88	0.044	1.41	0.229
1426994_at	PH domain and leucine rich repeat protein phosphatase	Phlpp	1.01	0.795	-2.06	0.019	-1.62	0.001	-1.88	0.000	-2.1	0.001
1444553_at	Postmeiotic segregation increased 1 (S. cerevisiae)	Pms1	1.27	0.415	1.24	0.319	1.4	0.760	-1.88	0.011	-1.43	0.022
1436910_at	RAS protein activator like 2	Rasal2	1.04	0.327	-2.91	0.008	-1.78	0.017	-1.88	0.001	-1.98	0.002
1438332_at	solute carrier family 22 (organic anion transporter), member 6	Slc22a6	-1.53	0.279	1.04	0.642	2.61	0.216	-1.88	0.012	1.86	0.768
1444412_at	Absent in melanoma 1	Aim1	1.19	0.939	-1.96	0.096	1.57	0.596	-1.87	0.005	2.82	0.206
1457790_at	Ankyrin repeat and SOCS box-containing protein 3	Asb3	1.08	0.759	-3.48	0.023	-1.25	0.109	-1.87	0.024	1.11	0.627
1420560_at	cholinergic receptor, nicotinic, epsilon polypeptide	Chrne	1.53	0.443	1.58	0.919	2.14	0.475	-1.87	0.004	1.15	0.316
1457685_at	RIKEN cDNA D330034E10 gene	D330034E10Rik	1.33	0.907	1.03	0.907	1.05	0.979	-1.87	0.014	-1.49	0.303
1429841_at	multiple EGF-like-domains 10	Megf10	-1.66	0.022	-2.13	0.020	1.22	0.769	-1.87	0.023	-1.41	0.127
1430612_at	RIKEN cDNA 1810033B17 gene	1810033B17Rik	1.6	0.681	1.81	0.919	1.43	0.249	-1.86	0.029	1	0.865
1459515_at	RIKEN cDNA 2610037D02 gene	2610037D02Rik	2.8	0.256	2.18	0.256	1.45	0.802	-1.86	0.015	-1.13	0.228
1453613_at	RIKEN cDNA A130006I12 gene	A130006I12Rik	2.07	0.757	1.62	0.331	1.17	0.949	-1.86	0.030	1.51	0.637
1416846_a_at	PDZ domain containing RING finger 3	Pdzrn3	1.32	0.624	-1.43	0.178	-1.71	0.011	-1.86	0.006	-2.09	0.001
1445984_at	PFTAIRE protein kinase 1	Pftk1	1.7	0.228	2.44	0.540	-2.56	0.029	-1.86	0.033	2.49	0.956
1422541_at	protein tyrosine phosphatase, receptor type, M	Ptprm	-1.47	0.055	-3.24	0.022	-1.9	0.005	-1.86	0.004	-2.27	0.004
1438055_at	retinoic acid receptor responder (tazarotene induced) 1	Rarres1	-1.05	0.811	-1.26	0.402	1.19	0.493	-1.86	0.026	1.25	0.179
1455967_at	sorbin and SH3 domain containing 1	Sorbs1	1.06	0.775	-1.22	0.260	-1.77	0.144	-1.86	0.025	-2.19	0.067
1432495_at	SRY-box containing gene 7	Sox7	1.92	0.994	2.24	0.419	-2.08	0.138	-1.86	0.019	1.77	0.384
1452714_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	Tanc1	1.07	0.602	-1.79	0.011	-1.62	0.004	-1.86	0.009	-1.89	0.001
1442343_at	Thioredoxin domain containing 11	Txndc11	-1.09	0.400	2.34	0.399	1.73	0.160	-1.86	0.014	3.7	0.198
1459785_at	Zinc finger protein 383	Zfp383	2.18	0.636	3.01	0.214	1.81	0.851	-1.86	0.012	-1.55	0.208
1455422_x_at	septin 4	4-Sep	1.55	0.401	-1.11	0.807	1.5	0.629	-1.85	0.047	-1.2	0.370
1431110_at	RIKEN cDNA 5430431D22 gene	5430431D22Rik	-1.28	0.197	-4.34	0.012	-1.93	0.004	-1.85	0.023	-1.89	0.015
1451628_a_at	ankyrin 3, epithelial	Ank3	1.05	0.758	-1.36	0.208	-1.86	0.004	-1.84	0.016	-1.36	0.128
1417318_at	deleted in bladder cancer 1 (human)	Dbc1	-1.37	0.141	-3.6	0.020	-1.99	0.004	-1.84	0.008	-2.43	0.006
1460662_at	period homolog 3 (Drosophila)	Per3	-1.3	0.403	-1.47	0.243	-1.09	0.436	-1.84	0.016	1.48	0.747
1456816_at	Retinoic acid induced 17	Rai17	-1.11	0.422	1.08	0.443	1.4	0.119	-1.84	0.027	-1.13	0.295
1450343_at	vomeronasal 1 receptor, D1	V1rd1	1.12	0.533	1.56	0.195	1.57	0.024	-1.84	0.041	1.36	0.714
1439812_at	RIKEN cDNA 4930402H24 gene	4930402H24Rik	-1.26	0.120	1.02	0.898	2.09	0.261	-1.83	0.032	-1.09	0.569
1451872_a_at	neuralized-like homolog (Drosophila)	Neurl	1.36	0.249	1.73	0.898	1.61	0.807	-1.83	0.014	-1.29	0.280
1441708_at	sperm associated antigen 16	Spag16	1.13	0.781	-1.21	0.380	1.53	0.703	-1.83	0.045	1.17	0.734
1454546_at	RIKEN cDNA 4933403L11 gene	4933403L11Rik	1.69	0.695	1.16	0.587	-1.34	0.403	-1.82	0.002	-2.86	0.004
1429549_at	procollagen, type XXVII, alpha 1	Col27a1	1.16	0.272	-2.07	0.122	-1.06	0.420	-1.82	0.011	1.19	0.933
1443939_at	similar to C05G5.5 /// similar to C05G5.5 /// similar to C05G5.5	LOC230628 /// LOC	-1.29	0.188	-2.16	0.065	-1.58	0.014	-1.82	0.008	-1.21	0.201
1428517_at	WD repeat and FYVE domain containing 3	Wdfy3	-1.13	0.058	-1.62	0.025	-1.23	0.120	-1.82	0.006	-1.91	0.002
1450182_at	chloride channel Ka	Clcnka	-1.13	0.536	-1.29	0.139	2.4	0.202	-1.81	0.018	-2.08	0.076
1456467_s_at	nemo like kinase	Nlk	-1.47	0.310	-1.65	0.264	-1.37	0.054	-1.81	0.002	-1.36	0.087
1420784_at	sodium channel, voltage-gated, type XI, alpha	Scn11a	1.48	0.122	-1.24	0.243	1.38	0.079	-1.81	0.015	1.68	0.381
1441226_at	spondin 1, (f-spondin) extracellular matrix protein	Spon1	-2.14	0.114	-1.55	0.239	1.03	0.472	-1.81	0.006	-1.63	0.197
1450046_at	transmembrane protein 59	Tmem59	-1.13	0.455	1.45	0.596	1.7	0.077	-1.81	0.021	-1.37	0.084
1428493_at	RIKEN cDNA 2610511M17 gene /// similar to signal-induced proliferatior	2610511M17Rik /// l	-1.17	0.275	-1.74	0.005	-1.4	0.047	-1.8	0.005	-1.63	0.000
1447674_at	RIKEN cDNA 2900080J11 gene	2900080J11Rik	1.55	0.700	1.08	0.809	-1.28	0.161	-1.8	0.005	1.41	0.336

1454272_at	RIKEN cDNA 9630015K15 gene	9630015K15Rik	2.5	0.334	1.23	0.755	1.4	0.673	-1.8	0.036	2.64	0.120
1431953_at	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	Atp8a2	-1.76	0.137	-1.4	0.330	-1.27	0.462	-1.8	0.049	1.55	0.459
1449220_at	GTPase, IMAP family member 3	Gimap3	-1.42	0.218	-1.09	0.405	-1.18	0.216	-1.8	0.014	3.55	0.316
1430137_at	mitogen-activated protein kinase kinase kinase 13	Map3k13	-1.11	0.466	1.02	0.720	1.13	0.718	-1.8	0.032	-1.3	0.289
1452762_at	RIKEN cDNA 8430436O14 gene	8430436O14Rik	-1.6	0.141	-3.44	0.061	-2.18	0.007	-1.79	0.002	-2.17	0.036
1444401_at	Expressed sequence C80913	C80913	-1.17	0.374	1.19	0.611	1.48	0.574	-1.79	0.022	1.46	0.610
1426463_at	gephyrin	Gphn	-1.17	0.284	-4.1	0.010	-1.84	0.001	-1.79	0.007	-1.9	0.012
1435521_at	Musashi homolog 2 (Drosophila)	Msi2	-1.34	0.215	-2.68	0.004	-1.28	0.126	-1.79	0.023	-1.34	0.097
1441836_x_at	RIKEN cDNA 1700006H03 gene	1700006H03Rik	1.3	0.357	1.76	0.238	1	0.688	-1.78	0.040	-1.03	0.727
1429598_at	RIKEN cDNA 2310042D19 gene	2310042D19Rik	-2.59	0.055	-1.57	0.090	1.34	0.505	-1.78	0.036	1.05	0.861
1430900_at	RIKEN cDNA 4930430O22 gene	4930430O22Rik	-1.1	0.403	1.21	0.966	-1.09	0.527	-1.78	0.000	-1.65	0.074
1454056_at	RIKEN cDNA 9030407P20 gene	9030407P20Rik	1.42	0.534	1.38	0.541	-1.94	0.102	-1.78	0.036	1.05	0.912
1417867_at	complement factor D (adipsin)	Cfd	1.37	0.653	1.55	0.685	-1.33	0.163	-1.78	0.021	-1.27	0.394
1438451_at	Rho GTPase-activating protein	Grit	-1.11	0.393	-2.11	0.035	-1.54	0.034	-1.78	0.004	-2.06	0.013
1439354_at	region containing RIKEN cDNA 2310008H09 gene; RIKEN cDNA A2300	LOC668373 /// LOC	-1.12	0.510	1.25	0.254	-1.22	0.311	-1.78	0.028	1.26	0.544
1452878_at	protein kinase C, epsilon	Prkce	-1.75	0.015	-5.11	0.011	-1.19	0.204	-1.78	0.034	-1.69	0.021
1434406_at	SLIT-ROBO Rho GTPase activating protein 2	Srgap2	-1.24	0.295	-2.21	0.074	-1.42	0.003	-1.78	0.001	-1.67	0.008
1453631_at	syntaxin 8	Stx8	-1.19	0.085	1.13	0.567	-1.41	0.034	-1.78	0.025	-1.27	0.299
1439913_at	RIKEN cDNA 1810053B01 gene	1810053B01Rik	-1.19	0.413	-1.11	0.505	1.22	0.190	-1.77	0.001	1.29	0.942
1442620_at	RIKEN cDNA 4931420C21 gene	4931420C21Rik	1.58	0.841	-1.09	0.269	2.77	0.120	-1.77	0.017	-1.61	0.190
1433291_at	RIKEN cDNA C030045M22 gene	C030045M22Rik	-1.42	0.179	1.14	0.830	-1.1	0.427	-1.77	0.043	1.34	0.998
1445534_at	Filamin, beta	Flnb	-1.11	0.277	-1.51	0.033	-2.03	0.045	-1.77	0.006	-2.31	0.001
1456067_at	GLI-Kruppel family member GLI3	Gli3	-1.02	0.632	-2.15	0.005	-1.56	0.025	-1.77	0.019	-1.8	0.008
1455825_s_at	ligand of numb-protein X 1	Lnx1	2.73	0.210	1.53	0.149	1.13	0.782	-1.77	0.043	1.11	0.862
1426158_at	T-cell receptor beta, variable 13	Tcrb-V13	1.35	0.368	2.13	0.080	-1.12	0.532	-1.77	0.014	1.36	0.237
1443669_at	Zinc finger, FYVE domain containing 28	Zfyve28	-1.04	0.465	1.23	0.802	2.32	0.525	-1.77	0.029	1.01	0.836
1453471_at	RIKEN cDNA 4833421E05 gene	4833421E05Rik	1.7	0.939	1.52	0.521	2.01	0.120	-1.76	0.025	1.37	0.930
1432265_at	RIKEN cDNA 4930445B16 gene	4930445B16Rik	-1.41	0.226	-1.57	0.064	1.29	0.521	-1.76	0.022	-1.06	0.558
1457682_at	RIKEN cDNA 9030420J04 gene	9030420J04Rik	-1.07	0.466	-2.49	0.032	-1.49	0.127	-1.76	0.032	-1.55	0.064
1454985_at	RIKEN cDNA D030051N19 gene	D030051N19Rik	1.41	0.379	1.09	0.863	-1.38	0.001	-1.76	0.003	-2.14	0.004
1455729_at	guanine nucleotide binding protein, alpha q polypeptide	Gnaq	-1.26	0.287	-2.02	0.098	-1.47	0.017	-1.76	0.008	-1.79	0.009
1446699_at	jumonji domain containing 2A	Jmjd2a	2.33	0.238	2.62	0.134	-1.09	0.409	-1.76	0.022	-1.43	0.117
1450786_x_at	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like	LOC669660	1.02	0.849	-1.74	0.031	-1.77	0.021	-1.76	0.004	-1.84	0.009
1441099_at	Pleckstrin homology domain containing, family G (with RhoGef domain)	Plekhg3	-1.26	0.384	1.39	0.620	2.26	0.087	-1.76	0.037	-1.45	0.250
1430102_at	ring finger protein 148	Rnf148	-1.31	0.084	1.18	0.187	1.13	0.631	-1.76	0.024	1.27	0.645
1439306_at	Small optic lobes homolog (Drosophila)	Solh	1.95	0.466	2.11	0.197	-1.52	0.193	-1.76	0.027	1.51	0.116
1430940_at	RIKEN cDNA 3110045A19 gene	3110045A19Rik	1.95	0.406	1.63	0.918	-1.25	0.141	-1.75	0.040	-2.12	0.079
1455709_at	RIKEN cDNA 4930422I22 gene	4930422I22Rik	1.32	0.843	1.33	0.690	-1.57	0.239	-1.75	0.031	-1.53	0.028
1452244_at	RIKEN cDNA 6330406I15 gene	6330406I15Rik	1.2	0.638	1.03	0.731	-1.53	0.068	-1.75	0.010	-1.61	0.006
1419300_at	FMS-like tyrosine kinase 1	Flt1	-1.01	0.942	-2.89	0.010	-1.83	0.031	-1.75	0.000	1.02	0.703
1437147_at	gamma-aminobutyric acid (GABA-A) receptor, subunit gamma 2	Gabrg2	1.76	0.910	-1.19	0.317	1.4	0.861	-1.75	0.027	-1.01	0.984
1441168_at	Interleukin 1 receptor accessory protein-like 2	Il1rapl2	-1.06	0.691	1.31	0.329	4.16	0.106	-1.75	0.045	-1.27	0.394
1432862_at	NK2 transcription factor related, locus 4 (Drosophila)	Nkx2-4	1.01	0.840	1.22	0.599	1.79	0.403	-1.75	0.019	1.32	0.525
1420819_at	src-like adaptor	Sla	1.09	0.525	1.36	0.219	1.55	0.082	-1.75	0.026	1.17	0.570
1445198_at	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	Utx	-1.67	0.085	-1.44	0.307	-1.18	0.214	-1.75	0.015	-1.13	0.410
1429987_at	RIKEN cDNA 9930013L23 gene	9930013L23Rik	-1.29	0.007	-3.17	0.004	-2.03	0.006	-1.74	0.000	-2.44	0.008
1447623_s_at	RIKEN cDNA C130009A20 gene	C130009A20Rik	-1.64	0.226	-4.15	0.099	-1.49	0.029	-1.74	0.005	-1.69	0.008
1442526_at	expressed sequence C77681	C77681	-1.07	0.563	-1.51	0.269	1.09	0.985	-1.74	0.035	1.83	0.378
1436380_at	Cdc42 binding protein kinase alpha	Cdc42bpa	1.13	0.236	-1.53	0.039	-1.83	0.021	-1.74	0.005	-1.62	0.026
1423953_at	CDK5 regulatory subunit associated protein 1-like 1	Cdkal1	-1.2	0.092	-2.66	0.005	-1.95	0.005	-1.74	0.017	-2.14	0.019
1457222_at	cAMP responsive element binding protein 5	Creb5	1.32	0.851	1.19	0.645	-1.35	0.152	-1.74	0.038	-1.61	0.027
1458832_at	Growth hormone receptor	Ghr	-1.1	0.402	-1.45	0.008	-1.23	0.279	-1.74	0.016	-1.78	0.099
1440343_at	ribosomal protein S6 kinase, polypeptide 5	Rps6ka5	1.02	0.567	-1.2	0.403	1.15	0.026	-1.74	0.009	1.2	0.510
1452222_at	utrophin	Utrn	-1.22	0.149	-2.52	0.017	-1.94	0.006	-1.74	0.003	-2.28	0.007
1460537_at	RIKEN cDNA 9430085L16 gene	9430085L16Rik	1.65	0.532	-1.12	0.564	-1.57	0.140	-1.73	0.046	-1.75	0.102
1458307_at	RIKEN cDNA B230334C09 gene	B230334C09Rik	-2.16	0.036	1.33	0.458	-1.46	0.157	-1.73	0.016	2.26	0.712
1452265_at	CLIP associating protein 1	Clasp1	-1.09	0.202	-1.71	0.006	-1.56	0.014	-1.73	0.001	-1.96	0.000
1444955_at	DNA segment, Chr 6, ERATO Doi 469, expressed	D6Ertd469e	1.28	0.609	1.22	0.625	-1.52	0.198	-1.73	0.005	-1.16	0.709

1421978_at	glutamic acid decarboxylase 2	Gad2	-1.11	0.396	-1.1	0.364	1.7	0.952	-1.73	0.043	-1.45	0.160
1453917_at	interferon induced transmembrane protein 7	Ifitm7	-1.04	0.586	1.33	0.322	1.83	0.541	-1.73	0.005	1.24	0.981
1456927_at	microtubule associated serine/threonine kinase 2	Mast2	-1.51	0.227	-1.34	0.235	-1.81	0.004	-1.73	0.013	-1.47	0.131
1435234_at	nuclear receptor coactivator 2	Ncoa2	-1.13	0.235	-2.47	0.031	1.01	0.584	-1.73	0.014	-1.55	0.122
1459473_at	Prenyl (solanesyl) diphosphate synthase, subunit 2	Pdss2	1.09	0.406	-1.63	0.266	-1.63	0.085	-1.73	0.037	-1.45	0.147
1425794_at	polymerase (DNA directed), alpha 2	Pola2	1.28	0.806	1.18	0.806	-1.47	0.143	-1.73	0.012	2.27	0.138
1457548_at	A disintegrin-like and metallopeptidase (reprolysin type) with thrombospo	Adamts6	-1.11	0.473	-2.14	0.092	-1.69	0.107	-1.72	0.011	-2.45	0.007
1458322_x_at	RIKEN cDNA E230008N13 gene	E230008N13Rik	2.16	0.754	1.66	0.502	1.03	0.958	-1.72	0.003	-1.13	0.619
1423028_at	interferon alpha 2	Ifna2	2.95	0.499	2	0.250	1.3	0.870	-1.72	0.037	-1.42	0.428
1429063_s_at	kinesin family member 16B	Kif16b	-1.31	0.259	-6.74	0.022	-1.24	0.046	-1.72	0.000	-2.03	0.053
1436356_at	lectin, galactose binding, soluble 7	Lgals7	1.06	0.633	-1.74	0.003	-1.83	0.004	-1.72	0.001	-2.08	0.013
1452632_at	hypothetical protein LOC637741	LOC637741	-1.13	0.490	-1.68	0.188	1.87	0.187	-1.72	0.010	-1.18	0.186
1434298_at	zinc finger homeobox 1b	Zfhx1b	-1.29	0.077	-1.57	0.002	1.03	0.687	-1.72	0.026	-1.34	0.075
1432120_at	RIKEN cDNA 4921513D11 gene	4921513D11Rik	-1.18	0.467	1.13	0.878	2.36	0.825	-1.71	0.012	1.47	0.341
1428902_at	carbohydrate sulfotransferase 11	Chst11	-1.24	0.125	-3.04	0.005	-1.85	0.002	-1.71	0.004	-1.91	0.001
1419894_at	Similar to proteasome (prosome, macropain) subunit, beta type 7	MGC107702	-1.03	0.437	1.31	0.646	1.11	0.862	-1.71	0.000	-1.35	0.119
1447577_x_at	propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	-1.38	0.236	-1.29	0.186	-1.27	0.168	-1.71	0.045	-1.13	0.314
1456214_at	protocadherin 7	Pcdh7	1.03	0.603	-1.47	0.021	-1.81	0.015	-1.71	0.019	-2.25	0.150
1420786_a_at	RNA binding motif protein, Y chromosome, family 1, member A1	Rbmy1a1	1.4	0.519	-1.21	0.542	-1	0.693	-1.71	0.033	1.52	0.958
1434222_at	signal-induced proliferation-associated 1 like 1	Sipa1l1	1.05	0.438	-1.77	0.001	-1.76	0.006	-1.71	0.008	-1.87	0.001
1435404_at	dispatched homolog 2 (Drosophila)	Disp2	2.37	0.061	3.3	0.002	2.2	0.265	-1.7	0.033	1.21	0.473
1438623_x_at	ring-box 1	Rbx1	-1.78	0.071	-1.47	0.164	-1.43	0.194	-1.7	0.011	1.38	0.149
1422696_at	tweety homolog 1 (Drosophila)	Ttyh1	-1.32	0.284	1.56	0.345	-1.02	0.935	-1.7	0.012	1.71	0.474
1438944_at	RIKEN cDNA 1700007J24 gene	1700007J24Rik	-1.05	0.625	-1.1	0.397	1.03	0.422	-1.69	0.048	1.11	0.668
1432687_at	RIKEN cDNA 4833406M21 gene	4833406M21Rik	-1.4	0.300	1.35	0.375	1.08	0.971	-1.69	0.036	1.19	0.504
1454535_at	RIKEN cDNA A430110A21 gene	A430110A21Rik	-1.5	0.217	1.03	0.904	1.27	0.184	-1.69	0.013	1.2	0.273
1437919_at	B double prime 1, subunit of RNA polymerase III transcription initiation fa	Bdp1	2.63	0.708	3.99	0.326	-1.41	0.163	-1.69	0.004	-1.43	0.029
1427043_s_at	cytosolic ovarian carcinoma antigen 1	Cova1	-1.41	0.049	-2.99	0.005	-1.37	0.065	-1.69	0.008	-1.63	0.041
1459377_at	paralemmin 2	Palm2	-1.35	0.342	-1.06	0.480	-1.62	0.212	-1.69	0.031	-1.48	0.210
1422271_at	pancreatic polypeptide receptor 1	Ppyr1	-1.29	0.350	1.15	0.555	-1.02	0.882	-1.69	0.022	1.29	0.871
1423428_at	receptor tyrosine kinase-like orphan receptor 2	Ror2	-1.29	0.243	-1.85	0.089	-1.14	0.299	-1.69	0.016	-1.29	0.037
1436602_x_at	calcium channel, voltage-dependent, N type, alpha 1B subunit	Cacna1b	1.82	0.732	-1.03	0.792	-2.82	0.048	-1.68	0.033	1.21	0.737
1434705_at	C-terminal binding protein 2 /// zinc finger, RAN-binding domain containin	Ctbp2 /// Zranb1	1.12	0.159	-1.13	0.339	-1.44	0.006	-1.68	0.000	-1.43	0.005
1434582_at	DNA segment, Chr 14, ERATO Doi 171, expressed	D14Ertd171e	-2.2	0.031	-3.44	0.041	-2.08	0.048	-1.68	0.048	-2.95	0.032
1417321_at	DNA segment, Chr 4, Wayne State University 132, expressed	D4Wsu132e	-1.22	0.383	-1.41	0.301	-1.24	0.025	-1.68	0.012	-1.81	0.019
1450768_at	discs, large homolog 1 (Drosophila)	Dlgh1	1.22	0.982	-1.55	0.096	-1.77	0.007	-1.68	0.005	-2.35	0.001
1435888_at	epidermal growth factor receptor	Egfr	-1.14	0.236	-1.8	0.024	-1.44	0.025	-1.68	0.006	-1.68	0.015
1434260_at	FCH and double SH3 domains 2	Fchsd2	-1.03	0.511	-1.63	0.031	-1.32	0.011	-1.68	0.000	-1.35	0.005
1437318_at	p21 (CDKN1A)-activated kinase 3	Pak3	-1.1	0.414	-3.06	0.036	-1.46	0.017	-1.68	0.009	-2.02	0.064
1437617_x_at	RIKEN cDNA 1110034G24 gene	1110034G24Rik	1.03	0.618	1.32	0.860	1.45	0.007	-1.67	0.016	1.36	0.019
1433453_a_at	ankyrin repeat and BTB (POZ) domain containing 2	Abtb2	-1.63	0.222	-3.36	0.105	-1.01	0.768	-1.67	0.005	-1.28	0.040
1455125_at	centaurin, beta 1	Centb1	1.6	0.994	-1.83	0.192	1.36	0.929	-1.67	0.047	3.66	0.324
1459704_at	DnaJ (Hsp40) homolog, subfamily C, member 7	Dnajc7	1.27	0.724	-1.2	0.348	-1.19	0.391	-1.67	0.021	-1.18	0.342
1424704_at	runt related transcription factor 2	Runx2	-1.11	0.370	-1.67	0.017	-1.44	0.001	-1.67	0.007	-1.65	0.016
1453583_at	zinc finger, ZZ-type with EF hand domain 1	Zzef1	-1.22	0.282	-1.33	0.313	-1.37	0.066	-1.67	0.001	-2.05	0.028
1435672_at	hypothetical protein 3830612M24	3830612M24	-1.16	0.404	-3.21	0.142	-1.32	0.001	-1.66	0.002	-1.43	0.104
1431638_at	RIKEN cDNA 4930592A05 gene	4930592A05Rik	-1.04	0.566	2.33	0.480	2.31	0.632	-1.66	0.041	1.92	0.145
1434856_at	ankyrin repeat domain 44	Ankrd44	1.15	0.495	-2.6	0.061	1.02	0.616	-1.66	0.011	-1.64	0.041
1449486_at	carboxylesterase 1	Ces1	-3.07	0.114	-2.25	0.076	-1.53	0.159	-1.66	0.031	2.27	0.728
1452253_at	cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	-1.29	0.150	-1.84	0.005	-1.44	0.102	-1.66	0.036	-1.07	0.751
1450781_at	high mobility group AT-hook 2	Hmga2	1.1	0.952	-1.72	0.056	-1.85	0.000	-1.66	0.007	-1.99	0.003
1434418_at	longevity assurance homolog 6 (S. cerevisiae)	Lass6	-1.22	0.024	-2.06	0.010	-1.58	0.020	-1.66	0.006	-1.87	0.015
1439198_at	PTK2 protein tyrosine kinase 2	Ptk2	-1.34	0.200	-1.13	0.349	2.16	0.837	-1.66	0.000	-1.51	0.070
1444689_at	WD repeat domain 67	Wdr67	1.54	0.637	-1	0.485	1.04	0.793	-1.66	0.041	1.33	0.118
1430459_at	RIKEN cDNA 4632428C04 gene	4632428C04Rik	1.18	0.965	-1.62	0.129	2.36	0.160	-1.65	0.037	1.11	0.510
1439066_at	angiopoietin 1	Angpt1	-1.1	0.545	-1.49	0.291	1.39	0.910	-1.65	0.036	-1.1	0.376
1455244_at	dishevelled associated activator of morphogenesis 1	Daam1	1.25	0.378	-1.32	0.171	-1.37	0.015	-1.65	0.002	-1.65	0.000
1445705_x_at	dipeptidylpeptidase 8	Dpp8	1.77	0.891	1	0.437	-1.35	0.227	-1.65	0.034	1.82	0.847

1416242_at	kelch-like 13 (Drosophila)	Klhl13	-1.43	0.057	-1.02	0.640	1.61	0.705	-1.65	0.024	2.37	0.608
1454969_at	LY6/PLAUR domain containing 6	Lypd6	1.05	0.651	-1.48	0.238	-1.4	0.141	-1.65	0.049	1.15	0.154
1452251_at	neurobeachin	Nbea	-1.44	0.152	-2.77	0.058	-1.57	0.024	-1.65	0.017	-2.22	0.014
1457276_at	SNF1-like kinase 2	Snf1lk2	1.03	0.801	-1.09	0.370	-1.2	0.218	-1.65	0.015	1.05	0.843
1450420_at	stromal antigen 1	Stag1	3.08	0.736	1.18	0.120	-1.44	0.066	-1.65	0.022	-1.82	0.019
1453024_at	WD repeat domain 37	Wdr37	-1	0.578	-1.16	0.366	-1.09	0.369	-1.65	0.004	-1.54	0.055
1447839_x_at	adrenomedullin	Adm	-1.45	0.226	-2.47	0.068	-1.57	0.012	-1.64	0.000	-1.95	0.008
1457425_at	RIKEN cDNA C130038G02 gene	C130038G02Rik	-1.82	0.090	-1.58	0.044	-1.16	0.421	-1.64	0.018	1.16	0.525
1455599_at	glucose-fructose oxidoreductase domain containing 1	Gfod1	-1.31	0.175	-1.73	0.128	-1.23	0.127	-1.64	0.038	-1.17	0.179
1431687_at	glia maturation factor, beta	Gmfb	-1.05	0.899	-1.84	0.098	-1.1	0.415	-1.64	0.005	1.62	0.906
1450723_at	ISL1 transcription factor, LIM/homeodomain	Isl1	1.22	0.601	1.19	0.726	2.55	0.216	-1.64	0.038	1.02	0.917
1422698_s_at	jumonji, AT rich interactive domain 2	Jarid2	1.11	0.755	-2.04	0.009	-1.58	0.007	-1.64	0.018	-1.7	0.034
1451255_at	lipolysis stimulated lipoprotein receptor	Lsr	2.58	0.253	1.85	0.314	1.6	0.438	-1.64	0.021	1.32	0.877
1459912_at	mitogen-activated protein kinase kinase kinase kinase 4	Map4k4	-1.1	0.452	-1.56	0.249	1.26	0.739	-1.64	0.014	-1.14	0.660
1459828_at	Serine/arginine repetitive matrix 1	Srrm1	1.45	0.995	1.66	0.409	1.78	0.015	-1.64	0.022	-1.16	0.326
1434603_at	thyroid hormone receptor associated protein 2	Thrap2	1.03	0.170	-1.49	0.000	-1.55	0.024	-1.64	0.014	-2.04	0.025
1429112_at	talin 2 /// similar to talin 2	Tln2 /// LOC639214	1.28	0.804	-1.44	0.183	-1.87	0.185	-1.64	0.019	-1.19	0.362
1431988_at	RIKEN cDNA 1700112E06 gene	1700112E06Rik	2.79	0.785	4.46	0.545	1.16	0.557	-1.63	0.033	1.04	0.795
1436805_at	RIKEN cDNA 2810457I06 gene	2810457I06Rik	-1.14	0.374	-1.3	0.012	-1.01	0.921	-1.63	0.004	-1.35	0.076
1459838_s_at	BTB (POZ) domain containing 11	Btbd11	-1.24	0.389	-3.27	0.145	-1.2	0.143	-1.63	0.000	-1.43	0.041
1420768_a_at	DNA segment, Chr 11, Lothar Hennighausen 2, expressed	D11Lgp2e	2.04	0.663	1.71	0.572	1.76	0.543	-1.63	0.014	-1.02	0.677
1459549_at	DPH5 homolog (S. cerevisiae)	Dph5	1.11	0.698	1.53	0.413	2.26	0.867	-1.63	0.025	1.13	0.851
1441835_x_at	myotubularin related protein 11	Mtmr11	-1.15	0.445	-1.34	0.259	1.03	0.735	-1.63	0.020	1.84	0.090
1449530_at	trichorhinophalangeal syndrome I (human)	Trps1	1.33	0.333	-1.92	0.043	-1.66	0.005	-1.63	0.004	-1.85	0.075
1424358_at	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	-1.34	0.163	-2.76	0.034	-1.43	0.014	-1.63	0.000	-1.7	0.001
1448611_at	WW, C2 and coiled-coil domain containing 2	Wwc2	-1	0.839	-1.42	0.007	-1.31	0.031	-1.63	0.031	-1.69	0.031
1458587_at	RIKEN cDNA 2310047D07 gene	2310047D07Rik	-1.02	0.846	-1.03	0.709	-1.31	0.156	-1.62	0.020	1.26	0.867
1428987_at	dynein light chain roadblock-type 2	Dynlrb2	1.41	0.625	1.47	0.854	-2.23	0.035	-1.62	0.042	-1.04	0.592
1443287_at	gene model 1337, (NCBI)	Gm1337	1.82	0.944	1.11	0.608	1.2	0.779	-1.62	0.013	1.03	0.850
1454958_at	glycogen synthase kinase 3 beta	Gsk3b	1.33	0.417	-1.09	0.447	-1.41	0.025	-1.62	0.001	-1.72	0.001
1456263_at	Notch gene homolog 4 (Drosophila)	Notch4	-1.51	0.114	1.15	0.095	-1.26	0.085	-1.62	0.012	1.21	0.904
1419107_at	oligophrenin 1	Ophn1	1.04	0.763	-1.52	0.047	-1.08	0.222	-1.62	0.012	-1.07	0.486
1425383_a_at	pre B-cell leukemia transcription factor 1 /// region containing RIKEN cDN	Pbx1 /// LOC67687	-1.12	0.389	-2.01	0.066	-1.32	0.059	-1.62	0.010	-2.16	0.000
1453891_at	polymerase I and transcript release factor	Ptrf	1.8	0.094	1.03	0.806	1.21	0.933	-1.62	0.018	1.06	0.976
1452833_at	Rap guanine nucleotide exchange factor (GEF) 2	Rapgef2	1.09	0.423	-1.19	0.211	-1.24	0.029	-1.62	0.000	-1.51	0.011
1427493_at	sodium channel and clathrin linker 1	Sclt1	-2.08	0.171	-1.08	0.437	1.12	0.804	-1.62	0.045	-1.27	0.168
1422118_at	syncoilin	Sync	1.6	0.261	1	0.961	-1.21	0.092	-1.62	0.039	-1.21	0.240
1439129_at	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	1110060D06Rik ///	1.14	0.981	-1.62	0.077	-1.36	0.040	-1.61	0.013	-1.99	0.014
1442966_at	RIKEN cDNA 5330421F07 gene	5330421F07Rik	2.11	0.603	1.96	0.201	1.6	0.168	-1.61	0.048	-1.16	0.313
1442232_at	RIKEN cDNA C530025M09 gene	C530025M09Rik	1.24	0.716	1.9	0.909	2.14	0.662	-1.61	0.043	-1.07	0.634
1436983_at	CREB binding protein	Crebbp	-1.11	0.421	-1.06	0.396	-1.45	0.057	-1.61	0.015	-1.29	0.086
1436090_at	ectonucleotide pyrophosphatase/phosphodiesterase 6	Enpp6	-1.42	0.123	1.12	0.763	2.35	0.956	-1.61	0.010	1.36	0.110
1416255_at	gap junction membrane channel protein alpha 4	Gja4	1.42	0.231	1.37	0.405	-1.31	0.169	-1.61	0.001	1.9	0.998
1458354_x_at	keratin 28	Krt28	1.39	0.523	2.09	0.197	-2.16	0.055	-1.61	0.045	-1.39	0.161
1439386_x_at	methionine adenosyltransferase II, alpha	Mat2a	-1.46	0.309	-1.69	0.278	1.55	0.936	-1.61	0.009	1.68	0.258
1455685_at	microtubule associated monoxygenase, calponin and LIM domain contai	Mical2	1.34	0.833	-1	0.305	-1.59	0.018	-1.61	0.029	-1.77	0.029
1456715_at	Pam, highwire, rpm 1	Phr1	1.36	0.291	-2.59	0.022	1.05	0.603	-1.61	0.028	-1.47	0.302
1439619_at	transcription factor 12	Tcf12	-1.2	0.081	-1.18	0.339	-1.42	0.176	-1.61	0.030	-1.24	0.182
1436499_at	transmembrane protein 23	Tmem23	-1.08	0.076	-1.53	0.023	-1.38	0.024	-1.61	0.001	-1.55	0.030
1442175_at	RIKEN cDNA C030027H14 gene	C030027H14Rik	-1.31	0.060	-4.62	0.014	-1.48	0.005	-1.6	0.022	-1.78	0.019
1444279_at	HECT, UBA and WWE domain containing 1	Huwe1	1.24	0.436	-1.54	0.030	1.27	0.870	-1.6	0.043	-1.83	0.072
1437339_s_at	proprotein convertase subtilisin/kexin type 5	Pcsk5	-1.24	0.386	-1.45	0.361	-1.1	0.365	-1.6	0.043	-1.77	0.053
1452209_at	plakophilin 4	Pkp4	-1.24	0.238	-2.01	0.027	-1.41	0.009	-1.6	0.000	-1.6	0.004
1437197_at	sorbin and SH3 domain containing 2	Sorbs2	1.18	0.863	-1.51	0.145	-1.6	0.006	-1.6	0.027	-1.55	0.007
1420726_x_at	trimethyllysine hydroxylase, epsilon	Tmlhe	1.07	0.783	-1.34	0.270	1.04	0.825	-1.6	0.008	-1.07	0.575
1446479_at	TNNI3 interacting kinase	Tnni3k	-1.16	0.411	1.83	0.768	1.81	0.736	-1.6	0.026	-1.56	0.233
1431991_at	RIKEN cDNA 2410004P03 gene	2410004P03Rik	-1.2	0.326	1.11	0.331	1.32	0.339	-1.59	0.044	1.12	0.827
1430633_s_at	RIKEN cDNA C430045I18 gene	C430045I18Rik	1.23	0.796	-1.01	0.413	-1.45	0.099	-1.59	0.003	-1.14	0.413

1438833_at	cancer susceptibility candidate 5 /// similar to cancer susceptibility candi	Casc5 /// LOC6772	1.23	0.282	1.12	0.570	-1.37	0.100	-1.59	0.019	-1.12	0.390
1425015_at	Eph receptor B2	Ephb2	-1.28	0.223	-1.82	0.189	-1.54	0.020	-1.59	0.048	-1.27	0.203
1452982_at	insulin-like growth factor I receptor	Igf1r	-1.05	0.553	-2.17	0.008	-1.54	0.002	-1.59	0.020	-1.84	0.022
1431254_at	kelch repeat and BTB (POZ) domain containing 11 /// similar to Protein K	Kbtbd11 /// LOC632	1.88	0.122	-1.4	0.264	-1.54	0.133	-1.59	0.044	1.27	0.565
1438666_at	low density lipoprotein receptor class A domain containing 3	Ldlrad3	-1.09	0.260	-2.56	0.005	-1.18	0.421	-1.59	0.007	-1.84	0.013
1437181_at	pellino 2	Peli2	-1.11	0.129	-2.09	0.005	-1.46	0.002	-1.59	0.002	-1.7	0.006
1450610_at	urocortin	Ucn	1.34	0.568	-1.06	0.580	-1.04	0.466	-1.59	0.014	1.07	0.962
1451577_at	zinc finger and BTB domain containing 20	Zbtb20	1.12	0.362	-2.11	0.005	-1.74	0.009	-1.59	0.040	-2.37	0.001
1456154_at	Zinc finger protein 444	Zfp444	1.15	0.760	-1.25	0.375	2.89	0.976	-1.59	0.007	1.12	0.871
1431398_at	RIKEN cDNA 5730446D14 gene	5730446D14Rik	-1.46	0.201	-1.31	0.126	-1.28	0.099	-1.58	0.041	-1.19	0.434
1437764_at	RIKEN cDNA A730011L01 gene	A730011L01Rik	1.18	0.747	-1.01	0.646	-1.04	0.585	-1.58	0.026	-1.01	0.764
1440372_at	ADP-ribosylation factor-like 15	Arl15	1.62	0.517	-1.37	0.370	-1.12	0.781	-1.58	0.048	-4.73	0.064
1436440_at	RIKEN cDNA B230107K20 gene	B230107K20Rik	-1.38	0.223	-1.67	0.187	-1.64	0.011	-1.58	0.030	-1.69	0.130
1427867_at	Myosin, heavy polypeptide 1, skeletal muscle, adult	Myh1	1.37	0.588	2.09	0.378	1.36	0.777	-1.58	0.005	1.24	0.728
1436907_at	neuron navigator 1	Nav1	-1.15	0.110	-2.36	0.006	-1.37	0.019	-1.58	0.000	-1.81	0.002
1459357_at	Neurofascin	Nfasc	1.4	0.741	-1.09	0.386	1.35	0.288	-1.58	0.030	1.37	0.173
1426455_at	serologically defined colon cancer antigen 10	Sdccag10	-1.26	0.198	-2.42	0.018	-1.52	0.077	-1.58	0.034	-1.51	0.059
1428822_a_at	sorting nexing 24	Snx24	-1.09	0.370	-1.98	0.016	-1.53	0.043	-1.58	0.015	-1.83	0.000
1433384_at	RIKEN cDNA 9330199C07 gene	9330199C07Rik	-1.97	0.052	1.69	0.597	2.27	0.817	-1.57	0.039	1.07	0.951
1455396_at	ATPase, class I, type 8B, member 1	Atp8b1	1.26	0.705	-1.8	0.073	-1.5	0.002	-1.57	0.012	-1.53	0.025
1448676_at	calcium/calmodulin-dependent protein kinase II, beta	Camk2b	-1.06	0.656	-1.14	0.433	-2.07	0.051	-1.57	0.019	1.04	0.650
1439493_at	RIKEN cDNA D630040G17 gene /// similar to zinc finger protein 64 (pre	D630040G17Rik ///	-1.16	0.298	-1.58	0.036	-1.24	0.041	-1.57	0.003	-1.31	0.047
1426911_at	desmocollin 2	Dsc2	2.29	0.370	1.49	0.290	2.27	0.793	-1.57	0.030	1.17	0.905
1436413_at	fyn-related kinase	Frk	1.28	0.668	1.07	0.959	1.13	0.880	-1.57	0.019	1.09	0.298
1459718_x_at	Kruppel-like factor 6	Klf6	-1.35	0.195	-1.54	0.107	1.17	0.997	-1.57	0.008	1.01	0.994
1443498_at	methylmalonic aciduria (cobalamin deficiency) type B homolog (human)	Mmab	-1.38	0.061	-1.13	0.248	-1.3	0.010	-1.57	0.044	-1.05	0.694
1452294_at	protocadherin 1	Pcdh1	-1.45	0.202	1.33	0.032	1	0.582	-1.57	0.034	1.42	0.783
1418390_at	PHD finger protein 21A	Phf21a	-1.08	0.374	-1.49	0.040	-1.16	0.245	-1.57	0.007	-1.42	0.046
1427231_at	roundabout homolog 1 (Drosophila)	Robo1	-1.33	0.075	-2.18	0.003	-1.25	0.068	-1.57	0.002	-1.37	0.018
1434096_at	solute carrier family 4 (anion exchanger), member 4	Slc4a4	1.18	0.982	-2.13	0.057	-1.4	0.075	-1.57	0.011	-1.95	0.008
1429037_at	RIKEN cDNA 1700019A02 gene	1700019A02Rik	-2.22	0.086	1.01	0.627	3.24	0.285	-1.56	0.039	1.49	0.925
1456831_at	AT rich interactive domain 5B (Mrf1 like)	Arid5b	1.5	0.020	1.73	0.222	-1.06	0.564	-1.56	0.026	-1.41	0.091
1442223_at	Enabled homolog (Drosophila)	Enah	1.03	0.462	-1.65	0.011	-1.65	0.111	-1.56	0.038	-2.05	0.035
1456698_s_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	-1.32	0.291	-1.5	0.199	-1.24	0.146	-1.56	0.012	-1.34	0.031
1454731_at	myosin X	Myo10	1.13	0.553	-1.34	0.164	-1.5	0.018	-1.56	0.039	-1.56	0.015
1421413_a_at	PDZ and LIM domain 5 /// similar to PDZ and LIM domain protein 5 (Eni	Pdlim5 /// LOC6696	12.26	0.588	7	0.464	-1.9	0.034	-1.56	0.045	-1.95	0.040
1449853_at	sideroflexin 2 /// similar to Sideroflexin-2	Sfxn2 /// LOC67714	-1.16	0.207	-1.24	0.099	1.28	0.350	-1.56	0.004	1.16	0.939
1426595_at	solute carrier family 18 (vesicular monoamine), member 1	Slc18a1	1.01	0.742	-1.18	0.535	-1.12	0.447	-1.56	0.014	1.38	0.430
1432502_at	RIKEN cDNA 1700028N14 gene	1700028N14Rik	1.08	0.471	2.02	0.686	-1.37	0.335	-1.55	0.027	-1.21	0.741
1452366_at	RIKEN cDNA 4732435N03 gene	4732435N03Rik	-1.29	0.286	-2.82	0.035	-1.64	0.017	-1.55	0.003	-1.94	0.000
1430933_at	RIKEN cDNA 5730433K22 gene	5730433K22Rik	1.08	0.773	-1.15	0.306	2.18	0.521	-1.55	0.025	-1.15	0.581
1429064_at	DIP2 disco-interacting protein 2 homolog C (Drosophila)	Dip2c	-1.44	0.104	-3.12	0.032	-1.41	0.002	-1.55	0.004	-1.99	0.008
1429021_at	Eph receptor A4	Epha4	1.24	0.055	-1.51	0.071	-1.04	0.380	-1.55	0.016	-1.41	0.042
1421729_a_at	fer (fms/fps related) protein kinase, testis specific 2	Fert2	1.64	0.793	-1.09	0.367	-1.58	0.002	-1.55	0.009	-1.46	0.031
1433485_x_at	G protein-coupled receptor 56	Gpr56	2.4	0.109	2.15	0.160	1.7	0.087	-1.55	0.040	2.14	0.940
1455314_at	LIM domain containing preferred translocation partner in lipoma	Lpp	-1.14	0.045	-1.94	0.001	-1.66	0.004	-1.55	0.000	-1.99	0.009
1443018_at	Neural cell adhesion molecule 1	Ncam1	1.06	0.759	-1.37	0.165	-1.12	0.329	-1.55	0.044	-1.95	0.081
1422673_at	protein kinase C, mu	Prkcm	-1.38	0.174	-2.74	0.022	-1.27	0.036	-1.55	0.003	-1.53	0.045
1453980_at	RIKEN cDNA 5330434G04 gene	5330434G04Rik	1.3	0.503	1.4	0.446	2.44	0.948	-1.54	0.040	-1.85	0.107
1455372_at	cytoplasmic polyadenylation element binding protein 3	Cpeb3	-1.2	0.324	-2.67	0.136	-1.25	0.158	-1.54	0.015	-1.45	0.132
1455078_at	Heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	1.04	0.800	-1.61	0.011	-1.37	0.008	-1.54	0.017	-1.38	0.016
1424125_at	potassium channel, subfamily K, member 13	Kcnk13	-1.29	0.084	1.05	0.813	1.6	0.069	-1.54	0.033	1.08	0.660
1457363_at	hypothetical protein LOC654469	LOC654469	1.13	0.874	1.1	0.894	1.18	0.119	-1.54	0.001	1.17	0.927
1436190_at	neural precursor cell expressed, developmentally down-regulated gene	Nedd10	1.31	0.962	-1.24	0.450	1.01	0.957	-1.54	0.008	-1.08	0.615
1455030_at	protein tyrosine phosphatase, receptor type, J	Ptprj	-1.5	0.018	-2.07	0.027	-1.36	0.207	-1.54	0.024	-1.88	0.004
1434563_at	ribosomal protein S6 kinase polypeptide 1	Rps6kc1	1	0.828	-1	0.607	-1.14	0.163	-1.54	0.006	-1.64	0.002
1438735_at	remodeling and spacing factor 1	Rsf1	-1.16	0.381	-1.16	0.246	-1.33	0.053	-1.54	0.006	-1.13	0.286
1442365_at	Reticulon 3	Rtn3	1.12	0.413	-1.29	0.108	1.36	0.217	-1.54	0.047	1.02	0.982

1441517_at	Sprouty protein with EVH-1 domain 1, related sequence	Spred1	-1.12	0.704	1.06	0.777	1.12	0.399	-1.54	0.032	1.01	0.717
1453015_at	RIKEN cDNA 5830471E12 gene	5830471E12Rik	-1.23	0.336	-1.78	0.137	-1.31	0.008	-1.53	0.001	-1.64	0.020
1433939_at	hypothetical protein A730046J16	A730046J16	-1.3	0.090	-2.39	0.020	-1.19	0.151	-1.53	0.014	-1.72	0.005
1446319_at	ankyrin repeat and SOCS box-containing protein 7	Asb7	1.42	0.645	1.25	0.609	-1.13	0.210	-1.53	0.042	-1.16	0.286
1438207_at	golgi-specific brefeldin A-resistance factor 1	Gbf1	2.51	0.908	2.49	0.332	-1.18	0.135	-1.53	0.008	-1.21	0.153
1451451_at	grancalcin	Gca	1.16	0.537	-1.22	0.650	-1.29	0.113	-1.53	0.024	1.38	0.423
1419603_at	similar to Interferon-activatable protein 204 (Ifi-204) (Interferon-inducible	LOC672547	-1.39	0.065	1.03	0.878	-1.22	0.477	-1.53	0.022	1.18	0.746
1446316_at	Lipin 2	Lpin2	1.99	0.569	2	0.816	1.28	0.982	-1.53	0.009	1.17	0.761
1437201_at	leucine rich repeat containing 4C	Lrrc4c	-1.26	0.266	-3.7	0.014	-1.38	0.012	-1.53	0.005	-1.52	0.076
1451474_a_at	poly (ADP-ribose) polymerase family, member 8	Parp8	1.15	0.213	-1.22	0.210	-1.55	0.006	-1.53	0.001	-1.59	0.005
1431680_a_at	protein tyrosine phosphatase, receptor type, K	Ptprk	1.35	0.650	-1.88	0.039	-1.7	0.073	-1.53	0.032	-1.72	0.189
1443762_s_at	SET binding factor 2	Sbf2	-1.32	0.225	-2.23	0.049	-1.33	0.004	-1.53	0.004	-1.55	0.007
1442482_at	RIKEN cDNA 1700106N22 gene	1700106N22Rik	-1.9	0.242	-1.23	0.377	1.28	0.449	-1.52	0.048	-1.3	0.280
1436302_at	RIKEN cDNA 2410193C02 gene	2410193C02Rik	-1.12	0.236	-2.26	0.003	-1.46	0.015	-1.52	0.001	-1.72	0.010
1444969_at	RIKEN cDNA 5033414K04 gene	5033414K04Rik	1.47	0.893	1.15	0.808	1.41	0.793	-1.52	0.031	1.34	0.844
1437542_at	RIKEN cDNA A730095J18 gene	A730095J18Rik	-1.01	0.715	-2.51	0.023	-1.08	0.350	-1.52	0.008	-1.51	0.043
1449827_at	aggrecan 1	Agc1	1.05	0.924	1.13	0.648	1.58	0.694	-1.52	0.009	1.5	0.625
1435648_at	RIKEN cDNA B430119L13 gene	B430119L13Rik	-1.44	0.189	-1.28	0.327	-1.15	0.470	-1.52	0.034	1.06	0.634
1448007_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	-1.3	0.188	1.14	0.875	1	0.855	-1.52	0.007	-1.02	0.503
1456692_at	Bromodomain containing 1	Brd1	1.01	0.988	-1.03	0.723	1.14	0.095	-1.52	0.050	1.82	0.428
1425555_at	Cdc2-related kinase, arginine/serine-rich	Crkrs	1.07	0.375	-1.21	0.288	1.1	0.810	-1.52	0.043	1.09	0.726
1415758_at	furry homolog-like (Drosophila)	Fryl	-1.15	0.322	-2.06	0.080	-1.35	0.045	-1.52	0.012	-1.47	0.059
1418125_at	INO80 complex homolog 1 (S. cerevisiae)	Inoc1	-1.12	0.462	-1.27	0.298	-1.33	0.010	-1.52	0.007	-1.17	0.162
1428644_at	mannoside acetylglucosaminyltransferase 5	Mgat5	-1.45	0.195	-2.39	0.128	-1.33	0.047	-1.52	0.022	-1.31	0.100
1425844_a_at	RNA guanylyltransferase and 5'-phosphatase	Rngtt	2.18	0.261	1.47	0.623	-1.17	0.264	-1.52	0.003	-1.51	0.094
1429523_a_at	solute carrier family 39 (metal ion transporter), member 5	Slc39a5	2.65	0.256	1.88	0.384	-2.07	0.106	-1.52	0.048	3.37	0.554
1450853_at	transducin-like enhancer of split 4, homolog of Drosophila E(spl)	Tle4	-1.21	0.393	-1.53	0.291	1.06	0.771	-1.52	0.003	-1.43	0.089
1457714_at	RIKEN cDNA 2310005N03 gene	2310005N03Rik	1.23	0.984	-1.2	0.335	1.62	0.512	-1.51	0.045	3.76	0.382
1432797_at	RIKEN cDNA 2900060N12 gene	2900060N12Rik	1.61	0.142	-1.33	0.109	1.76	0.030	-1.51	0.008	1.41	0.808
1449439_at	Kruppel-like factor 7 (ubiquitous)	Klf7	-1.11	0.187	-1.5	0.041	-1.47	0.008	-1.51	0.026	-1.51	0.046
1426759_at	mitogen-activated protein kinase kinase kinase kinase 3 /// similar to mit	Map4k3 /// LOC675	1.12	0.152	-1.2	0.049	-1.41	0.047	-1.51	0.007	-1.69	0.001
1447895_x_at	PAN3 polyA specific ribonuclease subunit homolog (S. cerevisiae)	Pan3	-1.01	0.519	-1.16	0.357	-1.01	0.719	-1.51	0.006	-1.19	0.269
1428710_at	Ras-like without CAAX 1	Rit1	-1.05	0.590	1.02	0.725	-1.06	0.399	-1.51	0.011	-1.31	0.082
1434149_at	transcription factor 4	Tcf4	1.19	0.836	-1.54	0.066	-1.42	0.030	-1.51	0.040	-1.37	0.058
1457492_at	Triple functional domain (PTPRF interacting)	Trio	1.05	0.957	1.04	0.889	-1.18	0.306	-1.51	0.007	-1.44	0.188
1434335_at	expressed sequence AI317237	AI317237	-1.17	0.067	-1.64	0.024	-1.18	0.003	-1.5	0.018	-1.38	0.003
1457069_at	activating signal cointegrator 1 complex subunit 3	Ascc3	-1.11	0.467	-2.11	0.148	-1.42	0.084	-1.5	0.016	-1.62	0.047
1440833_at	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	-1.34	0.308	-1.56	0.243	-1.28	0.177	-1.5	0.019	-1.37	0.087
1438255_at	checkpoint suppressor 1	Ches1	-1	0.861	-1.7	0.014	-1.35	0.012	-1.5	0.039	-1.3	0.060
1421331_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Hs3st3b1	-1.32	0.285	-1.09	0.509	1.64	0.552	-1.5	0.013	1.27	0.487
1454389_at	Leucine-rich repeats and calponin homology (CH) domain containing 4	Lrch4	-1.33	0.330	-1.12	0.563	1.87	0.949	-1.5	0.003	1.06	0.489
1429911_at	microcephaly, primary autosomal recessive 1	Mcph1	-1.16	0.037	-2.34	0.006	-1.49	0.034	-1.5	0.032	-1.41	0.010
1429197_s_at	RAB GTPase activating protein 1-like	Rabgap1l	-1.8	0.008	-2.32	0.006	-1.41	0.160	-1.5	0.005	-1.61	0.052
1419447_s_at	TBC1 domain family, member 1	Tbc1d1	1.17	0.447	-1.26	0.126	-1.31	0.003	-1.5	0.001	-1.43	0.009
1440791_x_at	transcription elongation factor A (SII), 2	Tcea2	1.55	0.858	2.1	0.986	-1.02	0.471	-1.5	0.008	-1.03	0.771
1433894_at	expressed sequence AI591476	AI591476	2.21	0.333	1.1	0.303	-1.73	0.017	-1.49	0.026	-1.68	0.077
1444514_at	RIKEN cDNA B930096F20 gene	B930096F20Rik	-2.16	0.021	-2.19	0.013	1.95	0.144	-1.49	0.028	2.05	0.284
1458602_at	bobby sox homolog (Drosophila)	Bbx	-1.23	0.145	-1.8	0.137	1.02	0.290	-1.49	0.043	1.6	0.143
1427488_a_at	baculoviral IAP repeat-containing 6	Birc6	1.04	0.600	1.03	0.687	-1.1	0.625	-1.49	0.011	-1.53	0.001
1424836_a_at	CLIP associating protein 2	Clasp2	-1	0.638	-1.72	0.133	-1.23	0.201	-1.49	0.002	-1.36	0.006
1449620_s_at	DNA segment, Chr 16, Wayne State University 65, expressed	D16Wsu65e	1.39	0.497	-1.18	0.341	1.13	0.371	-1.49	0.043	-1.07	0.395
1439263_at	fibroblast growth factor inducible 15	Fin15	1.11	0.497	-1.3	0.267	1.03	0.652	-1.49	0.046	-1.03	0.661
1428579_at	formin-like 2	Fmnl2	1.26	0.449	-2.45	0.034	-1.45	0.031	-1.49	0.007	-1.81	0.018
1454780_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosamin	Galntl4	-1.13	0.099	-1.97	0.000	-1.73	0.000	-1.49	0.000	-1.89	0.000
1452690_at	KH-type splicing regulatory protein	Khsrp	1.29	0.661	1.22	0.244	1.08	0.857	-1.49	0.001	1.81	0.155
1432177_a_at	menage a trois 1	Mnat1	1.11	0.613	-1.31	0.082	-1.29	0.024	-1.49	0.022	-1.61	0.003
1445230_at	Nuclear receptor co-repressor 1	Ncor1	2.07	0.049	-1.12	0.532	1.1	0.977	-1.49	0.017	-1.43	0.055
1449315_at	odd Oz/ten-m homolog 3 (Drosophila)	Odz3	-1.5	0.113	-1.99	0.098	-1.61	0.184	-1.49	0.009	-1.33	0.168

1422744_at	phosphorylase kinase alpha 1	Phka1	1.25	0.608	-1.58	0.078	-1.1	0.367	-1.49	0.044	-1.35	0.321
1434005_at	RNA binding motif, single stranded interacting protein 1	Rbms1	-1.01	0.888	-1.53	0.001	-1.37	0.002	-1.49	0.003	-1.58	0.005
1458064_at	Ring finger protein 34	Rnf34	1.59	0.970	1.71	0.834	1.43	0.928	-1.49	0.012	2.05	0.094
1452502_at	small EDRK-rich factor 1	Serf1	1.28	0.673	-1.14	0.372	-1.05	0.631	-1.49	0.049	1.39	0.257
1454894_at	SMAD specific E3 ubiquitin protein ligase 2	Smurf2	1.12	0.422	-1.07	0.536	-1.37	0.000	-1.49	0.004	-1.44	0.002
1419551_s_at	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	1.16	0.921	-1.85	0.012	-1.17	0.132	-1.49	0.027	-1.39	0.052
1423434_at	TEA domain family member 1	Tead1	1.11	0.694	-1.47	0.146	-1.28	0.088	-1.49	0.017	-1.76	0.011
1435028_at	WD repeat domain 7	Wdr7	-1.17	0.172	-2.29	0.008	-1.39	0.055	-1.49	0.014	-1.68	0.007
1444705_at	Amyloid beta (A4) precursor protein	App	-1.08	0.371	-1.21	0.266	-1.43	0.114	-1.48	0.025	-1.06	0.525
1452023_at	ankyrin repeat and SOCS box-containing 16	Asb16	-1.32	0.098	1.08	0.835	-1.07	0.106	-1.48	0.009	2.1	0.569
1455082_at	Casitas B-lineage lymphoma b	Cblb	-1.07	0.213	-1.69	0.007	-1.41	0.018	-1.48	0.044	-1.97	0.041
1457470_at	DNA segment, Chr 3, ERATO Doi 452, expressed	D3Ertd452e	-1.13	0.414	-1.18	0.393	-1.51	0.097	-1.48	0.027	-1.81	0.035
1431354_a_at	phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	1.04	0.699	-2.29	0.027	-1.51	0.022	-1.48	0.030	-2.01	0.002
1450063_at	formin 2	Fmn2	-1.57	0.024	-2.47	0.003	-1.77	0.006	-1.48	0.012	-1.74	0.007
1447640_s_at	pre B-cell leukemia transcription factor 3	Pbx3	-1.17	0.432	-2.01	0.182	-1.28	0.004	-1.48	0.009	-1.39	0.029
1450167_at	RAB37, member of RAS oncogene family	Rab37	-1.56	0.134	-1.3	0.201	-1.1	0.454	-1.48	0.006	1.64	0.842
1429449_at	sterile alpha motif domain containing 4	Samd4	1.3	0.449	-1.28	0.218	-1.71	0.009	-1.48	0.013	-1.7	0.010
1452868_at	ubiquitin specific peptidase 24	Usp24	-1	0.854	-1.08	0.068	-1.22	0.000	-1.48	0.002	-1.33	0.005
1439751_at	zinc finger protein 708	Zfp708	2.78	0.688	1.25	0.425	1.95	0.701	-1.48	0.040	-1.23	0.432
1436116_x_at	RIKEN cDNA 2900057D21 gene	2900057D21Rik	-1.53	0.252	-1.5	0.284	-1.07	0.570	-1.47	0.019	-1.26	0.223
1433048_at	RIKEN cDNA 4933428L01 gene	4933428L01Rik	-1.01	0.748	1.01	0.904	1.3	0.470	-1.47	0.026	1.31	0.912
1434221_at	cDNA sequence BC030863	BC030863	1.68	0.351	1.02	0.505	-1.25	0.018	-1.47	0.003	-1.43	0.015
1439850_at	cDNA sequence BC066028	BC066028	1.11	0.594	1.85	0.195	1.22	0.859	-1.47	0.022	-1.19	0.368
1434645_at	RIKEN cDNA C530008M17 gene	C530008M17Rik	1.29	0.356	-1.85	0.032	-1.15	0.144	-1.47	0.007	-1.23	0.011
1444970_at	expressed sequence C79870	C79870	-1.33	0.340	1.64	0.954	-1.42	0.128	-1.47	0.026	1.2	0.800
1454795_at	Cobl-like 1	Cobll1	1.02	0.912	-1.54	0.052	-1.03	0.647	-1.47	0.006	-1.19	0.039
1436624_at	dynamin 3	Dnm3	-1.67	0.102	-2.35	0.004	-1.06	0.468	-1.47	0.004	-1.22	0.343
1450932_s_at	dedicator of cytokinesis 9 /// similar to Dedicator of cytokinesis protein 9	Dock9 /// LOC67030	1.06	0.582	-3.95	0.010	-1.3	0.114	-1.47	0.005	-1.76	0.006
1436341_at	homeobox containing 1	Hmbox1	-1.14	0.053	-1.2	0.235	1.03	0.669	-1.47	0.009	-1.67	0.001
1451496_at	metastasis suppressor 1	Mtss1	-1.02	0.500	1.27	0.795	1.07	0.915	-1.47	0.024	1.34	0.561
1434640_at	neurensin 2	Nrsn2	1.68	0.385	1.42	0.340	1.22	0.989	-1.47	0.014	-1.27	0.297
1449260_at	RAB3D, member RAS oncogene family	Rab3d	1.3	0.816	1.95	0.554	1.08	0.443	-1.47	0.026	1.08	0.842
1448918_at	solute carrier organic anion transporter family, member 3a1	Slco3a1	1.29	0.754	-2.13	0.042	-1.37	0.092	-1.47	0.044	-1.54	0.078
1430407_at	RIKEN cDNA 3110035C09 gene	3110035C09Rik	1.2	0.767	1.04	0.596	-1.38	0.039	-1.46	0.028	-1.27	0.204
1436597_at	ankyrin repeat and KH domain containing 1	Ankhd1	1.55	0.126	1.28	0.487	-1.31	0.143	-1.46	0.015	-1.26	0.288
1428806_at	casein kinase 1, gamma 1	Csnk1g1	1	0.927	-1.06	0.482	-1.29	0.001	-1.46	0.002	-1.41	0.005
1422887_a_at	C-terminal binding protein 2	Ctbp2	1.03	0.459	-1.22	0.068	-1.39	0.009	-1.46	0.000	-1.37	0.012
1434380_at	guanylate binding protein 7	Gbp7	1.77	0.056	1.34	0.464	1.11	0.971	-1.46	0.018	-1.09	0.605
1454693_at	Histone deacetylase 4	Hdac4	1.19	0.393	-1.21	0.069	-1.41	0.049	-1.46	0.023	-1.77	0.053
1418265_s_at	interferon regulatory factor 2	Irf2	1.01	0.987	-1.21	0.383	-1.33	0.084	-1.46	0.000	-1.11	0.442
1458351_s_at	kelch-like 2, Mayven (Drosophila)	Klhl2	-1.3	0.327	-1.8	0.161	-1.1	0.165	-1.46	0.011	-1.32	0.046
1428647_at	region containing RIKEN cDNA 2310056B04 gene; pre B-cell leukemia t	LOC676870	1.49	0.973	-1.62	0.142	-1.34	0.114	-1.46	0.027	-1.88	0.043
1452056_s_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	-1.21	0.023	-2.15	0.008	-1.25	0.127	-1.46	0.006	-1.37	0.001
1420766_at	suppressor of cytokine signaling 7	Socs7	-1.02	0.722	1.39	0.100	-1.35	0.142	-1.46	0.022	1.33	0.607
1448639_a_at	spermatogenesis associated 5	Spata5	-1.23	0.262	-1.19	0.268	-1.35	0.013	-1.46	0.005	-1.58	0.001
1456976_at	wingless-related MMTV integration site 5A	Wnt5a	-1.1	0.511	1.04	0.687	-1.4	0.123	-1.46	0.049	1.05	0.973
1429228_at	RIKEN cDNA 4930534B04 gene	4930534B04Rik	1.5	0.612	-1.56	0.125	1.06	0.656	-1.45	0.044	-1.54	0.031
1430685_at	RIKEN cDNA 6330503C03 gene	6330503C03Rik	-1.05	0.881	1.67	0.296	1.04	0.936	-1.45	0.050	3.09	0.170
1435975_at	expressed sequence AI115600	AI115600	-1.14	0.090	-1.28	0.042	1.15	0.251	-1.45	0.015	-1.33	0.119
1442257_at	RIKEN cDNA B130021B11 gene	B130021B11Rik	-1.37	0.215	-2.33	0.141	-1.38	0.102	-1.45	0.015	-1.63	0.067
1443099_at	CDNA sequence BC087945	BC087945	-1.21	0.085	1.05	0.922	1.19	0.853	-1.45	0.008	-1.04	0.515
1429329_at	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farne	Cox10	-1.07	0.535	-1.14	0.423	-1.2	0.241	-1.45	0.018	-1.39	0.009
1457839_at	DEAH (Asp-Glu-Ala-His) box polypeptide 40	Dhx40	1.41	0.071	1.41	0.048	1.23	0.112	-1.45	0.012	1.18	0.345
1448665_at	dystrophin, muscular dystrophy	Dmd	-1.02	0.519	-1.49	0.028	-1.33	0.015	-1.45	0.039	-1.39	0.019
1434489_at	engulfment and cell motility 3, ced-12 homolog (C. elegans)	Elmo3	-1.33	0.148	1.15	0.505	1.22	0.339	-1.45	0.009	1.55	0.143
1425500_x_at	Hypothetical protein LOC625794	LOC625794	1.59	0.831	1.63	0.858	1.99	0.319	-1.45	0.025	1.33	0.885
1435185_at	leucine rich repeat and coiled-coil domain containing 1	Lrrcc1	2.51	0.498	1.67	0.560	1.42	0.425	-1.45	0.013	-1.41	0.046
1455941_s_at	mitogen activated protein kinase kinase 5	Map2k5	-1.32	0.257	-2.33	0.102	-1.22	0.016	-1.45	0.004	-1.31	0.030

1426850_a_at	mitogen activated protein kinase kinase 6	Map2k6	-1.33	0.169	-1.46	0.113	-1.27	0.324	-1.45	0.001	-1.03	0.738
1442853_at	Mitogen-activated protein kinase 8 interacting protein 3	Mapk8ip3	-1.04	0.915	-1	0.852	1.05	0.847	-1.45	0.023	-1.06	0.356
1427212_at	mitogen-activated protein kinase associated protein 1	Mapkap1	1.39	0.788	-1.39	0.111	-1.29	0.016	-1.45	0.003	-1.48	0.007
1449298_a_at	phosphodiesterase 1A, calmodulin-dependent	Pde1a	-1.07	0.396	-1.2	0.312	1.21	0.113	-1.45	0.040	1.58	0.102
1421594_a_at	synaptotagmin-like 2	Sytl2	-1.09	0.141	-2.02	0.004	-1.33	0.004	-1.45	0.027	-1.43	0.026
1423186_at	T-cell lymphoma invasion and metastasis 2	Tiam2	1.52	0.298	1.06	0.614	-1.28	0.052	-1.45	0.013	-1.69	0.001
1456385_x_at	UBX domain containing 3	Ubxd3	-1.12	0.495	-1.35	0.379	1.55	0.777	-1.45	0.050	1.12	0.745
1446365_at	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	1.35	0.054	1.39	0.293	-1.05	0.474	-1.45	0.023	1.02	0.613
1427980_at	RIKEN cDNA 4933407C03 gene	4933407C03Rik	1.3	0.240	-1.06	0.740	-1.37	0.002	-1.44	0.019	-1.4	0.001
1457371_at	RIKEN cDNA 5230400G24 gene	5230400G24Rik	-1.32	0.431	1.04	0.563	1.14	0.779	-1.44	0.039	1.88	0.998
1432902_at	RIKEN cDNA 9130414P19 gene	9130414P19Rik	-1.1	0.596	1.24	0.763	1.9	0.456	-1.44	0.046	-1.52	0.083
1458434_at	RIKEN cDNA A730009L09 gene	A730009L09Rik	1.5	0.637	1.11	0.553	-1.12	0.409	-1.44	0.031	-1.31	0.273
1456111_at	RIKEN cDNA D930028F11 gene	D930028F11Rik	-1.25	0.301	-4.25	0.058	-1.1	0.421	-1.44	0.032	-1.45	0.149
1424586_at	EH domain binding protein 1	Ehbp1	-1.19	0.028	-2.61	0.004	-1.37	0.008	-1.44	0.014	-1.71	0.031
1418242_at	Fas-associated factor 1	Faf1	-1.27	0.202	-2.28	0.058	-1.41	0.002	-1.44	0.007	-1.69	0.002
1452280_at	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-	Farp1	1.44	0.705	-1.2	0.200	-1.3	0.019	-1.44	0.000	-1.65	0.000
1422018_at	human immunodeficiency virus type I enhancer binding protein 2	Hivep2	1.23	0.748	-1.12	0.303	-1.39	0.018	-1.44	0.025	-1.92	0.000
1454066_at	myc induced nuclear antigen	Mina	-1.25	0.294	-1.07	0.486	1.28	0.485	-1.44	0.042	-1.15	0.013
1434900_at	MKL (megakaryoblastic leukemia)/myocardin-like 1	Mkl1	1.31	0.483	1.25	0.647	-1.32	0.001	-1.44	0.018	-1.3	0.155
1439205_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	Nfatc2	-1.28	0.173	-1.49	0.165	-1.32	0.163	-1.44	0.013	-1.16	0.208
1455936_a_at	RNA binding protein gene with multiple splicing	Rbpms	-1.34	0.314	-1.88	0.150	-1.29	0.026	-1.44	0.001	-1.24	0.098
1445781_at	SH3 domain protein D19	Sh3d19	1.08	0.732	-1.41	0.120	-1.1	0.493	-1.44	0.047	-1.3	0.343
1442753_at	tumor necrosis factor, alpha-induced protein 8	Tnfaip8	1.18	0.862	1.75	0.425	1.02	0.616	-1.44	0.025	1.67	0.732
1433460_at	tetratricopeptide repeat domain 7B	Ttc7b	1.73	0.492	-1.04	0.307	-1.37	0.006	-1.44	0.002	-1.52	0.024
1437556_at	zinc finger homeodomain 4	Zfhx4	1.16	0.224	-2.53	0.001	-1.04	0.694	-1.44	0.010	-1.57	0.007
1438515_at	zinc finger protein 207	Zfp207	1.12	0.873	1.11	0.877	-1.1	0.373	-1.44	0.024	1.66	0.080
1420469_at	RIKEN cDNA 4933411G06 gene	4933411G06Rik	1.47	0.730	1.47	0.849	1.77	0.159	-1.43	0.009	-1.09	0.721
1457218_at	RIKEN cDNA 6430510M02 gene	6430510M02Rik	1.08	0.821	-1.05	0.511	1.27	0.564	-1.43	0.013	1.16	0.622
1456948_at	adaptor-related protein complex AP-4, epsilon 1	Ap4e1	-1.61	0.125	1.11	0.742	1.42	0.230	-1.43	0.037	-1.9	0.066
1450460_at	aquaporin 3	Aqp3	1.32	0.524	1.19	0.941	-1.13	0.515	-1.43	0.019	1.51	0.704
1425099_a_at	aryl hydrocarbon receptor nuclear translocator-like	Arntl	-1.08	0.412	-1.56	0.015	-1.38	0.020	-1.43	0.010	-1.77	0.007
1436030_at	cache domain containing 1	Cachd1	-1.32	0.315	-2.49	0.095	-1.15	0.239	-1.43	0.002	-1.44	0.027
1459457_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	1.01	0.580	-1.39	0.296	-1.51	0.027	-1.43	0.048	-2.13	0.014
1451972_at	glucocorticoid induced transcript 1	Glcci1	2.13	0.745	-1.36	0.164	1.37	0.303	-1.43	0.001	1.16	0.345
1435332_at	5-hydroxytryptamine (serotonin) receptor 7	Htr7	-1.06	0.425	-1.01	0.949	-1.04	0.558	-1.43	0.034	-1.03	0.409
1457030_at	miRNA containing gene	Mirg	1.21	0.599	-1.45	0.074	1.36	0.690	-1.43	0.023	-1.38	0.081
1459665_s_at	MRV integration site 1	Mrvi1	-1.73	0.120	-1.91	0.138	-1.47	0.019	-1.43	0.035	-1.21	0.118
1431701_a_at	PDZ domain containing 1	Pdzk1	1.17	0.687	2.07	0.729	1.04	0.738	-1.43	0.032	1.72	0.157
1431539_at	SAM domain, SH3 domain and nuclear localization signals, 1	Samsn1	-1.45	0.167	-1.01	0.562	-1.08	0.392	-1.43	0.046	1.46	0.913
1430433_at	RIKEN cDNA 4933406J08 gene /// hypothetical protein LOC640572	4933406J08Rik /// L	1.55	0.591	-1.05	0.570	-1.09	0.167	-1.42	0.043	-1.36	0.250
1436143_at	RIKEN cDNA 4933425L03 gene	4933425L03Rik	-1.28	0.050	-1.93	0.063	-1.57	0.004	-1.42	0.024	-1.67	0.025
1451891_a_at	dysferlin	Dysf	1.56	0.787	1.26	0.965	1.01	0.955	-1.42	0.001	-1.22	0.124
1449514_at	G protein-coupled receptor kinase 5	Gprk5	1.09	0.933	-1.61	0.085	-1.31	0.074	-1.42	0.023	-1.46	0.008
1435671_at	mirror-image polydactyly gene 1 homolog (human)	Mipol1	-1	0.554	-2.13	0.119	-1.22	0.140	-1.42	0.012	-1.31	0.162
1445134_at	MKL/myocardin-like 2	Mkl2	1.22	0.219	-1.35	0.208	1.56	0.427	-1.42	0.020	-1.63	0.200
1436262_x_at	OTU domain containing 5	Otud5	2.75	0.524	2.01	0.493	-1.02	0.812	-1.42	0.017	-1.2	0.384
1449405_at	tensin 1	Tns1	-1.04	0.500	-1.32	0.040	-1.53	0.004	-1.42	0.008	-1.46	0.006
1435110_at	unc-5 homolog B (C. elegans)	Unc5b	-1.12	0.240	-1.45	0.063	-1.16	0.223	-1.42	0.024	-1.31	0.030
1421778_at	vomeronasal 1, receptor B2	V1rb2	-1.19	0.653	1.37	0.970	1.09	0.501	-1.42	0.048	1.18	0.524
1452274_at	zinc finger, AN1-type domain 3	Zfand3	-1.12	0.345	-1.63	0.103	-1.58	0.011	-1.42	0.002	-1.58	0.004
1438798_at	RIKEN cDNA 4931406P16 gene	4931406P16Rik	-1.1	0.554	1.05	0.705	-1.09	0.664	-1.41	0.016	1.09	0.886
1460080_at	expressed sequence AI645535	AI645535	1.54	0.829	1.8	0.723	-1.05	0.585	-1.41	0.007	-1.26	0.134
1458604_at	Rho/rac guanine nucleotide exchange factor (GEF) 18	Arhgef18	1.36	0.990	2.06	0.067	-1.41	0.182	-1.41	0.020	-1.15	0.563
1418815_at	cadherin 2	Cdh2	-1.23	0.104	-1.75	0.007	-1.22	0.038	-1.41	0.028	-1.28	0.018
1452291_at	centaurin, delta 1	Centd1	1.18	0.806	1.01	0.711	-1.06	0.513	-1.41	0.042	-1.61	0.015
1449419_at	dedicator of cytokinesis 8	Dock8	-1.18	0.231	-1.56	0.022	-1.28	0.123	-1.41	0.035	1.01	0.741
1439688_at	fibulin 1	Fbln1	1.64	0.293	-1.61	0.149	1.24	0.209	-1.41	0.015	-1.69	0.035
1422742_at	human immunodeficiency virus type I enhancer binding protein 1	Hivep1	-1.14	0.273	-1.49	0.041	-1.08	0.395	-1.41	0.022	-1.22	0.205

1422445_at	integrin alpha 6	Itga6	1.02	0.995	-1.67	0.034	-1.16	0.047	-1.41	0.002	-1.33	0.008
1435884_at	intersectin 1 (SH3 domain protein 1A)	Itsn1	-1.32	0.354	-1.33	0.345	-1.06	0.466	-1.41	0.033	-1.07	0.920
1460723_at	melanocortin 5 receptor	Mc5r	-1.06	0.749	1.29	0.159	-1.47	0.265	-1.41	0.036	1.2	0.806
1416891_at	numb gene homolog (Drosophila)	Numb	-1.01	0.740	-1.39	0.011	-1.2	0.050	-1.41	0.008	-1.4	0.002
1446821_at	Protocadherin 17	Pcdh17	1.88	0.862	1.99	0.264	1.22	0.843	-1.41	0.038	1.5	0.878
1434653_at	PTK2 protein tyrosine kinase 2 beta	Ptk2b	-1.05	0.703	-1.83	0.010	-1.29	0.003	-1.41	0.026	-1.29	0.125
1438163_x_at	Rhomboid domain containing 2	Rhbdd2	1.58	0.333	2.75	0.505	1.04	0.977	-1.41	0.039	1.64	0.624
1427650_a_at	runt related transcription factor 1	Runx1	-1.15	0.124	-1.08	0.515	-1.16	0.266	-1.41	0.013	-1.67	0.084
1423658_at	signal peptide peptidase 3	Sppl3	-1.12	0.361	-1.29	0.084	-1.25	0.048	-1.41	0.050	-1.26	0.047
1447624_s_at	storkhead box 2	Stox2	-1.04	0.568	-1.31	0.063	-1.06	0.446	-1.41	0.000	-1.26	0.005
1450117_at	transcription factor 3	Tcf3	-1.23	0.318	-1.51	0.155	1.03	0.879	-1.41	0.019	-1.53	0.016
1426435_at	transmembrane protein 135	Tmem135	1.05	0.836	-2.18	0.005	-1.16	0.031	-1.41	0.019	-1.92	0.001
1458438_at	RIKEN cDNA 4933415L06 gene	4933415L06Rik	-1.37	0.235	-1.68	0.010	1.05	0.996	-1.4	0.008	1.01	0.904
1448460_at	activin A receptor, type 1	Acvr1	1.31	0.908	1.14	0.453	-1.3	0.043	-1.4	0.003	-1.55	0.001
1437659_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate	Als2cr11	1.25	0.268	1.3	0.264	1.29	0.568	-1.4	0.002	-1.27	0.338
1424842_a_at	Rho GTPase activating protein 24	Arhgap24	1.1	0.360	-1.17	0.214	-1.2	0.129	-1.4	0.017	-1.51	0.033
1437645_at	activating transcription factor 7	Atf7	1.21	0.780	1.38	0.657	-1.06	0.558	-1.4	0.035	-1.33	0.123
1427505_a_at	CASP2 and RIPK1 domain containing adaptor with death domain	Cradd	-1.47	0.206	-2.71	0.105	-1.01	0.699	-1.4	0.034	-1.55	0.080
1449884_at	EF-hand calcium binding domain 2	Efcab2	1.13	0.960	-1.28	0.151	-1.08	0.423	-1.4	0.026	1.83	0.284
1432260_at	G protein-coupled receptor 39	Gpr39	1.48	0.508	1.08	0.449	-1.23	0.152	-1.4	0.027	1.01	0.892
1455746_at	kinesin family member 13A	Kif13a	1.23	0.061	-1.86	0.020	-1.19	0.008	-1.4	0.003	-1.42	0.033
1451846_at	nebulette	Nebl	1.6	0.415	1.14	0.473	-2.21	0.080	-1.4	0.015	1.01	0.898
1419053_at	peroxisomal biogenesis factor 14	Pex14	-1	0.770	-1.59	0.035	-1.13	0.263	-1.4	0.001	-1.38	0.048
1449799_s_at	plakophilin 2	Pkp2	-1.15	0.378	-1.67	0.092	-1.28	0.054	-1.4	0.000	-1.4	0.002
1439774_at	paired related homeobox 1	Prrx1	-1.1	0.501	-1.33	0.206	-1.14	0.182	-1.4	0.010	-1.33	0.028
1447672_x_at	protein serine kinase H1	Pskh1	-1.29	0.348	-1.33	0.300	1.1	0.981	-1.4	0.028	1.34	0.098
1452324_at	plasmacytoma variant translocation 1	Pvt1	-1.19	0.408	-1.3	0.382	-1.39	0.067	-1.4	0.015	-1.79	0.004
1455181_at	RAS p21 protein activator 2	Rasa2	-1.01	0.704	-1.38	0.135	-1.29	0.032	-1.4	0.020	-1.5	0.020
1437700_at	Schwannomin interacting protein 1	Schip1	1.23	0.630	-1.08	0.416	-1.11	0.284	-1.4	0.011	-1.46	0.069
1427685_a_at	synaptojanin 2	Synj2	1.13	0.819	1.09	0.910	-1.32	0.018	-1.4	0.002	-1.25	0.000
1434393_at	ubiquitin specific peptidase 34	Usp34	1.57	0.150	1.09	0.548	-1.29	0.011	-1.4	0.014	-1.83	0.015
1436746_at	WNK lysine deficient protein kinase 1	Wnk1	-1.29	0.169	-1.72	0.009	-1.62	0.046	-1.4	0.041	-1.23	0.085
1426053_a_at	xenotropic and polytropic retrovirus receptor 1	Xpr1	1.15	0.950	-1.23	0.120	1.05	0.904	-1.4	0.039	-1.33	0.080
1421301_at	Zic finger protein of the cerebellum 2	Zic2	-1.03	0.504	-1.64	0.150	1.2	0.845	-1.4	0.019	-1.22	0.315
1453087_at	RIKEN cDNA 6330403L08 gene	6330403L08Rik	1.45	0.800	1.05	0.696	-1.24	0.173	-1.39	0.048	1.04	0.966
1434197_at	attractin	Atrn	1.14	0.239	-1.46	0.027	-1.17	0.004	-1.39	0.033	-1.26	0.179
1455352_at	expressed sequence AU023006	AU023006	1.72	0.255	1.43	0.670	-1.15	0.014	-1.39	0.024	-1.33	0.062
1449165_at	calpain 5	Capn5	-1.4	0.385	-1.33	0.275	1.12	0.810	-1.39	0.041	1.03	0.962
1437385_at	collagen and calcium binding EGF domains 1	Ccbe1	1.06	0.906	-2.99	0.186	-1.86	0.045	-1.39	0.045	-1.92	0.106
1448001_x_at	cell division cycle associated 3	Cdca3	-1.25	0.288	-1.51	0.258	1.22	0.898	-1.39	0.031	1.02	0.893
1418071_s_at	chromodomain protein, Y chromosome-like	Cdyl	-1.05	0.426	-1.37	0.034	-1.27	0.080	-1.39	0.004	-1.39	0.022
1429028_at	dedicator of cytokinesis 11	Dock11	-1.02	0.630	-1.9	0.083	-1.26	0.008	-1.39	0.028	-1.48	0.014
1424295_at	developmental pluripotency-associated 3	Dppa3	1.13	0.559	1.18	0.647	1.23	0.252	-1.39	0.032	1.3	0.954
1442920_at	Kruppel-like factor 3 (basic)	Klf3	1.13	0.747	-1.01	0.566	1.03	0.872	-1.39	0.030	-1.38	0.222
1455486_at	protein inhibitor of activated STAT 1	Pias1	-1.07	0.593	-1.49	0.191	1.53	0.415	-1.39	0.008	-1.3	0.177
1455149_at	SH3 domain containing ring finger 1	Sh3rf1	-1.13	0.423	-1.29	0.143	-1.1	0.364	-1.39	0.015	-1.23	0.043
1428251_at	SMC hinge domain containing 1	Smchd1	-1.11	0.464	-1.52	0.067	-1.19	0.040	-1.39	0.035	-1.33	0.015
1455309_at	transmembrane protein 16F	Tmem16f	1.27	0.404	-1.31	0.185	-1.51	0.070	-1.39	0.019	-1.56	0.007
1418926_at	zinc finger homeobox 1a	Zfhx1a	1.16	0.474	-1.47	0.076	-1.37	0.003	-1.39	0.005	-1.68	0.011
1454723_at	RIKEN cDNA 1110033M05 gene	1110033M05Rik	1.06	0.927	-1.57	0.007	-1.53	0.004	-1.38	0.011	-1.67	0.003
1456563_at	RIKEN cDNA 4933429F08 gene	4933429F08Rik	-1.4	0.285	-1.24	0.381	-1.18	0.159	-1.38	0.022	1.21	0.217
1434932_at	adenosine deaminase, RNA-specific, B1	Adarb1	1.56	0.599	-3.87	0.025	-2.05	0.044	-1.38	0.002	-1.34	0.323
1435594_at	ADP-ribosylation factor-like 6 interacting protein 2	Arl6ip2	1.13	0.766	1.29	0.961	-1.07	0.481	-1.38	0.021	1.35	0.545
1436304_at	RIKEN cDNA C030003D03 gene	C030003D03Rik	-1.07	0.276	-1.05	0.522	-1.04	0.517	-1.38	0.022	-1.15	0.309
1432229_a_at	chromodomain protein, Y chromosome-like 2	Cdyl2	3.69	0.439	2.14	0.536	1.16	0.545	-1.38	0.010	-1.35	0.051
1451723_at	CCR4-NOT transcription complex, subunit 6-like	Cnot6l	1.12	0.636	-1.23	0.174	-1.08	0.140	-1.38	0.019	-1.15	0.072
1436866_at	ephrin A5	Efna5	-1.19	0.114	-2.62	0.015	1.02	0.954	-1.38	0.044	-1.35	0.048
1425710_a_at	homer homolog 1 (Drosophila)	Homer1	2.01	0.274	-1.11	0.403	-1.02	0.773	-1.38	0.035	-1.03	0.641

1448352_at	leucine zipper protein 1	Luzp1	-1.42	0.297	-1.26	0.359	-1.34	0.128	-1.38	0.033	1.09	0.546
1425755_at	mature T-cell proliferation 1	Mtcp1	1.11	0.839	1.16	0.764	1.01	0.656	-1.38	0.020	1.02	0.970
1453271_at	PHD finger protein 14	Phf14	-1.26	0.345	-1.82	0.180	-1.18	0.130	-1.38	0.004	-1.54	0.019
1453163_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	1.66	0.346	1.21	0.570	-1.33	0.056	-1.38	0.045	-1.78	0.050
1425060_s_at	restin (Reed-Steinberg cell-expressed intermediate filament-associated p	Rsn	-1.09	0.467	-1.43	0.127	-1.24	0.232	-1.38	0.028	1.01	0.655
1459903_at	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor,	Sema7a	-1.21	0.128	-1.85	0.049	-1.35	0.013	-1.38	0.018	-1.41	0.005
1454284_at	solute carrier family 25 (mitochondrial carrier, phosphate carrier), membe	Slc25a25	1.58	0.261	1.15	0.355	3.33	0.536	-1.38	0.017	1.57	0.210
1416977_at	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Stam2	1.03	0.857	-1.14	0.495	-1.01	0.855	-1.38	0.049	-1.54	0.050
1455042_at	Transducin (beta)-like 1 X-linked	Tbl1x	1.36	0.550	-1.02	0.467	-1.37	0.007	-1.38	0.003	-1.56	0.006
1432183_at	transmembrane protein 116	Tmem116	-1.14	0.065	-1.05	0.727	-1.04	0.482	-1.38	0.004	-1.25	0.120
1440424_at	Troponin T2, cardiac	Tnnt2	-1.15	0.329	1.87	0.364	1.04	0.566	-1.38	0.007	1.15	0.859
1425388_a_at	thiamine pyrophosphokinase	Tpk1	-1.26	0.057	-2.32	0.003	-1.05	0.558	-1.38	0.032	-1.32	0.042
1456946_at	RIKEN cDNA 4831416G18 gene	4831416G18Rik	1.09	0.567	-1.19	0.483	1.15	0.790	-1.37	0.000	-1.43	0.143
1443923_at	A kinase (PRKA) anchor protein 13	Akap13	-1.06	0.575	-1.31	0.322	-1.47	0.078	-1.37	0.006	-1.19	0.159
1435879_at	thymoma viral proto-oncogene 3	Akt3	-1.12	0.272	-2.7	0.030	-1.51	0.004	-1.37	0.010	-1.65	0.005
1428369_s_at	Rho GTPase activating protein 21	Arhgap21	-1.03	0.670	-1.19	0.179	-1.22	0.000	-1.37	0.006	-1.3	0.002
1434951_at	armadillo repeat containing 8	Armc8	-1.02	0.544	-1.19	0.364	-1.18	0.329	-1.37	0.007	-1.34	0.138
1455164_at	Cdc42 GTPase-activating protein	Cdgap	1.07	0.324	-1.29	0.083	-1.43	0.014	-1.37	0.001	-1.61	0.001
1447538_at	CREB regulated transcription coactivator 1	Crtc1	1.39	0.994	1.17	0.974	1.01	0.687	-1.37	0.013	-1.11	0.571
1458770_at	DNA segment, Chr 11, ERATO Doi 4, expressed	D11Ertd4e	1.36	0.770	1.16	0.429	1.85	0.761	-1.37	0.042	3.06	0.046
1452635_x_at	Josephin domain containing 3	Josd3	-1.36	0.326	-1.07	0.498	1.06	0.482	-1.37	0.012	1.05	0.551
1426025_s_at	lysosomal-associated protein transmembrane 5	Laptm5	1.19	0.691	1.36	0.721	1.07	0.898	-1.37	0.016	1.19	0.174
1451982_at	mitogen activated protein kinase kinase 4	Map2k4	1.01	0.781	-1.19	0.171	-1.14	0.128	-1.37	0.018	-1.19	0.044
1457416_at	Methionine aminopeptidase 2	Metap2	-1.63	0.173	-1.13	0.429	1.12	0.620	-1.37	0.034	-1.12	0.330
1457316_at	microtubule-associated protein 6	Mtap6	-1.19	0.017	-1.58	0.001	-1.47	0.075	-1.37	0.007	-1.7	0.006
1434884_at	Metadherin	Mtdh	-1.09	0.395	-1.13	0.370	-1.02	0.678	-1.37	0.010	-1.01	0.667
1453576_at	Nipped-B homolog (Drosophila)	Nipbl	-1.14	0.425	-1.55	0.287	-1.43	0.009	-1.37	0.010	-1.35	0.108
1460615_at	5'-nucleotidase domain containing 1	Nt5dc1	1	0.918	-1.66	0.006	-1.19	0.023	-1.37	0.023	-1.66	0.014
1433694_at	phosphodiesterase 3B, cGMP-inhibited	Pde3b	-1.46	0.265	-2.6	0.104	-1.02	0.696	-1.37	0.019	1.15	0.784
1434924_at	PHD finger protein 2	Phf2	-1	0.883	-1.25	0.030	1.09	0.060	-1.37	0.015	-1.22	0.211
1454862_at	pleckstrin homology-like domain, family B, member 2	Phldb2	-1.06	0.576	-1.35	0.115	-1.23	0.048	-1.37	0.008	-1.37	0.011
1456261_at	SH3-domain kinase binding protein 1	Sh3kbp1	-1.15	0.333	-1.67	0.057	-1.26	0.012	-1.37	0.040	-1.29	0.049
1436892_at	sprouty-related, EVH1 domain containing 2	Spred2	1.13	0.527	1.27	0.472	-1.13	0.265	-1.37	0.005	1.2	0.026
1451332_at	zinc finger protein 521	Zfp521	-1.06	0.376	-3.24	0.019	-1.62	0.003	-1.37	0.009	-1.77	0.001
1460455_at	RIKEN cDNA 1110059H15 gene	1110059H15Rik	-1.06	0.452	-1.27	0.011	-1.02	0.546	-1.36	0.020	-1.39	0.084
1447913_x_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	1.52	0.526	-1.39	0.070	-1.31	0.200	-1.36	0.041	-1.12	0.632
1437633_at	ankyrin repeat domain 11	Ankrd11	1.04	0.397	-1.1	0.339	-1.82	0.025	-1.36	0.016	-1.4	0.046
1454763_at	ankyrin repeat domain 17	Ankrd17	1.59	0.304	1.63	0.542	-1.28	0.004	-1.36	0.005	-1.46	0.001
1435108_at	Rho GTPase activating protein 22	Arhgap22	-1.69	0.084	-1.09	0.760	1.98	0.249	-1.36	0.006	2.29	0.420
1441572_at	RIKEN cDNA C030036D22 gene	C030036D22Rik	1.18	0.111	1.06	0.898	-1.6	0.117	-1.36	0.042	1.02	0.878
1455467_at	RIKEN cDNA C330043M08 gene	C330043M08Rik	1.44	0.874	1.23	0.308	-1.11	0.516	-1.36	0.003	1.35	0.634
1443486_at	Component of oligomeric golgi complex 7	Cog7	-1.56	0.173	-1.95	0.100	1.28	0.809	-1.36	0.026	1.06	0.243
1420384_at	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Col4a3bp	-1.16	0.339	-1.26	0.104	-1.22	0.106	-1.36	0.017	-1.22	0.036
1419935_s_at	casein kinase 2, alpha prime polypeptide	Csnk2a2	-1.03	0.461	1.07	0.391	-1.19	0.109	-1.36	0.001	-1.01	0.769
1452220_at	dedicator of cyto-kinesis 1	Dock1	-1	0.781	-1.98	0.022	-1.39	0.024	-1.36	0.017	-1.61	0.008
1455057_at	guanine monphosphate synthetase	Gmps	1.03	0.885	-1.09	0.072	-1.17	0.168	-1.36	0.025	-1.25	0.008
1425589_at	hydroxysteroid (17-beta) dehydrogenase 13	Hsd17b13	1.99	0.847	1.52	0.959	1.15	0.587	-1.36	0.032	1.85	0.774
1453126_at	leucine rich repeat and fibronectin type III domain containing 2	Lrfn2	-1.1	0.804	-1.25	0.325	1.35	0.141	-1.36	0.038	1.35	0.754
1434179_at	myeloid/lymphoid or mixed-lineage leukemia 3	Mll3	-1.06	0.375	-2.61	0.014	-1.32	0.046	-1.36	0.017	-1.88	0.009
1436502_at	mitochondrial tumor suppressor 1	Mtus1	1.34	0.921	-1.14	0.255	1.16	0.428	-1.36	0.031	-1.03	0.756
1454851_at	nuclear receptor subfamily 2, group C, member 2	Nr2c2	-1.13	0.161	-1.36	0.021	-1.22	0.096	-1.36	0.014	-1.3	0.001
1426933_at	oxidative-stress responsive 1	Oxsr1	-1.02	0.538	-1.36	0.164	-1.06	0.748	-1.36	0.011	-1.14	0.286
1452788_at	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	Ppp2r5e	3.82	0.240	3.44	0.799	-1.32	0.049	-1.36	0.045	-1.61	0.012
1432057_a_at	PR domain containing 5	Prdm5	1.02	0.684	-1.34	0.097	-1.33	0.003	-1.36	0.023	-1.27	0.031
1417400_at	retinoic acid induced 14	Rai14	-1.08	0.204	-1.69	0.008	-1.32	0.013	-1.36	0.016	-1.5	0.014
1424084_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	1.03	0.487	-1.08	0.157	-1.11	0.215	-1.36	0.011	-1.07	0.868
1423881_at	SAPS domain family, member 3	Saps3	1.12	0.554	-1.1	0.525	-1.29	0.022	-1.36	0.033	-1.43	0.001
1460735_at	supervillin	Svil	1.1	0.774	-1.41	0.101	-1.25	0.026	-1.36	0.005	-1.43	0.003

1439766_x_at	vascular endothelial growth factor C	Vegfc	-1.42	0.265	-1.47	0.256	1.18	0.466	-1.36	0.017	-1.16	0.160
1453593_at	RIKEN cDNA 1700110N18 gene	1700110N18Rik	-1.08	0.317	-1.28	0.001	-1.19	0.048	-1.35	0.006	-1.27	0.005
1428696_at	RIKEN cDNA 2310015N21 gene	2310015N21Rik	-1.2	0.056	-2.17	0.001	-1.14	0.075	-1.35	0.034	-1.45	0.021
1445896_at	RIKEN cDNA 2810433D01 gene	2810433D01Rik	1.2	0.749	1.27	0.999	-1.5	0.238	-1.35	0.039	3.52	0.016
1453543_at	RIKEN cDNA 4930556H04 gene	4930556H04Rik	-1.38	0.281	1.39	0.462	1.43	0.849	-1.35	0.004	-1.31	0.186
1447465_at	RIKEN cDNA 4930558N01 gene	4930558N01Rik	1.35	0.478	1.33	0.436	-1.05	0.449	-1.35	0.042	-1.34	0.168
1434797_at	RIKEN cDNA 6720469N11 gene	6720469N11Rik	-1.03	0.586	-1.26	0.044	-1.28	0.066	-1.35	0.003	-1.32	0.010
1432681_at	RIKEN cDNA 9130009M17 gene	9130009M17Rik	-1.13	0.330	1.31	0.216	-1.29	0.328	-1.35	0.046	-1.33	0.180
1427692_a_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Cask	2.84	0.743	1.5	0.203	-1.41	0.021	-1.35	0.045	-1.65	0.090
1455072_at	centrosomal protein 350	Cep350	1.06	0.133	-1.25	0.005	-1.13	0.185	-1.35	0.023	-1.46	0.008
1423271_at	gap junction membrane channel protein beta 2	Gjb2	-1.17	0.069	-1.79	0.017	-1.29	0.089	-1.35	0.003	-1.46	0.013
1450050_at	histone cell cycle regulation defective homolog A (S. cerevisiae)	Hira	1.49	0.115	1.25	0.338	-1.32	0.293	-1.35	0.046	-1.66	0.070
1435490_at	hexokinase 3	Hk3	-1.32	0.694	1.59	0.226	1.23	0.620	-1.35	0.044	-1.45	0.249
1449328_at	lymphocyte antigen 75	Ly75	-1.37	0.126	-1.34	0.250	1.06	0.940	-1.35	0.016	-1.05	0.661
1416092_a_at	microtubule-associated protein 4	Mtap4	1.18	0.617	-1.29	0.091	-1.34	0.044	-1.35	0.016	-1.44	0.031
1448944_at	neuropilin 1	Nrp1	1.21	0.393	-1.23	0.355	-1.52	0.018	-1.35	0.011	-1.54	0.017
1457225_at	olfactory receptor 288	Olfr288	1.15	0.839	2.08	0.143	1.86	0.090	-1.35	0.031	1.06	0.983
1452759_s_at	PTPRF interacting protein, binding protein 1 (liprin beta 1)	Ppfibp1	-1.04	0.586	-1.17	0.059	-1.29	0.099	-1.35	0.021	-1.38	0.055
1448020_at	RAS-related protein-1a	Rap1a	-1.02	0.635	-1.18	0.368	-1.19	0.022	-1.35	0.033	-1.17	0.081
1434509_at	Rap guanine nucleotide exchange factor (GEF) 6	Rapgef6	-1.05	0.564	-1.57	0.000	-1.21	0.025	-1.35	0.011	-1.4	0.008
1428657_at	ras responsive element binding protein 1	Rreb1	-1.02	0.655	-1.05	0.581	-1.11	0.080	-1.35	0.004	-1.11	0.020
1439515_at	SET domain containing 5	Setd5	1.14	0.469	-1.3	0.053	-1.4	0.014	-1.35	0.025	-1.51	0.037
1458803_at	schlafen 9 /// similar to schlafen 9	Slfn9 /// LOC67761	-1.13	0.681	-1.17	0.373	-1.01	0.990	-1.35	0.019	-1.02	0.870
1437155_a_at	WW domain containing transcription regulator 1	Wwtr1	-1.05	0.470	-1.46	0.005	-1.38	0.007	-1.35	0.023	-1.25	0.001
1455483_at	zinc finger protein 148	Zfp148	-1.2	0.337	-1.25	0.299	-1.19	0.023	-1.35	0.002	-1.35	0.023
1429089_s_at	RIKEN cDNA 2900026A02 gene	2900026A02Rik	-1.14	0.108	-1.88	0.018	-1.47	0.007	-1.34	0.010	-1.52	0.001
1433151_at	RIKEN cDNA 4933415B22 gene	4933415B22Rik	1.03	0.876	1.22	0.715	1.16	0.619	-1.34	0.047	1.66	0.243
1442098_at	expressed sequence AU022434	AU022434	-1.31	0.291	-1.84	0.077	-1.15	0.369	-1.34	0.043	1.06	0.986
1460439_at	cDNA sequence BC033915	BC033915	-1.07	0.605	-1.95	0.001	-1.44	0.017	-1.34	0.010	-1.49	0.044
1447608_x_at	BTB (POZ) domain containing 14A	Btbd14a	-1.1	0.250	-1.17	0.519	1.58	0.575	-1.34	0.032	1.15	0.586
1445843_at	chromodomain helicase DNA binding protein 2	Chd2	-1.25	0.315	-1.33	0.313	-1.53	0.022	-1.34	0.028	-1.17	0.454
1457424_at	eyes absent 1 homolog (Drosophila)	Eya1	-1.29	0.132	-1.94	0.087	1.12	0.802	-1.34	0.018	1.25	0.584
1442453_at	FCH domain only 2	Fcho2	1.33	0.106	1.49	0.264	1.23	0.776	-1.34	0.023	-1.24	0.216
1455242_at	forkhead box P1	Foxp1	1.35	0.401	1.08	0.560	-1.22	0.027	-1.34	0.009	-1.36	0.003
1449099_at	LPS-responsive beige-like anchor	Lrba	-1.14	0.097	-1.5	0.013	-1.21	0.075	-1.34	0.014	-1.32	0.065
1425510_at	MAP/microtubule affinity-regulating kinase 1	Mark1	2.03	0.981	2.13	0.881	1.05	0.846	-1.34	0.005	-1.46	0.084
1448989_a_at	myosin IB	Myo1b	1.07	0.968	-1.39	0.071	-1.29	0.029	-1.34	0.005	-1.5	0.000
1432592_at	pregnancy-associated plasma protein A	Pappa	-1.12	0.352	-1.62	0.022	-1.72	0.052	-1.34	0.015	-1.58	0.006
1449404_at	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	Pip5k2a	-1.2	0.260	-2.02	0.055	-1.26	0.008	-1.34	0.003	-1.37	0.006
1451618_at	rhodopsin	Rho	-1.05	0.537	1	0.586	-1.19	0.123	-1.34	0.044	1.07	0.819
1423776_s_at	TBC1 domain family, member 22a	Tbc1d22a	-1.19	0.292	-2.65	0.057	-1.3	0.138	-1.34	0.012	-2.03	0.001
1458963_at	RIKEN cDNA 1810054D07 gene	1810054D07Rik	1.04	0.788	-1.12	0.356	-1.19	0.018	-1.33	0.012	-1.4	0.006
1437041_at	RIKEN cDNA 5730406M06 gene	5730406M06Rik	1.35	0.251	-1.01	0.386	1.05	0.781	-1.33	0.038	-1.26	0.075
1442063_at	RIKEN cDNA 5930437A14 gene	5930437A14Rik	-1.09	0.220	-1.31	0.157	-1.23	0.181	-1.33	0.029	-1.7	0.008
1455342_at	RIKEN cDNA A230083H22 gene	A230083H22Rik	1.05	0.887	-1.13	0.295	-1.03	0.467	-1.33	0.044	-1.34	0.147
1450915_at	adaptor-related protein complex 3, beta 1 subunit	Ap3b1	1.11	0.514	-1.29	0.107	-1.33	0.032	-1.33	0.047	-1.35	0.012
1447606_x_at	aquaporin 11	Aqp11	1.02	0.808	1.17	0.908	1.33	0.846	-1.33	0.045	-1.2	0.622
1449709_s_at	arginine-tRNA-protein transferase 1	Ate1	1.07	0.569	-1.22	0.145	-1.29	0.031	-1.33	0.026	-1.51	0.004
1439948_at	cDNA sequence BC046401	BC046401	1.15	0.521	1.17	0.954	1.39	0.783	-1.33	0.010	-1	0.434
1456505_at	Braf transforming gene	Braf	1.48	0.850	1.26	0.628	-1.16	0.364	-1.33	0.030	-1.24	0.191
1451447_at	CUE domain containing 1	Cuedc1	-1.32	0.086	-1.29	0.276	-1.09	0.453	-1.33	0.008	-1.12	0.376
1437141_x_at	dymeclin	Dym	-1.28	0.361	-1.51	0.276	-1.14	0.135	-1.33	0.003	-1.15	0.240
1418349_at	heparin-binding EGF-like growth factor	Hbegf	-1.05	0.581	-1.44	0.006	-1.22	0.029	-1.33	0.036	-1.22	0.025
1449242_s_at	histidine-rich glycoprotein	Hrg	-1.01	0.800	1.72	0.248	-1.05	0.397	-1.33	0.030	1.25	0.310
1439582_at	Microtubule-actin crosslinking factor 1	Macf1	-1.23	0.360	-1.43	0.219	-1.02	0.680	-1.33	0.002	1.1	0.606
1420870_at	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolo	Mllt10	1.12	0.303	-1	0.933	-1.26	0.070	-1.33	0.017	-1.79	0.002
1437295_at	protein kinase N2	Pkn2	1.19	0.183	-1.04	0.510	-1.27	0.024	-1.33	0.016	-1.32	0.021
1448502_at	solute carrier family 16 (monocarboxylic acid transporters), member 7	Slc16a7	1.09	0.904	-1.26	0.152	-1.15	0.118	-1.33	0.006	-1.83	0.085

1450916_at	staufen (RNA binding protein) homolog 2 (Drosophila)	Stau2	1.04	0.892	-1.99	0.050	-1.28	0.043	-1.33	0.018	-1.35	0.016
1429428_at	transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	-1.03	0.449	-1.67	0.017	1.01	0.619	-1.33	0.005	-1.26	0.029
1435235_at	thioredoxin-like 1	Txnl1	-1.11	0.492	-1.24	0.320	-1.25	0.002	-1.33	0.006	-1.21	0.107
1443924_at	WNK lysine deficient protein kinase 3	Wnk3	-1.21	0.252	-2.2	0.017	1.41	0.251	-1.33	0.042	-1	0.650
1430012_at	RIKEN cDNA 1110050K14 gene	1110050K14Rik	2.21	0.396	-1.08	0.376	1.78	0.245	-1.32	0.019	1.18	0.249
1428539_at	RIKEN cDNA 2610207I05 gene	2610207I05Rik	1.09	0.768	-1.01	0.722	-1.15	0.167	-1.32	0.023	-1.43	0.008
1430252_at	RIKEN cDNA 3110027N22 gene	3110027N22Rik	-1.21	0.357	-1.59	0.244	-1.33	0.152	-1.32	0.027	-1.41	0.100
1431158_at	RIKEN cDNA 8430406H22 gene	8430406H22Rik	1.16	0.682	1.05	0.772	1.03	0.955	-1.32	0.045	1.12	0.662
1456634_at	RIKEN cDNA 9830001H06 gene	9830001H06Rik	1.22	0.912	1.28	0.954	-1.34	0.012	-1.32	0.042	-1.04	0.704
1429140_at	RIKEN cDNA 9830002I17 gene	9830002I17Rik	-1.24	0.260	1.03	0.848	-1.08	0.605	-1.32	0.024	1.39	0.753
1437216_at	RIKEN cDNA A430106J12 gene	A430106J12Rik	1.11	0.222	-1.3	0.181	-1.35	0.021	-1.32	0.037	-1.7	0.043
1440838_at	Expressed sequence AI852064	AI852064	2.22	0.643	1.36	0.440	-1.12	0.556	-1.32	0.013	-1.19	0.063
1419939_at	Rho guanine nucleotide exchange factor (GEF) 17	Arhgef17	1.05	0.633	1.11	0.746	1.4	0.228	-1.32	0.019	1.12	0.312
1427482_a_at	carbonic anhydrase 8 /// similar to Carbonic anhydrase-related protein (C	Car8 /// LOC676792	-1.02	0.538	-1.8	0.070	-1.19	0.157	-1.32	0.027	-1.03	0.845
1457672_at	chromodomain helicase DNA binding protein 9	Chd9	-1.09	0.413	-1.51	0.090	-1.5	0.003	-1.32	0.026	-1.71	0.031
1460576_at	exocyst complex component 6	Exoc6	-1.34	0.352	-3.53	0.194	1.01	0.709	-1.32	0.020	1.25	0.512
1452232_at	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosamir	Galnt7	1.04	0.812	-1.74	0.002	-1.08	0.276	-1.32	0.003	-1.19	0.069
1434009_at	glucocorticoid receptor DNA binding factor 1	Grlf1	-1	0.676	-1.17	0.031	-1.03	0.623	-1.32	0.001	-1.22	0.141
1419302_at	hairy/enhancer-of-split related with YRPW motif-like	Heyl	1.08	0.567	-1.19	0.399	-1.23	0.153	-1.32	0.005	-1.2	0.170
1428787_at	NCK associated protein 1 like	Nckap1l	1.23	0.993	-1.03	0.438	-1.23	0.270	-1.32	0.021	1.5	0.691
1438684_at	NUAK family, SNF1-like kinase, 1	Nuak1	-1.22	0.248	-1.41	0.152	-1.3	0.006	-1.32	0.030	-1.4	0.010
1425824_a_at	proprotein convertase subtilisin/kexin type 4	Pcsk4	-1.22	0.369	1.18	0.967	-1.05	0.570	-1.32	0.003	1.18	0.155
1450819_at	poliovirus receptor-related 1	Pvrl1	1.29	0.687	1.27	0.662	-1.2	0.324	-1.32	0.013	-1.19	0.235
1427017_at	special AT-rich sequence binding protein 2	Satb2	1.49	0.412	-1.21	0.243	-1.32	0.181	-1.32	0.003	-1.81	0.037
1434261_at	signal-induced proliferation-associated 1 like 2	Sipa1l2	1.02	0.688	-1.38	0.041	-1.2	0.014	-1.32	0.011	-1.47	0.002
1438147_at	scavenger receptor cysteine rich domain containing, group B (4 domains	Srcrb4d	-1.33	0.336	-1.45	0.292	1.09	0.740	-1.32	0.027	1.07	0.548
1452604_at	serologically defined colon cancer antigen 13	Stard13	1.63	0.499	1.52	0.528	-1.31	0.030	-1.32	0.029	-1.52	0.014
1430535_at	TSC22 domain family 2	Tsc22d2	1.02	0.986	-1.31	0.060	-1.23	0.021	-1.32	0.000	-1.31	0.000
1452964_at	tubulin tyrosine ligase-like family, member 11	Ttll11	-1.15	0.202	-1.93	0.021	-1.29	0.046	-1.32	0.017	-1.55	0.032
1439302_at	ubiquitin-activating enzyme E1-like 2	Ube1l2	-1.06	0.526	-1.57	0.038	-1.49	0.015	-1.32	0.003	-1.47	0.018
1434184_s_at	RIKEN cDNA 9430080K19 gene	9430080K19Rik	1.1	0.319	-1.13	0.137	-1.23	0.048	-1.31	0.000	-1.35	0.007
1455059_at	RIKEN cDNA 9430093I07 gene	9430093I07Rik	1.42	0.217	1.12	0.980	-1.12	0.069	-1.31	0.044	-1.09	0.431
1456790_at	EST AA407452	AA407452	1.09	0.487	1.04	0.660	1.05	0.645	-1.31	0.025	1.07	0.698
1442132_at	CDNA sequence BC057552	BC057552	1.35	0.703	1.24	0.770	1.69	0.413	-1.31	0.012	1.21	0.535
1441137_at	bicaudal C homolog 1 (Drosophila)	Bicc1	1.08	0.730	-1.49	0.057	-1.23	0.003	-1.31	0.006	-1.35	0.043
1427973_s_at	Vcell division cycle 73, Paf1/RNA polymerase II complex component, ho	Cdc73	1.75	0.011	1.46	0.127	-1.3	0.097	-1.31	0.023	-1.2	0.210
1439824_at	choroidermia	Chm	-1.15	0.410	-1.43	0.180	-1.09	0.103	-1.31	0.011	-1.19	0.209
1430936_at	CHMP family, member 7	Chmp7	1.14	0.982	2.08	0.449	2.57	0.460	-1.31	0.009	1.09	0.622
1440657_at	Contactin 3	Cntn3	-1.2	0.326	-1.3	0.199	1.25	0.968	-1.31	0.009	1.06	0.875
1430676_at	procollagen, type XIX, alpha 1	Col19a1	1.31	0.947	1.29	0.739	2.51	0.358	-1.31	0.032	1.06	0.835
1426153_a_at	desmoglein 2	Dsg2	-1.19	0.220	1.38	0.177	-1.17	0.267	-1.31	0.048	1.01	0.763
1451924_a_at	endothelin 1	Edn1	-1.27	0.204	-1.45	0.075	-1.9	0.053	-1.31	0.046	-1.29	0.103
1421299_a_at	lymphoid enhancer binding factor 1	Lef1	1.15	0.357	-1.52	0.101	-1.5	0.090	-1.31	0.040	-1.08	0.217
1434185_at	similar to acetyl-coenzyme A carboxylase alpha	LOC672245	-1.15	0.293	-1.61	0.062	-1.13	0.007	-1.31	0.029	-1.25	0.021
1452320_at	low density lipoprotein receptor-related protein 2	Lrp2	-1.27	0.022	-1.36	0.144	-1.41	0.027	-1.31	0.000	-1.13	0.148
1451318_a_at	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog /// similar to Yam	Lyn /// LOC676654	-1.11	0.448	-1.52	0.241	-1.15	0.098	-1.31	0.033	-1.11	0.246
1452347_at	myocyte enhancer factor 2A	Mef2a	1.53	0.466	1.1	0.619	-1.32	0.082	-1.31	0.010	-1.46	0.030
1453622_s_at	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog	Mllt3	1.25	0.845	1.05	0.333	1.06	0.768	-1.31	0.029	-1.67	0.162
1418031_at	myosin IXb	Myo9b	1	0.730	-1.32	0.226	-1.21	0.114	-1.31	0.004	-1.18	0.136
1446429_at	purinergic receptor P2X, ligand-gated ion channel 4	P2rx4	1.45	0.755	-1.1	0.405	-1.12	0.555	-1.31	0.032	1.01	0.744
1460729_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	-1.01	0.911	-1.18	0.118	-1.05	0.413	-1.31	0.006	-1.34	0.017
1437246_x_at	ribosomal protein S6 /// similar to 40S ribosomal protein S6 /// similar to 4	Rps6 /// LOC214738	-1.31	0.044	-1.06	0.527	1.17	0.162	-1.31	0.046	1.14	0.200
1427096_s_at	signal sequence receptor, delta	Ssr4	1.5	0.388	1.46	0.723	1.31	0.051	-1.31	0.003	1.4	0.629
1419181_at	zinc finger protein 326	Zfp326	-1.09	0.387	-1.12	0.105	-1.05	0.369	-1.31	0.023	-1.38	0.044
1456789_at	Zinc finger protein 462	Zfp462	-1.03	0.620	-1.39	0.150	-1.15	0.256	-1.31	0.004	-1.17	0.101
1455732_at	RIKEN cDNA 1700025G04 gene	1700025G04Rik	-1.08	0.148	-2.2	0.012	-1.16	0.020	-1.3	0.045	-1.5	0.016
1459879_at	RIKEN cDNA 4921513D23 gene	4921513D23Rik	1.09	0.764	1	0.897	1.04	0.926	-1.3	0.039	-1.09	0.479
1428413_at	RIKEN cDNA 5730405I09 gene	5730405I09Rik	-1.18	0.391	-1.33	0.314	-1.23	0.006	-1.3	0.005	-1.15	0.118

1446586_at	RIKEN cDNA 8030463A06 gene	8030463A06Rik	1.84	0.291	1.44	0.760	1.51	0.206	-1.3	0.040	-1.75	0.122
1436795_at	RIKEN cDNA 9630058J23 gene	9630058J23Rik	-1.06	0.233	-1.3	0.065	-1.04	0.569	-1.3	0.005	-1.3	0.001
1423177_a_at	abl-interactor 1	Abi1	1.17	0.508	1.04	0.806	-1.12	0.161	-1.3	0.002	-1.27	0.005
1440668_at	ADAMTS-like 3	Adamtsl3	-1.07	0.730	-1.19	0.061	-1.34	0.074	-1.3	0.023	-1.31	0.052
1422700_at	arachidonate 12-lipoxygenase	Alox12	-1.03	0.497	1.12	0.884	1.09	0.914	-1.3	0.049	1.8	0.430
1441897_at	RIKEN cDNA B230120H23 gene	B230120H23Rik	-1.54	0.048	-1.76	0.101	1.36	0.316	-1.3	0.016	1	0.957
1440304_at	BTB and CNC homology 2	Bach2	1.39	0.971	2.6	0.595	1.14	0.547	-1.3	0.041	1.02	0.903
1446293_at	B-cell CLL/lymphoma 11A (zinc finger protein)	Bcl11a	-1.34	0.276	1.11	0.763	1.09	0.842	-1.3	0.006	1.2	0.647
1438806_at	B-cell CLL/lymphoma 9-like	Bcl9l	1.45	0.739	2.19	0.843	-1.01	0.496	-1.3	0.020	-1.25	0.280
1450757_at	cadherin 11	Cdh11	1.18	0.506	-1.18	0.213	-1.32	0.004	-1.3	0.001	-1.35	0.007
1449167_at	erythrocyte protein band 4.1-like 4a	Epb4.1l4a	-1.05	0.400	-1.42	0.114	-1.14	0.136	-1.3	0.041	-1.35	0.014
1460574_at	FAT tumor suppressor homolog 4 (Drosophila)	Fat4	1.74	0.692	-1.31	0.172	-1.47	0.053	-1.3	0.015	-1.64	0.092
1418508_a_at	growth factor receptor bound protein 2	Grb2	-1.45	0.044	-1.28	0.019	1.17	0.510	-1.3	0.026	1.12	0.447
1452443_s_at	helicase with zinc finger domain	Helz	-1.28	0.271	-1.29	0.270	-1.14	0.145	-1.3	0.043	-1.3	0.054
1439764_s_at	insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	-1.2	0.400	-1.58	0.311	-1.22	0.070	-1.3	0.027	-1.15	0.263
1434825_at	similar to CAGL79	LOC381742	-1.02	0.654	-1.06	0.510	-1.28	0.001	-1.3	0.026	-1.12	0.288
1422574_at	Max dimerization protein 4	Mxd4	-1.25	0.355	1.19	0.407	1.17	0.689	-1.3	0.020	1.03	0.740
1448893_at	nuclear receptor co-repressor 2	Ncor2	1.2	0.542	1.01	0.752	-1.24	0.060	-1.3	0.040	-1.32	0.052
1420583_a_at	RAR-related orphan receptor alpha	Rora	-1.02	0.705	-1.29	0.080	-1.09	0.553	-1.3	0.030	-1.27	0.167
1453389_a_at	SH2B adaptor protein 2	Sh2b2	1.69	0.399	2.43	0.305	1.78	0.269	-1.3	0.044	1.6	0.080
1460204_at	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	Tec	1.02	0.754	-1.32	0.003	-1.04	0.396	-1.3	0.027	-1.24	0.090
1441968_at	tetraspanin 9	Tspan9	3.33	0.191	1.5	0.595	-1.35	0.175	-1.3	0.003	1.14	0.789
1438971_x_at	ubiquitin-conjugating enzyme E2H	Ube2h	-1.38	0.230	-1.5	0.199	-1.15	0.196	-1.3	0.013	-1.25	0.004
1453343_s_at	vaccinia related kinase 2	Vrk2	-1	0.945	-1.32	0.031	-1.19	0.104	-1.3	0.007	-1.21	0.048
1435608_at	zinc and ring finger 3 /// similar to Goliath homolog precursor (Ring finge	Znrf3 /// LOC63180	-1.05	0.634	-1.27	0.008	-1.05	0.584	-1.3	0.001	-1.21	0.040
1452840_at	RIKEN cDNA 1500009L16 gene	1500009L16Rik	1.14	0.584	1.17	0.186	1.28	0.024	-1.29	0.009	1.16	0.365
1454913_at	RIKEN cDNA 9930104L06 gene	9930104L06Rik	1.11	0.924	-1.04	0.573	1.16	0.946	-1.29	0.028	1.05	0.723
1454810_s_at	expressed sequence AI315068	AI315068	-1.2	0.376	-1.56	0.204	-1.25	0.071	-1.29	0.038	1.03	0.729
1447985_s_at	ankyrin repeat and IBR domain containing 1	Ankib1	-1.38	0.358	-1.29	0.389	1.27	0.513	-1.29	0.001	1.01	0.971
1443340_at	calcium binding atopy-related autoantigen 1	Cbara1	1.5	0.186	1.17	0.848	1.14	0.923	-1.29	0.021	-1.13	0.591
1457104_at	RIKEN cDNA D930036F22 gene	D930036F22Rik	1.18	0.791	1.02	0.794	-1.85	0.005	-1.29	0.017	-1.43	0.139
1452718_at	E3 ubiquitin protein ligase, HECT domain containing, 1	Edd1	-1.05	0.481	-1.13	0.125	-1.26	0.021	-1.29	0.021	-1.39	0.006
1438658_a_at	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	Edg3	-1.43	0.285	-2	0.181	-1.31	0.006	-1.29	0.020	-1.37	0.015
1451263_a_at	fatty acid binding protein 4, adipocyte	Fabp4	-1.51	0.205	-1.04	0.663	-1.09	0.336	-1.29	0.023	1.69	0.021
1453746_at	formin binding protein 1	Fnbp1	-1.27	0.369	-1.42	0.298	-1.25	0.021	-1.29	0.023	-1.2	0.042
1448223_at	fatso	Fto	-1.12	0.224	-1.74	0.002	-1.23	0.030	-1.29	0.043	-1.29	0.041
1434754_at	GTPase activating RANGAP domain-like 4	Garnl4	-1.14	0.012	-1.41	0.009	-1.26	0.014	-1.29	0.011	-1.55	0.005
1435282_at	gene model 967, (NCBI)	Gm967	-1.33	0.250	-1.44	0.152	1.14	0.479	-1.29	0.020	-1.19	0.217
1460203_at	inositol 1,4,5-triphosphate receptor 1	Itpr1	-1.24	0.068	-2.05	0.011	-1.32	0.029	-1.29	0.030	-1.46	0.037
1436056_at	kinesin family member 13B	Kif13b	-1.05	0.446	-1.29	0.153	-1.19	0.126	-1.29	0.002	-1.25	0.114
1444451_at	pappalysin 2	Pappa2	-1.32	0.196	-1.12	0.377	-1.21	0.379	-1.29	0.026	-1.36	0.182
1436970_a_at	platelet derived growth factor receptor, beta polypeptide	Pdgfrb	-1.3	0.257	-1.4	0.060	-1.2	0.074	-1.29	0.011	-1.19	0.127
1416390_at	regulator of chromosome condensation (RCC1) and BTB (POZ) domain	Rcbtb2	1.09	0.485	1.05	0.590	1.09	0.594	-1.29	0.020	1.26	0.184
1427299_at	ribosomal protein S6 kinase polypeptide 3	Rps6ka3	-1.05	0.287	-1.42	0.011	-1.37	0.010	-1.29	0.039	-1.42	0.005
1435964_a_at	TAO kinase 3	Taok3	-1.36	0.326	-1.6	0.253	-1.07	0.475	-1.29	0.002	-1.31	0.008
1421683_at	t-complex-associated testis expressed 3	Tcte3	1.16	0.623	-1.13	0.462	1.15	0.748	-1.29	0.049	-1.22	0.376
1440348_at	zinc finger, FYVE domain containing 9	Zfyve9	-1.13	0.144	-1.31	0.002	-1.17	0.011	-1.29	0.038	-1.1	0.006
1436631_at	RIKEN cDNA 2010010M04 gene	2010010M04Rik	-1.12	0.326	1.04	0.921	1.02	0.597	-1.28	0.001	-1.14	0.241
1431831_at	RIKEN cDNA 2210009G21 gene	2210009G21Rik	1.8	0.871	1.38	0.385	-1.51	0.027	-1.28	0.029	-1.17	0.150
1433249_at	RIKEN cDNA 4931409D07 gene	4931409D07Rik	1.9	0.250	2.61	0.408	1.83	0.419	-1.28	0.011	1.62	0.428
1429579_at	RIKEN cDNA 6330407I18 gene	6330407I18Rik	1.37	0.889	-1.46	0.112	-1.4	0.047	-1.28	0.037	-1.76	0.015
1452009_at	RIKEN cDNA 9130422G05 gene	9130422G05Rik	1.1	0.566	-1.38	0.131	-1.2	0.022	-1.28	0.014	-1.33	0.005
1418403_at	a disintegrin and metallopeptidase domain 19 (meltrin beta)	Adam19	6.69	0.600	3.65	0.560	-1.41	0.006	-1.28	0.023	-1.54	0.010
1434265_s_at	ankyrin 2, brain	Ank2	-1.27	0.145	-1.91	0.049	-1.3	0.098	-1.28	0.041	-1.34	0.131
1435959_at	Rho GTPase activating protein 15	Arhgap15	2.65	0.498	1.8	0.710	1.27	0.817	-1.28	0.016	-1.16	0.445
1434410_at	cDNA sequence BC043118	BC043118	1.25	0.402	-1.07	0.279	-1.27	0.172	-1.28	0.049	-1.02	0.240
1444607_at	Corneodesmosin	Cdsn	-1.11	0.275	1.09	0.695	1.28	0.389	-1.28	0.025	1.23	0.346
1434917_at	cordon-bleu	Cobl	-1.09	0.319	-1.14	0.242	1.09	0.480	-1.28	0.018	-1.56	0.016

1437448_s_at	catenin (cadherin associated protein), delta 1	Ctnnd1	1.27	0.658	1.06	0.757	-1.16	0.306	-1.28	0.004	-1.37	0.004
1450756_s_at	cullin 3	Cul3	3.04	0.568	2.14	0.912	-1.33	0.021	-1.28	0.010	-1.55	0.000
1451977_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	1.65	0.575	1.47	0.658	-1.3	0.009	-1.28	0.022	-1.29	0.035
1418285_at	ephrin B1	Efnb1	-1.33	0.061	-1.5	0.010	-1.42	0.019	-1.28	0.002	-1.11	0.115
1451264_at	FERM domain containing 6	Frmd6	1.16	0.580	-1.06	0.583	-1.31	0.016	-1.28	0.014	-1.37	0.002
1440238_at	glioma tumor suppressor candidate region gene 1	Gltscr1	-1.33	0.231	-1.14	0.370	-1.02	0.982	-1.28	0.010	-1.21	0.140
1435992_at	IQ motif containing with AAA domain	Iqca	1.62	0.608	2.47	0.286	1.22	0.979	-1.28	0.029	1.92	0.818
1453317_a_at	KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	-1.12	0.055	-1.73	0.007	-1.44	0.002	-1.28	0.011	-1.45	0.000
1447308_at	longevity assurance homolog 5 (S. cerevisiae)	Lass5	1.15	0.333	1.2	0.766	1.16	0.226	-1.28	0.013	1.23	0.218
1427485_at	leiomodin 1 (smooth muscle)	Lmod1	-1.06	0.242	-1.33	0.079	-1.11	0.377	-1.28	0.044	-1.11	0.335
1448870_at	latent transforming growth factor beta binding protein 1	Ltbp1	-1.13	0.155	-1.35	0.038	-1.28	0.009	-1.28	0.007	-1.41	0.018
1436165_at	LUC7-like 2 (S. cerevisiae)	Luc7l2	1.05	0.354	-1.1	0.038	-1.02	0.841	-1.28	0.014	-1.29	0.077
1440708_at	myosin, heavy polypeptide 9, non-muscle	Myh9	-1.2	0.412	-1.57	0.184	-1.32	0.102	-1.28	0.028	-1.45	0.025
1454809_at	nuclear receptor coactivator 7	Ncoa7	1.11	0.489	-1.66	0.018	-1.09	0.454	-1.28	0.011	-1.19	0.365
1448435_at	positive cofactor 2, multiprotein complex, glutamine/Q-rich-associated pr	Pcqap	1.17	0.271	1.08	0.697	-1.18	0.195	-1.28	0.010	-1.27	0.071
1423129_at	soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	1.38	0.397	1.22	0.671	-1.34	0.008	-1.28	0.036	-1.45	0.025
1433911_at	Smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans)	Smg6	-1.06	0.434	-1.32	0.057	-1.15	0.289	-1.28	0.010	-1.21	0.083
1440314_at	Thyroid hormone receptor interactor 12	Trip12	-1.22	0.390	-1.2	0.421	-1.31	0.200	-1.28	0.007	-1.71	0.011
1434517_at	WD repeat and FYVE domain containing 2	Wdfy2	-1.27	0.328	-1.84	0.174	-1.29	0.016	-1.28	0.003	-1.21	0.194
1433343_at	RIKEN cDNA 4930448K20 gene	4930448K20Rik	1.54	0.697	1.9	0.457	-1.52	0.020	-1.27	0.006	1.32	0.928
1438869_at	RIKEN cDNA 4930515G01 gene	4930515G01Rik	1.12	0.491	1.24	0.565	-1.07	0.314	-1.27	0.046	-1.12	0.273
1442115_at	RIKEN cDNA 9430028L06 gene	9430028L06Rik	-1.4	0.111	-1.88	0.050	-1.44	0.142	-1.27	0.008	-1.01	0.522
1440950_at	Thymoma viral proto-oncogene 1	Akt1	1.08	0.834	1.21	0.095	-1.1	0.554	-1.27	0.033	1.08	0.417
1448789_at	aldehyde dehydrogenase family 1, subfamily A3	Aldh1a3	-1.04	0.532	-1.62	0.005	-1.2	0.053	-1.27	0.001	-1.17	0.011
1451159_at	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	1.47	0.419	1.01	0.617	-1.1	0.322	-1.27	0.014	-1.38	0.004
1437491_at	bicaudal D homolog 2 (Drosophila)	Bicd2	1.64	0.341	1.75	0.165	-1.21	0.321	-1.27	0.047	-1.06	0.519
1460324_at	DNA methyltransferase 3A	Dnmt3a	-1.44	0.074	-1.94	0.041	1.01	0.951	-1.27	0.026	-1.19	0.129
1418492_at	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	Grem2	1.13	0.632	-1.16	0.309	-1.26	0.031	-1.27	0.013	-1.33	0.004
1438430_at	high mobility group box transcription factor 1	Hbp1	-1.29	0.109	-1.7	0.058	-1.08	0.097	-1.27	0.035	-1.36	0.011
1438328_at	host cell factor C2	Hcfc2	1.24	0.656	-1.07	0.382	1.02	0.943	-1.27	0.020	-1.06	0.553
1446430_at	HECT domain containing 2	Hectd2	-1.09	0.550	1.05	0.985	1.21	0.647	-1.27	0.046	-1.23	0.199
1433731_at	insulin-like growth factor 2 mRNA binding protein 3	Igf2bp3	-1.3	0.181	-1.42	0.118	-1.43	0.006	-1.27	0.042	-1	0.963
1455404_at	junctophilin 2	Jph2	-1.05	0.450	-1.33	0.003	-1.14	0.117	-1.27	0.006	-1.29	0.174
1418232_s_at	LIM and senescent cell antigen-like domains 1	Lims1	1.55	0.387	1.08	0.804	-1.27	0.004	-1.27	0.009	-1.44	0.008
1455827_at	muscleblind-like 2	Mbnl2	1.45	0.445	-1.01	0.501	-1.47	0.012	-1.27	0.001	-1.63	0.019
1448061_at	macrophage scavenger receptor 1	Msr1	1.53	0.346	1.3	0.493	-1.21	0.065	-1.27	0.012	2.35	0.591
1451352_s_at	metastasis associated 3	Mta3	1.37	0.241	-1.12	0.337	-1.09	0.075	-1.27	0.008	-1.27	0.073
1433768_at	palladin, cytoskeletal associated protein	Palld	1.23	0.688	-1.11	0.305	-1.21	0.037	-1.27	0.008	-1.28	0.000
1419757_at	phosphatidylinositol transfer protein, membrane-associated 2	Pitpnm2	-1.16	0.315	-1.27	0.088	1	0.855	-1.27	0.000	-1.27	0.111
1429514_at	phosphatidic acid phosphatase type 2B	Ppap2b	1.01	0.882	-1.45	0.010	-1.14	0.085	-1.27	0.023	-1.25	0.037
1451179_a_at	quaking	Qk	-1.04	0.550	-1.36	0.003	-1.2	0.001	-1.27	0.004	-1.26	0.001
1447557_at	RAB interacting factor	Rabif	-1.25	0.339	1.01	0.976	1.09	0.752	-1.27	0.036	1.63	0.422
1451041_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	1.25	0.474	-1.39	0.145	-1.5	0.010	-1.27	0.009	-1.6	0.014
1455549_at	SEC14 and spectrin domains 1	Sestd1	-1.01	0.773	-1.33	0.021	-1.1	0.103	-1.27	0.012	-1.32	0.002
1426247_at	serine/threonine kinase 24 (STE20 homolog, yeast)	Stk24	1.04	0.823	-1.06	0.629	-1.21	0.127	-1.27	0.019	-1.35	0.001
1453302_at	transmembrane protein 81	Tmem81	1.2	0.941	1.04	0.718	1.71	0.528	-1.27	0.019	-1.03	0.776
1439539_at	translocating chain-associating membrane protein 2	Tram2	-1.15	0.163	-1.5	0.068	-1.07	0.150	-1.27	0.005	-1.14	0.212
1427258_at	tripartite motif protein 24	Trim24	1.05	0.838	-1.05	0.664	-1.07	0.046	-1.27	0.030	-1.31	0.009
1435091_at	zinc finger protein 568	Zfp568	1.22	0.527	1.13	0.591	-1.22	0.191	-1.27	0.007	-1.45	0.005
1452977_at	zinc fingers and homeoboxes 3	Zhx3	2.76	0.990	1.67	0.399	-1.07	0.380	-1.27	0.007	-1.33	0.069
1433872_at	RIKEN cDNA 2410042D21 gene	2410042D21Rik	1.02	0.857	1.01	0.986	1.05	0.604	-1.26	0.020	-1.12	0.050
1436729_at	RIKEN cDNA 2600003E23 gene	2600003E23Rik	1.06	0.528	-1.09	0.406	-1.17	0.004	-1.26	0.024	-1.29	0.003
1428829_at	RIKEN cDNA 6820401H01 gene	6820401H01Rik	-1.15	0.406	-2.32	0.129	-1.18	0.002	-1.26	0.044	-1.36	0.000
1450879_at	ATPas, class II, type 9B	Atp9b	1.12	0.754	-1.43	0.082	-1.34	0.052	-1.26	0.038	-1.8	0.018
1435883_at	expressed sequence AW413431	AW413431	2.56	0.454	-1.53	0.096	1	0.821	-1.26	0.048	-1.51	0.103
1422533_at	cytochrome P450, family 51	Cyp51	-1.16	0.311	-1.37	0.089	1.02	0.961	-1.26	0.014	1.01	0.942
1424198_at	discs, large homolog 5 (Drosophila)	Dlg5	1.23	0.345	1.17	0.800	-1.07	0.449	-1.26	0.001	-1.16	0.076
1448606_at	endothelial differentiation, lysophosphatidic acid G-protein-coupled recep	Edg2	-1.12	0.365	-1.52	0.069	-1.19	0.003	-1.26	0.001	-1.18	0.001

1417408_at	coagulation factor III	F3	1.05	0.896	-1.15	0.186	-1.14	0.051	-1.26	0.024	-1.3	0.026
1437468_x_at	F-box and WD-40 domain protein 11	Fbxw11	-1.11	0.379	-1.16	0.330	-1.05	0.338	-1.26	0.006	-1.18	0.053
1438405_at	fibroblast growth factor 7	Fgf7	1.25	0.173	1.09	0.571	-1.28	0.001	-1.26	0.003	-1.21	0.102
1460319_at	fucosyltransferase 8	Fut8	1.29	0.810	-1.67	0.056	-1.32	0.076	-1.26	0.030	-1.7	0.011
1455476_a_at	genetic suppressor element 1	Gse1	1.78	0.505	1.37	0.860	-1.22	0.089	-1.26	0.042	-1.2	0.115
1416029_at	Kruppel-like factor 10	Klf10	1.2	0.592	-1.1	0.209	-1.03	0.557	-1.26	0.001	-1.06	0.113
1435463_s_at	myosin ID	Myo1d	-1.18	0.000	-2.15	0.003	-1.29	0.000	-1.26	0.004	-1.31	0.014
1422466_at	nucleoredoxin	Nxn	-1.14	0.074	-1.25	0.153	-1.18	0.022	-1.26	0.039	-1.23	0.099
1460325_at	pumilio 1 (Drosophila)	Pum1	1.04	0.556	1.14	0.245	-1.13	0.063	-1.26	0.005	-1.17	0.036
1455310_at	RNA binding motif protein 16	Rbm16	-1.08	0.509	-1.24	0.324	-1.21	0.001	-1.26	0.000	-1.25	0.012
1419717_at	sema domain, immunoglobulin domain (Ig), short basic domain, secretec	Sema3e	1.07	0.584	-1.74	0.113	-1.2	0.358	-1.26	0.036	-1.57	0.040
1456479_at	sorting nexin family member 30	Snx30	-1.02	0.746	-1	0.965	-1.06	0.074	-1.26	0.004	-1.28	0.000
1423246_at	thioredoxin domain containing 4 (endoplasmic reticulum)	Txndc4	1.18	0.955	-1.02	0.465	-1.02	0.759	-1.26	0.041	-1.27	0.131
1416487_a_at	yes-associated protein 1	Yap1	1.29	0.502	1.03	0.746	-1.42	0.009	-1.26	0.028	-1.39	0.035
1441822_at	RIKEN cDNA 1700008F19 gene	1700008F19Rik	-1.12	0.432	-1.03	0.639	1.36	0.967	-1.25	0.016	1.56	0.086
1438379_x_at	RIKEN cDNA 2310007F21 gene	2310007F21Rik	-1.22	0.400	-1.5	0.319	-1.32	0.220	-1.25	0.020	1.24	0.359
1430419_at	RIKEN cDNA 2310031A07 gene	2310031A07Rik	1.23	0.776	1.9	0.033	-1.69	0.154	-1.25	0.006	1.12	0.385
1425913_a_at	RIKEN cDNA 2810022L02 gene	2810022L02Rik	1.14	0.835	-1.58	0.032	-1.12	0.089	-1.25	0.024	-1.31	0.028
1429691_at	RIKEN cDNA 5430405N12 gene	5430405N12Rik	1.17	0.640	-1.5	0.027	-1.62	0.027	-1.25	0.000	-1.57	0.211
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	-1.38	0.031	-2.43	0.034	-1.39	0.004	-1.25	0.012	-1.34	0.049
1438292_x_at	adenosine kinase	Adk	-1.23	0.199	-1.48	0.109	-1.15	0.107	-1.25	0.015	-1.17	0.082
1425640_at	AF4/FMR2 family, member 1	Aff1	1.4	0.353	1.09	0.857	-1.94	0.038	-1.25	0.037	-1.41	0.109
1424956_at	AT hook, DNA binding motif, containing 1	Ahdc1	1.03	0.815	1.14	0.879	-1.08	0.550	-1.25	0.039	-1.04	0.861
1440193_at	ankyrin repeat domain 12	Ankrd12	-1.17	0.413	-1.28	0.334	-1.22	0.104	-1.25	0.005	1.04	0.661
1434630_at	ankyrin repeat domain 28	Ankrd28	1.02	0.452	-1.28	0.044	-1.15	0.035	-1.25	0.025	-1.4	0.003
1438143_s_at	ataxin 2	Atxn2	-1.17	0.410	-1.11	0.450	-1.16	0.049	-1.25	0.002	-1.11	0.056
1456523_at	expressed sequence C77713	C77713	1.61	0.624	1.13	0.488	-1.28	0.002	-1.25	0.032	-1.3	0.003
1431146_a_at	copine VIII	Cpne8	1.41	0.693	-1.02	0.331	-1.19	0.158	-1.25	0.008	-1.11	0.125
1421897_at	ELK1, member of ETS oncogene family	Elk1	1.12	0.619	1.19	0.253	-1.16	0.345	-1.25	0.046	1.29	0.296
1422028_a_at	E26 avian leukemia oncogene 1, 5' domain	Ets1	-1.26	0.342	1.16	0.652	-1.27	0.083	-1.25	0.030	-1.14	0.264
1433605_at	inositol polyphosphate-5-phosphatase A	Inpp5a	-1.08	0.409	-1.43	0.015	-1.23	0.000	-1.25	0.001	-1.31	0.021
1444322_at	lipocalin 11	Lcn11	-1.35	0.179	-1.14	0.321	-1.47	0.098	-1.25	0.018	1.87	0.242
1427705_a_at	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	Nfkb1	1.08	0.418	-1.06	0.673	-1.27	0.005	-1.25	0.007	-1.3	0.009
1435881_at	poly(rC) binding protein 2	Pcbp2	-1.2	0.171	-1.45	0.072	-1.11	0.091	-1.25	0.044	1.04	0.208
1432820_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	Psmd7	2.09	0.288	1.03	0.846	2.34	0.086	-1.25	0.032	-1.06	0.841
1453406_a_at	RAB28, member RAS oncogene family	Rab28	1.06	0.835	-1.17	0.260	-1.09	0.524	-1.25	0.026	-1.17	0.126
1424330_at	SUMO1/sentrin specific peptidase 1	Senp1	-1.03	0.572	1.26	0.840	1.33	0.310	-1.25	0.009	-1.07	0.636
1448847_at	serine incorporator 3	Serinc3	1.57	0.149	1.19	0.307	1.02	0.732	-1.25	0.032	1.67	0.214
1426637_a_at	sine oculis-related homeobox 3 homolog (Drosophila)	Six3	1.2	0.203	1.44	0.013	1.03	0.995	-1.25	0.031	1.29	0.331
1454938_at	sorting nexin 13	Snx13	1.19	0.129	-1.1	0.374	-1.17	0.017	-1.25	0.008	-1.31	0.014
1427917_s_at	single-stranded DNA binding protein 3	Ssbp3	-1.21	0.148	-1.69	0.036	-1.13	0.096	-1.25	0.032	-1.07	0.397
1450406_a_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 3	St3gal3	1.09	0.508	-1.3	0.082	-1.38	0.012	-1.25	0.021	-1.26	0.094
1452061_s_at	spermatid perinuclear RNA binding protein	Strbp	-1.32	0.329	-1.57	0.218	-1.12	0.300	-1.25	0.050	-1.24	0.204
1422566_at	transcription factor EB	Tcfeb	-1.26	0.319	-1.15	0.486	2.18	0.473	-1.25	0.029	-1.07	0.603
1424652_at	transmembrane protein 166	Tmem166	1.15	0.276	1.24	0.147	-1.27	0.000	-1.25	0.004	-1.19	0.095
1427348_at	zinc finger CCCH type containing 12A	Zc3h12a	-1.1	0.391	1.01	0.876	1.23	0.754	-1.25	0.035	1.16	0.777
1419924_at	RIKEN cDNA A730024A03 gene	A730024A03Rik	-1.3	0.168	-1.09	0.488	1.12	0.927	-1.24	0.004	-1.07	0.530
1415927_at	actin, alpha, cardiac	Actc1	1.38	0.781	1.53	1.000	-1.13	0.448	-1.24	0.013	1.13	0.046
1455340_at	Expressed sequence AI852444	AI852444	1.21	0.340	-1.18	0.378	-1.09	0.139	-1.24	0.004	-1.18	0.327
1415684_at	autophagy-related 5 (yeast)	Atg5	-1.03	0.595	-1.03	0.811	-1.04	0.728	-1.24	0.014	-1.22	0.141
1435034_at	expressed sequence AW060207	AW060207	1.1	0.365	-1.23	0.254	-1.09	0.433	-1.24	0.034	-1.05	0.638
1435248_a_at	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot	Btaf1	1.09	0.044	1.07	0.348	-1.24	0.001	-1.24	0.009	-1.37	0.005
1451382_at	ChaC, cation transport regulator-like 1 (E. coli)	Chac1	-1.22	0.007	-2.44	0.001	-1.18	0.052	-1.24	0.002	-1.32	0.001
1458263_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	1.08	0.701	1.3	0.881	1.02	0.735	-1.24	0.025	-1.07	0.556
1431618_a_at	DNA segment, Chr 14, ERATO Doi 581, expressed	D14Ertd581e	4.82	0.443	3.57	0.925	-1.42	0.009	-1.24	0.037	-1.67	0.107
1438045_at	early endosome antigen 1	Eea1	1.27	0.275	-1.34	0.109	-1.29	0.027	-1.24	0.012	-1.59	0.038
1428470_at	exocyst complex component 2	Exoc2	1.09	0.046	-1.23	0.027	-1.16	0.292	-1.24	0.004	-1.13	0.443
1442059_at	fragile X mental retardation gene 1, autosomal homolog	Fxr1h	1.04	0.559	1.19	0.732	-1.22	0.064	-1.24	0.023	-1.2	0.299

1425969_a_at	Huntington disease gene homolog	Hdh	-1.27	0.254	-1.45	0.160	-1.24	0.029	-1.24	0.034	-1.41	0.002
1425142_a_at	heterogeneous nuclear ribonucleoprotein D	Hnrpd	-1.11	0.036	-1.3	0.026	-1.29	0.008	-1.24	0.008	-1.19	0.103
1435720_at	potassium voltage-gated channel, Shal-related family, member 3	Kcnd3	1.2	0.975	1.77	0.239	1.12	0.981	-1.24	0.031	1.22	0.930
1418594_a_at	nuclear receptor coactivator 1	Ncoa1	-1.11	0.410	-2.39	0.051	-1.23	0.026	-1.24	0.028	-1.63	0.009
1443319_at	phosphoprotein associated with glycosphingolipid microdomains 1	Pag1	1.83	0.166	2.55	0.079	1.96	0.167	-1.24	0.008	-1.07	0.846
1437360_at	protocadherin 19	Pcdh19	-1.09	0.301	-1.94	0.011	-1.42	0.026	-1.24	0.034	-1.48	0.003
1460263_at	Programmed cell death 6 interacting protein	Pdcd6ip	-1.25	0.329	-1.21	0.313	1.04	0.519	-1.24	0.048	1.09	0.197
1418406_at	phosphodiesterase 8A	Pde8a	1.09	0.309	-1.25	0.126	-1.22	0.072	-1.24	0.002	-1.16	0.017
1435836_at	pyruvate dehydrogenase kinase, isoenzyme 1	Pdk1	-1.03	0.499	1.04	0.407	1.15	0.131	-1.24	0.044	1.09	0.056
1438854_x_at	phosphatidylinositol membrane-associated 1	Pitpnm1	1.08	0.738	1.11	0.509	1.05	0.914	-1.24	0.030	1.32	0.029
1436616_at	expressed sequence R74740	R74740	1.22	0.245	-1.14	0.343	1.09	0.582	-1.24	0.013	1.06	0.776
1424188_at	RAB GTPase activating protein 1	Rabgap1	1.18	0.270	1.14	0.433	-1.12	0.122	-1.24	0.005	-1.45	0.001
1448689_at	related RAS viral (r-ras) oncogene homolog 2	Rras2	1.06	0.308	-1.18	0.079	-1.24	0.005	-1.24	0.007	-1.4	0.002
1427640_a_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	Runx1t1	1.09	0.464	-1.58	0.153	-1.22	0.207	-1.24	0.027	-1.46	0.050
1444644_x_at	TatD DNase domain containing 1	Tatdn1	-1.18	0.327	1.05	0.890	-1.04	0.286	-1.24	0.041	1.21	0.150
1444004_at	THO complex 2	Thoc2	-1.03	0.614	-1.19	0.354	-1.26	0.140	-1.24	0.041	-1.31	0.017
1448396_at	transmembrane protein 131	Tmem131	-1.06	0.182	-1.16	0.104	-1.11	0.472	-1.24	0.044	-1.25	0.000
1434560_at	WD and tetratricopeptide repeats 1	Wdtc1	1.44	0.829	-1.43	0.241	1.27	0.310	-1.24	0.018	1.62	0.010
1435072_at	zinc finger, FYVE domain containing 1	Zfyve1	1.19	0.279	1.22	0.162	-1.13	0.423	-1.24	0.006	1.13	0.344
1439967_at	RIKEN cDNA 1700071A11 gene	1700071A11Rik	-1.21	0.345	-1.2	0.391	1.23	0.704	-1.23	0.001	1.06	0.795
1434620_s_at	RIKEN cDNA 2610024E20 gene	2610024E20Rik	-1.05	0.532	-1.15	0.157	-1.18	0.105	-1.23	0.035	-1.25	0.182
1421172_at	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	Adam12	1.01	0.686	-1.48	0.109	-1.38	0.024	-1.23	0.050	-1.53	0.001
1436640_x_at	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid a	Agpat4	-1.12	0.373	-1.41	0.232	1.01	0.968	-1.23	0.008	-1.3	0.039
1455306_at	cDNA sequence BC037112	BC037112	1.11	0.674	1.18	0.418	-1.06	0.448	-1.23	0.029	-1.46	0.000
1434757_at	core-binding factor, runt domain, alpha subunit 2, translocated to, 2 hom	Cbfa2t2h	-1.1	0.404	-1.05	0.469	1.01	0.942	-1.23	0.002	-1.16	0.071
1429455_at	GTPase activating protein and VPS9 domains 1	Gapvd1	1.05	0.856	1.07	0.628	1.12	0.098	-1.23	0.018	-1.05	0.423
1423569_at	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	Gatm	1.26	0.148	1.11	0.532	1.36	0.573	-1.23	0.033	1.02	0.837
1429088_at	limb-bud and heart	Lbh	-1.1	0.117	-1.42	0.025	-1.13	0.057	-1.23	0.048	-1.24	0.055
1422706_at	similar to Nedd4 WW binding protein 4	LOC637870	-1.1	0.144	-1.44	0.004	-1.14	0.047	-1.23	0.004	-1.16	0.030
1425029_a_at	membrane bound O-acyltransferase domain containing 2	Mboat2	-1.35	0.196	-1.6	0.076	-1.1	0.202	-1.23	0.004	-1.06	0.805
1456772_at	neutrophil cytosolic factor 1	Ncf1	1.12	0.614	1.06	0.808	1.04	0.665	-1.23	0.032	1.76	0.213
1415729_at	3-phosphoinositide dependent protein kinase-1	Pdpk1	-1.11	0.214	-1.25	0.017	-1.02	0.513	-1.23	0.003	-1.16	0.047
1460398_at	PHD finger protein 8	Phf8	1.06	0.855	1.01	0.748	1.01	0.928	-1.23	0.001	-1.35	0.007
1427006_at	Rap guanine nucleotide exchange factor (GEF) 1	Rapgef1	-1.09	0.110	-1.27	0.032	-1.04	0.685	-1.23	0.021	-1.19	0.214
1454962_at	spire homolog 1 (Drosophila)	Spire1	1.1	0.264	-1.21	0.048	-1.14	0.030	-1.23	0.038	-1.39	0.006
1418755_at	T-box 15	Tbx15	-1.06	0.513	-1.1	0.253	1.15	0.548	-1.23	0.024	-1.39	0.033
1418145_at	tuftelin interacting protein 11	Tfip11	1.38	0.249	1.35	0.444	-1.21	0.170	-1.23	0.011	1.36	0.243
1431827_a_at	tousled-like kinase 2 (Arabidopsis)	Tlk2	4.49	0.363	3.56	0.513	-1.15	0.087	-1.23	0.027	-1.58	0.015
1449033_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegeri	Tnfrsf11b	-1.12	0.257	-1.21	0.170	1.01	0.954	-1.23	0.030	1.35	0.058
1436982_at	trinucleotide repeat containing 6b	Tnrc6b	1.03	0.876	-1.34	0.049	-1.09	0.190	-1.23	0.033	-1.29	0.015
1456623_at	tropomyosin 1, alpha	Tpm1	-1.04	0.504	-1.27	0.015	-1.28	0.212	-1.23	0.025	-1.15	0.141
1448146_at	WW domain containing E3 ubiquitin protein ligase 2	Wwp2	-1.28	0.291	-1.29	0.321	-1.03	0.675	-1.23	0.014	-1.3	0.150
1435669_at	zinc finger protein 532	Zfp532	1.93	0.373	1.69	0.624	-1.15	0.037	-1.23	0.025	-1.25	0.035
1459722_at	Zinc finger, SWIM domain containing 6	Zswim6	-1.26	0.337	-1.27	0.300	1.13	0.493	-1.23	0.004	-1.95	0.011
1452415_at	actinin, alpha 1	Actn1	1.28	0.818	-1	0.411	-1.19	0.056	-1.22	0.049	-1.29	0.009
1460712_s_at	adaptor protein complex AP-1, gamma 1 subunit	Ap1g1	-1.19	0.254	-1.13	0.053	-1.03	0.569	-1.22	0.028	-1.31	0.008
1454916_s_at	ADP-ribosylation factor interacting protein 1	Arfip1	1.01	0.891	-1.38	0.004	-1.19	0.078	-1.22	0.002	-1.4	0.022
1439814_at	ATPase, class I, type 8B, member 4	Atp8b4	-1.01	0.572	-1.56	0.153	-1.02	0.669	-1.22	0.009	-1.19	0.048
1417861_at	cyclin C	Ccnc	1.91	0.450	1.76	0.661	1.09	0.247	-1.22	0.047	1.04	0.651
1459118_at	hypothetical protein D230038C21	D230038C21	-1.1	0.733	-1.05	0.572	-1.06	0.501	-1.22	0.037	-1.29	0.195
1431011_at	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarat	Dlst	-1.03	0.491	-1.15	0.212	1.31	0.299	-1.22	0.019	1.35	0.285
1433776_at	lipoma HMGIC fusion partner	Lhfp	-1.01	0.728	-1.35	0.002	-1.23	0.000	-1.22	0.037	-1.29	0.005
1449362_a_at	misshapen-like kinase 1 (zebrafish)	Mink1	-1.17	0.350	-1.14	0.278	1.07	0.845	-1.22	0.030	1.27	0.056
1425504_at	myosin, light polypeptide kinase	Mylk	12.03	0.493	9.38	0.686	-1.01	0.977	-1.22	0.016	-1.02	0.539
1439154_at	nucleoporin 98	Nup98	1.1	0.307	-1.03	0.635	-1.13	0.100	-1.22	0.050	-1.41	0.012
1420851_at	par-6 partitioning defective 6 homolog gamma (C. elegans)	Pard6g	1.08	0.545	1.09	0.792	-1.03	0.546	-1.22	0.016	-1.08	0.225
1418036_at	DNA primase, p58 subunit	Prim2	1.02	0.738	-1.47	0.005	-1.1	0.249	-1.22	0.042	-1.37	0.005
1455359_at	protein tyrosine phosphatase, non-receptor type 14	Ptpn14	-1.07	0.367	-1.2	0.086	1.04	0.148	-1.22	0.020	-1.21	0.004

1425266_a_at	RAP1, GTP-GDP dissociation stimulator 1	Rap1gds1	1.21	0.584	-1.07	0.398	-1.11	0.057	-1.22	0.032	-1.21	0.002
1437378_x_at	scavenger receptor class B, member 1	Scarb1	-1.27	0.293	-1.18	0.403	-1.1	0.306	-1.22	0.003	-1.08	0.463
1428929_s_at	solute carrier family 25 (mitochondrial carrier, phosphate carrier), membe	Slc25a26	-1.1	0.527	-1.42	0.018	-1.06	0.677	-1.22	0.045	-1.09	0.464
1423621_a_at	solute carrier family 33 (acetyl-CoA transporter), member 1	Slc33a1	-1.28	0.164	-1.29	0.100	-1.15	0.141	-1.22	0.004	-1.11	0.367
1433648_at	sperm associated antigen 9	Spag9	1.08	0.400	-1.4	0.049	-1.34	0.002	-1.22	0.021	-1.36	0.006
1420043_s_at	THO complex 1	Thoc1	-1.14	0.370	1.29	0.591	1.22	0.264	-1.22	0.020	1.41	0.020
1459666_at	trafficking protein, kinesin binding 1	Trak1	-1.26	0.096	-1.4	0.005	-1.36	0.020	-1.22	0.046	-1.4	0.044
1426881_at	ubiquitin protein ligase E3C	Ube3c	1.02	0.543	-1.19	0.225	-1.19	0.002	-1.22	0.021	-1.36	0.052
1426700_a_at	ubiquitin specific peptidase 52	Usp52	1.38	0.344	1.32	0.261	1.09	0.859	-1.22	0.039	1.2	0.559
1425074_at	Werner syndrome homolog (human)	Wrn	-1.05	0.530	-1.61	0.006	-1.23	0.210	-1.22	0.021	-1.06	0.699
1459048_s_at	zinc finger protein 142	Zfp142	-1.19	0.272	-1.01	0.725	1.13	0.267	-1.22	0.001	1.12	0.311
1444107_at	RIKEN cDNA 9430029N19 gene	9430029N19Rik	-1.11	0.144	-1.15	0.181	-1.05	0.585	-1.21	0.032	1.02	0.620
1434447_at	expressed sequence AI838057	AI838057	1.12	0.150	-1.23	0.171	1.14	0.718	-1.21	0.031	-1.17	0.120
1438270_at	expressed sequence AI846148	AI846148	1.07	0.839	1.09	0.601	-1.06	0.668	-1.21	0.021	1.08	0.273
1426301_at	activated leukocyte cell adhesion molecule	Alcam	1.05	0.985	-1.47	0.130	-1.16	0.145	-1.21	0.005	-1.08	0.390
1450717_at	angiogenin, ribonuclease A family, member 1	Ang1	1.39	0.202	1.37	0.023	-1.19	0.065	-1.21	0.038	-1.19	0.043
1454745_at	Rho GTPase activating protein 29	Arhgap29	1.03	0.217	-1.1	0.074	-1.22	0.048	-1.21	0.009	-1.3	0.015
1434215_at	RIKEN cDNA B230308N11 gene	B230308N11Rik	-1.04	0.651	-1.32	0.123	-1.17	0.031	-1.21	0.022	-1.25	0.013
1451729_at	bone morphogenetic protein receptor, type 1A	Bmpr1a	-1.31	0.335	-1.46	0.283	-1.24	0.087	-1.21	0.040	1.27	0.198
1454874_at	BTB (POZ) domain containing 7	Btbd7	1.05	0.276	-1.01	0.788	-1.02	0.663	-1.21	0.015	-1.27	0.007
1426669_at	RIKEN cDNA C530044N13 gene	C530044N13Rik	-1.06	0.501	1.1	0.425	1.04	0.757	-1.21	0.020	1.17	0.271
1423942_a_at	calcium/calmodulin-dependent protein kinase II gamma	Camk2g	1.31	0.471	1.02	0.759	-1.08	0.408	-1.21	0.014	-1.16	0.012
1446399_at	cadherin 10	Cdh10	2.4	0.365	2.16	0.284	-1.24	0.243	-1.21	0.032	1.32	0.133
1438211_s_at	D site albumin promoter binding protein	Dbp	-1.04	0.577	1.24	0.490	1.11	0.993	-1.21	0.003	1.55	0.032
1437763_at	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisia	Dcun1d3	-1.01	0.648	-1.01	0.672	-1.06	0.310	-1.21	0.007	-1.06	0.560
1422738_at	discoidin domain receptor family, member 2	Ddr2	-1.03	0.652	-1.54	0.081	-1.34	0.119	-1.21	0.003	-1.2	0.060
1433490_s_at	erythrocyte protein band 4.1-like 2	Epb4.1l2	1.08	0.509	-1.23	0.099	-1.25	0.006	-1.21	0.013	-1.32	0.000
1420933_a_at	eyes absent 3 homolog (Drosophila)	Eya3	-1.1	0.342	-1.12	0.221	-1.09	0.266	-1.21	0.015	-1.22	0.063
1449121_at	FUS interacting protein (serine-arginine rich) 1	Fusip1	1.06	0.950	-1.12	0.191	1.37	0.446	-1.21	0.045	1.22	0.277
1447470_at	haloacid dehalogenase-like hydrolase domain containing 2	Hdhd2	1.06	0.387	1.25	0.636	1.25	0.261	-1.21	0.020	1.58	0.481
1452237_at	HIV-1 Rev binding protein	Hrb	1.16	0.116	1.09	0.461	-1.15	0.038	-1.21	0.040	-1.26	0.023
1436510_a_at	leucine rich repeat (in FLII) interacting protein 2	Lrrfip2	-1.2	0.403	-1.72	0.278	-1.16	0.046	-1.21	0.043	-1.23	0.054
1456462_x_at	protein phosphatase 1, catalytic subunit, beta isoform	Ppp1cb	-1.37	0.220	-1.14	0.385	-1	0.890	-1.21	0.013	1.25	0.191
1417850_at	retinoblastoma 1	Rb1	1	0.850	-1.5	0.074	1.08	0.263	-1.21	0.001	-1.11	0.380
1434336_s_at	REST corepressor 1	Rcor1	-1.01	0.527	1.09	0.277	-1.03	0.664	-1.21	0.040	-1.12	0.356
1457116_at	REX1, RNA exonuclease 1 homolog (S. cerevisiae)	Rexo1	-1.33	0.177	-1.03	0.696	-1.19	0.355	-1.21	0.017	1.45	0.182
1436660_at	ribosome binding protein 1	Rrbp1	-1.18	0.172	-1.33	0.030	-1.17	0.270	-1.21	0.004	-1.4	0.090
1452261_at	SNF2 histone linker PHD RING helicase	Shprh	2.02	0.449	2.76	0.467	1.14	0.411	-1.21	0.036	-1.26	0.050
1427916_at	suppression of tumorigenicity 7-like	St7l	1.28	0.367	1.05	0.778	-1.19	0.136	-1.21	0.007	-1.2	0.068
1450923_at	transforming growth factor, beta 2	Tgfb2	-1.01	0.934	-1.63	0.002	-1.18	0.125	-1.21	0.022	-1.27	0.025
1422705_at	transmembrane, prostate androgen induced RNA	Tmepai	1.45	0.421	1.05	0.543	-1.34	0.014	-1.21	0.029	-1.18	0.012
1447522_s_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	Tnks2	-1.2	0.364	-1.23	0.314	-1.02	0.678	-1.21	0.046	-1.12	0.272
1426771_at	taurine upregulated gene 1	Tug1	-1.07	0.473	-1.19	0.055	-1.03	0.710	-1.21	0.046	-1.31	0.091
1454643_at	ubiquitin associated protein 2-like	Ubap2l	-1.17	0.331	-1.25	0.227	-1.08	0.262	-1.21	0.041	-1.23	0.041
1455094_s_at	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	1.02	0.835	-1.12	0.169	-1.06	0.283	-1.21	0.029	-1.25	0.043
1422759_a_at	exportin 6	Xpo6	1.18	0.709	1.06	0.826	-1.15	0.114	-1.21	0.043	-1.36	0.000
1439411_a_at	exportin 7	Xpo7	-1.23	0.378	-1.64	0.211	-1.08	0.053	-1.21	0.040	-1.29	0.003
1440999_at	zinc finger protein 697	Zfp697	1.16	0.470	1.01	0.896	-1.12	0.132	-1.21	0.003	-1.2	0.104
1427112_at	RIKEN cDNA 2700049H19 gene	2700049H19Rik	3.15	0.543	3.29	0.201	1.1	0.180	-1.2	0.036	1.04	0.198
1451434_s_at	RIKEN cDNA 5430405G24 gene	5430405G24Rik	1.06	0.730	1.28	0.228	-1.12	0.407	-1.2	0.035	-1	0.893
1436353_at	RIKEN cDNA A230046K03 gene	A230046K03Rik	-1.15	0.068	1.02	0.768	-1.21	0.094	-1.2	0.001	1.02	0.804
1452359_at	expressed sequence AA536743	AA536743	-1.15	0.368	-1.43	0.211	-1.02	0.504	-1.2	0.039	-1.11	0.046
1451526_at	Rho GTPase activating protein 12	Arhgap12	-1.12	0.450	-1.3	0.253	-1.17	0.175	-1.2	0.010	-1.29	0.013
1436498_at	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Dro	Arih1	1.44	0.410	1.05	0.737	-1.35	0.007	-1.2	0.046	-1.51	0.018
1454952_s_at	RIKEN cDNA B130055D15 gene	B130055D15Rik	-1.11	0.490	-1.14	0.384	-1.03	0.559	-1.2	0.016	-1.05	0.434
1434656_at	RIKEN cDNA B230339M05 gene	B230339M05Rik	1	0.631	-1.19	0.342	-1.06	0.420	-1.2	0.031	-1.24	0.058
1443899_at	cDNA sequence BC028799 /// RIKEN cDNA 4922501C03 gene	BC028799 /// 49225	1.14	0.855	-1.06	0.598	1.24	0.422	-1.2	0.041	1.02	0.515
1452381_at	cAMP responsive element binding protein 3-like 2	Creb3l2	1.01	0.996	-1.42	0.052	-1.22	0.042	-1.2	0.046	-1.43	0.010

1453372_at	DnaJ (Hsp40) homolog, subfamily C, member 1	Dnajc1	1.05	0.384	-1.35	0.013	-1.38	0.031	-1.2	0.010	-1.51	0.009
1417164_at	dual specificity phosphatase 10	Dusp10	-1.02	0.615	1.01	0.682	-1.17	0.069	-1.2	0.011	-1.11	0.133
1437199_at	dual specificity phosphatase 5	Dusp5	-1.05	0.880	-1.21	0.082	-1.02	0.856	-1.2	0.014	1.01	0.619
1433474_at	EGF-like repeats and discoidin I-like domains 3	Edil3	-1.13	0.248	-1.27	0.077	-1.13	0.115	-1.2	0.024	-1.35	0.015
1416916_at	E74-like factor 3	Elf3	1.26	0.541	1.61	0.180	1.13	0.850	-1.2	0.007	1.16	0.768
1448797_at	ELK3, member of ETS oncogene family	Elk3	-1.03	0.447	-1.14	0.156	-1.03	0.505	-1.2	0.002	-1.17	0.099
1456378_s_at	F-box and leucine-rich repeat protein 20	Fbxl20	-1.23	0.305	-1.32	0.173	-1.04	0.471	-1.2	0.007	-1.08	0.103
1424050_s_at	fibroblast growth factor receptor 1	Fgfr1	-1.25	0.071	-1.24	0.207	-1.07	0.361	-1.2	0.040	-1.01	0.893
1437718_x_at	fibromodulin	Fmod	-1.33	0.350	-1.16	0.438	-1	0.654	-1.2	0.040	1.01	0.687
1453851_a_at	growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	1.03	0.571	-1.08	0.152	-1.21	0.101	-1.2	0.018	-1.32	0.004
1423267_s_at	integrin alpha 5 (fibronectin receptor alpha)	Itga5	1.14	0.849	-1.29	0.191	-1.17	0.144	-1.2	0.050	-1.24	0.082
1451783_a_at	kinesin-associated protein 3	Kifap3	-1.13	0.263	-1.42	0.046	-1.1	0.078	-1.2	0.025	-1.11	0.033
1429005_at	malignant fibrous histiocytoma amplified sequence 1	Mfhas1	-1.16	0.321	-1.23	0.236	-1.1	0.167	-1.2	0.015	-1.18	0.126
1437055_x_at	Major facilitator superfamily domain containing 1	Mfsd1	-1.27	0.255	-1.13	0.618	1.2	0.621	-1.2	0.028	1.21	0.042
1448528_at	programmed cell death 10	Pdcd10	-1.08	0.488	-1.04	0.534	-1.34	0.123	-1.2	0.023	-1.43	0.024
1434948_at	RAB11 family interacting protein 2 (class I)	Rab11fip2	1.22	0.425	1.36	0.493	1.03	0.713	-1.2	0.025	-1.04	0.708
1438505_s_at	ribonuclease III, nuclear	Rnasen	-1.47	0.328	-1.4	0.344	-1.03	0.801	-1.2	0.003	-1	0.815
1426972_at	SEC24 related gene family, member D (S. cerevisiae)	Sec24d	1.5	0.429	1.13	0.627	-1.21	0.081	-1.2	0.026	-1.33	0.002
1454683_at	splicing factor, arginine/serine-rich 8	Sfrs8	-1.2	0.138	1.07	0.499	-1.13	0.608	-1.2	0.032	-1.07	0.690
1423865_at	solute carrier family 44, member 1	Slc44a1	-1.23	0.117	-1.07	0.491	1.16	0.424	-1.2	0.003	1.01	0.949
1424659_at	slit homolog 2 (Drosophila)	Slit2	-1.27	0.100	-1.7	0.044	-1.22	0.043	-1.2	0.015	-1.22	0.025
1421849_at	stromal antigen 2	Stag2	1.11	0.101	-1.19	0.133	-1.13	0.081	-1.2	0.016	-1.3	0.002
1423535_at	striatin, calmodulin binding protein 3	Strn3	1.07	0.353	-1.03	0.634	-1.23	0.015	-1.2	0.005	-1.24	0.071
1455024_at	tousled-like kinase 1	Tlk1	1.18	0.269	1.03	0.989	-1.13	0.003	-1.2	0.006	-1.21	0.045
1435030_at	UPF2 regulator of nonsense transcripts homolog (yeast)	Upf2	-1.04	0.617	-1.16	0.380	-1.11	0.265	-1.2	0.019	-1.4	0.027
1418479_at	vacuolar protein sorting 54 (yeast)	Vps54	1.05	0.658	-1.17	0.013	-1.23	0.003	-1.2	0.023	-1.35	0.019
1418083_at	RIKEN cDNA 0610009B22 gene	0610009B22Rik	1.1	0.149	1.28	0.264	1.15	0.281	1.2	0.040	1.22	0.182
1432848_a_at	RIKEN cDNA 1200004M23 gene	1200004M23Rik	1.57	0.351	1.87	0.146	1.08	0.391	1.2	0.001	1.11	0.107
1419660_at	RIKEN cDNA 1600012F09 gene	1600012F09Rik	1.2	0.080	1.36	0.009	1.09	0.063	1.2	0.028	1.15	0.111
1451334_at	RIKEN cDNA 1810009O10 gene	1810009O10Rik	-1.01	0.786	1.3	0.078	1.13	0.010	1.2	0.005	1.23	0.048
1435238_x_at	RIKEN cDNA 2310009A05 gene	2310009A05Rik	-1.07	0.504	1.04	0.746	1.1	0.376	1.2	0.020	1.11	0.320
1417218_at	RIKEN cDNA 2810048G17 gene	2810048G17Rik	1.1	0.459	1.22	0.180	1.23	0.047	1.2	0.004	1.12	0.000
1428128_at	RIKEN cDNA 4921506J03 gene	4921506J03Rik	-1.06	0.484	1.14	0.236	1.11	0.021	1.2	0.019	1.18	0.029
1434601_at	adhesion molecule with Ig like domain 2	Amigo2	1.8	0.196	2.14	0.237	2.63	0.690	1.2	0.044	2.06	0.224
1438661_a_at	ADP-ribosylation factor 2	Arf2	1.98	0.417	1.94	0.028	-1.07	0.358	1.2	0.011	1.12	0.183
1439063_at	additional sex combs like 2 (Drosophila)	Asxl2	1.02	0.903	1.54	0.026	1.15	0.362	1.2	0.033	-1.03	0.558
1451246_s_at	aurora kinase B	Aurkb	1.11	0.005	1.36	0.019	1.18	0.041	1.2	0.005	1.29	0.028
1452628_at	BCL2-associated athanogene 5	Bag5	1.16	0.278	1.35	0.074	1.01	0.863	1.2	0.001	1.05	0.512
1420632_a_at	Bernardinelli-Seip congenital lipodystrophy 2 homolog (human)	Bscl2	-1.15	0.255	-1.04	0.591	-1.05	0.510	1.2	0.015	1.01	0.647
1450846_at	basic leucine zipper and W2 domains 1	Bzw1	4.33	0.253	4.76	0.324	1.02	0.757	1.2	0.038	1.01	0.982
1428759_s_at	coiled-coil domain containing 49	Ccdc49	1.3	0.436	1.49	0.059	-1	0.890	1.2	0.049	1.08	0.694
1428131_a_at	CDC42 small effector 1	Cdc42se1	-1.1	0.226	-1.03	0.578	1.08	0.255	1.2	0.036	1.13	0.135
1435863_at	COMM domain containing 6	Commd6	1.44	0.059	1.63	0.012	1.12	0.038	1.2	0.044	1.26	0.012
1429078_a_at	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsi	Cops7a	1.34	0.362	1.32	0.290	1.01	0.850	1.2	0.033	1.05	0.306
1433859_at	RIKEN cDNA D030070L09 gene	D030070L09Rik	1.42	0.240	1.52	0.180	1.1	0.122	1.2	0.004	1.09	0.021
1425228_a_at	deoxyguanosine kinase	Dguok	2.35	0.354	2.32	0.136	1.09	0.310	1.2	0.003	1.25	0.060
1452797_at	FAST kinase domains 3	Fastkd3	1.14	0.345	1.49	0.007	1.21	0.005	1.2	0.009	1.02	0.430
1420374_at	forkhead box J2	Foxj2	-1.24	0.347	-1.15	0.377	1.17	0.420	1.2	0.001	1.12	0.182
1426783_at	GCN5 general control of amino acid synthesis-like 2 (yeast)	Gcn5l2	-1.08	0.345	1.12	0.446	1.14	0.018	1.2	0.026	1.31	0.031
1435925_at	G protein-coupled receptor kinase-interactor 2	Git2	-1.04	0.573	1.01	0.802	1.01	0.824	1.2	0.032	1.11	0.242
1416708_a_at	GRAM domain containing 1A	Gramd1a	-1.03	0.284	1.1	0.024	1.18	0.052	1.2	0.011	1.2	0.048
1423382_a_at	heterogeneous nuclear ribonucleoprotein F /// similar to heterogeneous r	Hnrpf /// LOC63700	1.83	0.327	1.86	0.222	1	0.853	1.2	0.022	1.02	0.738
1454996_at	hydroxysteroid dehydrogenase like 1	Hsdl1	-1.05	0.435	1.15	0.383	1.26	0.017	1.2	0.000	1.33	0.050
1419455_at	interleukin 10 receptor, beta	Il10rb	1.67	0.199	1.91	0.049	1.28	0.128	1.2	0.002	1.31	0.001
1415911_at	imprinted and ancient	Impact	1.25	0.155	1.35	0.085	1.04	0.585	1.2	0.044	1.14	0.021
1426111_x_at	interferon regulatory factor 3	Irf3	-1.12	0.280	-1.09	0.258	-1.01	0.630	1.2	0.008	1.08	0.040
1451214_at	kelch repeat and BTB (POZ) domain containing 2	Kbtbd2	1.15	0.412	1.22	0.284	1.15	0.035	1.2	0.033	1.05	0.285
1416106_at	KTI12 homolog, chromatin associated (S. cerevisiae)	Kti12	1.11	0.270	1.43	0.013	1.16	0.005	1.2	0.008	1.22	0.013

1450204_a_at	myoneurin	Mynn	1.2	0.321	1.22	0.089	1.1	0.963	1.2	0.042	-1.04	0.660
1419666_x_at	nuclear protein 1	Nupr1	1.33	0.310	1.16	0.663	1.06	0.433	1.2	0.010	1.01	0.957
1422488_at	NTF2-related export protein 1	Nxt1	1	0.969	1.29	0.020	1.11	0.019	1.2	0.042	1.1	0.390
1419760_a_at	open reading frame 5	ORF5	-1.11	0.347	1.04	0.717	1.05	0.640	1.2	0.035	1.1	0.061
1450630_at	queuine tRNA-ribosyltransferase 1	Qtrt1	1.31	0.241	1.39	0.014	1.11	0.759	1.2	0.024	1.26	0.106
1429528_at	RAE1 RNA export 1 homolog (S. pombe)	Rae1	2.41	0.293	2.69	0.217	1.09	0.387	1.2	0.026	1.1	0.313
1426426_at	RNA binding motif protein 13	Rbm13	1.14	0.266	1.39	0.052	1.15	0.030	1.2	0.008	1.2	0.017
1418859_at	regulatory factor X-associated protein	Rfxap	1.01	0.612	1.27	0.032	1.05	0.637	1.2	0.000	1.08	0.201
1422668_at	serine (or cysteine) peptidase inhibitor, clade B, member 9b	Serpinb9b	1.2	0.069	1.2	0.156	1.22	0.202	1.2	0.009	1.17	0.115
1448132_at	solute carrier family 19 (sodium/hydrogen exchanger), member 1	Slc19a1	1.85	0.455	2.16	0.165	1.13	0.572	1.2	0.030	1.26	0.087
1436007_a_at	THUMP domain containing 1	Thumpd1	1.81	0.548	2.13	0.234	1.11	0.278	1.2	0.050	1.05	0.129
1416346_at	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	Timm8a1	1.14	0.110	1.36	0.014	1.14	0.003	1.2	0.006	1.16	0.141
1454836_at	transmembrane protein 18	Tmem18	1.03	0.718	1.17	0.156	1.18	0.136	1.2	0.026	1.24	0.009
1454861_at	taxilin alpha	Txlna	1.01	0.906	1.32	0.068	1.18	0.089	1.2	0.006	1.26	0.004
1435824_at	YY1 transcription factor	Yy1	-1.02	0.725	-1.1	0.317	1.04	0.451	1.2	0.003	1.05	0.189
1451277_at	zinc binding alcohol dehydrogenase, domain containing 2	Zadh2	-1.03	0.595	1.13	0.515	1.26	0.005	1.2	0.032	1.22	0.076
1457285_at	zinc finger protein 187	Zfp187	1.33	0.116	1.58	0.070	1.2	0.088	1.2	0.016	1.25	0.011
1424892_at	zinc finger protein 95	Zfp95	1.17	0.399	1.53	0.031	1.25	0.032	1.2	0.031	1.47	0.023
1428593_at	RIKEN cDNA 1700029F09 gene	1700029F09Rik	1.06	0.328	1.19	0.125	1.16	0.044	1.21	0.035	1.14	0.036
1435076_at	RIKEN cDNA 2310047D13 gene	2310047D13Rik	1.2	0.442	1.31	0.162	1.25	0.025	1.21	0.009	1.05	0.487
1416439_at	RIKEN cDNA 2410015N17 gene	2410015N17Rik	1.13	0.046	1.36	0.032	1.15	0.232	1.21	0.016	1.26	0.148
1455878_at	RIKEN cDNA 2700023E23 gene	2700023E23Rik	1.04	0.772	1.03	0.992	1.04	0.581	1.21	0.021	1.11	0.364
1434870_at	RIKEN cDNA 2810004N23 gene	2810004N23Rik	-1.06	0.490	1.09	0.885	1.08	0.555	1.21	0.014	1.09	0.386
1453028_at	RIKEN cDNA 4631424J17 gene	4631424J17Rik	1.72	0.142	2.19	0.094	1.18	0.033	1.21	0.020	1	0.852
1437089_at	RIKEN cDNA 4833409A17 gene	4833409A17Rik	1.2	0.077	1.03	0.820	1.2	0.735	1.21	0.009	-1.02	0.544
1454621_s_at	RIKEN cDNA 5730472N09 gene	5730472N09Rik	1.21	0.373	1.33	0.349	1.08	0.435	1.21	0.026	1.08	0.613
1428457_at	RIKEN cDNA 5830472M02 gene	5830472M02Rik	1.29	0.161	1.57	0.024	1.18	0.058	1.21	0.005	1.24	0.016
1442093_at	Arginine decarboxylase	Adc	-1.05	0.449	1.07	0.463	-1.01	0.804	1.21	0.029	1.41	0.373
1434544_at	bolA-like 2 (E. coli)	Bola2	1.02	0.825	1.01	0.750	1.19	0.121	1.21	0.009	1.09	0.487
1452414_s_at	coiled-coil domain containing 86	Ccdc86	1.2	0.320	1.66	0.012	1.11	0.228	1.21	0.028	1.3	0.066
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	1.16	0.333	1.69	0.005	1.25	0.005	1.21	0.002	1.29	0.003
1454641_at	CGG triplet repeat binding protein 1	Cggbp1	-1.02	0.715	1.08	0.264	1.15	0.244	1.21	0.020	1.16	0.014
1455723_at	DNA segment, Chr 1, ERATO Doi 448, expressed	D1Ertd448e	1.95	0.648	2.24	0.125	1.33	0.060	1.21	0.018	1.23	0.046
1455757_at	DNA segment, Chr 3, ERATO Doi 254, expressed	D3Ertd254e	1.11	0.415	1.28	0.212	1.01	0.935	1.21	0.019	1.21	0.048
1417506_at	geminin	Gmnn	1.06	0.876	1.21	0.429	1.24	0.081	1.21	0.015	1.13	0.027
1424617_at	interferon-induced protein 35	Ifi35	2.33	0.156	2.85	0.106	1.01	0.849	1.21	0.044	1.13	0.510
1417064_at	jagunal homolog 1 (Drosophila)	Jagn1	1.42	0.463	1.46	0.106	1.08	0.373	1.21	0.024	1.05	0.399
1450747_at	kelch-like ECH-associated protein 1	Keap1	2.39	0.403	3.27	0.287	1.16	0.364	1.21	0.027	-1.01	0.891
1416621_at	lethal giant larvae homolog 1 (Drosophila)	Llgl1	-1.19	0.302	-1.05	0.515	1.09	0.071	1.21	0.018	1.14	0.202
1442246_at	hypothetical protein LOC668224 /// hypothetical protein LOC669738 /// h	LOC668224 /// LOC	-2.16	0.143	-1.48	0.258	-1.27	0.328	1.21	0.035	3.31	0.268
1429176_at	leucine rich repeat and sterile alpha motif containing 1	Lrsam1	1.98	0.183	1.68	0.138	1.25	0.577	1.21	0.009	1.65	0.034
1437630_at	large subunit GTPase 1 homolog (S. cerevisiae)	Lsg1	1.41	0.295	1.57	0.054	1.05	0.633	1.21	0.049	1.05	0.340
1424001_at	Mki67 (FHA domain) interacting nucleolar phosphoprotein	Mki67ip	1.16	0.375	1.38	0.030	1.1	0.013	1.21	0.019	1.15	0.120
1419272_at	myeloid differentiation primary response gene 88	Myd88	1.2	0.295	1.43	0.068	1.18	0.166	1.21	0.002	1.16	0.077
1436189_at	NAD(P)H dehydrogenase, quinone 2	Nqo2	1.42	0.175	1.6	0.242	1.65	0.006	1.21	0.001	1.34	0.790
1422034_a_at	paralemmin	Palm	1.01	0.980	-1.02	0.907	1.03	0.865	1.21	0.014	1.07	0.096
1427241_at	poly(A) polymerase gamma	Papolg	1.08	0.814	1.18	0.040	-1.02	0.755	1.21	0.012	1.1	0.499
1444288_at	polyribonucleotide nucleotidyltransferase 1	Pnpt1	1.74	0.561	1.57	0.322	1.79	0.742	1.21	0.000	-1.01	0.595
1424473_at	polymerase (RNA) II (DNA directed) polypeptide H	Polr2h	1.25	0.115	1.58	0.000	1.27	0.005	1.21	0.041	1.22	0.054
1431506_s_at	peptidyl prolyl isomerase H /// similar to peptidyl prolyl isomerase H /// sir	Ppih /// LOC433064	1.61	0.164	1.73	0.048	1.09	0.245	1.21	0.013	1.04	0.680
1428892_at	peptidylprolyl isomerase (cyclophilin)-like 1	Ppil1	1.1	0.453	1.27	0.027	1.03	0.776	1.21	0.027	1.05	0.063
1418181_at	protein tyrosine phosphatase 4a3	Ptp4a3	1.66	0.306	2.48	0.035	1.24	0.080	1.21	0.045	1.38	0.036
1419061_at	ras homolog gene family, member D	Rhod	1.33	0.344	2.09	0.012	1.26	0.021	1.21	0.049	1.5	0.005
1439780_at	ribosomal protein L7-like 1	Rpl7l1	1.03	0.777	1.18	0.891	1.23	0.006	1.21	0.009	1.28	0.048
1428133_at	Smad nuclear interacting protein 1	Snip1	1.22	0.206	1.33	0.121	1.18	0.423	1.21	0.025	1.11	0.131
1460743_at	tigger transposable element derived 5	Tigd5	1.48	0.170	1.1	0.598	1.2	0.644	1.21	0.049	1.28	0.541
1431789_s_at	transmembrane emp24 protein transport domain containing 5	Tmed5	5.26	0.312	4.91	0.582	1.04	0.564	1.21	0.006	-1	0.776
1455116_at	tumor necrosis factor receptor superfamily, member 19-like /// similar to (	Tnfrsf19l /// LOC671	1.07	0.920	1.29	0.271	1.28	0.054	1.21	0.023	1.15	0.223

1435202_at	zinc finger protein 574	Zfp574	1.05	0.865	1.21	0.617	1.35	0.083	1.21	0.039	1.28	0.049
1449546_a_at	zinc finger protein 617	Zfp617	1.09	0.014	1.32	0.194	1.17	0.051	1.21	0.003	1.16	0.171
1423224_at	RIKEN cDNA 4432405B04 gene	4432405B04Rik	1.09	0.665	-1.22	0.265	1.04	0.828	1.22	0.013	1.03	0.911
1452340_at	RIKEN cDNA 6820424L24 gene	6820424L24Rik	-1.01	0.325	1.11	0.165	1.17	0.129	1.22	0.026	1.22	0.058
1428275_at	abhydrolase domain containing 13	Abhd13	1.01	0.818	1.26	0.075	1.08	0.325	1.22	0.003	1.2	0.047
1457606_x_at	expressed sequence AU015228	AU015228	1.67	0.175	1.22	0.368	1.56	0.322	1.22	0.009	2.13	0.161
1455166_at	expressed sequence AW146430	AW146430	1.12	0.140	1.03	0.600	1.18	0.041	1.22	0.005	1.09	0.212
1426083_a_at	B-cell translocation gene 1, anti-proliferative	Btg1	-1.03	0.604	1.19	0.033	1.3	0.018	1.22	0.035	1.37	0.011
1452829_at	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dil	Cad	1.26	0.510	1.4	0.202	1.1	0.080	1.22	0.005	1.13	0.331
1454733_at	caspase recruitment domain 4	Card4	2.45	0.635	2.67	0.568	1.05	0.529	1.22	0.024	1.05	0.748
1424143_a_at	chromatin licensing and DNA replication factor 1	Cdt1	-1.13	0.390	1.17	0.640	1.2	0.025	1.22	0.031	1.24	0.017
1424495_a_at	chemokine-like factor	Cklf	1.16	0.107	1.19	0.115	1.19	0.071	1.22	0.017	1.17	0.236
1454935_at	RIKEN cDNA D930001I22 gene	D930001I22Rik	-1.1	0.401	1.11	0.656	1.07	0.511	1.22	0.026	1.13	0.207
1417903_at	deafness, autosomal dominant 5 homolog (human)	Dfna5h	4.55	0.518	2.12	0.879	1.45	0.081	1.22	0.035	1.11	0.768
1456502_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	Dyrk2	1.12	0.086	1.02	0.714	1.02	0.661	1.22	0.007	1.08	0.208
1450934_at	eukaryotic translation initiation factor 4A2	Eif4a2	1.41	0.317	1.51	0.459	1.14	0.164	1.22	0.028	1.03	0.712
1417699_at	general transcription factor IIF, polypeptide 1	Gtf2f1	1.92	0.614	2.12	0.120	1.11	0.086	1.22	0.043	1.05	0.434
1448679_at	hyaluronoglucosaminidase 2	Hyal2	-1.15	0.045	1.08	0.095	1.08	0.744	1.22	0.045	1.48	0.016
1416956_at	potassium voltage-gated channel, shaker-related subfamily, beta membe	Kcnab2	-1.05	0.313	-1.65	0.169	2.01	0.832	1.22	0.039	-1.04	0.919
1437226_x_at	MARCKS-like 1	Marcksl1	1.07	0.012	1.46	0.000	1.24	0.000	1.22	0.019	1.28	0.076
1420845_at	mitochondrial ribosomal protein S2	Mrps2	11.34	0.299	12.33	0.089	1.01	0.890	1.22	0.011	1.15	0.269
1417483_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibit	Nfkbiz	1	0.723	1.28	0.164	1.5	0.016	1.22	0.030	1.37	0.034
1450147_at	neuronal pentraxin receptor	Nptxr	-1.11	0.319	1.06	0.913	-1.03	0.665	1.22	0.046	-1	0.977
1450854_at	proliferation-associated 2G4	Pa2g4	1.36	0.424	1.99	0.188	1.12	0.754	1.22	0.018	1.18	0.001
1428228_at	phosphoglucomutase 3	Pgm3	1.15	0.379	-1.01	0.895	1.05	0.636	1.22	0.043	1.07	0.353
1424671_at	pleckstrin homology domain containing, family F (with FYVE domain) me	Plekhf1	1.03	0.997	1.17	0.091	1.09	0.289	1.22	0.016	1.13	0.108
1418203_at	phorbol-12-myristate-13-acetate-induced protein 1	Pmaip1	1.33	0.093	2.85	0.020	1.42	0.015	1.22	0.008	1.68	0.090
1426838_at	polymerase (DNA-directed), delta 3, accessory subunit	Pold3	-1.03	0.616	1.19	0.967	1.22	0.339	1.22	0.002	1.08	0.497
1448899_s_at	RAD51 associated protein 1	Rad51ap1	1.21	0.064	1.38	0.022	1.06	0.392	1.22	0.033	1.21	0.029
1426968_a_at	retinol dehydrogenase 10 (all-trans)	Rdh10	1.14	0.315	1.33	0.244	1.16	0.048	1.22	0.021	1.18	0.143
1456383_at	ribosomal L1 domain containing 1	Rsl1d1	1.86	0.233	2.16	0.059	1.06	0.340	1.22	0.001	1.12	0.443
1428496_at	SECIS binding protein 2	Secisbp2	1.02	0.815	1.21	0.189	1.03	0.484	1.22	0.023	1.02	0.793
1447573_at	Solute carrier family 32 (GABA vesicular transporter), member 1	Slc32a1	1.01	0.999	-1.11	0.281	-1.22	0.323	1.22	0.036	1.04	0.592
1449959_x_at	small proline rich-like 9	Sprrl9	-1.16	0.390	-1.12	0.342	1.28	0.094	1.22	0.011	1.25	0.292
1420509_at	serum response factor binding protein 1	Srfbp1	1.29	0.527	1.49	0.222	-1.01	0.789	1.22	0.043	-1.07	0.370
1437283_at	transportin 2 (importin 3, karyopherin beta 2b)	Tnpo2	2.46	0.342	2.46	0.473	1.15	0.228	1.22	0.012	1.1	0.595
1423176_at	transducer of ErbB-2.1	Tob1	1.01	0.995	1.32	0.013	1.56	0.016	1.22	0.039	1.63	0.000
1452374_at	zinc finger protein 322a	Zfp322a	-1.05	0.595	1.09	0.931	1.2	0.130	1.22	0.007	1.02	0.996
1433946_at	zinc finger protein interacting with K protein 1	Zik1	1.13	0.031	1.44	0.041	1.36	0.002	1.22	0.041	1.23	0.015
1438205_at	RIKEN cDNA 1110014N23 gene	1110014N23Rik	1.94	0.315	2.24	0.301	-1.13	0.437	1.23	0.023	1.27	0.262
1429243_at	RIKEN cDNA 1110054O05 gene	1110054O05Rik	1.13	0.320	1.33	0.223	1.03	0.883	1.23	0.047	1.2	0.461
1447063_at	RIKEN cDNA 1700017B05 gene	1700017B05Rik	1.08	0.529	1.21	0.202	1.06	0.560	1.23	0.036	1.13	0.202
1447572_at	RIKEN cDNA 1700052I22 gene	1700052I22Rik	1.72	0.975	1.18	0.650	1.67	0.885	1.23	0.036	2.12	0.034
1418996_a_at	RIKEN cDNA 4930469P12 gene	4930469P12Rik	1.14	0.118	1.19	0.201	1.18	0.037	1.23	0.011	1.24	0.037
1423072_at	RIKEN cDNA 6720475J19 gene /// similar to putative retrovirus-related g	6720475J19Rik /// L	-1.05	0.636	1.11	0.443	1.09	0.684	1.23	0.029	1.28	0.027
1455616_at	expressed sequence AI586002	AI586002	1.12	0.506	1.36	0.926	1.21	0.100	1.23	0.014	-1.02	0.438
1451131_at	ADP-ribosylation factor-like 6 interacting protein 1	Arl6ip1	-1.01	0.788	1.03	0.361	1	0.722	1.23	0.030	1.14	0.196
1416227_at	actin related protein 2/3 complex, subunit 1B /// similar to Actin-related p	Arpc1b /// LOC4347	-1.21	0.266	1.14	0.249	1.53	0.071	1.23	0.034	1.43	0.222
1451747_a_at	autophagy-related 12 (yeast)	Atg12	1.05	0.129	1.35	0.001	1.16	0.287	1.23	0.038	1.04	0.701
1437879_at	expressed sequence AU045404	AU045404	1.14	0.468	1.12	0.664	1.07	0.073	1.23	0.015	1.02	0.980
1451583_a_at	cDNA sequence BC025076	BC025076	1.56	0.135	1.75	0.191	1.15	0.287	1.23	0.036	1.23	0.092
1429784_at	RIKEN cDNA C130032J12 gene	C130032J12Rik	1.07	0.429	1.09	0.554	1.03	0.875	1.23	0.042	1	0.976
1427844_a_at	CCAAT/enhancer binding protein (C/EBP), beta	Cebpb	1.54	0.581	1.28	0.451	-1.24	0.008	1.23	0.034	1.13	0.042
1423233_at	CCAAT/enhancer binding protein (C/EBP), delta	Cebpd	-1.06	0.480	1.13	0.515	1.21	0.266	1.23	0.048	1.18	0.267
1454112_a_at	centrosomal protein 27	Cep27	1.33	0.301	1.78	0.045	1.09	0.276	1.23	0.045	1.13	0.567
1440715_s_at	DNA segment, Chr 11, ERATO Doi 497, expressed	D11Ertd497e	1.11	0.029	1.12	0.086	1.19	0.001	1.23	0.004	1.1	0.081
1447805_s_at	DNA segment, Chr 11, ERATO Doi 730, expressed	D11Ertd730e	-1.16	0.158	1.11	0.952	1.14	0.068	1.23	0.017	1.11	0.867
1437284_at	frizzled homolog 1 (Drosophila)	Fzd1	1.03	0.393	1.27	0.017	1.34	0.060	1.23	0.012	1.39	0.042

1455904_at	growth arrest specific 5	Gas5	1.01	0.711	-1.03	0.544	1.22	0.002	1.23	0.038	1.1	0.140
1426995_a_at	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	Gfer	-1.03	0.547	1.49	0.079	1.08	0.277	1.23	0.050	1.38	0.077
1426523_a_at	glucosamine-6-phosphate deaminase 2	Gnpda2	1.07	0.020	1.24	0.052	1.05	0.474	1.23	0.024	1.24	0.065
1452774_at	heterogeneous nuclear ribonucleoprotein A3	Hnrpa3	-1.03	0.610	-1.19	0.396	1.12	0.203	1.23	0.008	1.09	0.367
1434012_at	integrator complex subunit 5	Ints5	-1.12	0.015	1.14	0.024	1.14	0.242	1.23	0.007	1.13	0.341
1449503_at	karyopherin (importin) alpha 1	Kpna1	1.19	0.222	1.24	0.138	1.07	0.325	1.23	0.041	1.03	0.737
1451464_at	microfibrillar-associated protein 3	Mfap3	3.26	0.352	3.67	0.062	1.2	0.333	1.23	0.049	1.05	0.801
1423711_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly facto	Ndufaf1	1.4	0.318	1.77	0.017	1.19	0.003	1.23	0.020	1.29	0.019
1449474_a_at	nasal embryonic LHRH factor	Nelf	-1.09	0.226	-1.05	0.555	1.12	0.537	1.23	0.033	1.23	0.148
1424019_at	nucleolar protein 1	Nol1	1.04	0.555	1.38	0.009	1.06	0.631	1.23	0.025	1.19	0.092
1423864_at	nuclear receptor binding protein	Nrbp	1.59	0.259	1.54	0.517	1.15	0.088	1.23	0.021	1.02	0.876
1449017_at	nuclear transport factor 2	Nutf2	1.22	0.263	1.52	0.011	1.16	0.093	1.23	0.004	1.24	0.002
1451069_at	proviral integration site 3	Pim3	1.91	0.665	1.61	0.611	1.12	0.380	1.23	0.031	1.24	0.006
1430780_a_at	phosphomannomutase 1	Pmm1	2.06	0.315	2.45	0.022	1.05	0.769	1.23	0.004	1.17	0.012
1435057_x_at	polymerase (RNA) I polypeptide E	Polr1e	-1.01	0.702	1.34	0.371	1.13	0.055	1.23	0.049	1.38	0.028
1417972_s_at	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)	Pop5	1.1	0.342	1.58	0.003	1.17	0.038	1.23	0.015	1.38	0.016
1449092_at	protein phosphatase 1D magnesium-dependent, delta isoform	Ppm1d	-1.03	0.558	1.5	0.007	1.16	0.026	1.23	0.015	1.29	0.024
1430979_a_at	peroxiredoxin 2	Prdx2	1.14	0.487	1.43	0.068	1.13	0.137	1.23	0.001	1.38	0.004
1452062_at	phosphoribosyl pyrophosphate synthetase-associated protein 2	Prpsap2	1.04	0.966	1.45	0.043	1.06	0.724	1.23	0.032	-1.1	0.203
1454142_a_at	PWP1 homolog (S. cerevisiae)	Pwp1	4.25	0.393	5.69	0.133	1.14	0.161	1.23	0.027	1.14	0.290
1417035_at	SAC3 domain containing 1	Sac3d1	1.04	0.715	1.36	0.026	1.23	0.034	1.23	0.023	1.28	0.048
1448874_a_at	SH2B adaptor protein 1	Sh2b1	1.35	0.280	1.64	0.114	1.19	0.028	1.23	0.020	1.27	0.058
1460168_at	stem-loop binding protein	Slbp	1.2	0.071	1.73	0.002	1.27	0.009	1.23	0.002	1.28	0.092
1416421_a_at	Sjogren syndrome antigen B	Ssb	1.19	0.316	1.35	0.040	1.06	0.815	1.23	0.009	1.09	0.600
1421469_a_at	signal transducer and activator of transcription 5A	Stat5a	2.21	0.224	2.57	0.087	1.11	0.409	1.23	0.025	1.42	0.067
1447159_at	Synaptic nuclear envelope 2	Syne2	1.44	0.440	1.05	0.897	1.35	0.050	1.23	0.023	-1.18	0.460
1452605_at	threonine synthase-like 1 (bacterial)	Thnsl1	2.63	0.335	2.8	0.103	1.11	0.551	1.23	0.035	1.08	0.395
1422740_at	tumor necrosis factor receptor superfamily, member 21	Tnfrsf21	-1.23	0.094	-1.32	0.160	1.24	0.131	1.23	0.001	1.36	0.589
1417755_at	topoisomerase I binding, arginine/serine-rich	Topors	1.03	0.814	1.14	0.477	-1.1	0.223	1.23	0.049	1.17	0.268
1454846_at	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Utp15	-1.08	0.475	1.21	0.151	1.24	0.003	1.23	0.010	1.23	0.038
1453034_at	zinc finger protein 251	Zfp251	1.09	0.999	1.3	0.558	1.08	0.552	1.23	0.035	1.36	0.049
1435556_at	zinc finger protein 597	Zfp597	-1.11	0.234	1.08	0.715	1.07	0.543	1.23	0.020	1	0.919
1424670_s_at	zinc finger, FYVE domain containing 21	Zfyve21	-1.02	0.552	1.09	0.455	1.13	0.047	1.23	0.001	1.25	0.018
1428798_s_at	RIKEN cDNA 0610039J04 gene	0610039J04Rik	-1.09	0.108	1.09	0.185	1.26	0.279	1.24	0.001	1.14	0.228
1423440_at	RIKEN cDNA 1110001A07 gene	1110001A07Rik	1.28	0.020	1.32	0.226	1.16	0.313	1.24	0.004	1.14	0.516
1433582_at	RIKEN cDNA 1190002N15 gene	1190002N15Rik	1.6	0.203	2.14	0.039	1.45	0.015	1.24	0.030	1.13	0.156
1419265_at	RIKEN cDNA 1200014M14 gene	1200014M14Rik	1.87	0.361	2	0.182	-1.09	0.320	1.24	0.008	1.01	0.924
1447993_a_at	RIKEN cDNA 1700026B20 gene	1700026B20Rik	-1.12	0.437	1.06	0.607	1.14	0.349	1.24	0.026	1.31	0.146
1426577_a_at	RIKEN cDNA 1810054G18 gene	1810054G18Rik	-1.1	0.367	1.22	0.083	1.18	0.238	1.24	0.042	1.19	0.067
1436105_at	RIKEN cDNA 2310015A05 gene	2310015A05Rik	1.01	0.594	1.34	0.120	1.13	0.645	1.24	0.008	1.83	0.067
1428350_at	RIKEN cDNA 2310061F22 gene	2310061F22Rik	1.1	0.135	1.15	0.074	-1.02	0.510	1.24	0.008	1.19	0.211
1456355_s_at	RIKEN cDNA 2810002G02 gene /// region containing RIKEN cDNA 2810	2810002G02Rik /// L	1.02	0.841	1.21	0.687	-1.11	0.271	1.24	0.009	1.17	0.182
1435267_at	RIKEN cDNA A430108E01 gene	A430108E01Rik	1.06	0.297	1.04	0.842	1.03	0.986	1.24	0.011	-1.16	0.137
1420717_at	RIKEN cDNA A930018P22 gene	A930018P22Rik	3	0.300	1.76	0.700	1.32	0.606	1.24	0.009	2.26	0.450
1429850_x_at	alkB, alkylation repair homolog 4 (E. coli)	Alkbh4	-1.21	0.372	1.05	0.631	1.17	0.102	1.24	0.022	1.23	0.033
1448199_at	ankyrin repeat domain 10	Ankrd10	-1.06	0.126	1.55	0.005	1.45	0.019	1.24	0.040	1.39	0.049
1417655_a_at	arsenate resistance protein 2	Ars2	-1.11	0.397	1.14	0.341	1.31	0.009	1.24	0.048	1.25	0.020
1433685_a_at	RIKEN cDNA C330011F01 gene /// RIKEN cDNA 6430706D22 gene	C330011F01Rik /// 6	2.21	0.393	2.25	0.362	1.04	0.601	1.24	0.017	1.13	0.015
1416873_a_at	cyclin-dependent kinase 2	Cdk2	1.13	0.194	1.26	0.002	1.16	0.221	1.24	0.041	1.13	0.214
1451505_at	coiled-coil-helix-coiled-coil-helix domain containing 5	Chchd5	1.06	0.346	1.12	0.514	-1.03	0.674	1.24	0.032	1.2	0.371
1452796_at	differentially expressed in FDCP 6	Def6	1.45	0.151	1.87	0.024	1.22	0.002	1.24	0.012	1.4	0.012
1454737_at	dual specificity phosphatase 9	Dusp9	1.03	0.928	1.58	0.049	1.37	0.022	1.24	0.014	1.45	0.045
1456756_at	RIKEN cDNA E430016P22 gene	E430016P22Rik	1.08	0.567	1.21	0.161	1.05	0.975	1.24	0.026	1.21	0.188
1436011_at	engulfment and cell motility 2, ced-12 homolog (C. elegans)	Elmo2	-1.2	0.238	1.07	0.972	1.49	0.004	1.24	0.038	1.16	0.406
1434991_at	F-box and WD-40 domain protein 17	Fbxw17	1.53	0.217	1.51	0.171	1.09	0.774	1.24	0.005	1.22	0.008
1455065_x_at	glucosamine-6-phosphate deaminase 1 /// similar to Glucosamine-6-phos	Gnpda1 /// LOC2319	-1.1	0.471	-1.01	0.541	1.31	0.050	1.24	0.001	1.35	0.018
1447612_x_at	Jumonji domain containing 3	Jmjd3	-1.21	0.397	-1.03	0.436	-1.03	0.675	1.24	0.026	1.23	0.150
1427317_at	antigenic determinant of rec-A protein	Kin	-1.22	0.395	-1.23	0.378	-1	0.904	1.24	0.006	1.01	0.900

1420530_at	neuronal d4 domain family member	Neud4	1.31	0.749	1.56	0.428	1.17	0.275	1.24	0.000	1.65	0.020
1423827_s_at	nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	1.34	0.377	1.46	0.068	-1.09	0.103	1.24	0.003	1.15	0.316
1422471_at	peroxisomal biogenesis factor 13	Pex13	1.07	0.714	1.47	0.013	1.17	0.012	1.24	0.000	1.21	0.008
1423861_at	pleckstrin homology domain containing, family F (with FYVE domain) me	Plekhf2	1.08	0.704	1.35	0.123	1.19	0.223	1.24	0.046	1.26	0.101
1417057_a_at	peptidylprolyl isomerase D (cyclophilin D) /// lysosomal-associated meml	Ppid /// Lamp3 /// LC	1.1	0.617	1.6	0.030	1.12	0.381	1.24	0.030	1.19	0.227
1428766_at	RNA methyltransferase like 1	Rnmtl1	1.03	0.383	1.23	0.018	1.17	0.150	1.24	0.002	1.32	0.004
1439237_a_at	slingshot homolog 1 (Drosophila)	Ssh1	1.37	0.928	-1.32	0.317	1.53	0.169	1.24	0.040	-1.38	0.460
1451423_at	tubulin-specific chaperone c	Tbcc	-1.83	0.262	-1.14	0.396	-1.19	0.257	1.24	0.037	-1.05	0.686
1448529_at	thrombomodulin	Thbd	1.11	0.415	1.31	0.047	1.29	0.101	1.24	0.010	1.15	0.222
1428660_s_at	torsin family 3, member A	Tor3a	-1.04	0.634	1.28	0.003	1.13	0.294	1.24	0.013	1.17	0.419
1436045_at	testis specific 10	Tsga10	1.06	0.816	-1.12	0.065	1.26	0.428	1.24	0.045	1.23	0.448
1421832_at	twisted gastrulation homolog 1 (Drosophila)	Twsg1	3.97	0.749	4.74	0.504	-1.08	0.116	1.24	0.040	1.05	0.997
1425384_a_at	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	Ube4a	2.75	0.348	2.94	0.322	-1.01	0.924	1.24	0.031	1.04	0.784
1415790_at	ubiquitin-like domain containing CTD phosphatase 1	Ublcp1	1.03	0.670	1.21	0.110	1.07	0.732	1.24	0.025	1.06	0.541
1451317_at	YTH domain family 2	Ythdf2	1.96	0.247	2.51	0.036	1.03	0.576	1.24	0.046	1.07	0.687
1439089_at	zinc finger and BTB domain containing 41 homolog	Zbtb41	1.07	0.768	1.2	0.208	1.14	0.107	1.24	0.020	1.13	0.120
1452025_a_at	zinc finger protein 2	Zfp2	2.47	0.221	1.92	0.307	-1.62	0.039	1.24	0.038	1.5	0.939
1424297_at	zinc finger protein 282	Zfp282	-1.05	0.467	1.17	0.300	-1.03	0.719	1.24	0.036	1.14	0.013
1416367_at	RIKEN cDNA 1110001J03 gene	1110001J03Rik	1.03	0.708	1.07	0.565	1.02	0.881	1.25	0.017	1.31	0.073
1452063_at	RIKEN cDNA 2410081M15 gene	2410081M15Rik	1.47	0.229	1.74	0.118	1.13	0.221	1.25	0.035	1.13	0.629
1428529_at	RIKEN cDNA 2810026P18 gene	2810026P18Rik	-1.08	0.541	1.06	0.993	1.15	0.204	1.25	0.023	1.16	0.082
1428903_at	RIKEN cDNA 3110037I16 gene	3110037I16Rik	-1.07	0.449	1.19	0.406	1.18	0.024	1.25	0.001	1.38	0.053
1427959_at	abhydrolase domain containing 10	Abhd10	1.04	0.551	1.38	0.026	1.27	0.027	1.25	0.029	1.29	0.029
1419188_s_at	chemokine (C-C motif) ligand 27	Ccl27	-1.11	0.398	1.04	0.853	1.09	0.773	1.25	0.037	1.16	0.705
1416802_a_at	cell division cycle associated 5	Cdca5	-1.1	0.469	1.21	0.618	1.15	0.079	1.25	0.004	1.24	0.072
1453137_at	F-box protein 30	Fbxo30	1.5	0.294	1.6	0.203	1.03	0.047	1.25	0.019	1.05	0.510
1448620_at	Fc receptor, IgG, low affinity III	Fcgr3	1.27	0.206	1.31	0.317	1.03	0.911	1.25	0.027	1.47	0.400
1421731_a_at	flap structure specific endonuclease 1	Fen1	1.18	0.546	1.56	0.001	1.28	0.003	1.25	0.030	1.27	0.001
1422430_at	fidgetin-like 1	Fignl1	1.14	0.108	1.33	0.116	1.34	0.052	1.25	0.018	1.24	0.045
1425196_a_at	histidine triad nucleotide binding protein 2	Hint2	-1.19	0.410	1.05	0.558	1.25	0.026	1.25	0.004	1.21	0.011
1416210_at	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Imp3	1.12	0.391	1.29	0.018	1.15	0.128	1.25	0.002	1.18	0.164
1449158_at	potassium channel, subfamily K, member 2	Kcnk2	1.28	0.180	1.36	0.162	1.28	0.038	1.25	0.006	1.04	0.314
1452625_at	potassium channel tetramerisation domain containing 2	Kctd2	-1.06	0.534	-1.07	0.509	1.1	0.142	1.25	0.038	1.16	0.025
1419951_at	Lectin, mannose-binding, 1	Lman1	-1.11	0.467	1.05	0.725	-1.27	0.030	1.25	0.046	1.03	0.877
1455324_at	hypothetical LOC433022	LOC433022	-1.06	0.519	1.1	0.944	1.17	0.007	1.25	0.025	1.29	0.013
1418300_a_at	MAP kinase-interacting serine/threonine kinase 2	Mknk2	-1.05	0.558	1.27	0.104	1.19	0.057	1.25	0.007	1.47	0.020
1449550_at	myosin IC	Myo1c	1.05	0.348	1.33	0.019	1.3	0.048	1.25	0.012	1.32	0.020
1451678_at	nuclear prelamin A recognition factor	Narf	3.1	0.356	3.42	0.272	1.23	0.199	1.25	0.034	1.15	0.098
1418329_at	pyroglutamyl-peptidase I	Pgpep1	1.34	0.309	1.71	0.059	1.26	0.038	1.25	0.020	1.29	0.055
1423703_at	peter pan homolog (Drosophila)	Ppan	-1.05	0.199	1.02	0.958	-1	0.706	1.25	0.005	1.11	0.191
1429639_at	preimplantation protein 4	Prei4	1.66	0.180	1.31	0.300	1.15	0.674	1.25	0.045	-1.11	0.454
1418539_a_at	protein tyrosine phosphatase, receptor type, E	Ptpre	1.03	0.695	1.02	0.910	1.11	0.586	1.25	0.032	1.15	0.123
1450180_a_at	retinoic acid receptor, alpha	Rara	2.22	0.650	2.36	0.755	-1.18	0.135	1.25	0.050	1.08	0.696
1439724_at	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	Ric8b	-1.13	0.378	-1.2	0.228	-1.4	0.148	1.25	0.045	-1.13	0.176
1438187_at	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transpor	Slc25a29	-1.17	0.308	-1.12	0.325	-1.02	0.585	1.25	0.001	1.16	0.322
1417684_at	THUMP domain containing 3	Thumpd3	-1.05	0.546	1.23	0.574	1.15	0.092	1.25	0.003	1.15	0.057
1416507_at	transmembrane protein 4	Tmem4	1.27	0.913	1.24	0.833	1.27	0.589	1.25	0.012	-1.2	0.400
1455692_x_at	RIKEN cDNA 1700097N02 gene	1700097N02Rik	-1.01	0.826	-1.17	0.438	1.05	0.929	1.26	0.026	-1.07	0.691
1455850_at	RIKEN cDNA 2310003H01 gene	2310003H01Rik	1.16	0.444	1.61	0.075	1.08	0.869	1.26	0.016	1.39	0.031
1453006_at	RIKEN cDNA 2610306H15 gene	2610306H15Rik	1.09	0.348	1.57	0.040	1.44	0.036	1.26	0.000	1.57	0.006
1418040_at	RIKEN cDNA 4432406C05 gene	4432406C05Rik	-1.03	0.513	1.11	0.901	1.25	0.194	1.26	0.031	1.22	0.240
1460624_at	RIKEN cDNA 6330564D18 gene	6330564D18Rik	-1.16	0.139	1.02	0.802	1.16	0.522	1.26	0.013	1.1	0.440
1438407_at	RIKEN cDNA 9330132E09 gene	9330132E09Rik	1.1	0.041	1.17	0.158	1.08	0.134	1.26	0.034	1.11	0.259
1426459_s_at	expressed sequence AW549877	AW549877	1.38	0.371	1.64	0.196	1.18	0.039	1.26	0.011	1.07	0.464
1444657_at	Bcl3 binding protein	B3bp	1.12	0.432	1.65	0.313	1.02	0.757	1.26	0.023	-1.07	0.282
1444016_at	RIKEN cDNA C430014K04 gene	C430014K04Rik	1.11	0.864	1.22	0.310	1.81	0.456	1.26	0.020	3.24	0.299
1423098_at	calpain 7	Capn7	1.46	0.230	1.46	0.321	1.07	0.724	1.26	0.005	1.11	0.049
1418542_s_at	centromere protein O	Cenpo	1.56	0.188	1.47	0.002	1.05	0.756	1.26	0.026	1.14	0.779

1436034_at	centrosomal protein 68	Cep68	-1.06	0.565	1.01	0.995	1.14	0.451	1.26	0.024	1.42	0.003
1432273_a_at	Duffy blood group, chemokine receptor	Darc	1.12	0.476	1.05	0.801	1.34	0.092	1.26	0.006	1.06	0.800
1434607_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	-1.02	0.626	1.27	0.145	1.15	0.066	1.26	0.006	1.22	0.030
1423799_at	eukaryotic translation initiation factor 1	Eif1	1.05	0.453	1.12	0.093	1.14	0.027	1.26	0.002	1.05	0.132
1436022_at	endonuclease G-like 1	Endogl1	1.29	0.460	1.7	0.070	1.08	0.146	1.26	0.018	1.16	0.015
1450935_at	excision repair cross-complementing rodent repair deficiency, compleme	Ercc5	-1.01	0.580	1.91	0.140	1.32	0.025	1.26	0.042	1.3	0.071
1435544_at	exosome component 6	Exosc6	-1.08	0.516	1.22	0.509	1.11	0.147	1.26	0.008	1.31	0.012
1434271_at	glucosidase beta 2	Gba2	1.65	0.320	1.82	0.070	1.17	0.056	1.26	0.017	1.4	0.286
1423071_x_at	hypothetical gene supported by BC019681; BC027236 /// hypothetical L	LOC270335 /// LOC	-1.06	0.518	1.02	0.874	1.28	0.001	1.26	0.008	1.2	0.023
1437061_at	methyl-CpG binding domain protein 1	Mbd1	1.14	0.529	1.38	0.054	1.14	0.222	1.26	0.035	1.16	0.265
1418150_at	myotubularin related protein 4	Mtmr4	3.93	0.772	4.49	0.360	1.11	0.071	1.26	0.013	1.23	0.047
1450401_at	nuclear receptor coactivator 6 interacting protein	Ncoa6ip	1.02	0.874	1.42	0.120	-1.03	0.633	1.26	0.003	1.23	0.056
1421321_a_at	neuroepithelial cell transforming gene 1	Net1	1.8	0.415	2.62	0.108	1.1	0.423	1.26	0.024	1.53	0.015
1416709_a_at	neugrin, neurite outgrowth associated	Ngrn	-1.15	0.179	-1.03	0.654	1.03	0.786	1.26	0.015	-1.03	0.502
1421965_s_at	Notch gene homolog 3 (Drosophila)	Notch3	-1.24	0.226	1.12	0.467	1.11	0.605	1.26	0.037	1.4	0.230
1447253_x_at	nucleoporin 54	Nup54	1.73	0.922	4.44	0.048	1.24	0.671	1.26	0.007	-1.14	0.709
1423534_at	programmed cell death 2	Pdcd2	-1.06	0.325	1.2	0.252	1.15	0.265	1.26	0.005	1.29	0.002
1431893_a_at	prenyl (solanesyl) diphosphate synthase, subunit 1	Pdss1	1.51	0.190	1.52	0.125	1.16	0.155	1.26	0.002	-1.07	0.183
1423044_at	proline synthetase co-transcribed	Prosc	1.36	0.306	1.71	0.013	1.12	0.034	1.26	0.020	1.19	0.005
1417166_at	PC4 and SFRS1 interacting protein 1	Psip1	1.04	0.933	1.06	0.731	1.23	0.014	1.26	0.035	1.27	0.027
1431068_at	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	Rmnd5a	1.13	0.422	1.24	0.768	1.48	0.459	1.26	0.046	1.2	0.723
1450778_a_at	RNA U, small nuclear RNA export adaptor	Rnuxa	1.1	0.042	1.48	0.014	1.18	0.027	1.26	0.014	1.15	0.086
1455292_x_at	Regulator of sex limited protein-Slp 1	Rsl1	3.18	0.321	2.86	0.112	1.27	0.226	1.26	0.048	1.27	0.328
1417719_at	sin3 associated polypeptide	Sap30	-1	0.875	1.29	0.182	1.14	0.206	1.26	0.012	1.37	0.006
1417406_at	SERTA domain containing 1	Sertad1	-1.06	0.513	1.14	0.969	1.3	0.007	1.26	0.006	1.34	0.021
1433789_at	small nucleolar RNA host gene (non-protein coding) 3 /// similar to RNA,	Snhg3 /// LOC67043	-1.16	0.347	1.04	0.797	1.22	0.079	1.26	0.029	1.12	0.170
1451339_at	sulfite oxidase	Suox	5.26	0.543	8.31	0.070	1.38	0.039	1.26	0.024	1.42	0.004
1422517_a_at	zinc ribbon domain containing, 1	Znrd1	-1.01	0.749	1.21	0.144	1.25	0.034	1.26	0.005	1.31	0.051
1460474_at	RIKEN cDNA 2610028L16 gene	2610028L16Rik	-1.05	0.559	1.06	0.709	1.11	0.696	1.27	0.018	-1.16	0.349
1453745_at	RIKEN cDNA 2700038G22 gene	2700038G22Rik	1.04	0.299	1.04	0.672	1.16	0.054	1.27	0.025	1.13	0.447
1422628_at	RIKEN cDNA 4632417K18 gene	4632417K18Rik	1.29	0.065	1.66	0.013	1.21	0.004	1.27	0.002	1.23	0.018
1429364_at	RIKEN cDNA 4930579G24 gene	4930579G24Rik	1.01	0.767	1.21	0.021	1.4	0.037	1.27	0.036	1.27	0.003
1432178_at	RIKEN cDNA 4933431I19 gene	4933431I19Rik	1.39	0.755	2.15	0.737	-1.75	0.231	1.27	0.032	1.35	0.975
1445558_at	RIKEN cDNA 5930430L01 gene	5930430L01Rik	-1.03	0.502	1.05	0.797	-1	0.889	1.27	0.028	-1.81	0.007
1451326_at	abhydrolase domain containing 14b	Abhd14b	-1.03	0.528	-1.07	0.523	1.17	0.304	1.27	0.007	1.24	0.339
1457265_at	RIKEN cDNA B230333C21 gene	B230333C21Rik	-1.02	0.599	1.05	0.854	1.1	0.316	1.27	0.021	-1.01	0.560
1425776_a_at	expressed sequence C87436	C87436	2.82	0.199	1.93	0.531	1.23	0.237	1.27	0.008	1.3	0.074
1422123_s_at	CEA-related cell adhesion molecule 1 /// CEA-related cell adhesion mole	Ceacam1 /// Ceacar	1.01	0.995	-1.27	0.290	1.4	0.434	1.27	0.000	1.31	0.151
1447860_x_at	component of oligomeric golgi complex 8	Cog8	-1.17	0.421	1.2	0.653	-1.1	0.354	1.27	0.003	1.2	0.326
1416019_at	down-regulator of transcription 1	Dr1	1.01	0.987	1.27	0.015	1.24	0.259	1.27	0.012	1.12	0.393
1435926_at	RIKEN cDNA E030003F13 gene	E030003F13Rik	-1.03	0.574	1.4	0.017	1.23	0.022	1.27	0.028	1.29	0.047
1440299_at	RIKEN cDNA E330016A19 gene	E330016A19Rik	-1.07	0.495	1.14	0.779	1.09	0.996	1.27	0.027	1.18	0.079
1418275_a_at	E74-like factor 2	Elf2	1.09	0.537	1.12	0.212	-1.05	0.632	1.27	0.003	1.04	0.656
1424854_at	histone 1, H4i	Hist1h4i	-1.25	0.225	1.04	0.781	1.04	0.791	1.27	0.047	1.19	0.069
1451021_a_at	Kruppel-like factor 5	Klf5	1.84	0.399	2.3	0.093	1.21	0.120	1.27	0.033	1.46	0.001
1417115_at	mitogen activated protein kinase kinase kinase 12	Map3k12	1.03	0.764	1.2	0.856	1.15	0.393	1.27	0.024	1.61	0.047
1433816_at	mitochondrial carrier triple repeat 1	Mcart1	1.15	0.367	1.23	0.108	1.06	0.773	1.27	0.025	1.08	0.109
1423196_at	neural precursor cell expressed, developmentally down-regulated gene 1	Nedd1	1.44	0.356	1.45	0.127	1.15	0.109	1.27	0.010	1.09	0.149
1428339_at	nudix (nucleoside diphosphate linked moiety X)-type motif 21	Nudt21	1.3	0.259	1.38	0.091	1.35	0.003	1.27	0.003	1.3	0.007
1429651_at	phosphatase and actin regulator 3	Phactr3	1.36	0.980	1.54	0.862	-1.04	0.420	1.27	0.014	1.31	0.748
1430286_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 14c	Ppp1r14c	1.16	0.903	1.43	0.647	1.11	0.838	1.27	0.025	1.27	0.735
1442911_at	RIO kinase 2 (yeast)	Riok2	-1.19	0.215	-1.28	0.334	1.28	0.717	1.27	0.028	-1.03	0.428
1420502_at	spermidine/spermine N1-acetyl transferase 1	Sat1	1.29	0.135	1.7	0.006	1.38	0.014	1.27	0.011	1.32	0.006
1451596_a_at	sphingosine kinase 1	Sphk1	1.07	0.348	1.33	0.015	1.19	0.192	1.27	0.000	1.37	0.022
1453351_at	T-box 20	Tbx20	2	0.425	1.18	0.658	1.56	0.288	1.27	0.016	1.75	0.860
1424929_a_at	tripartite motif protein 26	Trim26	1.12	0.472	1.5	0.027	1.2	0.079	1.27	0.005	1.12	0.134
1455873_a_at	vacuolar protein sorting 18 (yeast)	Vps18	1.44	0.567	1.87	0.069	1.04	0.757	1.27	0.017	1	0.897
1436548_at	RIKEN cDNA 1810012P15 gene	1810012P15Rik	-1.18	0.335	-1.06	0.637	1.27	0.288	1.28	0.029	1.3	0.413

1433112_at	RIKEN cDNA 4933424L07 gene	4933424L07Rik	-1.08	0.463	1.18	0.675	1.08	0.423	1.28	0.010	1.05	0.732
1432509_at	RIKEN cDNA 5033430I15 gene	5033430I15Rik	1.23	0.217	1.32	0.211	1.21	0.137	1.28	0.040	1.39	0.025
1430701_a_at	RIKEN cDNA 5730528L13 gene	5730528L13Rik	3.17	0.244	3.24	0.084	1.18	0.105	1.28	0.013	1.25	0.030
1426292_at	RIKEN cDNA 6330581L23 gene	6330581L23Rik	-1.09	0.377	1.08	0.705	1.03	0.902	1.28	0.037	1.07	0.474
1454682_at	RIKEN cDNA A430005L14 gene	A430005L14Rik	-1.06	0.546	1.19	0.876	1.2	0.077	1.28	0.007	1.21	0.033
1418854_at	baculoviral IAP repeat-containing 2	Birc2	-1.24	0.342	-1.09	0.495	1.16	0.316	1.28	0.031	1.14	0.173
1417955_at	coiled-coil domain containing 71	Ccdc71	1	0.845	1.13	0.487	1.12	0.118	1.28	0.029	1.19	0.102
1435320_at	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small	Ctdspl2	1.22	0.087	1.4	0.029	1.09	0.344	1.28	0.014	1.04	0.889
1435866_s_at	histone 3, H2a	Hist3h2a	-1.05	0.609	1.21	0.041	1.21	0.013	1.28	0.008	1.25	0.005
1455305_x_at	heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	1.14	0.786	1.2	0.801	-1.02	0.739	1.28	0.004	-1.03	0.174
1418045_at	inositol polyphosphate-1-phosphatase	Inpp1	1.43	0.559	1.71	0.102	1.15	0.242	1.28	0.005	1.23	0.307
1456200_at	inositol polyphosphate multikinase	Ipmk	-1.06	0.495	1.1	0.830	1.33	0.039	1.28	0.008	1.1	0.255
1447864_s_at	pogo transposable element with KRAB domain	Pogk	-1.16	0.422	1.24	0.845	1.11	0.010	1.28	0.010	1.26	0.016
1450862_at	RAD54 like (S. cerevisiae)	Rad54l	1.49	0.138	1.51	0.036	1.04	0.678	1.28	0.002	-1.09	0.270
1433683_at	RNA binding motif protein 35b	Rbm35b	1.23	0.670	1.31	0.259	-1	0.943	1.28	0.033	2.94	0.121
1424333_at	RNA (guanine-9-) methyltransferase domain containing 1	Rg9mtd1	1.08	0.136	1.38	0.148	1.16	0.068	1.28	0.031	1.17	0.060
1437052_s_at	solute carrier family 2 (facilitated glucose transporter), member 3	Slc2a3	-1.03	0.686	-1	0.594	1.26	0.090	1.28	0.016	1.29	0.020
1452789_at	stannin	Snn	1.05	0.805	1.5	0.010	1.2	0.229	1.28	0.002	1.42	0.012
1448040_at	TCF3 (E2A) fusion partner	Tfpt	-1.8	0.075	-1.43	0.235	1.03	0.935	1.28	0.027	-1.03	0.639
1426527_at	target of EGR1, member 1 (nuclear)	Toe1	-1.05	0.345	1.3	0.467	1.04	0.736	1.28	0.005	1.1	0.056
1438669_at	WD repeat domain 40A	Wdr40a	1.02	0.775	1.35	0.004	1.1	0.537	1.28	0.010	1.03	0.917
1429560_at	zinc finger protein 422, related sequence 1	Zfp422-rs1	1.19	0.477	1.55	0.194	1.11	0.479	1.28	0.017	1.07	0.768
1455633_at	zinc finger protein 647	Zfp647	-1.08	0.542	1.08	0.927	1.15	0.038	1.28	0.017	1.43	0.049
1431252_a_at	zinc finger protein 655	Zfp655	1.21	0.383	1.43	0.044	1.06	0.799	1.28	0.015	1.23	0.120
1428836_at	RIKEN cDNA 2300009A05 gene	2300009A05Rik	1	0.984	1.16	0.046	1.22	0.016	1.29	0.014	1.37	0.002
1432013_a_at	RIKEN cDNA 2610016C23 gene	2610016C23Rik	1.34	0.050	1.75	0.165	1.51	0.023	1.29	0.043	1.18	0.241
1430905_at	RIKEN cDNA 4921504E06 gene	4921504E06Rik	-1.04	0.634	1.14	0.093	1.12	0.883	1.29	0.035	1.15	0.951
1424003_at	RIKEN cDNA 4930444A02 gene	4930444A02Rik	1.05	0.313	1.42	0.076	1.26	0.014	1.29	0.001	1.21	0.175
1431523_at	RIKEN cDNA 4930564K09 gene	4930564K09Rik	1.41	0.454	2.35	0.980	1.07	0.877	1.29	0.006	-1.54	0.113
1451571_s_at	RIKEN cDNA 9130019O22 gene /// RIKEN cDNA E430018J23 gene /// F	9130019O22Rik /// E	-1.03	0.672	1.13	0.750	1.08	0.543	1.29	0.006	1.12	0.433
1416835_s_at	S-adenosylmethionine decarboxylase 1 /// S-adenosylmethionine decarb	Amd1 /// Amd2	1.51	0.214	1.8	0.076	1.15	0.082	1.29	0.019	1.23	0.151
1435033_at	Rho guanine nucleotide exchange factor (GEF) 4	Arhgef4	1.46	0.144	2.28	0.026	-1.13	0.407	1.29	0.008	1.31	0.421
1451340_at	AT rich interactive domain 5A (Mrf1 like)	Arid5a	-1.12	0.302	-1.07	0.695	-1.23	0.231	1.29	0.004	-1.06	0.634
1436422_at	cDNA sequence BC026590	BC026590	1.33	0.507	1.82	0.058	1.35	0.019	1.29	0.003	1.48	0.005
1440906_at	B-cell CLL/lymphoma 7C	Bcl7c	-1.29	0.173	1.16	0.337	1.29	0.641	1.29	0.040	1.6	0.119
1453740_a_at	cyclin L2	Ccnl2	1.66	0.355	1.61	0.566	1.01	0.952	1.29	0.035	-1.09	0.388
1459053_at	centaurin, gamma 2	Centg2	-1.31	0.218	-1.19	0.336	-1.03	0.921	1.29	0.011	1.12	0.549
1457233_at	DnaJ (Hsp40) homolog, subfamily A, member 2	Dnaja2	-1.02	0.581	-1.03	0.585	1.41	0.063	1.29	0.013	1.01	0.928
1459546_s_at	ectonucleotide pyrophosphatase/phosphodiesterase 1	Enpp1	-1.04	0.393	-1.07	0.493	-1.11	0.371	1.29	0.025	-1.09	0.221
1429493_at	methyltransferase like 4	Mettl4	1.12	0.212	1.11	0.109	1.05	0.346	1.29	0.038	-1.02	0.650
1424908_at	mitochondrial methionyl-tRNA formyltransferase	Mtfmt	1.15	0.059	1.33	0.033	1.17	0.061	1.29	0.004	1.19	0.010
1419753_at	nuclear transcription factor, X-box binding 1	Nfx1	1.14	0.468	1.33	0.034	1.22	0.245	1.29	0.007	1.21	0.101
1418082_at	N-myristoyltransferase 1	Nmt1	-1.05	0.578	1.36	0.554	-1.14	0.299	1.29	0.043	1.02	0.847
1420535_a_at	negative regulator of ubiquitin-like proteins 1	Nub1	1.45	0.471	1.57	0.063	1.12	0.449	1.29	0.024	1.27	0.096
1454120_a_at	polycomb group ring finger 6	Pcgf6	2.78	0.693	2.89	0.119	1.58	0.166	1.29	0.019	1.41	0.094
1416388_at	phosphatidylinositol-4-phosphate 5-kinase, type II, gamma	Pip5k2c	1.92	0.733	2.47	0.249	1.38	0.207	1.29	0.012	1.16	0.799
1435253_at	RAB11B, member RAS oncogene family	Rab11b	-1.11	0.429	1.02	0.605	1.11	0.196	1.29	0.029	1.13	0.297
1430367_at	Stam binding protein like 1	Stambpl1	-1.2	0.231	-1.14	0.424	-1.03	0.602	1.29	0.018	-1.01	0.624
1434022_at	zinc finger and BTB domain containing 33	Zbtb33	-1.01	0.735	1.16	0.437	1.26	0.003	1.29	0.009	1.25	0.013
1426896_at	zinc finger protein 191	Zfp191	1.43	0.477	1.35	0.661	1.05	0.615	1.29	0.008	1.25	0.290
1455778_at	zinc finger protein 192	Zfp192	1.1	0.364	1.07	0.634	1.22	0.225	1.29	0.039	1.05	0.696
1424261_at	zinc finger protein 672	Zfp672	1.64	0.729	1.81	0.117	1.17	0.052	1.29	0.004	1.41	0.026
1432114_at	RIKEN cDNA 1110035E04 gene	1110035E04Rik	-1.17	0.340	-1.23	0.159	1.4	0.814	1.3	0.001	1.27	0.454
1429536_at	RIKEN cDNA 2310040C09 gene	2310040C09Rik	-1.17	0.310	-1.29	0.290	-1.16	0.482	1.3	0.010	1.28	0.451
1429126_at	RIKEN cDNA 2600001M11 gene	2600001M11Rik	1.27	0.249	1.33	0.121	-1.11	0.232	1.3	0.033	1.2	0.134
1424692_at	RIKEN cDNA 2810055F11 gene	2810055F11Rik	1.53	0.251	1.83	0.018	1.25	0.007	1.3	0.039	1.47	0.008
1427085_at	RIKEN cDNA 2810432D09 gene	2810432D09Rik	1.03	0.905	1.5	0.162	1.3	0.046	1.3	0.003	1.25	0.090
1455852_at	RIKEN cDNA 4833432M17 gene	4833432M17Rik	1.92	0.197	2.44	0.010	1.12	0.593	1.3	0.030	1.04	0.997

1454028_at	RIKEN cDNA 4931402H11 gene	4931402H11Rik	1.47	0.227	-1.46	0.141	1.01	0.867	1.3	0.003	1.01	0.683
1416912_at	RIKEN cDNA 6330407G11 gene	6330407G11Rik	1.32	0.316	1.4	0.369	1.07	0.099	1.3	0.007	1	0.992
1455334_at	RIKEN cDNA 9830167H18 gene	9830167H18Rik	1.33	0.301	1.86	0.016	1.15	0.259	1.3	0.019	1.02	0.716
1452273_at	expressed sequence AA409316	AA409316	1.23	0.209	1.58	0.035	1.42	0.014	1.3	0.012	1.55	0.033
1451347_at	coiled-coil domain containing 95	Ccdc95	2.65	0.408	3.34	0.053	1.36	0.078	1.3	0.004	1.3	0.085
1416511_a_at	CDC42 effector protein (Rho GTPase binding) 4	Cdc42ep4	1.12	0.476	1.27	0.158	1.22	0.271	1.3	0.008	1.23	0.178
1446915_at	DNA segment, Chr 7, ERATO Doi 316, expressed	D7Ertd316e	-1.34	0.253	1.97	0.421	-1.33	0.373	1.3	0.047	1.86	0.031
1452097_a_at	dual specificity phosphatase 7 /// similar to dual specificity phosphatase	Dusp7 /// LOC67494	1.5	0.314	2.06	0.091	1.19	0.144	1.3	0.017	1.23	0.031
1416268_at	E26 avian leukemia oncogene 2, 3' domain	Ets2	1.03	0.898	1.32	0.027	1.26	0.064	1.3	0.047	1.2	0.020
1424300_at	gem (nuclear organelle) associated protein 6	Gemin6	1.19	0.010	1.32	0.005	1.2	0.030	1.3	0.003	1.16	0.027
1431333_at	histone 1, H4h	Hist1h4h	-1.72	0.138	1.18	0.583	1.82	0.634	1.3	0.039	1.79	0.213
1439637_at	kinesin family member 7	Kif7	3.47	0.739	3.19	0.204	1.06	0.319	1.3	0.012	1.13	0.580
1425280_at	leukocyte receptor cluster (LRC) member 1	Leng1	-1.05	0.494	1.12	0.670	1.05	0.537	1.3	0.043	1.16	0.133
1455700_at	MTERF domain containing 3	Mterfd3	1.15	0.061	1.23	0.199	1.24	0.111	1.3	0.045	1.25	0.168
1417971_at	nurim (nuclear envelope membrane protein)	Nrm	2.01	0.612	1.79	0.285	1.16	0.414	1.3	0.037	1.05	0.817
1455387_at	nuclear fragile X mental retardation protein interacting protein 2	Nufip2	1.1	0.136	1.23	0.279	1.03	0.006	1.3	0.021	1.2	0.711
1422890_at	protocadherin 18	Pcdh18	-1.07	0.833	1.41	0.138	1.79	0.039	1.3	0.036	1.3	0.124
1428345_at	phosphatidic acid phosphatase type 2 domain containing 2	Ppapdc2	1.06	0.865	1.29	0.206	1.81	0.092	1.3	0.013	1.04	0.686
1423387_at	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	Psmd9	1.3	0.716	1.69	0.832	1.08	0.879	1.3	0.004	1.68	0.234
1452736_at	R3H domain and coiled-coil containing 1	R3hcc1	1.95	0.295	2.37	0.052	1.21	0.054	1.3	0.003	1.26	0.029
1438397_a_at	RNA binding motif protein 39	Rbm39	4.39	0.296	4.04	0.101	-1.06	0.615	1.3	0.023	-1.04	0.453
1454011_a_at	replication protein A2	Rpa2	4.17	0.273	4.99	0.007	1.09	0.455	1.3	0.013	1.13	0.222
1451190_a_at	SH3-binding kinase 1	Sbk1	-1.29	0.317	1.43	0.673	1.82	0.072	1.3	0.005	1.61	0.024
1443158_at	Sex comb on midleg homolog 1	Scmh1	1.76	0.189	1.75	0.046	1.32	0.220	1.3	0.035	-1.01	0.908
1435887_at	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, a	Serpina11	-1.19	0.354	-1.23	0.342	1.44	0.292	1.3	0.026	1.25	0.453
1439041_at	solute carrier family 39 (zinc transporter), member 10	Slc39a10	5.22	0.379	4.58	0.292	1.12	0.026	1.3	0.003	-1.05	0.658
1421012_at	signal recognition particle receptor, B subunit	Srprb	-1.18	0.393	1.25	0.745	1.46	0.013	1.3	0.024	1.33	0.133
1421528_a_at	surfeit gene 5	Surf5	1.03	0.625	1.42	0.007	1.34	0.007	1.3	0.009	1.48	0.025
1434552_at	WD repeat domain 77	Wdr77	-1.1	0.347	1.2	0.335	1.37	0.000	1.3	0.001	1.34	0.000
1436978_at	wingless-type MMTV integration site 9A	Wnt9a	-1.05	0.438	1.23	0.459	1.31	0.496	1.3	0.036	1.13	0.354
1418291_at	zinc finger protein 87	Zfp87	1.15	0.786	1.48	0.060	1.28	0.125	1.3	0.050	1.29	0.369
1421031_a_at	RIKEN cDNA 2310016C08 gene	2310016C08Rik	1.12	0.597	1.47	0.003	1.29	0.067	1.31	0.002	1.21	0.066
1453081_at	RIKEN cDNA 2410022M11 gene	2410022M11Rik	-1.19	0.397	-1.11	0.458	1.01	0.920	1.31	0.026	1.67	0.002
1437110_at	RIKEN cDNA 2810474O19 gene	2810474O19Rik	1.07	0.362	1.4	0.166	-1.05	0.593	1.31	0.014	1.27	0.034
1432583_at	RIKEN cDNA 2900042E19 gene	2900042E19Rik	1.63	0.913	1.05	0.617	-1.01	0.988	1.31	0.021	2.12	0.172
1417734_at	A kinase (PRKA) anchor protein 8-like	Akap8l	1.11	0.783	1.48	0.034	-1.03	0.487	1.31	0.044	1.11	0.365
1453736_s_at	RIKEN cDNA B230219D22 gene	B230219D22Rik	2.8	0.359	3.24	0.300	1.14	0.328	1.31	0.021	-1.03	0.447
1442052_at	RIKEN cDNA C330019G07 gene	C330019G07Rik	1.3	0.199	1.1	0.554	-1.15	0.128	1.31	0.038	-1.12	0.692
1415995_at	caspase 6	Casp6	2.7	0.210	3.5	0.114	1.18	0.060	1.31	0.001	1.35	0.083
1448382_at	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogena	Ehhadh	1.67	0.075	1.12	0.718	1.63	0.105	1.31	0.004	-1.08	0.416
1455108_at	eukaryotic translation initiation factor 4E member 2	Eif4e2	-1.01	0.966	1.21	0.033	1.15	0.118	1.31	0.044	1.12	0.256
1436623_at	ectonucleoside triphosphate diphosphohydrolase 7	Entpd7	1.56	0.148	1.25	0.121	1.05	0.630	1.31	0.022	1.09	0.459
1453102_at	fibronectin leucine rich transmembrane protein 3	Flrt3	1.6	0.437	2.79	0.025	1.33	0.001	1.31	0.032	1.5	0.013
1425713_a_at	ring finger protein 146	Rnf146	1.97	0.426	2.44	0.185	1.02	0.831	1.31	0.002	1.06	0.645
1433892_at	sperm associated antigen 5	Spag5	1.03	0.396	1.22	0.128	1.08	0.575	1.31	0.004	1.14	0.271
1418074_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalacto	St6galnac4	1	0.884	1.25	0.242	1.16	0.144	1.31	0.031	1.35	0.039
1421485_at	tau tubulin kinase 2	Ttbk2	-1.51	0.277	-1.48	0.272	1.34	0.912	1.31	0.022	-1.09	0.720
1428218_a_at	RIKEN cDNA 1600012H06 gene	1600012H06Rik	1.18	0.230	1.4	0.041	1.12	0.365	1.32	0.011	1.17	0.159
1429961_at	RIKEN cDNA 1700021C14 gene	1700021C14Rik	1.42	0.279	1.16	0.640	1.28	0.557	1.32	0.046	1.07	0.885
1428400_at	RIKEN cDNA 2200002K05 gene	2200002K05Rik	-1.14	0.434	-1.18	0.422	1.51	0.070	1.32	0.049	1.16	0.235
1427050_at	RIKEN cDNA 5730420B22 gene	5730420B22Rik	1.58	0.373	1.29	0.512	-1.16	0.172	1.32	0.018	-1.13	0.323
1419831_at	expressed sequence AA416453	AA416453	1.04	0.669	1.39	0.483	1.12	0.569	1.32	0.031	-1.5	0.198
1438816_at	AT hook containing transcription factor 1	Ahctf1	1.04	0.561	1.1	0.581	1.11	1.000	1.32	0.026	-1.04	0.502
1416374_at	adaptor-related protein complex 3, mu 1 subunit /// similar to AP-3 compl	Ap3m1 /// LOC6718	7.8	0.167	7.78	0.103	1.13	0.229	1.32	0.036	1.1	0.715
1444408_at	RIKEN cDNA B130040O20 gene	B130040O20Rik	-1.49	0.275	-1.01	0.524	1.29	0.942	1.32	0.000	-1.07	0.443
1424971_at	coiled-coil domain containing 99	Ccdc99	1.1	0.336	1.19	0.307	1.25	0.191	1.32	0.034	1.12	0.124
1439023_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 55	Ddx55	1.1	0.242	1.1	0.107	1.05	0.934	1.32	0.007	-1.08	0.472
1448969_at	FtsJ homolog 2 (E. coli)	Ftsj2	1.13	0.993	1.54	0.175	1.38	0.280	1.32	0.009	1.14	0.305

1460206_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffold pro	Grasp	6.01	0.281	7.21	0.134	1.54	0.046	1.32	0.014	1.19	0.173
1442183_at	similar to carnitine deficiency-associated gene expressed in ventricle 3 is	LOC236069	1.58	0.190	-1.09	0.581	1.18	0.811	1.32	0.034	-1.03	0.593
1417234_at	matrix metallopeptidase 11	Mmp11	1.62	0.315	1.57	0.252	1.16	0.160	1.32	0.031	1.31	0.017
1450087_a_at	nucleolar and coiled-body phosphoprotein 1	Nolc1	1.68	0.346	1.89	0.020	-1	0.959	1.32	0.022	1.11	0.357
1434469_at	OTU domain containing 4	Otud4	1.64	0.325	1.8	0.157	1.09	0.224	1.32	0.016	-1.1	0.340
1422026_at	peptidase inhibitor 16	Pi16	-1.03	0.540	1.2	0.756	-1.1	0.420	1.32	0.001	1.28	0.094
1432538_a_at	replication factor C (activator 1) 3	Rfc3	4.97	0.204	6.5	0.028	1.34	0.099	1.32	0.025	1.24	0.015
1437476_at	ribonucleotide reductase M2 B (TP53 inducible)	Rrm2b	3.12	0.359	3.14	0.575	1.18	0.386	1.32	0.001	-1.07	0.635
1434520_at	sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. ce	Sc5d	1.91	0.241	1.77	0.119	1.25	0.102	1.32	0.012	1.28	0.069
1455511_at	selenophosphate synthetase 1	Sephs1	1.09	0.608	1.47	0.128	1.87	0.074	1.32	0.001	1.47	0.038
1424920_at	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	Slc37a3	-1.01	0.644	1.08	0.746	1.06	0.644	1.32	0.025	1.19	0.557
1428010_at	translocase of inner mitochondrial membrane 9 homolog (yeast)	Timm9	1.25	0.224	1.17	0.989	1.21	0.301	1.32	0.015	1.13	0.932
1451192_a_at	tetratricopeptide repeat domain 4	Ttc4	17.81	0.432	16.49	0.112	1.07	0.505	1.32	0.043	1.09	0.472
1456043_at	ubiquitin specific peptidase 22	Usp22	17.33	0.441	20.36	0.403	1.12	0.228	1.32	0.036	1.16	0.156
1436004_at	ubiquitin specific peptidase 27, X chromosome	Usp27x	-1.09	0.488	1.32	0.380	1.35	0.153	1.32	0.018	1.76	0.024
1417088_at	zinc finger protein 346	Zfp346	-1.03	0.622	1.14	0.331	1.44	0.080	1.32	0.003	1.38	0.005
1450410_a_at	RIKEN cDNA 4930570C03 gene	4930570C03Rik	1.3	0.411	1.37	0.196	1.08	0.042	1.33	0.029	1.59	0.037
1454302_at	RIKEN cDNA 5730410E19 gene	5730410E19Rik	1.44	0.648	1.48	0.640	-1.14	0.367	1.33	0.017	1.08	0.778
1431495_at	RIKEN cDNA 6030440G07 gene	6030440G07Rik	1.05	0.551	-1.36	0.296	-1.45	0.216	1.33	0.007	1.22	0.406
1442007_at	RIKEN cDNA 9830124H08 gene	9830124H08Rik	1.03	0.648	1.18	0.866	1.17	0.080	1.33	0.042	1.42	0.046
1436753_at	aarF domain containing kinase 5	Adck5	-1.03	0.263	1.1	0.192	1.18	0.380	1.33	0.014	1.47	0.104
1442745_x_at	expressed sequence C79248	C79248	1.25	0.340	1.31	0.112	1.09	0.943	1.33	0.019	-1.17	0.060
1451702_at	CKLF-like MARVEL transmembrane domain containing 7	Cmtm7	-1.07	0.440	1.29	0.028	1	0.945	1.33	0.023	1.19	0.281
1452210_at	DNA2 DNA replication helicase 2-like (yeast)	Dna2l	1.34	0.235	1.84	0.087	1.35	0.078	1.33	0.022	1.33	0.056
1452638_s_at	dynamin 1-like	Dnm1l	2.65	0.431	1.8	0.994	-1.1	0.382	1.33	0.026	1.03	0.943
1451308_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-	Elovl4	1.03	0.959	1.12	0.401	1.19	0.310	1.33	0.006	1.45	0.319
1445898_at	gamma-glutamyl carboxylase	Ggcx	1.3	0.381	1.07	0.751	1.07	0.733	1.33	0.004	-1	0.968
1416481_s_at	HIG1 domain family, member 1A	Higd1a	1.06	0.697	1.32	0.206	1.58	0.077	1.33	0.017	1.32	0.011
1423104_at	insulin receptor substrate 1	Irs1	1.41	0.165	1.98	0.109	1.32	0.007	1.33	0.004	1.23	0.017
1444651_at	hypothetical LOC553089	LOC553089	-1.09	0.464	-1.06	0.614	1.02	0.565	1.33	0.049	-1.13	0.309
1458508_at	matrin 3	Matr3	1.14	0.231	1.22	0.273	-1.01	0.792	1.33	0.012	-1.3	0.141
1419676_at	myxovirus (influenza virus) resistance 2	Mx2	1.81	0.290	1.38	0.568	1.17	0.482	1.33	0.023	1.06	0.982
1420554_a_at	RAS-related C3 botulinum substrate 3	Rac3	1.06	0.764	1.14	0.286	-1.01	0.810	1.33	0.008	1.32	0.058
1451517_at	Rho-related BTB domain containing 2	Rhobtb2	1.26	0.139	1.85	0.256	1.1	0.643	1.33	0.041	1.43	0.073
1426958_at	ribosomal protein S9 /// similar to ribosomal protein S9	Rps9 /// LOC272691	1.26	0.192	1.4	0.405	1.28	0.275	1.33	0.001	1.13	0.445
1424317_at	solute carrier family 25 (mitochondrial deoxynucleotide carrier), member	Slc25a19	-1.17	0.429	1.56	0.948	1.29	0.670	1.33	0.001	1.1	0.992
1448706_at	Traf and Tnf receptor associated protein	Ttrap	1.35	0.128	1.38	0.004	1.13	0.120	1.33	0.012	1.17	0.100
1427831_s_at	zinc finger protein 260 /// similar to Zinc finger protein OZF (Zinc finger p	Zfp260 /// LOC6350	3.59	0.366	3.31	0.461	1.08	0.292	1.33	0.000	-1.05	0.714
1450644_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	-1.03	0.752	1.4	0.022	1.55	0.030	1.33	0.016	1.57	0.000
1451281_at	zinc finger protein 96	Zfp96	-1.05	0.613	1.24	0.331	1.25	0.051	1.33	0.019	1.27	0.072
1439087_a_at	RIKEN cDNA 1500004A08 gene	1500004A08Rik	1.48	0.114	2.08	0.017	1.13	0.476	1.34	0.024	-1.02	0.812
1425297_at	cDNA sequence BC012278	BC012278	1.26	0.542	1.52	0.092	1.04	0.272	1.34	0.036	1.19	0.123
1438089_a_at	BCL2-associated transcription factor 1	Bclaf1	1.48	0.140	1.54	0.154	-1	0.898	1.34	0.028	-1.08	0.343
1437210_a_at	bromodomain containing 2	Brd2	-1.06	0.299	1.16	0.120	1.07	0.706	1.34	0.002	1.39	0.039
1426002_a_at	cell division cycle 7 (S. cerevisiae)	Cdc7	1.12	0.274	1.35	0.010	1.24	0.275	1.34	0.019	1.22	0.272
1420545_a_at	chimerin (chimaerin) 1	Chn1	2.35	0.165	1.35	0.341	-1.01	0.685	1.34	0.036	1.05	0.872
1426714_at	DNA segment, Chr 11, ERATO Doi 18, expressed	D11Ertd18e	2.26	0.532	1.37	0.510	-1.04	0.633	1.34	0.004	1.03	0.901
1438488_at	esterase D/formylglutathione hydrolase	Esd	-1.09	0.370	-1.07	0.640	1.05	0.336	1.34	0.029	1.12	0.340
1460673_at	folylpolyglutamyl synthetase	Fpgs	-1.03	0.575	1.37	0.251	1.22	0.375	1.34	0.013	1.37	0.004
1427554_at	helicase, mus308-like (Drosophila)	Hel308	3.24	0.105	2.46	0.183	3.15	0.033	1.34	0.044	-1.03	0.610
1440965_at	Phosphatidylinositol glycan, class L	Pigl	1.09	0.989	1.16	0.572	1.24	0.040	1.34	0.006	1.06	0.022
1449480_at	Sin3-associated polypeptide 18	Sap18	1.17	0.290	1.48	0.203	1.31	0.038	1.34	0.017	1.31	0.192
1450034_at	signal transducer and activator of transcription 1	Stat1	1.02	0.705	-1.07	0.816	1.16	0.491	1.34	0.027	1.12	0.419
1448458_at	topoisomerase (DNA) II beta	Top2b	3.51	0.223	2.16	0.394	1.01	0.652	1.34	0.047	-1.2	0.465
1449391_at	zinc finger protein 37	Zfp37	1.6	0.298	1.66	0.042	1.51	0.276	1.34	0.002	1.41	0.024
1425522_at	RIKEN cDNA 2600011C06 gene	2600011C06Rik	1.75	0.111	1.17	0.751	-1.37	0.100	1.35	0.037	-1.26	0.217
1431528_at	RIKEN cDNA 5830427D02 gene	5830427D02Rik	-1.1	0.448	-1.03	0.491	1.03	0.654	1.35	0.043	1	0.646
1450716_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospo	Adamts1	1.09	0.215	1.27	0.083	1.35	0.001	1.35	0.039	1.49	0.059

1441172_at	AF4/FMR2 family, member 3	Aff3	-1.12	0.418	-1.25	0.336	1.73	0.000	1.35	0.036	1.32	0.712
1454736_at	ankyrin repeat domain 57	Ankrd57	1.06	0.862	1.27	0.133	1.22	0.081	1.35	0.001	1.41	0.017
1454617_at	arrestin domain containing 3	Arrdc3	-1.05	0.719	1.4	0.142	1.58	0.007	1.35	0.021	1.71	0.025
1423512_at	expressed sequence AW209491	AW209491	1.2	0.274	1.35	0.136	1.1	0.423	1.35	0.001	1.01	0.460
1433452_at	RIKEN cDNA B630019K06 gene	B630019K06Rik	2.92	0.088	3.74	0.035	1.47	0.084	1.35	0.033	1.06	0.660
1440462_at	RIKEN cDNA B930068K11 gene	B930068K11Rik	-1.37	0.370	-1.23	0.399	1.19	0.566	1.35	0.011	1.04	0.987
1436585_at	expressed sequence BB182297	BB182297	1.6	0.412	1.44	0.453	1.06	0.826	1.35	0.045	-1.14	0.375
1444416_at	Centromere autoantigen A	Cenpa	-1.92	0.065	1.04	0.710	1.79	0.149	1.35	0.019	-1.04	0.687
1460665_a_at	CCR4-NOT transcription complex, subunit 7	Cnot7	1.46	0.325	1.37	0.354	1.03	0.802	1.35	0.020	-1.06	0.468
1452391_at	coxsackievirus and adenovirus receptor	Cxadr	-1	0.700	1.11	0.857	1.21	0.566	1.35	0.011	1.39	0.644
1433622_at	gem (nuclear organelle) associated protein 4	Gemin4	1.82	0.236	2.11	0.013	1.24	0.013	1.35	0.009	1.39	0.005
1423566_a_at	heat shock protein 110	Hsp110	1.77	0.352	1.91	0.103	1.09	0.719	1.35	0.003	1.15	0.141
1431026_at	N-acetyltransferase 12	Nat12	-1.17	0.434	1.21	0.886	1.25	0.237	1.35	0.005	1.68	0.037
1455035_s_at	nucleolar protein 5A	Nol5a	-1.09	0.417	1.26	0.522	1.18	0.067	1.35	0.002	1.23	0.011
1432012_a_at	NOL1/NOP2/Sun domain family 6	Nsun6	3.27	0.017	3.56	0.020	1.36	0.583	1.35	0.022	-1.24	0.038
1428615_at	purinergic receptor P2Y, G-protein coupled, 5	P2ry5	1.24	0.018	1.7	0.043	1.44	0.019	1.35	0.009	1.52	0.011
1451624_a_at	phosphatase, orphan 2	Phospho2	1.03	0.988	1.39	0.251	1.22	0.020	1.35	0.028	1.63	0.029
1451106_at	RNA binding motif protein 21	Rbm21	1.18	0.165	1.55	0.028	1.17	0.242	1.35	0.014	1.44	0.023
1438516_at	Rap1 interacting factor 1 homolog (yeast)	Rif1	1.47	0.302	1.21	0.691	1.14	0.554	1.35	0.007	-1.2	0.288
1440986_at	RNA polymerase II associated protein 1	Rpap1	1.86	0.163	1.57	0.025	2.5	0.587	1.35	0.042	1.61	0.522
1428805_at	solute carrier family 35, member E3	Slc35e3	1.93	0.233	3.11	0.012	1.18	0.069	1.35	0.006	1.52	0.003
1429194_at	tigger transposable element derived 2	Tigd2	-1.09	0.464	-1.03	0.525	1.09	0.281	1.35	0.043	1.38	0.010
1428074_at	transmembrane protein 158	Tmem158	-1.13	0.479	1.64	0.129	1.67	0.107	1.35	0.034	1.71	0.027
1434495_at	zinc finger protein 278	Zfp278	1.93	0.263	2.46	0.069	1.14	0.736	1.35	0.021	1.72	0.007
1447403_a_at	Zinc finger, MYND domain containing 19	Zmynd19	-1.1	0.476	1.31	0.040	1.12	0.443	1.35	0.015	1.26	0.034
1451189_at	zinc finger, SWIM domain containing 1	Zswim1	1.12	0.522	1.45	0.012	1.12	0.044	1.35	0.015	1.41	0.045
1429869_at	RIKEN cDNA 1110020C03 gene	1110020C03Rik	1.31	0.871	1.46	0.588	1.72	0.647	1.36	0.033	-1.28	0.277
1456430_at	coiled-coil domain containing 39	Ccdc39	1.09	0.925	1.29	0.894	1.09	0.536	1.36	0.028	-1.11	0.733
1417019_a_at	cell division cycle 6 homolog (S. cerevisiae)	Cdc6	-1.15	0.186	1.51	0.080	1.19	0.170	1.36	0.006	1.31	0.026
1449408_at	junction adhesion molecule 2	Jam2	-1.14	0.676	-1.09	0.704	1.04	0.697	1.36	0.023	-1.06	0.488
1423218_a_at	mitochondrial ribosomal protein L49	Mrpl49	1.31	0.017	1.85	0.007	1.24	0.006	1.36	0.009	1.29	0.096
1457264_at	PHD finger protein 20-like 1	Phf20l1	1.05	0.610	1.03	0.588	1.24	0.951	1.36	0.023	-1.14	0.359
1436366_at	protein phosphatase 1, regulatory (inhibitor) subunit 15b	Ppp1r15b	1.45	0.237	1.6	0.452	1.16	0.982	1.36	0.047	1.53	0.071
1422552_at	reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	1.6	0.294	4.18	0.007	1.31	0.022	1.36	0.042	2.34	0.011
1442129_at	RIKEN cDNA 1810058I24 gene	1810058I24Rik	-1.32	0.145	1.04	0.922	1.14	0.101	1.37	0.026	1.13	0.337
1452268_at	RIKEN cDNA 2810485I05 gene	2810485I05Rik	2.47	0.226	2.27	0.362	1.22	0.018	1.37	0.007	1.09	0.340
1434532_at	cDNA sequence BC035295	BC035295	-1.07	0.499	1.44	0.752	1.31	0.000	1.37	0.013	1.43	0.002
1449147_at	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	Chst1	-1.15	0.441	-1.07	0.620	1.62	0.092	1.37	0.046	1.23	0.674
1444378_at	Casein kinase 1, delta	Csnk1d	1.26	0.132	1.1	0.524	1.1	0.319	1.37	0.041	1.15	0.231
1435348_at	RIKEN cDNA D930009K15 gene	D930009K15Rik	1.05	0.722	1.27	0.073	1.28	0.030	1.37	0.011	1.37	0.003
1431422_a_at	dual specificity phosphatase 14	Dusp14	1.88	0.299	2.21	0.031	1.32	0.019	1.37	0.006	1.27	0.039
1453689_at	Fanconi anemia, complementation group E	Fance	1.67	0.665	1.44	0.824	1.08	0.740	1.37	0.045	1.14	0.471
1435213_at	NHL repeat containing 1	Nhlrc1	-1.04	0.561	2.11	0.038	-1.06	0.579	1.37	0.038	1.01	0.975
1423522_at	nucleoplasmin 3 /// nucleoplasmin 3, pseudogene 1 /// similar to Nucleop	Npm3 /// Npm3-ps1	1.36	0.055	1.55	0.054	1.12	0.701	1.37	0.011	1.25	0.078
1451773_s_at	polymerase (RNA) III (DNA directed) polypeptide F	Polr3f	2.42	0.270	2.74	0.048	-1.04	0.706	1.37	0.039	-1.03	0.810
1424906_at	PQ loop repeat containing	Pqlc3	2.88	0.360	4.08	0.081	1.43	0.145	1.37	0.021	1.46	0.018
1428172_at	PRP39 pre-mRNA processing factor 39 homolog (yeast)	Prpf39	1.43	0.120	1.76	0.047	1.32	0.050	1.37	0.021	1.06	0.278
1439747_at	prostaglandin E synthase	Ptges	1.81	0.616	1.97	0.350	1.47	0.096	1.37	0.008	1.28	0.472
1455002_at	protein tyrosine phosphatase 4a1	Ptp4a1	1.06	0.052	1.38	0.047	1.21	0.058	1.37	0.010	1.29	0.002
1429399_at	ring finger protein 125	Rnf125	-1.36	0.067	-1.21	0.181	1.48	0.050	1.37	0.008	1.49	0.054
1424581_at	SH3 and cysteine rich domain 2	Stac2	1.01	0.842	1.02	0.899	1.09	0.245	1.37	0.031	1.37	0.165
1418163_at	toll-like receptor 4	Tlr4	1.13	0.110	1.22	0.289	1.11	0.570	1.37	0.032	1.11	0.204
1431504_at	RIKEN cDNA 2310061N02 gene	2310061N02Rik	-1.55	0.121	-1.03	0.775	1.25	0.749	1.38	0.001	1.36	0.675
1449122_at	RIKEN cDNA 3110003A22 gene	3110003A22Rik	1.36	0.496	1.98	0.021	1.36	0.005	1.38	0.040	1.08	0.535
1422535_at	cyclin E2	Ccne2	1.07	0.667	1.54	0.097	1.26	0.060	1.38	0.043	1.39	0.029
1448364_at	cyclin G2	Ccng2	4.9	0.271	5.52	0.140	1.37	0.002	1.38	0.035	1.18	0.306
1449402_at	carbohydrate (N-acetylglucosamino) sulfotransferase 7	Chst7	-1.01	0.414	-1.06	0.962	1.14	0.343	1.38	0.037	1.41	0.128
1454648_s_at	DNA segment, Chr 10, Wayne State University 102, expressed	D10Wsu102e	1.35	0.463	1.72	0.014	1.18	0.012	1.38	0.006	1.3	0.026

1417412_at	factor 8-associated gene A	F8a	2.33	0.320	3.02	0.086	1.23	0.328	1.38	0.019	2.26	0.280
1418060_a_at	mitogen activated protein kinase 7	Mapk7	1.42	0.154	1.82	0.080	1.2	0.249	1.38	0.033	1.33	0.084
1416505_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	1.34	0.031	2.01	0.033	1.48	0.004	1.38	0.001	1.56	0.010
1423666_s_at	ribosomal protein L5 /// similar to 60S ribosomal protein L5 /// similar to 6	Rpl5 /// LOC382740	-1.1	0.256	1.27	0.032	1.21	0.047	1.38	0.002	1.31	0.063
1432027_a_at	TBC1 domain family, member 14	Tbc1d14	3.07	0.770	4.08	0.160	1.06	0.447	1.38	0.014	1.23	0.653
1421139_a_at	zinc finger protein 386 (Kruppel-like)	Zfp386	12.01	0.399	17.29	0.112	1.12	0.030	1.38	0.020	1.1	0.308
1426564_at	zinc finger protein 553	Zfp553	-1.14	0.301	1.27	0.576	1.26	0.118	1.38	0.021	1.23	0.405
1422954_at	zinc finger protein 60	Zfp60	2.22	0.869	1.82	0.936	-1.35	0.105	1.38	0.008	1.26	0.191
1441871_at	RIKEN cDNA 1810044D09 gene	1810044D09Rik	-1.43	0.216	-1.32	0.150	1.07	0.949	1.39	0.035	-1.25	0.055
1420989_at	RIKEN cDNA 4933411K20 gene	4933411K20Rik	1.07	0.999	1.44	0.096	1.11	0.617	1.39	0.024	2.65	0.035
1419070_at	cystin 1	Cys1	1.8	0.191	1.91	0.001	1.06	0.752	1.39	0.032	1.4	0.474
1454229_a_at	exonuclease domain containing 1	Exod1	1.88	0.010	2.25	0.095	1.06	0.906	1.39	0.030	-1.06	0.818
1415842_at	G protein beta subunit-like	Gbl	1.18	0.526	1.45	0.461	1.32	0.145	1.39	0.014	1.22	0.131
1449169_at	hyaluronan synthase 2	Has2	1.41	0.023	1.81	0.113	1.36	0.005	1.39	0.003	1.38	0.023
1449262_s_at	lin-7 homolog C (C. elegans)	Lin7c	1.95	0.195	2.02	0.289	1.29	0.156	1.39	0.044	1.25	0.557
1433575_at	similar to Transcription factor SOX-4	LOC672274	1.53	0.189	2.22	0.048	1.45	0.012	1.39	0.011	1.56	0.000
1428950_s_at	nucleolar protein 8	Nol8	1.16	0.659	1.44	0.322	-1	0.900	1.39	0.006	1.06	0.974
1438070_at	PHD finger protein 3	Phf3	2.42	0.278	3.06	0.214	1.09	0.625	1.39	0.006	1.01	0.951
1424336_at	phosphopantothenoylcysteine decarboxylase	Ppcdc	1.43	0.628	-1.01	0.267	1.08	0.756	1.39	0.042	1.48	0.011
1435167_at	RAN binding protein 6	Ranbp6	-1.35	0.276	1.23	0.846	1.2	0.091	1.39	0.021	1.46	0.082
1425974_a_at	tripartite motif protein 25	Trim25	1.2	0.507	1.43	0.017	1.26	0.089	1.39	0.001	1.5	0.023
1441412_s_at	tripartite motif-containing 45	Trim45	-1.05	0.493	-1.07	0.532	1.53	0.014	1.39	0.015	1.17	0.189
1446855_at	vacuolar protein sorting 13 D (yeast)	Vps13d	1.11	0.963	1.09	0.830	1.88	0.097	1.39	0.035	1.15	0.859
1429734_at	RIKEN cDNA 4632434I11 gene	4632434I11Rik	1.45	0.010	2.17	0.002	1.35	0.157	1.4	0.002	1.57	0.048
1457260_at	RIKEN cDNA 7530403E16 gene	7530403E16Rik	-1.02	0.552	1.14	0.596	1.46	0.004	1.4	0.024	1.29	0.182
1436021_at	RIKEN cDNA A930031D07 gene	A930031D07Rik	1.25	0.600	1.41	0.735	2.66	0.240	1.4	0.040	2.48	0.087
1421690_s_at	agouti related protein	Agrp	1.5	0.818	2.33	0.543	1.78	0.955	1.4	0.031	1.41	0.972
1442977_at	Procollagen, type III, alpha 1	Col3a1	1.03	0.595	1.34	0.921	1.19	0.687	1.4	0.002	1.14	0.112
1455087_at	DNA segment, Chr 7, ERATO Doi 715, expressed	D7Ertd715e	1.31	0.310	-1.01	0.875	1.36	0.777	1.4	0.010	1.43	0.132
1439673_at	RIKEN cDNA E230008O15 gene	E230008O15Rik	1.87	0.222	1.44	0.167	-1.01	0.845	1.4	0.024	1.05	0.782
1450608_at	histone 1, H1t	Hist1h1t	-1.44	0.120	2.28	0.919	-1.01	0.435	1.4	0.040	2.06	0.116
1427679_at	large tumor suppressor	Lats1	1.57	0.261	1.7	0.027	1.04	0.992	1.4	0.034	1.07	0.815
1437198_at	ligase III, DNA, ATP-dependent	Lig3	1.1	0.640	1.19	0.155	1.13	0.096	1.4	0.019	1.08	0.559
1460348_at	MAD2 mitotic arrest deficient-like 2 (yeast)	Mad2l2	1.62	0.452	2.42	0.108	1.19	0.384	1.4	0.007	1.15	0.520
1455238_at	melanoma associated antigen (mutated) 1-like 1	Mum1l1	1.36	0.100	1.63	0.045	1.46	0.009	1.4	0.011	1.1	0.240
1448722_s_at	phosphopantothenoylcysteine synthetase	Ppcs	-1.09	0.494	1.15	0.775	1.36	0.013	1.4	0.011	1.35	0.039
1460447_at	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	Pus7l	-1.06	0.109	1.21	0.059	1.16	0.112	1.4	0.007	1.19	0.100
1448885_at	RAP2B, member of RAS oncogene family	Rap2b	-1.1	0.614	1.11	0.672	1.2	0.256	1.4	0.000	1.41	0.087
1453843_at	THAP domain containing 6	Thap6	2.89	0.625	2.46	0.058	1.58	0.087	1.4	0.013	-1.21	0.418
1440560_at	Yippee-like 2 (Drosophila)	Ypel2	1.66	0.245	1.2	0.722	2.7	0.332	1.4	0.035	1.07	0.715
1435333_at	RIKEN cDNA 1110007M04 gene	1110007M04Rik	1.12	0.087	1.39	0.101	1.27	0.005	1.41	0.027	1.3	0.015
1454556_at	RIKEN cDNA 2700057C20 gene	2700057C20Rik	2.26	0.204	1.39	0.985	-1.01	0.828	1.41	0.008	2.28	0.678
1433801_at	RIKEN cDNA 9930012K11 gene	9930012K11Rik	1.1	0.598	1.39	0.054	1.26	0.255	1.41	0.026	1.51	0.059
1451631_at	cDNA sequence BC021395	BC021395	2.69	0.345	1.91	0.249	1.04	0.970	1.41	0.028	-1.03	0.507
1436543_at	cDNA sequence BC034507	BC034507	1.34	0.145	1.55	0.009	1.06	0.548	1.41	0.010	1.22	0.254
1428968_at	centrosomal protein 57	Cep57	1.53	0.213	1.72	0.055	1.16	0.086	1.41	0.014	1.26	0.178
1437341_x_at	cyclic nucleotide phosphodiesterase 1	Cnp1	-1.03	0.558	-1.06	0.431	1.26	0.286	1.41	0.037	1.04	0.786
1445260_at	DCUN1D1 DCN1, defective in cullin neddylation 1, domain containing 1	Dcun1d1	-1.19	0.416	-1.1	0.441	1.15	0.329	1.41	0.013	-1.04	0.464
1424435_a_at	phosphoribosylglycinamide formyltransferase	Gart	11.14	0.656	8.09	0.846	-1	0.887	1.41	0.006	1.06	0.888
1425553_s_at	huntingtin interacting protein 1 related	Hip1r	1.21	0.903	-1.12	0.399	1.18	0.864	1.41	0.015	1.05	0.911
1441239_at	potassium channel tetramerisation domain containing 18	Kctd18	-1.02	0.757	-1.04	0.506	1.21	0.368	1.41	0.050	-1.01	0.647
1457083_at	PRP31 pre-mRNA processing factor 31 homolog (yeast)	Prpf31	1.59	0.196	2.41	0.030	1.35	0.032	1.41	0.043	1.74	0.020
1418851_at	tripartite motif protein 39	Trim39	1.05	0.788	1.34	0.080	1.17	0.354	1.41	0.032	1.17	0.471
1436819_at	septin 6	6-Sep	1.42	0.101	-1.22	0.341	-1.02	0.753	1.42	0.039	1.18	0.554
1440486_at	RIKEN cDNA 2310037I24 gene	2310037I24Rik	1.55	0.352	1.3	0.378	1.64	0.743	1.42	0.040	1.23	0.504
1437427_at	RIKEN cDNA 4933405O20 gene	4933405O20Rik	1.25	0.284	1.1	0.827	-1.01	0.496	1.42	0.043	1.38	0.177
1455218_at	RIKEN cDNA 6330503K22 gene	6330503K22Rik	4.6	0.321	6.4	0.063	1.31	0.321	1.42	0.020	1.25	0.114
1451552_at	Similar to lipoyltransferase	MGC28431	1.43	0.443	1.67	0.015	1.25	0.046	1.42	0.027	1.44	0.103

1434737_at	oligonucleotide/oligosaccharide-binding fold containing 1	Obfc1	1.59	0.023	1.85	0.060	1.2	0.371	1.42	0.013	1.3	0.073
1423314_s_at	phosphodiesterase 7A	Pde7a	1.86	0.892	1.97	0.945	1.04	0.603	1.42	0.038	-1.11	0.616
1448743_at	synovial sarcoma, X breakpoint 2 interacting protein	Ssx2ip	1.5	0.407	1.25	0.838	1.48	0.113	1.42	0.035	1.25	0.057
1429502_at	stress 70 protein chaperone, microsome-associated, human homolog	Stch	2.21	0.246	2.49	0.191	1.22	0.099	1.42	0.006	1.04	0.800
1450090_at	zinc finger protein 101	Zfp101	1.36	0.002	1.19	0.136	1.12	0.507	1.42	0.037	-1.08	0.374
1428550_at	RIKEN cDNA 1810015A11 gene	1810015A11Rik	1.06	0.364	1.27	0.025	1.34	0.004	1.43	0.017	1.41	0.040
1424872_at	RIKEN cDNA 2310001H12 gene /// similar to zinc finger protein 709 /// si	2310001H12Rik /// L	1.23	0.925	1.91	0.127	1.27	0.012	1.43	0.042	1.13	0.080
1432736_at	RIKEN cDNA 4933430H06 gene	4933430H06Rik	1.1	0.955	1.02	0.862	-1.12	0.536	1.43	0.013	1.15	0.889
1428694_at	RIKEN cDNA 5033413D16 gene	5033413D16Rik	1.13	0.391	1.17	0.735	1.18	0.396	1.43	0.016	1.21	0.605
1433298_at	RIKEN cDNA 5830461L22 gene	5830461L22Rik	1.79	0.967	2.98	0.501	-1.05	0.524	1.43	0.007	1.36	0.440
1437684_at	CDNA sequence BC025546	BC025546	1.63	0.589	1.54	0.801	1.76	0.059	1.43	0.036	1.13	0.028
1424229_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3	2.16	0.096	3.82	0.004	1.72	0.023	1.43	0.038	1.89	0.003
1445334_at	similar to signal recognition particle 54	LOC665155	1.02	0.861	1.13	0.837	1.31	0.700	1.43	0.041	1.18	0.419
1420710_at	reticuloendotheliosis oncogene	Rel	1.53	0.097	2.11	0.013	-1.44	0.111	1.43	0.035	1.14	0.696
1453711_at	R-spondin family, member 4	Rspo4	1.21	0.864	1.47	0.260	1.11	0.920	1.43	0.024	-1.17	0.372
1452489_at	vacuolar protein sorting 11 (yeast)	Vps11	1.21	0.938	-1.35	0.268	-1.2	0.302	1.43	0.015	-1.45	0.139
1427985_at	RIKEN cDNA 9630042H07 gene	9630042H07Rik	1.06	0.755	1.36	0.032	1.39	0.145	1.44	0.016	1.63	0.002
1459937_at	Argininosuccinate synthetase 1	Ass1	1.06	0.953	1.46	0.090	-1.17	0.316	1.44	0.017	-1.12	0.490
1429444_at	RAS-like, family 11, member A	Rasl11a	3.42	0.655	4.68	0.179	1.25	0.868	1.44	0.048	1.5	0.090
1443882_at	Solute carrier family 26 (sulfate transporter), member 2	Slc26a2	-1.05	0.512	1.13	0.678	1.17	0.047	1.44	0.037	1.1	0.967
1447657_s_at	synaptopodin 2-like	Synpo2l	1.1	0.893	1.82	0.027	1.17	0.816	1.44	0.005	1.46	0.229
1458311_at	ubiquitin specific peptidase 36	Usp36	-1.09	0.477	-1.14	0.364	-1.03	0.630	1.44	0.038	1.33	0.132
1417803_at	RIKEN cDNA 1110032A04 gene	1110032A04Rik	1.16	0.340	1.62	0.399	1.16	0.561	1.45	0.036	-1.12	0.537
1423888_at	RIKEN cDNA 1200003M09 gene	1200003M09Rik	1.79	0.756	1.79	0.505	1.23	0.117	1.45	0.028	1.33	0.531
1428370_at	RIKEN cDNA 1500011B03 gene	1500011B03Rik	1.81	0.975	1.92	0.947	1.2	0.023	1.45	0.005	1.26	0.196
1460672_at	RIKEN cDNA 2410002F23 gene	2410002F23Rik	2.09	0.469	2.41	0.052	1.22	0.055	1.45	0.047	1.19	0.136
1454466_at	RIKEN cDNA 4933407I18 gene	4933407I18Rik	1.92	0.852	1.43	0.575	1.59	0.816	1.45	0.021	1.07	0.639
1426670_at	agrin	Agrin	1.86	0.700	2.13	0.452	1.15	0.864	1.45	0.001	1.22	0.340
1458500_at	expressed sequence AU021034	AU021034	-1.48	0.197	-1.6	0.156	1.25	0.982	1.45	0.001	1.21	0.360
1445281_a_at	RIKEN cDNA B230311B06 gene	B230311B06Rik	-1.27	0.164	-1.53	0.220	1.26	0.829	1.45	0.005	-1.09	0.698
1440340_at	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	B3galt6	-1.31	0.193	-1.01	0.727	1.33	0.569	1.45	0.038	1.68	0.201
1437878_s_at	coiled-coil domain containing 39 /// tetratricopeptide repeat domain 14	Ccdc39 /// Ttc14	1.69	0.176	2.05	0.316	1.11	0.939	1.45	0.021	-1.05	0.284
1420249_s_at	chemokine (C-C motif) ligand 6	Ccl6	1.5	0.315	1.49	0.208	-1	0.656	1.45	0.001	3.12	0.042
1419744_at	histocompatibility 2, class II, locus Mb2	H2-DMb2	1.02	0.626	-1.01	0.596	1.04	0.657	1.45	0.045	1.81	0.045
1424988_at	myosin regulatory light chain interacting protein	Mylip	1.01	0.556	1.05	0.498	1.33	0.015	1.45	0.007	1.33	0.038
1444634_at	NOL1/NOP2/Sun domain family 3	Nsun3	2.49	0.396	1.86	0.029	1.03	0.708	1.45	0.005	1.1	0.724
1417890_at	pyridoxal (pyridoxine, vitamin B6) phosphatase	Pdxp	1.03	0.382	1.42	0.004	1.27	0.074	1.45	0.004	1.38	0.105
1417237_at	phospholipase D2	Pld2	-1.04	0.692	-1.03	0.859	1.05	0.112	1.45	0.009	1.12	0.128
1424950_at	SRY-box containing gene 9	Sox9	2.02	0.348	2.18	0.320	1.38	0.479	1.45	0.039	1.27	0.265
1450403_at	signal transducer and activator of transcription 2	Stat2	1.14	0.961	1.2	0.888	1.34	0.638	1.45	0.047	-1.04	0.569
1416926_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.12	0.621	2.52	0.002	1.79	0.000	1.45	0.047	1.69	0.003
1460488_at	zinc finger and BTB domain containing 4	Zbtb4	-1.26	0.180	-1.26	0.462	-1.29	0.216	1.45	0.005	1.02	0.478
1447976_at	expressed sequence AI596198	AI596198	1.84	0.298	2.36	0.398	-1.02	0.659	1.46	0.043	-1.11	0.310
1429897_a_at	DNA segment, Chr 16, ERATO Doi 472, expressed	D16Ertd472e	1.43	0.283	1.42	0.347	1.08	0.637	1.46	0.015	1.19	0.188
1423100_at	FBJ osteosarcoma oncogene	Fos	-1.01	0.953	1.62	0.005	1.36	0.029	1.46	0.003	1.53	0.003
1418876_at	forkhead box D1	Foxd1	1.28	0.530	-1.07	0.545	1.12	0.786	1.46	0.046	-1.48	0.266
1436648_at	nanos homolog 1 (Drosophila)	Nanos1	2.01	0.042	2.82	0.165	2.48	0.098	1.46	0.042	1.84	0.044
1455315_at	tumor protein p53 inducible protein 13	Trp53i13	-1.1	0.444	1.03	0.878	1.28	0.099	1.46	0.002	1.19	0.468
1436796_at	RIKEN cDNA 1110061A14 gene	1110061A14Rik	-1.01	0.774	1.22	0.333	1.16	0.060	1.47	0.020	1.27	0.011
1435565_at	RIKEN cDNA 1500011H22 gene	1500011H22Rik	1.08	0.642	1.64	0.699	1.33	0.008	1.47	0.009	1.35	0.066
1423672_at	RIKEN cDNA 2510042P03 gene	2510042P03Rik	1.28	0.475	1.38	0.121	1.18	0.293	1.47	0.017	1.24	0.054
1430248_at	RIKEN cDNA 4930415O11 gene	4930415O11Rik	1.46	0.300	2.27	0.116	1.61	0.765	1.47	0.044	1.48	0.476
1427167_at	expressed sequence AI448196	AI448196	1.22	0.321	1.32	0.185	1.23	0.022	1.47	0.043	1.44	0.057
1448309_at	adaptor-related protein complex 3, mu 1 subunit	Ap3m1	7.34	0.308	7.34	0.147	1.07	0.562	1.47	0.045	1.14	0.718
1428750_at	CDC42 effector protein (Rho GTPase binding) 2	Cdc42ep2	4.51	0.388	6.99	0.211	1.19	0.376	1.47	0.049	1.13	0.238
1441003_at	excision repair cross-complementing rodent repair deficiency, compleme	Ercc4	1.15	0.792	-1.7	0.147	-1.07	0.503	1.47	0.032	-1.25	0.045
1424772_at	H2A histone family, member J /// similar to H2A histone family, member	H2afj /// LOC632401	2.52	0.510	3.71	0.037	1.71	0.057	1.47	0.045	1.52	0.113
1453995_a_at	HpaII tiny fragments locus 9c	Htf9c	1.55	0.115	1.78	0.054	1.23	0.425	1.47	0.042	1.44	0.036

1416915_at	mutS homolog 6 (E. coli)	Msh6	1.1	0.060	2.15	0.000	1.51	0.047	1.47	0.029	1.4	0.023
1444647_at	phospholipase A2, activating protein	Plaa	1.46	0.811	1.12	0.693	1.36	0.448	1.47	0.011	1.04	0.616
1449231_at	zinc finger protein 296	Zfp296	-1.01	0.813	1.49	0.041	1.21	0.105	1.47	0.019	1.81	0.019
1435449_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	2.18	0.144	3.9	0.071	1.26	0.248	1.48	0.015	1.46	0.059
1421933_at	chromobox homolog 5 (Drosophila HP1a)	Cbx5	1.3	0.328	1.16	0.506	1.04	0.730	1.48	0.021	1.4	0.294
1439117_at	calmin	Clmn	-1.02	0.940	-1.45	0.134	1.14	0.602	1.48	0.024	1.94	0.637
1417001_a_at	DNA segment, Chr 4, Wayne State University 53, expressed	D4Wsu53e	-1.3	0.167	-1.21	0.359	1.04	0.937	1.48	0.010	1.17	0.476
1443136_at	hypothetical gene supported by AK082906	LOC432459	1.57	0.904	3.66	0.379	1.15	0.836	1.48	0.014	1.33	0.885
1442886_at	transformer 2 alpha homolog (Drosophila)	Tra2a	1.48	0.104	1.14	0.879	1.5	0.262	1.48	0.026	1.35	0.155
1448952_at	RIKEN cDNA A030009H04 gene	A030009H04Rik	1.06	0.609	1.67	0.078	1.3	0.115	1.49	0.044	1.78	0.080
1440436_at	hypothetical protein A730030A06	A730030A06	2.61	0.697	3.73	0.992	-1.08	0.537	1.49	0.016	-1.08	0.565
1430826_s_at	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	Gcnt2	2.22	0.178	2.59	0.088	1.15	0.453	1.49	0.034	1.38	0.337
1425937_a_at	hexamethylene bis-acetamide inducible 1	Hexim1	1.05	0.729	1.52	0.009	1.39	0.015	1.49	0.002	1.41	0.015
1446311_at	membrane bound C2 domain containing protein	Mbc2	-1.24	0.379	-1.52	0.263	-1.06	0.585	1.49	0.021	1.12	0.921
1438933_x_at	RAS, guanyl releasing protein 2	Rasgrp2	-1.14	0.147	1.28	0.069	1.06	0.902	1.49	0.022	1.16	0.545
1416154_at	signal recognition particle 54 /// similar to signal recognition particle 54	Srp54 /// LOC66515	1.17	0.292	-1.14	0.535	1.04	0.683	1.49	0.011	-1.1	0.730
1417169_at	ubiquitin specific peptidase 2	Usp2	1.2	0.876	1.24	0.954	1.33	0.095	1.49	0.014	1.4	0.029
1451323_at	zinc finger protein 7	Zfp7	1.25	0.645	1.71	0.062	1.52	0.002	1.49	0.006	1.61	0.046
1429927_at	RIKEN cDNA 5830409B07 gene	5830409B07Rik	-1.3	0.044	-2.19	0.063	-1.13	0.444	1.5	0.032	1.21	0.408
1452367_at	coronin, actin binding protein 2A	Coro2a	-1.05	0.467	-1.3	0.232	1.37	0.206	1.5	0.008	1.28	0.700
1418322_at	cAMP responsive element modulator	Crem	1.11	0.936	1.25	0.275	1.32	0.048	1.5	0.013	1.34	0.243
1419728_at	chemokine (C-X-C motif) ligand 5	Cxcl5	1.27	0.843	1.27	0.877	1.43	0.090	1.5	0.028	1.06	0.356
1432181_s_at	endothelial cell growth factor 1 (platelet-derived)	Ecgf1	1.17	0.185	1.72	0.003	1.5	0.155	1.5	0.006	1.67	0.016
1419128_at	integrin alpha X	Itgax	1.3	0.882	1.9	0.009	-1.05	0.359	1.5	0.017	-1.79	0.190
1455200_at	p21 (CDKN1A)-activated kinase 6	Pak6	1.01	0.442	-1.31	0.378	-1.51	0.237	1.5	0.038	-1.07	0.613
1449370_at	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	Sox4 /// LOC672274	1.04	0.137	1.63	0.065	1.78	0.033	1.5	0.022	1.78	0.018
1457951_at	RIKEN cDNA 4930434E21 gene	4930434E21Rik	1.37	0.601	-1.37	0.202	1.41	0.562	1.51	0.010	-1.26	0.217
1457913_at	RIKEN cDNA 5730601F06 gene	5730601F06Rik	-1.07	0.424	1.12	0.787	1.19	0.037	1.51	0.026	1.27	0.440
1447952_at	AU RNA binding protein/enoyl-coenzyme A hydratase	Auh	1.22	0.639	1.53	0.073	1.12	0.732	1.51	0.034	1.03	0.854
1450140_a_at	cyclin-dependent kinase inhibitor 2A	Cdkn2a	1.21	0.288	1.15	0.468	1.38	0.962	1.51	0.041	1.22	0.479
1422787_at	FK506 binding protein-like	Fkbpl	1.04	0.743	1.49	0.059	-1.03	0.647	1.51	0.004	1.07	0.846
1418477_at	matrilin 1, cartilage matrix protein 1	Matn1	1.6	0.462	1.51	0.698	1.08	0.719	1.51	0.006	-1.42	0.223
1451809_s_at	RWD domain containing 3	Rwdd3	-1.1	0.234	-1.36	0.101	1.39	0.628	1.51	0.027	1.24	0.106
1449293_a_at	S-phase kinase-associated protein 2 (p45)	Skp2	3.54	0.088	4.4	0.022	1.25	0.260	1.51	0.048	1.25	0.224
1447228_at	RIKEN cDNA 1110051M20 gene	1110051M20Rik	-1.05	0.625	-1.28	0.108	-1.16	0.181	1.52	0.002	1.11	0.074
1449252_at	RIKEN cDNA 9030611O19 gene	9030611O19Rik	2.23	0.112	3.49	0.061	2.43	0.039	1.52	0.006	1.69	0.213
1457697_at	RIKEN cDNA A330021E22 gene	A330021E22Rik	2.04	0.108	1.61	0.906	1.18	0.623	1.52	0.049	1.11	0.403
1436074_at	cDNA sequence AY078069	AY078069	-1.04	0.469	1.88	0.896	2.56	0.042	1.52	0.040	1.64	0.491
1422127_at	desert hedgehog	Dhh	-1.04	0.615	-1.1	0.508	1.16	0.674	1.52	0.039	1.23	0.506
1449989_at	mast cell protease 2	Mcpt2	2.46	0.551	2.5	0.239	-1.85	0.136	1.52	0.025	1.43	0.397
1438479_at	zinc finger protein 213	Zfp213	2.83	0.130	1.98	0.908	1.79	0.529	1.52	0.035	3.34	0.133
1458483_at	RIKEN cDNA A330102I10 gene	A330102I10Rik	1.2	0.537	1.1	0.493	-1.01	0.615	1.53	0.015	1.16	0.587
1457658_x_at	annexin A4	Anxa4	1.39	0.067	1.51	0.070	1.22	0.138	1.53	0.015	1.13	0.613
1425362_at	HIV-1 Rev binding protein-like	Hrbl	1.03	0.785	1	0.907	1.3	0.374	1.53	0.016	-1.05	0.614
1428033_at	hypothetical protein LOC245174	LOC245174	-1.2	0.410	1.25	0.671	1.19	0.447	1.53	0.029	1.23	0.315
1423012_at	synaptotagmin VII	Syt7	1.23	0.341	1.09	0.518	1.36	0.170	1.53	0.048	1.03	0.794
1460085_at	Zinc finger protein 281	Zfp281	-1.61	0.101	-1.19	0.255	1.41	0.075	1.53	0.039	1.48	0.120
1424546_at	cDNA sequence BC003965	BC003965	1.62	0.180	1.19	0.175	1.05	0.477	1.54	0.036	1.34	0.356
1456318_at	C-type lectin domain family 1, member a	Clec1a	1.33	0.490	1.46	0.278	1.86	0.646	1.54	0.027	2.48	0.422
1431049_at	islet cell autoantigen 1-like	Ica1l	1.13	0.332	2.46	0.219	1.14	0.374	1.54	0.005	2.59	0.125
1425145_at	interleukin 1 receptor-like 1	Il1rl1	1.07	0.958	1.49	0.240	1.24	0.055	1.54	0.003	1.33	0.063
1449160_at	natriuretic peptide receptor 1	Npr1	-1.34	0.361	-1.34	0.321	-1.37	0.307	1.54	0.020	1.07	0.698
1455197_at	Rho family GTPase 1	Rnd1	1.18	0.366	1.27	0.074	1.28	0.084	1.54	0.002	1.34	0.008
1437585_x_at	zinc finger protein 161	Zfp161	-1.11	0.415	1.16	0.664	1.23	0.350	1.54	0.039	1.38	0.054
1421478_a_at	zinc finger protein 318	Zfp318	-1.83	0.090	1.05	0.736	1.11	0.252	1.54	0.015	1.4	0.048
1440226_at	zinc finger protein 760	Zfp760	1.18	0.606	1.22	0.475	1.38	0.061	1.54	0.034	1.17	0.229
1446122_at	RIKEN cDNA 4732416N19 gene	4732416N19Rik	1.32	0.920	-1.18	0.128	1.17	0.772	1.55	0.044	1.22	0.601
1431173_at	RIKEN cDNA A930008G19 gene	A930008G19Rik	1.27	0.904	1.5	0.361	1.13	0.567	1.55	0.021	1.23	0.899

1429948_x_at	crystallin, gamma F	Crygf	1.38	0.956	1.41	0.866	1.68	0.720	1.55	0.017	-1.9	0.082
1427361_at	homeo box C6	Hoxc6	1.46	0.547	1.9	0.379	-1.15	0.205	1.55	0.028	1.12	0.773
1454075_s_at	nudix (nucleoside diphosphate linked moiety X)-type motif 13	Nudt13	1.23	0.251	1.04	0.691	1.3	0.417	1.55	0.022	1.53	0.072
1430242_at	RWD domain containing 1	Rwdd1	-1.23	0.438	1.15	0.690	1.12	0.567	1.55	0.031	1.99	0.089
1420095_s_at	zinc finger proliferation 1	Zipro1	-1.08	0.472	1.27	0.948	1.2	0.026	1.55	0.016	1.24	0.001
1445919_at	expressed sequence AA409261	AA409261	1.03	0.682	1.66	0.519	-1.01	0.752	1.56	0.013	1.43	0.090
1454880_s_at	Bcl2 modifying factor	Bmf	-1.24	0.298	-1.49	0.268	1.7	0.486	1.56	0.029	-1.35	0.037
1447820_x_at	carnitine palmitoyltransferase 2	Cpt2	1.34	0.670	1.39	0.699	-1.09	0.558	1.56	0.047	-1.02	0.999
1444079_at	defensin beta 8	Defb8	-1.61	0.317	-1.17	0.423	1.07	0.965	1.56	0.038	1.15	0.178
1429408_at	TBC1 domain family, member 21	Tbc1d21	-1.91	0.133	1.63	0.326	-1.02	0.482	1.56	0.013	1.23	0.601
1455705_at	transmembrane protein 161A	Tmem161a	1.41	0.408	1.42	0.405	1.57	0.367	1.56	0.047	-1.19	0.227
1448738_at	calbindin-28K	Calb1	1.39	0.751	1.75	0.503	2	0.204	1.57	0.047	2	0.207
1427088_at	cyclin T2	Ccnt2	-1.22	0.057	1.07	0.979	1.22	0.048	1.57	0.014	1.39	0.024
1417590_at	cytochrome P450, family 27, subfamily a, polypeptide 1	Cyp27a1	1.28	0.831	-1.19	0.202	1.76	0.092	1.57	0.009	-1.83	0.030
1426291_at	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	Dimt1	1.04	0.960	-1.16	0.312	-1.21	0.039	1.57	0.022	1.28	0.166
1417860_a_at	spondin 2, extracellular matrix protein	Spon2	-1.16	0.336	-1.08	0.726	1.74	0.862	1.57	0.048	2.03	0.761
1428803_at	RIKEN cDNA 4632408A20 gene	4632408A20Rik	2.11	0.278	2.53	0.038	-1.09	0.460	1.58	0.006	1.25	0.078
1431621_at	RIKEN cDNA 4930420G21 gene	4930420G21Rik	1.24	0.671	1.37	0.586	1.6	0.165	1.58	0.045	1.68	0.841
1440886_at	cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	1.07	0.879	1.44	0.141	1.7	0.043	1.58	0.024	1.52	0.007
1440900_at	G protein-coupled receptor 174	Gpr174	-1.67	0.063	1.16	0.171	1.41	0.826	1.58	0.019	1.22	0.838
1454857_at	ring finger protein 122	Rnf122	3	0.333	4.85	0.042	1.39	0.024	1.58	0.034	1.83	0.017
1428905_at	Ras-related GTP binding A	Rraga	1.41	0.300	1.58	0.012	1.12	0.009	1.58	0.002	1.23	0.012
1419537_at	transcription factor EC	Tcfec	2.4	0.144	1.16	0.557	1.36	0.034	1.58	0.041	1.1	0.699
1454633_at	ethanolamine kinase 1	Etnk1	1.05	0.693	1.26	0.518	-1.06	0.540	1.59	0.018	1.06	0.575
1418343_at	GTF2I repeat domain containing 2	Gtf2ird2	-1.16	0.358	-1.36	0.207	1.04	0.834	1.6	0.020	1.26	0.433
1445570_at	NOL1/NOP2/Sun domain family, member 4	Nsun4	-1.46	0.144	-1.16	0.463	1.06	0.609	1.6	0.032	1.14	0.389
1426082_a_at	solute carrier family 16 (monocarboxylic acid transporters), member 4	Slc16a4	-1.38	0.274	1.04	0.799	2.07	0.155	1.6	0.002	1.04	0.902
1432963_at	RIKEN cDNA 2410049M19 gene	2410049M19Rik	-1.64	0.200	1.25	0.634	1.01	0.653	1.61	0.044	1.65	0.292
1431775_at	RIKEN cDNA 3100002H09 gene	3100002H09Rik	-1.25	0.329	2.05	0.433	2.39	0.328	1.61	0.015	1.52	0.526
1459500_at	expressed sequence C85351	C85351	-2.54	0.049	-1.47	0.205	1.42	0.412	1.61	0.048	1.49	0.721
1439332_at	DNA-damage-inducible transcript 4-like	Ddit4l	1.72	0.024	3.45	0.004	2.23	0.002	1.61	0.014	2.04	0.169
1443940_at	leucine rich repeat containing 22	Lrrc22	1.67	0.490	1.23	0.926	-1.45	0.205	1.61	0.005	2.06	0.309
1437833_at	latent transforming growth factor beta binding protein 3	Ltbp3	-1.97	0.039	-1.42	0.443	2.45	0.198	1.61	0.026	-1.29	0.472
1459299_at	myosin IIIB	Myo3b	1.68	0.124	1.1	0.961	1.07	0.841	1.61	0.043	3.14	0.242
1421646_a_at	protein inhibitor of activated STAT 3	Pias3	3.78	0.568	4.94	0.426	1.16	0.067	1.61	0.046	1.38	0.040
1439675_at	RIKEN cDNA 4933429D07 gene	4933429D07Rik	-1.27	0.375	1.43	0.699	-1.17	0.419	1.62	0.002	-1.1	0.562
1442998_at	Cytidine 5'-triphosphate synthase 2	Ctps2	1.03	0.830	-2.45	0.037	2.53	0.509	1.62	0.025	2.34	0.076
1417587_at	timeless homolog (Drosophila)	Timeless	1.01	0.990	1.2	0.450	1.23	0.094	1.62	0.017	1.3	0.072
1433823_at	expressed sequence AW456874	AW456874	1.14	0.187	-1.13	0.510	1.48	0.092	1.63	0.026	-1.03	0.843
1433043_at	chondroitin sulfate proteoglycan 2	Cspg2	1.64	0.623	3.13	0.124	-1.05	0.505	1.63	0.032	2.75	0.003
1437337_x_at	fucokinase	Fuk	-1.11	0.482	1.15	0.826	1.26	0.742	1.63	0.024	1.35	0.380
1441271_at	Isocitrate dehydrogenase 3 (NAD+) beta	Idh3b	2.2	0.014	1.33	0.459	1.21	0.862	1.63	0.038	1.51	0.143
1455034_at	Nuclear receptor subfamily 4, group A, member 2	Nr4a2	1.28	0.905	2.01	0.042	2.06	0.003	1.63	0.002	2.37	0.002
1437713_x_at	RIKEN cDNA 1500010J02 gene	1500010J02Rik	1.71	0.756	1.43	0.589	-1.1	0.482	1.64	0.002	-1.4	0.277
1432890_at	RIKEN cDNA 2610011E03 gene	2610011E03Rik	-1.03	0.811	-1.36	0.241	-2.01	0.063	1.64	0.041	1.98	0.098
1457122_at	Adaptor protein complex AP-2, mu1	Ap2m1	1.31	0.641	1.37	0.193	1.04	0.827	1.64	0.040	-1.11	0.310
1435942_at	potassium voltage-gated channel, subfamily Q, member 2	Kcnq2	-1.01	0.684	1.11	0.445	-1.29	0.374	1.64	0.045	-1.39	0.266
1449261_at	pre B-cell leukemia transcription factor 2	Pbx2	5.72	0.649	4.51	0.615	-1.01	0.941	1.64	0.011	1.04	0.695
1442956_at	Protein phosphatase 1, regulatory (inhibitor) subunit 13B	Ppp1r13b	-1.23	0.159	-1.72	0.088	1.1	0.625	1.64	0.036	-1	0.422
1439610_at	RAB27b, member RAS oncogene family	Rab27b	-1.08	0.456	-1.31	0.311	1.49	0.127	1.64	0.018	1.39	0.323
AFFX-TransRecMu	transferrin receptor	Tfrc	2.11	0.401	1.56	0.720	-1.14	0.548	1.64	0.045	1.22	0.263
1430099_at	RIKEN cDNA 4930509E16 gene	4930509E16Rik	-1.17	0.688	2.51	0.105	-1.41	0.350	1.65	0.011	2.08	0.526
1457049_at	VATPase, H+ transporting, lysosomal V1 subunit E1	Atp6v1e1	1.46	0.098	2.51	0.315	1.61	0.212	1.65	0.037	1.54	0.358
1454839_a_at	coiled-coil domain containing 84	Ccdc84	1.28	0.840	1.26	0.946	-1.07	0.408	1.65	0.012	1.13	0.675
1457550_at	RIKEN cDNA 9530059O14 gene	9530059O14Rik	-1.95	0.079	-2.36	0.139	1.87	0.534	1.66	0.034	1.86	0.872
1415999_at	hairy/enhancer-of-split related with YRPW motif 1	Hey1	1.19	0.654	1.19	0.535	1.14	0.912	1.66	0.017	1.25	0.363
1427550_at	paternally expressed 10	Peg10	1.62	0.599	1.69	0.265	1.17	0.668	1.67	0.006	-1.3	0.227
1438950_x_at	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	-1.15	0.450	-1.11	0.641	2.04	0.469	1.67	0.016	-1.32	0.445

1446687_at	splicing factor 3a, subunit 1	Sf3a1	1.1	0.856	1	0.686	1.39	0.031	1.67	0.016	1.03	0.980
1439241_x_at	steroid 5 alpha-reductase 2-like	Srd5a2l	-1.55	0.092	-1.29	0.314	-1.17	0.301	1.67	0.031	1.28	0.545
1424968_at	RIKEN cDNA 2210023G05 gene	2210023G05Rik	1.26	0.964	1.29	0.300	1.31	0.719	1.68	0.034	-1.22	0.418
1433388_at	RIKEN cDNA 2900022M07 gene	2900022M07Rik	1.57	0.813	-1	0.515	-1.24	0.348	1.68	0.006	1.83	0.969
1446021_at	expressed sequence AU018466	AU018466	1.16	0.401	1.03	0.951	2.07	0.494	1.68	0.048	1.07	0.684
1430409_at	N-ethylmaleimide sensitive fusion protein	Nsf	1.29	0.566	1.39	0.362	-1	0.781	1.68	0.009	1.08	0.611
1436240_at	sclerostin	Sost	1.06	0.449	1.19	0.356	1.28	0.113	1.68	0.012	1.04	0.596
1443837_x_at	B-cell leukemia/lymphoma 2	Bcl2	1.47	0.499	-1.23	0.383	4.44	0.216	1.69	0.035	1.75	0.029
1435905_at	DNA segment, Chr 3, ERATO Doi 300, expressed	D3Ertd300e	1.03	0.795	1.22	0.587	1.06	0.569	1.69	0.032	1.36	0.134
1460609_at	Integrator complex subunit 8	Ints8	1.9	0.103	1.45	0.420	-1.29	0.227	1.69	0.034	1.08	0.801
1443999_at	NIMA (never in mitosis gene a)-related expressed kinase 2	Nek2	-1.3	0.086	1.05	0.957	1.71	0.083	1.69	0.008	1.36	0.505
1438341_at	transglutaminase 4 (prostate)	Tgm4	2.49	0.317	2.22	0.805	-1.92	0.208	1.69	0.003	1.13	0.757
1428926_at	RIKEN cDNA 1110003O08 gene	1110003O08Rik	-1.17	0.300	-1	0.616	1.32	0.029	1.7	0.047	1.03	0.915
1426894_s_at	RIKEN cDNA C230093N12 gene	C230093N12Rik	1.27	0.315	1.72	0.038	1.43	0.108	1.71	0.000	1.61	0.089
1421288_at	coagulation factor II (thrombin) receptor-like 3	F2rl3	-2.61	0.060	1.47	0.136	2.57	0.496	1.71	0.041	1.83	0.409
1429396_at	autophagy related 16 like 2 (S. cerevisiae)	Atg16l2	3.92	0.728	5.78	0.189	3.78	0.142	1.72	0.015	2.42	0.382
1456219_at	similar to zinc finger protein of the cerebellum 5	LOC624168	1.03	0.932	1.16	0.853	1.14	0.960	1.72	0.022	1.95	0.556
1447179_at	RIKEN cDNA 2210412D01 gene	2210412D01Rik	1.15	0.970	-1.43	0.196	2.27	0.227	1.73	0.022	1.51	0.571
1431525_at	RIKEN cDNA 9130002K18 gene	9130002K18Rik	-1.35	0.259	-2.17	0.031	1.97	0.963	1.73	0.050	-1.11	0.514
1454885_at	cDNA sequence BC063263	BC063263	1.14	0.871	1.64	0.092	1.3	0.248	1.73	0.011	1.71	0.111
1418992_at	coagulation factor X	F10	1.15	0.538	1.71	0.699	1.17	0.918	1.73	0.045	1.22	0.823
1441593_at	Phosphatase and tensin homolog	Pten	-1.06	0.898	-1.83	0.077	1.1	0.961	1.73	0.011	1.12	0.996
1450374_at	tuberoinfundibular peptide of 39 residues (TIP39) preprohormone	Tifp39	1.37	0.556	-1.03	0.861	1.08	0.705	1.73	0.001	1.11	0.898
1438541_at	RIKEN cDNA 4933439F18 gene	4933439F18Rik	1.95	0.248	2.67	0.230	-2.3	0.008	1.74	0.049	3.69	0.227
1456328_at	B-cell scaffold protein with ankyrin repeats 1	Bank1	1.29	0.814	-1.08	0.397	1	0.997	1.74	0.010	1.05	0.744
1444761_at	Coiled-coil domain containing 8	Ccdc8	1	0.498	1.11	0.736	1.24	0.312	1.74	0.002	1.16	0.090
1432377_x_at	shroom family member 3	Shroom3	1.2	0.748	1.4	0.554	1.08	0.970	1.74	0.023	2.41	0.583
1451696_at	zinc finger protein 64	Zfp64	-1.09	0.335	1.31	0.640	1.11	0.980	1.74	0.032	-1.27	0.392
1453706_at	RIKEN cDNA 2900042A17 gene	2900042A17Rik	-1.1	0.427	1.41	0.636	1.24	0.644	1.75	0.036	-1.56	0.075
1436219_at	RIKEN cDNA 4933403F05 gene	4933403F05Rik	1.4	0.038	2.63	0.005	1.56	0.008	1.75	0.002	1.69	0.008
1449993_at	cDNA sequence AF119384	AF119384	1.27	0.993	-1.39	0.149	-1.04	0.606	1.75	0.039	1.1	0.679
1430744_at	napsin A aspartic peptidase	Napsa	1.72	0.536	3.18	0.857	2.04	0.783	1.75	0.004	1.15	0.501
1422401_at	small proline-rich protein 3	Sprr3	2.35	0.815	1.3	0.855	1.48	0.908	1.75	0.019	-1.34	0.136
1439311_at	RIKEN cDNA B830012L14 gene	B830012L14Rik	-1.19	0.426	1.22	0.460	1.25	0.631	1.76	0.030	-1.17	0.363
1436374_x_at	F11 receptor	F11r	-1.79	0.246	-1.73	0.202	1.37	0.685	1.76	0.027	1.15	0.894
1451792_a_at	praja1, RING-H2 motif containing	Pja1	5.03	0.551	5.77	0.346	1.27	0.229	1.76	0.035	1.12	0.405
1441236_at	solute carrier family 9 (sodium/hydrogen exchanger), member 3	Slc9a3	-1.19	0.411	-2.13	0.230	1.05	0.882	1.76	0.005	1.15	0.797
1420294_at	Acyltransferase like 2	Aytl2	2.03	0.184	1.68	0.105	-2.56	0.055	1.77	0.016	-1.59	0.256
1442531_at	DNA segment, Chr 12, ERATO Doi 123, expressed	D12Ertd123e	1.69	0.428	1.9	0.874	1.5	0.436	1.77	0.007	2.35	0.253
1422122_at	Fc receptor, IgE, low affinity II, alpha polypeptide	Fcer2a	1.26	0.813	1.66	0.599	1.21	0.973	1.77	0.029	-1.49	0.290
1420461_at	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	Mst1r	2.23	0.614	1.11	0.587	1.41	0.700	1.77	0.037	-1.49	0.070
1457320_at	Wings apart-like homolog (Drosophila)	Wapal	-1.52	0.425	1.23	0.929	-1.11	0.380	1.77	0.041	1.99	0.374
1444144_at	RIKEN cDNA 5530400K22 gene	5530400K22Rik	2.06	0.419	2.16	0.498	1.24	0.206	1.78	0.024	-1.02	0.704
1459922_at	expressed sequence AI646383	AI646383	2.2	0.717	1.75	0.381	1.18	0.633	1.78	0.030	1.19	0.994
1446991_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	Gcn1l1	2.58	0.266	1.8	0.973	1.38	0.883	1.78	0.026	2.33	0.543
1419325_at	neuromedin U	Nmu	1.13	0.977	1.23	0.763	-1.25	0.243	1.78	0.016	1.52	0.251
1425298_a_at	baculoviral IAP repeat-containing 1a	Birc1a	1.02	0.939	-2.06	0.081	2.13	0.025	1.79	0.017	1.32	0.458
1446324_at	Calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	1.11	0.154	1.33	0.489	1.03	0.812	1.79	0.024	1.01	0.952
1451799_at	coiled-coil domain containing 25	Ccdc25	1.64	0.424	1.4	0.555	-1.03	0.432	1.79	0.030	-1.35	0.174
1458277_at	Chemokine (C-C motif) ligand 25	Ccl25	-1.55	0.082	-1.29	0.155	1.41	0.655	1.79	0.044	1.08	0.912
1446492_at	transmembrane protein 132D	Tmem132d	2.11	0.954	1.17	0.701	1.32	0.842	1.79	0.000	1.85	0.487
1428581_at	RIKEN cDNA 1700024G10 gene	1700024G10Rik	-1.15	0.363	1.21	0.877	-1.18	0.385	1.8	0.018	1.4	0.439
1459194_at	RIKEN cDNA 2210408I21 gene	2210408I21Rik	-1.32	0.130	-1.04	0.704	-1.07	0.423	1.8	0.040	-1.64	0.106
1419306_at	coiled-coil domain containing 96	Ccdc96	-1.02	0.549	1.36	0.792	-1.23	0.239	1.8	0.004	1.26	0.659
1442182_at	DnaJ (Hsp40) homolog, subfamily C, member 19	Dnajc19	1.1	0.937	1.45	0.662	1.52	0.026	1.8	0.049	1.63	0.118
1441148_at	Fukuyama type congenital muscular dystrophy homolog (human)	Fcmd	-1.54	0.192	1.07	0.571	-1.18	0.310	1.8	0.031	1.26	0.864
1440396_at	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	Mpp6	1.15	0.937	1.69	0.677	-1.53	0.222	1.8	0.017	-1.28	0.479
1455894_at	peptidyl-tRNA hydrolase 2	Ptrh2	1.57	0.223	2.77	0.009	1.65	0.003	1.8	0.019	1.56	0.012

1430361_at	RIKEN cDNA 2610005M20 gene	2610005M20Rik	1.82	0.985	-1.22	0.378	2.19	0.579	1.81	0.039	1.55	0.408
1458000_at	desmoglein 1 alpha	Dsg1a	-2.26	0.039	1.16	0.964	1.01	0.521	1.81	0.027	2.01	0.750
1431748_a_at	ring finger and FYVE like domain containing protein	Rffl	2.6	0.085	1.4	0.190	1.45	0.921	1.81	0.033	1.91	0.045
1420658_at	uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	1.61	0.883	1.87	0.104	1.41	0.905	1.81	0.004	-1.23	0.465
1439325_at	Bleomycin hydrolase	Blmh	-1.29	0.417	1	0.704	2.56	0.082	1.82	0.040	-1.56	0.075
1450441_at	leucine rich repeat containing 50	Lrrc50	-1.52	0.103	-1.12	0.649	1.32	0.376	1.82	0.046	-1.45	0.198
1429379_at	extra cellular link domain-containing 1	Xlkd1	2.17	0.522	1.01	0.541	1.31	0.742	1.82	0.039	2.07	0.591
1429751_at	zinc finger, SWIM domain containing 2	Zswim2	1.53	0.949	1.75	0.458	-1.18	0.445	1.82	0.024	1.2	0.765
1431234_at	RIKEN cDNA 1700041B20 gene	1700041B20Rik	1.04	0.951	-1.01	0.940	1.13	0.547	1.83	0.008	1.07	0.550
1441440_at	autophagy-related 4C (yeast)	Atg4c	1.4	0.986	1.2	0.664	-1.08	0.612	1.83	0.001	1.15	0.807
1456450_at	Cystinosis, nephropathic	Ctns	-1.02	0.504	1.06	0.620	-1.37	0.190	1.83	0.048	1.13	0.821
1436133_at	RIKEN cDNA 0610011N22 gene	0610011N22Rik	1.09	0.401	1.69	0.019	1.55	0.192	1.84	0.021	2.06	0.028
1460607_at	immunoglobulin superfamily, member 11	Igsf11	-1.06	0.189	-1.02	0.704	1.57	0.108	1.84	0.021	1.55	0.101
1440483_at	Pleckstrin homology domain containing, family M (with RUN domain) me	Plekhm2	1.89	0.623	2.97	0.246	2.27	0.883	1.84	0.021	-1.29	0.400
1431427_at	RIKEN cDNA 5430427M07 gene	5430427M07Rik	1.96	0.667	1.01	0.370	-1	0.351	1.85	0.045	1.8	0.509
1419185_a_at	MLX interacting protein-like	Mlxipl	1.12	0.206	1.51	0.222	1.58	0.496	1.85	0.036	1.7	0.497
1457815_at	Nucleoporin 214	Nup214	1.24	0.793	1.38	0.813	1.93	0.128	1.85	0.020	-1.47	0.140
1431161_at	Rho-guanine nucleotide exchange factor	Rgnef	1.42	0.500	1.87	0.742	1.17	0.848	1.85	0.016	1.31	0.796
1428283_at	cytochrome P450, family 2, subfamily s, polypeptide 1	Cyp2s1	-1.65	0.107	2.08	0.429	1.03	0.857	1.86	0.034	1.78	0.047
1457847_at	Regulatory factor X domain containing 2 homolog (human)	Rfxdc2	2.37	0.114	2.62	0.106	1.04	0.852	1.86	0.002	-1.07	0.922
1433108_at	T-cell receptor beta, joining region /// T-cell receptor beta, variable 8.2 ///	Tcrb-J /// Tcrb-V8.2	1.51	0.547	2.66	0.884	1.59	0.835	1.86	0.044	1.78	0.250
1443806_x_at	Erythrocyte protein band 4.1-like 1	Epb4.1l1	-1.22	0.274	2.53	0.693	1.33	0.893	1.87	0.034	1.29	0.754
1440450_at	Heat shock protein 1-like	Hspa1l	1.1	0.985	1.08	0.786	-1	0.879	1.87	0.049	1.55	0.118
1458618_at	Iron responsive element binding protein 2	Ireb2	1.74	0.378	2.43	0.134	1.08	0.692	1.87	0.006	-1.05	0.428
1450195_at	N-deacetylase/N-sulfotransferase (heparin glucosaminyl) 4	Ndst4	1.74	0.766	3.04	0.947	1.32	0.742	1.89	0.048	1.76	0.285
1428780_at	threonine aldolase 1	Tha1	-1.09	0.444	-2.18	0.097	1.09	0.787	1.89	0.007	1.09	0.832
1437260_at	multimerin 1	Mmrn1	1.12	0.708	-1.02	0.967	2.82	0.379	1.91	0.014	-1	0.967
1437018_at	paraneoplastic antigen MA2	Pnma2	-1.18	0.380	-1.23	0.322	1.14	0.904	1.91	0.021	-1.01	0.761
1445235_at	YTH domain family 3	Ythdf3	1.15	0.531	1.39	0.015	-1.36	0.190	1.91	0.026	-1.02	0.857
1435022_at	cartilage homeo protein 1	Cart1	-2.26	0.194	-1.11	0.405	1.05	0.894	1.92	0.029	1.7	0.588
1453794_at	fer-1-like 4 (C. elegans)	Fer1l4	1.68	0.105	1.4	0.081	-1.07	0.583	1.92	0.028	2.21	0.142
1457593_at	RIKEN cDNA 2610202C22 gene	2610202C22Rik	-1.22	0.053	-1.1	0.600	-1.19	0.524	1.94	0.003	-1.06	0.953
1419334_at	cytotoxic T-lymphocyte-associated protein 4	Ctla4	2.61	0.683	3.94	0.800	1.36	0.823	1.94	0.014	1.02	0.963
1458908_at	Dystrobrevin alpha	Dtna	-1.02	0.439	1.35	0.554	1.76	0.750	1.94	0.038	1.45	0.375
1417043_at	lecithin cholesterol acyltransferase	Lcat	1.36	0.136	1	0.785	1.51	0.068	1.94	0.020	-1.14	0.503
1438363_at	similar to KIAA1183 protein	LOC434128	3.05	0.452	1.94	0.933	2.11	0.151	1.94	0.043	-1.09	0.417
1442158_at	microtubule associated serine/threonine kinase family member 4	Mast4	-1.18	0.396	1.41	0.775	1.03	0.674	1.94	0.046	-1.03	0.788
1441215_at	TraB domain containing	Trabd	1.29	0.712	1.2	0.783	-2.93	0.009	1.94	0.043	1.42	0.855
1428358_at	RIKEN cDNA 1810010M01 gene	1810010M01Rik	-1.24	0.181	-1.2	0.368	1.87	0.385	1.95	0.032	1.16	0.829
1446537_at	Dendritic cell protein GA17	Ga17	1.35	0.516	1.37	0.456	-1.14	0.371	1.95	0.038	1.16	0.599
1429968_at	RIKEN cDNA 2310047L11 gene	2310047L11Rik	-1.03	0.523	1.4	0.804	2.7	0.392	1.96	0.026	1.71	0.302
1455679_at	RIKEN cDNA 5830411E10 gene	5830411E10Rik	1.93	0.264	3.7	0.007	1.83	0.053	1.96	0.005	1.84	0.005
1456296_at	RIKEN cDNA 5830418K08 gene	5830418K08Rik	1.03	0.718	1.21	0.753	1.72	0.041	1.96	0.023	-1.47	0.169
1444410_at	acid phosphatase 6, lysophosphatidic	Acp6	1.31	0.877	1.03	0.449	1.01	0.564	1.96	0.040	1.13	0.559
1429268_at	RIKEN cDNA 2610318N02 gene	2610318N02Rik	2.21	0.003	1.71	0.022	-1.18	0.469	1.97	0.024	1.27	0.089
1444666_at	brix domain containing 1	Bxdc1	1.2	0.562	-1.42	0.057	-1.02	0.413	1.97	0.044	1.59	0.179
1441279_at	RIKEN cDNA C430002E04 gene	C430002E04Rik	-1.09	0.665	-1.02	0.933	1.8	0.904	1.97	0.026	-1.61	0.073
1452353_at	G protein-coupled receptor 155	Gpr155	1.47	0.670	1.35	0.628	2.24	0.101	1.97	0.008	2.45	0.011
1427813_at	iduronate 2-sulfatase	Ids	2.22	0.501	1.8	0.312	1.97	0.338	1.97	0.049	1.02	0.792
1450446_a_at	suppressor of cytokine signaling 1	Socs1	-1.07	0.351	1.91	0.580	1.86	0.387	1.97	0.032	1.35	0.561
1432277_at	RIKEN cDNA 4930565D16 gene	4930565D16Rik	1.21	0.984	1.74	0.856	-1.24	0.171	1.98	0.030	1.6	0.142
1449971_a_at	CD209f antigen	Cd209f	-2.15	0.217	1.13	0.460	2.04	0.042	1.98	0.035	-1.36	0.231
1424303_at	DEP domain containing 7	Depdc7	1.07	0.576	1.07	0.288	3.42	0.033	1.98	0.020	2.96	0.026
1447033_at	gene model 829, (NCBI)	Gm829	1.47	0.909	1.37	0.991	1.2	0.807	1.98	0.015	2.4	0.159
1450273_at	interleukin 1 receptor-like 2	Il1rl2	1.88	0.496	1.05	0.502	-1.12	0.411	1.98	0.039	1.24	0.675
1444429_at	leucine-rich repeats and transmembrane domains 1	Lrtm1	1.44	0.613	1.7	0.736	1.01	0.827	1.98	0.035	-1.26	0.192
1457893_at	Protein tyrosine phosphatase-like A domain containing 2	Ptplad2	-1.9	0.095	-1.62	0.154	2.28	0.587	1.98	0.039	1.06	0.828
1445156_at	expressed sequence C81001	C81001	-1.31	0.465	1.63	0.064	1.71	0.578	1.99	0.037	1.16	0.803

1427528_a_at	Eph receptor A7	Epha7	-2.01	0.091	1.17	0.687	1.02	0.709	2	0.036	-1.36	0.239
1455489_at	leucine rich repeat transmembrane neuronal 2	Lrrtm2	1.4	0.016	2.63	0.018	1.71	0.103	2	0.012	2.11	0.055
1458591_at	RAS and EF hand domain containing	Rasef	1.36	0.627	-1	0.440	1.04	0.616	2	0.032	-2.48	0.046
1446760_at	thyroid hormone receptor interactor 13	Trip13	1.05	0.926	-1.59	0.021	1.03	0.790	2	0.049	-1	0.914
1422253_at	procollagen, type X, alpha 1	Col10a1	1.96	0.066	2.6	0.069	2.02	0.127	2.02	0.049	2.65	0.083
1434227_at	keratinocyte differentiation associated protein	Krtdap	1.22	0.419	1.73	0.634	-1.27	0.391	2.02	0.047	-1.1	0.293
1445097_at	Phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	Pik3r3	1.14	0.796	-1.06	0.526	2.88	0.163	2.03	0.027	1.13	0.842
1434425_at	trichohyalin	Tchh	1.71	0.526	2.22	0.651	1.6	0.304	2.03	0.011	1.86	0.390
1441033_at	transmembrane and tetratricopeptide repeat containing 2	Tmtc2	-1.09	0.482	-1.09	0.627	1.65	0.034	2.03	0.040	-1.03	0.561
1445895_at	T-cell receptor beta, variable 8.2	Tcrb-V8.2	1.07	0.470	1.15	0.801	-1.32	0.321	2.04	0.025	1.3	0.636
1443556_at	RIKEN cDNA 1110007F12 gene	1110007F12Rik	1.74	0.452	1.76	0.287	1.01	0.642	2.05	0.023	1.54	0.592
1430201_at	RIKEN cDNA 9130017K11 gene	9130017K11Rik	1.69	0.454	-1.18	0.412	1.14	0.940	2.05	0.015	1.26	0.922
1447725_at	RIKEN cDNA C030034E14 gene	C030034E14Rik	-1.54	0.108	1.02	0.718	2.09	0.204	2.05	0.048	1.17	0.865
1421773_at	ets variant gene 2	Etv2	2.54	0.237	2.49	0.584	1.62	0.443	2.05	0.026	-1.02	0.716
1421575_at	RIKEN cDNA 2310057N15 gene	2310057N15Rik	2.16	0.179	2.99	0.203	1.24	0.686	2.06	0.050	1.29	0.877
1431940_at	hypothetical protein LOC74457	LOC74457	2.42	0.091	1.71	0.509	1.19	0.592	2.06	0.012	1.32	0.888
1436058_at	radical S-adenosyl methionine domain containing 2	Rsad2	-1.18	0.325	1.78	0.608	2.09	0.561	2.06	0.044	-1.55	0.414
1430094_at	RIKEN cDNA 4931440L10 gene	4931440L10Rik	1.22	0.532	-1.17	0.370	1.23	0.843	2.07	0.020	1.18	0.758
1433348_at	RIKEN cDNA 2810414N06 gene	2810414N06Rik	1.19	0.383	-1.09	0.520	2.5	0.384	2.08	0.037	1.45	0.984
1454649_at	steroid 5 alpha-reductase 1	Srd5a1	-1.11	0.283	-1.37	0.087	-1.03	0.675	2.08	0.044	1.44	0.001
1458684_at	synovial sarcoma translocation, Chromosome 18	Ss18	-1.52	0.233	-1.52	0.135	1.06	0.827	2.08	0.019	1.11	0.821
1426702_at	RIKEN cDNA 4632419K20 gene	4632419K20Rik	1.44	0.487	-1.04	0.629	1.35	0.914	2.09	0.045	-1.03	0.543
1448675_at	DNA segment, Chr 1, ERATO Doi 161, expressed	D1Ertd161e	2.27	0.608	2.32	0.933	-1.14	0.292	2.09	0.044	1.23	0.333
1454261_at	RIKEN cDNA E130304I02 gene	E130304I02Rik	1.43	0.173	-1.29	0.172	1.67	0.318	2.09	0.024	2.06	0.162
1426154_s_at	major urinary protein 1 /// major urinary protein 3	Mup1 /// Mup3	1.2	0.650	-1.5	0.307	1.14	0.533	2.09	0.023	1.38	0.495
1419429_at	ciliary neurotrophic factor receptor	Cntfr	-1.09	0.673	1.56	0.071	1.29	0.011	2.1	0.036	1.68	0.835
1439294_at	hypothetical protein D530008I22	D530008I22	1.87	0.839	1.18	0.730	-1.61	0.229	2.1	0.003	1.37	0.552
1441479_at	Protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	1.01	0.882	1.21	0.839	1.16	0.920	2.1	0.034	-1.3	0.256
1417172_at	ubiquitin-conjugating enzyme E2L 6	Ube2l6	-1.52	0.188	1.52	0.381	1.25	0.452	2.1	0.041	1.19	0.716
1437955_at	RIKEN cDNA 4922504M18 gene	4922504M18Rik	-2.03	0.062	1.07	0.529	2.51	0.828	2.11	0.002	-1.64	0.112
1442500_at	expressed sequence C77406	C77406	1.39	0.914	1.37	0.973	1.02	0.871	2.11	0.011	-1.11	0.331
1441095_at	RIKEN cDNA A430041B07 gene	A430041B07Rik	-1.09	0.287	-1.01	0.352	1.01	0.698	2.12	0.016	1.74	0.598
1437584_at	Cyclin D3	Ccnd3	-1.44	0.116	1.58	0.173	1.66	0.689	2.12	0.047	1.58	0.457
1431851_at	RIKEN cDNA 4930534P07 gene	4930534P07Rik	1.02	0.594	1.52	0.898	-1.74	0.043	2.13	0.040	1.22	0.377
1436172_at	hypothetical protein 9530028C05	9530028C05	1.43	0.904	1.09	0.488	1.26	0.319	2.13	0.017	2.72	0.549
1457507_at	Neuregulin 3	Nrg3	1.79	0.292	1.56	0.366	1.19	0.684	2.13	0.037	1.5	0.399
1454220_at	RIKEN cDNA 9330185C12 gene	9330185C12Rik	-1.15	0.590	-1.11	0.346	-1.4	0.375	2.14	0.038	1.67	0.706
1453856_at	BTB (POZ) domain containing 4	Btbd4	2.08	0.972	1.86	0.850	1.62	0.921	2.15	0.029	1.29	0.699
1456768_a_at	multimerin 2	Mmrn2	-1.04	0.578	-1.03	0.478	-1	0.546	2.16	0.031	1.92	0.390
1429929_at	meiosis defective 1	Mei1	-1.09	0.288	-1.52	0.181	1.97	0.008	2.17	0.002	-1.36	0.255
1452112_a_at	RNA binding motif protein 4B	Rbm4b	1.2	0.458	2.08	0.004	1.34	0.206	2.17	0.004	1.29	0.385
1454187_at	polycystic kidney disease 1 like 2	Pkd1l2	3.4	0.558	1.18	0.826	1.46	0.949	2.18	0.044	1.2	0.841
1434226_at	cytochrome b-561 domain containing 1	Cyb561d1	-1.02	0.482	1.36	0.110	-1.45	0.212	2.19	0.009	1.49	0.810
1425595_at	gamma-aminobutyric acid (GABA-B) receptor, 1	Gabbr1	-1.22	0.248	1.42	0.323	-1.22	0.345	2.19	0.007	1.08	0.950
1420385_at	guanine nucleotide binding protein, alpha 14	Gna14	1.25	0.962	1.33	0.870	1.2	0.689	2.19	0.031	-1.01	0.793
1451632_a_at	immunoglobulin heavy chain 1a (serum IgG2a)	Igh-1a	1.82	0.261	1.25	0.513	1.27	0.367	2.19	0.017	1.05	0.811
1447119_at	Transcription termination factor, RNA polymerase II	Ttf2	1.92	0.322	2.57	0.128	1.37	0.964	2.19	0.050	1.29	0.378
1442518_at	RIKEN cDNA C030044O21 gene	C030044O21Rik	-2.52	0.084	1.03	0.840	1.03	0.812	2.2	0.041	1.74	0.569
1440979_at	Insulin-like growth factor 2 receptor	Igf2r	2.05	0.407	1.66	0.639	1.1	0.790	2.2	0.044	1.21	0.526
1440399_at	Ubiquitin specific peptidase 32	Usp32	1.25	0.975	1.84	0.198	1.05	0.806	2.21	0.021	1.31	0.241
1438893_at	RIKEN cDNA 5530601H04 gene	5530601H04Rik	1.54	0.209	2.36	0.030	2.13	0.758	2.22	0.035	-1.1	0.875
1430453_a_at	Bcl2-like 2	Bcl2l2	1.92	0.210	1.82	0.239	2.2	0.316	2.22	0.036	2	0.108
1427422_at	similar to hepatocellular carcinoma-associated gene TD26	LOC624219	2.91	0.631	1.06	0.388	1.64	0.987	2.22	0.009	-1.08	0.470
1454651_x_at	myelin basic protein	Mbp	1.24	0.551	-1.33	0.255	1.79	0.648	2.22	0.031	-1.12	0.488
1429285_at	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase,	Serpina9	1.99	0.464	1.65	0.539	1.72	0.325	2.22	0.012	1.88	0.578
1431792_a_at	serine/threonine kinase 11 interacting protein	Stk11ip	1.45	0.649	1.66	0.339	1.39	0.463	2.22	0.024	1.89	0.794
1438240_at	calicin	Ccin	-1.83	0.134	1.76	0.513	1.79	0.245	2.23	0.038	1.14	0.794
1435370_a_at	carboxylesterase 3	Ces3	-1.24	0.245	1.14	0.629	-1.22	0.389	2.23	0.028	-1.06	0.589

1434818_at	hypothetical protein 9330159K06	9330159K06	1.31	0.675	1.06	0.532	2.48	0.673	2.24	0.042	-1.14	0.532
1451704_at	androgen binding protein delta	Abpd	1.14	0.543	1.71	0.907	2.2	0.332	2.24	0.025	1.81	0.380
1425463_at	GATA binding protein 6	Gata6	1.63	0.857	2.51	0.075	1.52	0.325	2.24	0.030	1.28	0.977
1430165_at	serine/threonine kinase 17b (apoptosis-inducing)	Stk17b	1.3	0.397	1.12	0.942	1.62	0.068	2.24	0.006	1.56	0.972
1420794_at	ADP-ribosyltransferase 2b	Art2b	-1.07	0.672	1.41	0.495	1.33	0.792	2.25	0.016	1.82	0.313
1441047_at	solute carrier family 45, member 4	Slc45a4	-1.64	0.068	-1.89	0.016	1.36	0.302	2.25	0.030	2.38	0.614
1447233_at	RIKEN cDNA D330027H18 gene	D330027H18Rik	-1.25	0.321	-1.7	0.002	1.35	0.976	2.26	0.006	1.49	0.079
1420289_at	expressed sequence T25656	T25656	1.98	0.897	3.7	0.404	2.05	0.276	2.26	0.017	2.64	0.543
1455122_at	patched domain containing 2	Ptchd2	1.38	0.149	1.39	0.042	-1.48	0.037	2.27	0.042	1.44	0.918
1455840_at	Rap guanine nucleotide exchange factor (GEF) 5	Rapgef5	1.17	0.784	1.65	0.042	1.69	0.633	2.27	0.023	-1.64	0.078
1438160_x_at	solute carrier organic anion transporter family, member 4a1	Slco4a1	-2.05	0.030	1.19	0.909	1.65	0.792	2.27	0.007	-1.17	0.284
1441669_at	centaurin, beta 2	Centb2	1.83	0.202	1.76	0.095	2.79	0.059	2.28	0.005	1.98	0.667
1429872_at	RIKEN cDNA 1700007N14 gene	1700007N14Rik	1.31	0.577	-1.15	0.360	2.22	0.809	2.29	0.002	2.08	0.215
1456408_x_at	RIKEN cDNA 4933439C10 gene	4933439C10Rik	4.79	0.630	3.49	0.525	2.54	0.290	2.29	0.016	1.13	0.837
1455088_at	similar to Ser/Thr protein kinase PAR-1A /// similar to serine/threonine ki	LOC381936 /// LOC	1.43	0.416	1.28	0.418	1.78	0.819	2.29	0.046	-1.01	0.501
1424510_at	nudix (nucleoside diphosphate linked moiety X)-type motif 6	Nudt6	1.12	0.445	1.33	0.134	1.13	0.201	2.29	0.002	1.09	0.835
1449032_at	prolactin-like protein M	Prlpm	-1.02	0.442	1.36	0.659	1.06	0.903	2.29	0.043	2.11	0.004
1459692_at	expressed sequence AI661323	AI661323	1.03	0.722	1.16	0.372	1.06	0.960	2.3	0.036	1.55	0.478
1460055_at	Ecotropic viral integration site 2a	Evi2a	-1.18	0.311	1.09	0.775	-1.05	0.654	2.3	0.014	1.9	0.491
1435154_at	similar to solute carrier family 7 (cationic amino acid transporter, y+ syste	LOC245128	1.62	0.725	1.72	0.908	-1.28	0.309	2.3	0.037	1.57	0.800
1440654_at	Hypothetical protein LOC574403	MGC99845	2.87	0.561	2.3	0.081	1.33	0.441	2.3	0.029	1.82	0.575
1431103_at	RIKEN cDNA 1700003P14 gene	1700003P14Rik	-1.94	0.073	1.14	0.330	-1.52	0.305	2.32	0.045	1.33	0.927
1445318_at	Kelch-like 4 (Drosophila)	Klhl4	1.35	0.945	-1.15	0.358	-2.84	0.043	2.32	0.034	-1.52	0.186
1428959_at	RIKEN cDNA 5830405N20 gene	5830405N20Rik	-1.05	0.424	-1	0.482	-1.13	0.189	2.33	0.043	-1.25	0.251
1433153_at	RIKEN cDNA 9030201C23 gene	9030201C23Rik	1.5	0.771	-1.4	0.334	-1	0.790	2.33	0.027	1.46	0.717
1420666_at	double C2, beta	Doc2b	-1.53	0.134	-1.49	0.207	1.43	0.699	2.33	0.023	1.21	0.791
1441346_at	RIKEN cDNA 2810421E14 gene	2810421E14Rik	2.21	0.021	2.52	0.326	-2.66	0.026	2.34	0.039	1.12	0.632
1431313_at	RIKEN cDNA 5730442P18 gene	5730442P18Rik	1.9	0.500	1.11	0.807	1.39	0.930	2.34	0.031	2.07	0.637
1425941_a_at	cDNA sequence BC025462	BC025462	-1.14	0.598	1.28	0.617	2.44	0.070	2.34	0.046	-1.82	0.059
1451553_at	ADP-ribosyltransferase 5	Art5	1.51	0.922	-1.44	0.215	-1.31	0.306	2.35	0.025	-1.69	0.166
1450555_at	testis expressed gene 13	Tex13	1.2	0.714	2.04	0.875	1.25	0.729	2.35	0.033	-1.05	0.429
1427018_at	translin-associated factor X (Tsnax) interacting protein 1	Tsnaxip1	2.74	0.377	3.04	0.449	-1.16	0.477	2.35	0.002	1.18	0.848
1432866_at	RIKEN cDNA 6030442K20 gene	6030442K20Rik	1.37	0.838	1.32	0.915	-1	0.493	2.36	0.028	-1.12	0.583
1442800_x_at	RIKEN cDNA A830059I20 gene	A830059I20Rik	2.24	0.921	2.44	0.437	2.37	0.057	2.36	0.013	1.81	0.426
1422708_at	phosphoinositide-3-kinase, catalytic, gamma polypeptide	Pik3cg	-1.54	0.162	-1.64	0.148	3.13	0.011	2.36	0.049	1.7	0.483
1446289_at	Serine/threonine kinase 3 (Ste20, yeast homolog)	Stk3	-1.17	0.412	1.02	0.432	1.44	0.549	2.36	0.045	1.75	0.916
1459798_x_at	RIKEN cDNA 4732479N06 gene	4732479N06Rik	-1.26	0.287	2.11	0.849	2.3	0.063	2.37	0.001	-1.24	0.318
1449854_at	nuclear receptor subfamily 0, group B, member 2	Nr0b2	1.66	0.356	-1.22	0.275	-1.04	0.649	2.37	0.027	-2.07	0.100
1428642_at	solute carrier family 35, member D3	Slc35d3	1.38	0.913	1.56	0.918	-1.27	0.608	2.37	0.019	-1.17	0.288
1455918_at	adrenergic receptor, beta 3	Adrb3	2.99	0.757	5.74	0.357	1.31	0.868	2.39	0.022	1.73	0.349
1453658_at	RIKEN cDNA 5830477G23 gene	5830477G23Rik	2.15	0.336	1.31	0.132	1.01	0.977	2.4	0.034	1.12	0.954
1446462_at	Histidyl tRNA synthetase 2	Hars2	1.63	0.719	1.4	0.738	1.22	0.861	2.4	0.035	1.18	0.748
1459236_at	expressed sequence AU022436	AU022436	2.14	0.569	1.05	0.620	-1.24	0.306	2.44	0.033	-1.14	0.305
1438998_at	RAS p21 protein activator 1	Rasa1	1.47	0.953	1.32	0.732	2.12	0.145	2.44	0.032	2.05	0.868
1430280_at	RIKEN cDNA 1810062G17 gene	1810062G17Rik	2.24	0.257	1.59	0.027	2.09	0.217	2.45	0.014	2.15	0.982
1449388_at	thrombospondin 4	Thbs4	-1.17	0.912	-1.11	0.922	-1.36	0.273	2.45	0.027	-1.24	0.940
1438436_at	RIKEN cDNA 6330407J23 gene	6330407J23Rik	2.17	0.863	1.59	0.938	-1.53	0.105	2.46	0.005	2.74	0.420
1458031_at	RIKEN cDNA B230315F11 gene	B230315F11Rik	1.58	0.764	2.16	0.296	1.34	0.816	2.46	0.026	1.66	0.133
1453561_x_at	RIKEN cDNA 8430431K14 gene	8430431K14Rik	-1.18	0.052	1.38	0.192	1.52	0.283	2.47	0.000	-1.01	0.670
1441826_x_at	Ubiquitin domain containing 1	Ubtd1	1.57	0.649	1.11	0.392	-2.96	0.010	2.47	0.008	1.94	0.261
1441531_at	phospholipase C, beta 4	Plcb4	1.87	0.343	2.44	0.351	1.07	0.864	2.48	0.032	1.63	0.115
1444453_at	Trp53 regulating kinase	Trp53rk	-1.26	0.424	-1.29	0.145	-1.42	0.032	2.48	0.031	1.37	0.838
1441434_at	RIKEN cDNA 2810426N06 gene	2810426N06Rik	1.81	0.689	1.7	0.438	2.05	0.493	2.49	0.028	1.29	0.734
1423458_at	solute carrier family 35, member A5	Slc35a5	1.24	0.765	1.86	0.386	1.88	0.479	2.51	0.031	1.46	0.510
1419411_at	tachykinin 2	Tac2	1.54	0.713	-1.23	0.343	1.31	0.756	2.54	0.026	2.47	0.059
1444192_at	RIKEN cDNA 9630020C08 gene	9630020C08Rik	-1.24	0.325	1.62	0.790	1.43	0.161	2.55	0.014	1.97	0.859
1450597_at	olfactory receptor 870	Olfr870	2.67	0.447	2.17	0.375	1.87	0.549	2.55	0.036	-1.39	0.299
1443234_at	CDNA sequence BC088983	BC088983	1.04	0.297	1.67	0.535	-1.07	0.708	2.56	0.018	-1.11	0.744

1445934_at	ariadne homolog 2 (Drosophila) /// similar to ariadne homolog 2	Arih2 /// LOC432565	2.47	0.328	2.44	0.139	1.11	0.767	2.57	0.046	2.09	0.803
1446710_at	expressed sequence C76669	C76669	1.82	0.714	1.82	0.301	-1.15	0.274	2.57	0.005	2.29	0.074
1460297_at	nephrosis 2 homolog, podocin (human)	Nphs2	-1.12	0.345	1.45	0.867	1.29	0.308	2.57	0.020	1.58	0.940
1447510_at	RIKEN cDNA C530014P21 gene	C530014P21Rik	2.79	0.110	2.46	0.055	3.88	0.088	2.59	0.000	1.52	0.376
1440598_at	syntrophin, gamma 1	Sntg1	1.26	0.949	-1.7	0.141	1.2	0.014	2.59	0.013	1.94	0.517
1420347_at	palate, lung, and nasal epithelium carcinoma associated	Plunc	1.47	0.670	1.51	0.890	1.16	0.724	2.6	0.046	1.57	0.234
1432267_at	RIKEN cDNA 6720483E21 gene	6720483E21Rik	-1.29	0.386	1.11	0.897	1.01	0.710	2.61	0.043	2.02	0.316
1435996_at	caspase recruitment domain family, member 11	Card11	-1.04	0.473	1.73	0.999	1.35	0.860	2.61	0.018	1.4	0.781
1457308_at	Ubiquitin specific petidase 45	Usp45	2.83	0.036	2.14	0.451	1.13	0.880	2.62	0.043	-1.78	0.064
1432348_at	RIKEN cDNA 4930524O07 gene	4930524O07Rik	1.32	0.664	-2.04	0.229	1.67	0.098	2.63	0.015	-1.15	0.554
1457807_at	Glucosamine-phosphate N-acetyltransferase 1	Gnpnat1	-1.12	0.551	1.13	0.959	1.3	0.589	2.63	0.001	1.66	0.854
1431620_at	RIKEN cDNA 4930442J19 gene	4930442J19Rik	1.2	0.808	1.17	0.701	1.02	0.720	2.64	0.039	2.2	0.500
1458799_at	RIKEN cDNA A330033J07 gene	A330033J07Rik	-1.26	0.267	-1.08	0.428	-1.83	0.085	2.64	0.009	1.24	0.745
1447166_at	RIKEN cDNA E230002P03 gene	E230002P03Rik	-2.13	0.107	-1.22	0.312	2.8	0.276	2.64	0.026	-1.17	0.324
1418303_at	RIKEN cDNA 1700113O17 gene	1700113O17Rik	1.08	0.485	1.18	0.730	1.2	0.837	2.65	0.009	-1.18	0.429
1455807_at	testis-specific protein, Y-encoded-like 5	Tspyl5	-1.1	0.433	1.39	0.643	1.75	0.902	2.65	0.045	3.18	0.013
1443386_at	expressed sequence C86727	C86727	-1.43	0.245	-1.63	0.317	2.01	0.388	2.66	0.000	1.12	0.398
1446994_at	Exosome component 2	Exosc2	-1.32	0.252	1.75	0.987	1.15	0.565	2.67	0.037	2.21	0.944
1453800_at	RIKEN cDNA 2500002L14 gene	2500002L14Rik	1.46	0.861	1.79	0.744	-1.16	0.582	2.7	0.008	1.06	0.895
1447659_x_at	ATPase, H+ transporting, lysosomal V1 subunit H	Atp6v1h	4.03	0.133	2.27	0.260	-1.63	0.118	2.7	0.024	-1.36	0.361
1459077_at	Cytochrome P450, family 2, subfamily d, polypeptide 26	Cyp2d26	1.94	0.519	1.79	0.254	1.12	0.912	2.7	0.040	1.43	0.498
1441668_at	RIKEN cDNA E130107B13 gene	E130107B13Rik	2.47	0.685	2.08	0.965	2.41	0.172	2.7	0.027	1.67	0.197
1432724_at	RIKEN cDNA 4930445G23 gene	4930445G23Rik	1.78	0.459	3.22	0.851	1.28	0.929	2.71	0.003	1.21	0.784
1453252_at	dihydrouridine synthase 4-like (S. cerevisiae)	Dus4l	1.73	0.033	2.08	0.005	1.44	0.627	2.72	0.013	1.27	0.260
1447326_s_at	zinc finger, MYM-type 3	Zmym3	1.57	0.428	2.28	0.580	2.63	0.197	2.72	0.024	1.55	0.513
1447116_at	Presenilin associated, rhomboid-like	Parl	-2.33	0.073	2.06	0.027	1.98	0.684	2.74	0.019	1.85	0.763
1454399_at	RIKEN cDNA 2010003H20 gene	2010003H20Rik	1.14	0.543	-1.73	0.178	1.03	0.990	2.75	0.007	-1.06	0.872
1446514_at	Dipeptidylpeptidase 10	Dpp10	1.62	0.718	-1.37	0.275	1.5	0.685	2.77	0.047	2.2	0.554
1436410_at	expressed sequence AI449023 /// gene model 941, (NCBI)	AI449023 /// Gm941	1.56	0.876	1.63	0.935	-1.11	0.856	2.78	0.016	1.91	0.405
1419827_s_at	kinesin family member 17	Kif17	1.27	0.961	2.13	0.508	1.15	0.690	2.78	0.044	1.44	0.574
1458144_at	CDNA sequence BC031353	BC031353	-1.35	0.423	1.53	0.499	1.52	0.506	2.79	0.024	1.78	0.079
1453845_at	RIKEN cDNA 4733401D01 gene	4733401D01Rik	-1.35	0.142	-1.66	0.187	1.66	0.356	2.81	0.047	-1.05	0.556
1430721_at	RIKEN cDNA 4931431C16 gene	4931431C16Rik	1.49	0.716	1.24	0.858	1.05	0.587	2.82	0.016	1.16	0.175
1441843_s_at	RIKEN cDNA 5230400M03 gene	5230400M03Rik	1.32	0.995	1.21	0.630	1.14	0.877	2.82	0.043	1.68	0.726
1425973_at	lysosomal trafficking regulator	Lyst	1.15	0.764	-1.46	0.112	-1.38	0.265	2.82	0.018	-1.72	0.110
1441120_at	CEA-related cell adhesion molecule 16	Ceacam16	2.26	0.934	2.64	0.700	2.72	0.324	2.83	0.038	-1.28	0.431
1445743_at	RIKEN cDNA E330024J20 gene	E330024J20Rik	-1.17	0.531	-1.02	0.808	1.56	0.736	2.85	0.002	2.03	0.106
1446279_at	Neuronal growth regulator 1	Negr1	-1.34	0.151	-1.22	0.391	2.1	0.283	2.85	0.007	3.1	0.028
1436476_at	DAN domain family, member 5	Dand5	1.09	0.475	1.29	0.759	1.03	0.578	2.86	0.023	-1.38	0.341
1453280_at	melanoma antigen, family B, 5 /// similar to Melanoma-associated antige	Mageb5 /// LOC629	-1.31	0.198	-1.18	0.288	-1.72	0.010	2.86	0.042	-1.03	0.804
1456010_x_at	hairy and enhancer of split 5 (Drosophila)	Hes5	3.31	0.100	2.51	0.020	1.1	0.679	2.87	0.015	1.21	0.883
1439333_at	potassium channel, subfamily V, member 1	Kcnv1	-2.68	0.007	-2.55	0.014	1.56	0.926	2.87	0.001	1.21	0.921
1445068_at	mucosa associated lymphoid tissue lymphoma translocation gene 1	Malt1	1.03	0.536	1.68	0.612	1.33	0.413	2.87	0.047	-1.02	0.619
1456720_at	RIKEN cDNA 1500041B16 gene	1500041B16Rik	-1.5	0.291	1.15	0.463	-1.07	0.574	2.88	0.039	1.39	0.428
1440917_at	RIKEN cDNA 2900093K20 gene	2900093K20Rik	2.7	0.215	3.14	0.138	2.3	0.524	2.88	0.022	1.09	0.796
1441837_at	cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal)	Chrnb2	3.08	0.588	1.47	0.443	2.26	0.109	2.88	0.040	1.73	0.223
1435585_at	transcription elongation factor A (SII)-like 7	Tceal7	1.92	0.432	4.49	0.455	1.24	0.854	2.88	0.011	1.4	0.455
1453190_at	ubiquitin specific peptidase 19	Usp19	-2.1	0.109	-1.22	0.343	1.68	0.246	2.9	0.014	1.44	0.357
1459568_at	Transmembrane and tetratricopeptide repeat containing 4	Tmtc4	1.54	0.905	1.61	0.909	1.49	0.706	2.91	0.006	1.07	0.798
1453041_at	Trp53 inducible protein 5	Trp53i5	1.36	0.983	1.44	0.412	-1.07	0.428	2.91	0.008	2.16	0.572
1448906_at	cadherin 16	Cdh16	1.02	0.755	1.93	0.405	-1.02	0.479	2.94	0.042	-1.75	0.116
1445594_at	Heterogeneous nuclear ribonucleoprotein L	Hnrpl	-1.3	0.225	1.47	0.915	1.22	0.880	2.96	0.012	-1.29	0.161
1453699_at	RIKEN cDNA 4930448D08 gene	4930448D08Rik	1.71	0.318	1.54	0.662	-1.32	0.187	2.98	0.030	1.74	0.873
1438274_at	zinc finger protein, subfamily 1A, 4 (Eos)	Zfpn1a4	-1.85	0.134	-1.47	0.178	1.55	0.922	2.98	0.021	1.11	0.511
1448930_at	RIKEN cDNA 3010026O09 gene	3010026O09Rik	2.66	0.173	3.97	0.065	1.16	0.637	2.99	0.008	1.85	0.088
1458116_at	RIKEN cDNA 9530079D04 gene	9530079D04Rik	-1.68	0.024	1.06	0.673	-1.51	0.076	2.99	0.039	-1.61	0.176
1430084_at	TLC domain containing 1	Tlcd1	2.02	0.345	1.22	0.914	1.4	0.180	3.01	0.037	3.89	0.052
1459988_at	methyl-CpG binding domain protein 3-like 2	Mbd3l2	2.45	0.911	2.31	0.979	1.93	0.992	3.02	0.000	-1.34	0.104

1450725_s_at	carbonic anhydrase 14	Car14	2.37	0.701	1.74	0.595	1.34	0.986	3.04	0.026	1.68	0.276
1431152_at	hyaluronan and proteoglycan link protein 3	Hapln3	-1.36	0.328	-1.46	0.110	1.32	0.693	3.05	0.007	1.25	0.593
1432975_at	RIKEN cDNA 2310038E17 gene	2310038E17Rik	2.71	0.453	1.22	0.746	-1.07	0.496	3.07	0.002	-1.28	0.543
1457837_at	cDNA sequence BC033606 /// similar to phospholipase B	BC033606 /// LOC6	1.24	0.759	-1.02	0.583	1.87	0.964	3.08	0.007	-1.03	0.404
1457290_at	mab-21-like 1 (C. elegans)	Mab21l1	-1.29	0.313	1.98	0.856	1.6	0.784	3.09	0.008	1.98	0.291
1432643_at	RIKEN cDNA 4933411E06 gene	4933411E06Rik	-1.48	0.085	1.26	0.409	1.08	0.424	3.11	0.044	1.16	0.891
1446096_at	RIKEN cDNA 2310001H17 gene	2310001H17Rik	-1.14	0.506	-1.98	0.045	1.46	0.784	3.12	0.020	-1.15	0.210
1426603_at	ribonuclease L (2', 5'-oligoisoadenylate synthetase-dependent)	Rnasel	2.5	0.056	2.04	0.505	2.16	0.540	3.13	0.012	1.27	0.788
1454094_at	RIKEN cDNA 4930471E19 gene	4930471E19Rik	1.13	0.400	1.07	0.545	-1.17	0.396	3.14	0.005	2.15	0.119
1440804_at	natural killer tumor recognition sequence	Nktr	1.35	0.805	1.5	0.841	1.04	0.529	3.14	0.030	2.09	0.127
1436686_at	zinc finger protein 706	Zfp706	1.81	0.639	1.62	0.664	1.4	0.943	3.14	0.044	2.91	0.404
1445131_at	F-box and leucine-rich repeat protein 13	Fbxl13	1.35	0.552	-1.14	0.371	1.05	0.818	3.15	0.037	1.45	0.735
1453790_at	RIKEN cDNA 5730403B10 gene	5730403B10Rik	-1.2	0.372	1.02	0.606	1.75	0.182	3.19	0.003	1.04	0.856
1442384_at	G elongation factor, mitochondrial 2	Gfm2	-1.22	0.474	-1.14	0.516	-1.26	0.444	3.22	0.015	1.03	0.702
1456836_at	IL2-inducible T-cell kinase	Itk	1.52	0.800	1.96	0.842	-1.08	0.546	3.22	0.042	1.33	0.253
1444114_at	Muskelin 1, intracellular mediator containing kelch motifs	Mkln1	-1.02	0.716	-1.14	0.584	1.86	0.695	3.22	0.001	1.22	0.656
1439595_at	RIKEN cDNA A430107P09 gene	A430107P09Rik	1.22	0.838	1.39	0.526	1.34	0.421	3.25	0.049	1.4	0.892
1453357_at	tudor domain containing 9	Tdrd9	2.26	0.441	-1.22	0.541	1.43	0.205	3.25	0.034	-1.23	0.321
1440542_at	RIKEN cDNA 7420416P09 gene	7420416P09Rik	1.83	0.131	1.23	0.153	1.1	0.901	3.26	0.011	-2.07	0.018
1432950_at	RIKEN cDNA 5330421F21 gene	5330421F21Rik	-1.37	0.356	-1.61	0.233	-1.26	0.284	3.32	0.032	2.09	0.636
1454176_at	excision repaiross-complementing rodent repair deficiency, complementa	Ercc8	1.55	0.597	2.15	0.141	-1.62	0.185	3.34	0.022	1.04	0.959
1417765_a_at	amylase 1, salivary	Amy1	-1.56	0.053	-2.67	0.073	1.31	0.926	3.38	0.000	1.02	0.663
1441760_at	similar to 40S ribosomal protein S25 /// similar to 40S ribosomal protein	LOC243302 /// LOC	1.02	0.644	-1.07	0.487	-1.12	0.656	3.38	0.049	-1.98	0.124
1441521_at	Calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	1.16	0.828	1.31	0.929	1.28	0.191	3.43	0.050	-1.02	0.611
1448409_at	lymphoid-restricted membrane protein	Lrmp	1.27	0.597	1.62	0.749	1.04	0.635	3.44	0.038	-1.2	0.295
1449919_at	keratin associated protein 6-2	Krtap6-2	1.79	0.662	2.15	0.833	-1.2	0.545	3.45	0.009	-1.34	0.163
1438311_at	RIKEN cDNA 2010002M12 gene	2010002M12Rik	1.13	0.775	1.47	0.670	1.57	0.190	3.47	0.018	1.47	0.382
1440126_at	cDNA sequence BC037704	BC037704	-1.17	0.363	1.56	0.382	-1.13	0.449	3.51	0.009	2.22	0.641
1424098_at	ELOVL family member 7, elongation of long chain fatty acids (yeast)	Elovl7	-2.64	0.059	-2.28	0.073	1.88	0.164	3.53	0.018	-1.65	0.176
1439006_x_at	RIKEN cDNA 6430550H21 gene	6430550H21Rik	2.66	0.445	2.41	0.123	1.3	0.536	3.56	0.016	1.24	0.659
1433222_at	RIKEN cDNA 2610311E24 gene	2610311E24Rik	-1.14	0.528	2.06	0.362	2.37	0.111	3.57	0.030	-1.7	0.171
1432415_at	RAB3C, member RAS oncogene family	Rab3c	2.73	0.171	2.08	0.462	1.22	0.628	3.62	0.004	2.11	0.227
1433178_at	RIKEN cDNA 4933427C19 gene	4933427C19Rik	1.65	0.967	1.3	0.858	1.15	0.771	3.65	0.002	1.72	0.577
1421280_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 1	Gabra1	-1.45	0.037	1.65	0.813	1.66	0.247	3.74	0.007	-1.16	0.395
1459926_at	expressed sequence C77068	C77068	2.41	0.658	1.64	0.856	1.78	0.477	3.75	0.023	1.26	0.604
1439712_at	integrator complex subunit 10	Ints10	2.77	0.588	2.61	0.790	-1.14	0.477	3.78	0.016	-1.4	0.179
1429718_at	SLIT and NTRK-like family, member 5	Slitrk5	1.39	0.995	1.31	0.892	1.49	0.851	3.93	0.040	2.35	0.367
1435408_at	RIKEN cDNA 2700092H06 gene	2700092H06Rik	-1.21	0.525	-1.48	0.233	2.35	0.105	3.95	0.042	1.39	0.167
1447567_at	RIKEN cDNA D130007H15 gene	D130007H15Rik	1.5	0.824	-1.54	0.243	1.02	0.670	3.97	0.001	1.59	0.903
1459966_at	Oxysterol binding protein-like 7	Osbpl7	1.05	0.831	2.7	0.408	1.14	0.964	4.03	0.023	1.23	0.671
1437310_at	Bardet-Biedl syndrome 1 homolog (human)	Bbs1	1.74	0.323	1.23	0.403	2.44	0.036	4.06	0.034	1.35	0.575
1449767_x_at	synaptotagmin VI	Syt6	-1.22	0.471	1.06	0.719	1.14	0.660	4.29	0.007	1.13	0.361
1419140_at	activin receptor IIB	Acvr2b	1.46	0.980	1.53	0.759	1.12	0.519	4.53	0.034	-1	0.782
1455347_at	regulator of telomere elongation helicase 1	Rtel1	6	0.837	1.49	0.408	4.35	0.797	5.78	0.002	2.4	0.072
1452552_at	neoplastic progression 2	Npn2	2.01	0.566	11.69	0.000	3.34	0.102	7.33	0.002	3.96	0.024

Supplementary table 5. List of significant expression profiles of DKO cells irradiated with 0.6J/m2 of UV (gray color) as compared to non-irradiated DKO cells

code	Gene Title	Symbol	WT_0.6J/m2	p	WT_4J/m2	p	XPA_0.6J/m2	p	CSB_0.6J/m2	p	DKO_0.6J/m2	p
1437371_at	RIKEN cDNA 9930021J17 gene	9930021J17Rik	1.26	0.940	1.44	0.868	-1.82	0.104	-1.46	0.243	-5.82	0.003
1450836_at	neurogenin 1	Neurog1	2.62	0.053	1.56	0.046	-1.25	0.336	1.79	0.610	-5.02	0.028
1438861_at	basonuclin 2	Bnc2	-1.43	0.148	-8.88	0.007	-2.42	0.029	-3.5	0.001	-4.02	0.002
1455040_s_at	RIKEN cDNA 1110062M06 gene	1110062M06Rik	1.03	0.783	-2.18	0.062	-1.6	0.065	1.24	0.887	-3.95	0.013
1427564_at	diaphanous homolog 2 (Drosophila)	Diap2	-1.62	0.060	-4.29	0.032	-2.65	0.025	-1.57	0.072	-3.92	0.023
1445111_at	Exocyst complex component 4	Exoc4	1.17	0.601	1.68	0.232	1.1	0.847	-1.94	0.045	-3.64	0.045
1437897_at	kelch-like 21 (Drosophila)	Klhl21	-2.03	0.111	-2.48	0.069	1.12	0.921	1.73	0.917	-3.61	0.010
1446698_at	Mortality factor 4 like 1	Morf4l1	1.65	0.350	-3.52	0.093	-1.85	0.105	-1.99	0.089	-3.6	0.037
1442435_at	Smg-6 homolog, nonsense mediated mRNA decay factor	Smg6	-1.26	0.340	-1.5	0.284	-1.29	0.209	2.31	0.310	-3.55	0.034
1417435_at	like-glycosyltransferase	Large	-1.14	0.255	-4.38	0.003	-2.64	0.009	-2.16	0.002	-3.49	0.001
1436765_at	par-3 (partitioning defective 3) homolog (C. elegans)	Pard3	3.12	0.674	-1.6	0.101	-1.75	0.064	-1.96	0.006	-3.48	0.003
1416302_at	early B-cell factor 1	Ebf1	2.21	0.743	-1.95	0.072	-3.29	0.002	-3.45	0.000	-3.44	0.006
1445695_at	Ataxin 1	Atxn1	1.04	0.451	-1.33	0.239	-1.31	0.210	-1.11	0.634	-3.33	0.029
1443373_at	Mitogen-activated protein kinase kinase kinase kinase 5	Map4k5	1.29	0.692	2.82	0.076	1.11	0.737	1.44	0.837	-3.31	0.012
1444740_at	RIKEN cDNA 4930550L11 gene	4930550L11Rik	-1.07	0.283	-1.57	0.153	-1.11	0.307	2.25	0.820	-3.27	0.021
1437010_a_at	ornithine decarboxylase antizyme 3	Oaz3	1.31	0.466	1.26	0.652	2.04	0.095	-1.03	0.619	-3.26	0.007
1455358_at	Ataxin 2 binding protein 1	A2bp1	1.24	0.723	-1.44	0.255	-1.52	0.196	-1.9	0.030	-3.22	0.007
1445991_at	Lipoma HMGIC fusion partner	Lhfp	2.9	0.251	1.48	0.827	-1.17	0.416	1.97	0.977	-3.15	0.006
1428204_at	RIKEN cDNA C030002O17 gene	C030002O17Rik	1.14	0.998	1.29	0.945	-1.11	0.480	1.2	0.987	-3.14	0.036
1449794_x_at	Cathepsin F	Ctsf	-1.28	0.336	-1.03	0.445	1.16	0.295	-3.58	0.050	-3.13	0.036
1452050_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-2.14	0.028	-5.47	0.022	-1.24	0.338	-2.13	0.093	-3.12	0.002
1453443_at	RIKEN cDNA 1110015O18 gene	1110015O18Rik	1.99	0.372	-1.17	0.460	1.19	0.676	3.58	0.083	-3.07	0.044
1443229_at	ATPase family, AAA domain containing 2	Atad2	1.31	0.849	2.97	0.094	1.71	0.587	3.27	0.100	-3.02	0.030
1458513_at	mitogen activated protein kinase 10	Mapk10	1.68	0.540	-1.41	0.090	1.71	0.620	1.45	0.889	-3.02	0.008
1444964_at	casein kinase 1, gamma 1	Csnk1g1	-1.12	0.633	1.06	0.625	-1.66	0.051	-1.23	0.225	-2.97	0.022
1459349_at	RIKEN cDNA A930011G23 gene	A930011G23Rik	1.52	0.967	1.94	0.671	1.43	0.759	1.29	0.800	-2.95	0.032
1449594_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	Abcb1b	1.19	0.837	2.36	0.160	1.22	0.566	1.3	0.791	-2.95	0.011
1434582_at	DNA segment, Chr 14, ERATO Doi 171, expressed	D14Ertd171e	-2.2	0.031	-3.44	0.041	-2.08	0.048	-1.68	0.048	-2.95	0.032
1427514_at	hypothetical protein LOC624295	LOC624295	1.66	0.767	-1.02	0.469	1.29	0.773	-1.21	0.394	-2.94	0.010
1438350_at	G protein-coupled receptor 64	Gpr64	3.38	0.167	3.1	0.025	1.68	0.224	-1.25	0.187	-2.88	0.031
1456423_at	methyl-CpG binding domain protein 5	Mbd5	-1.34	0.162	-6.08	0.005	-2.29	0.026	-2.69	0.001	-2.88	0.005
1454546_at	RIKEN cDNA 4933403L11 gene	4933403L11Rik	1.69	0.695	1.16	0.587	-1.34	0.403	-1.82	0.002	-2.86	0.004
1424625_a_at	DENN/MADD domain containing 1A	Dennd1a	-1.06	0.474	-2.94	0.002	-1.95	0.016	-2.58	0.012	-2.85	0.032
1442086_at	Metastasis associated 3	Mta3	-1.26	0.316	1.57	0.296	1.52	0.742	1.85	0.252	-2.83	0.012
1460509_at	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	B3galt1	1.24	0.904	1.72	0.579	-1.72	0.159	1.15	0.694	-2.82	0.005
1459372_at	neuronal PAS domain protein 4	Npas4	1.76	0.147	1.24	0.963	-1.57	0.038	-1.01	0.762	-2.81	0.016
1452342_at	amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	-1.24	0.242	-4.81	0.045	-2.12	0.007	-2.59	0.000	-2.8	0.010
1433301_at	RIKEN cDNA 4930478M09 gene	4930478M09Rik	1.56	0.251	-1.07	0.006	-1.14	0.624	-1.3	0.199	-2.78	0.007
1438531_at	RIKEN cDNA A730054J21 gene	A730054J21Rik	-1.34	0.080	-3.96	0.006	-2.15	0.001	-2.14	0.003	-2.72	0.004
1431653_at	T-cell receptor beta, joining region	Tcrb-J	1.18	0.686	1.96	0.652	-1.5	0.152	1.09	0.786	-2.72	0.003
1452783_at	fibronectin type III domain containing 3B	Fndc3b	1.16	0.796	-1.44	0.119	-2.16	0.005	-2.1	0.000	-2.71	0.002
1444538_at	Expressed sequence AL033314	AL033314	-1.39	0.242	-1.91	0.160	-2.67	0.059	-1.49	0.126	-2.69	0.006
1443654_at	Ankyrin repeat and FYVE domain containing 1	Ankfy1	1.37	0.615	-1.05	0.386	-1.42	0.245	-1.13	0.227	-2.68	0.017
1457524_at	Transcription factor 12	Tcf12	1.28	0.802	1.83	0.774	-1.24	0.542	1.5	0.570	-2.68	0.012
1429417_at	RIKEN cDNA 4833446K15 gene	4833446K15Rik	-1.34	0.062	-4.38	0.016	-1.62	0.080	-2.05	0.003	-2.67	0.001
1438449_at	Cdc42 binding protein kinase alpha	Cdc42bpa	-1.04	0.699	-1.38	0.325	1.35	0.177	-1.15	0.527	-2.67	0.007
1430439_at	multiple C2 domains, transmembrane 1	Mctp1	1.87	0.340	2.08	0.360	1.51	0.552	1.37	0.914	-2.67	0.004
1442437_at	PTK2 protein tyrosine kinase 2 beta	Ptk2b	1.51	0.858	2.06	0.107	-1.45	0.098	-1.58	0.264	-2.67	0.033
1438828_at	Rap guanine nucleotide exchange factor (GEF) 6	Rapgef6	2.43	0.775	1.19	0.410	-1.19	0.463	1.25	0.774	-2.66	0.029
1449314_at	zinc finger protein, multitype 2	Zfpm2	-1.07	0.482	-8.16	0.005	-2.11	0.007	-2.19	0.002	-2.66	0.026
1458298_at	Ca<2+>dependent activator protein for secretion	Cadps	2.57	0.078	3.06	0.104	2.01	0.387	3.84	0.199	-2.65	0.049
1448152_at	insulin-like growth factor 2	Igf2	-1.16	0.520	1.34	0.891	-1.42	0.119	3.08	0.123	-2.65	0.008
1423439_at	phosphoenolpyruvate carboxykinase 1, cytosolic	Pck1	-1.08	0.393	-1.79	0.296	1.85	0.199	1.28	0.975	-2.65	0.004

1430408_at	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	Cacna1a	1.65	0.364	1.44	0.712	1.79	0.129	1.11	0.670	-2.64	0.013
1436778_at	cytochrome b-245, beta polypeptide	Cybb	1.97	0.779	1.56	0.827	-1.29	0.193	-1.13	0.502	-2.64	0.004
1427421_at	t-complex protein 10b	Tcp10b	1.04	0.961	-1.08	0.271	1.24	0.007	-1.32	0.182	-2.64	0.005
1443989_at	tripartite motif protein 9	Trim9	1.05	0.883	-1.03	0.364	-2.3	0.076	-1.18	0.335	-2.64	0.007
1437135_at	F-box and WD-40 domain protein 10	Fbxw10	1.07	0.569	1.02	0.468	1.28	0.659	1.01	0.770	-2.62	0.038
1434685_at	DNA segment, Chr 3, Brigham & Women's Genetics 0562 expressed	D3Bwg0562e	2.42	0.481	-1.02	0.535	2.5	0.621	2.85	0.405	-2.6	0.010
1457876_at	DNA segment, Chr 9, ERATO Doi 496, expressed	D9Ertd496e	1.48	0.379	-1.01	0.761	-1.02	0.605	1.8	0.438	-2.6	0.021
1422392_at	vomeronasal 1 receptor, C6	V1rc6	1.22	0.694	1.34	0.694	2.87	0.039	1.91	0.512	-2.59	0.003
1450945_at	protein kinase C, alpha	Prkca	1.16	0.926	-2.39	0.042	-2.09	0.001	-2.13	0.001	-2.58	0.005
1434878_at	SLIT and NTRK-like family, member 4	Slitrk4	1.76	0.036	-1.88	0.025	2.16	0.897	1.87	0.331	-2.58	0.033
1426027_a_at	Rho GTPase activating protein 10	Arhgap10	4.61	0.736	1.98	0.336	-1.54	0.114	-1.9	0.000	-2.56	0.012
1440246_at	longevity assurance homolog 6 (S. cerevisiae)	Lass6	1.35	0.638	-1.49	0.154	1.08	0.837	-1.08	0.283	-2.56	0.020
1432019_at	TruB pseudouridine (psi) synthase homolog 1 (E. coli)	Trub1	-1.6	0.139	1.11	0.980	1.89	0.230	1.67	0.591	-2.56	0.003
1449763_at	Doublesex and mab-3 related transcription factor 3	Dmrt3	-1.01	0.670	-1.92	0.033	1.44	0.929	-1.82	0.126	-2.54	0.030
1436515_at	RIKEN cDNA E030004N02 gene	E030004N02Rik	-1.01	0.682	-5.74	0.001	-1.46	0.218	-2.17	0.026	-2.54	0.032
1439397_at	formin 1	Fmn1	-1.32	0.348	-4.27	0.117	-1.6	0.001	-2.56	0.002	-2.54	0.000
1431203_at	serologically defined colon cancer antigen 8	Sdccag8	1.85	0.269	1.23	0.267	-1.32	0.308	-1.07	0.406	-2.53	0.003
1450278_at	tachykinin receptor 3	Tacr3	1.7	0.260	1.76	0.261	1.14	0.754	2.32	0.365	-2.53	0.013
1452860_at	F-box and leucine-rich repeat protein 17	Fbxl17	-1.28	0.074	-4.57	0.011	-1.87	0.000	-2.24	0.002	-2.52	0.000
1424953_at	cDNA sequence BC021614	BC021614	1.26	0.589	2.08	0.250	-1.02	0.326	-1.91	0.087	-2.51	0.012
1429138_at	neuronal PAS domain protein 3	Npas3	1.03	0.485	1.89	0.861	1.63	0.637	1.04	0.995	-2.51	0.010
1430632_at	ankyrin repeat and SOCS box-containing protein 1	Asb1	3.77	0.538	1.45	0.427	1.48	0.767	1.65	0.554	-2.5	0.041
1440969_at	cDNA sequence BC030308	BC030308	1.1	0.748	1.56	0.872	1.18	0.969	1.5	0.458	-2.49	0.011
1445359_at	adenylate cyclase 1	Adcy1	1.85	0.946	2.21	0.966	1.45	0.298	1.61	0.965	-2.48	0.022
1440645_at	similar to deleted in malignant brain tumors 1 isoform c precursor	LOC546006	2.29	0.046	4.08	0.018	2.49	0.340	-1.05	0.328	-2.48	0.015
1416043_at	nuclear autoantigenic sperm protein (histone-binding)	Nasp	1.29	0.351	1.75	0.158	1	0.502	1.31	0.956	-2.48	0.022
1458591_at	RAS and EF hand domain containing	Rasef	1.36	0.627	-1	0.440	1.04	0.616	2	0.032	-2.48	0.046
1451567_a_at	interferon activated gene 203	Ifi203	-1.16	0.374	1.55	0.605	2.44	0.463	-1.25	0.505	-2.47	0.019
1437422_at	semaphorin 5A	Sema5a	1.06	0.756	-1.14	0.448	-2.96	0.072	-2.18	0.068	-2.47	0.044
1454127_at	RIKEN cDNA 1010001I08 gene	1010001I08Rik	-1.79	0.140	1	0.351	-1.79	0.227	1.33	0.873	-2.46	0.002
1433165_at	RIKEN cDNA 4930570E01 gene	4930570E01Rik	1.54	0.961	1.96	0.468	1.04	0.849	-1.33	0.331	-2.46	0.004
1437393_at	expressed sequence AI875142	AI875142	-1.31	0.125	-3.91	0.004	-2.18	0.001	-2.12	0.006	-2.46	0.005
1457548_at	A disintegrin-like and metallopeptidase with thrombospondin type 1	Adamts6	-1.11	0.473	-2.14	0.092	-1.69	0.107	-1.72	0.011	-2.45	0.007
1426442_at	glycoprotein m6a	Gpm6a	3.56	0.327	-1.5	0.306	1.17	0.603	1.57	0.944	-2.45	0.002
1436611_at	solute carrier family 39 (zinc transporter), member 12	Slc39a12	1.2	0.909	3.48	0.232	1.18	0.551	-1.3	0.327	-2.45	0.039
1438619_x_at	zinc finger, DHHC domain containing 14	Zdhhc14	-1.47	0.288	-5.73	0.136	-1.7	0.068	-2.57	0.001	-2.45	0.026
1429987_at	RIKEN cDNA 9930013L23 gene	9930013L23Rik	-1.29	0.007	-3.17	0.004	-2.03	0.006	-1.74	0.000	-2.44	0.008
1436047_at	gene model 672, (NCBI)	Gm672	-1.12	0.226	-2.63	0.015	-1.69	0.000	-2.21	0.001	-2.44	0.000
1417318_at	deleted in bladder cancer 1 (human)	Dbc1	-1.37	0.141	-3.6	0.020	-1.99	0.004	-1.84	0.008	-2.43	0.006
1442320_at	hypothetical LOC553096	LOC553096	1.02	0.546	-1.03	0.516	1.04	0.683	1.31	0.194	-2.42	0.002
1442693_at	similar to tripartite motif protein TRIM5	LOC667823	1.84	0.618	1.55	0.873	1.26	0.572	1.32	0.051	-2.42	0.031
1453512_at	RIKEN cDNA 5830407P18 gene	5830407P18Rik	1.19	0.430	-1.14	0.529	-1.65	0.049	-1.33	0.247	-2.41	0.013
1417730_at	exostoses (multiple) 1	Ext1	1.33	0.686	-1.75	0.098	-2.36	0.002	-2.41	0.001	-2.41	0.013
1427687_at	protocadherin alpha 10	Pcdha10	-1.93	0.087	1.52	0.470	2.08	0.772	2.11	0.304	-2.41	0.030
1460384_a_at	AT rich interactive domain 4B (Rbp1 like)	Arid4b	1.38	0.070	1.17	0.899	1.03	0.852	-1.38	0.164	-2.39	0.005
1436737_a_at	sorbin and SH3 domain containing 1	Sorbs1	-1.33	0.230	-2.35	0.052	-1.86	0.006	-2.22	0.000	-2.38	0.005
1430994_at	membrane-associated ring finger (C3HC4) 5	5-Mar	1.03	0.641	-1.59	0.085	-1.2	0.159	-1.42	0.212	-2.37	0.040
1418173_at	keratin 25	Krt25	-1.25	0.426	1.65	0.325	1.38	0.547	1.35	0.782	-2.37	0.032
1451577_at	zinc finger and BTB domain containing 20	Zbtb20	1.12	0.362	-2.11	0.005	-1.74	0.009	-1.59	0.040	-2.37	0.001
1451333_a_at	proacrosin binding protein	Acrbp	1.4	0.717	1.16	0.423	2.75	0.138	1.06	0.550	-2.36	0.004
1457629_at	cDNA sequence BC060631	BC060631	2.05	0.639	2.34	0.459	1.16	0.674	1.36	0.340	-2.35	0.022
1450768_at	discs, large homolog 1 (Drosophila)	Dlgh1	1.22	0.982	-1.55	0.096	-1.77	0.007	-1.68	0.005	-2.35	0.001
1420455_at	glial cells missing homolog 2 (Drosophila)	Gcm2	-1.24	0.133	1.13	0.321	-1.29	0.252	2.6	0.708	-2.35	0.008
1444386_at	phosphodiesterase 1C	Pde1c	2.52	0.122	2.08	0.443	-1.88	0.057	-1.22	0.424	-2.35	0.009
1434880_at	ets variant gene 6 (TEL oncogene)	Etv6	1.08	0.579	-1.4	0.093	-1.66	0.003	-1.93	0.003	-2.34	0.001
1457236_at	G protein-coupled receptor 62	Gpr62	-1.45	0.218	2.11	0.693	1.38	0.822	-1.43	0.188	-2.34	0.041
1447566_at	Histone deacetylase 4	Hdac4	2.13	0.817	-1.04	0.229	1.18	0.547	-1.02	0.724	-2.34	0.031
1443809_at	Pleiotrophin	Ptn	1.7	0.985	1.36	0.894	1.08	0.802	-1.2	0.332	-2.34	0.015

1422261_a_at	mutS homolog 3 (E. coli)	Msh3	-1.39	0.131	-1.25	0.279	1.36	0.382	1.29	0.079	-2.33	0.031
1440703_at	RIKEN cDNA 2810429I04 gene	2810429I04Rik	1.34	0.427	-1.71	0.006	1.23	0.768	-1.6	0.173	-2.32	0.033
1436369_at	RIKEN cDNA 2900076A07 gene	2900076A07Rik	1.53	0.824	-1.51	0.139	1.65	0.990	1.84	0.930	-2.32	0.023
1453893_at	RIKEN cDNA 4933412O06 gene	4933412O06Rik	1.56	0.861	-1.13	0.312	1.94	0.267	2.63	0.102	-2.32	0.049
1429229_s_at	RIKEN cDNA 4930534B04 gene	4930534B04Rik	-1.21	0.524	-2	0.005	1.65	0.810	-1.14	0.387	-2.31	0.002
1457463_at	Down syndrome cell adhesion molecule-like 1	Dscaml1	-1.72	0.202	1.03	0.430	1.85	0.243	-1.58	0.150	-2.31	0.001
1441620_at	Growth factor receptor bound protein 10	Grb10	1.97	0.061	1.13	0.957	-1.4	0.235	-1.26	0.345	-2.31	0.029
1450284_at	phosphodiesterase 3A, cGMP inhibited	Pde3a	2.84	0.875	1.44	0.373	1.26	0.726	-1.71	0.159	-2.31	0.038
1429939_at	SAPS domain family, member 3	Saps3	-1.31	0.261	-1.19	0.409	1.01	0.999	-1.31	0.181	-2.31	0.008
1454711_at	triple functional domain (PTPRF interacting)	Trio	1.12	0.560	-1.51	0.126	-1.68	0.005	-2.53	0.002	-2.31	0.001
1450558_at	vomeronasal 1 receptor, A1	V1ra1	1.26	0.891	1.43	0.972	2.64	0.368	1.16	0.556	-2.31	0.042
1457821_at	RIKEN cDNA 2610511M17 gene	2610511M17Rik	1.82	0.593	1.7	0.912	-1.18	0.336	-2.02	0.093	-2.3	0.017
1447709_at	Erythrocyte protein band 4.1-like 3	Epb4.1l3	2.1	0.125	3.07	0.077	-1.33	0.296	1.1	0.797	-2.3	0.008
1444828_at	Protein phosphatase 2, regulatory subunit B (B56), gamma isoform	Ppp2r5c	2.06	0.120	1.52	0.615	-1.22	0.266	1.62	0.675	-2.3	0.031
1458450_at	zinc finger RNA binding protein	Zfr	2.42	0.329	1.62	0.809	1.12	0.610	-1.16	0.327	-2.3	0.027
1440317_at	RIKEN cDNA C130068B02 gene	C130068B02Rik	1.02	0.602	-1.13	0.252	-1.24	0.181	-1.37	0.107	-2.29	0.044
1455256_at	TRAF2 and NCK interacting kinase	Tnik /// LOC66511	-1.48	0.160	-3.74	0.050	-1.76	0.160	-3.01	0.002	-2.29	0.029
1459491_at	DNA segment, Chr 12, ERATO Doi 673, expressed	D12Ertd673e	-2.06	0.019	1.02	0.944	-1.17	0.354	1.55	0.221	-2.28	0.038
1452222_at	utrophin	Utrn	-1.22	0.149	-2.52	0.017	-1.94	0.006	-1.74	0.003	-2.28	0.007
1427716_at	RIKEN cDNA 1700036D21 gene	1700036D21Rik	1.47	0.432	1.95	0.285	-1.17	0.296	-1.37	0.148	-2.27	0.005
1422541_at	protein tyrosine phosphatase, receptor type, M	Ptprm	-1.47	0.055	-3.24	0.022	-1.9	0.005	-1.86	0.004	-2.27	0.004
1435930_at	zinc finger protein 291	Zfp291	-1.82	0.225	-3.26	0.140	-1.53	0.005	-1.9	0.019	-2.27	0.016
1420801_at	neuronal PAS domain protein 1	Npas1	1.01	0.567	1.16	0.730	-1.1	0.423	-1.23	0.355	-2.26	0.045
1440762_at	synapsin II	Syn2	1.98	0.573	1.61	0.963	-1.14	0.817	1.39	0.097	-2.26	0.048
1440209_at	membrane-associated ring finger (C3HC4) 1	1-Mar	1.32	0.360	1.06	0.646	-1.08	0.674	1.54	0.488	-2.25	0.011
1458452_at	ankyrin repeat domain 11	Ankrd11	-1.08	0.604	-1.59	0.081	-1.45	0.022	-1.22	0.261	-2.25	0.012
1446227_at	G protein-coupled receptor 180	Gpr180	1.47	0.904	1.43	0.754	2.39	0.126	-1.04	0.601	-2.25	0.029
1440568_at	protection of telomeres 1	Pot1	2.27	0.170	1.69	0.589	1.45	0.684	-1.31	0.331	-2.25	0.005
1445866_at	microtubule associated serine/threonine kinase family member 4	Mast4	1.02	0.901	-1.14	0.275	-1.68	0.046	-1.24	0.167	-2.24	0.007
1434571_at	vacuolar protein sorting 13B	Vps13b /// LOC66	-1.03	0.556	-2.27	0.040	-1.87	0.009	-2.07	0.001	-2.24	0.019
1442623_at	LysM, putative peptidoglycan-binding, domain containing 4	Lysmd4	1.22	0.924	-1.19	0.339	1.04	0.673	1.71	0.728	-2.23	0.009
1438433_at	WAS protein homology region 2 domain containing 1	Whdc1	1.36	0.675	2.3	0.461	2.53	0.513	-1.06	0.512	-2.23	0.028
1459998_at	zinc finger protein 407	Zfp407	1.05	0.681	-3.13	0.001	-1.74	0.002	-2.18	0.004	-2.23	0.012
1417574_at	chemokine (C-X-C motif) ligand 12	Cxcl12	-1.29	0.129	-1.64	0.093	-1.06	0.689	-1.14	0.712	-2.22	0.044
1452251_at	neurobeachin	Nbea	-1.44	0.152	-2.77	0.058	-1.57	0.024	-1.65	0.017	-2.22	0.014
1446240_at	Kinesin 2	Kns2	1.52	0.956	1.11	0.624	-1.37	0.296	1.85	0.889	-2.21	0.017
1453116_at	zinc finger protein 689	Zfp689	1.54	0.040	1.33	0.254	-1.27	0.404	1.14	0.773	-2.21	0.031
1430975_at	RIKEN cDNA 8430416G17 gene	8430416G17Rik	1	0.660	-1.71	0.205	1.1	0.883	1.14	0.974	-2.2	0.033
1445821_at	Interleukin 1 receptor accessory protein-like 1	Il1rapl1	2.92	0.565	2.81	0.464	1.54	0.727	2.01	0.642	-2.2	0.018
1437602_at	similar to Hypothetical protein MGC26988	RP23-273O7.4	-1.22	0.363	-1.39	0.387	-1.54	0.017	1.93	0.558	-2.19	0.028
1445416_at	Testis specific gene A14	Tsga14	1.42	0.374	2.48	0.298	1.55	0.540	2.43	0.314	-2.19	0.046
1452343_at	DNA segment, Chr 18, ERATO Doi 653, expressed	D18Ertd653e	1.21	0.888	-1.57	0.124	-1.75	0.006	-2.07	0.045	-2.18	0.002
1452762_at	RIKEN cDNA 8430436O14 gene	8430436O14Rik	-1.6	0.141	-3.44	0.061	-2.18	0.007	-1.79	0.002	-2.17	0.036
1459948_at	Growth hormone receptor	Ghr	2.27	0.314	1.74	0.466	1.14	0.736	1.9	0.889	-2.17	0.046
1419249_at	PFTAIRE protein kinase 1	Pftk1	1.03	0.439	-2.55	0.043	-1.68	0.003	-1.76	0.007	-2.17	0.015
1455204_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-1.07	0.436	-3.71	0.010	-1.77	0.040	-2.02	0.012	-2.17	0.007
1456230_at	RIKEN cDNA 4933422H20 gene	4933422H20Rik	1.44	0.900	1.41	0.789	-1.06	0.620	-1.15	0.163	-2.16	0.003
1441851_x_at	lymphocyte antigen 6 complex, locus G6C	Ly6g6c	2.32	0.431	1.7	0.799	1.67	0.382	1.09	0.883	-2.16	0.033
1425383_a_at	pre B-cell leukemia transcription factor 1 /// region containing RIKEN cDNA	Pbx1 /// LOC67687	-1.12	0.389	-2.01	0.066	-1.32	0.059	-1.62	0.010	-2.16	0.000
1446974_at	phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III	Pip5k3	2.21	0.125	2.35	0.309	1.9	0.395	-2.01	0.097	-2.16	0.002
1423278_at	protein tyrosine phosphatase, receptor type, K	Ptprk	-1.49	0.031	-2.67	0.015	-2.26	0.030	-2.01	0.007	-2.16	0.014
1437788_at	trans-acting transcription factor 6	Sp6	-1.1	0.456	2.43	0.131	1.72	0.193	1.43	0.871	-2.16	0.048
1444062_at	RIKEN cDNA 2900056L01 gene	2900056L01Rik	-1.07	0.354	-2.97	0.136	1.44	0.263	-1.87	0.056	-2.15	0.033
1460006_at	AT motif binding factor 1	Atbf1	-1.14	0.107	-1.9	0.002	-1.76	0.002	-1.99	0.000	-2.15	0.002
1440232_at	similar to KIAA1913 /// similar to KIAA1913	LOC622645 /// LO	-1.04	0.609	1.84	0.069	2.79	0.238	1.17	0.891	-2.15	0.022
1423953_at	CDK5 regulatory subunit associated protein 1-like 1	Cdkal1	-1.2	0.092	-2.66	0.005	-1.95	0.005	-1.74	0.017	-2.14	0.019
1459457_at	calcium/calmodulin-dependent protein kinase II, delta	Camk2d	1.01	0.580	-1.39	0.296	-1.51	0.027	-1.43	0.048	-2.13	0.014
1438301_at	Development and differentiation enhancing	Ddef1	1.23	0.350	1.17	0.994	-1.95	0.077	-1.33	0.173	-2.13	0.034

1456220_at	F-box and leucine-rich repeat protein 7	Fbxl7	1	0.539	-6.34	0.021	-1.82	0.043	-2.23	0.000	-2.13	0.005
1428643_at	mannoside acetylglucosaminyltransferase 5	Mgat5	-1.35	0.080	-2.8	0.007	-1.41	0.061	-1.57	0.005	-2.13	0.025
1440489_at	BTB (POZ) domain containing 4	Btbd4	1.34	0.939	1.22	0.932	1.07	0.963	-1.2	0.196	-2.12	0.037
1426412_at	neurogenic differentiation 1	Neurod1	2.23	0.471	3.34	0.006	-2.09	0.004	1.26	0.839	-2.11	0.049
1449520_at	tetratricopeptide repeat domain 28	Ttc28	-1.28	0.065	-2.61	0.020	-1.74	0.010	-1.92	0.002	-2.11	0.036
1448765_at	Fyn proto-oncogene	Fyn	-1.15	0.180	-2.22	0.004	-1.66	0.007	-1.92	0.000	-2.1	0.002
1447651_x_at	mitochondrial ribosomal protein L30 /// similar to mitochondrial ribosomal p	Mrpl30 /// LOC621	1.02	0.693	1.33	0.591	-1.11	0.725	1.2	0.175	-2.1	0.047
1426994_at	PH domain and leucine rich repeat protein phosphatase	Phlpp	1.01	0.795	-2.06	0.019	-1.62	0.001	-1.88	0.000	-2.1	0.001
1447135_at	Protein tyrosine phosphatase, receptor type, T	Ptprt	-1.25	0.338	1.17	0.807	-1.32	0.522	-1.19	0.314	-2.1	0.027
1452014_a_at	insulin-like growth factor 1	Igf1	1.45	0.482	1.53	0.793	1.33	0.411	-1.05	0.765	-2.09	0.036
1456997_at	Nuclear receptor coactivator 5	Ncoa5	1.11	0.697	-1.08	0.362	1.2	0.403	1.45	0.277	-2.09	0.003
1451497_at	casein kinase 1, alpha 1	Csnk1a1	-1.12	0.304	1.5	0.269	1.68	0.863	-1.08	0.420	-2.08	0.017
1417901_a_at	islet cell autoantigen 1	Ica1	1.23	0.591	-1.72	0.121	1.6	0.605	1.43	0.906	-2.08	0.045
1436356_at	lectin, galactose binding, soluble 7	Lgals7	1.06	0.633	-1.74	0.003	-1.83	0.004	-1.72	0.001	-2.08	0.013
1453905_at	RIKEN cDNA 5033415L01 gene	5033415L01Rik	1.09	0.780	-1.34	0.303	-1.18	0.164	-1.12	0.342	-2.07	0.034
1440542_at	RIKEN cDNA 7420416P09 gene	7420416P09Rik	1.83	0.131	1.23	0.153	1.1	0.901	3.26	0.011	-2.07	0.018
1440990_at	cDNA sequence BC056349	BC056349	-1.84	0.199	-4.12	0.094	-1.94	0.002	-2.52	0.009	-2.07	0.013
1451648_a_at	folate receptor 2 (fetal)	Folr2	1.19	0.968	1.32	0.107	-1.18	0.517	-1.21	0.397	-2.07	0.014
1450823_at	OG9 homeobox gene	Og9x	-1.43	0.459	1.07	0.596	-2.45	0.000	1.71	0.919	-2.07	0.022
1424221_at	sushi domain containing 4	Susd4	1.21	0.738	-1.04	0.884	-1.36	0.199	2.29	0.192	-2.07	0.012
1438451_at	Rho GTPase-activating protein	Grit	-1.11	0.393	-2.11	0.035	-1.54	0.034	-1.78	0.004	-2.06	0.013
1434804_at	SEC15-like 2 (S. cerevisiae)	Sec15l2	-1.23	0.223	-3.11	0.051	-1.76	0.009	-1.92	0.002	-2.06	0.002
1436513_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	Tanc2	-1.2	0.128	-5.67	0.022	-1.44	0.082	-1.61	0.098	-2.06	0.005
1446426_at	Enabled homolog (Drosophila)	Enah	1.19	0.330	-1.17	0.231	-1.34	0.149	-1.14	0.249	-2.05	0.013
1454593_at	FYVE, RhoGEF and PH domain containing 3	Fgd3	-1.17	0.487	-1.18	0.407	1.86	0.184	1.17	0.975	-2.05	0.029
1453583_at	zinc finger, ZZ-type with EF hand domain 1	Zzef1	-1.22	0.282	-1.33	0.313	-1.37	0.066	-1.67	0.001	-2.05	0.028
1432308_at	RIKEN cDNA 1700058C13 gene	1700058C13Rik	-1.15	0.192	1.54	0.794	1.81	0.437	1.43	0.563	-2.04	0.006
1440993_at	Expressed sequence AW111846	AW111846	-1.2	0.406	-1.58	0.274	1.08	0.009	-1.01	0.792	-2.04	0.046
1445900_at	Kalirin, RhoGEF kinase	Kalrn	1.11	0.422	1.07	0.876	-1.06	0.518	-1.7	0.007	-2.04	0.024
1451893_s_at	membrane associated guanylate kinase, WW and PDZ domain containing	Magi1	-1.72	0.219	-4.1	0.103	-1.16	0.197	-2.92	0.005	-2.04	0.005
1424588_at	SLIT-ROBO Rho GTPase activating protein 3	Srgap3	-1.21	0.287	-3.26	0.022	-1.62	0.011	-1.92	0.002	-2.04	0.022
1434603_at	thyroid hormone receptor associated protein 2	Thrap2	1.03	0.170	-1.49	0.000	-1.55	0.024	-1.64	0.014	-2.04	0.025
1454185_at	RIKEN cDNA 4933436E23 gene	4933436E23Rik	2.24	0.339	1.42	0.311	1.87	0.885	1.37	0.950	-2.03	0.034
1455979_at	AT rich interactive domain 1B (Swi1 like)	Arid1b	-1.36	0.229	-3.04	0.030	-1.49	0.017	-2.25	0.001	-2.03	0.009
1451279_at	ELKS/RAB6-interacting/CAST family member 1	Erc1	-1.21	0.161	-2.67	0.006	-1.54	0.012	-1.96	0.011	-2.03	0.004
1455803_at	solute carrier organic anion transporter family, member 4a1	Slco4a1	-1.16	0.232	1.27	0.638	-1.09	0.614	1.09	0.693	-2.03	0.018
1423776_s_at	TBC1 domain family, member 22a	Tbc1d22a	-1.19	0.292	-2.65	0.057	-1.3	0.138	-1.34	0.012	-2.03	0.001
1441050_at	Striatin, calmodulin binding protein 3	Strn3	1.66	0.400	1.61	0.456	-1.08	0.485	1.23	0.487	-2.02	0.046
1440581_at	RIKEN cDNA A530088H08 gene	A530088H08Rik	-1.92	0.135	-1.75	0.115	3.47	0.139	1.01	0.726	-2.01	0.046
1426605_at	BRCA1/BRCA2-containing complex, subunit 3	Brcc3	-1	0.627	-1.24	0.053	2.04	0.474	-1.02	0.785	-2.01	0.025
1430911_at	DNA segment, Chr 19, ERATO Doi 652, expressed	D19Ertd652e	-1.15	0.751	-1.01	0.490	1.28	0.794	1.51	0.317	-2.01	0.040
1431354_a_at	phenylalanine-tRNA synthetase 2 (mitochondrial)	Fars2	1.04	0.699	-2.29	0.027	-1.51	0.022	-1.48	0.030	-2.01	0.002
1456022_at	homeodomain interacting protein kinase 2	Hipk2	1.01	0.934	-1.81	0.048	-1.76	0.024	-1.99	0.001	-2.01	0.024
1449378_at	keratin 27	Krt27	1.59	0.333	2.39	0.207	-1.42	0.231	1.68	0.390	-2.01	0.048
1434286_at	trichorhinophalangeal syndrome I (human)	Trps1	1.21	0.279	-1.78	0.021	-1.37	0.130	-1.43	0.048	-2.01	0.028
1439211_at	uromodulin-like 1	Umodl1	2.49	0.126	1.89	0.161	-1.13	0.714	1.5	0.590	-2.01	0.028
1443203_at	Zinc finger homeobox 1a	Zfhx1a	1.75	0.386	1	0.743	2.12	0.806	3.08	0.421	-2.01	0.042
1430973_at	zinc finger protein 558	Zfp558	-1.16	0.434	1.07	0.799	1.43	0.995	1.39	0.369	-2.01	0.014
1439129_at	RIKEN cDNA 1110060D06 gene /// dedicator of cytokinesis 5	1110060D06Rik ///	1.14	0.981	-1.62	0.077	-1.36	0.040	-1.61	0.013	-1.99	0.014
1432126_at	RIKEN cDNA 1700072H12 gene	1700072H12Rik	1.32	0.889	1.08	0.449	-1.01	0.775	-1.16	0.529	-1.99	0.049
1429064_at	DIP2 disco-interacting protein 2 homolog C (Drosophila)	Dip2c	-1.44	0.104	-3.12	0.032	-1.41	0.002	-1.55	0.004	-1.99	0.008
1441898_at	RIKEN cDNA E530011F12 gene	E530011F12Rik	1.09	0.981	-1.11	0.662	1.39	0.644	1.06	0.939	-1.99	0.025
1450781_at	high mobility group AT-hook 2	Hmga2	1.1	0.952	-1.72	0.056	-1.85	0.000	-1.66	0.007	-1.99	0.003
1455314_at	LIM domain containing preferred translocation partner in lipoma	Lpp	-1.14	0.045	-1.94	0.001	-1.66	0.004	-1.55	0.000	-1.99	0.009
1459453_at	Roundabout homolog 1 (Drosophila)	Robo1	1.77	0.487	1.71	0.436	-1.02	0.445	-1.03	0.835	-1.99	0.011
1431485_at	RIKEN cDNA 4833447I15 gene	4833447I15Rik	1.49	0.931	-1.54	0.175	-1.13	0.217	1.07	0.930	-1.98	0.012
1432725_at	RIKEN cDNA 4930445G23 gene	4930445G23Rik	-1.06	0.513	-1.11	0.468	1.55	0.495	1.45	0.078	-1.98	0.046
1429284_at	RIKEN cDNA 8430436F23 gene	8430436F23Rik	1.16	0.698	-1.13	0.609	-1.2	0.186	1.8	0.700	-1.98	0.007

1440614_at	Rho GTPase activating protein 23	Arhgap23	-1.03	0.676	1.05	0.917	1.14	0.907	-1.02	0.367	-1.98	0.028
1439757_s_at	Eph receptor A4	Epha4	-1.3	0.342	-1.44	0.263	-1.03	0.566	-1.42	0.117	-1.98	0.013
1436910_at	RAS protein activator like 2	Rasal2	1.04	0.327	-2.91	0.008	-1.78	0.017	-1.88	0.001	-1.98	0.002
1441596_at	RIKEN cDNA 5730601F06 gene	5730601F06Rik	-1.11	0.387	1.78	0.379	1.25	0.775	1.75	0.581	-1.97	0.036
1437640_at	RIKEN cDNA 6430704M03 gene	6430704M03Rik	-1.32	0.300	1.1	0.746	2.53	0.242	1.45	0.947	-1.97	0.036
1455082_at	Casitas B-lineage lymphoma b	Cblb	-1.07	0.213	-1.69	0.007	-1.41	0.018	-1.48	0.044	-1.97	0.041
1435432_at	centaurin, gamma 2	Centg2	-1.23	0.014	-2.53	0.001	-1.91	0.009	-1.57	0.005	-1.97	0.018
1418948_at	fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus pur	Fscn3	-1.85	0.007	-1.07	0.540	1.14	0.612	-1.27	0.089	-1.97	0.040
1419108_at	oligophrenin 1	Ophn1	-1.08	0.508	-1.58	0.032	-1.44	0.080	-1.14	0.238	-1.97	0.031
1447980_s_at	RUN and TBC1 domain containing 2	Rutbc2	-1.43	0.137	-1.33	0.351	1.36	0.493	1.08	0.893	-1.97	0.013
1442019_at	RIKEN cDNA B230343A10 gene	B230343A10Rik	2.28	0.025	1.28	0.290	-2.66	0.046	-1.1	0.739	-1.96	0.038
1452265_at	CLIP associating protein 1	Clasp1	-1.09	0.202	-1.71	0.006	-1.56	0.014	-1.73	0.001	-1.96	0.000
1435954_at	zinc finger protein 710	Zfp710	-1.05	0.697	2.57	0.560	-1.32	0.379	1.45	0.622	-1.96	0.036
1443089_at	RIKEN cDNA 4930506C02 gene	4930506C02Rik	2.21	0.219	2.08	0.210	1.85	0.832	2.5	0.559	-1.95	0.014
1447839_x_at	adrenomedullin	Adm	-1.45	0.226	-2.47	0.068	-1.57	0.012	-1.64	0.000	-1.95	0.008
1444497_at	cDNA sequence BC059050	BC059050	-1.24	0.310	-1.92	0.158	1.34	0.786	-1.26	0.228	-1.95	0.044
1437939_s_at	cathepsin C	Ctsc	1.23	0.601	1.35	0.130	-1.1	0.211	1.33	0.968	-1.95	0.027
1429783_at	PDZ and LIM domain 5	Pdlim5	-1.3	0.170	-1.51	0.040	-1.84	0.005	-1.89	0.000	-1.95	0.046
1421413_a_at	PDZ and LIM domain 5 /// similar to PDZ and LIM domain protein 5 (Enigm	Pdlim5 /// LOC669	12.26	0.588	7	0.464	-1.9	0.034	-1.56	0.045	-1.95	0.040
1434096_at	solute carrier family 4 (anion exchanger), member 4	Slc4a4	1.18	0.982	-2.13	0.057	-1.4	0.075	-1.57	0.011	-1.95	0.008
1440698_at	Unc-5 homolog C (C. elegans)	Unc5c	-1.44	0.145	-1.71	0.170	-1.27	0.125	-1.09	0.722	-1.95	0.004
1459722_at	Zinc finger, SWIM domain containing 6	Zswim6	-1.26	0.337	-1.27	0.300	1.13	0.493	-1.23	0.004	-1.95	0.011
1452366_at	RIKEN cDNA 4732435N03 gene	4732435N03Rik	-1.29	0.286	-2.82	0.035	-1.64	0.017	-1.55	0.003	-1.94	0.000
1454486_at	RIKEN cDNA 9530002O20 gene	9530002O20Rik	1.31	0.784	-1.16	0.414	1.19	0.630	-1.13	0.291	-1.94	0.014
1430316_at	RIKEN cDNA 4930579E17 gene	4930579E17Rik	-1.23	0.145	-4.72	0.003	-1.17	0.251	-1.26	0.065	-1.93	0.001
1428083_at	RIKEN cDNA 2310043N10 gene	2310043N10Rik	-1.05	0.461	-1.81	0.049	-1.28	0.151	-1.42	0.178	-1.92	0.023
1456870_at	RIKEN cDNA A430107D22 gene	A430107D22Rik	1.35	0.692	1.27	0.488	1.08	0.944	2.48	0.516	-1.92	0.030
1444641_at	Adenylate cyclase 3	Adcy3	2	0.379	2.25	0.990	1.13	0.815	-1.19	0.078	-1.92	0.013
1441653_at	RIKEN cDNA D030022P06 gene	D030022P06Rik	1.36	0.697	1.18	0.886	1.58	0.176	1.39	0.689	-1.92	0.014
1422018_at	human immunodeficiency virus type I enhancer binding protein 2	Hivep2	1.23	0.748	-1.12	0.303	-1.39	0.018	-1.44	0.025	-1.92	0.000
1451908_a_at	SEC14-like 1 (S. cerevisiae)	Sec14l1	-1	0.584	-1.09	0.434	1.43	0.802	1.04	0.952	-1.92	0.029
1426435_at	transmembrane protein 135	Tmem135	1.05	0.836	-2.18	0.005	-1.16	0.031	-1.41	0.019	-1.92	0.001
1444652_at	RIKEN cDNA B830004H01 gene	B830004H01Rik	1.88	0.363	1.56	0.097	1.36	0.887	1.93	0.232	-1.91	0.035
1428902_at	carbohydrate sulfotransferase 11	Chst11	-1.24	0.125	-3.04	0.005	-1.85	0.002	-1.71	0.004	-1.91	0.001
1439238_at	unc-84 homolog B (C. elegans)	Unc84b	-1.23	0.324	1.09	0.798	-1.4	0.194	1.28	0.792	-1.91	0.026
1434719_at	alpha-2-macroglobulin /// hypothetical protein LOC677369	A2m /// LOC67736	1.05	0.559	1.13	0.938	1.16	0.604	-1.2	0.223	-1.9	0.024
1429569_a_at	coiled-coil domain containing 46	Ccdc46	1.3	0.953	1.2	0.631	1.17	0.743	-1.36	0.288	-1.9	0.048
1420806_at	fibroblast growth factor 16	Fgf16	-1.03	0.182	2.72	0.756	1.93	0.841	1.35	0.054	-1.9	0.010
1443335_at	PDZ domain containing RING finger 3	Pdzrn3	-1.26	0.324	-1.26	0.249	-1.01	0.764	1.16	0.936	-1.9	0.004
1431110_at	RIKEN cDNA 5430431D22 gene	5430431D22Rik	-1.28	0.197	-4.34	0.012	-1.93	0.004	-1.85	0.023	-1.89	0.015
1445848_at	hypothetical protein 9630009C16	9630009C16	1.47	0.625	1.01	0.462	-1.51	0.183	-1.18	0.414	-1.89	0.034
1444071_at	RIKEN cDNA 9630013A20 gene	9630013A20Rik	1.12	0.580	2.36	0.590	-1.15	0.321	1.42	0.149	-1.89	0.040
1454780_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminylt	Galntl4	-1.13	0.099	-1.97	0.000	-1.73	0.000	-1.49	0.000	-1.89	0.000
1452714_at	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	Tanc1	1.07	0.602	-1.79	0.011	-1.62	0.004	-1.86	0.009	-1.89	0.001
1439033_at	zinc finger, CCHC domain containing 7	Zcchc7	1.41	0.032	-1	0.703	-1.42	0.078	-1.14	0.134	-1.89	0.009
1442226_at	hypothetical protein 6430702L12	6430702L12	1.29	0.734	-1.23	0.202	-1.15	0.231	-1.07	0.414	-1.88	0.024
1444432_at	RIKEN cDNA D330040H18 gene	D330040H18Rik	1.79	0.937	1.49	0.327	1.18	0.736	2.12	0.836	-1.88	0.046
1428647_at	region containing RIKEN cDNA 2310056B04 gene; pre B-cell leukemia tra	LOC676870	1.49	0.973	-1.62	0.142	-1.34	0.114	-1.46	0.027	-1.88	0.043
1434179_at	myeloid/lymphoid or mixed-lineage leukemia 3	Mll3	-1.06	0.375	-2.61	0.014	-1.32	0.046	-1.36	0.017	-1.88	0.009
1455030_at	protein tyrosine phosphatase, receptor type, J	Ptprj	-1.5	0.018	-2.07	0.027	-1.36	0.207	-1.54	0.024	-1.88	0.004
1416966_at	solute carrier family 22 (organic anion transporter), member 8	Slc22a8	2.16	0.087	2.81	0.058	1.68	0.184	-1.16	0.504	-1.88	0.023
1455469_at	solute carrier family 6 (neurotransmitter transporter, L-proline), member 7	Slc6a7	1.05	0.986	1.78	0.359	2.33	0.054	-1.3	0.210	-1.88	0.002
1443531_at	RIKEN cDNA A930005I04 gene	A930005I04Rik	1.14	0.960	1.39	0.789	1.44	0.991	1.52	0.853	-1.87	0.014
1441055_at	paralemmin 2	Palm2	-1.3	0.362	-1.73	0.295	-1.42	0.015	-1.89	0.010	-1.87	0.004
1425724_at	protein tyrosine phosphatase, receptor type, N polypeptide 2	Ptprn2	2.25	0.767	1.58	0.101	-1.14	0.463	1.55	0.733	-1.87	0.044
1434222_at	signal-induced proliferation-associated 1 like 1	Sipa1l1	1.05	0.438	-1.77	0.001	-1.76	0.006	-1.71	0.008	-1.87	0.001
1424934_at	UDP glucuronosyltransferase 2 family, polypeptide B1	Ugt2b1	-2.01	0.090	1.01	0.562	1.42	0.593	1.13	0.699	-1.87	0.046
1454069_at	RIKEN cDNA 9030409C19 gene	9030409C19Rik	3.2	0.624	2.8	0.791	-1.29	0.132	1.27	0.991	-1.86	0.050

1447394_at	chloride channel calcium activated 6 /// expressed sequence AI747448 /// s	Clca6 /// AI747448	-1	0.525	-1.32	0.251	2.64	0.686	-1.13	0.534	-1.86	0.032
1442282_at	Similar to vomeronasal 2, receptor, 2	LOC625068	1.18	0.463	-1.27	0.414	-1.37	0.269	1.54	0.733	-1.86	0.042
1449351_s_at	platelet-derived growth factor, C polypeptide	Pdgfc	1.07	0.742	-1.92	0.015	-1.75	0.012	-1.91	0.007	-1.86	0.000
1447054_at	expressed sequence C85395	C85395	-1.27	0.320	-1.37	0.183	-1.05	0.743	-1.46	0.138	-1.85	0.028
1459098_at	Dystonin	Dst	1.34	0.287	1.34	0.243	-1.27	0.231	-1.11	0.501	-1.85	0.038
1421689_at	keratin associated protein 8-2	Krtap8-2	1.8	0.997	1.95	0.342	1.75	0.605	1.08	0.856	-1.85	0.020
1441264_x_at	RIKEN cDNA A930005H10 gene	A930005H10Rik	2.64	0.005	1.33	0.867	3.65	0.233	1.06	0.882	-1.84	0.041
1446679_at	Glutamate receptor, metabotropic 5	Grm5	1.08	0.588	1.17	0.635	1.16	0.567	-1.21	0.254	-1.84	0.002
1452982_at	insulin-like growth factor I receptor	Igf1r	-1.05	0.553	-2.17	0.008	-1.54	0.002	-1.59	0.020	-1.84	0.022
1438666_at	low density lipoprotein receptor class A domain containing 3	Ldlrad3	-1.09	0.260	-2.56	0.005	-1.18	0.421	-1.59	0.007	-1.84	0.013
1450786_x_at	similar to PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like F	LOC669660	1.02	0.849	-1.74	0.031	-1.77	0.021	-1.76	0.004	-1.84	0.009
1451839_a_at	phosphodiesterase 7A	Pde7a	1.24	0.227	1.3	0.699	-1.21	0.208	-1.11	0.305	-1.84	0.025
1433282_at	RIKEN cDNA 4930529H12 gene	4930529H12Rik	-1.54	0.305	1.05	0.469	2.66	0.108	1.44	0.238	-1.83	0.018
1455136_at	ATPase, Na+/K+ transporting, alpha 2 polypeptide	Atp1a2	-1.27	0.242	1.82	0.589	1.6	0.657	1.9	0.748	-1.83	0.006
1459804_at	CREB binding protein	Crebbp	2.63	0.394	2.59	0.284	-1.91	0.158	-1	0.776	-1.83	0.007
1417590_at	cytochrome P450, family 27, subfamily a, polypeptide 1	Cyp27a1	1.28	0.831	-1.19	0.202	1.76	0.092	1.57	0.009	-1.83	0.030
1430353_at	GLIS family zinc finger 3	Glis3	-1.28	0.287	-2.82	0.062	-1.49	0.008	-1.88	0.020	-1.83	0.000
1437273_at	HtrA serine peptidase 4	Htra4	-1.32	0.165	1.41	0.569	-1.37	0.284	1.03	0.724	-1.83	0.024
1424933_at	myosin VC	Myo5c	-1.2	0.299	1.05	0.949	1.44	0.890	-1.27	0.225	-1.83	0.017
1437069_at	oxysterol binding protein-like 8	Osbpl8	-1.17	0.236	-1.76	0.075	-1.21	0.151	-1.17	0.207	-1.83	0.014
1428822_a_at	sorting nexing 24	Snx24	-1.09	0.370	-1.98	0.016	-1.53	0.043	-1.58	0.015	-1.83	0.000
1434393_at	ubiquitin specific peptidase 34	Usp34	1.57	0.150	1.09	0.548	-1.29	0.011	-1.4	0.014	-1.83	0.015
1435240_at	bromodomain adjacent to zinc finger domain, 2B	Baz2b	-1.06	0.442	-2.05	0.015	-1.06	0.385	-1.57	0.026	-1.82	0.028
1443595_at	CCR4-NOT transcription complex, subunit 6-like	Cnot6l	1.54	0.832	-1.62	0.106	2.6	0.112	1.22	0.716	-1.82	0.035
1435298_at	component of oligomeric golgi complex 5	Cog5	2.41	0.668	1.53	0.839	1.82	0.854	1.07	0.877	-1.82	0.010
1447295_at	Cut-like 1 (Drosophila)	Cutl1	-1.25	0.384	-1.19	0.400	-1.33	0.183	-1.13	0.504	-1.82	0.012
1450420_at	stromal antigen 1	Stag1	3.08	0.736	1.18	0.120	-1.44	0.066	-1.65	0.022	-1.82	0.019
1445558_at	RIKEN cDNA 5930430L01 gene	5930430L01Rik	-1.03	0.502	1.05	0.797	-1	0.889	1.27	0.028	-1.81	0.007
1457470_at	DNA segment, Chr 3, ERATO Doi 452, expressed	D3Ertd452e	-1.13	0.414	-1.18	0.393	-1.51	0.097	-1.48	0.027	-1.81	0.035
1417321_at	DNA segment, Chr 4, Wayne State University 132, expressed	D4Wsu132e	-1.22	0.383	-1.41	0.301	-1.24	0.025	-1.68	0.012	-1.81	0.019
1440111_at	Formin-like 2	Fmnl2	3.19	0.637	4.49	0.483	1.13	0.671	4.05	0.488	-1.81	0.006
1422319_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminylt	Galnt11	1.14	0.939	1.88	0.607	-1.5	0.072	-1.75	0.065	-1.81	0.031
1446053_at	G patch domain and KOW motifs	Gpkow	-1.64	0.014	-1.15	0.250	-1.4	0.056	-1.36	0.232	-1.81	0.005
1441321_at	hypothetical LOC552911	LOC552911	1.17	0.691	1.05	0.494	-1.23	0.215	1.15	0.602	-1.81	0.035
1437636_at	Similar to Interferon-activatable protein 203 (Ifi-203) (Interferon-inducible p	LOC623121	-1.54	0.225	-1.48	0.091	-1.02	0.837	1.71	0.372	-1.81	0.041
1436907_at	neuron navigator 1	Nav1	-1.15	0.110	-2.36	0.006	-1.37	0.019	-1.58	0.000	-1.81	0.002
1418749_at	pleckstrin and Sec7 domain containing 3	Psd3	-1.11	0.309	-2.21	0.043	-1.5	0.008	-1.4	0.051	-1.81	0.001
1427017_at	special AT-rich sequence binding protein 2	Satb2	1.49	0.412	-1.21	0.243	-1.32	0.181	-1.32	0.003	-1.81	0.037
1425906_a_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted,	Sema3e	6.51	0.487	1.79	0.735	-1.23	0.164	-1.38	0.055	-1.81	0.035
1457715_at	RIKEN cDNA 1010001B22 gene	1010001B22Rik	1.02	0.914	2.22	0.479	1.32	0.406	-1.03	0.507	-1.8	0.041
1455276_x_at	RIKEN cDNA 1110004E09 gene	1110004E09Rik	-1.05	0.515	1.25	0.338	1.62	0.431	1.64	0.198	-1.8	0.030
1450879_at	ATPas, class II, type 9B	Atp9b	1.12	0.754	-1.43	0.082	-1.34	0.052	-1.26	0.038	-1.8	0.018
1419320_at	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5	Chst5	-1.1	0.248	1.31	0.677	-1.67	0.110	1.79	0.448	-1.8	0.044
1456067_at	GLI-Kruppel family member GLI3	Gli3	-1.02	0.632	-2.15	0.005	-1.56	0.025	-1.77	0.019	-1.8	0.008
1452344_at	synaptojanin 2	Synj2	-1.19	0.166	-1.11	0.442	-1.49	0.081	-1.25	0.174	-1.8	0.029
1443896_at	TBC1 domain family, member 5	Tbc1d5	-1.07	0.568	-2.53	0.002	-1.67	0.015	-1.32	0.087	-1.8	0.003
1456021_at	activating transcription factor 6	Atf6	1.15	0.680	-1.5	0.046	-1.37	0.013	-1.28	0.133	-1.79	0.005
1455729_at	guanine nucleotide binding protein, alpha q polypeptide	Gnaq	-1.26	0.287	-2.02	0.098	-1.47	0.017	-1.76	0.008	-1.79	0.009
1435229_at	GRAM domain containing 1B	Gramd1b	1.67	0.750	-1.63	0.224	3.21	0.959	1.2	0.465	-1.79	0.047
1442278_at	Jumonji, AT rich interactive domain 1B (Rbp2 like)	Jarid1b	1.33	0.173	1.09	0.959	-1.41	0.167	1.29	0.062	-1.79	0.014
1455260_at	ligand dependent nuclear receptor corepressor-like	Lcorl	-1.28	0.315	-2.02	0.101	-1.09	0.453	-1.39	0.100	-1.79	0.011
1444406_at	Mitogen-activated protein kinase kinase kinase kinase 3	Map4k3	-1.39	0.282	-1.53	0.184	1.24	0.367	1.71	0.841	-1.79	0.003
1420870_at	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (	Mllt10	1.12	0.303	-1	0.933	-1.26	0.070	-1.33	0.017	-1.79	0.002
1452324_at	plasmacytoma variant translocation 1	Pvt1	-1.19	0.408	-1.3	0.382	-1.39	0.067	-1.4	0.015	-1.79	0.004
1452082_at	RIKEN cDNA 6430548M08 gene	6430548M08Rik	1.22	0.791	-1.18	0.331	1.42	0.723	1.26	0.458	-1.78	0.046
1442175_at	RIKEN cDNA C030027H14 gene	C030027H14Rik	-1.31	0.060	-4.62	0.014	-1.48	0.005	-1.6	0.022	-1.78	0.019
1457176_at	GTPase activating RANGAP domain-like 1	Garnl1	1.67	0.040	1.42	0.244	-1.2	0.001	-1.21	0.063	-1.78	0.029
1449542_at	pre B-cell leukemia transcription factor 1	Pbx1	-1.74	0.083	-2.25	0.056	-1.89	0.074	-1.57	0.076	-1.78	0.011

1454900_s_at	pam, highwire, rpm 1	Phr1	-1.13	0.417	-1.97	0.055	-1.37	0.024	-1.64	0.005	-1.78	0.026
1453984_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 2 (p85 beta)	Pik3r2 /// Ifi30	1.83	0.805	2.37	0.583	-1.02	0.553	1.31	0.264	-1.78	0.019
1454345_at	RIKEN cDNA 1700081H04 gene	1700081H04Rik	-1.61	0.280	-1.55	0.188	1.54	0.308	1.37	0.492	-1.77	0.045
1453491_at	RIKEN cDNA 4833409A17 gene	4833409A17Rik	1.22	0.881	1.94	0.328	1.17	0.905	-1.31	0.237	-1.77	0.039
1440163_at	RIKEN cDNA 6030490B17 gene	6030490B17Rik	-1.12	0.131	1.05	0.787	1.08	0.333	1.26	0.339	-1.77	0.014
1425099_a_at	aryl hydrocarbon receptor nuclear translocator-like	Arntl	-1.08	0.412	-1.56	0.015	-1.38	0.020	-1.43	0.010	-1.77	0.007
1438989_s_at	RIKEN cDNA B130021B11 gene	B130021B11Rik	-1.5	0.357	-3.71	0.279	-1.66	0.090	-1.37	0.031	-1.77	0.044
1437765_at	cytoplasmic polyadenylation element binding protein 3	Cpeb3	1.38	0.568	-1.48	0.165	-1.01	0.432	-1.4	0.057	-1.77	0.028
1458226_at	filamin, beta	Flnb	2.27	0.394	2.09	0.658	-1	0.552	-1.21	0.152	-1.77	0.042
1455685_at	microtubule associated monoxygenase, calponin and LIM domain containi	Mical2	1.34	0.833	-1	0.305	-1.59	0.018	-1.61	0.029	-1.77	0.029
1444232_at	protein kinase, cGMP-dependent, type I	Prkg1	-1.62	0.014	-2.34	0.001	-1.58	0.011	-1.35	0.096	-1.77	0.016
1435537_at	protein tyrosine phosphatase, receptor type, D	Ptprd	-1.57	0.115	-1.44	0.139	-1.33	0.330	-1.64	0.111	-1.77	0.029
1434062_at	RAB GTPase activating protein 1-like	Rabgap1l	-1.46	0.191	-1.5	0.185	-1.18	0.522	-1.21	0.283	-1.77	0.041
1451332_at	zinc finger protein 521	Zfp521	-1.06	0.376	-3.24	0.019	-1.62	0.003	-1.37	0.009	-1.77	0.001
1431424_at	RIKEN cDNA 2810055G20 gene	2810055G20Rik	-1.02	0.934	1.22	0.703	1.49	0.732	-1.02	0.896	-1.76	0.049
1453540_at	RIKEN cDNA 5430404G13 gene	5430404G13Rik	-1.18	0.409	-1.4	0.219	-1.1	0.403	-1.22	0.146	-1.76	0.040
1429579_at	RIKEN cDNA 6330407I18 gene	6330407I18Rik	1.37	0.889	-1.46	0.112	-1.4	0.047	-1.28	0.037	-1.76	0.015
1430448_at	RIKEN cDNA 6720418B01 gene	6720418B01Rik	1.1	0.726	-1.16	0.436	1	0.468	-1.11	0.650	-1.76	0.043
1441980_at	RIKEN cDNA C030007I09 gene	C030007I09Rik	-1.15	0.394	-2.11	0.127	-1.33	0.031	-1.38	0.102	-1.76	0.003
1450932_s_at	dedicator of cytokinesis 9 /// similar to Dedicator of cytokinesis protein 9 (C	Dock9 /// LOC670	1.06	0.582	-3.95	0.010	-1.3	0.114	-1.47	0.005	-1.76	0.006
1455989_at	gap junction membrane channel protein alpha 12	Gja12	1.3	0.431	-1.08	0.467	1.19	0.999	-1.2	0.383	-1.76	0.034
1449098_a_at	polymerase (DNA directed), iota	Poli	3.5	0.486	3.63	0.433	1.09	0.501	-1.27	0.341	-1.76	0.015
1423471_at	polypyrimidine tract binding protein 2	Ptbp2	1.03	0.701	-1.04	0.520	-1.41	0.232	-1.24	0.244	-1.76	0.027
1416674_at	protein tyrosine phosphatase, receptor type, U	Ptpru	1.56	0.832	1.6	0.670	1.36	0.459	-1.45	0.087	-1.76	0.015
1418792_at	SH3-domain GRB2-like 2	Sh3gl2	-1.1	0.452	-1.06	0.442	2.12	0.921	-1.04	0.204	-1.76	0.039
1419092_a_at	STE20-like kinase (yeast)	Slk	1.09	0.021	1.55	0.183	1.21	0.565	1.27	0.496	-1.76	0.017
1425290_at	syntaxin 19	Stx19	2.11	0.562	1.29	0.662	-1.27	0.376	1.28	0.573	-1.76	0.034
1423434_at	TEA domain family member 1	Tead1	1.11	0.694	-1.47	0.146	-1.28	0.088	-1.49	0.017	-1.76	0.011
1433795_at	transforming growth factor, beta receptor III	Tgfbr3	1.36	0.587	-2.63	0.151	-1.31	0.119	-1.35	0.127	-1.76	0.030
1456658_at	actin, alpha 2, smooth muscle, aorta	Acta2	2.03	0.590	2.06	0.931	-1.22	0.014	-1.12	0.480	-1.75	0.014
1457506_at	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 1	Als2cr19	-1.02	0.858	1.13	0.487	-1.22	0.234	2.06	0.958	-1.75	0.002
1458724_at	RIKEN cDNA E230008O15 gene	E230008O15Rik	3.77	0.189	3.84	0.129	2.47	0.099	1.17	0.837	-1.75	0.046
1421486_at	early growth response 3	Egr3	-1.42	0.377	2.11	0.539	1.65	0.942	-1.22	0.354	-1.75	0.016
1425252_a_at	mitotic arrest deficient 1-like 1	Mad1l1	1.48	0.971	-2.23	0.048	-1.28	0.088	-1.28	0.202	-1.75	0.011
1425924_at	MyoD family inhibitor	Mdfi	-1.27	0.228	1.06	0.488	1.3	0.776	1.59	0.104	-1.75	0.027
1416980_at	methyltransferase like 7B	Mettl7b	1.84	0.790	1.66	0.755	1.33	0.995	-1.02	0.502	-1.75	0.032
1439467_at	Microtubule-associated protein 4	Mtap4	1.05	0.612	-1.02	0.940	-1.5	0.021	-1.17	0.436	-1.75	0.045
1419189_at	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	Vti1a	2.05	0.554	-1.83	0.137	-1.28	0.324	-1.36	0.139	-1.75	0.008
1436925_at	checkpoint suppressor 1	Ches1	-1.25	0.262	-2.11	0.048	-1.12	0.452	-1.46	0.081	-1.74	0.014
1450063_at	formin 2	Fmn2	-1.57	0.024	-2.47	0.003	-1.77	0.006	-1.48	0.012	-1.74	0.007
1457707_at	gene model 489, (NCBI)	Gm489	1.1	0.900	1.02	0.892	1.56	0.351	-1.1	0.381	-1.74	0.050
1433431_at	pancreatic lipase	Pnlip	-1.12	0.308	1.56	0.730	1.53	0.790	2.29	0.101	-1.74	0.030
1440379_at	solute carrier family 1 (neutral amino acid transporter), member 5	Slc1a5	-1.31	0.359	1.24	0.105	-1.24	0.164	1.01	0.883	-1.74	0.048
1454706_at	UV radiation resistance associated gene	Uvrag	-1.04	0.271	-1.95	0.005	-1.53	0.005	-1.98	0.004	-1.73	0.000
1436302_at	RIKEN cDNA 2410193C02 gene	2410193C02Rik	-1.12	0.236	-2.26	0.003	-1.46	0.015	-1.52	0.001	-1.72	0.010
1437869_at	RIKEN cDNA 3222402P14 gene	3222402P14Rik	-1.12	0.021	-1.88	0.005	-1.29	0.159	-1.14	0.287	-1.72	0.040
1433939_at	hypothetical protein A730046J16	A730046J16	-1.3	0.090	-2.39	0.020	-1.19	0.151	-1.53	0.014	-1.72	0.005
1458238_at	AT rich interactive domain 5B (Mrf1 like)	Arid5b	-1	0.920	2.2	0.817	1.24	0.976	-1.16	0.288	-1.72	0.046
1454958_at	glycogen synthase kinase 3 beta	Gsk3b	1.33	0.417	-1.09	0.447	-1.41	0.025	-1.62	0.001	-1.72	0.001
1456062_at	natriuretic peptide precursor type A	Nppa	-1.07	0.477	-1.07	0.440	2.45	0.031	-1.21	0.388	-1.72	0.046
1439187_at	vacuolar protein sorting 13 D (yeast)	Vps13d	1.26	0.453	-1.27	0.211	-1.59	0.003	-1.59	0.001	-1.72	0.001
1429556_at	RIKEN cDNA 2610024B07 gene	2610024B07Rik	-1.01	0.892	-1.47	0.030	-1.46	0.030	-1.52	0.052	-1.71	0.012
1457672_at	chromodomain helicase DNA binding protein 9	Chd9	-1.09	0.413	-1.51	0.090	-1.5	0.003	-1.32	0.026	-1.71	0.031
1449291_a_at	discoidin, CUB and LCCL domain containing 1	Dcbld1	2.23	0.514	1.75	0.697	-1.1	0.430	-1.17	0.142	-1.71	0.002
1424586_at	EH domain binding protein 1	Ehbp1	-1.19	0.028	-2.61	0.004	-1.37	0.008	-1.44	0.014	-1.71	0.031
1451804_a_at	leucine rich repeat containing 16	Lrrc16	1	0.759	-3.49	0.004	-1.37	0.018	-1.96	0.005	-1.71	0.014
1441823_at	retinoic acid induced 17	Rai17	-1.16	0.427	-1.6	0.214	-1.2	0.221	-1.19	0.282	-1.71	0.028
1457357_at	tousled-like kinase 2 (Arabidopsis)	Tlk2	1.07	0.695	-1.21	0.270	1.11	0.738	1.09	0.654	-1.71	0.011

1440314_at	Thyroid hormone receptor interactor 12	Trip12	-1.22	0.390	-1.2	0.421	-1.31	0.200	-1.28	0.007	-1.71	0.011
1431576_at	RIKEN cDNA 4933404K08 gene	4933404K08Rik	1.44	0.937	-1.75	0.162	1.4	0.794	1.27	0.919	-1.7	0.042
1442063_at	RIKEN cDNA 5930437A14 gene	5930437A14Rik	-1.09	0.220	-1.31	0.157	-1.23	0.181	-1.33	0.029	-1.7	0.008
1437216_at	RIKEN cDNA A430106J12 gene	A430106J12Rik	1.11	0.222	-1.3	0.181	-1.35	0.021	-1.32	0.037	-1.7	0.043
1434264_at	ankyrin 2, brain	Ank2	1.43	0.875	-1.18	0.227	-1.17	0.359	-1.06	0.447	-1.7	0.012
1447272_s_at	ATPase, class V, type 10A	Atp10a	2.18	0.766	-1.82	0.084	-1.33	0.150	-1.31	0.106	-1.7	0.030
1460319_at	fucosyltransferase 8	Fut8	1.29	0.810	-1.67	0.056	-1.32	0.076	-1.26	0.030	-1.7	0.011
1422698_s_at	jumonji, AT rich interactive domain 2	Jarid2	1.11	0.755	-2.04	0.009	-1.58	0.007	-1.64	0.018	-1.7	0.034
1457316_at	microtubule-associated protein 6	Mtap6	-1.19	0.017	-1.58	0.001	-1.47	0.075	-1.37	0.007	-1.7	0.006
1437181_at	pellino 2	Peli2	-1.11	0.129	-2.09	0.005	-1.46	0.002	-1.59	0.002	-1.7	0.006
1429449_at	sterile alpha motif domain containing 4	Samd4	1.3	0.449	-1.28	0.218	-1.71	0.009	-1.48	0.013	-1.7	0.010
1424358_at	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	-1.34	0.163	-2.76	0.034	-1.43	0.014	-1.63	0.000	-1.7	0.001
1447623_s_at	RIKEN cDNA C130009A20 gene	C130009A20Rik	-1.64	0.226	-4.15	0.099	-1.49	0.029	-1.74	0.005	-1.69	0.008
1449558_at	coagulation factor VIII	F8	1.15	0.968	1.05	0.630	1.04	0.684	1.02	0.881	-1.69	0.030
1439688_at	fibulin 1	Fbln1	1.64	0.293	-1.61	0.149	1.24	0.209	-1.41	0.015	-1.69	0.035
1419297_at	histocompatibility 2, O region alpha locus	H2-Oa	-1	0.591	1.13	0.827	-1.01	0.234	1.58	0.508	-1.69	0.015
1427073_at	lactation elevated 1	Lace1	-1.2	0.172	-1.94	0.081	-1.19	0.097	-1.09	0.479	-1.69	0.023
1426759_at	mitogen-activated protein kinase kinase kinase kinase 3 /// similar to mitog	Map4k3 /// LOC67	1.12	0.152	-1.2	0.049	-1.41	0.047	-1.51	0.007	-1.69	0.001
1419599_s_at	membrane-spanning 4-domains, subfamily A, member 11	Ms4a11	1.39	0.425	1.1	0.744	1.52	0.399	-1.02	0.928	-1.69	0.013
1421597_a_at	homeo box, msh-like 3	Msx3	1.02	0.465	1.6	0.957	1.69	0.605	1.25	0.948	-1.69	0.019
1449270_at	plexin domain containing 2	Plxdc2	-1.29	0.125	-1.65	0.033	-1.27	0.207	-1.68	0.062	-1.69	0.046
1452878_at	protein kinase C, epsilon	Prkce	-1.75	0.015	-5.11	0.011	-1.19	0.204	-1.78	0.034	-1.69	0.021
1439635_at	regulator of G-protein signaling 9	Rgs9	1.33	0.886	1.21	0.017	2.39	0.248	-1.14	0.228	-1.69	0.019
1423186_at	T-cell lymphoma invasion and metastasis 2	Tiam2	1.52	0.298	1.06	0.614	-1.28	0.052	-1.45	0.013	-1.69	0.001
1448611_at	WW, C2 and coiled-coil domain containing 2	Wwc2	-1	0.839	-1.42	0.007	-1.31	0.031	-1.63	0.031	-1.69	0.031
1443720_s_at	bone morphogenetic protein receptor, type 1B	Bmpr1b	-1.05	0.476	-1.91	0.100	-1.27	0.122	-1.41	0.213	-1.68	0.014
1441637_at	RIKEN cDNA F730047E07 gene	F730047E07Rik	1	0.660	-1.22	0.258	-1.32	0.138	1.57	0.424	-1.68	0.034
1435461_at	membrane associated guanylate kinase, WW and PDZ domain containing	Magi3	-1.16	0.207	-3.3	0.018	-1.37	0.020	-1.46	0.094	-1.68	0.004
1437735_at	protein phosphatase 1, regulatory (inhibitor) subunit 12A	Ppp1r12a	-1.16	0.388	-1.53	0.127	-1.42	0.038	-1.69	0.015	-1.68	0.006
1435028_at	WD repeat domain 7	Wdr7	-1.17	0.172	-2.29	0.008	-1.39	0.055	-1.49	0.014	-1.68	0.007
1456771_at	zyg-11 homolog B (C. elegans)-like	Zyg11bl	2.09	0.740	2.18	0.538	-1.01	0.470	-1.16	0.776	-1.68	0.001
1454723_at	RIKEN cDNA 1110033M05 gene	1110033M05Rik	1.06	0.927	-1.57	0.007	-1.53	0.004	-1.38	0.011	-1.67	0.003
1430675_at	RIKEN cDNA 2900055J20 gene	2900055J20Rik	-1.55	0.053	-1.74	0.193	1.19	0.426	2.15	0.392	-1.67	0.048
1436143_at	RIKEN cDNA 4933425L03 gene	4933425L03Rik	-1.28	0.050	-1.93	0.063	-1.57	0.004	-1.42	0.024	-1.67	0.025
1434769_at	BTB (POZ) domain containing 9	Btbd9	-1.34	0.267	-2.53	0.139	-1.32	0.049	-1.95	0.022	-1.67	0.034
1427479_at	eukaryotic translation initiation factor 1A /// similar to Eukaryotic translation	Eif1a /// MGC1075	1.87	0.102	1.43	0.639	-1.37	0.062	4.54	0.361	-1.67	0.004
1458039_at	Nuclear receptor coactivator 3	Ncoa3	1.61	0.329	1.07	0.896	1.17	0.727	1.15	0.760	-1.67	0.008
1420558_at	selectin, platelet	Selp	1.03	0.954	1.18	0.626	-1.01	0.308	-1.07	0.828	-1.67	0.025
1434406_at	SLIT-ROBO Rho GTPase activating protein 2	Srgap2	-1.24	0.295	-2.21	0.074	-1.42	0.003	-1.78	0.001	-1.67	0.008
1430853_a_at	RIKEN cDNA 3110045G13 gene	3110045G13Rik	1.37	0.216	1.09	0.674	2.74	0.061	4.23	0.330	-1.66	0.046
1438730_at	cDNA sequence BC028801	BC028801	-1.18	0.257	-3.23	0.032	-1.51	0.152	-1.37	0.056	-1.66	0.040
1450005_x_at	EGF-like-domain, multiple 9	Egfl9	1.06	0.589	1.55	0.474	1.09	0.913	1.15	0.784	-1.66	0.044
1442756_at	Linker of T-cell receptor pathways	Lnk	1.79	0.981	2.22	0.701	-1.38	0.240	1.33	0.270	-1.66	0.017
1441297_at	mucin 6, gastric	Muc6	1.86	0.952	1.17	0.745	-1.57	0.216	1.55	0.475	-1.66	0.025
1460615_at	5'-nucleotidase domain containing 1	Nt5dc1	1	0.918	-1.66	0.006	-1.19	0.023	-1.37	0.023	-1.66	0.014
1435879_at	thymoma viral proto-oncogene 3	Akt3	-1.12	0.272	-2.7	0.030	-1.51	0.004	-1.37	0.010	-1.65	0.005
1435480_at	Braf transforming gene	Braf	-1.02	0.889	-1.46	0.026	-1.22	0.163	-1.2	0.133	-1.65	0.031
1440543_at	RIKEN cDNA D930036F22 gene	D930036F22Rik	-1.08	0.415	-1.18	0.445	1.04	0.707	1.07	0.418	-1.65	0.034
1455244_at	dishevelled associated activator of morphogenesis 1	Daam1	1.25	0.378	-1.32	0.171	-1.37	0.015	-1.65	0.002	-1.65	0.000
1452280_at	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-de	Farp1	1.44	0.705	-1.2	0.200	-1.3	0.019	-1.44	0.000	-1.65	0.000
1457374_at	neural precursor cell expressed, developmentally down-regulated gene 4-l	Nedd4l	-1.07	0.387	-1.8	0.089	-1.13	0.418	-1.04	0.637	-1.65	0.039
1456303_at	PHD finger protein 14	Phf14	-1	0.759	-1	0.954	-1.28	0.034	1.12	0.990	-1.65	0.043
1453286_at	plexin A2	Plxna2	-1.08	0.544	-4.11	0.016	-1.17	0.129	-1.37	0.144	-1.65	0.002
1424704_at	runt related transcription factor 2	Runx2	-1.11	0.370	-1.67	0.017	-1.44	0.001	-1.67	0.007	-1.65	0.016
1439857_at	Ubiquitin specific peptidase 32	Usp32	-1.08	0.467	-1.41	0.285	1.09	0.829	-1.22	0.066	-1.65	0.047
1430878_at	RIKEN cDNA 2210406H18 gene	2210406H18Rik	1.45	0.516	-1.67	0.180	-1.32	0.196	-1.2	0.412	-1.64	0.026
1453015_at	RIKEN cDNA 5830471E12 gene	5830471E12Rik	-1.23	0.336	-1.78	0.137	-1.31	0.008	-1.53	0.001	-1.64	0.020
1460003_at	expressed sequence AI956758	AI956758	1.14	0.990	-1.69	0.081	-1.08	0.455	-1.76	0.116	-1.64	0.028

1434856_at	ankyrin repeat domain 44	Ankrd44	1.15	0.495	-2.6	0.061	1.02	0.616	-1.66	0.011	-1.64	0.041
1426951_at	cysteine rich transmembrane BMP regulator 1 (chordin like)	Crim1	-1.11	0.025	-2.12	0.000	-1.99	0.027	-1.7	0.004	-1.64	0.011
1456667_at	Huntington disease gene homolog	Hdh	-1.07	0.501	-1.27	0.081	-1.43	0.109	-1.36	0.214	-1.64	0.026
1434563_at	ribosomal protein S6 kinase polypeptide 1	Rps6kc1	1	0.828	-1	0.607	-1.14	0.163	-1.54	0.006	-1.64	0.002
1447443_at	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan 2	Spock2	1.89	0.940	1.64	0.835	-1.2	0.311	-1.51	0.172	-1.64	0.040
1450038_s_at	ubiquitin specific peptidase 9, X chromosome	Usp9x	2.99	0.333	1.83	0.437	-1.29	0.102	1.13	0.375	-1.64	0.004
1458142_at	zinc finger, DHHC domain containing 9	Zdhhc9	-1.64	0.061	-1.54	0.086	-1.18	0.069	1.35	0.904	-1.64	0.012
1428493_at	RIKEN cDNA 2610511M17 gene /// similar to signal-induced proliferation-a	2610511M17Rik //	-1.17	0.275	-1.74	0.005	-1.4	0.047	-1.8	0.005	-1.63	0.000
1446244_at	RIKEN cDNA 2810482G21 gene	2810482G21Rik	1.99	0.746	1.8	0.612	2.38	0.077	1.15	0.446	-1.63	0.002
1427016_at	RIKEN cDNA 4932438A13 gene /// similar to CG4841-PA	4932438A13Rik ///	-1.49	0.016	-1.91	0.029	-1.19	0.136	-1.22	0.270	-1.63	0.031
1427043_s_at	cytosolic ovarian carcinoma antigen 1	Cova1	-1.41	0.049	-2.99	0.005	-1.37	0.065	-1.69	0.008	-1.63	0.041
1455827_at	muscleblind-like 2	Mbnl2	1.45	0.445	-1.01	0.501	-1.47	0.012	-1.27	0.001	-1.63	0.019
1418594_a_at	nuclear receptor coactivator 1	Ncoa1	-1.11	0.410	-2.39	0.051	-1.23	0.026	-1.24	0.028	-1.63	0.009
1422894_at	Scm-like with four mbt domains 1	Sfmbt1	2.35	0.082	2.1	0.651	-1.03	0.686	-1.05	0.640	-1.63	0.024
1451055_at	solute carrier family 45, member 2	Slc45a2	-1.21	0.303	1.17	0.725	1.7	0.129	2.13	0.450	-1.63	0.028
1419496_at	solute carrier organic anion transporter family, member 1a6	Slco1a6	2.34	0.752	-1.48	0.167	-1.09	0.413	2.36	0.946	-1.63	0.033
1435065_x_at	Vav2 oncogene	Vav2	1.15	0.992	-1.13	0.453	-1.45	0.079	1.32	0.907	-1.63	0.010
1420328_at	RIKEN cDNA 2210417D09 gene	2210417D09Rik	1.09	0.943	1.07	0.416	-1.14	0.273	-1.09	0.437	-1.62	0.047
1455802_x_at	anterior gradient 2 (Xenopus laevis)	Agr2	1.57	0.671	1.51	0.913	1.33	0.937	1.88	0.214	-1.62	0.040
1457069_at	activating signal cointegrator 1 complex subunit 3	Ascc3	-1.11	0.467	-2.11	0.148	-1.42	0.084	-1.5	0.016	-1.62	0.047
1451440_at	chondrolectin	Chodl	1.38	0.822	1.59	0.528	1.59	0.693	1.38	0.335	-1.62	0.050
1434370_s_at	Fas-associated factor 1	Faf1	3.07	0.347	1.66	0.363	-1.3	0.108	-1.26	0.078	-1.62	0.031
1443185_at	lipoma HMGIC fusion partner-like 2	Lhfpl2	-1.08	0.503	-1.15	0.449	-1.26	0.297	1.31	0.478	-1.62	0.001
1446421_at	Schwannomin interacting protein 1	Schip1	-1.18	0.324	-1.05	0.967	-1.36	0.078	-1.45	0.104	-1.62	0.008
1456153_at	slingshot homolog 2 (Drosophila)	Ssh2	1.21	0.251	-1.46	0.012	-1.3	0.002	-1.26	0.087	-1.62	0.007
1452244_at	RIKEN cDNA 6330406I15 gene	6330406I15Rik	1.2	0.638	1.03	0.731	-1.53	0.068	-1.75	0.010	-1.61	0.006
1443986_at	Vcell division cycle 73, Paf1/RNA polymerase II complex component, hom	Cdc73	1.41	0.545	1.16	0.708	-1.38	0.035	-1.11	0.300	-1.61	0.003
1455164_at	Cdc42 GTPase-activating protein	Cdgap	1.07	0.324	-1.29	0.083	-1.43	0.014	-1.37	0.001	-1.61	0.001
1452291_at	centaurin, delta 1	Centd1	1.18	0.806	1.01	0.711	-1.06	0.513	-1.41	0.042	-1.61	0.015
1457222_at	cAMP responsive element binding protein 5	Creb5	1.32	0.851	1.19	0.645	-1.35	0.152	-1.74	0.038	-1.61	0.027
1452220_at	dedicator of cyto-kinesis 1	Dock1	-1	0.781	-1.98	0.022	-1.39	0.024	-1.36	0.017	-1.61	0.008
1455375_at	similar to Protein enabled homolog (NPC-derived proline-rich protein 1) (N	LOC669787	1.04	0.712	-2.01	0.091	-1.06	0.335	-1.17	0.289	-1.61	0.012
1441316_at	similar to wingless related MMTV integration site 8b	LOC677060	-1.2	0.328	-1.37	0.169	2.19	0.469	2.25	0.864	-1.61	0.049
1432177_a_at	menage a trois 1	Mnat1	1.11	0.613	-1.31	0.082	-1.29	0.024	-1.49	0.022	-1.61	0.003
1440414_at	metal response element binding transcription factor 1	Mtf1	1.99	0.132	1.28	0.095	-1.5	0.078	1.16	0.681	-1.61	0.018
1452788_at	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	Ppp2r5e	3.82	0.240	3.44	0.799	-1.32	0.049	-1.36	0.045	-1.61	0.012
1447610_at	transmembrane protein 34	Tmem34	-1.09	0.408	1.4	0.689	-1.32	0.386	1.41	0.411	-1.61	0.030
1442121_at	cyclic AMP-regulated phosphoprotein, 21	Arpp21	1.37	0.706	2.16	0.068	1.23	0.998	1.54	0.933	-1.6	0.016
1438750_at	Alpha thalassemia/mental retardation syndrome X-linked homolog (human	Atrx	-1.13	0.092	-1.08	0.557	-1.27	0.186	-1.27	0.090	-1.6	0.006
1433643_at	calcium channel, voltage-dependent, alpha2/delta subunit 1	Cacna2d1	1.1	0.731	-1.6	0.041	-1.13	0.065	-1.05	0.559	-1.6	0.003
1441165_s_at	calsyntenin 2	Clstn2	1.52	0.959	1.26	0.935	-1.35	0.320	1.62	0.980	-1.6	0.012
1419538_at	FMS-like tyrosine kinase 3	Flt3	1.31	0.726	-1.62	0.151	-1.67	0.230	1.8	0.913	-1.6	0.028
1436827_at	gene model 944, (NCBI)	Gm944	-1.06	0.498	-2.23	0.038	-1.31	0.053	-1.13	0.320	-1.6	0.007
1434290_at	glycosyltransferase-like domain containing 1	Gtdc1	-1.3	0.199	-2.16	0.048	-1.57	0.046	-1.58	0.107	-1.6	0.005
1421905_at	nuclear receptor coactivator 6 interacting protein	Ncoa6ip	1.41	0.898	2.01	0.621	1.18	0.667	1.16	0.701	-1.6	0.021
1417626_at	phosphodiesterase 4D interacting protein (myomegalin)	Pde4dip	-1.02	0.713	-1.72	0.005	-1.42	0.003	-1.48	0.000	-1.6	0.007
1452209_at	plakophilin 4	Pkp4	-1.24	0.238	-2.01	0.027	-1.41	0.009	-1.6	0.000	-1.6	0.004
1437397_at	prolactin receptor	Prlr	1.64	0.004	1.43	0.313	1.5	0.952	-1.05	0.296	-1.6	0.048
1451041_at	Rho-associated coiled-coil containing protein kinase 2	Rock2	1.25	0.474	-1.39	0.145	-1.5	0.010	-1.27	0.009	-1.6	0.014
1419550_a_at	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	Stk39	-1.1	0.297	-1.94	0.015	-1.43	0.034	-1.44	0.003	-1.6	0.014
1435700_at	talin 2	Tln2	-1.04	0.562	-1.59	0.092	-1.45	0.017	-1.38	0.086	-1.6	0.024
1455764_at	RIKEN cDNA B930007L02 gene	B930007L02Rik	1.73	0.525	1.9	0.291	-1.64	0.104	1.15	0.750	-1.59	0.028
1438045_at	early endosome antigen 1	Eea1	1.27	0.275	-1.34	0.109	-1.29	0.027	-1.24	0.012	-1.59	0.038
1421053_at	kinesin family member 1A	Kif1a	1.73	0.676	1.4	0.909	-1.15	0.255	1	0.839	-1.59	0.020
1434674_at	lysosomal trafficking regulator	Lyst	1.54	0.537	-1.59	0.107	-1.29	0.034	-1.38	0.063	-1.59	0.012
1437158_at	Nipped-B homolog (Drosophila)	Nipbl	-1.15	0.389	-1.57	0.096	-1.33	0.049	-1.32	0.046	-1.59	0.046
1451474_a_at	poly (ADP-ribose) polymerase family, member 8	Parp8	1.15	0.213	-1.22	0.210	-1.55	0.006	-1.53	0.001	-1.59	0.005
1440878_at	runt related transcription factor 1	Runx1	-1.18	0.261	-1.22	0.180	-1.1	0.536	-1.25	0.061	-1.59	0.014

1430797_at	exportin 4	Xpo4	2.2	0.140	2.54	0.014	1.4	0.823	-2.25	0.028	-1.59	0.048
1424602_s_at	X-ray repair complementing defective repair in Chinese hamster cells 4	Xrcc4	-1.26	0.129	-1.9	0.030	-1.35	0.115	-1.22	0.050	-1.59	0.018
1443453_at	zinc finger protein 651	Zfp651	-1.12	0.493	1.43	0.287	-1.04	0.527	-1.2	0.309	-1.59	0.049
1431800_at	RIKEN cDNA 1300010F03 gene	1300010F03Rik	1.6	0.040	-1.09	0.660	2	0.050	1	0.564	-1.58	0.010
1458386_at	RIKEN cDNA C030009J22 gene	C030009J22Rik	-1.23	0.427	-1.47	0.149	2.02	0.830	1.23	0.726	-1.58	0.006
1452413_at	RIKEN cDNA C230081A13 gene	C230081A13Rik	2.41	0.236	1.82	0.931	-1.08	0.397	-1.25	0.117	-1.58	0.034
1445090_at	Glutamate receptor, ionotropic, kainate 2 (beta 2)	Grik2	1.73	0.173	2.68	0.314	2.92	0.251	1.89	0.813	-1.58	0.048
1451023_at	hyperpolarization-activated, cyclic nucleotide-gated K+ 3	Hcn3	1.07	0.749	1.11	0.975	-1.49	0.119	-1.3	0.110	-1.58	0.028
1448050_s_at	mitogen-activated protein kinase kinase kinase kinase 4	Map4k4	-1.34	0.242	-1.59	0.224	-1.2	0.109	-1.25	0.078	-1.58	0.029
1439328_at	nuclear factor of activated T-cells 5	Nfat5	1.35	0.415	1.45	0.567	1	0.556	-1.28	0.081	-1.58	0.006
1435349_at	neuropilin 2	Nrp2	-1.16	0.184	-2.35	0.024	-1.34	0.119	-1.45	0.010	-1.58	0.001
1432592_at	pregnancy-associated plasma protein A	Pappa	-1.12	0.352	-1.62	0.022	-1.72	0.052	-1.34	0.015	-1.58	0.006
1448065_at	protoporphyrinogen oxidase	Ppox	1.14	0.707	1.71	0.997	2.25	0.441	1.3	0.850	-1.58	0.040
1434005_at	RNA binding motif, single stranded interacting protein 1	Rbms1	-1.01	0.888	-1.53	0.001	-1.37	0.002	-1.49	0.003	-1.58	0.005
1448639_a_at	spermatogenesis associated 5	Spata5	-1.23	0.262	-1.19	0.268	-1.35	0.013	-1.46	0.005	-1.58	0.001
1452274_at	zinc finger, AN1-type domain 3	Zfand3	-1.12	0.345	-1.63	0.103	-1.58	0.011	-1.42	0.002	-1.58	0.004
1428220_at	RIKEN cDNA 5730419I09 gene	5730419I09Rik	1.03	0.509	-1.66	0.068	-1.43	0.174	1.55	0.693	-1.57	0.032
1452124_at	ankyrin 3, epithelial /// RIKEN cDNA 2900054D09 gene	Ank3 /// 2900054D	-1.6	0.167	-2.46	0.120	-1.26	0.197	-1.27	0.128	-1.57	0.001
1433642_at	ADP-ribosylation factor-like 15	Arl15	-1.31	0.059	-3.42	0.013	-1.21	0.196	-1.53	0.009	-1.57	0.021
1446730_at	Expressed sequence C79267	C79267	1.37	0.836	1.62	0.583	-1.06	0.449	1.12	0.833	-1.57	0.004
1447084_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1	Nfatc1	-1.41	0.222	-1.52	0.022	-1.25	0.165	1.07	0.952	-1.57	0.031
1419073_at	transmembrane protein with EGF-like and two follistatin-like domains 2	Tmeff2	-1.14	0.194	-2.11	0.017	-1.34	0.023	-1.21	0.080	-1.57	0.001
1437556_at	zinc finger homeodomain 4	Zfhx4	1.16	0.224	-2.53	0.001	-1.04	0.694	-1.44	0.010	-1.57	0.007
1441403_at	RIKEN cDNA 6430501K19 gene	6430501K19Rik	1.08	0.963	-1.02	0.478	1.66	0.110	1.11	0.961	-1.56	0.003
1431995_at	anthrax toxin receptor 1	Antxr1	-1.24	0.275	-1.63	0.060	-1.07	0.494	-1.05	0.690	-1.56	0.047
1447928_at	carbonic anhydrase 5b, mitochondrial	Car5b	1.06	0.615	-2.13	0.062	1.33	0.879	1.11	0.432	-1.56	0.002
1420380_at	chemokine (C-C motif) ligand 2	Ccl2	1.21	0.920	1.13	0.461	-1.34	0.021	-1.14	0.131	-1.56	0.019
1435155_at	cingulin	Cgn	-2.14	0.001	-1.51	0.138	1.05	0.730	-1.11	0.619	-1.56	0.032
1434917_at	cordon-bleu	Cobl	-1.09	0.319	-1.14	0.242	1.09	0.480	-1.28	0.018	-1.56	0.016
1440642_at	RIKEN cDNA D630042P16 gene	D630042P16Rik	3.13	0.433	1.45	0.756	1.16	0.422	1.73	0.157	-1.56	0.045
1454731_at	myosin X	Myo10	1.13	0.553	-1.34	0.164	-1.5	0.018	-1.56	0.039	-1.56	0.015
1440426_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	Nfatc2	2.74	0.124	2.72	0.345	1	0.890	1.38	0.110	-1.56	0.005
1455042_at	Transducin (beta)-like 1 X-linked	Tbl1x	1.36	0.550	-1.02	0.467	-1.37	0.007	-1.38	0.003	-1.56	0.006
1458681_at	Transmembrane 9 superfamily member 3	Tm9sf3	1.19	0.475	-1.1	0.420	1.27	0.895	-1.35	0.115	-1.56	0.043
1455309_at	transmembrane protein 16F	Tmem16f	1.27	0.404	-1.31	0.185	-1.51	0.070	-1.39	0.019	-1.56	0.007
1431869_at	RIKEN cDNA 5730419F03 gene	5730419F03Rik	1.2	0.529	1.76	0.937	2.75	0.009	-1.26	0.164	-1.55	0.011
1448460_at	activin A receptor, type 1	Acvr1	1.31	0.908	1.14	0.453	-1.3	0.043	-1.4	0.003	-1.55	0.001
1427461_at	cDNA sequence BC005561	BC005561	2.2	0.018	2.82	0.269	-1.14	0.631	-1.25	0.341	-1.55	0.027
1450756_s_at	cullin 3	Cul3	3.04	0.568	2.14	0.912	-1.33	0.021	-1.28	0.010	-1.55	0.000
1434754_at	GTPase activating RANGAP domain-like 4	Garnl4	-1.14	0.012	-1.41	0.009	-1.26	0.014	-1.29	0.011	-1.55	0.005
1439153_at	IBR domain containing 2	Ibrdc2	-1.1	0.337	-1.06	0.603	1.4	0.001	1.08	0.730	-1.55	0.008
1453578_at	phosphotriesterase related	Pter	-1.11	0.383	-2.51	0.136	1.04	0.957	-1.1	0.251	-1.55	0.020
1448046_at	Rab9 effector protein with kelch motifs	Rabepk	1.94	0.804	1.67	0.986	1.13	0.833	-1.26	0.181	-1.55	0.042
1443762_s_at	SET binding factor 2	Sbf2	-1.32	0.225	-2.23	0.049	-1.33	0.004	-1.53	0.004	-1.55	0.007
1437197_at	sorbin and SH3 domain containing 2	Sorbs2	1.18	0.863	-1.51	0.145	-1.6	0.006	-1.6	0.027	-1.55	0.007
1452964_at	tubulin tyrosine ligase-like family, member 11	Ttll11	-1.15	0.202	-1.93	0.021	-1.29	0.046	-1.32	0.017	-1.55	0.032
1444717_at	ZW10 interactor	Zwint	1.38	0.732	1.77	0.652	-1.26	0.295	-1.01	0.767	-1.55	0.004
1418403_at	a disintegrin and metallopeptidase domain 19 (meltrin beta)	Adam19	6.69	0.600	3.65	0.560	-1.41	0.006	-1.28	0.023	-1.54	0.010
1439501_at	calcium binding atopy-related autoantigen 1	Cbara1	1.16	0.828	1.27	0.862	-1.18	0.282	-1.05	0.492	-1.54	0.006
1447174_at	Dachshund 1 (Drosophila)	Dach1	-1.16	0.337	1.55	0.892	3.48	0.139	2.15	0.176	-1.54	0.036
1429368_at	leucine-rich repeats and immunoglobulin-like domains 3	Lrig3	1.28	0.232	-1.2	0.261	1.23	0.581	1.17	0.991	-1.54	0.037
1457632_s_at	myeloid ecotropic viral integration site-related gene 1	Mrg1	-1.46	0.281	-3.35	0.131	-1.42	0.028	-1.99	0.015	-1.54	0.006
1439123_at	PHD finger protein 21A	Phf21a	-1.35	0.151	1.08	0.256	2.41	0.163	1.62	0.422	-1.54	0.047
1424089_a_at	transcription factor 4	Tcf4	1.05	0.260	-1.49	0.036	-1.31	0.026	-1.3	0.023	-1.54	0.024
1429607_at	trafficking protein, kinesin binding 2	Trak2	1.37	0.434	1.45	0.885	-1.04	0.582	1.04	0.641	-1.54	0.017
1455709_at	RIKEN cDNA 4930422I22 gene	4930422I22Rik	1.32	0.843	1.33	0.690	-1.57	0.239	-1.75	0.031	-1.53	0.028
1432325_at	RIKEN cDNA 4930502M04 gene	4930502M04Rik	-1.39	0.358	-1.26	0.380	-1.5	0.109	1.1	0.626	-1.53	0.017
1421172_at	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	Adam12	1.01	0.686	-1.48	0.109	-1.38	0.024	-1.23	0.050	-1.53	0.001

1455396_at	ATPase, class I, type 8B, member 1	Atp8b1	1.26	0.705	-1.8	0.073	-1.5	0.002	-1.57	0.012	-1.53	0.025
1427488_a_at	baculoviral IAP repeat-containing 6	Birc6	1.04	0.600	1.03	0.687	-1.1	0.625	-1.49	0.011	-1.53	0.001
1417067_s_at	chaperone, ABC1 activity of bc1 complex like (S. pombe)	Cabc1	1.18	0.584	-1.8	0.232	1.4	0.651	-1.31	0.188	-1.53	0.016
1418659_at	circadian locomoter output cycles kaput	Clock	-1.01	0.769	-1.28	0.024	-1.2	0.137	-1.16	0.160	-1.53	0.032
1422944_a_at	diaphanous homolog 3 (Drosophila)	Diap3	-1.46	0.136	-2.67	0.017	-1.86	0.010	-1.51	0.109	-1.53	0.041
1441630_at	E1A binding protein p400	Ep400	1.29	0.413	1.16	0.821	1.45	0.073	-1.45	0.243	-1.53	0.036
1417568_at	neurocalcin delta	Ncald	-1.05	0.723	1.17	0.555	1.04	0.828	-1.22	0.289	-1.53	0.033
1442603_at	Polybromo 1	Pb1	2.55	0.020	2.99	0.036	-1.33	0.259	-1.11	0.598	-1.53	0.028
1429770_at	protein geranylgeranyltransferase type I, beta subunit	Pggt1b	2.52	0.757	2.93	0.801	1.24	0.256	1.08	0.819	-1.53	0.031
1422673_at	protein kinase C, mu	Prkcm	-1.38	0.174	-2.74	0.022	-1.27	0.036	-1.55	0.003	-1.53	0.045
1450117_at	transcription factor 3	Tcf3	-1.23	0.318	-1.51	0.155	1.03	0.879	-1.41	0.019	-1.53	0.016
1420753_at	tolloid-like	Tll1	1.16	0.742	-1.38	0.149	1.12	0.629	-1.15	0.329	-1.53	0.018
1422932_a_at	vav 1 oncogene	Vav1	2.2	0.126	1.72	0.283	1.05	0.406	2.17	0.737	-1.53	0.048
1443916_at	RIKEN cDNA 2900026A02 gene	2900026A02Rik	-1.31	0.007	-2.11	0.000	-1.07	0.428	-1.05	0.602	-1.52	0.015
1451923_at	RIKEN cDNA 3222401M22 gene	3222401M22Rik	-2.09	0.078	1.12	0.778	-2.72	0.052	-3.08	0.087	-1.52	0.028
1439895_at	expressed sequence AU021025	AU021025	1.26	0.805	1.11	0.944	-1.17	0.351	1.36	0.184	-1.52	0.034
1429330_at	gamma-aminobutyric acid (GABA-A) receptor, subunit alpha 4	Gabra4	1.57	0.945	1.41	0.762	1.57	0.901	1.15	0.743	-1.52	0.047
1433891_at	leucine-rich repeat-containing G protein-coupled receptor 4 /// similar to Le	Lgr4 /// LOC66958	1.15	0.218	-1.34	0.086	-1.08	0.574	-1.17	0.181	-1.52	0.007
1453759_at	NOL1/NOP2/Sun domain family 2	Nsun2	2.12	0.249	2.4	0.153	-1.27	0.344	1.44	0.599	-1.52	0.022
1457465_at	shroom family member 4	Shroom4	-1.04	0.665	-1.26	0.060	-1.34	0.060	-1.9	0.003	-1.52	0.012
1452604_at	serologically defined colon cancer antigen 13	Stard13	1.63	0.499	1.52	0.528	-1.31	0.030	-1.32	0.029	-1.52	0.014
1459770_at	TAO kinase 1	Taok1	-1.04	0.583	1.73	0.362	1.12	0.443	1.86	0.386	-1.52	0.040
1433460_at	tetratricopeptide repeat domain 7B	Ttc7b	1.73	0.492	-1.04	0.307	-1.37	0.006	-1.44	0.002	-1.52	0.024
1437542_at	RIKEN cDNA A730095J18 gene	A730095J18Rik	-1.01	0.715	-2.51	0.023	-1.08	0.350	-1.52	0.008	-1.51	0.043
1446566_at	Adaptor-related protein complex 2, beta 1 subunit	Ap2b1	-1.17	0.464	-1.35	0.363	1.06	0.950	-1.33	0.164	-1.51	0.027
1424842_a_at	Rho GTPase activating protein 24	Arhgap24	1.1	0.360	-1.17	0.214	-1.2	0.129	-1.4	0.017	-1.51	0.033
1436498_at	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Dros	Arih1	1.44	0.410	1.05	0.737	-1.35	0.007	-1.2	0.046	-1.51	0.018
1449709_s_at	arginine-tRNA-protein transferase 1	Ate1	1.07	0.569	-1.22	0.145	-1.29	0.031	-1.33	0.026	-1.51	0.004
1453372_at	DnaJ (Hsp40) homolog, subfamily C, member 1	Dnajc1	1.05	0.384	-1.35	0.013	-1.38	0.031	-1.2	0.010	-1.51	0.009
1442909_at	Potassium voltage-gated channel, subfamily Q, member 4	Kcnq4	1.16	0.741	1.43	0.296	-1.24	0.425	1.41	0.906	-1.51	0.046
1449439_at	Kruppel-like factor 7 (ubiquitous)	Klf7	-1.11	0.187	-1.5	0.041	-1.47	0.008	-1.51	0.026	-1.51	0.046
1452833_at	Rap guanine nucleotide exchange factor (GEF) 2	Rapgef2	1.09	0.423	-1.19	0.211	-1.24	0.029	-1.62	0.000	-1.51	0.011
1457097_at	src family associated phosphoprotein 2	Scap2	-1.37	0.216	-1.41	0.025	-1.06	0.618	-1.1	0.495	-1.51	0.044
1439515_at	SET domain containing 5	Setd5	1.14	0.469	-1.3	0.053	-1.4	0.014	-1.35	0.025	-1.51	0.037
1455493_at	synaptic nuclear envelope 1	Syne1	-1.16	0.375	-2.54	0.079	-1.32	0.039	-1.19	0.136	-1.51	0.018
1418057_at	T-cell lymphoma invasion and metastasis 1	Tiam1	-1.28	0.188	-2.08	0.033	-1.3	0.024	-1.19	0.362	-1.51	0.048
1449431_at	transient receptor potential cation channel, subfamily C, member 6	Trpc6	1.06	0.811	-1.93	0.045	1.69	0.913	-1.35	0.091	-1.51	0.006
1455732_at	RIKEN cDNA 1700025G04 gene	1700025G04Rik	-1.08	0.148	-2.2	0.012	-1.16	0.020	-1.3	0.045	-1.5	0.016
1441059_at	RIKEN cDNA 1700049G17 gene	1700049G17Rik	1.26	0.966	1.24	0.939	-1.32	0.164	-1	0.727	-1.5	0.022
1454878_at	RIKEN cDNA 2310047C04 gene	2310047C04Rik	-1.18	0.410	-1.71	0.159	-1.21	0.003	-1.3	0.119	-1.5	0.040
1429215_at	RIKEN cDNA 2310058N22 gene	2310058N22Rik	1.13	0.876	1.25	0.860	-1.21	0.335	-1.07	0.722	-1.5	0.007
1453174_at	RIKEN cDNA 2310076G13 gene	2310076G13Rik	-1	0.844	-1.51	0.000	-1.27	0.107	-1.27	0.057	-1.5	0.039
1433722_at	A kinase (PRKA) anchor protein 13	Akap13	1.01	0.771	-1.11	0.396	-1.29	0.049	-1.4	0.025	-1.5	0.003
1449244_at	cadherin 2	Cdh2	1	0.807	-1.33	0.020	-1.37	0.040	-1.18	0.146	-1.5	0.002
1445940_at	DNA segment, Chr 4, ERATO Doi 298, expressed	D4Ertd298e	1.16	0.591	-1.25	0.228	2.08	0.161	-1.18	0.395	-1.5	0.038
1425574_at	Eph receptor A3	Epha3	3.47	0.615	-1.13	0.357	-1.69	0.072	1.59	0.463	-1.5	0.038
1448989_a_at	myosin IB	Myo1b	1.07	0.968	-1.39	0.071	-1.29	0.029	-1.34	0.005	-1.5	0.000
1455181_at	RAS p21 protein activator 2	Rasa2	-1.01	0.704	-1.38	0.135	-1.29	0.032	-1.4	0.020	-1.5	0.020
1454293_at	retinoblastoma-like 1 (p107)	Rbl1	-1.25	0.365	1.43	0.950	2.03	0.818	-1.49	0.118	-1.5	0.048
1429111_at	talin 2 /// similar to talin 2	Tln2 /// LOC63921	-1.2	0.033	-1.68	0.002	-1.46	0.005	-1.41	0.006	-1.5	0.005
1420339_at	RIKEN cDNA 0610016J10 gene	0610016J10Rik	-1.04	0.706	-1.54	0.003	-1.39	0.006	-1.18	0.024	-1.49	0.010
1456045_at	RIKEN cDNA 1700106N22 gene	1700106N22Rik	-1.65	0.139	-2.12	0.044	-1.64	0.004	-1.03	0.662	-1.49	0.044
1458376_at	RIKEN cDNA B930025B16 gene	B930025B16Rik	1.05	0.655	1.01	0.972	-1.13	0.246	-1.03	0.679	-1.49	0.013
1460439_at	cDNA sequence BC033915	BC033915	-1.07	0.605	-1.95	0.001	-1.44	0.017	-1.34	0.010	-1.49	0.044
1429273_at	BMP-binding endothelial regulator	Bmper	-1.36	0.087	-2.3	0.047	-1.13	0.124	-1.14	0.297	-1.49	0.038
1444439_at	Bri3 binding protein	Bri3bp	1.34	0.941	1.88	0.580	-1.05	0.206	-1.15	0.659	-1.49	0.004
1423466_at	chemokine (C-C motif) receptor 7	Ccr7	1.12	0.769	-1.23	0.403	-1.62	0.205	-1.32	0.295	-1.49	0.043
1446118_at	DNA segment, Chr 17, ERATO Doi 165, expressed	D17Ertd165e	-1.21	0.619	1.39	0.711	-1.09	0.516	2.41	0.130	-1.49	0.011

1442604_at	excision repair cross-complementing rodent repair deficiency, complement	Ercc6	1.13	0.408	1.46	0.419	1.56	0.255	2.19	0.285	-1.49	0.034
1438700_at	formin binding protein 4	Fnbp4	1.24	0.408	-1.13	0.337	1.48	0.208	1.12	0.220	-1.49	0.038
1453222_at	genetic suppressor element 1	Gse1	6.11	0.725	5.76	0.922	-1.18	0.094	-1.16	0.071	-1.49	0.002
1452449_at	homeobox containing 1	Hmbox1	6.97	0.565	5.84	0.717	-1.2	0.280	-1.15	0.264	-1.49	0.017
1435622_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	Hs3st3a1	1.44	0.732	1.73	0.201	-1.22	0.239	1.32	0.650	-1.49	0.005
1422235_at	5-hydroxytryptamine (serotonin) receptor 7	Htr7	-1.96	0.115	-1.54	0.088	1.53	0.502	1.59	0.839	-1.49	0.042
1444750_at	Restin (Reed-Steinberg cell-expressed intermediate filament-associated pı	Rsn	3.15	0.275	1.56	0.429	1.03	0.745	1.05	0.812	-1.49	0.017
1455353_at	transmembrane and coiled coil domains 1	Tmcc1	1.28	0.054	1.03	0.682	-1.28	0.023	-1.02	0.713	-1.49	0.001
1425043_s_at	RIKEN cDNA 0610037D15 gene	0610037D15Rik	1.08	0.837	1.11	0.947	1.35	0.249	1.16	0.319	-1.48	0.042
1456557_at	RIKEN cDNA 1700041C02 gene	1700041C02Rik	1.21	0.873	1.42	0.987	1.36	0.695	1.28	0.379	-1.48	0.034
1455657_at	RIKEN cDNA 2610207I05 gene	2610207I05Rik	1.04	0.778	1.02	0.741	-1.18	0.118	-1.25	0.130	-1.48	0.028
1456050_at	expressed sequence C80998	C80998	2.52	0.149	1.7	0.503	-1.34	0.176	-1.23	0.122	-1.48	0.018
1422519_at	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	Cask	2.26	0.411	1.22	0.345	-1.25	0.109	-1.29	0.044	-1.48	0.024
1425445_a_at	claudin 18	Cldn18	1.07	0.906	-1.04	0.617	-1.08	0.873	1.3	0.524	-1.48	0.038
1429028_at	dedicator of cytokinesis 11	Dock11	-1.02	0.630	-1.9	0.083	-1.26	0.008	-1.39	0.028	-1.48	0.014
1433491_at	erythrocyte protein band 4.1-like 2	Epb4.1l2	22.4	0.418	14.39	0.732	-1.4	0.005	-1.14	0.175	-1.48	0.027
1420080_a_at	glutamine fructose-6-phosphate transaminase 1	Gfpt1	1.03	0.954	-2.35	0.001	1.53	0.440	-1.07	0.598	-1.48	0.018
1428640_at	heat shock transcription factor 2 binding protein	Hsf2bp	-1.5	0.059	1.51	0.129	1.17	0.837	1.07	0.497	-1.48	0.035
1440582_at	itchy /// RIKEN cDNA 8030492O04 gene	Itch /// 8030492O0	-1.06	0.468	-1.75	0.015	-1.06	0.512	-1.04	0.753	-1.48	0.036
1427212_at	mitogen-activated protein kinase associated protein 1	Mapkap1	1.39	0.788	-1.39	0.111	-1.29	0.016	-1.45	0.003	-1.48	0.007
1435184_at	natriuretic peptide receptor 3	Npr3	-1.17	0.158	-1.96	0.042	-1.23	0.034	-1.09	0.188	-1.48	0.022
1439137_at	solute carrier family 4, sodium bicarbonate cotransporter, member 9	Slc4a9	1.29	0.772	1.02	0.555	1.1	0.551	-1.19	0.582	-1.48	0.041
1445777_at	UPF2 regulator of nonsense transcripts homolog (yeast)	Upf2	2.86	0.465	2.69	0.201	2.13	0.044	-1.37	0.241	-1.48	0.019
1417848_at	zinc finger protein 704	Zfp704	-1.37	0.262	-3.26	0.102	-1.38	0.003	-1.36	0.109	-1.48	0.005
1457592_x_at	RIKEN cDNA 2210018M03 gene	2210018M03Rik	1.25	0.450	1.41	0.735	1.02	0.789	-1.29	0.198	-1.47	0.028
1432925_at	RIKEN cDNA 4933416A02 gene	4933416A02Rik	1.05	0.867	-1.29	0.271	-1.02	0.709	-1.06	0.556	-1.47	0.044
1418332_a_at	ATP/GTP binding protein 1 /// similar to ATP/GTP binding protein 1	Agtpbp1 /// LOC67	-1.18	0.384	-1.27	0.232	1.02	0.934	-1.03	0.831	-1.47	0.040
1431239_at	non-POU-domain-containing, octamer binding protein	Nono	1.32	0.215	1.23	0.140	1.03	0.813	1.22	0.201	-1.47	0.044
1443204_at	RNA binding motif, single stranded interacting protein	Rbms3	1.02	0.375	-1.37	0.274	-1.01	0.592	-1.31	0.264	-1.47	0.044
1434261_at	signal-induced proliferation-associated 1 like 2	Sipa1l2	1.02	0.688	-1.38	0.041	-1.2	0.014	-1.32	0.011	-1.47	0.002
1439302_at	ubiquitin-activating enzyme E1-like 2	Ube1l2	-1.06	0.526	-1.57	0.038	-1.49	0.015	-1.32	0.003	-1.47	0.018
1426977_at	ubiquitin specific peptidase 47	Usp47	1.16	0.321	-1.06	0.572	-1.28	0.025	-1.18	0.026	-1.47	0.017
1459907_a_at	Wolf-Hirschhorn syndrome candidate 1-like 1 (human)	Whsc1l1	-1.11	0.278	-1.36	0.073	-1.16	0.255	-1.35	0.247	-1.47	0.046
1456389_at	zinc finger homeobox 1b	Zfhx1b	1.06	0.363	-1.39	0.029	-1.3	0.015	-1.31	0.075	-1.47	0.022
1438862_at	RIKEN cDNA A630005I04 gene	A630005I04Rik	1.35	0.111	-1.34	0.161	-1.09	0.263	-1.21	0.222	-1.46	0.005
1454763_at	ankyrin repeat domain 17	Ankrd17	1.59	0.304	1.63	0.542	-1.28	0.004	-1.36	0.005	-1.46	0.001
1430820_a_at	bobby sox homolog (Drosophila)	Bbx	-1.27	0.136	-2.12	0.039	-1.43	0.155	-1.17	0.218	-1.46	0.032
1455306_at	cDNA sequence BC037112	BC037112	1.11	0.674	1.18	0.418	-1.06	0.448	-1.23	0.029	-1.46	0.000
1455072_at	centrosomal protein 350	Cep350	1.06	0.133	-1.25	0.005	-1.13	0.185	-1.35	0.023	-1.46	0.008
1421729_a_at	fer (fms/fps related) protein kinase, testis specific 2	Fert2	1.64	0.793	-1.09	0.367	-1.58	0.002	-1.55	0.009	-1.46	0.031
1423271_at	gap junction membrane channel protein beta 2	Gjb2	-1.17	0.069	-1.79	0.017	-1.29	0.089	-1.35	0.003	-1.46	0.013
1449514_at	G protein-coupled receptor kinase 5	Gprk5	1.09	0.933	-1.61	0.085	-1.31	0.074	-1.42	0.023	-1.46	0.008
1460203_at	inositol 1,4,5-triphosphate receptor 1	Itpr1	-1.24	0.068	-2.05	0.011	-1.32	0.029	-1.29	0.030	-1.46	0.037
1452347_at	myocyte enhancer factor 2A	Mef2a	1.53	0.466	1.1	0.619	-1.32	0.082	-1.31	0.010	-1.46	0.030
1426864_a_at	neural cell adhesion molecule 1	Ncam1	-1.26	0.227	-1.87	0.094	-1.34	0.014	-1.23	0.075	-1.46	0.014
1427640_a_at	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	Runx1t1	1.09	0.464	-1.58	0.153	-1.22	0.207	-1.24	0.027	-1.46	0.050
1449405_at	tensin 1	Tns1	-1.04	0.500	-1.32	0.040	-1.53	0.004	-1.42	0.008	-1.46	0.006
1431530_a_at	tetraspanin 5	Tspan5	1.22	0.696	-1.3	0.203	-1.11	0.213	-1.23	0.123	-1.46	0.044
1436088_at	RIKEN cDNA 0910001A06 gene	0910001A06Rik	-1.03	0.577	-1.03	0.599	-1.1	0.555	-1.14	0.200	-1.45	0.001
1428696_at	RIKEN cDNA 2310015N21 gene	2310015N21Rik	-1.2	0.056	-2.17	0.001	-1.14	0.075	-1.35	0.034	-1.45	0.021
1456906_at	RIKEN cDNA 4833432P19 gene	4833432P19Rik	-1.4	0.031	-1.17	0.226	1.25	0.267	1.16	0.448	-1.45	0.016
1432971_at	RIKEN cDNA 4921518B13 gene	4921518B13Rik	1.02	0.953	-1.2	0.331	1.89	0.331	1.18	0.531	-1.45	0.040
1433524_at	expressed sequence AU042671	AU042671	1.61	0.555	1.05	0.543	-1.16	0.167	1.03	0.748	-1.45	0.002
1443782_x_at	cytochrome P450, family 20, subfamily A, polypeptide 1	Cyp20a1	1.33	0.898	-1.03	0.513	-1.07	0.655	1.54	0.306	-1.45	0.014
1420775_at	haloacid dehalogenase-like hydrolase domain	Hdhd1a	-1.6	0.225	1.08	0.573	1.12	0.783	1.07	0.392	-1.45	0.047
1436089_at	integrator complex subunit 6	Ints6	1.16	0.284	1.16	0.547	-1.17	0.100	-1.14	0.209	-1.45	0.036
1453317_a_at	KH domain containing, RNA binding, signal transduction associated 3	Khdrbs3	-1.12	0.055	-1.73	0.007	-1.44	0.002	-1.28	0.011	-1.45	0.000
1440708_at	myosin, heavy polypeptide 9, non-muscle	Myh9	-1.2	0.412	-1.57	0.184	-1.32	0.102	-1.28	0.028	-1.45	0.025

1457765_at	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	Psmd14	1.26	0.133	1.23	0.243	-1.1	0.499	-1.01	0.945	-1.45	0.043
1424188_at	RAB GTPase activating protein 1	Rabgap1	1.18	0.270	1.14	0.433	-1.12	0.122	-1.24	0.005	-1.45	0.001
1431391_at	Ral GEF with PH domain and SH3 binding motif 1	Ralgps1	-1.4	0.102	-1.39	0.228	1.22	0.521	-1.25	0.273	-1.45	0.010
1459627_at	Sterol-C4-methyl oxidase-like	Sc4mol	1.38	0.220	1.49	0.891	1.38	0.554	-1.2	0.611	-1.45	0.008
1423129_at	soc-2 (suppressor of clear) homolog (C. elegans)	Shoc2	1.38	0.397	1.22	0.671	-1.34	0.008	-1.28	0.036	-1.45	0.025
1444089_at	spectrin beta 2	Spnb2	-1.11	0.265	-1.45	0.010	-1.37	0.101	-1.15	0.145	-1.45	0.005
1445109_at	WD repeat domain 4	Wdr4	1.01	0.576	-1.04	0.322	-1.22	0.170	-1.18	0.478	-1.45	0.048
1435091_at	zinc finger protein 568	Zfp568	1.22	0.527	1.13	0.591	-1.22	0.191	-1.27	0.007	-1.45	0.005
1433427_at	RIKEN cDNA 1700111A04 gene	1700111A04Rik	1.56	0.345	1.42	0.089	-1.13	0.351	-1.14	0.434	-1.44	0.028
1454872_at	RIKEN cDNA B230308N11 gene	B230308N11Rik	-1.03	0.583	-1.26	0.110	-1	0.750	1.08	0.928	-1.44	0.019
1434310_at	bone morphogenic protein receptor, type II (serine/threonine kinase)	Bmpr2	-1.04	0.375	-1.49	0.014	-1.25	0.013	-1.18	0.127	-1.44	0.005
1420683_at	BCL2/adenovirus E1B 19kD interacting protein like	Bnipl	1.73	0.195	-1.02	0.896	-1.11	0.508	1.03	0.836	-1.44	0.045
1443083_at	Cleavage and polyadenylation specific factor 2	Cpsf2	1.43	0.682	-1.05	0.546	-1.21	0.332	2.67	0.238	-1.44	0.012
1437119_at	Endoplasmic reticulum (ER) to nucleus signalling 1	Ern1	-1.28	0.252	-1.68	0.148	-1.47	0.011	-1.1	0.276	-1.44	0.001
1455182_at	kinesin family member 1B	Kif1b	1.04	0.350	-1.04	0.774	-1.23	0.034	-1.21	0.083	-1.44	0.003
1436307_at	myosin IXa	Myo9a	-1.08	0.466	-1.67	0.074	-1.14	0.213	-1.1	0.300	-1.44	0.022
1418561_at	splicing factor 3b, subunit 1	Sf3b1	-1.1	0.478	-1.61	0.065	-1.16	0.003	-1.12	0.288	-1.44	0.001
1454894_at	SMAD specific E3 ubiquitin protein ligase 2	Smurf2	1.12	0.422	-1.07	0.536	-1.37	0.000	-1.49	0.004	-1.44	0.002
1433778_at	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	Tnks	2.19	0.337	1.55	0.860	-1.15	0.176	-1.19	0.035	-1.44	0.003
1457662_x_at	thiamine pyrophosphokinase	Tpk1	-1.62	0.031	-1.61	0.116	-1.2	0.264	-1.74	0.064	-1.44	0.039
1450163_a_at	Werner syndrome homolog (human)	Wrn	4.26	0.348	2.08	0.346	-1.13	0.159	-1.03	0.592	-1.44	0.003
1441816_at	RIKEN cDNA 2900056M20 gene	2900056M20Rik	-1.66	0.112	-1.78	0.152	1.65	0.944	-1.12	0.494	-1.43	0.005
1434949_at	armadillo repeat containing 8	Armc8	-1.07	0.545	-1.13	0.217	-1.32	0.005	-1.29	0.048	-1.43	0.034
1434221_at	cDNA sequence BC030863	BC030863	1.68	0.351	1.02	0.505	-1.25	0.018	-1.47	0.003	-1.43	0.015
1437919_at	B double prime 1, subunit of RNA polymerase III transcription initiation fact	Bdp1	2.63	0.708	3.99	0.326	-1.41	0.163	-1.69	0.004	-1.43	0.029
1452321_at	bromodomain and WD repeat domain containing 1	Brwd1	-1	0.904	-1.02	0.601	-1.08	0.440	-1.1	0.295	-1.43	0.038
1459838_s_at	BTB (POZ) domain containing 11	Btbd11	-1.24	0.389	-3.27	0.145	-1.2	0.143	-1.63	0.000	-1.43	0.041
1455287_at	cyclin-dependent kinase 6	Cdk6	-1.14	0.298	-1.85	0.073	-1.2	0.034	-1.26	0.053	-1.43	0.000
1445511_at	centrin 4 /// similar to centrin 4	Cetn4 /// LOC6328	-1.06	0.475	1.32	0.613	-1.23	0.318	1.62	0.746	-1.43	0.047
1452381_at	cAMP responsive element binding protein 3-like 2	Creb3l2	1.01	0.996	-1.42	0.052	-1.22	0.042	-1.2	0.046	-1.43	0.010
1434705_at	C-terminal binding protein 2 /// zinc finger, RAN-binding domain containing	Ctbp2 /// Zranb1	1.12	0.159	-1.13	0.339	-1.44	0.006	-1.68	0.000	-1.43	0.005
1444706_at	RIKEN cDNA E430014L09 gene	E430014L09Rik	1.18	0.846	-1.03	0.542	-1.34	0.269	-1.95	0.047	-1.43	0.049
1427199_at	furry homolog-like (Drosophila)	Fryl	-1.07	0.138	-2.02	0.005	-1.61	0.012	-1.39	0.091	-1.43	0.008
1457849_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminylt	Galnt4	-1.53	0.187	-1	0.429	1.9	0.050	1	0.989	-1.43	0.046
1434935_at	hypothetical protein LOC637741	LOC637741	-1.18	0.402	-1.75	0.184	-1.19	0.007	-1.32	0.001	-1.43	0.000
1434112_at	latrophilin 2	Lphn2	-1.15	0.327	-1.88	0.022	-1.34	0.002	-1.14	0.113	-1.43	0.019
1419386_at	mucin 13, epithelial transmembrane	Muc13	1.36	0.549	1.17	0.609	-1.2	0.352	-1.29	0.318	-1.43	0.036
1448528_at	programmed cell death 10	Pdcd10	-1.08	0.488	-1.04	0.534	-1.34	0.123	-1.2	0.023	-1.43	0.024
1455773_at	Phosphatidylinositol binding clathrin assembly protein	Picalm	1.77	0.154	2.08	0.320	-1.18	0.206	1.06	0.844	-1.43	0.024
1444553_at	Postmeiotic segregation increased 1 (S. cerevisiae)	Pms1	1.27	0.415	1.24	0.319	1.4	0.760	-1.88	0.011	-1.43	0.022
1444884_at	palmitoyl-protein thioesterase 1	Ppt1	-2.14	0.089	-1.4	0.149	1.56	0.515	1.68	0.329	-1.43	0.001
1426550_at	SID1 transmembrane family, member 1	Sidt1	-1.06	0.463	1.1	0.819	1.38	0.278	-1.17	0.464	-1.43	0.010
1434963_at	suppressor of Ty 3 homolog (S. cerevisiae)	Supt3h	2.07	0.747	1.65	0.551	-1.19	0.179	-1.03	0.676	-1.43	0.014
1460735_at	supervillin	Svil	1.1	0.774	-1.41	0.101	-1.25	0.026	-1.36	0.005	-1.43	0.003
1421594_a_at	synaptotagmin-like 2	Sytl2	-1.09	0.141	-2.02	0.004	-1.33	0.004	-1.45	0.027	-1.43	0.026
1419447_s_at	TBC1 domain family, member 1	Tbc1d1	1.17	0.447	-1.26	0.126	-1.31	0.003	-1.5	0.001	-1.43	0.009
1429253_at	zinc finger, MYM-type 4	Zmym4	1.03	0.914	-1.25	0.150	-1.15	0.093	-1.37	0.056	-1.43	0.007
1432094_a_at	RIKEN cDNA 1700034M03 gene	1700034M03Rik	2.05	0.407	1.41	0.911	-1.09	0.307	-1.1	0.360	-1.42	0.010
1441773_at	RIKEN cDNA 1700061N14 gene	1700061N14Rik	1.45	0.808	-1	0.432	1.11	0.964	2.86	0.123	-1.42	0.024
1447459_at	Apoptosis antagonizing transcription factor	Aatf	-1.37	0.315	-1.21	0.427	-1.18	0.286	-1.29	0.351	-1.42	0.032
1454918_at	alkylglycerone phosphate synthase	Agps	1.02	0.854	-1.26	0.007	-1.2	0.172	-1.29	0.072	-1.42	0.003
1443868_at	ATPase type 13A3	Atp13a3	1.62	0.060	1.12	0.501	-1.25	0.421	-1.1	0.419	-1.42	0.031
1434671_at	RIKEN cDNA B230337E12 gene	B230337E12Rik	-1.19	0.308	-1.93	0.024	-1.05	0.719	-1.38	0.097	-1.42	0.027
1457464_at	hypothetical LOC403342	C130015C19	1.52	0.176	1.4	0.208	-1.05	0.530	1.33	0.337	-1.42	0.023
1435005_at	centromere protein E	Cenpe	1.14	0.139	-1.18	0.211	-1.23	0.146	1.02	0.717	-1.42	0.021
1425016_at	Eph receptor B2	Ephb2	1.03	0.961	-1.91	0.017	-1.17	0.262	-1.14	0.298	-1.42	0.027
1428933_at	histone deacetylase 8	Hdac8	1.2	0.707	-1.5	0.082	-1.33	0.024	-1.24	0.221	-1.42	0.042
1455746_at	kinesin family member 13A	Kif13a	1.23	0.061	-1.86	0.020	-1.19	0.008	-1.4	0.003	-1.42	0.033

1427800_at	keratin associated protein 16-2	Krtap16-2	1.14	0.841	-1.22	0.483	-1.79	0.147	-1.22	0.219	-1.42	0.027
1427299_at	ribosomal protein S6 kinase polypeptide 3	Rps6ka3	-1.05	0.287	-1.42	0.011	-1.37	0.010	-1.29	0.039	-1.42	0.005
1459951_at	ribosomal protein S6 kinase, polypeptide 1	Rps6kb1	-1.28	0.320	-1.27	0.351	-1	0.769	-1.16	0.562	-1.42	0.034
1423077_at	sorting nexin 9	Snx9	1.87	0.466	1.3	0.660	-1.34	0.004	-1.18	0.007	-1.42	0.016
1418651_at	spermatogenesis associated 6	Spata6	-1.16	0.207	-1.86	0.032	1.03	0.894	-1.2	0.163	-1.42	0.042
1447411_at	UDP-glucose dehydrogenase	Ugdh	-1.19	0.218	1.06	0.505	1.1	0.889	1.17	0.884	-1.42	0.005
1455407_at	zinc finger protein 236	Zfp236	1.09	0.299	-1.36	0.102	-1.27	0.009	-1.3	0.067	-1.42	0.021
1439216_at	RIKEN cDNA 2900075B16 gene	2900075B16Rik	1.16	0.816	-1.37	0.340	-1.03	0.524	1.51	0.113	-1.41	0.020
1432916_at	RIKEN cDNA 5730407I07 gene	5730407I07Rik	5.57	0.269	3.49	0.250	-1.11	0.529	1.35	0.828	-1.41	0.047
1443752_at	RIKEN cDNA E230008N13 gene	E230008N13Rik	1.75	0.050	2.17	0.342	1.4	0.949	-1.45	0.242	-1.41	0.043
1445266_at	excision repair cross-complementing rodent repair deficiency, complement	Ercc1	1.82	0.544	3.26	0.155	-1.09	0.440	-1.34	0.252	-1.41	0.050
1415757_at	golgi-specific brefeldin A-resistance factor 1	Gbf1	1.48	0.816	1	0.364	-1.25	0.010	-1.21	0.002	-1.41	0.001
1435185_at	leucine rich repeat and coiled-coil domain containing 1	Lrrcc1	2.51	0.498	1.67	0.560	1.42	0.425	-1.45	0.013	-1.41	0.046
1448870_at	latent transforming growth factor beta binding protein 1	Ltbp1	-1.13	0.155	-1.35	0.038	-1.28	0.009	-1.28	0.007	-1.41	0.018
1429911_at	microcephaly, primary autosomal recessive 1	Mcph1	-1.16	0.037	-2.34	0.006	-1.49	0.034	-1.5	0.032	-1.41	0.010
1455179_at	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	Mpp7	1.18	0.815	-2.63	0.004	-1.12	0.402	-1.29	0.110	-1.41	0.010
1438067_at	neurofibromatosis 1	Nf1	-1.09	0.470	-1.29	0.232	-1.44	0.078	-1.31	0.082	-1.41	0.008
1439154_at	nucleoporin 98	Nup98	1.1	0.307	-1.03	0.635	-1.13	0.100	-1.22	0.050	-1.41	0.012
1436780_at	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosa	Ogt	2.54	0.339	1.9	0.682	1.2	0.327	1.11	0.710	-1.41	0.021
1441026_at	poly (ADP-ribose) polymerase family, member 4	Parp4	1.24	0.331	-1.19	0.528	-1.23	0.369	-1.31	0.197	-1.41	0.032
1444422_at	protocadherin 19	Pcdh19	-1.21	0.242	-1.87	0.022	-1.34	0.002	-1.26	0.078	-1.41	0.006
1428725_at	protein inhibitor of activated STAT 2	Pias2	-1.14	0.412	-1.52	0.123	-1.15	0.137	-1.14	0.096	-1.41	0.002
1459903_at	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (s	Sema7a	-1.21	0.128	-1.85	0.049	-1.35	0.013	-1.38	0.018	-1.41	0.005
1457778_at	storkhead box 2	Stox2	1.5	0.464	1.39	0.622	-1.15	0.093	-1.14	0.118	-1.41	0.046
1449821_a_at	RIKEN cDNA 0610016J10 gene /// hypothetical LOC619602	0610016J10Rik ///	1.17	0.587	-1.14	0.284	-1.2	0.024	-1.19	0.021	-1.4	0.014
1458963_at	RIKEN cDNA 1810054D07 gene	1810054D07Rik	1.04	0.788	-1.12	0.356	-1.19	0.018	-1.33	0.012	-1.4	0.006
1434817_s_at	RIKEN cDNA 4930535B03 gene	4930535B03Rik	-1.06	0.231	-1.16	0.240	-1.03	0.726	-1.31	0.119	-1.4	0.045
1427980_at	RIKEN cDNA 4933407C03 gene	4933407C03Rik	1.3	0.240	-1.06	0.740	-1.37	0.002	-1.44	0.019	-1.4	0.001
1419758_at	ATP-binding cassette, sub-family B (MDR/TAP), member 1A	Abcb1a	1.52	0.187	1.33	0.750	1.49	0.621	1.88	0.356	-1.4	0.011
1454916_s_at	ADP-ribosylation factor interacting protein 1	Arfip1	1.01	0.891	-1.38	0.004	-1.19	0.078	-1.22	0.002	-1.4	0.022
1456257_at	RIKEN cDNA C130065N10 gene	C130065N10Rik	1.14	0.362	1.12	0.661	-1.42	0.031	-1.06	0.299	-1.4	0.034
1447156_at	Choroidermia	Chm	2.49	0.149	1.37	0.965	1	0.608	1.5	0.544	-1.4	0.003
1428563_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	Ddx10	1.08	0.830	-1.2	0.178	-1.1	0.290	-1.08	0.215	-1.4	0.001
1451530_at	epidermal growth factor receptor	Egfr	1.42	0.610	1.02	0.413	-1.22	0.165	-1.28	0.095	-1.4	0.047
1442116_at	G protein-coupled receptor 176	Gpr176	-1.15	0.045	-1.59	0.001	-1.22	0.062	-1.18	0.068	-1.4	0.020
1426491_at	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and F	Herc2	-1.13	0.065	-1.32	0.050	-1.25	0.001	-1.3	0.054	-1.4	0.006
1435139_at	NMDA receptor-regulated gene 1	Narg1	1	0.997	-1.16	0.062	-1.31	0.024	-1.15	0.275	-1.4	0.027
1438684_at	NUAK family, SNF1-like kinase, 1	Nuak1	-1.22	0.248	-1.41	0.152	-1.3	0.006	-1.32	0.030	-1.4	0.010
1416891_at	numb gene homolog (Drosophila)	Numb	-1.01	0.740	-1.39	0.011	-1.2	0.050	-1.41	0.008	-1.4	0.002
1428484_at	oxysterol binding protein-like 3	Osbpl3	-1.03	0.297	-1.59	0.026	-1.28	0.005	-1.25	0.078	-1.4	0.000
1417148_at	platelet derived growth factor receptor, beta polypeptide	Pdgfrb	1.19	0.743	1.01	0.722	-1.27	0.041	-1.14	0.230	-1.4	0.001
1449799_s_at	plakophilin 2	Pkp2	-1.15	0.378	-1.67	0.092	-1.28	0.054	-1.4	0.000	-1.4	0.002
1426047_a_at	protein tyrosine phosphatase, receptor type, R	Ptprr	1.22	0.402	1.4	0.522	1.41	0.713	1.59	0.788	-1.4	0.027
1448689_at	related RAS viral (r-ras) oncogene homolog 2	Rras2	1.06	0.308	-1.18	0.079	-1.24	0.005	-1.24	0.007	-1.4	0.002
1449815_a_at	single-stranded DNA binding protein 2	Ssbp2	-1.2	0.017	-2.62	0.010	-1.42	0.033	-1.2	0.086	-1.4	0.001
1428546_at	synaptotagmin binding, cytoplasmic RNA interacting protein	Syncrip	-1.1	0.384	-1.3	0.090	-1.21	0.031	-1.27	0.053	-1.4	0.004
1459666_at	trafficking protein, kinesin binding 1	Trak1	-1.26	0.096	-1.4	0.005	-1.36	0.020	-1.22	0.046	-1.4	0.044
1433676_at	WNK lysine deficient protein kinase 1	Wnk1	-1.02	0.347	-1.37	0.002	-1.26	0.017	-1.3	0.016	-1.4	0.001
1433653_at	cDNA sequence BC029169	BC029169	1.14	0.690	-1.26	0.172	-1.17	0.117	-1	0.861	-1.39	0.033
1418071_s_at	chromodomain protein, Y chromosome-like	Cdyl	-1.05	0.426	-1.37	0.034	-1.27	0.080	-1.39	0.004	-1.39	0.022
1459005_at	RIKEN cDNA D030051N19 gene	D030051N19Rik	-1.14	0.377	-1.28	0.369	-1.56	0.029	-1.16	0.356	-1.39	0.010
1448665_at	dystrophin, muscular dystrophy	Dmd	-1.02	0.519	-1.49	0.028	-1.33	0.015	-1.45	0.039	-1.39	0.019
1452718_at	E3 ubiquitin protein ligase, HECT domain containing, 1	Edd1	-1.05	0.481	-1.13	0.125	-1.26	0.021	-1.29	0.021	-1.39	0.006
1455257_at	integrin beta 3	Itgb3	-1.26	0.246	-2.22	0.121	-1.24	0.077	-1.13	0.081	-1.39	0.002
1434194_at	microtubule-associated protein 2	Mtap2	1.05	0.869	-1.37	0.250	-1.05	0.551	1.25	0.243	-1.39	0.043
1454824_s_at	mitochondrial tumor suppressor 1	Mtus1	1.65	0.248	1.22	0.624	-1.29	0.197	-1.34	0.054	-1.39	0.010
1447640_s_at	pre B-cell leukemia transcription factor 3	Pbx3	-1.17	0.432	-2.01	0.182	-1.28	0.004	-1.48	0.009	-1.39	0.029
1419716_a_at	POU domain, class 2, transcription factor 1	Pou2f1	1.84	0.732	1.6	0.751	-1.16	0.410	-1	0.823	-1.39	0.042

1424632_a_at	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like (S. cerev	Rev3l	-1.15	0.441	-1.88	0.143	-1.05	0.584	-1.03	0.600	-1.39	0.021
1449865_at	sema domain, immunoglobulin domain (Ig), short basic domain, secreted,	Sema3a	1.23	0.725	-1.53	0.043	-1.23	0.081	-1.17	0.076	-1.39	0.047
1418755_at	T-box 15	Tbx15	-1.06	0.513	-1.1	0.253	1.15	0.548	-1.23	0.024	-1.39	0.033
1416487_a_at	yes-associated protein 1	Yap1	1.29	0.502	1.03	0.746	-1.42	0.009	-1.26	0.028	-1.39	0.035
1430154_at	RIKEN cDNA 4930543C13 gene	4930543C13Rik	-1.28	0.126	-1.3	0.100	-1.16	0.189	-1.11	0.500	-1.38	0.003
1457513_at	RIKEN cDNA 6330569M22 gene	6330569M22Rik	1.82	0.704	1.82	0.453	-1.1	0.413	1.16	0.122	-1.38	0.002
1434335_at	expressed sequence AI317237	AI317237	-1.17	0.067	-1.64	0.024	-1.18	0.003	-1.5	0.018	-1.38	0.003
1451159_at	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	1.47	0.419	1.01	0.617	-1.1	0.322	-1.27	0.014	-1.38	0.004
1446326_at	procollagen, type I, alpha 2	Col1a2	-1.2	0.315	-1.99	0.141	1.09	0.749	1.14	0.533	-1.38	0.005
1417960_at	cytoplasmic polyadenylation element binding protein 1	Cpeb1	1.56	0.558	1.12	0.517	-1.1	0.135	-1.18	0.140	-1.38	0.006
1427318_s_at	dysferlin /// fer-1-like 3, myoferlin (C. elegans)	Dysf /// Fer1l3	1.89	0.421	1.47	0.857	-1.15	0.061	-1.15	0.030	-1.38	0.002
1435362_at	forkhead box J3	Foxj3	-1.09	0.413	1.02	0.787	-1.19	0.054	-1.12	0.337	-1.38	0.045
1455078_at	Heat shock protein 90kDa alpha (cytosolic), class A member 1	Hsp90aa1	1.04	0.800	-1.61	0.011	-1.37	0.008	-1.54	0.017	-1.38	0.016
1419053_at	peroxisomal biogenesis factor 14	Pex14	-1	0.770	-1.59	0.035	-1.13	0.263	-1.4	0.001	-1.38	0.048
1459209_at	Ring finger protein 10	Rnf10	1.22	0.664	1.86	0.613	1.03	0.573	1.01	0.589	-1.38	0.013
1419181_at	zinc finger protein 326	Zfp326	-1.09	0.387	-1.12	0.105	-1.05	0.369	-1.31	0.023	-1.38	0.044
1447947_at	zinc finger, FYVE domain containing 16	Zfyve16	1.24	0.094	1.23	0.174	1.1	0.523	-1.13	0.250	-1.38	0.021
1417361_at	ankyrin repeat and SOCS box-containing protein 3	Asb3	1.21	0.588	-1.48	0.104	-1.16	0.085	-1.25	0.108	-1.37	0.042
1436031_at	cache domain containing 1	Cachd1	-1.26	0.126	-2.63	0.036	-1.18	0.118	-1.13	0.307	-1.37	0.035
1455440_at	chloride channel 6	Clcn6	1.02	0.952	-1.26	0.012	-1.29	0.025	-1.2	0.188	-1.37	0.013
1422887_a_at	C-terminal binding protein 2	Ctbp2	1.03	0.459	-1.22	0.068	-1.39	0.009	-1.46	0.000	-1.37	0.012
1437448_s_at	catenin (cadherin associated protein), delta 1	Ctnnd1	1.27	0.658	1.06	0.757	-1.16	0.306	-1.28	0.004	-1.37	0.004
1438658_a_at	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	Edg3	-1.43	0.285	-2	0.181	-1.31	0.006	-1.29	0.020	-1.37	0.015
1424986_s_at	F-box and WD-40 domain protein 7, archipelago homolog (Drosophila)	Fbxw7	-1.07	0.439	1.09	0.930	1.03	0.957	-1.11	0.407	-1.37	0.035
1451264_at	FERM domain containing 6	Frmd6	1.16	0.580	-1.06	0.583	-1.31	0.016	-1.28	0.014	-1.37	0.002
1425942_a_at	glycoprotein m6b	Gpm6b	3.55	0.039	2.88	0.316	-1.2	0.376	-1.09	0.912	-1.37	0.025
1437103_at	insulin-like growth factor 2 mRNA binding protein 2	Igf2bp2	1.01	0.898	-1.27	0.042	-1.26	0.003	-1.25	0.001	-1.37	0.009
1454862_at	pleckstrin homology-like domain, family B, member 2	Phldb2	-1.06	0.576	-1.35	0.115	-1.23	0.048	-1.37	0.008	-1.37	0.011
1449404_at	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	Pip5k2a	-1.2	0.260	-2.02	0.055	-1.26	0.008	-1.34	0.003	-1.37	0.006
1439797_at	peroxisome proliferator activator receptor delta	Ppard	-1.14	0.224	-1.14	0.164	1.2	0.307	-1.11	0.187	-1.37	0.008
1452056_s_at	protein phosphatase 3, catalytic subunit, alpha isoform	Ppp3ca	-1.21	0.023	-2.15	0.008	-1.25	0.127	-1.46	0.006	-1.37	0.001
1418036_at	DNA primase, p58 subunit	Prim2	1.02	0.738	-1.47	0.005	-1.1	0.249	-1.22	0.042	-1.37	0.005
1420885_a_at	seizure related gene 6	Sez6	1.73	0.950	1.73	0.434	1.32	0.109	1.22	0.059	-1.37	0.026
1452373_at	RIKEN cDNA 1700081L11 gene	1700081L11Rik	1.79	0.433	2.12	0.414	-1.03	0.574	-1.14	0.094	-1.36	0.003
1429475_at	RIKEN cDNA 2810457I06 gene	2810457I06Rik	1.31	0.051	-1.43	0.106	-1.34	0.165	-1.3	0.095	-1.36	0.007
1428691_at	RIKEN cDNA 5630401D06 gene	5630401D06Rik	-1	0.828	-1.14	0.200	-1.23	0.007	-1.07	0.168	-1.36	0.044
1428829_at	RIKEN cDNA 6820401H01 gene	6820401H01Rik	-1.15	0.406	-2.32	0.129	-1.18	0.002	-1.26	0.044	-1.36	0.000
1438895_at	RIKEN cDNA A430102J17 gene	A430102J17Rik	-1.07	0.563	-1.07	0.482	1.07	0.916	1.14	0.622	-1.36	0.028
1427197_at	ataxia telangiectasia and Rad3 related	Atr	-1.1	0.361	-1.71	0.065	-1.03	0.592	-1.17	0.244	-1.36	0.026
1424836_a_at	CLIP associating protein 2	Clasp2	-1	0.638	-1.72	0.133	-1.23	0.201	-1.49	0.002	-1.36	0.006
1423699_at	DNA segment, Chr 15, ERATO Doi 785, expressed	D15Ertd785e	-1.01	0.731	1.05	0.810	-1.36	0.018	1.01	0.971	-1.36	0.017
1455242_at	forkhead box P1	Foxp1	1.35	0.401	1.08	0.560	-1.22	0.027	-1.34	0.009	-1.36	0.003
1441208_at	Haloacid dehalogenase-like hydrolase domain containing 2	Hdhd2	1.12	0.318	-1.14	0.219	1.26	0.315	1.22	0.576	-1.36	0.039
1457377_at	L(3)mbt-like 3 (Drosophila)	L3mbtl3	1.17	0.873	3.17	0.024	-1.36	0.204	-1.09	0.606	-1.36	0.040
1424893_at	nuclear distribution gene E-like homolog 1 (A. nidulans)	Ndel1	1	0.842	-1.11	0.103	-1.06	0.564	-1.09	0.277	-1.36	0.037
1422465_a_at	nucleoredoxin	Nxn	-1.02	0.832	-1.47	0.016	-1.27	0.015	-1.25	0.001	-1.36	0.019
1445137_at	PTK2 protein tyrosine kinase 2	Ptk2	1.16	0.792	1.31	0.035	1.17	0.393	-1.07	0.268	-1.36	0.045
1448584_at	arginine/serine-rich coiled-coil 1	Rsrc1	-1.09	0.255	-1.42	0.067	-1.27	0.010	-1.17	0.008	-1.36	0.015
1433648_at	sperm associated antigen 9	Spag9	1.08	0.400	-1.4	0.049	-1.34	0.002	-1.22	0.021	-1.36	0.006
AFFX-ThrX-3_at	---	---	1.37	0.461	-1.03	0.535	-1.36	0.245	1.51	0.149	-1.35	0.011
1424784_at	RIKEN cDNA 1700029I01 gene /// similar to zinc finger protein 665 /// simil	1700029I01Rik ///	-1.09	0.301	-1.06	0.590	-1.02	0.761	-1.09	0.258	-1.35	0.046
1434184_s_at	RIKEN cDNA 9430080K19 gene	9430080K19Rik	1.1	0.319	-1.13	0.137	-1.23	0.048	-1.31	0.000	-1.35	0.007
1450915_at	adaptor-related protein complex 3, beta 1 subunit	Ap3b1	1.11	0.514	-1.29	0.107	-1.33	0.032	-1.33	0.047	-1.35	0.012
1429433_at	BAT2 domain containing 1	Bat2d	1.12	0.469	1.17	0.620	-1.31	0.136	-1.06	0.283	-1.35	0.022
1441137_at	bicaudal C homolog 1 (Drosophila)	Bicc1	1.08	0.730	-1.49	0.057	-1.23	0.003	-1.31	0.006	-1.35	0.043
1454880_s_at	Bcl2 modifying factor	Bmf	-1.24	0.298	-1.49	0.268	1.7	0.486	1.56	0.029	-1.35	0.037
1450757_at	cadherin 11	Cdh11	1.18	0.506	-1.18	0.213	-1.32	0.004	-1.3	0.001	-1.35	0.007
1427274_at	RIKEN cDNA D130054N24 gene	D130054N24Rik	-1.07	0.484	1.16	0.730	-1.05	0.623	-1.12	0.432	-1.35	0.006

1433474_at	EGF-like repeats and discoidin I-like domains 3	Edil3	-1.13	0.248	-1.27	0.077	-1.13	0.115	-1.2	0.024	-1.35	0.015
1436866_at	ephrin A5	Efna5	-1.19	0.114	-2.62	0.015	1.02	0.954	-1.38	0.044	-1.35	0.048
1460562_at	elongation factor Tu GTP binding domain containing 1	Eftud1	-1.05	0.470	-1.21	0.220	-1.07	0.533	-1.17	0.144	-1.35	0.029
1449167_at	erythrocyte protein band 4.1-like 4a	Epb4.1l4a	-1.05	0.400	-1.42	0.114	-1.14	0.136	-1.3	0.041	-1.35	0.014
1434260_at	FCH and double SH3 domains 2	Fchsd2	-1.03	0.511	-1.63	0.031	-1.32	0.011	-1.68	0.000	-1.35	0.005
1439396_x_at	glycerol-3-phosphate dehydrogenase 1 (soluble)	Gpd1	1.34	0.764	2.53	0.516	-1.43	0.210	1.69	0.815	-1.35	0.004
1416722_at	high mobility group 20A	Hmg20a	1.13	0.618	-1.26	0.090	-1.08	0.229	-1.1	0.317	-1.35	0.000
1434690_at	lysocardiolipin acyltransferase	Lycat	1.28	0.484	-1.19	0.210	-1.13	0.214	-1.18	0.005	-1.35	0.004
1426686_s_at	mitogen activated protein kinase kinase kinase 3	Map3k3	1.06	0.945	-1.03	0.582	-1.08	0.314	-1.09	0.239	-1.35	0.021
1454997_at	methionine sulfoxide reductase B3	Msrb3	1.15	0.383	-1.24	0.083	-1.18	0.007	-1.21	0.072	-1.35	0.006
1420521_at	papilin, proteoglycan-like sulfated glycoprotein	Papln	1.4	0.970	-1.15	0.438	-1.13	0.452	1.28	0.465	-1.35	0.018
1460398_at	PHD finger protein 8	Phf8	1.06	0.855	1.01	0.748	1.01	0.928	-1.23	0.001	-1.35	0.007
1421560_at	snail homolog 3 (Drosophila)	Snai3	1.05	0.449	-1.08	0.478	1.14	0.333	1.16	0.692	-1.35	0.001
1450916_at	staufen (RNA binding protein) homolog 2 (Drosophila)	Stau2	1.04	0.892	-1.99	0.050	-1.28	0.043	-1.33	0.018	-1.35	0.016
1420895_at	transforming growth factor, beta receptor I	Tgfbr1	1.14	0.544	-1.13	0.268	-1.24	0.097	-1.19	0.079	-1.35	0.016
1459414_at	WD repeat and FYVE domain containing 3	Wdfy3	1.04	0.840	-1.18	0.447	-1.18	0.463	1.23	0.454	-1.35	0.044
1455483_at	zinc finger protein 148	Zfp148	-1.2	0.337	-1.25	0.299	-1.19	0.023	-1.35	0.002	-1.35	0.023
1429121_at	RIKEN cDNA 4921517N04 gene	4921517N04Rik	1.08	0.024	1.06	0.450	-1.08	0.362	-1.06	0.328	-1.34	0.008
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	Abcc4	-1.38	0.031	-2.43	0.034	-1.39	0.004	-1.25	0.012	-1.34	0.049
1460374_at	a disintegrin and metallopeptidase domain 2	Adam2	1.96	0.252	1.6	0.303	-1.14	0.403	1.42	0.081	-1.34	0.045
1436739_at	angiotensin II receptor, type 1a	Agtr1a	1.23	0.130	1	0.839	-1.02	0.744	-1.18	0.002	-1.34	0.001
1435280_at	expressed sequence AI452195	AI452195	-1.14	0.398	-1.32	0.249	-1.31	0.019	-1.13	0.031	-1.34	0.009
1435769_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	-1.03	0.630	-1.71	0.022	-1.34	0.031	-1.31	0.030	-1.34	0.036
1420992_at	ankyrin repeat domain 1 (cardiac muscle)	Ankrd1	1.13	0.325	-1.1	0.343	-1.17	0.138	-1.07	0.128	-1.34	0.018
1436161_at	androgen-induced proliferation inhibitor	Aprin	1.12	0.419	-1.37	0.011	-1.08	0.288	-1.19	0.214	-1.34	0.027
1435209_at	cDNA sequence BC057079	BC057079	-1.27	0.145	-1.84	0.051	-1.15	0.117	-1.11	0.340	-1.34	0.007
1455609_at	RIKEN cDNA C030025P15 gene	C030025P15Rik	-1.1	0.401	-1.42	0.207	-1.04	0.820	-1.31	0.126	-1.34	0.021
1451504_at	coiled-coil-helix-coiled-coil-helix domain containing 3	Chchd3	1.43	0.467	1.04	0.646	-1.14	0.025	-1.05	0.213	-1.34	0.010
1432462_a_at	cofactor required for Sp1 transcriptional activation, subunit 8	Crsp8	3.66	0.324	2.29	0.583	-1.23	0.115	-1.29	0.078	-1.34	0.024
1429612_at	echinoderm microtubule associated protein like 4	Eml4	1.03	0.766	-1.06	0.475	-1.09	0.239	-1.06	0.370	-1.34	0.028
1456698_s_at	heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	-1.32	0.291	-1.5	0.199	-1.24	0.146	-1.56	0.012	-1.34	0.031
1419109_at	histidine rich calcium binding protein	Hrc	1.27	0.594	1.04	0.960	-1.22	0.234	1.13	0.668	-1.34	0.016
1433758_at	nischarin	Nisch	1.08	0.145	-1.02	0.743	-1.11	0.425	1.05	0.503	-1.34	0.037
1460729_at	Rho-associated coiled-coil containing protein kinase 1	Rock1	-1.01	0.911	-1.18	0.118	-1.05	0.413	-1.31	0.006	-1.34	0.017
1420492_s_at	submaxillary gland androgen regulated protein 1 /// submaxillary gland anc	Smr1 /// Smr3	-1.4	0.303	1.21	0.813	-1.03	0.671	-1.45	0.080	-1.34	0.030
1450663_at	thrombospondin 2	Thbs2	1.21	0.786	-1.17	0.325	-1.03	0.697	-1.04	0.444	-1.34	0.022
1419898_s_at	zinc finger CCCH type containing 7 A	Zc3h7a	1.27	0.203	1.03	0.778	-1.09	0.351	1.02	0.911	-1.34	0.029
1417792_at	zinc finger, matrin-like	Zfml	1.05	0.488	1.16	0.332	-1.24	0.153	-1.06	0.385	-1.34	0.047
1452376_at	zinc finger protein 444	Zfp444	3.68	0.343	7.03	0.143	1.03	0.945	1.11	0.243	-1.34	0.016
1429355_at	RIKEN cDNA 3300001K11 gene	3300001K11Rik	1.23	0.413	-1.07	0.731	-1.18	0.295	1.8	0.359	-1.33	0.008
1452009_at	RIKEN cDNA 9130422G05 gene	9130422G05Rik	1.1	0.566	-1.38	0.131	-1.2	0.022	-1.28	0.014	-1.33	0.005
1442358_at	expressed sequence AA409587	AA409587	1.38	0.140	1.64	0.138	1.06	0.986	1.1	0.449	-1.33	0.010
1435543_at	adenomatosis polyposis coli	Apc	-1.03	0.531	-1.05	0.534	-1.04	0.666	-1.07	0.486	-1.33	0.017
1426418_at	atonal homolog 8 (Drosophila)	Atoh8	1.88	0.509	1.2	0.568	-1.22	0.040	-1.17	0.099	-1.33	0.034
1419178_at	CD3 antigen, gamma polypeptide	Cd3g	1.63	0.273	1.96	0.365	1.27	0.698	1.19	0.883	-1.33	0.044
1428982_at	RIKEN cDNA D530031C13 gene	D530031C13Rik	1.11	0.319	-1.04	0.659	-1.12	0.245	-1.21	0.095	-1.33	0.010
1451708_at	G protein-coupled receptor 33	Gpr33	1.06	0.931	1.06	0.806	-1.19	0.144	1.19	0.932	-1.33	0.035
1418492_at	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	Grem2	1.13	0.632	-1.16	0.309	-1.26	0.031	-1.27	0.013	-1.33	0.004
1422445_at	integrin alpha 6	Itga6	1.02	0.995	-1.67	0.034	-1.16	0.047	-1.41	0.002	-1.33	0.008
1417324_at	microtubule associated serine/threonine kinase 2	Mast2	1.01	0.920	-1.48	0.002	-1.3	0.009	-1.21	0.003	-1.33	0.004
1439774_at	paired related homeobox 1	Prrx1	-1.1	0.501	-1.33	0.206	-1.14	0.182	-1.4	0.010	-1.33	0.028
1417401_at	retinoic acid induced 14	Rai14	1.34	0.362	-1.08	0.349	-1.44	0.028	-1.19	0.179	-1.33	0.047
1457613_at	Regulatory factor X domain containing 1	Rfxdc1	-1.12	0.453	-1.18	0.492	1.25	0.852	-1.08	0.627	-1.33	0.032
1434958_at	sacsin	Sacs	-1.09	0.493	-1.26	0.224	-1.21	0.070	-1.11	0.164	-1.33	0.017
1426972_at	SEC24 related gene family, member D (S. cerevisiae)	Sec24d	1.5	0.429	1.13	0.627	-1.21	0.081	-1.2	0.026	-1.33	0.002
1428251_at	SMC hinge domain containing 1	Smchd1	-1.11	0.464	-1.52	0.067	-1.19	0.040	-1.39	0.035	-1.33	0.015
1455829_at	ubiquitin specific peptidase 14	Usp14	1.07	0.114	-1.06	0.480	-1.1	0.117	1	0.976	-1.33	0.017
1452868_at	ubiquitin specific peptidase 24	Usp24	-1	0.854	-1.08	0.068	-1.22	0.000	-1.48	0.002	-1.33	0.005

1427894_at	vasorin	Vasn	-1.23	0.033	-1.29	0.091	-1.19	0.031	-1.1	0.118	-1.33	0.034
1456705_at	Zinc finger protein 532	Zfp532	-1.48	0.096	-1.63	0.041	1.04	0.566	1.43	0.186	-1.33	0.032
1457746_at	RIKEN cDNA 2610028H07 gene	2610028H07Rik	2.85	0.112	1.73	0.402	-1.02	0.688	1.17	0.077	-1.32	0.030
1430404_at	RIKEN cDNA 4833416J08 gene	4833416J08Rik	-1.23	0.391	-1.44	0.346	1.05	0.899	-1.01	0.937	-1.32	0.006
1434797_at	RIKEN cDNA 6720469N11 gene	6720469N11Rik	-1.03	0.586	-1.26	0.044	-1.28	0.066	-1.35	0.003	-1.32	0.010
1450072_at	ash1 (absent, small, or homeotic)-like (Drosophila)	Ash1l	-1.11	0.394	-1.11	0.392	-1.12	0.228	-1.23	0.080	-1.32	0.005
1419922_s_at	attractin like 1	Atrnl1	-1.14	0.030	-1.39	0.048	-1.18	0.109	-1.17	0.261	-1.32	0.013
1451382_at	ChaC, cation transport regulator-like 1 (E. coli)	Chac1	-1.22	0.007	-2.44	0.001	-1.18	0.052	-1.24	0.002	-1.32	0.001
1437349_at	cytoskeleton associated protein 5	Ckap5	1.68	0.291	1.47	0.830	-1.16	0.088	-1.14	0.034	-1.32	0.030
1448582_at	catenin, beta like 1	Ctnnbl1	-1.06	0.461	-1.43	0.059	-1.13	0.065	-1.14	0.131	-1.32	0.015
1428384_at	DNA segment, Chr 4, Brigham & Women's Genetics 0951 expressed	D4Bwg0951e	1.49	0.399	1.15	0.774	-1.24	0.015	-1.09	0.051	-1.32	0.002
1453851_a_at	growth arrest and DNA-damage-inducible 45 gamma	Gadd45g	1.03	0.571	-1.08	0.152	-1.21	0.101	-1.2	0.018	-1.32	0.004
1458351_s_at	kelch-like 2, Mayven (Drosophila)	Klhl2	-1.3	0.327	-1.8	0.161	-1.1	0.165	-1.46	0.011	-1.32	0.046
1448487_at	leucine rich repeat (in FLII) interacting protein 1	Lrrfip1	1.06	0.425	-1.21	0.051	-1.13	0.030	-1.09	0.020	-1.32	0.003
1452620_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	Pck2	-1.16	0.276	-1.15	0.372	-1.1	0.446	1.07	0.757	-1.32	0.050
1437295_at	protein kinase N2	Pkn2	1.19	0.183	-1.04	0.510	-1.27	0.024	-1.33	0.016	-1.32	0.021
1441386_at	Rap guanine nucleotide exchange factor (GEF) 1	Rapgef1	1.34	0.360	-1.16	0.371	1.05	0.817	1.16	0.174	-1.32	0.028
1460706_s_at	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	Rer1	-1.26	0.240	-1.13	0.445	1.1	0.590	-1.04	0.667	-1.32	0.001
1452862_at	ras responsive element binding protein 1	Rreb1	2.17	0.327	1.95	0.574	-1.26	0.154	-1.1	0.352	-1.32	0.047
1455549_at	SEC14 and spectrin domains 1	Sestd1	-1.01	0.773	-1.33	0.021	-1.1	0.103	-1.27	0.012	-1.32	0.002
1429220_at	WD40 repeat domain 85	Wdr85	-1.07	0.417	1.07	0.797	-1.16	0.419	1.26	0.411	-1.32	0.037
1453029_s_at	RIKEN cDNA 1110059H15 gene	1110059H15Rik	-1.03	0.548	-1.23	0.029	-1.14	0.017	-1.28	0.012	-1.31	0.027
1435572_at	RIKEN cDNA 2310014L17 gene	2310014L17Rik	-1.11	0.470	-1.02	0.545	-1.02	0.818	1.09	0.392	-1.31	0.050
1458706_at	RIKEN cDNA 2610035D17 gene	2610035D17Rik	1.05	0.865	-1.28	0.292	1.5	0.722	-1.26	0.078	-1.31	0.010
1425913_a_at	RIKEN cDNA 2810022L02 gene	2810022L02Rik	1.14	0.835	-1.58	0.032	-1.12	0.089	-1.25	0.024	-1.31	0.028
1460712_s_at	adaptor protein complex AP-1, gamma 1 subunit	Ap1g1	-1.19	0.254	-1.13	0.053	-1.03	0.569	-1.22	0.028	-1.31	0.008
1424770_at	caldesmon 1	Cald1	-1.18	0.327	-1.51	0.043	-1.42	0.036	-1.15	0.077	-1.31	0.001
1451154_a_at	CUG triplet repeat, RNA binding protein 2	Cugbp2	-1.3	0.252	-2.2	0.047	-1.19	0.037	-1.3	0.003	-1.31	0.018
1434454_at	DNA segment, Chr 16, Wayne State University 65, expressed	D16Wsu65e	1.52	0.378	-1.01	0.925	1.19	0.202	-1.27	0.092	-1.31	0.050
1441229_at	RIKEN cDNA D230019N24 gene	D230019N24Rik	-1.38	0.189	1.17	0.843	1.08	0.748	1.05	0.699	-1.31	0.001
1439493_at	RIKEN cDNA D630040G17 gene /// similar to zinc finger protein 64 (predic	D630040G17Rik //	-1.16	0.298	-1.58	0.036	-1.24	0.041	-1.57	0.003	-1.31	0.047
1434285_at	FERM domain containing 4A	Frmd4a	-1.07	0.386	-1.15	0.109	-1.26	0.017	-1.27	0.077	-1.31	0.042
1458566_at	G patch domain containing 2	Gpatc2	1.25	0.735	1.22	0.784	-1.25	0.278	-1.45	0.213	-1.31	0.008
1420420_at	hydroxyacid oxidase 1, liver	Hao1	1.28	0.669	-1.16	0.410	-1.46	0.280	-1.32	0.226	-1.31	0.014
1438307_at	High mobility group box 2	Hmgb2	-1.09	0.510	-1.15	0.449	1.17	0.310	1.07	0.634	-1.31	0.025
1452238_at	HIV-1 Rev binding protein	Hrb	1.11	0.205	-1.03	0.465	-1.14	0.318	-1.16	0.059	-1.31	0.031
1456434_x_at	heat shock protein 8	Hspb8	-1.15	0.462	-1.08	0.464	1.18	0.734	-1.05	0.595	-1.31	0.040
1433605_at	inositol polyphosphate-5-phosphatase A	Inpp5a	-1.08	0.409	-1.43	0.015	-1.23	0.000	-1.25	0.001	-1.31	0.021
1419308_at	inversin	Invs	-1.14	0.426	-2.63	0.083	-1.27	0.038	-1.09	0.372	-1.31	0.021
1433747_at	leucyl/cystinyl aminopeptidase	Lnpep	1.04	0.394	-1.34	0.036	-1.21	0.073	-1.12	0.105	-1.31	0.010
1455941_s_at	mitogen activated protein kinase kinase 5	Map2k5	-1.32	0.257	-2.33	0.102	-1.22	0.016	-1.45	0.004	-1.31	0.030
1423508_at	MYST histone acetyltransferase monocytic leukemia 4	Myst4	1.01	0.712	-1.6	0.002	-1	0.710	-1.13	0.300	-1.31	0.029
1431086_s_at	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	Pcmt1	-1.07	0.539	-1.12	0.464	-1.17	0.012	-1.11	0.061	-1.31	0.002
1434181_at	pleckstrin homology domain containing, family C (with FERM domain) mer	Plekhc1	1.19	0.374	-1.2	0.223	-1.25	0.008	-1.17	0.011	-1.31	0.039
1450122_at	protein tyrosine phosphatase, receptor type, G	Ptprg	3.12	0.668	2.32	0.778	-1.3	0.016	-1.16	0.195	-1.31	0.040
1434360_s_at	protein tyrosine phosphatase, receptor type, G /// similar to protein tyrosine	Ptprg /// LOC6326	1.42	0.865	-1.02	0.334	-1.27	0.045	-1.24	0.063	-1.31	0.007
1418017_at	pumilio 2 (Drosophila)	Pum2	1.32	0.311	1.27	0.739	-1.09	0.320	-1.11	0.048	-1.31	0.047
1437161_x_at	RNA binding protein gene with multiple splicing	Rbpms	-1.03	0.655	-1.59	0.019	-1.27	0.017	-1.33	0.007	-1.31	0.014
1455819_at	ROD1 regulator of differentiation 1 (S. pombe)	Rod1	1.08	0.142	-1.18	0.169	-1.17	0.189	-1.1	0.187	-1.31	0.014
1428760_at	small nuclear RNA activating complex, polypeptide 3	Snapc3	1.15	0.334	1.2	0.393	-1.18	0.087	-1.09	0.139	-1.31	0.008
1454938_at	sorting nexin 13	Snx13	1.19	0.129	-1.1	0.374	-1.17	0.017	-1.25	0.008	-1.31	0.014
1435964_a_at	TAO kinase 3	Taok3	-1.36	0.326	-1.6	0.253	-1.07	0.475	-1.29	0.002	-1.31	0.008
1435292_at	TBC1 domain family, member 4	Tbc1d4	1.39	0.683	-2.18	0.033	2.62	0.734	1.76	0.325	-1.31	0.023
1444004_at	THO complex 2	Thoc2	-1.03	0.614	-1.19	0.354	-1.26	0.140	-1.24	0.041	-1.31	0.017
1427258_at	tripartite motif protein 24	Trim24	1.05	0.838	-1.05	0.664	-1.07	0.046	-1.27	0.030	-1.31	0.009
1430535_at	TSC22 domain family 2	Tsc22d2	1.02	0.986	-1.31	0.060	-1.23	0.021	-1.32	0.000	-1.31	0.000
1427163_at	ubiquitin protein ligase E3 component n-recognin 2	Ubr2	1.24	0.436	1.21	0.306	-1.2	0.049	-1.15	0.012	-1.31	0.011
1449095_at	vacuolar protein sorting 54 (yeast)	Vps54	-1	0.790	-1.2	0.112	-1.04	0.312	-1.04	0.384	-1.31	0.042

1459490_at	RIKEN cDNA 1110032E23 gene	1110032E23Rik	1.19	0.243	1.1	0.558	-1.11	0.372	1.07	0.614	-1.3	0.046
1435089_at	RIKEN cDNA 2010111I01 gene	2010111I01Rik	1.02	0.990	-1.09	0.376	-1.11	0.213	-1.11	0.108	-1.3	0.031
1453038_at	RIKEN cDNA 4930422G04 gene	4930422G04Rik	2.23	0.261	2.2	0.185	-1.13	0.107	-1.08	0.379	-1.3	0.028
1429999_at	RIKEN cDNA 4933403M19 gene	4933403M19Rik	2.12	0.553	1.36	0.545	1.25	0.591	1.03	0.781	-1.3	0.036
1428419_at	RIKEN cDNA 5430411K18 gene	5430411K18Rik	1.04	0.516	-1.08	0.255	-1.11	0.030	-1.15	0.043	-1.3	0.014
1436795_at	RIKEN cDNA 9630058J23 gene	9630058J23Rik	-1.06	0.233	-1.3	0.065	-1.04	0.569	-1.3	0.005	-1.3	0.001
1439827_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospon	Adamts12	1.22	0.304	-1.02	0.634	-1.28	0.003	-1.07	0.078	-1.3	0.019
1436640_x_at	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acy	Agpat4	-1.12	0.373	-1.41	0.232	1.01	0.968	-1.23	0.008	-1.3	0.039
1428369_s_at	Rho GTPase activating protein 21	Arhgap21	-1.03	0.670	-1.19	0.179	-1.22	0.000	-1.37	0.006	-1.3	0.002
1454745_at	Rho GTPase activating protein 29	Arhgap29	1.03	0.217	-1.1	0.074	-1.22	0.048	-1.21	0.009	-1.3	0.015
1449119_at	ariadne homolog 2 (Drosophila)	Arih2	1.2	0.348	1.21	0.411	-1.19	0.022	-1.14	0.091	-1.3	0.006
1426582_at	activating transcription factor 2	Atf2	-1.03	0.650	-1.1	0.169	-1.19	0.020	-1.09	0.479	-1.3	0.029
1456523_at	expressed sequence C77713	C77713	1.61	0.624	1.13	0.488	-1.28	0.002	-1.25	0.032	-1.3	0.003
1444787_at	Chromodomain helicase DNA binding protein 1	Chd1	1.03	0.834	-1.03	0.886	2.71	0.726	1.03	0.869	-1.3	0.024
1458984_at	RIKEN cDNA E130308A19 gene	E130308A19Rik	-1.13	0.468	-1.83	0.068	1.02	0.954	-1.2	0.051	-1.3	0.005
1417408_at	coagulation factor III	F3	1.05	0.896	-1.15	0.186	-1.14	0.051	-1.26	0.024	-1.3	0.026
1435985_at	FERM, RhoGEF and pleckstrin domain protein 2	Farp2	-1.02	0.679	-1.19	0.164	-1.16	0.156	-1.12	0.296	-1.3	0.004
1433482_a_at	far upstream element (FUSE) binding protein 1	Fubp1	1.08	0.679	-1.15	0.179	-1.28	0.016	-1.16	0.030	-1.3	0.009
1434158_at	GDP-mannose 4, 6-dehydratase	Gmds	-1.3	0.036	-1.34	0.039	-1.4	0.009	-1.13	0.033	-1.3	0.012
1424141_at	HECT domain containing 1	Hectd1	1.44	0.207	1.21	0.479	-1.13	0.177	-1.02	0.572	-1.3	0.015
1452360_a_at	jumonji, AT rich interactive domain 1A (Rbp2 like)	Jarid1a	1.08	0.077	1.07	0.155	-1.04	0.631	-1.15	0.015	-1.3	0.016
1423885_at	laminin, gamma 1	Lamc1	2.79	0.581	1.58	0.584	-1.15	0.014	-1.2	0.073	-1.3	0.004
1427705_a_at	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	Nfkb1	1.08	0.418	-1.06	0.673	-1.27	0.005	-1.25	0.007	-1.3	0.009
1454851_at	nuclear receptor subfamily 2, group C, member 2	Nr2c2	-1.13	0.161	-1.36	0.021	-1.22	0.096	-1.36	0.014	-1.3	0.001
1440223_at	RNA binding motif protein 6	Rbm6	1.05	0.969	-1.01	0.786	-1.21	0.180	-1.01	0.621	-1.3	0.036
1421849_at	stromal antigen 2	Stag2	1.11	0.101	-1.19	0.133	-1.13	0.081	-1.2	0.016	-1.3	0.002
1419708_at	wingless-related MMTV integration site 6	Wnt6	-1.29	0.316	-1	0.614	1.42	0.190	1.04	0.918	-1.3	0.048
1434846_at	RIKEN cDNA 1700065A05 gene	1700065A05Rik	1.06	0.631	-1.16	0.016	-1.07	0.254	-1.19	0.078	-1.29	0.010
1444790_at	RIKEN cDNA 1810005K13 gene	1810005K13Rik	-1.08	0.487	-1.09	0.495	1.06	0.821	-1.15	0.349	-1.29	0.012
1436729_at	RIKEN cDNA 2600003E23 gene	2600003E23Rik	1.06	0.528	-1.09	0.406	-1.17	0.004	-1.26	0.024	-1.29	0.003
1439484_at	RIKEN cDNA 4930431H11 gene	4930431H11Rik	-1.02	0.711	-1.01	0.881	1.24	0.645	-1.08	0.264	-1.29	0.011
1428971_at	RIKEN cDNA 5730405I09 gene	5730405I09Rik	1.3	0.317	1.02	0.737	-1.04	0.693	-1.14	0.130	-1.29	0.025
1452233_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	Abcc1	-1.01	0.811	-1.22	0.119	-1.23	0.010	-1.16	0.035	-1.29	0.016
1452415_at	actinin, alpha 1	Actn1	1.28	0.818	-1	0.411	-1.19	0.056	-1.22	0.049	-1.29	0.009
1436185_at	expressed sequence AI314180	AI314180	-1.09	0.433	-1.35	0.210	1.16	0.334	-1.12	0.290	-1.29	0.026
1460573_at	expressed sequence AI848100	AI848100	1.81	0.352	1.57	0.834	-1	0.926	-1.1	0.233	-1.29	0.014
1451526_at	Rho GTPase activating protein 12	Arhgap12	-1.12	0.450	-1.3	0.253	-1.17	0.175	-1.2	0.010	-1.29	0.013
1416961_at	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	Bub1b	1.18	0.539	1	0.711	-1.16	0.207	1.07	0.410	-1.29	0.016
1460389_at	cyclin-dependent kinase 8	Cdk8	1.01	0.512	-1.08	0.256	-1.13	0.074	-1.11	0.140	-1.29	0.025
1434251_at	CCR4-NOT transcription complex, subunit 1	Cnot1	1.1	0.103	-1	0.856	-1.13	0.139	-1.19	0.006	-1.29	0.001
1456576_x_at	CCR4-NOT transcription complex, subunit 2	Cnot2	-1.12	0.436	-1.02	0.501	-1.05	0.577	-1.14	0.134	-1.29	0.006
1438891_at	Catenin (cadherin associated protein), delta 2	Ctnnd2	1.43	0.039	1.77	0.200	-1.26	0.386	1.19	0.511	-1.29	0.009
1427941_at	Dicer1, Dcr-1 homolog (Drosophila)	Dicer1	-1.13	0.217	-1.07	0.392	-1.18	0.069	-1.05	0.459	-1.29	0.004
1451977_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	Dyrk1a	1.65	0.575	1.47	0.658	-1.3	0.009	-1.28	0.022	-1.29	0.035
1448223_at	fatso	Fto	-1.12	0.224	-1.74	0.002	-1.23	0.030	-1.29	0.043	-1.29	0.041
1428774_at	glypican 6	Gpc6	-1.15	0.095	-1.43	0.036	-1.22	0.012	-1.27	0.054	-1.29	0.008
1452424_at	G protein-coupled receptor 23	Gpr23	2.62	0.387	1.42	0.833	-1.02	0.460	1.58	0.067	-1.29	0.040
1454905_at	inhibitor of Bruton agammaglobulinemia tyrosine kinase	Ibtk	-1.02	0.660	-1.2	0.204	-1.2	0.082	-1.09	0.455	-1.29	0.042
1422611_s_at	insulin-like growth factor 2 mRNA binding protein 3	Igf2bp3	2.84	0.499	1.84	0.831	1.08	0.510	-1.24	0.003	-1.29	0.044
1451985_at	leucine-rich repeat kinase 1	Lrrk1	-1.11	0.205	-1.23	0.097	-1.23	0.033	-1.15	0.112	-1.29	0.027
1426369_at	male sterility domain containing 2	Mlstd2	-1.01	0.808	-1.35	0.024	-1.09	0.270	-1.16	0.134	-1.29	0.037
1418664_at	multiple PDZ domain protein	Mpdz	-1.08	0.341	-1.4	0.031	-1.15	0.168	-1.17	0.055	-1.29	0.046
1423428_at	receptor tyrosine kinase-like orphan receptor 2	Ror2	-1.29	0.243	-1.85	0.089	-1.14	0.299	-1.69	0.016	-1.29	0.037
1432029_a_at	stromal membrane-associated protein 1	Smap1	1.9	0.307	1.64	0.635	-1.03	0.701	-1.07	0.162	-1.29	0.006
1429288_x_at	syntaxin 18	Stx18	1	0.844	-1.16	0.130	-1.14	0.144	-1.05	0.459	-1.29	0.017
1436982_at	trinucleotide repeat containing 6b	Tnrc6b	1.03	0.876	-1.34	0.049	-1.09	0.190	-1.23	0.033	-1.29	0.015
1439411_a_at	exportin 7	Xpo7	-1.23	0.378	-1.64	0.211	-1.08	0.053	-1.21	0.040	-1.29	0.003
1429807_at	RIKEN cDNA 1700011H22 gene	1700011H22Rik	-1.1	0.469	1.95	0.273	1.79	0.213	1.13	0.313	-1.28	0.020

1426708_at	anthrax toxin receptor 2	Antxr2	1.08	0.542	-1.35	0.094	-1.19	0.029	-1.16	0.038	-1.28	0.007
1426967_at	axin 1	Axin1	3.09	0.473	4.28	0.262	-1.05	0.151	-1	0.909	-1.28	0.018
1434459_at	cDNA sequence BC057627	BC057627	-1.01	0.624	-1.12	0.053	-1.06	0.527	-1.09	0.155	-1.28	0.049
1437022_at	RIKEN cDNA D130059P03 gene	D130059P03Rik	1.03	0.584	-1.02	0.524	1.05	0.573	-1.04	0.068	-1.28	0.003
1458769_at	DNA segment, Chr 7, ERATO Doi 558, expressed	D7Ertd558e	-1.38	0.284	-1.23	0.343	1.24	0.092	-2.17	0.115	-1.28	0.024
1426833_at	eukaryotic translation initiation factor 4 gamma, 3	Eif4g3	-1.14	0.128	-1.39	0.027	-1.19	0.063	-1.16	0.220	-1.28	0.048
1437363_at	homer homolog 1 (Drosophila)	Homer1	-1.04	0.442	-1.56	0.026	-1.13	0.089	-1.02	0.550	-1.28	0.012
1450992_a_at	myeloid ecotropic viral integration site 1	Meis1	-1	0.849	-1.92	0.006	-1.43	0.029	-1.49	0.077	-1.28	0.049
1443279_at	Nemo like kinase	Nlk	-1.13	0.398	-1.36	0.380	1.42	0.806	1.51	0.376	-1.28	0.047
1433768_at	palladin, cytoskeletal associated protein	Palld	1.23	0.688	-1.11	0.305	-1.21	0.037	-1.27	0.008	-1.28	0.000
1426614_at	protein kinase C binding protein 1	Prkcbp1	-1.06	0.509	-1.05	0.539	-1.08	0.324	-1.07	0.240	-1.28	0.031
1418758_a_at	pleckstrin homology, Sec7 and coiled-coil domains 3	Pscd3	1.11	0.530	-1.15	0.333	-1.15	0.056	-1.16	0.016	-1.28	0.002
1415850_at	RAS p21 protein activator 3	Rasa3	1.04	0.391	-1.45	0.004	-1.09	0.244	-1.18	0.020	-1.28	0.015
1426912_at	ring finger and WD repeat domain 2 /// similar to constitutive photomorpho	Rfwd2 /// LOC6212	1.22	0.333	1.05	0.966	-1.2	0.018	-1.17	0.014	-1.28	0.004
1454991_at	solute carrier family 7 (cationic amino acid transporter, y+ system), membe	Slc7a1	-1.15	0.265	-1.4	0.053	-1.11	0.124	-1.12	0.022	-1.28	0.011
1456479_at	sorting nexin family member 30	Snx30	-1.02	0.746	-1	0.965	-1.06	0.074	-1.26	0.004	-1.28	0.000
1448782_at	thioredoxin domain containing 11	Txndc11	1.07	0.348	-1.16	0.074	-1.14	0.016	-1.03	0.475	-1.28	0.002
1428861_at	RIKEN cDNA 4631422O05 gene /// similar to downregulated in ovarian ca	4631422O05Rik ///	1.5	0.614	1.18	0.626	-1.22	0.003	-1.11	0.039	-1.27	0.039
1423177_a_at	abl-interactor 1	Abi1	1.17	0.508	1.04	0.806	-1.12	0.161	-1.3	0.002	-1.27	0.005
1418135_at	AF4/FMR2 family, member 1	Aff1	-1.14	0.218	-1.28	0.111	-1.1	0.061	-1.34	0.009	-1.27	0.001
1443665_at	Expressed sequence AI852444	AI852444	-1.07	0.549	-1.53	0.049	1.1	0.191	-1.27	0.131	-1.27	0.034
1431848_at	angiopoietin-like 2	Angptl2	1.45	0.410	1.22	0.790	-1.13	0.394	1.01	0.959	-1.27	0.003
1425492_at	bone morphogenetic protein receptor, type 1A	Bmpr1a	1.09	0.375	-1.07	0.531	1.01	0.992	-1.1	0.031	-1.27	0.016
1454874_at	BTB (POZ) domain containing 7	Btbd7	1.05	0.276	-1.01	0.788	-1.02	0.663	-1.21	0.015	-1.27	0.007
1452476_at	calcium channel, voltage-dependent, beta 2 subunit	Cacnb2	1.14	0.346	1.45	0.512	1.32	0.627	1	0.924	-1.27	0.037
1435220_s_at	CDC42 small effector 2	Cdc42se2	1.02	0.678	1	0.955	1.02	0.137	-1.13	0.022	-1.27	0.006
1418599_at	procollagen, type XI, alpha 1	Col11a1	-1.15	0.385	-1.55	0.301	-1.11	0.349	-1.04	0.384	-1.27	0.043
1434038_at	DnaJ (Hsp40) homolog, subfamily C, member 13	Dnajc13	1.02	0.591	-1.2	0.082	-1.21	0.009	-1.14	0.027	-1.27	0.000
1425462_at	F-box and WD-40 domain protein 11	Fbxw11	1.09	0.436	1.08	0.678	-1.22	0.043	-1.3	0.004	-1.27	0.011
1448185_at	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-	Herpud1	1.05	0.857	-2.02	0.023	-1.22	0.004	-1.05	0.109	-1.27	0.003
1450730_at	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	1.03	0.695	-1.27	0.006	-1.2	0.003	-1.04	0.474	-1.27	0.007
1415769_at	itchy	Itch	1.09	0.401	-1.06	0.625	-1.22	0.221	-1.2	0.127	-1.27	0.000
1443947_at	LIM and senescent cell antigen-like domains 1	Lims1	-1.76	0.115	-1.1	0.579	1.01	0.618	-1.08	0.498	-1.27	0.018
1453836_a_at	monoglyceride lipase	Mgll	1.56	0.450	1.05	0.674	-1.28	0.137	-1.09	0.229	-1.27	0.020
1460436_at	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	Ndst1	-1.04	0.367	-1.12	0.221	-1.17	0.008	-1.12	0.045	-1.27	0.049
1442834_at	Protein phosphatase 4, regulatory subunit 2	Ppp4r2	-1.05	0.533	-1.47	0.125	-1.21	0.097	1.03	0.719	-1.27	0.037
1432057_a_at	PR domain containing 5	Prdm5	1.02	0.684	-1.34	0.097	-1.33	0.003	-1.36	0.023	-1.27	0.031
1454722_at	phosphatase and tensin homolog	Pten	1.62	0.389	1.4	0.628	-1.18	0.158	-1.06	0.233	-1.27	0.043
1426504_a_at	ring finger protein 121	Rnf121	1.18	0.325	1.13	0.275	-1.08	0.213	-1.06	0.323	-1.27	0.018
1452445_at	solute carrier family 41, member 2	Slc41a2	1.17	0.245	-1.23	0.043	-1.15	0.024	-1.13	0.022	-1.27	0.002
1426457_at	sarcolemma associated protein	Slmap	1.17	0.296	-1.03	0.724	-1.12	0.070	-1.18	0.022	-1.27	0.004
1450923_at	transforming growth factor, beta 2	Tgfb2	-1.01	0.934	-1.63	0.002	-1.18	0.125	-1.21	0.022	-1.27	0.025
1454889_x_at	transmembrane and coiled coil domains 3	Tmcc3	1.03	0.784	-1.07	0.508	-1.11	0.179	-1.13	0.117	-1.27	0.024
1434724_at	ubiquitin specific peptidase 31	Usp31	1.02	0.746	-1.14	0.004	1.01	0.788	-1.09	0.229	-1.27	0.046
1435636_at	RIKEN cDNA 2310051F07 gene	2310051F07Rik	1.48	0.549	1.45	0.814	-1.04	0.486	-1.06	0.138	-1.26	0.006
1441005_at	RIKEN cDNA 2610304G08 gene	2610304G08Rik	-1.09	0.317	2.99	0.740	1.29	0.750	1.5	0.228	-1.26	0.038
1428122_s_at	RIKEN cDNA 2610528K11 gene	2610528K11Rik	-1.27	0.117	-2.3	0.050	-1.08	0.365	-1.24	0.057	-1.26	0.049
1455159_at	RIKEN cDNA 2900057D21 gene	2900057D21Rik	-1.02	0.639	-1.52	0.076	-1.05	0.492	-1.12	0.375	-1.26	0.021
1420679_a_at	androgen-induced 1	Aig1	-1.03	0.730	-1.63	0.032	-1.14	0.180	-1.16	0.011	-1.26	0.000
1459234_at	Arachidonate 5-lipoxygenase activating protein	Alox5ap	-1.42	0.275	-1.49	0.199	1.15	0.980	-1.35	0.136	-1.26	0.048
1429193_at	ankyrin repeat and IBR domain containing 1	Ankib1	1.02	0.716	-1.19	0.053	-1.08	0.034	-1.21	0.009	-1.26	0.028
1456917_at	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-i	Arfgef1	-1	0.715	1.03	0.799	1.16	0.695	1.17	0.935	-1.26	0.030
1428311_at	coiled-coil domain containing 6	Ccdc6	1.02	0.898	-1.24	0.058	-1.19	0.028	-1.25	0.050	-1.26	0.007
1456042_s_at	Crm, cramped-like (Drosophila)	Cramp1l	1.02	0.749	1.19	0.232	1	0.726	-1.12	0.165	-1.26	0.017
1460458_at	cysteine-rich secretory protein LCCL domain containing 2	Crispld2	1.05	0.735	-1.21	0.109	1.11	0.130	-1.07	0.238	-1.26	0.041
1460208_at	fibrillin 1	Fbn1	1.14	0.560	-1.14	0.286	-1.16	0.028	-1.07	0.038	-1.26	0.002
1439786_at	growth factor receptor bound protein 2-associated protein 2	Gab2	-1.18	0.314	-1.62	0.115	-1.25	0.226	-1.21	0.223	-1.26	0.047
1445480_at	G protein-coupled receptor 19	Gpr19	1.14	0.534	1.13	0.854	-1.19	0.312	1.13	0.451	-1.26	0.039

1435023_at	intersectin 2	Itsn2	-1.11	0.470	-1.29	0.222	-1.11	0.322	-1.08	0.237	-1.26	0.044
1450052_at	kinesin family member 2A	Kif2a	1.27	0.190	1.14	0.489	-1.06	0.087	-1.18	0.016	-1.26	0.018
1455434_a_at	kinectin 1	Ktn1	-1.01	0.770	-1.26	0.051	-1.12	0.107	-1.13	0.105	-1.26	0.029
1450253_a_at	mitogen activated protein kinase kinase kinase 4	Map3k4	5	0.453	5.04	0.849	-1.25	0.037	-1.11	0.389	-1.26	0.018
1428900_s_at	methyltransferase 5 domain containing 1	Mett5d1	-1.36	0.125	-2.65	0.017	-1.2	0.142	-1.25	0.087	-1.26	0.049
1436908_at	pericentriolar material 1	Pcm1	1.04	0.533	1.09	0.860	-1.24	0.044	-1.13	0.301	-1.26	0.001
1434786_at	protein phosphatase 1, regulatory (inhibitor) subunit 12B	Ppp1r12b	-1	0.878	-1.16	0.006	1.02	0.994	-1.18	0.044	-1.26	0.026
1451179_a_at	quaking	Qk	-1.04	0.550	-1.36	0.003	-1.2	0.001	-1.27	0.004	-1.26	0.001
1458182_at	RNA binding motif protein 18	Rbm18	-1.18	0.267	-1.5	0.037	1.15	0.342	-1.05	0.518	-1.26	0.037
1460337_at	SH3-domain kinase binding protein 1	Sh3kbp1	1.04	0.176	-1.22	0.001	-1.19	0.008	-1.18	0.067	-1.26	0.018
1417329_at	solute carrier family 23 (nucleobase transporters), member 2	Slc23a2	1.09	0.390	-1.01	0.720	-1.07	0.300	-1.04	0.168	-1.26	0.022
1428396_at	SMAD specific E3 ubiquitin protein ligase 1 /// similar to Smad ubiquitinatic	Smurf1 /// LOC640	2.4	0.944	2.7	0.838	-1.27	0.048	1.08	0.289	-1.26	0.010
1416525_at	speckle-type POZ protein	Spop	3.11	0.528	2.55	0.855	-1.23	0.021	-1.08	0.179	-1.26	0.038
1423658_at	signal peptide peptidase 3	Sppl3	-1.12	0.361	-1.29	0.084	-1.25	0.048	-1.41	0.050	-1.26	0.047
1418546_a_at	Stam binding protein like 1	Stambpl1	1.23	0.597	1.22	0.684	-1.1	0.232	-1.08	0.099	-1.26	0.009
1445186_at	stanniocalcin 2	Stc2	-1.13	0.261	-1.24	0.266	-1.11	0.378	1.17	0.549	-1.26	0.038
1429428_at	transcription factor 7-like 2, T-cell specific, HMG-box	Tcf7l2	-1.03	0.449	-1.67	0.017	1.01	0.619	-1.33	0.005	-1.26	0.029
1417455_at	transforming growth factor, beta 3	Tgfb3	1.37	0.786	1.01	0.373	-1.19	0.010	-1.09	0.007	-1.26	0.015
1426949_s_at	translocated promoter region	Tpr	1.07	0.128	-1.01	0.856	-1.12	0.028	-1.02	0.696	-1.26	0.048
1422604_at	urate oxidase	Uox	1.65	0.187	1.4	0.786	1.12	0.903	1.16	0.866	-1.26	0.001
1418143_at	vacuolar protein sorting 45 (yeast)	Vps45	1.14	0.345	-1.23	0.203	-1.03	0.635	-1.02	0.347	-1.26	0.025
1428519_at	RIKEN cDNA 2610528E23 gene	2610528E23Rik	-1.13	0.370	-1.65	0.205	-1.08	0.381	-1.19	0.198	-1.25	0.021
1433993_at	RIKEN cDNA 4931406P16 gene	4931406P16Rik	1.02	0.788	1.05	0.658	-1.05	0.410	-1.18	0.085	-1.25	0.000
1452809_at	RIKEN cDNA 9030607L17 gene	9030607L17Rik	1.08	0.523	1.07	0.538	1.15	0.642	1.02	0.932	-1.25	0.030
1438402_at	RIKEN cDNA 9630050M13 gene	9630050M13Rik	4.73	0.647	3.55	0.937	-1.11	0.061	-1.16	0.017	-1.25	0.000
1427251_at	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Atp2a2	3.1	0.596	2.53	0.874	-1.1	0.109	-1	0.953	-1.25	0.011
1438695_at	RIKEN cDNA C230091D08 gene	C230091D08Rik	-1.02	0.706	-1.25	0.181	1.03	0.932	-1.16	0.078	-1.25	0.038
1452867_at	procollagen, type IV, alpha 3 (Goodpasture antigen) binding protein	Col4a3bp	1.07	0.314	-1.24	0.022	-1.13	0.090	-1.22	0.095	-1.25	0.003
1441103_at	DNA segment, Chr 12, ERATO Doi 551, expressed	D12Ertd551e	-1.11	0.697	-1.54	0.087	1.56	0.601	2.02	0.216	-1.25	0.012
1434297_at	RIKEN cDNA E130304F04 gene	E130304F04Rik	1.38	0.484	2.83	0.644	2.44	0.478	1.46	0.870	-1.25	0.047
1441003_at	excision repair cross-complementing rodent repair deficiency, complement	Ercc4	1.15	0.792	-1.7	0.147	-1.07	0.503	1.47	0.032	-1.25	0.045
1433857_at	fat tumor suppressor homolog (Drosophila) /// similar to fat tumor suppress	Fath /// LOC67212	1.13	0.597	-1.01	0.680	-1.11	0.023	-1.09	0.069	-1.25	0.005
1455057_at	guanine monphosphate synthetase	Gmps	1.03	0.885	-1.09	0.072	-1.17	0.168	-1.36	0.025	-1.25	0.008
1415703_at	HECT, UBA and WWE domain containing 1	Huwe1	1.55	0.221	1.3	0.724	-1.15	0.048	-1.14	0.084	-1.25	0.017
1421991_a_at	insulin-like growth factor binding protein 4	Igfbp4	5.56	0.525	5.9	0.645	-1.1	0.534	1.1	0.255	-1.25	0.024
1434185_at	similar to acetyl-coenzyme A carboxylase alpha	LOC672245	-1.15	0.293	-1.61	0.062	-1.13	0.007	-1.31	0.029	-1.25	0.021
1429514_at	phosphatidic acid phosphatase type 2B	Ppap2b	1.01	0.882	-1.45	0.010	-1.14	0.085	-1.27	0.023	-1.25	0.037
1428392_at	Ras association (RalGDS/AF-6) domain family 2	Rassf2	1.23	0.784	2.32	0.409	1.72	0.089	1.21	0.786	-1.25	0.036
1455310_at	RNA binding motif protein 16	Rbm16	-1.08	0.509	-1.24	0.324	-1.21	0.001	-1.26	0.000	-1.25	0.012
1428555_at	SET domain containing 2	Setd2	1.09	0.680	1.3	0.328	1.06	0.480	-1.02	0.714	-1.25	0.038
1450889_at	SWI/SNF related, matrix associated, actin dependent regulator of chromat	Smarca3	-1.14	0.074	-1.29	0.055	-1.09	0.070	-1.06	0.462	-1.25	0.040
1448396_at	transmembrane protein 131	Tmem131	-1.06	0.182	-1.16	0.104	-1.11	0.472	-1.24	0.044	-1.25	0.000
1423474_at	topoisomerase (DNA) I	Top1	1.02	0.531	-1.03	0.652	-1.13	0.054	-1.17	0.081	-1.25	0.002
1448548_at	tubby like protein 4	Tulp4	1.09	0.337	-1.07	0.272	-1.12	0.037	-1.13	0.083	-1.25	0.001
1455094_s_at	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, C. elegans)	Ube2g1	1.02	0.835	-1.12	0.169	-1.06	0.283	-1.21	0.029	-1.25	0.043
1438971_x_at	ubiquitin-conjugating enzyme E2H	Ube2h	-1.38	0.230	-1.5	0.199	-1.15	0.196	-1.3	0.013	-1.25	0.004
1427235_at	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	Utx	1.04	0.816	1	0.881	-1.15	0.026	-1.12	0.118	-1.25	0.018
1437155_a_at	WW domain containing transcription regulator 1	Wwtr1	-1.05	0.470	-1.46	0.005	-1.38	0.007	-1.35	0.023	-1.25	0.001
1454668_at	zinc finger, UBR1 type 1	Zubr1	1.12	0.533	1.1	0.706	-1.09	0.302	-1.16	0.014	-1.25	0.027
1428551_at	RIKEN cDNA 2410075D05 gene	2410075D05Rik	1.31	0.065	1.13	0.478	1.02	0.953	1.05	0.881	-1.24	0.005
1428897_at	RIKEN cDNA 2610029I01 gene	2610029I01Rik	1.09	0.598	-1.03	0.678	-1.03	0.643	1.01	0.869	-1.24	0.003
1454841_at	RIKEN cDNA 4921511H13 gene	4921511H13Rik	-1.26	0.188	-1.13	0.210	-1.07	0.163	1.02	0.869	-1.24	0.027
1435006_s_at	ATP-binding cassette, sub-family B (MDR/TAP), member 7	Abcb7	-1.02	0.624	-1.77	0.006	-1.02	0.669	-1.15	0.306	-1.24	0.019
1450627_at	progressive ankylosis	Ank	1.11	0.755	-1.55	0.074	-1.17	0.091	-1.14	0.056	-1.24	0.005
1426534_a_at	ADP-ribosylation factor GTPase activating protein 3	Arfgap3	1.04	0.590	-1.23	0.007	-1.19	0.007	-1.08	0.097	-1.24	0.027
1421042_at	rho/rac guanine nucleotide exchange factor (GEF) 2	Arhgef2	1.23	0.776	1.07	0.787	-1.19	0.060	1.01	0.998	-1.24	0.031
1448135_at	activating transcription factor 4	Atf4	1.06	0.784	-1.26	0.128	-1.07	0.309	-1.08	0.009	-1.24	0.002
1455206_at	Hypothetical protein C130006E23	C130006E23	-1.01	0.641	-1.65	0.154	-1.08	0.124	-1.1	0.347	-1.24	0.048

1434479_at	Procollagen, type V, alpha 1	Col5a1	-1.04	0.371	-1.27	0.057	-1.18	0.021	-1.11	0.094	-1.24	0.008
1455627_at	procollagen, type VIII, alpha 1	Col8a1	-1.1	0.228	-1.5	0.018	-1.2	0.084	-1.17	0.032	-1.24	0.036
1438133_a_at	cysteine rich protein 61	Cyr61	1.71	0.674	1.51	0.919	-1.14	0.132	-1.14	0.019	-1.24	0.014
1440985_at	RIKEN cDNA D130023J23 gene	D130023J23Rik	1.45	0.357	2.79	0.600	1	0.518	-1.37	0.205	-1.24	0.010
1451469_at	RIKEN cDNA D530005L17 gene	D530005L17Rik	1.12	0.688	-1.16	0.357	-1.17	0.221	1.1	0.189	-1.24	0.009
1448892_at	dedicator of cytokinesis 7	Dock7	-1.05	0.118	-1.44	0.001	-1.08	0.068	-1.21	0.065	-1.24	0.002
1436550_at	F-box protein 30	Fbxo30	-1.17	0.333	1	0.962	1.05	0.582	1.08	0.587	-1.24	0.045
1426908_at	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminy	Galnt7	1.16	0.625	-1.46	0.065	-1.14	0.260	-1.01	0.770	-1.24	0.024
1446737_a_at	hook homolog 3 (Drosophila)	Hook3	-1.06	0.430	1.05	0.861	-1.1	0.324	-1.11	0.040	-1.24	0.024
1450692_at	kinesin family member 4	Kif4	1.03	0.388	-1.19	0.131	-1.31	0.009	-1.19	0.075	-1.24	0.041
1416904_at	muscleblind-like 1 (Drosophila)	Mbnl1	1.12	0.155	-1.19	0.135	-1.17	0.019	-1.18	0.001	-1.24	0.005
1417675_a_at	midasin homolog (yeast)	Mdn1	1.02	0.797	-1.04	0.727	-1.12	0.304	-1.13	0.141	-1.24	0.040
1432012_a_at	NOL1/NOP2/Sun domain family 6	Nsun6	3.27	0.017	3.56	0.020	1.36	0.583	1.35	0.022	-1.24	0.038
1449214_a_at	optic atrophy 1 homolog (human)	Opa1	1.51	0.444	1.37	0.579	-1.15	0.023	-1.17	0.130	-1.24	0.005
1446272_at	PCTAIRE-motif protein kinase 2	Pctk2	-1.11	0.454	-1.14	0.499	-1.25	0.353	1.11	0.442	-1.24	0.049
1448558_a_at	phospholipase A2, group IVA (cytosolic, calcium-dependent)	Pla2g4a	1.12	0.093	-1.19	0.113	-1.12	0.071	-1.1	0.147	-1.24	0.020
1418446_at	solute carrier family 16 (monocarboxylic acid transporters), member 2	Slc16a2	3.66	0.085	2.37	0.450	1.11	0.556	1.19	0.983	-1.24	0.033
1435304_at	superoxide dismutase 1, soluble	Sod1	-1.09	0.507	-1.22	0.285	-1.06	0.260	-1.09	0.030	-1.24	0.001
1460243_at	serine palmitoyltransferase, long chain base subunit 2	Sptlc2	1.01	0.892	-1.27	0.013	-1.18	0.169	-1.11	0.048	-1.24	0.022
1428372_at	suppression of tumorigenicity 5	St5	1.1	0.176	-1.05	0.443	-1.13	0.227	-1.19	0.101	-1.24	0.028
1427441_a_at	succinate-Coenzyme A ligase, GDP-forming, beta subunit	Suclg2	3.51	0.466	1.95	0.784	-1.16	0.167	1.02	0.896	-1.24	0.036
1421870_at	tripartite motif-containing 44	Trim44	1.11	0.302	-1.15	0.188	-1.07	0.174	-1.19	0.017	-1.24	0.044
1435133_at	UDP-glucose ceramide glucosyltransferase	Ugcg	1.12	0.406	-1.32	0.019	-1.19	0.087	-1.16	0.084	-1.24	0.006
1460620_at	zinc finger protein 592	Zfp592	-1.03	0.392	1.26	0.459	1.1	0.302	-1.05	0.388	-1.24	0.033
1429623_at	zinc finger protein 644	Zfp644	1.52	0.283	1.6	0.361	-1.13	0.084	-1.11	0.132	-1.24	0.038
1430543_at	RIKEN cDNA 1500005P14 gene	1500005P14Rik	1.35	0.267	1.26	0.279	-1.05	0.434	-1.06	0.024	-1.23	0.016
1434613_at	RIKEN cDNA 1810013L24 gene	1810013L24Rik	-1.14	0.432	-1.46	0.151	-1	0.842	-1.13	0.304	-1.23	0.030
1430028_at	RIKEN cDNA 2210018M11 gene	2210018M11Rik	1.18	0.201	1.31	0.098	-1.09	0.306	-1	0.877	-1.23	0.041
1443980_at	agrin	Agrin	-1.08	0.478	1.09	0.376	1.41	0.937	-1.05	0.505	-1.23	0.008
1427245_at	ADP-ribosylation factor GTPase activating protein 1	Arfgap1	-1.2	0.299	-1.2	0.267	-1.17	0.036	-1.15	0.003	-1.23	0.031
1457575_at	expressed sequence AU021128	AU021128	1.15	0.735	-1.28	0.455	1.76	0.454	2.27	0.654	-1.23	0.037
1457568_at	hypothetical protein C230004L04	C230004L04	1.03	0.819	-1.22	0.300	1.3	0.397	-1.01	0.722	-1.23	0.019
1434645_at	RIKEN cDNA C530008M17 gene	C530008M17Rik	1.29	0.356	-1.85	0.032	-1.15	0.144	-1.47	0.007	-1.23	0.011
1440617_at	carboxypeptidase A6	Cpa6	-1.06	0.677	-1.19	0.122	1.03	0.919	1.05	0.785	-1.23	0.005
1452155_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	Ddx17	1.06	0.682	-1.06	0.523	-1.12	0.113	-1.06	0.007	-1.23	0.032
1426590_at	G elongation factor, mitochondrial 2	Gfm2	1.56	0.330	1.47	0.304	1.08	0.639	1.04	0.726	-1.23	0.021
1459622_at	gene model 22, (NCBI)	Gm22	-1.04	0.244	-1.25	0.048	-1.06	0.346	-1.14	0.005	-1.23	0.014
1439030_at	GDP-mannose pyrophosphorylase B	Gmppb	-1.11	0.270	-1.51	0.019	-1.08	0.020	-1.11	0.116	-1.23	0.004
1417810_a_at	potassium voltage gated channel, Shab-related subfamily, member 1 /// pr	Kcnb1 /// Pacsin2	-1.09	0.292	-1.3	0.057	-1.12	0.056	-1.19	0.012	-1.23	0.007
1435772_at	kinesin family member 21B	Kif21b	-1.15	0.296	-1.57	0.164	-1.27	0.103	-1.01	0.630	-1.23	0.048
1422771_at	similar to Mothers against decapentaplegic homolog 6 (SMAD 6) (Mothers	LOC670044	1.5	0.608	1.22	0.633	-1.14	0.113	-1.12	0.254	-1.23	0.043
1423251_at	LUC7-like 2 (S. cerevisiae)	Luc7l2	-1.02	0.542	-1.11	0.149	-1.07	0.277	-1.22	0.005	-1.23	0.036
1454740_at	mindbomb homolog 1 (Drosophila)	Mib1	-1.13	0.432	-1.41	0.125	-1.06	0.323	-1.21	0.077	-1.23	0.007
1434110_x_at	major urinary protein 1	Mup1	1.17	0.145	1.36	0.065	-1.32	0.325	1.38	0.174	-1.23	0.035
1423374_at	nuclear receptor coactivator 6	Ncoa6	1.03	0.828	1.05	0.768	1.01	0.446	-1.15	0.026	-1.23	0.032
1415830_at	origin recognition complex, subunit 5-like (S. cerevisiae)	Orc5l	1.08	0.491	1.22	0.165	1.02	0.970	-1.13	0.091	-1.23	0.010
1451669_at	protein phosphatase 1B, magnesium dependent, beta isoform	Ppm1b	-1.15	0.247	-1.34	0.097	-1.12	0.136	-1.16	0.096	-1.23	0.009
1438012_at	protein phosphatase 1 (formerly 2C)-like	Ppm1l	1.05	0.891	-1.37	0.119	-1.21	0.028	-1.22	0.058	-1.23	0.010
1418039_at	RAB, member of RAS oncogene family-like 3	Rabl3	-1.13	0.061	-1.22	0.009	-1.12	0.060	-1.17	0.019	-1.23	0.014
1449292_at	RB1-inducible coiled-coil 1	Rb1cc1	-1.16	0.389	-1.19	0.272	-1.43	0.032	-1.23	0.160	-1.23	0.024
1450173_at	receptor (TNFRSF)-interacting serine-threonine kinase 2	Ripk2	1.62	0.397	1.29	0.824	-1.11	0.267	-1.18	0.020	-1.23	0.002
1433608_at	sec1 family domain containing 2	Scfd2	-1.14	0.062	-1.87	0.029	-1.11	0.304	-1.21	0.093	-1.23	0.021
1455149_at	SH3 domain containing ring finger 1	Sh3rf1	-1.13	0.423	-1.29	0.143	-1.1	0.364	-1.39	0.015	-1.23	0.043
1448568_a_at	solute carrier family 20, member 1	Slc20a1	-1.02	0.679	-1.26	0.001	-1.1	0.033	-1.11	0.000	-1.23	0.005
1422133_at	sialophorin	Spn	1.51	0.280	2.29	0.692	1.22	0.712	1.04	0.863	-1.23	0.045
1424053_a_at	transcription factor 25 (basic helix-loop-helix)	Tcf25	1.4	0.864	1.44	0.888	-1.12	0.114	1.08	0.418	-1.23	0.009
1453160_at	thyroid hormone receptor associated protein 1	Thrap1	1.13	0.030	1.18	0.404	1.02	0.880	-1.05	0.451	-1.23	0.028
1454643_at	ubiquitin associated protein 2-like	Ubap2l	-1.17	0.331	-1.25	0.227	-1.08	0.262	-1.21	0.041	-1.23	0.041

1417846_at	Unc-51 like kinase 2 (C. elegans)	Ulk2	1.06	0.955	-1.03	0.606	-1.07	0.313	-1.06	0.490	-1.23	0.003
1453269_at	unc-5 homolog B (C. elegans)	Unc5b	-1.24	0.135	-1.65	0.038	-1.28	0.156	-1.17	0.065	-1.23	0.032
1422032_a_at	zinc finger, AN1-type domain 6	Zfand6	1	0.981	-1.26	0.011	-1.04	0.413	-1.08	0.085	-1.23	0.008
1455294_at	RIKEN cDNA 1110029L17 gene	1110029L17Rik	1.19	0.741	-1.05	0.443	-1.1	0.236	-1.12	0.061	-1.22	0.034
1427906_at	RIKEN cDNA 1110037F02 gene	1110037F02Rik	1.15	0.331	1.12	0.404	-1.07	0.342	-1.07	0.275	-1.22	0.017
1453122_at	RIKEN cDNA 4921533L14 gene	4921533L14Rik	1.19	0.442	-1.08	0.591	-1.09	0.243	-1.09	0.171	-1.22	0.011
1429669_at	RIKEN cDNA 4930488L21 gene	4930488L21Rik	1.07	0.769	2.34	0.096	1.86	0.289	1.35	0.687	-1.22	0.029
1454801_at	ankyrin repeat domain 28	Ankrd28	1.05	0.595	-1.21	0.198	-1.27	0.205	-1.26	0.087	-1.22	0.045
1454990_at	AT rich interactive domain 2 (Arid-rfx like)	Arid2	-1.03	0.543	1	0.995	1.06	0.728	-1.13	0.195	-1.22	0.028
1435953_at	BTAF1 RNA polymerase II, B-TFIID transcription factor-associated, (Mot1	Btaf1	1.27	0.155	1.22	0.348	-1.08	0.202	-1.08	0.246	-1.22	0.034
1434301_at	RIKEN cDNA D330050I23 gene	D330050I23Rik	-1.05	0.641	-1.19	0.124	-1.02	0.675	-1.09	0.267	-1.22	0.042
1454995_at	dimethylarginine dimethylaminohydrolase 1	Ddah1	1.01	0.966	-1.19	0.093	-1.07	0.369	-1.11	0.245	-1.22	0.008
1434564_at	E2F transcription factor 3	E2f3	-1.05	0.489	1.07	0.544	-1.14	0.075	-1.23	0.085	-1.22	0.039
1417238_at	Ewing sarcoma breakpoint region 1	Ewsr1	1.69	0.501	1.43	0.802	-1.08	0.439	1.04	0.330	-1.22	0.023
1419159_at	golgi autoantigen, golgin subfamily a, 3	Golga3	-1.01	0.693	-1.16	0.118	-1.13	0.087	-1.02	0.661	-1.22	0.025
1417293_at	heparan sulfate 6-O-sulfotransferase 1	Hs6st1	1.3	0.555	1.35	0.568	-1.07	0.415	-1.07	0.066	-1.22	0.014
1450047_at	heparan sulfate 6-O-sulfotransferase 2	Hs6st2	1.01	0.944	-1.18	0.082	-1.19	0.032	-1.16	0.058	-1.22	0.024
1444158_at	jumonji, AT rich interactive domain 1C (Rbp2 like)	Jarid1c	-1.09	0.306	-1.08	0.468	-1.03	0.445	-1.07	0.325	-1.22	0.019
1455398_at	leucine rich repeat containing 8 family, member C	Lrrc8c	-1.14	0.225	-1.55	0.040	-1.04	0.452	-1.19	0.016	-1.22	0.026
1448647_at	mannosidase 2, alpha 1	Man2a1	1.01	0.847	-1.3	0.008	-1.13	0.055	-1.09	0.114	-1.22	0.000
1434746_at	MAX gene associated	Mga	-1.01	0.752	1.03	0.896	-1.02	0.774	1.08	0.844	-1.22	0.023
1428817_at	MON2 homolog (yeast)	Mon2	1.05	0.106	-1.12	0.075	-1.1	0.160	-1.19	0.013	-1.22	0.006
1419754_at	myosin Va	Myo5a	1.2	0.310	-1.15	0.225	-1.12	0.003	-1.07	0.350	-1.22	0.018
1433942_at	myosin VI	Myo6	1.51	0.511	1.3	0.948	-1.09	0.467	1.03	0.630	-1.22	0.011
1422567_at	niban protein	Niban	1.18	0.643	-1.11	0.344	-1.2	0.023	-1.09	0.098	-1.22	0.046
1451379_at	RAB22A, member RAS oncogene family	Rab22a	-1.1	0.001	-1.08	0.024	-1.07	0.088	-1.12	0.036	-1.22	0.001
1454915_at	RAB3 GTPase activating protein subunit 2	Rab3gap2	1.09	0.494	-1.24	0.100	-1.21	0.020	-1.12	0.132	-1.22	0.015
1426799_at	RAB8B, member RAS oncogene family	Rab8b	-1.05	0.308	-1.21	0.049	-1.08	0.322	-1.07	0.415	-1.22	0.010
1422736_at	RAN binding protein 9	Ranbp9	3.75	0.269	2.84	0.294	-1.08	0.324	-1.02	0.627	-1.22	0.041
1451365_at	RNA binding motif protein 19	Rbm19	-1.05	0.250	-1.1	0.219	-1.11	0.046	-1.09	0.097	-1.22	0.026
1417542_at	ribosomal protein S6 kinase, polypeptide 2	Rps6ka2	-1.22	0.011	-1.66	0.014	-1.05	0.435	-1.09	0.009	-1.22	0.048
1424659_at	slit homolog 2 (Drosophila)	Slit2	-1.27	0.100	-1.7	0.044	-1.22	0.043	-1.2	0.015	-1.22	0.025
1430133_at	TBC1 domain family, member 8B	Tbc1d8b	1.06	0.927	-1.4	0.195	-1.1	0.205	-1.13	0.194	-1.22	0.005
1455128_x_at	trinucleotide repeat containing 6a	Tnrc6a	1.21	0.256	1.27	0.305	-1.03	0.592	-1.08	0.287	-1.22	0.002
1448925_at	twist homolog 2 (Drosophila)	Twist2	-1.06	0.022	-1.28	0.038	-1.14	0.162	-1.11	0.134	-1.22	0.015
1427105_at	RIKEN cDNA 2610510J17 gene	2610510J17Rik	1.53	0.078	1.28	0.949	1.11	0.824	1.07	0.898	-1.21	0.035
1428300_at	RIKEN cDNA 4932439K10 gene	4932439K10Rik	1.03	0.583	-1	0.966	-1.16	0.132	-1.1	0.153	-1.21	0.008
1460342_s_at	expressed sequence AA536749	AA536749	1.43	0.569	1.27	0.986	-1.14	0.015	-1.11	0.008	-1.21	0.028
1454982_at	ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin A-	Arfgef2 /// LOC670	-1.03	0.504	-1.26	0.063	-1.08	0.046	-1.11	0.061	-1.21	0.017
1426330_at	calcium channel, voltage-dependent, gamma subunit 5	Cacng5	1.15	0.668	2.21	0.338	-1.03	0.436	-1.09	0.359	-1.21	0.017
1449858_at	CD86 antigen	Cd86	1.6	0.214	1.08	0.979	1.28	0.159	-1.13	0.449	-1.21	0.014
1450625_at	procollagen, type V, alpha 2	Col5a2	-1	0.861	-1.28	0.009	-1.17	0.003	-1.18	0.026	-1.21	0.013
1420617_at	cytoplasmic polyadenylation element binding protein 4	Cpeb4	1.29	0.254	1.07	0.978	-1.01	0.933	-1.06	0.242	-1.21	0.026
1448149_at	catenin (cadherin associated protein), alpha 1	Ctnna1	-1.06	0.189	-1.22	0.016	-1.03	0.453	-1.06	0.186	-1.21	0.004
1435542_s_at	CTTNBP2 N-terminal like	Cttnbp2nl	-1.09	0.286	1.02	0.655	-1.1	0.111	-1.1	0.184	-1.21	0.012
1437550_at	DEAH (Asp-Glu-Ala-His) box polypeptide 36	Dhx36	1.02	0.985	1.08	0.699	1.06	0.546	1.08	0.647	-1.21	0.049
1428374_at	glucuronyl C5-epimerase	Glce	-1	0.800	-1.34	0.010	-1.07	0.316	-1.05	0.512	-1.21	0.045
1428096_at	importin 11	Ipo11	1.37	0.185	-1.01	0.697	-1.02	0.617	-1.08	0.241	-1.21	0.043
1423268_at	integrin alpha 5 (fibronectin receptor alpha)	Itga5	32.88	0.967	24.24	0.357	-1.32	0.066	-1.12	0.226	-1.21	0.043
1419362_at	mitochondrial ribosomal protein L35	Mrpl35	3.08	0.670	2.11	0.302	-1.05	0.643	1.39	0.262	-1.21	0.039
1417624_at	Ngfi-A binding protein 1	Nab1	1.01	0.959	-1.21	0.037	1.06	0.406	1.02	0.894	-1.21	0.041
1421080_at	nuclear receptor subfamily 4, group A, member 3	Nr4a3	1.79	0.193	1.29	0.271	-1.22	0.208	1.25	0.486	-1.21	0.017
1438672_at	parvin, beta	Parvb	1.13	0.651	-1.01	0.956	-1.04	0.623	-1.16	0.049	-1.21	0.049
1455359_at	protein tyrosine phosphatase, non-receptor type 14	Ptpn14	-1.07	0.367	-1.2	0.086	1.04	0.148	-1.22	0.020	-1.21	0.004
1451037_at	protein tyrosine phosphatase, non-receptor type 9	Ptpn9	1.23	0.490	1.16	0.861	-1.12	0.004	-1.15	0.012	-1.21	0.002
1419945_s_at	RAB2, member RAS oncogene family	Rab2	-1.03	0.303	-1.25	0.007	-1.13	0.068	-1.09	0.018	-1.21	0.049
1423990_at	RAB28, member RAS oncogene family	Rab28	-1.02	0.506	-1.41	0.005	-1.1	0.045	-1.16	0.106	-1.21	0.003
1427448_at	rabaptin, RAB GTPase binding effector protein 1	Rabep1	-1.17	0.293	1.02	0.895	-1.17	0.161	-1.04	0.578	-1.21	0.047

1425266_a_at	RAP1, GTP-GDP dissociation stimulator 1	Rap1gds1	1.21	0.584	-1.07	0.398	-1.11	0.057	-1.22	0.032	-1.21	0.002
1455024_at	tousled-like kinase 1	Tlk1	1.18	0.269	1.03	0.989	-1.13	0.003	-1.2	0.006	-1.21	0.045
1416731_at	topoisomerase (DNA) II beta	Top2b	1.11	0.299	-1.14	0.276	-1.08	0.285	-1.07	0.352	-1.21	0.045
1448551_a_at	tripartite motif protein 2	Trim2	1.04	0.902	-1.53	0.014	1.03	0.934	-1.05	0.552	-1.21	0.043
1424274_at	vesicle docking protein	Vdp	1.22	0.427	-1.05	0.491	-1.13	0.003	-1.08	0.114	-1.21	0.004
1445514_at	von Hippel-Lindau syndrome homolog	Vhlh	-1.07	0.484	1.06	0.885	-1.07	0.618	1.2	0.590	-1.21	0.024
1453343_s_at	vaccinia related kinase 2	Vrk2	-1	0.945	-1.32	0.031	-1.19	0.104	-1.3	0.007	-1.21	0.048
1449515_at	zinc finger protein 292	Zfp292	-1.07	0.526	1	0.943	-1.11	0.341	1.04	0.502	-1.21	0.027
1435608_at	zinc and ring finger 3 /// similar to Goliath homolog precursor (Ring finger p	Znrf3 /// LOC6318	-1.05	0.634	-1.27	0.008	-1.05	0.584	-1.3	0.001	-1.21	0.040
1429898_at	RIKEN cDNA 2310008M10 gene	2310008M10Rik	-1.24	0.249	-1.5	0.144	-1.21	0.125	1.14	0.246	-1.2	0.049
1441155_at	RIKEN cDNA 2810446P07 gene	2810446P07Rik	1.13	0.985	-1.1	0.342	-1.03	0.457	-1.01	0.691	-1.2	0.031
1434126_at	RIKEN cDNA 4930402H24 gene	4930402H24Rik	1.08	0.782	-1.12	0.290	-1.27	0.114	-1.19	0.081	-1.2	0.020
1454195_at	RIKEN cDNA 4933433G19 gene	4933433G19Rik	-1.29	0.298	-1.02	0.386	1.03	0.624	1.13	0.549	-1.2	0.040
1453186_at	RIKEN cDNA 5730406M06 gene	5730406M06Rik	2.06	0.444	1.75	0.317	-1.22	0.030	-1.1	0.332	-1.2	0.043
1458416_at	RIKEN cDNA A330048O09 gene	A330048O09Rik	-1.09	0.526	1.32	0.605	-1.1	0.508	-1.02	0.713	-1.2	0.030
1435990_at	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospon	Adamts2	-1.03	0.553	-1.41	0.060	-1.1	0.372	1.09	0.183	-1.2	0.022
1422573_at	AMP deaminase 3	Ampd3	-1.05	0.212	-1.35	0.001	-1.11	0.050	-1.17	0.022	-1.2	0.024
1454717_at	Ankyrin repeat domain 27 (VPS9 domain)	Ankrd27	1.12	0.808	-1.16	0.348	-1.1	0.228	-1.05	0.320	-1.2	0.004
1436921_at	ATPase, Cu++ transporting, alpha polypeptide	Atp7a	-1.25	0.114	-1.48	0.011	1.04	0.894	-1.11	0.033	-1.2	0.013
1447930_at	bromodomain adjacent to zinc finger domain 1A	Baz1a	1.07	0.137	1.12	0.233	-1.39	0.035	-1.07	0.032	-1.2	0.020
1419911_at	Coronin, actin binding protein 1C	Coro1c	-1.01	0.567	1.01	0.626	-1.17	0.384	-1.13	0.085	-1.2	0.040
1428969_at	RIKEN cDNA D030074E01 gene	D030074E01Rik	1.3	0.274	1.2	0.901	-1.13	0.071	-1.15	0.016	-1.2	0.010
1444744_at	Death inducer-obliterator 1	Dido1	1.1	0.657	1.14	0.712	1.03	0.938	1.72	0.198	-1.2	0.021
1451591_a_at	ephrin B1	Efnb1	-1.03	0.393	-1.11	0.315	-1.18	0.120	-1.13	0.156	-1.2	0.050
1419184_a_at	four and a half LIM domains 2	Fhl2	1.2	0.393	-1.01	0.606	-1.1	0.006	-1.12	0.027	-1.2	0.020
1453746_at	formin binding protein 1	Fnbp1	-1.27	0.369	-1.42	0.298	-1.25	0.021	-1.29	0.023	-1.2	0.042
1428354_at	forkhead box K2	Foxk2	-1.06	0.076	-1.22	0.003	-1.04	0.436	-1.1	0.055	-1.2	0.029
1456532_at	Platelet-derived growth factor, D polypeptide	Pdgfd	1.31	0.392	-1.01	0.513	-1.14	0.055	-1.11	0.002	-1.2	0.042
1454090_at	prenyl (solanesyl) diphosphate synthase, subunit 1	Pdss1	1.22	0.140	1.25	0.245	-1.13	0.131	1.07	0.649	-1.2	0.040
1451576_at	protein kinase, DNA activated, catalytic polypeptide	Prkdc	-1.54	0.136	-2.07	0.103	-1.13	0.355	-1.01	0.879	-1.2	0.009
1452211_at	proteasome (prosome, macropain) activator subunit 4	Psme4	1.3	0.333	1.07	0.955	-1.05	0.122	-1.09	0.165	-1.2	0.003
1448957_at	recombining binding protein suppressor of hairless (Drosophila)	Rbpsuh	1.08	0.414	-1.03	0.681	-1.04	0.529	-1.19	0.010	-1.2	0.017
1460567_at	regulatory factor X domain containing 2 homolog (human)	Rfxdc2	1.01	0.713	1.08	0.885	-1.15	0.215	-1.25	0.142	-1.2	0.009
1453054_at	secretory carrier membrane protein 1	Scamp1	1.33	0.915	1.02	0.578	-1.13	0.219	1.21	0.214	-1.2	0.042
1427035_at	solute carrier family 39 (zinc transporter), member 14	Slc39a14	1.05	0.863	-1.02	0.687	-1.09	0.254	-1.08	0.035	-1.2	0.023
1422486_a_at	MAD homolog 4 (Drosophila)	Smad4	-1.11	0.449	-1.27	0.334	-1.03	0.296	-1.17	0.005	-1.2	0.012
1428527_at	sorting nexin 7	Snx7	1.21	0.471	1.03	0.741	-1.16	0.082	-1.13	0.025	-1.2	0.007
1451272_a_at	ubiquitin-conjugating enzyme E2F (putative)	Ube2f	-1.12	0.417	-1.23	0.319	-1.11	0.088	-1.15	0.065	-1.2	0.003
1416156_at	vinculin	Vcl	-1.05	0.137	-1.4	0.008	-1.17	0.015	-1.19	0.001	-1.2	0.001
1437358_at	WD repeat and FYVE domain containing 1	Wdfy1	1.07	0.506	-1.07	0.237	-1.21	0.036	-1.09	0.099	-1.2	0.010
1425972_a_at	zinc finger protein X-linked	Zfx	-1.02	0.668	-1.04	0.113	1.01	0.866	1.02	0.924	-1.2	0.002
1426531_at	zinc finger, MYND domain containing 11	Zmynd11	-1.13	0.227	-1.23	0.039	-1.09	0.203	-1.02	0.574	-1.2	0.040
1428679_s_at	RIKEN cDNA 0610010K14 gene	0610010K14Rik	1.18	0.340	1.24	0.003	1.09	0.385	1.03	0.772	1.2	0.039
1449902_at	RIKEN cDNA 1110058A15 gene	1110058A15Rik	1.64	0.927	1.95	0.615	1.71	0.246	1.1	0.189	1.2	0.019
1451313_a_at	RIKEN cDNA 1110067D22 gene	1110067D22Rik	-1.1	0.487	1.04	0.629	1.26	0.430	1.02	0.463	1.2	0.035
1428144_at	RIKEN cDNA 1200011O22 gene	1200011O22Rik	-1	0.774	1.03	0.933	1.06	0.735	1.07	0.509	1.2	0.041
1423266_at	RIKEN cDNA 2810405K02 gene	2810405K02Rik	-1.09	0.433	1.01	0.723	1.16	0.085	1.01	0.583	1.2	0.040
1424533_a_at	RIKEN cDNA 3110023B02 gene	3110023B02Rik	1.05	0.689	1.23	0.071	1.17	0.054	1.19	0.128	1.2	0.003
1434681_at	RIKEN cDNA 4932441K18 gene	4932441K18Rik	1.51	0.190	1.29	0.305	1.01	0.820	1.14	0.132	1.2	0.049
1417142_at	RIKEN cDNA 4932442K08 gene	4932442K08Rik	1.17	0.063	1.37	0.059	1.05	0.880	1.17	0.003	1.2	0.017
1434313_at	RIKEN cDNA 6330407D12 gene	6330407D12Rik	-1.17	0.320	-1.16	0.365	1.29	0.060	-1.04	0.483	1.2	0.005
1435163_at	RIKEN cDNA 9030612M13 gene	9030612M13Rik	1.08	0.210	1.23	0.077	1.07	0.640	1.12	0.165	1.2	0.026
1424212_at	RIKEN cDNA 9430023L20 gene	9430023L20Rik	-1.03	0.712	1.32	0.024	1.16	0.016	1.07	0.091	1.2	0.027
1428275_at	abhydrolase domain containing 13	Abhd13	1.01	0.818	1.26	0.075	1.08	0.325	1.22	0.003	1.2	0.047
1424182_at	acetyl-Coenzyme A acetyltransferase 1	Acat1	-1.09	0.238	-1.16	0.365	-1.09	0.299	1.05	0.784	1.2	0.036
1416631_at	adaptor-related protein complex AP-4, beta 1	Ap4b1	1.22	0.516	1.38	0.031	1.28	0.009	1.08	0.246	1.2	0.002
1460328_at	bromodomain containing 3	Brd3	1.03	0.839	1.18	0.369	1.03	0.818	1.14	0.045	1.2	0.049
1448326_a_at	cellular retinoic acid binding protein I	Crabp1	1.05	0.270	1.08	0.307	1.07	0.539	1.03	0.586	1.2	0.035

1449443_at	2,4-dienoyl CoA reductase 1, mitochondrial	Decr1	-1.21	0.322	-1.17	0.394	1	0.986	1.01	0.941	1.2	0.014
1426473_at	DnaJ (Hsp40) homolog, subfamily C, member 9	Dnajc9	1.24	0.075	1.89	0.007	1.12	0.448	1.23	0.082	1.2	0.008
1433797_at	RIKEN cDNA E130309D02 gene	E130309D02Rik	-1.03	0.599	1.1	0.427	1.09	0.400	1.2	0.090	1.2	0.022
1416268_at	E26 avian leukemia oncogene 2, 3' domain	Ets2	1.03	0.898	1.32	0.027	1.26	0.064	1.3	0.047	1.2	0.020
1416708_a_at	GRAM domain containing 1A	Gramd1a	-1.03	0.284	1.1	0.024	1.18	0.052	1.2	0.011	1.2	0.048
1451412_a_at	intraflagellar transport 20 homolog (Chlamydomonas)	Ift20	-1.01	0.538	-1.05	0.451	-1.01	0.787	1.05	0.005	1.2	0.000
1441300_at	potassium voltage-gated channel, subfamily F, member 1	Kcnf1	-1.18	0.362	-1.27	0.294	1.01	0.953	1.06	0.550	1.2	0.019
1423071_x_at	hypothetical gene supported by BC019681; BC027236 /// hypothetical LO	LOC270335 /// LO	-1.06	0.518	1.02	0.874	1.28	0.001	1.26	0.008	1.2	0.023
1449705_x_at	minichromosome maintenance deficient 3 (S. cerevisiae) /// similar to DNA	Mcm3 /// LOC6719	1.03	0.602	1.28	0.080	1.21	0.142	-1.07	0.588	1.2	0.008
1423492_at	mitochondrial ribosomal protein L45	Mrpl45	-1.01	0.680	1.1	0.003	1.12	0.198	1.08	0.082	1.2	0.010
1423219_a_at	mitochondrial ribosomal protein L49	Mrpl49	1.02	0.997	1.18	0.440	1.08	0.431	1.11	0.198	1.2	0.025
1416543_at	nuclear factor, erythroid derived 2, like 2	Nfe2l2	1.18	0.148	1.43	0.035	1.1	0.265	1.15	0.019	1.2	0.018
1418763_at	nitrilase family, member 2	Nit2	1.57	0.399	1.69	0.155	1.13	0.127	1.13	0.222	1.2	0.049
1455330_at	nucleolar protein 9	Nol9	1.14	0.446	1.32	0.012	1.04	0.198	1.14	0.009	1.2	0.019
1423627_at	NAD(P)H dehydrogenase, quinone 1	Nqo1	1.05	0.458	1.09	0.200	1.1	0.421	1.13	0.152	1.2	0.033
1428344_at	phosphatidic acid phosphatase type 2 domain containing 2	Ppapdc2	1.12	0.151	1.13	0.338	1.32	0.237	1.22	0.090	1.2	0.037
1426426_at	RNA binding motif protein 13	Rbm13	1.14	0.266	1.39	0.052	1.15	0.030	1.2	0.008	1.2	0.017
1417438_at	retinol dehydrogenase 14 (all-trans and 9-cis)	Rdh14	-1.03	0.643	1.17	0.137	1.19	0.221	1.14	0.007	1.2	0.018
1438665_at	sphingomyelin phosphodiesterase 3, neutral	Smpd3	-1.2	0.513	1.24	0.692	-1.46	0.036	1.65	0.222	1.2	0.031
1432526_a_at	SNF8, ESCRT-II complex subunit, homolog (S. cerevisiae)	Snf8	1.1	0.162	1.02	0.850	1.07	0.597	1.02	0.673	1.2	0.037
1417648_s_at	sorting nexin 5	Snx5	-1.02	0.698	1.01	0.747	1.16	0.092	1.16	0.013	1.2	0.041
1424427_at	transcriptional adaptor 1 (HFI1 homolog, yeast) like	Tada1l	1.68	0.188	1.78	0.069	1.31	0.059	1.13	0.081	1.2	0.040
1448882_at	transmembrane protein 93	Tmem93	1.03	0.298	1.26	0.011	1.13	0.022	1.16	0.014	1.2	0.012
1426427_at	tubulin tyrosine ligase-like 1	Ttll1	1.99	0.673	2.15	0.458	-1.05	0.362	-1.01	0.776	1.2	0.002
1422714_at	ubiquitin-conjugating enzyme E2I /// similar to Chain A, Human Ubiquitin-C	Ube2i /// LOC5462	-1.28	0.329	-1.08	0.529	1.1	0.233	1.05	0.212	1.2	0.011
1415810_at	ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	1.18	0.367	1.64	0.002	1.21	0.207	1.04	0.715	1.2	0.018
1448162_at	vascular cell adhesion molecule 1	Vcam1	1.22	0.191	1.34	0.014	1.38	0.091	1.17	0.071	1.2	0.016
1429634_at	zinc finger protein 580	Zfp580	1.04	0.899	1.07	0.977	-1.03	0.648	1.07	0.114	1.2	0.031
1452756_at	RIKEN cDNA 0610009J22 gene	0610009J22Rik	-1.09	0.414	-1.01	0.758	1.17	0.025	1.09	0.235	1.21	0.026
1453485_s_at	RIKEN cDNA 1110005A03 gene	1110005A03Rik	1.3	0.347	1.27	0.267	1.12	0.131	1.02	0.741	1.21	0.027
1452225_at	RIKEN cDNA 2010106G01 gene	2010106G01Rik	1.02	0.815	1.12	0.628	1.06	0.028	1.03	0.703	1.21	0.044
1423767_at	RIKEN cDNA 2810410M20 gene	2810410M20Rik	1.08	0.145	1.27	0.007	1.16	0.056	1.06	0.162	1.21	0.018
1441960_x_at	RIKEN cDNA 5730494M16 gene	5730494M16Rik	-1.11	0.447	-1.09	0.467	1.2	0.001	1.01	0.758	1.21	0.000
1454682_at	RIKEN cDNA A430005L14 gene	A430005L14Rik	-1.06	0.546	1.19	0.876	1.2	0.077	1.28	0.007	1.21	0.033
1421292_a_at	RIKEN cDNA A730008L03 gene	A730008L03Rik	1.19	0.572	1.22	0.445	1.07	0.391	1.14	0.120	1.21	0.012
1453257_at	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acy	Agpat5	1.05	0.578	1.16	0.198	1.04	0.052	1.04	0.093	1.21	0.007
1424545_at	cDNA sequence BC003965	BC003965	-1.07	0.499	1.11	0.933	1.13	0.052	1.18	0.003	1.21	0.025
1451533_at	cDNA sequence BC022687	BC022687	1.27	0.827	1.81	0.093	1.35	0.006	1.13	0.046	1.21	0.038
1439422_a_at	C1q domain containing 2	C1qdc2	-1.17	0.366	1.07	0.821	1.09	0.063	1.08	0.090	1.21	0.042
1428485_at	carbonic anyhydrase 12	Car12	1.18	0.505	1.23	0.232	1.03	0.879	-1.01	0.774	1.21	0.010
1452937_s_at	coiled coil domain containing 28B	Ccdc28b	2.22	0.740	1.59	0.311	1.36	0.057	-1.07	0.316	1.21	0.050
1455757_at	DNA segment, Chr 3, ERATO Doi 254, expressed	D3Ertd254e	1.11	0.415	1.28	0.212	1.01	0.935	1.21	0.019	1.21	0.048
1423571_at	endothelial differentiation sphingolipid G-protein-coupled receptor 1	Edg1	2.03	0.454	3.08	0.114	1.1	0.570	1.01	0.788	1.21	0.045
1429411_a_at	enhancer of yellow 2 homolog (Drosophila)	Eny2	-1.16	0.435	1.01	0.797	1.15	0.406	-1	0.946	1.21	0.048
1435561_at	Ets2 repressor factor	Erf	-1.1	0.160	-1.05	0.638	1.18	0.054	-1.03	0.594	1.21	0.047
1438945_x_at	gap junction membrane channel protein alpha 1	Gja1	-1.15	0.494	1.04	0.901	1.27	0.110	1	0.896	1.21	0.046
1436887_x_at	glutamate-rich WD repeat containing 1	Grwd1	-1.28	0.376	-1.01	0.553	1.04	0.926	1.1	0.262	1.21	0.041
1425196_a_at	histidine triad nucleotide binding protein 2	Hint2	-1.19	0.410	1.05	0.558	1.25	0.026	1.25	0.004	1.21	0.011
1427100_at	meteorin, glial cell differentiation regulator	Metrn	-1.11	0.261	1.01	0.983	-1.02	0.947	-1.01	0.853	1.21	0.009
1422471_at	peroxisomal biogenesis factor 13	Pex13	1.07	0.714	1.47	0.013	1.17	0.012	1.24	0.000	1.21	0.008
1426085_a_at	paxillin	Pxn	2	0.697	1.61	0.749	1.03	0.786	1.21	0.240	1.21	0.044
1448899_s_at	RAD51 associated protein 1	Rad51ap1	1.21	0.064	1.38	0.022	1.06	0.392	1.22	0.033	1.21	0.029
1416229_at	riboflavin kinase	Rfk	1.2	0.282	1.37	0.067	1.05	0.719	1.19	0.062	1.21	0.033
1424837_at	ring finger protein 113A1	Rnf113a1	1.55	0.149	1.73	0.061	1.04	0.444	1.06	0.633	1.21	0.022
1455060_at	Ras-GTPase-activating protein SH3-domain binding protein	RP23-336J1.4	2.38	0.486	2.69	0.479	1.1	0.207	1.19	0.042	1.21	0.047
1417041_at	RNA polymerase 1-1	Rpo1-1	-1.02	0.381	1.18	0.199	1.1	0.283	1.13	0.010	1.21	0.006
1422676_at	SWI/SNF related, matrix associated, actin dependent regulator of chromat	Smarce1	1.04	0.501	1.27	0.002	1.18	0.048	1.14	0.035	1.21	0.013
1441415_at	Sprouty-related, EVH1 domain containing 2	Spred2	1.15	0.864	1.12	0.876	1.08	0.762	1.43	0.347	1.21	0.011

1417334_at	serine/threonine kinase 19	Stk19	1.22	0.124	1.22	0.052	1.07	0.172	1.12	0.240	1.21	0.033
1455871_s_at	Tax1 (human T-cell leukemia virus type I) binding protein 3 /// ribosomal pr	Tax1bp3 /// Rpl13	-1.09	0.441	1.11	0.573	1.15	0.067	1.1	0.004	1.21	0.027
1425249_a_at	TYRO3 protein tyrosine kinase 3	Tyro3	1.61	0.698	1.78	0.857	1.38	0.100	1.1	0.451	1.21	0.014
1452880_at	zinc finger, HIT type 3	Znhit3	1.19	0.211	1.43	0.003	1.22	0.043	1.1	0.274	1.21	0.017
1434697_at	RIKEN cDNA 1110001P04 gene	1110001P04Rik	1.22	0.127	1.62	0.013	1.13	0.241	1.07	0.108	1.22	0.004
1428675_at	RIKEN cDNA 1110049F12 gene	1110049F12Rik	1.02	0.878	1.22	0.092	1.24	0.021	1.08	0.378	1.22	0.041
1428381_a_at	RIKEN cDNA 2700038C09 gene	2700038C09Rik	1.03	0.501	1.18	0.156	1.08	0.342	1.02	0.640	1.22	0.028
1435200_at	RIKEN cDNA 6330419J24 gene	6330419J24Rik	1.37	0.832	1.84	0.202	2.08	0.527	1.76	0.222	1.22	0.029
1438941_x_at	adenosine monophosphate deaminase 2 (isoform L)	Ampd2	-1.28	0.349	1.02	0.650	1.15	0.152	1.17	0.026	1.22	0.041
1447903_x_at	adaptor-related protein complex 1, sigma 2 subunit	Ap1s2	-1.09	0.473	1.11	0.762	1.2	0.015	1.19	0.028	1.22	0.041
1416960_at	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	B3gat3	1.15	0.633	1.14	0.597	1.2	0.056	1.21	0.055	1.22	0.047
1427947_at	cDNA sequence BC028440	BC028440	1.12	0.043	1.12	0.115	1.09	0.054	-1.05	0.120	1.22	0.001
1421122_at	Casitas B-lineage lymphoma-like 1	Cbll1	-1.02	0.677	1.14	0.819	1.02	0.641	1.13	0.070	1.22	0.033
1452702_at	chloride channel 7	Clcn7	-1.12	0.398	1.01	0.817	1.1	0.543	1.08	0.209	1.22	0.015
1415920_at	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	Cstf2t	-1.06	0.459	1.23	0.181	1.15	0.199	1.17	0.022	1.22	0.002
1434607_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	Ddx52	-1.02	0.626	1.27	0.145	1.15	0.066	1.26	0.006	1.22	0.030
1417167_at	exosome component 5	Exosc5	1.77	0.238	1.91	0.280	-1.01	0.843	1.11	0.254	1.22	0.045
1434991_at	F-box and WD-40 domain protein 17	Fbxw17	1.53	0.217	1.51	0.171	1.09	0.774	1.24	0.005	1.22	0.008
1416046_a_at	fucosidase, alpha-L- 2, plasma	Fuca2	1.27	0.344	1.39	0.339	1.15	0.158	1.08	0.213	1.22	0.009
1438195_at	glycerol-3-phosphate dehydrogenase 1-like /// similar to glycerol-3-phosph	Gpd1l /// LOC6725	1.13	0.298	-1.03	0.547	1.06	0.465	1.09	0.230	1.22	0.015
1448273_at	glutathione synthetase	Gss	1.1	0.504	1.29	0.007	1.15	0.005	1.11	0.003	1.22	0.028
1417101_at	heat shock protein 2	Hspa2	-1.34	0.171	-1.05	0.549	1.08	0.053	-1.01	0.919	1.22	0.044
1453784_at	integrin-linked kinase-associated serine/threonine phosphatase 2C	Ilkap	-1.01	0.658	-1.08	0.446	-1.1	0.322	1	0.927	1.22	0.011
1416106_at	KTI12 homolog, chromatin associated (S. cerevisiae)	Kti12	1.11	0.270	1.43	0.013	1.16	0.005	1.2	0.008	1.22	0.013
1437014_x_at	similar to Peroxiredoxin 1 (Thioredoxin peroxidase 2) (Thioredoxin-depend	LOC545161 /// LO	-1.34	0.286	-1.12	0.513	1.06	0.672	-1.13	0.317	1.22	0.035
1437481_at	hypothetical LOC623451	LOC623451	-1.24	0.255	1.24	0.604	1.25	0.047	1.14	0.103	1.22	0.023
1422498_at	melanoma antigen, family H, 1	Mageh1	1.21	0.209	1.07	0.279	-1.14	0.170	1.22	0.225	1.22	0.039
1434676_at	myotubularin related protein 9	Mtmr9	-1.17	0.349	-1.15	0.330	1.05	0.407	1.03	0.518	1.22	0.034
1416536_at	melanoma associated antigen (mutated) 1	Mum1	-1.17	0.312	1.04	0.887	1.18	0.184	1.18	0.067	1.22	0.019
1416750_at	opioid receptor, sigma 1	Oprs1	1.39	0.476	1.58	0.160	1.15	0.030	1.13	0.206	1.22	0.042
1451969_s_at	poly (ADP-ribose) polymerase family, member 3	Parp3	1.12	0.444	1.12	0.335	-1.07	0.265	1.1	0.178	1.22	0.002
1425042_s_at	proline, glutamic acid and leucine rich protein 1	Pelp1	-1.44	0.236	-1.14	0.412	1.06	0.764	1.02	0.949	1.22	0.024
1439266_a_at	polymerase (RNA) III (DNA directed) polypeptide K	Polr3k	-1.03	0.626	1.16	0.855	1.19	0.055	1.16	0.005	1.22	0.011
1439403_x_at	ring finger protein 12	Rnf12	-1.34	0.346	-1.14	0.445	1.04	0.673	-1.03	0.588	1.22	0.015
1448674_at	ring finger protein 25	Rnf25	1.08	0.939	1.3	0.041	1.15	0.083	1.17	0.081	1.22	0.031
1419814_s_at	S100 calcium binding protein A1	S100a1	-1.02	0.564	-1.01	0.884	1.08	0.560	1.07	0.189	1.22	0.008
1430300_at	SCO cytochrome oxidase deficient homolog 1 (yeast)	Sco1	-1.25	0.125	1.03	0.997	1.04	0.397	-1.1	0.430	1.22	0.011
1424776_a_at	solute carrier family 25, member 28	Slc25a28	-1.08	0.487	1.08	0.844	1.11	0.199	1.16	0.004	1.22	0.034
1428597_at	TBC1 domain family, member 9B	Tbc1d9b	-1.11	0.088	-1.03	0.586	1.21	0.269	1.12	0.298	1.22	0.029
1441926_x_at	transmembrane inner ear	Tmie	1.15	0.335	-1.43	0.021	2.32	0.448	1.4	0.785	1.22	0.021
1428678_s_at	WD repeat domain 73	Wdr73	-1.01	0.808	1.25	0.047	1.24	0.016	1.2	0.055	1.22	0.024
1430134_a_at	tyrosyl-tRNA synthetase 2 (mitochondrial)	Yars2	1.26	0.195	1.47	0.011	1.11	0.412	1.05	0.589	1.22	0.020
1433503_at	zinc binding alcohol dehydrogenase, domain containing 1	Zadh1	-1.01	0.734	1.11	0.421	1.09	0.251	1.1	0.048	1.22	0.014
1418820_s_at	zinc finger, CCHC domain containing 10	Zcchc10	-1.12	0.451	1.13	0.619	1.23	0.178	1.07	0.405	1.22	0.013
1438026_at	zinc finger protein 560	Zfp560	-1.03	0.584	1.04	0.754	1.16	0.092	1.04	0.759	1.22	0.039
1448760_at	zinc finger protein 68	Zfp68	1.09	0.626	1.39	0.196	1.12	0.406	1.05	0.987	1.22	0.002
1438793_x_at	RIKEN cDNA 1200007D18 gene	1200007D18Rik	1.17	0.801	1.24	0.901	-1.08	0.480	-1.17	0.375	1.23	0.014
1451334_at	RIKEN cDNA 1810009O10 gene	1810009O10Rik	-1.01	0.786	1.3	0.078	1.13	0.010	1.2	0.005	1.23	0.048
1436339_at	RIKEN cDNA 1810058I24 gene	1810058I24Rik	-1.04	0.667	-1.27	0.161	1.08	0.569	-1.15	0.248	1.23	0.014
1456204_at	RIKEN cDNA 2010107H07 gene	2010107H07Rik	-1.14	0.449	1.04	0.603	1.14	0.051	1.11	0.188	1.23	0.017
1424687_at	RIKEN cDNA 2700008B19 gene	2700008B19Rik	1.5	0.485	1.7	0.255	-1.09	0.542	1.01	0.733	1.23	0.021
1422628_at	RIKEN cDNA 4632417K18 gene	4632417K18Rik	1.29	0.065	1.66	0.013	1.21	0.004	1.27	0.002	1.23	0.018
1429172_a_at	RIKEN cDNA 5730507H05 gene	5730507H05Rik	-1.08	0.651	-1.14	0.345	1.08	0.408	1.13	0.403	1.23	0.008
1435497_at	RIKEN cDNA 5730590G19 gene	5730590G19Rik	2.57	0.108	2.69	0.011	1.14	0.437	1.09	0.390	1.23	0.037
1448318_at	adipose differentiation related protein	Adfp	-1	0.917	1.22	0.056	1.2	0.034	1.14	0.108	1.23	0.002
1429850_x_at	alkB, alkylation repair homolog 4 (E. coli)	Alkbh4	-1.21	0.372	1.05	0.631	1.17	0.102	1.24	0.022	1.23	0.033
1453681_at	ATPase inhibitory factor 1	Atpif1	1.1	0.835	1.16	0.723	1.24	0.586	1.19	0.158	1.23	0.022
1424429_s_at	coiled-coil domain containing 95	Ccdc95	-1.04	0.555	1.33	0.001	1.17	0.385	1.25	0.003	1.23	0.023

1448182_a_at	CD24a antigen	Cd24a	-1.07	0.528	1.14	0.794	1.37	0.048	1.18	0.011	1.23	0.013
1455723_at	DNA segment, Chr 1, ERATO Doi 448, expressed	D1Ertd448e	1.95	0.648	2.24	0.125	1.33	0.060	1.21	0.018	1.23	0.046
1448270_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	Ddx21	-1.03	0.469	1.2	0.053	1.17	0.048	1.07	0.168	1.23	0.032
1452097_a_at	dual specificity phosphatase 7 /// similar to dual specificity phosphatase 7	Dusp7 /// LOC674	1.5	0.314	2.06	0.091	1.19	0.144	1.3	0.017	1.23	0.031
1460679_at	exosome component 4	Exosc4	-1.2	0.094	1.11	0.523	1.21	0.100	1.12	0.103	1.23	0.015
1432211_a_at	f-box only protein 9	Fbxo9	1.13	0.969	-1.02	0.445	1.2	0.296	-1.05	0.580	1.23	0.013
1448241_at	GM2 ganglioside activator protein	Gm2a	-1.24	0.360	-1.26	0.329	1.08	0.592	-1.01	0.735	1.23	0.005
1419205_x_at	G patch domain containing 4	Gpatc4	-1.14	0.053	1.14	0.545	1.11	0.106	1.18	0.334	1.23	0.047
1435948_at	G protein-coupled receptor 178	Gpr178	1.09	0.147	1.18	0.167	1.16	0.082	1.06	0.291	1.23	0.024
1456032_x_at	H2A histone family, member Z /// similar to H2A histone family, member Z	H2afz /// LOC6666	-1.3	0.257	-1.2	0.377	1.09	0.564	-1.11	0.293	1.23	0.025
1451252_at	interferon regulatory factor 2 binding protein 1	Irf2bp1	-1.14	0.013	1.12	0.240	1.12	0.129	1.14	0.197	1.23	0.005
1423104_at	insulin receptor substrate 1	Irs1	1.41	0.165	1.98	0.109	1.32	0.007	1.33	0.004	1.23	0.017
1421344_a_at	ajuba	Jub	1.34	0.383	1.51	0.121	1.21	0.104	1.04	0.427	1.23	0.023
1424372_at	mitochondrial ribosomal protein L32	Mrpl32	1.17	0.156	1.46	0.034	1.21	0.146	1.24	0.053	1.23	0.021
1459874_s_at	myotubularin related protein 4	Mtmr4	-1.22	0.383	-1.03	0.560	1.17	0.028	1.11	0.140	1.23	0.002
1455035_s_at	nucleolar protein 5A	Nol5a	-1.09	0.417	1.26	0.522	1.18	0.067	1.35	0.002	1.23	0.011
1434216_a_at	nudix (nucleoside diphosphate linked moiety X)-type motif 19	Nudt19	1.04	0.206	1.12	0.190	1.13	0.057	1.13	0.039	1.23	0.021
1428080_at	phosphoglycerate mutase family member 5	Pgam5	1.08	0.783	1.26	0.023	1.07	0.384	1.13	0.033	1.23	0.037
1435821_s_at	protein phosphatase 1, regulatory (inhibitor) subunit 8	Ppp1r8	-1.17	0.420	1.24	0.745	1.26	0.058	1.03	0.669	1.23	0.033
1420664_s_at	protein C receptor, endothelial	Procr	-1.07	0.028	1.09	0.361	1.17	0.247	1.08	0.132	1.23	0.032
1456566_x_at	RNA binding motif protein 14	Rbm14	-1.31	0.280	1.06	0.705	1.01	0.907	1.16	0.011	1.23	0.036
1428905_at	Ras-related GTP binding A	Rraga	1.41	0.300	1.58	0.012	1.12	0.009	1.58	0.002	1.23	0.012
1426241_a_at	sex comb on midleg homolog 1	Scmh1	1.08	0.440	1.53	0.022	1.13	0.010	1.22	0.008	1.23	0.035
1428364_at	sodium channel modifier 1	Scnm1	1.21	0.176	1.33	0.189	-1.04	0.542	1.03	0.915	1.23	0.042
1430388_a_at	sulfatase 2	Sulf2	1.8	0.377	1.86	0.125	1.04	0.302	1.03	0.891	1.23	0.045
1424213_at	UbiA prenyltransferase domain containing 1	Ubiad1	1.2	0.311	1.3	0.134	1.09	0.532	1.2	0.067	1.23	0.043
1434859_at	uridine monophosphate synthetase	Umps	-1.01	0.737	1.25	0.283	1.16	0.006	1.18	0.033	1.23	0.037
1454846_at	UTP15, U3 small nucleolar ribonucleoprotein, homolog (yeast)	Utp15	-1.08	0.475	1.21	0.151	1.24	0.003	1.23	0.010	1.23	0.038
1457736_at	vacuolar protein sorting 37D (yeast)	Vps37d	-1.18	0.099	1.09	0.184	1.11	0.489	-1.13	0.384	1.23	0.024
1451728_at	WD repeat domain 13	Wdr13	1.16	0.298	1.15	0.166	1.18	0.021	1.16	0.197	1.23	0.001
1438218_at	zinc finger and BTB domain containing 24	Zbtb24	-1.07	0.498	-1.1	0.405	1.05	0.634	1.08	0.253	1.23	0.032
1449972_s_at	zinc finger protein 97 /// cDNA sequence BC018101	Zfp97 /// BC01810	1.03	0.591	1.3	0.101	1.14	0.495	1.2	0.058	1.23	0.031
1436554_at	zinc finger protein, subfamily 1A, 5	Zfpn1a5	-1.01	0.667	1.24	0.667	1.1	0.285	-1.07	0.256	1.23	0.002
1433946_at	zinc finger protein interacting with K protein 1	Zik1	1.13	0.031	1.44	0.041	1.36	0.002	1.22	0.041	1.23	0.015
1428332_at	RIKEN cDNA 1500004A08 gene	1500004A08Rik	2.22	0.272	2.95	0.231	1.13	0.118	1.24	0.290	1.24	0.028
1450057_at	RIKEN cDNA 2610042O14 gene	2610042O14Rik	1.13	0.410	1.07	0.757	1.02	0.902	1.06	0.641	1.24	0.006
1453226_at	RIKEN cDNA 3000004C01 gene	3000004C01Rik	1.15	0.254	1.37	0.062	1.13	0.392	1.13	0.034	1.24	0.041
1429165_at	RIKEN cDNA 3110001I22 gene	3110001I22Rik	-1.05	0.500	1.18	0.984	-1.03	0.757	-1.01	0.750	1.24	0.043
1418996_a_at	RIKEN cDNA 4930469P12 gene	4930469P12Rik	1.14	0.118	1.19	0.201	1.18	0.037	1.23	0.011	1.24	0.037
1428457_at	RIKEN cDNA 5830472M02 gene	5830472M02Rik	1.29	0.161	1.57	0.024	1.18	0.058	1.21	0.005	1.24	0.016
1444061_at	RIKEN cDNA A030004J04 gene	A030004J04Rik	1.23	0.715	1.49	0.677	1.21	0.069	1.3	0.058	1.24	0.003
1441068_at	RIKEN cDNA A130001G05 gene	A130001G05Rik	1.77	0.697	1.86	0.664	-1.09	0.818	1.78	0.142	1.24	0.012
1456336_at	RIKEN cDNA A330102K23 gene	A330102K23Rik	1.24	0.894	-1.22	0.367	-1.07	0.592	-1.46	0.234	1.24	0.035
1418279_a_at	A kinase (PRKA) anchor protein 1	Akap1	2.75	0.439	3.76	0.218	1.19	0.271	1.36	0.007	1.24	0.017
1419115_at	asparagine-linked glycosylation 14 homolog (yeast)	Alg14	-1.06	0.540	-1.08	0.537	1.14	0.504	-1.06	0.495	1.24	0.030
1418250_at	ADP-ribosylation factor 4-like	Arfl4	1.06	0.604	1.05	0.560	-1.01	0.401	1.13	0.271	1.24	0.024
1454197_a_at	coiled-coil domain containing 86	Ccdc86	1.61	0.509	2.12	0.035	1.04	0.332	1.14	0.094	1.24	0.010
1424144_at	chromatin licensing and DNA replication factor 1	Cdt1	1.34	0.456	1.63	0.057	1.13	0.002	1.23	0.096	1.24	0.007
1426886_at	ceroid-lipofuscinosis, neuronal 5	Cln5	1.65	0.194	1.86	0.160	1.2	0.015	1.1	0.210	1.24	0.012
1435281_at	carnitine palmitoyltransferase 1c	Cpt1c	1.16	0.207	1.35	0.020	1.18	0.159	1.1	0.139	1.24	0.046
1419645_at	cleavage stimulation factor, 3' pre-RNA subunit 2	Cstf2	1.23	0.163	1.33	0.023	1.14	0.043	1.09	0.063	1.24	0.003
1440085_at	ectodysplasin A2 isoform receptor	Eda2r	1.43	0.232	2.18	0.029	1.35	0.006	1.15	0.032	1.24	0.006
1422430_at	fidgetin-like 1	Fignl1	1.14	0.108	1.33	0.116	1.34	0.052	1.25	0.018	1.24	0.045
1429403_x_at	glycosyltransferase 8 domain containing 2	Glt8d2	-1.03	0.658	1.05	0.971	-1.07	0.476	-1.01	0.784	1.24	0.046
1436930_x_at	hydroxymethylbilane synthase /// similar to hydroxymethylbilane synthase	Hmbs /// LOC6238	-1.06	0.457	1.01	0.657	1.34	0.173	-1.09	0.378	1.24	0.016
1448167_at	interferon gamma receptor 1	Ifngr1	-1.03	0.687	1.23	0.237	1.27	0.182	1.13	0.009	1.24	0.010
1452144_a_at	mitochondrial ribosomal protein L44	Mrpl44	-1.12	0.459	-1.03	0.549	-1	0.801	1.05	0.099	1.24	0.022
1449559_at	homeo box, msh-like 2	Msx2	1.21	0.051	1.4	0.002	1.13	0.346	1.13	0.015	1.24	0.015

1448967_at	nipsnap homolog 3A (C. elegans)	Nipsnap3a	1.14	0.276	1.28	0.113	1.16	0.110	1.04	0.232	1.24	0.031
1424839_a_at	NOL1/NOP2/Sun domain family, member 4	Nsun4	1.23	0.051	1.59	0.009	1.28	0.047	1.31	0.001	1.24	0.002
1449017_at	nuclear transport factor 2	Nutf2	1.22	0.263	1.52	0.011	1.16	0.093	1.23	0.004	1.24	0.002
1425784_a_at	olfactomedin 1	Olfm1	-1.22	0.025	-1.18	0.259	1.19	0.287	-1.03	0.527	1.24	0.047
1451069_at	proviral integration site 3	Pim3	1.91	0.665	1.61	0.611	1.12	0.380	1.23	0.031	1.24	0.006
1441848_at	Phosphomannomutase 2	Pmm2	1.06	0.500	1.17	0.594	1.07	0.337	1.49	0.062	1.24	0.005
1450519_a_at	protein kinase, cAMP dependent, catalytic, alpha	Prkaca	-1.13	0.284	-1.02	0.771	1.11	0.426	-1.07	0.380	1.24	0.043
1417323_at	proline/serine-rich coiled-coil 1	Psrc1	1.09	0.506	1.46	0.007	1.22	0.004	1.16	0.006	1.24	0.009
1439440_x_at	protein tyrosine kinase 9-like (A6-related protein)	Ptk9l	-1.2	0.402	-1.02	0.583	1.22	0.096	1.02	0.863	1.24	0.016
1432538_a_at	replication factor C (activator 1) 3	Rfc3	4.97	0.204	6.5	0.028	1.34	0.099	1.32	0.025	1.24	0.015
1452399_at	regulator of G-protein signaling 6	Rgs6	1.11	0.313	1.22	0.286	1.1	0.043	1.12	0.479	1.24	0.013
1453752_at	ribosomal protein L17	Rpl17	-1.12	0.453	1.02	0.655	1.14	0.286	1.04	0.190	1.24	0.035
1448868_at	SCAN domain-containing 1	Scand1	-1.03	0.657	1.13	0.322	1.15	0.097	1.14	0.122	1.24	0.044
1451044_at	survivor of motor neuron protein interacting protein 1	Sip1	-1.11	0.386	1.06	0.800	1.03	0.946	1.15	0.008	1.24	0.042
1436324_at	START domain containing 9 /// similar to StAR-related lipid transfer protein	Stard9 /// LOC668	1.16	0.935	-1.25	0.434	1.39	0.164	-1.12	0.049	1.24	0.038
1416345_at	translocase of inner mitochondrial membrane 8 homolog a1 (yeast)	Timm8a1	1.03	0.760	1.25	0.019	1.2	0.038	1.16	0.025	1.24	0.007
1454836_at	transmembrane protein 18	Tmem18	1.03	0.718	1.17	0.156	1.18	0.136	1.2	0.026	1.24	0.009
1430045_at	translin-associated factor X	Tsnax	-1.13	0.172	1.01	0.760	1.44	0.103	-1.09	0.303	1.24	0.026
1428402_at	zinc finger, CCHC domain containing 3	Zcchc3	1.31	0.591	1.47	0.318	1.51	0.501	1.34	0.309	1.24	0.022
1434085_at	zinc finger protein 523	Zfp523	-1.05	0.585	1.01	0.829	1.01	0.887	-1.02	0.820	1.24	0.035
1420095_s_at	zinc finger proliferation 1	Zipro1	-1.08	0.472	1.27	0.948	1.2	0.026	1.55	0.016	1.24	0.001
1433936_at	RIKEN cDNA 0610010E21 gene	0610010E21Rik	1.15	0.022	1.46	0.010	1.19	0.133	1.19	0.008	1.25	0.019
1455545_at	RIKEN cDNA 1110065P20 gene	1110065P20Rik	1.08	0.440	1.29	0.006	1.03	0.675	1.19	0.000	1.25	0.003
1428684_at	RIKEN cDNA 1500001M20 gene	1500001M20Rik	1.03	0.799	-1.04	0.568	1.07	0.116	1.15	0.066	1.25	0.038
1442137_at	RIKEN cDNA 2010000I03 gene	2010000I03Rik	1.06	0.816	1.28	0.927	1.02	0.757	1.11	0.328	1.25	0.049
1441796_at	RIKEN cDNA 2010309E21 gene	2010309E21Rik	-1.06	0.575	1.12	0.677	1	0.995	1	0.927	1.25	0.020
1428619_at	RIKEN cDNA 2310005N03 gene	2310005N03Rik	-1.05	0.582	1.17	0.427	1.18	0.191	1.02	0.256	1.25	0.019
1452093_at	RIKEN cDNA 2500001K11 gene	2500001K11Rik	1.11	0.483	1.28	0.092	1.15	0.129	1.17	0.030	1.25	0.021
1460641_a_at	RIKEN cDNA 3100004P22 gene /// RIKEN cDNA 2310022K01 gene	3100004P22Rik ///	1.21	0.486	1.3	0.307	1.03	0.505	1.04	0.248	1.25	0.041
1456602_at	RIKEN cDNA 4932417I16 gene	4932417I16Rik	-1.03	0.779	-1.01	0.780	1.06	0.677	1.09	0.382	1.25	0.001
1430701_a_at	RIKEN cDNA 5730528L13 gene	5730528L13Rik	3.17	0.244	3.24	0.084	1.18	0.105	1.28	0.013	1.25	0.030
1423893_x_at	amyloid beta (A4) precursor protein-binding, family B, member 1	Apbb1	-1.05	0.458	-1.08	0.150	1.18	0.204	-1.05	0.576	1.25	0.001
1417655_a_at	arsenate resistance protein 2	Ars2	-1.11	0.397	1.14	0.341	1.31	0.009	1.24	0.048	1.25	0.020
1439036_a_at	ATPase, Na+/K+ transporting, beta 1 polypeptide	Atp1b1	1.32	0.285	1.52	0.222	1.17	0.180	1.09	0.435	1.25	0.018
1434711_at	cDNA sequence BC030867	BC030867	1.07	0.755	1.2	0.142	1.2	0.003	1.19	0.038	1.25	0.015
1429561_at	BRF2, subunit of RNA polymerase III transcription initiation factor, BRF1-li	Brf2	-1.07	0.448	1.24	0.642	1.2	0.039	1.16	0.023	1.25	0.004
1426165_a_at	caspase 3	Casp3	2.04	0.430	2.21	0.230	1.16	0.354	1.29	0.121	1.25	0.042
1456085_x_at	CD151 antigen	Cd151	-1.11	0.314	1.09	0.673	1.15	0.123	1.12	0.109	1.25	0.017
1419590_at	cytochrome P450, family 2, subfamily b, polypeptide 9	Cyp2b9	-1.18	0.283	1.31	0.695	1.09	0.954	1.14	0.681	1.25	0.036
1451641_at	debranching enzyme homolog 1 (S. cerevisiae)	Dbr1	-1.07	0.528	1.21	0.873	1.14	0.103	1.18	0.024	1.25	0.015
1416751_a_at	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	Ddx20	1.12	0.539	1.35	0.024	1.06	0.181	1.17	0.010	1.25	0.024
1434695_at	denticleless homolog (Drosophila)	Dtl	1.33	0.004	1.55	0.013	1.12	0.272	1.05	0.294	1.25	0.031
1424697_at	DTW domain containing 1	Dtwd1	1.06	0.013	1.13	0.124	1.2	0.024	1.06	0.049	1.25	0.025
1437187_at	E2F transcription factor 7	E2f7	-1.02	0.730	1.37	0.145	1.35	0.022	1.12	0.238	1.25	0.036
1452639_at	ectonucleotide pyrophosphatase/phosphodiesterase 4	Enpp4	1.19	0.823	1.47	0.335	1.05	0.839	-1.02	0.631	1.25	0.002
1428120_at	F-box and WD-40 domain protein 9	Fbxw9	-1.06	0.385	1.17	0.183	1.1	0.373	-1.07	0.496	1.25	0.001
1418361_at	growth arrest specific 8	Gas8	1.06	0.847	1.37	0.163	1.28	0.200	-1.05	0.419	1.25	0.037
1416593_at	glutaredoxin	Glrx	4.58	0.267	6.04	0.097	1.1	0.152	1.27	0.062	1.25	0.043
1448942_at	guanine nucleotide binding protein (G protein), gamma 11	Gng11	-1.07	0.407	1.07	0.381	1.17	0.002	-1.03	0.558	1.25	0.000
1427027_a_at	general transcription factor III A	Gtf3a	1.32	0.532	1.38	0.112	1.08	0.228	1.14	0.025	1.25	0.024
1435451_at	helicase, mus308-like (Drosophila)	Hel308	1.18	0.761	1.24	0.223	1.19	0.602	1.2	0.184	1.25	0.046
1435866_s_at	histone 3, H2a	Hist3h2a	-1.05	0.609	1.21	0.041	1.21	0.013	1.28	0.008	1.25	0.005
1417948_s_at	interleukin enhancer binding factor 2	Ilf2	1.13	0.157	1.31	0.018	1.18	0.054	1.05	0.161	1.25	0.008
1438095_x_at	Nucleolar complex associated 4 homolog (S. cerevisiae)	Noc4l	-1.16	0.402	-1.03	0.704	1.04	0.226	1.21	0.182	1.25	0.048
1454934_at	protein phosphatase 1F (PP2C domain containing)	Ppm1f	1.08	0.536	1.3	0.098	1.07	0.650	1.05	0.376	1.25	0.036
1437234_x_at	protein arginine N-methyltransferase 2	Prmt2	-1.31	0.301	-1.11	0.461	1.21	0.054	1.12	0.004	1.25	0.018
1450639_at	solute carrier family 28 (sodium-coupled nucleoside transporter), member	Slc28a2 /// LOC38	-1.29	0.376	-1.25	0.352	-1.28	0.067	1.03	0.724	1.25	0.027
1426429_at	THAP domain containing 7	Thap7	-1.07	0.377	1.11	0.841	-1	0.798	1.48	0.110	1.25	0.026

1428634_at	TWIST neighbor	Twistnb	-1.04	0.695	1.2	0.435	1.12	0.501	1.12	0.212	1.25	0.029
1451080_at	ubiquitin specific peptdiase 1	Usp1	1.38	0.036	1.7	0.011	1.28	0.022	1.17	0.029	1.25	0.042
1427933_at	vacuolar protein sorting 33B (yeast)	Vps33b	3.28	0.344	3.82	0.149	1.24	0.398	1.19	0.167	1.25	0.018
1416224_at	zinc finger and BTB domain containing 17	Zbtb17	-1.3	0.234	-1.15	0.391	-1.14	0.208	1.02	0.778	1.25	0.033
1434022_at	zinc finger and BTB domain containing 33	Zbtb33	-1.01	0.735	1.16	0.437	1.26	0.003	1.29	0.009	1.25	0.013
1457285_at	zinc finger protein 187	Zfp187	1.33	0.116	1.58	0.070	1.2	0.088	1.2	0.016	1.25	0.011
1424670_s_at	zinc finger, FYVE domain containing 21	Zfyve21	-1.02	0.552	1.09	0.455	1.13	0.047	1.23	0.001	1.25	0.018
1448540_a_at	RIKEN cDNA 0610012G03 gene /// hypothetical protein LOC638521	0610012G03Rik //	-1.06	0.577	1.08	0.985	1.14	0.186	1.11	0.031	1.26	0.044
1424106_at	RIKEN cDNA 1200003C05 gene	1200003C05Rik	1.15	0.065	1.14	0.104	1.13	0.104	1.1	0.170	1.26	0.041
1430846_at	RIKEN cDNA 1700061G19 gene	1700061G19Rik	1.21	0.472	1.12	0.921	-1.08	0.489	1.13	0.962	1.26	0.017
1428202_at	RIKEN cDNA 1810037C20 gene	1810037C20Rik	-1.02	0.701	-1.04	0.647	-1.08	0.144	-1.12	0.079	1.26	0.032
1421498_a_at	RIKEN cDNA 2010204K13 gene	2010204K13Rik	-1.13	0.484	-1	0.720	1.14	0.604	1.15	0.036	1.26	0.044
1460456_at	RIKEN cDNA 2010316F05 gene	2010316F05Rik	-1.15	0.422	1.28	0.592	-1	0.675	1.08	0.747	1.26	0.031
1452847_at	RIKEN cDNA 2410008K03 gene	2410008K03Rik	-1.02	0.673	-1.07	0.472	1.07	0.663	1.06	0.665	1.26	0.017
1453314_x_at	RIKEN cDNA 2610039C10 gene	2610039C10Rik	-1.14	0.408	1.09	0.997	1.16	0.482	1.07	0.287	1.26	0.021
1439901_at	RIKEN cDNA 2610208M17 gene	2610208M17Rik	-1.12	0.462	-1.17	0.427	1.12	0.050	-1.01	0.776	1.26	0.016
1438321_x_at	RIKEN cDNA 4930504E06 gene	4930504E06Rik	-1.15	0.405	1.02	0.689	1.18	0.038	1.1	0.150	1.26	0.027
1428821_at	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acy	Agpat2	1.51	0.249	1.8	0.047	1.21	0.012	1.18	0.042	1.26	0.006
1424322_at	apurinic/apyrimidinic endonuclease 2	Apex2	2.25	0.463	2.89	0.070	-1.24	0.128	1.03	0.874	1.26	0.042
1424513_at	ATPase, H+ transporting, lysosomal V0 subunit A2	Atp6v0a2	1.28	0.897	1.36	0.096	-1.01	0.786	1.04	0.425	1.26	0.011
1416250_at	B-cell translocation gene 2, anti-proliferative	Btg2	1.54	0.167	2.46	0.018	1.32	0.271	1.18	0.137	1.26	0.002
1434529_x_at	checkpoint with forkhead and ring finger domains	Chfr	-1.23	0.379	-1.13	0.450	1.13	0.383	1.02	0.527	1.26	0.030
1435863_at	COMM domain containing 6	Commd6	1.44	0.059	1.63	0.012	1.12	0.038	1.2	0.044	1.26	0.012
1419872_at	colony stimulating factor 1 receptor	Csf1r	-1.15	0.307	-1.29	0.161	1.13	0.377	1.05	0.931	1.26	0.038
1456891_at	DENN/MADD domain containing 2C	Dennd2c	1.56	0.475	2.04	0.021	1.04	0.921	1.09	0.374	1.26	0.023
1434027_at	Down syndrome critical region gene 1-like 2	Dscr1l2	1.1	0.354	-1.01	0.798	1.44	0.037	1.19	0.006	1.26	0.027
1452681_at	deoxythymidylate kinase	Dtymk	1.14	0.009	1.29	0.018	1.17	0.088	1.18	0.005	1.26	0.016
1418649_at	EGL nine homolog 3 (C. elegans)	Egln3	-1.04	0.642	-1.03	0.754	1.09	0.822	-1.05	0.275	1.26	0.005
1450898_at	hippocampus abundant gene transcript 1	Hiat1	1.26	0.630	1.4	0.449	1.12	0.223	1.1	0.160	1.26	0.034
1423068_at	intraflagellar transport 172 homolog (Chlamydomonas)	Ift172	1.41	0.622	-1.05	0.410	-1.07	0.271	1.28	0.077	1.26	0.013
1456846_at	similar to RP58 protein	LOC382639	1.09	0.570	1.11	0.619	1.32	0.225	1.18	0.121	1.26	0.040
1442818_at	hypothetical protein LOC671796 /// hypothetical protein LOC675117	LOC671796 /// LO	-1.03	0.915	1.14	0.922	1.48	0.306	1.15	0.902	1.26	0.005
1438563_s_at	mitochondrial ribosomal protein S24	Mrps24	-1.18	0.412	-1	0.559	1.1	0.470	1.04	0.507	1.26	0.035
1416914_s_at	mammary tumor virus receptor 2	Mtvr2	1.76	0.506	1.95	0.184	1.14	0.027	1.12	0.402	1.26	0.029
1432187_at	nucleoporin 43	Nup43	-1.11	0.480	1.05	0.836	1.11	0.168	1.06	0.634	1.26	0.004
1424081_at	polycomb group ring finger 6	Pcgf6	1.21	0.147	1.48	0.009	1.16	0.049	1.2	0.002	1.26	0.048
1447864_s_at	pogo transposable element with KRAB domain	Pogk	-1.16	0.422	1.24	0.845	1.11	0.010	1.28	0.010	1.26	0.016
1448315_a_at	pyrroline-5-carboxylate reductase family, member 2	Pycr2	-1.12	0.446	1.07	0.711	1.1	0.120	1.07	0.432	1.26	0.038
1452736_at	R3H domain and coiled-coil containing 1	R3hcc1	1.95	0.295	2.37	0.052	1.21	0.054	1.3	0.003	1.26	0.029
1434427_a_at	ring finger protein 157	Rnf157	-1.27	0.267	1.01	0.548	1.13	0.378	1.09	0.278	1.26	0.029
1417811_at	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	Slc24a6	1.01	0.500	1.21	0.822	1.07	0.966	-1.15	0.098	1.26	0.002
1438426_at	transmembrane protein 58	Tmem58	-1.11	0.497	1.05	0.853	1.21	0.087	1.09	0.041	1.26	0.010
1454861_at	taxilin alpha	Txlna	1.01	0.906	1.32	0.068	1.18	0.089	1.2	0.006	1.26	0.004
1442192_at	thymidylate synthase	Tyms	1.19	0.977	1.26	0.970	-1	0.887	1.09	0.929	1.26	0.042
1453039_at	zinc finger protein 335	Zfp335	-1.13	0.380	1.03	0.932	1.02	0.981	1.06	0.379	1.26	0.021
1418033_s_at	zinc finger protein 535	Zfp535	-1.03	0.780	1.2	0.137	1.3	0.182	1.19	0.274	1.26	0.034
1447403_a_at	Zinc finger, MYND domain containing 19	Zmynd19	-1.1	0.476	1.31	0.040	1.12	0.443	1.35	0.015	1.26	0.034
1436747_at	RIKEN cDNA 1110014K08 gene /// hypothetical protein LOC664786 /// hyp	1110014K08Rik ///	1	0.953	-1.05	0.144	1.06	0.462	1.06	0.234	1.27	0.037
1436796_at	RIKEN cDNA 1110061A14 gene	1110061A14Rik	-1.01	0.774	1.22	0.333	1.16	0.060	1.47	0.020	1.27	0.011
1453822_at	RIKEN cDNA 1700010H15 gene	1700010H15Rik	1.1	0.806	-1.26	0.142	-1.29	0.349	1.28	0.273	1.27	0.036
1437110_at	RIKEN cDNA 2810474O19 gene	2810474O19Rik	1.07	0.362	1.4	0.166	-1.05	0.593	1.31	0.014	1.27	0.034
1417479_at	RIKEN cDNA 4930511A21 gene	4930511A21Rik	3.38	0.288	2.52	0.032	1.34	0.127	1.14	0.456	1.27	0.042
1457939_at	RIKEN cDNA 4930578N16 gene	4930578N16Rik	1.07	0.582	1.46	0.889	-1.02	0.606	-1.28	0.149	1.27	0.046
1429364_at	RIKEN cDNA 4930579G24 gene	4930579G24Rik	1.01	0.767	1.21	0.021	1.4	0.037	1.27	0.036	1.27	0.003
1443344_at	RIKEN cDNA 4932409I22 gene	4932409I22Rik	-1.19	0.298	1.6	0.430	1.16	0.279	-1.18	0.501	1.27	0.029
1441779_at	RIKEN cDNA 9530006C21 gene	9530006C21Rik	1.04	0.919	1.21	0.884	1.13	0.402	1.17	0.417	1.27	0.024
1438036_x_at	expressed sequence AW061290	AW061290	-1.5	0.306	-1.46	0.262	-1.06	0.220	-1.08	0.572	1.27	0.003
1440831_at	BTB and CNC homology 1	Bach1	-1.05	0.574	1.13	0.939	1.23	0.042	1.12	0.099	1.27	0.014

1431079_at	C1q and tumor necrosis factor related protein 2	C1qtnf2	1.19	0.401	1.13	0.692	-1.07	0.242	1.02	0.796	1.27	0.025
1424475_at	calcium/calmodulin-dependent protein kinase kinase 2, beta	Camkk2	-1.14	0.293	1.01	0.949	1.02	0.937	1.14	0.377	1.27	0.005
1424529_s_at	cell growth regulator with EF hand domain 1	Cgref1	-1.23	0.223	1.18	0.672	1.13	0.079	1.16	0.011	1.27	0.048
1448657_a_at	DnaJ (Hsp40) homolog, subfamily B, member 10	Dnajb10	-1.07	0.425	1.1	0.788	1.17	0.144	1.03	0.840	1.27	0.043
1431422_a_at	dual specificity phosphatase 14	Dusp14	1.88	0.299	2.21	0.031	1.32	0.019	1.37	0.006	1.27	0.039
1431190_x_at	fumarylacetoacetate hydrolase domain containing 2A	Fahd2a	-1.07	0.545	-1.04	0.537	-1.04	0.606	-1.04	0.449	1.27	0.002
1421731_a_at	flap structure specific endonuclease 1	Fen1	1.18	0.546	1.56	0.001	1.28	0.003	1.25	0.030	1.27	0.001
1429942_at	glucocorticoid modulatory element binding protein 1	Gmeb1	1.17	0.869	1.1	0.953	1.28	0.063	-1.02	0.738	1.27	0.043
1419462_s_at	gene trap locus 3	Gtl3	1.08	0.213	1.26	0.120	1.19	0.121	1.14	0.029	1.27	0.020
1450746_at	kelch-like ECH-associated protein 1	Keap1	-1.14	0.383	-1.05	0.555	1.09	0.155	1.06	0.482	1.27	0.027
1448758_at	similar to nuclear receptor binding factor 2 /// similar to nuclear receptor bir	LOC627232 /// LO	-1.08	0.155	-1.01	0.823	1.04	0.869	1.05	0.000	1.27	0.008
1417931_at	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	Ndst2	1.34	0.412	1.38	0.459	1.14	0.323	1.09	0.119	1.27	0.023
1418289_at	nestin	Nes	-1.25	0.373	-1.2	0.449	-1.11	0.570	-1.12	0.147	1.27	0.007
1417166_at	PC4 and SFRS1 interacting protein 1	Psip1	1.04	0.933	1.06	0.731	1.23	0.014	1.26	0.035	1.27	0.027
1418666_at	pentraxin related gene	Ptx3	-1.23	0.052	1.18	0.362	-1.04	0.972	1.29	0.181	1.27	0.026
1437742_at	RAB21, member RAS oncogene family	Rab21	-1.06	0.258	1.21	0.136	1.13	0.334	1.09	0.754	1.27	0.005
1431090_at	Ssu72 RNA polymerase II CTD phosphatase homolog (yeast)	Ssu72	1.21	0.710	1.12	0.370	-1.34	0.198	-1.07	0.510	1.27	0.033
1429590_at	transforming, acidic coiled-coil containing protein 1	Tacc1	1.12	0.442	1.18	0.428	1.35	0.569	-1.07	0.311	1.27	0.031
1458244_at	transmembrane and coiled-coil domains 5	Tmco5	-1.05	0.879	-1.45	0.090	-1.87	0.082	-1.18	0.094	1.27	0.019
1424990_at	transmembrane protein 142A	Tmem142a	1.04	0.627	1.06	0.442	1.15	0.108	1.09	0.052	1.27	0.025
1451321_a_at	RIKEN cDNA 0610033I05 gene	0610033I05Rik	-1.07	0.482	1.64	0.066	1.34	0.009	1.07	0.148	1.28	0.040
1429259_a_at	RIKEN cDNA 1810014B01 gene	1810014B01Rik	-1.07	0.531	-1.07	0.528	1.07	0.575	1.05	0.361	1.28	0.048
1455529_at	RIKEN cDNA 2700083E18 gene	2700083E18Rik	1.04	0.254	1.28	0.015	1.08	0.082	1.15	0.004	1.28	0.013
1441086_at	RIKEN cDNA 4930451I11 gene	4930451I11Rik	1.93	0.066	2.56	0.234	1.92	0.422	-1.96	0.084	1.28	0.009
1429955_at	RIKEN cDNA 5031434O11 gene	5031434O11Rik	-1.13	0.472	-1.05	0.426	1.15	0.780	-1.14	0.467	1.28	0.016
1423072_at	RIKEN cDNA 6720475J19 gene /// similar to putative retrovirus-related ga	6720475J19Rik ///	-1.05	0.636	1.11	0.443	1.09	0.684	1.23	0.029	1.28	0.027
1443175_at	RIKEN cDNA A830010M09 gene	A830010M09Rik	1.11	0.790	1.39	0.956	-1.53	0.111	2.8	0.581	1.28	0.027
1436099_at	expressed sequence AI836003	AI836003	1.07	0.686	1.31	0.411	1.35	0.078	1.39	0.236	1.28	0.033
1434045_at	cyclin-dependent kinase inhibitor 1B	Cdkn1b	-1.12	0.410	-1.35	0.154	1.16	0.316	-1.04	0.881	1.28	0.019
1427183_at	epidermal growth factor-containing fibulin-like extracellular matrix protein 1	Efemp1	1.1	0.726	1.29	0.958	1.41	0.283	-1.1	0.307	1.28	0.007
1452085_at	GATA zinc finger domain containing 1	Gatad1	1.07	0.456	1.2	0.131	1.13	0.674	1.01	0.905	1.28	0.031
1441894_s_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffold prote	Grasp	-1.19	0.391	-1	0.573	1.24	0.021	1.34	0.002	1.28	0.007
1428985_at	integrator complex subunit 12	Ints12	1.2	0.026	1.36	0.029	1.29	0.080	1.2	0.218	1.28	0.027
1421903_at	intersex-like (Drosophila)	Ixl	1.3	0.143	1.31	0.046	-1	0.950	1.1	0.417	1.28	0.041
1436915_x_at	lysosomal-associated protein transmembrane 4B	Laptm4b	-1.29	0.314	-1.22	0.358	1.21	0.346	-1.07	0.184	1.28	0.031
1416503_at	latexin	Lxn	1.12	0.056	1.31	0.015	1.14	0.197	1.16	0.043	1.28	0.014
1422431_at	melanoma antigen, family E, 1	Magee1	1.29	0.484	1.65	0.052	1.24	0.074	1.04	0.314	1.28	0.000
1416671_a_at	mucolipin 1	Mcoln1	2.53	0.328	2.74	0.246	1.07	0.073	1.02	0.766	1.28	0.037
1450458_at	nuclear receptor coactivator 2	Ncoa2	-1.21	0.436	-1.53	0.063	-1.15	0.372	1.4	0.599	1.28	0.037
1428277_at	OTU domain containing 6B	Otud6b	1.19	0.044	1.36	0.032	1.02	0.989	1.08	0.432	1.28	0.040
1441967_at	Parkinson disease 7 domain containing 1	Pddc1	1.3	0.531	1.27	0.446	1.31	0.264	1.08	0.640	1.28	0.012
1436198_at	prolyl endopeptidase	Prep	-1.21	0.156	1.15	0.485	1.54	0.266	1.15	0.582	1.28	0.011
1433533_x_at	protein kinase, AMP-activated, gamma 1 non-catalytic subunit	Prkag1	-1.38	0.202	-1.15	0.391	-1.03	0.404	1.06	0.458	1.28	0.020
1417035_at	SAC3 domain containing 1	Sac3d1	1.04	0.715	1.36	0.026	1.23	0.034	1.23	0.023	1.28	0.048
1434291_a_at	small EDRK-rich factor 1	Serf1	-1.22	0.332	-1.03	0.689	1.21	0.693	-1.11	0.112	1.28	0.014
1415802_at	solute carrier family 16 (monocarboxylic acid transporters), member 1	Slc16a1	1.16	0.411	1.35	0.023	1.17	0.009	1.19	0.001	1.28	0.010
1439369_x_at	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	Slc9a3r2	-1.13	0.475	-1.07	0.641	1.02	0.737	1.12	0.620	1.28	0.014
1457680_a_at	transmembrane protein 69	Tmem69	1.06	0.898	1.19	0.682	1.08	0.001	1.01	0.833	1.28	0.024
1427593_at	tripartite motif protein 8	Trim8	1.32	0.749	1.1	0.667	2.77	0.281	1.14	0.811	1.28	0.016
1421050_at	vacuolar protein sorting 25 (yeast)	Vps25	-1.07	0.501	1.25	0.927	1.15	0.292	-1.17	0.218	1.28	0.037
1451244_a_at	zinc finger protein 422	Zfp422	1.15	0.006	1.32	0.020	1.18	0.114	1.04	0.258	1.28	0.007
1435202_at	zinc finger protein 574	Zfp574	1.05	0.865	1.21	0.617	1.35	0.083	1.21	0.039	1.28	0.049
1429541_at	RIKEN cDNA 2500002G23 gene	2500002G23Rik	-1.19	0.005	1.31	0.181	1.37	0.228	-1.11	0.465	1.29	0.021
1438982_s_at	RIKEN cDNA 2810417J12 gene	2810417J12Rik	-1.59	0.254	-1.39	0.345	1.88	0.163	1.11	0.844	1.29	0.025
1444450_at	RIKEN cDNA 9530096D07 gene	9530096D07Rik	1.22	0.541	1.01	0.686	1.59	0.623	-1.12	0.371	1.29	0.020
1427959_at	abhydrolase domain containing 10	Abhd10	1.04	0.551	1.38	0.026	1.27	0.027	1.25	0.029	1.29	0.029
1435498_at	ADP-ribosylation factor interacting protein 2	Arfip2	1.03	0.733	1.18	0.064	1.19	0.035	1.27	0.091	1.29	0.005
1454814_s_at	expressed sequence AU021838	AU021838	1.26	0.123	1.58	0.015	1.17	0.023	1.28	0.052	1.29	0.007

1451246_s_at	aurora kinase B	Aurkb	1.11	0.005	1.36	0.019	1.18	0.041	1.2	0.005	1.29	0.028
1435454_a_at	cDNA sequence BC006779	BC006779	-1.1	0.378	1.11	0.622	1.21	0.211	1.14	0.177	1.29	0.000
1452216_at	cDNA sequence BC025519	BC025519	1.07	0.485	1.11	0.276	1.11	0.422	1.23	0.081	1.29	0.021
1415975_at	calcium regulated heat stable protein 1	Carhsp1	1.61	0.152	1.91	0.034	1.22	0.024	1.17	0.056	1.29	0.008
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	1.16	0.333	1.69	0.005	1.25	0.005	1.21	0.002	1.29	0.003
1454640_at	coiled-coil-helix-coiled-coil-helix domain containing 7	Chchd7	-1.02	0.649	-1.04	0.656	1.2	0.142	1.19	0.131	1.29	0.038
1415948_at	cellular repressor of E1A-stimulated genes 1	Creg1	1.12	0.264	1.17	0.053	1.06	0.875	1.27	0.208	1.29	0.005
1417583_a_at	charged amino acid rich leucine zipper 1	Crlz1	1	0.712	1.51	0.086	1.04	0.879	1.11	0.520	1.29	0.034
1436126_at	dynein, axonemal, light intermediate polypeptide 1	Dnali1	-1.18	0.226	-1.16	0.113	-1.07	0.267	-1.04	0.561	1.29	0.032
1435926_at	RIKEN cDNA E030003F13 gene	E030003F13Rik	-1.03	0.574	1.4	0.017	1.23	0.022	1.27	0.028	1.29	0.047
1454963_at	RIKEN cDNA E430028B21 gene	E430028B21Rik	1.17	0.113	1.5	0.005	1.2	0.060	1.16	0.012	1.29	0.027
1434263_at	RIKEN cDNA F630110N24 gene	F630110N24Rik	-1.11	0.425	-1.09	0.518	-1.11	0.350	1.01	0.909	1.29	0.035
1458753_at	gene model 941, (NCBI)	Gm941	1.04	0.560	1.09	0.599	1.1	0.996	1.49	0.075	1.29	0.021
1455324_at	hypothetical LOC433022	LOC433022	-1.06	0.519	1.1	0.944	1.17	0.007	1.25	0.025	1.29	0.013
1460441_at	similar to Zinc finger X-linked protein ZXDB	LOC668166	-1.12	0.354	1.09	0.944	1.22	0.070	1.02	0.751	1.29	0.033
1415922_s_at	MARCKS-like 1	Marcksl1	1.24	0.395	1.56	0.153	1.17	0.112	1.14	0.008	1.29	0.012
1428608_at	myosin light chain, regulatory B	Mylc2b	1.04	0.566	1.36	0.015	1.15	0.117	1.14	0.119	1.29	0.004
1423711_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor	Ndufaf1	1.4	0.318	1.77	0.017	1.19	0.003	1.23	0.020	1.29	0.019
1428951_at	nucleolar protein 8	Nol8	-1.02	0.720	1.16	0.601	1.11	0.520	1.05	0.812	1.29	0.014
1423534_at	programmed cell death 2	Pdcd2	-1.06	0.325	1.2	0.252	1.15	0.265	1.26	0.005	1.29	0.002
1451210_at	phosphatidic acid phosphatase type 2c	Ppap2c	-1.12	0.220	-1.01	0.824	1.1	0.264	1.15	0.100	1.29	0.043
1449092_at	protein phosphatase 1D magnesium-dependent, delta isoform	Ppm1d	-1.03	0.558	1.5	0.007	1.16	0.026	1.23	0.015	1.29	0.024
1455002_at	protein tyrosine phosphatase 4a1	Ptp4a1	1.06	0.052	1.38	0.047	1.21	0.058	1.37	0.010	1.29	0.002
1437052_s_at	solute carrier family 2 (facilitated glucose transporter), member 3	Slc2a3	-1.03	0.686	-1	0.594	1.26	0.090	1.28	0.016	1.29	0.020
1417725_a_at	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	Sssca1	-1.18	0.414	-1.02	0.531	1.19	0.444	1.05	0.230	1.29	0.006
1418370_at	troponin C, cardiac/slow skeletal	Tnnc1	-1.16	0.430	1.1	0.817	1.25	0.229	1.07	0.260	1.29	0.034
1459618_at	Three prime repair exonuclease 1	Trex1	1.85	0.451	1.93	0.080	1.14	0.579	-1.09	0.427	1.29	0.027
1436533_at	TROVE domain family, member 2	Trove2	1.18	0.172	1.02	0.999	1.15	0.341	1.12	0.108	1.29	0.032
1437414_at	zinc finger protein 217	Zfp217	1.06	0.126	1.22	0.005	1.01	0.888	1.17	0.006	1.29	0.005
1416651_at	zinc finger, HIT domain containing 2	Znhit2	-1.03	0.683	1.14	0.126	1.07	0.389	1.1	0.067	1.29	0.030
1435333_at	RIKEN cDNA 1110007M04 gene	1110007M04Rik	1.12	0.087	1.39	0.101	1.27	0.005	1.41	0.027	1.3	0.015
1432290_at	RIKEN cDNA 1700040G22 gene	1700040G22Rik	1.34	0.834	1.95	0.463	1.82	0.628	-1.4	0.165	1.3	0.022
1434321_at	RIKEN cDNA 6620401K05 gene	6620401K05Rik	1.47	0.754	1.98	0.105	1.14	0.847	1.12	0.166	1.3	0.044
1439859_at	RIKEN cDNA 9630033F20 gene	9630033F20Rik	-1.21	0.385	-1.03	0.520	1.08	0.553	1.21	0.112	1.3	0.033
1419113_at	adaptor protein complex AP-1, gamma 2 subunit	Ap1g2	-1.2	0.358	-1.11	0.478	-1.07	0.559	1.16	0.437	1.3	0.037
1422168_a_at	brain derived neurotrophic factor	Bdnf	1.23	0.273	1.56	0.011	1.1	0.089	1.18	0.033	1.3	0.043
1428490_at	core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyl	C1galt1	1.14	0.264	1.17	0.174	1.2	0.049	1.17	0.284	1.3	0.049
1436352_at	centrosomal protein 78	Cep78	-1	0.799	1.03	0.874	1.32	0.050	1	0.946	1.3	0.022
1457846_at	COX11 homolog, cytochrome c oxidase assembly protein (yeast)	Cox11	-1.07	0.620	1.41	0.387	-1.04	0.694	1.59	0.455	1.3	0.019
1454648_s_at	DNA segment, Chr 10, Wayne State University 102, expressed	D10Wsu102e	1.35	0.463	1.72	0.014	1.18	0.012	1.38	0.006	1.3	0.026
1452805_at	DNA segment, Chr 11, Wayne State University 47, expressed	D11Wsu47e	-1.06	0.542	1.12	0.978	1.21	0.105	1.12	0.401	1.3	0.045
1439772_at	DNA segment, Chr 1, Brigham & Women's Genetics 0212 expressed	D1Bwg0212e	1.03	0.790	1.49	0.129	1.07	0.681	1.14	0.242	1.3	0.033
1418321_at	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenyme A iso	Dci	-1.05	0.496	1.04	0.977	1.03	0.621	1.06	0.074	1.3	0.010
1429093_at	DNA-damage inducible protein 2	Ddi2	-1.08	0.555	1.02	0.907	-1.03	0.845	1.02	0.829	1.3	0.006
1429499_at	F-box only protein 5	Fbxo5	-1.02	0.801	1.21	0.433	1.13	0.163	1.36	0.077	1.3	0.029
1427416_x_at	similar to dual specificity phosphatase 7	LOC674944	1.12	0.335	1.27	0.053	1.19	0.067	1.17	0.102	1.3	0.016
1459842_x_at	nucleotide binding protein 2	Nubp2	-1.23	0.273	1.05	0.844	1.12	0.478	-1.04	0.575	1.3	0.039
1428339_at	nudix (nucleoside diphosphate linked moiety X)-type motif 21	Nudt21	1.3	0.259	1.38	0.091	1.35	0.003	1.27	0.003	1.3	0.007
1449162_at	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	Pop7	1.21	0.208	1.4	0.014	1.17	0.119	1.11	0.043	1.3	0.017
1451538_at	SRY-box containing gene 9	Sox9	1.48	0.373	1.04	0.915	1.29	0.276	-1.03	0.237	1.3	0.041
1451935_a_at	serine protease inhibitor, Kunitz type 2	Spint2	1.2	0.613	1.19	0.877	1.14	0.194	1.03	0.778	1.3	0.008
1441917_s_at	transmembrane protein 40	Tmem40	1.16	0.856	1.18	0.803	1.12	0.366	-1.22	0.095	1.3	0.030
1456724_x_at	WD repeat domain 79	Wdr79	-1.23	0.396	-1.11	0.453	1.09	0.697	-1.02	0.800	1.3	0.028
1420012_at	X-box binding protein 1	Xbp1	-1.08	0.489	-1.1	0.492	-1.01	0.787	-1.17	0.060	1.3	0.003
1434355_at	zinc finger protein 617	Zfp617	1.25	0.062	1.42	0.034	1.09	0.715	1.21	0.031	1.3	0.006
1455192_at	RIKEN cDNA A230078I05 gene	A230078I05Rik	1.41	0.999	1.47	0.983	1.16	0.192	1.01	0.939	1.31	0.001
1427091_at	expressed sequence AI481105	AI481105	1.99	0.232	2.79	0.192	1.16	0.352	1.15	0.114	1.31	0.013
1447104_at	AT rich interactive domain 1A (Swi1 like)	Arid1a	-1.04	0.543	-1.46	0.176	-1.72	0.042	1.35	0.867	1.31	0.028

1439743_at	expressed sequence AW048948	AW048948	-1.17	0.456	-1.11	0.451	-1.2	0.242	-1.25	0.126	1.31	0.046
1451620_at	C1q-like 3	C1ql3	1.4	0.103	1.22	0.228	1.37	0.159	1.15	0.092	1.31	0.017
1417019_a_at	cell division cycle 6 homolog (S. cerevisiae)	Cdc6	-1.15	0.186	1.51	0.080	1.19	0.170	1.36	0.006	1.31	0.026
1449152_at	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	Cdkn2b	-1.01	0.641	1.19	0.515	1.14	0.082	1.11	0.020	1.31	0.010
1448995_at	chemokine (C-X-C motif) ligand 4	Cxcl4	-1.25	0.146	1.04	0.572	1.09	0.073	-1.04	0.177	1.31	0.013
1455384_x_at	RIKEN cDNA D030056L22 gene	D030056L22Rik	-1.13	0.478	-1.05	0.576	1.4	0.193	1.1	0.216	1.31	0.030
1438822_at	dorso-medial telencephalon gene 2	Dmt2	-1.42	0.292	1.06	0.499	1.5	0.143	-1.28	0.306	1.31	0.013
1431170_at	ephrin A3	Efna3	-1.23	0.171	1.03	0.749	1.09	0.875	-1.04	0.268	1.31	0.010
1435544_at	exosome component 6	Exosc6	-1.08	0.516	1.22	0.509	1.11	0.147	1.26	0.008	1.31	0.012
1426783_at	GCN5 general control of amino acid synthesis-like 2 (yeast)	Gcn5l2	-1.08	0.345	1.12	0.446	1.14	0.018	1.2	0.026	1.31	0.031
1434047_x_at	heterogeneous nuclear ribonucleoprotein A2/B1	Hnrpa2b1	-1.16	0.385	-1.01	0.759	1.16	0.202	1.15	0.205	1.31	0.014
1419455_at	interleukin 10 receptor, beta	Il10rb	1.67	0.199	1.91	0.049	1.28	0.128	1.2	0.002	1.31	0.001
1456092_at	potassium channel tetramerisation domain containing 7	Kctd7	1.55	0.486	1.39	0.258	2.05	0.140	1.71	0.103	1.31	0.006
1429965_at	LON peptidase N-terminal domain and ring finger 2	Lonrf2	-2.01	0.178	-1.64	0.298	1.08	0.999	-1.29	0.178	1.31	0.021
1426516_a_at	lipin 1	Lpin1	1.86	0.108	2.06	0.097	1.27	0.724	1.01	0.971	1.31	0.003
1453264_at	MARVEL (membrane-associating) domain containing 3	Marveld3	-1.3	0.082	1.01	0.813	1.39	0.617	1.23	0.858	1.31	0.035
1417234_at	matrix metallopeptidase 11	Mmp11	1.62	0.315	1.57	0.252	1.16	0.160	1.32	0.031	1.31	0.017
1416852_a_at	neurochondrin	Ncdn	-1.23	0.380	1.13	0.692	1.26	0.191	1.1	0.247	1.31	0.035
1447694_x_at	neogenin	Neo1	-1.2	0.175	-1.08	0.345	1.47	0.358	-1.01	0.655	1.31	0.025
1434836_at	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 in	Nfatc2ip	-1.06	0.550	1.11	0.821	1.27	0.023	1.12	0.145	1.31	0.015
1438951_x_at	nucleoporin 54	Nup54	-1.05	0.567	1.21	0.979	1.3	0.005	1.03	0.647	1.31	0.001
1452329_at	pleckstrin homology domain containing, family N member 1	Plekhn1	1.07	0.963	1.16	0.838	-1.07	0.619	1.05	0.835	1.31	0.035
1449040_a_at	selenophosphate synthetase 2	Sephs2	-1.11	0.467	1.14	0.683	1.15	0.382	1.03	0.866	1.31	0.024
1415908_at	testis-specific protein, Y-encoded-like 1	Tspyl1	-1.06	0.073	1.29	0.016	1.16	0.340	-1.05	0.352	1.31	0.017
1434689_at	zinc finger protein 637	Zfp637	1.36	0.042	1.48	0.006	1.26	0.027	1.11	0.310	1.31	0.020
1417840_at	RIKEN cDNA 1500031L02 gene	1500031L02Rik	-1.01	0.586	1.17	0.993	1.22	0.058	1.24	0.085	1.32	0.018
1420329_at	RIKEN cDNA 4930455C21 gene	4930455C21Rik	1.07	0.973	-1.18	0.345	1.01	0.959	-1.03	0.571	1.32	0.024
1455682_at	expressed sequence AA536808	AA536808	-1.01	0.635	1.18	0.112	1.06	0.787	1.14	0.312	1.32	0.007
1417130_s_at	angiopoietin-like 4	Angptl4	1.07	0.207	1.29	0.054	1.13	0.171	1.14	0.084	1.32	0.004
1416488_at	cyclin G2	Ccng2	-1	0.828	1.31	0.030	1.21	0.045	1.26	0.003	1.32	0.003
1451848_a_at	crystallin, zeta	Cryz	1.05	0.975	1.32	0.313	1.53	0.113	-1.04	0.612	1.32	0.002
1429914_at	enhancer of polycomb homolog 1 (Drosophila)	Epc1	-1.1	0.492	1.07	0.879	1.39	0.023	1.2	0.154	1.32	0.026
1422193_at	guanylate cyclase 2e	Gucy2e	-1.13	0.178	-1.01	0.854	-1.01	0.772	-1.03	0.559	1.32	0.007
1416597_at	hepatoma-derived growth factor, related protein 2	Hdgfrp2	-1.1	0.264	1.1	0.642	-1.14	0.097	1.13	0.157	1.32	0.045
1416481_s_at	HIG1 domain family, member 1A	Higd1a	1.06	0.697	1.32	0.206	1.58	0.077	1.33	0.017	1.32	0.011
1437589_x_at	Lck interacting transmembrane adaptor 1	Lime1	1.63	0.180	1.96	0.052	1.07	0.717	1.09	0.609	1.32	0.008
1439415_x_at	similar to 40S ribosomal protein S21	LOC622373	-1.45	0.280	-1.24	0.388	1.05	0.876	-1.17	0.191	1.32	0.011
1434278_at	X-linked myotubular myopathy gene 1	Mtm1	1.14	0.445	1.54	0.123	1.13	0.397	1.31	0.215	1.32	0.049
1434807_s_at	metaxin 3	Mtx3	-1.04	0.564	1.09	0.728	1.32	0.194	1.24	0.238	1.32	0.017
1449550_at	myosin IC	Myo1c	1.05	0.348	1.33	0.019	1.3	0.048	1.25	0.012	1.32	0.020
1425902_a_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p	Nfkb2	2.95	0.560	5.06	0.326	1.15	0.723	1.09	0.059	1.32	0.005
1428661_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor	Nfkbil2	-1.36	0.003	1.12	0.293	-1.04	0.572	1.15	0.369	1.32	0.027
1422707_at	phosphoinositide-3-kinase, catalytic, gamma polypeptide	Pik3cg	-1.12	0.038	-1.32	0.028	1.12	0.437	1.16	0.057	1.32	0.031
1438854_x_at	phosphatidylinositol membrane-associated 1	Pitpnm1	1.08	0.738	1.11	0.509	1.05	0.914	-1.24	0.030	1.32	0.029
1422624_at	REV1-like (S. cerevisiae)	Rev1l	1.57	0.398	2.37	0.102	1.48	0.384	1.15	0.446	1.32	0.019
1428766_at	RNA methyltransferase like 1	Rnmtl1	1.03	0.383	1.23	0.018	1.17	0.150	1.24	0.002	1.32	0.004
1420502_at	spermidine/spermine N1-acetyl transferase 1	Sat1	1.29	0.135	1.7	0.006	1.38	0.014	1.27	0.011	1.32	0.006
1441315_s_at	solute carrier family 19 (thiamine transporter), member 2	Slc19a2	1.03	0.634	1.47	0.531	1.27	0.017	1.08	0.012	1.32	0.044
1451013_at	solute carrier family 29 (nucleoside transporters), member 3	Slc29a3	1.01	0.686	1.2	0.072	2.36	0.023	2.34	0.057	1.32	0.045
1451181_at	transmembrane protein 121	Tmem121	1.2	0.600	1.69	0.278	1.59	0.769	-1.18	0.350	1.32	0.010
1417888_at	tripartite motif protein 13	Trim13	1.5	0.063	1.64	0.054	1.23	0.001	1.14	0.255	1.32	0.006
1427476_a_at	tripartite motif protein 32	Trim32	-1.06	0.493	1.31	0.241	1.17	0.112	1.18	0.194	1.32	0.027
1455268_at	zinc finger, CSL domain containing 2	Zcsl2	1.11	0.191	1.4	0.003	1.22	0.046	1.17	0.168	1.32	0.018
1428441_at	RIKEN cDNA 1500009M05 gene	1500009M05Rik	1.03	0.791	1.13	0.801	1.22	0.077	1.16	0.120	1.33	0.008
1429451_at	RIKEN cDNA 2610301B20 gene	2610301B20Rik	4.28	0.264	3.69	0.117	1.26	0.049	1.12	0.445	1.33	0.025
1434591_at	RIKEN cDNA 4732460K03 gene	4732460K03Rik	-1.17	0.084	-1.07	0.500	1.23	0.062	-1.01	0.833	1.33	0.040
1453768_a_at	RIKEN cDNA 5430432M24 gene	5430432M24Rik	1.48	0.750	1.99	0.143	1.17	0.114	1.18	0.050	1.33	0.047
1428145_at	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme	Acaa2	1.34	0.334	1.34	0.057	1.31	0.133	1.05	0.718	1.33	0.004

1435793_at	anterior pharynx defective 1b homolog (C. elegans)	Aph1b	1.14	0.447	1.16	0.542	1.07	0.946	1.03	0.623	1.33	0.030
1421164_a_at	Rho guanine nucleotide exchange factor (GEF) 1	Arhgef1	-1.09	0.295	-1.13	0.249	-1.03	0.687	-1.14	0.262	1.33	0.002
1434350_at	AXIN1 up-regulated 1	Axud1	1.03	0.547	1.16	0.089	1.09	0.369	1	0.944	1.33	0.044
1424757_at	cDNA sequence BC018242	BC018242	-1.02	0.601	1.11	0.846	1.17	0.520	-1.1	0.250	1.33	0.025
1436639_at	bolA-like 2 (E. coli)	Bola2	1.01	0.725	1.14	0.810	1.03	0.871	1.15	0.382	1.33	0.004
1458330_x_at	Cyclin M3	Cnnm3	1.27	0.999	1.74	0.652	1.01	0.954	1.66	0.163	1.33	0.020
1451052_at	component of oligomeric golgi complex 8	Cog8	1.02	0.770	1.32	0.645	1.14	0.231	1.13	0.237	1.33	0.028
1446958_at	DNA segment, Chr 13, ERATO Doi 150, expressed	D13Ertd150e	-1.21	0.464	-1.01	0.802	1.12	0.615	-1.18	0.364	1.33	0.039
1450886_at	germ cell-specific gene 2	Gsg2	1.98	0.429	2.15	0.005	1.14	0.177	1.22	0.084	1.33	0.019
1456610_at	jumonji domain containing 3	Jmjd3	1.18	0.366	1.39	0.092	1.02	0.920	1.18	0.406	1.33	0.047
1424988_at	myosin regulatory light chain interacting protein	Mylip	1.01	0.556	1.05	0.498	1.33	0.015	1.45	0.007	1.33	0.038
1419147_at	REC8-like 1 (yeast)	Rec8L1	-1.42	0.344	-1.1	0.445	1.09	0.767	1.08	0.938	1.33	0.017
1429462_at	solute carrier family 25, member 32	Slc25a32	1.15	0.574	1.02	0.851	1.13	0.789	1.3	0.330	1.33	0.047
1429596_at	solute carrier family 7, member 6 opposite strand	Slc7a6os	1.03	0.666	1.4	0.833	1.22	0.291	1.12	0.015	1.33	0.027
1449125_at	tumor necrosis factor, alpha-induced protein 8-like 1	Tnfaip8l1	-1.25	0.277	-1.09	0.504	1.24	0.267	1.18	0.052	1.33	0.013
1428746_a_at	tRNA selenocysteine associated protein 1	Trspap1	-1.1	0.453	1.14	0.611	1.18	0.139	1.07	0.180	1.33	0.024
1452418_at	RIKEN cDNA 1200016E24 gene	1200016E24Rik	-1.29	0.020	1.03	0.472	-1.08	0.608	1.05	0.925	1.34	0.035
1435690_at	RIKEN cDNA 2310008H09 gene	2310008H09Rik	1.19	0.265	1.62	0.054	1.24	0.109	1.43	0.063	1.34	0.005
1449274_at	RIKEN cDNA 2310038H17 gene	2310038H17Rik	1.12	0.378	1.07	0.484	1.15	0.356	1.07	0.161	1.34	0.003
1432454_at	RIKEN cDNA 2410137M14 gene	2410137M14Rik	-1.21	0.401	-1.09	0.467	1.31	0.152	-1.23	0.400	1.34	0.036
1456331_at	RIKEN cDNA 9130023H24 gene	9130023H24Rik	-1.16	0.378	-1.05	0.506	1.08	0.506	1.15	0.048	1.34	0.004
1456643_at	RIKEN cDNA 9230114K14 gene	9230114K14Rik	1.79	0.015	3.25	0.006	1.22	0.409	1.12	0.323	1.34	0.003
1417212_at	RIKEN cDNA 9530058B02 gene	9530058B02Rik	1.01	0.486	1.54	0.528	1.08	0.674	1.26	0.109	1.34	0.020
1425994_a_at	N-acylsphingosine amidohydrolase 2	Asah2	-1.58	0.281	-1.23	0.318	1.15	0.891	1.09	0.914	1.34	0.007
1427912_at	carbonyl reductase 3	Cbr3	-1.03	0.630	1.43	0.160	1.25	0.019	1.16	0.073	1.34	0.004
1433782_at	claudin 12	Cldn12	-1.05	0.373	1.2	0.058	1.19	0.079	1.12	0.013	1.34	0.004
1454921_at	gene model 561, (NCBI)	Gm561	-1.07	0.520	1.12	0.931	1.06	0.432	1.14	0.208	1.34	0.033
1423525_at	microtubule associated serine/threonine kinase-like	Mastl	2.66	0.377	3.91	0.514	1.46	0.007	1.02	0.910	1.34	0.021
1422474_at	phosphodiesterase 4B, cAMP specific	Pde4b	1.26	0.166	1.57	0.053	1.2	0.000	1.27	0.079	1.34	0.031
1459733_at	Phosphoprotein enriched in astrocytes 15	Pea15	1.03	0.678	1.43	0.058	-1.2	0.131	1.3	0.106	1.34	0.022
1425021_a_at	peroxisome biogenesis factor 16	Pex16	1.12	0.263	1.21	0.451	-1.11	0.276	1.09	0.151	1.34	0.037
1456482_at	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide 3 (p55)	Pik3r3	-1.09	0.283	1.15	0.200	1.07	0.090	1.21	0.111	1.34	0.034
1418404_at	RAD9 homolog (S. pombe)	Rad9	1.12	0.323	1.4	0.190	1.1	0.664	1.05	0.385	1.34	0.019
1455197_at	Rho family GTPase 1	Rnd1	1.18	0.366	1.27	0.074	1.28	0.084	1.54	0.002	1.34	0.008
1434490_at	scavenger receptor class F, member 1	Scarf1	1.02	0.930	-1.03	0.638	1.1	0.209	-1.11	0.461	1.34	0.039
1417406_at	SERTA domain containing 1	Sertad1	-1.06	0.513	1.14	0.969	1.3	0.007	1.26	0.006	1.34	0.021
1423809_at	transcription factor 19	Tcf19	1.14	0.094	1.51	0.034	1.33	0.254	1.15	0.037	1.34	0.031
1452132_at	TLC domain containing 1	Tlcd1	1.3	0.230	1.66	0.043	1.26	0.157	1.2	0.076	1.34	0.023
1430576_at	tripeptidyl peptidase II	Tpp2	-1.47	0.263	1.08	0.619	1.32	0.408	1.53	0.202	1.34	0.010
1423869_s_at	thioredoxin reductase 3	Txnrd3	1.14	0.376	1.01	0.940	1.12	0.319	-1.09	0.209	1.34	0.002
1418545_at	WASP family 1	Wasf1	-1.36	0.270	-1.19	0.355	1.47	0.003	1.15	0.086	1.34	0.046
1434552_at	WD repeat domain 77	Wdr77	-1.1	0.347	1.2	0.335	1.37	0.000	1.3	0.001	1.34	0.000
1460572_a_at	zinc finger protein 511	Zfp511	1.21	0.313	1.48	0.263	-1	0.938	1.12	0.181	1.34	0.019
1455544_at	zinc finger, RAN-binding domain containing 3	Zranb3	1.93	0.117	-1.22	0.338	-1.12	0.559	-1.25	0.168	1.34	0.034
1428366_at	RIKEN cDNA 1600027N09 gene	1600027N09Rik	1.01	0.807	1.06	0.965	1.08	0.857	1.17	0.299	1.35	0.016
1426012_a_at	RIKEN cDNA 2610301G19 gene	2610301G19Rik	1.09	0.871	1.26	0.321	-1.02	0.886	1.09	0.366	1.35	0.030
1432883_at	RIKEN cDNA 4932431P20 gene	4932431P20Rik	1.07	0.967	1.32	0.456	1.06	0.740	1.06	0.805	1.35	0.005
1428502_at	ARP6 actin-related protein 6 homolog (yeast)	Actr6	-1.09	0.550	1.1	0.528	1.32	0.040	1.18	0.100	1.35	0.012
1437629_at	Rho guanine nucleotide exchange factor (GEF) 19	Arhgef19	1.71	0.326	1.94	0.084	1.12	0.614	1.02	0.775	1.35	0.022
1431496_at	RIKEN cDNA B230104F01 gene	B230104F01Rik	-1.03	0.697	-1.47	0.009	1.16	0.368	1.14	0.686	1.35	0.015
1457277_at	cDNA sequence BC038925	BC038925	1.03	0.930	1.3	0.325	-1.27	0.162	1.09	0.618	1.35	0.032
1435488_at	RIKEN cDNA C630010D07 gene /// similar to methylenetetrahydrofolate de	C630010D07Rik //	-1.03	0.730	1.24	0.024	1.26	0.091	1.21	0.136	1.35	0.019
1419523_at	cytochrome P450, family 3, subfamily a, polypeptide 13	Cyp3a13	-1.27	0.222	-1.07	0.344	1.42	0.459	1.75	0.915	1.35	0.030
1428015_at	DNA segment, Chr 12, Wayne State University 118, expressed	D12Wsu118e	-1.46	0.237	-1.33	0.120	1.01	0.831	1.12	0.811	1.35	0.040
1439012_a_at	deoxycytidine kinase	Dck	-1.12	0.481	1.16	0.943	1.5	0.063	1.05	0.250	1.35	0.021
1442135_at	Gene model 237, (NCBI)	Gm237	1.05	0.510	1.23	0.036	1.18	0.176	1.3	0.059	1.35	0.027
1455065_x_at	glucosamine-6-phosphate deaminase 1 /// similar to Glucosamine-6-phosp	Gnpda1 /// LOC23	-1.1	0.471	-1.01	0.541	1.31	0.050	1.24	0.001	1.35	0.018
1429670_a_at	leucine-rich repeats and IQ motif containing 2	Lrriq2	-1.09	0.510	1.19	0.157	1.13	0.575	1.47	0.115	1.35	0.020

1447361_at	Metaxin 1	Mtx1	-1.21	0.271	1.33	0.689	1.71	0.003	-1.04	0.812	1.35	0.047
1456748_a_at	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein	Nipsnap1	1.26	0.041	1.2	0.727	2.93	0.134	1.11	0.782	1.35	0.002
1428896_at	platelet-derived growth factor receptor-like	Pdgfrl	1.04	0.801	1.02	0.845	-1.05	0.395	1.03	0.842	1.35	0.044
1429527_a_at	phospholipid scramblase 1 /// hypothetical LOC433328 /// hypothetical prot	Plscr1 /// LOC4333	1.15	0.777	1.31	0.457	1.27	0.319	1	0.894	1.35	0.015
1448722_s_at	phosphopantothenoylcysteine synthetase	Ppcs	-1.09	0.494	1.15	0.775	1.36	0.013	1.4	0.011	1.35	0.039
1436589_x_at	protein kinase D2	Prkd2	-1.02	0.601	1.38	0.168	1.25	0.169	1.22	0.086	1.35	0.039
1445749_at	Ring finger protein 4	Rnf4	1.41	0.880	1.58	0.933	2.17	0.269	1.96	0.515	1.35	0.038
1433680_x_at	Cd27 binding protein (Hindu God of destruction)	Siva	-1.14	0.415	1.16	0.873	1.12	0.754	1.27	0.082	1.35	0.044
1418074_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactos	St6galnac4	1	0.884	1.25	0.242	1.16	0.144	1.31	0.031	1.35	0.039
1424191_a_at	transmembrane protein 41a	Tmem41a	-1.13	0.162	1.31	0.135	1.07	0.648	1.55	0.271	1.35	0.009
1428313_at	zinc finger, SWIM domain containing 3	Zswim3	-1.06	0.450	1.03	0.768	1.05	0.458	1	0.872	1.35	0.002
1437617_x_at	RIKEN cDNA 1110034G24 gene	1110034G24Rik	1.03	0.618	1.32	0.860	1.45	0.007	-1.67	0.016	1.36	0.019
1423656_x_at	RIKEN cDNA 1500010J02 gene	1500010J02Rik	1.12	0.237	1.29	0.079	-1.09	0.491	1.05	0.037	1.36	0.027
1435776_at	RIKEN cDNA 2310009B15 gene	2310009B15Rik	-1.1	0.334	1.2	0.938	1.18	0.153	1.06	0.585	1.36	0.006
1426935_at	RIKEN cDNA 6330590E21 gene	6330590E21Rik	1.12	0.518	1.25	0.479	1.18	0.705	-1.29	0.140	1.36	0.026
1446935_at	RIKEN cDNA 9130011E15 gene	9130011E15Rik	-1.19	0.234	1.02	0.379	1.37	0.829	3.15	0.222	1.36	0.011
1442452_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2	Als2cr2	1.07	0.754	-1.14	0.263	2.26	0.455	1.28	0.753	1.36	0.006
1424682_at	ATP binding domain 1 family, member C	Atpbd1c	-1.03	0.490	1.19	0.467	1.23	0.154	1.17	0.043	1.36	0.005
1451654_x_at	cDNA sequence BC012278	BC012278	1.69	0.120	1.52	0.057	-1.06	0.780	1.18	0.057	1.36	0.042
1431692_a_at	Casitas B-lineage lymphoma c	Cblc	-1.43	0.076	-1.3	0.199	-1.03	0.662	1.13	0.601	1.36	0.026
1418762_at	CD55 antigen	Cd55	-1.2	0.655	1.07	0.705	2.01	0.884	1.65	0.339	1.36	0.005
1450833_at	cholinergic receptor, muscarinic 1, CNS	Chrm1	-1.57	0.071	-1.13	0.458	1.1	0.566	-1.27	0.196	1.36	0.004
1436926_at	estrogen related receptor, beta	Esrrb	-1.13	0.548	-1.24	0.112	-1.07	0.641	-1.49	0.149	1.36	0.040
1424793_a_at	phosphatidylethanolamine binding protein 2	Pbp2	1.01	0.733	1.25	0.156	1.25	0.006	1.26	0.243	1.36	0.011
1454738_x_at	peroxisomal biogenesis factor 6	Pex6	-1.28	0.368	1.03	0.536	1.23	0.060	1.05	0.490	1.36	0.045
1433668_at	proline-rich nuclear receptor coactivator 1	Pnrc1	1	0.913	1.29	0.129	1.27	0.031	1.19	0.005	1.36	0.010
1434940_x_at	regulator of G-protein signaling 19	Rgs19	-1.31	0.277	-1.01	0.633	1.08	0.474	-1	0.942	1.36	0.039
1425439_a_at	solute carrier family 41, member 3	Slc41a3	1.09	0.533	1.15	0.045	1.04	0.868	1	0.953	1.36	0.033
1453034_at	zinc finger protein 251	Zfp251	1.09	0.999	1.3	0.558	1.08	0.552	1.23	0.035	1.36	0.049
1429758_at	RIKEN cDNA 1700017B05 gene /// hypothetical protein LOC640563	1700017B05Rik ///	1.13	0.499	1.27	0.173	1.05	0.376	1.23	0.158	1.37	0.040
1454124_at	RIKEN cDNA 1700067K01 gene	1700067K01Rik	3.25	0.442	5.74	0.288	-1.26	0.346	1.11	0.598	1.37	0.031
1428836_at	RIKEN cDNA 2300009A05 gene	2300009A05Rik	1	0.984	1.16	0.046	1.22	0.016	1.29	0.014	1.37	0.002
1425240_at	cDNA sequence BC011426	BC011426	1.1	0.718	1	0.489	1.22	0.737	-1.04	0.529	1.37	0.039
1434171_at	RIKEN cDNA C330011K17 gene	C330011K17Rik	1.31	0.509	1.99	0.022	1.15	0.357	1.28	0.110	1.37	0.026
1450691_at	cask-interacting protein 2	Caskin2	1.17	0.879	-1.03	0.561	-1.14	0.046	1.17	0.301	1.37	0.016
1428069_at	cell division cycle associated 7	Cdca7	1.26	0.680	1.67	0.007	1.49	0.040	1.09	0.294	1.37	0.010
1441943_x_at	Cytokine induced apoptosis inhibitor 1	Ciapin1	-1.39	0.355	-1.19	0.409	1.13	0.532	1.08	0.687	1.37	0.036
1437146_x_at	coronin 7	Coro7	-1.03	0.649	-1.04	0.575	-1.19	0.067	1.03	0.761	1.37	0.006
1435348_at	RIKEN cDNA D930009K15 gene	D930009K15Rik	1.05	0.722	1.27	0.073	1.28	0.030	1.37	0.011	1.37	0.003
1426593_a_at	F-box only protein 22	Fbxo22	-1.32	0.311	1.05	0.792	1.2	0.217	1.06	0.269	1.37	0.010
1460673_at	folylpolyglutamyl synthetase	Fpgs	-1.03	0.575	1.37	0.251	1.22	0.375	1.34	0.013	1.37	0.004
1440817_x_at	RIKEN cDNA G630024C07 gene	G630024C07Rik	-1.12	0.443	1.07	0.714	1.15	0.335	1.21	0.015	1.37	0.050
1420499_at	GTP cyclohydrolase 1	Gch1	-1.2	0.272	-1.16	0.208	1.07	0.830	1.03	0.951	1.37	0.041
1417477_at	gene trap locus F3b	Gtlf3b	-1.11	0.340	1.19	0.500	1.32	0.004	1.17	0.001	1.37	0.016
1452166_a_at	keratin 10	Krt10	1.07	0.957	1.32	0.247	1.31	0.018	1.22	0.099	1.37	0.012
1435705_at	similar to hypothetical protein FLJ12895	LOC232875	1	0.640	1.25	0.709	1.35	0.226	1.14	0.207	1.37	0.018
1435198_at	hypothetical protein LOC545228	LOC545228	1.09	0.505	1.09	0.705	-1.08	0.472	1.23	0.423	1.37	0.023
1417483_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor	Nfkbiz	1	0.723	1.28	0.164	1.5	0.016	1.22	0.030	1.37	0.034
1451077_at	ribosomal protein L5 /// similar to 60S ribosomal protein L5 /// similar to 60S	Rpl5 /// LOC38274	1.3	0.277	1.64	0.060	1.36	0.054	1.2	0.398	1.37	0.012
1417719_at	sin3 associated polypeptide	Sap30	-1	0.875	1.29	0.182	1.14	0.206	1.26	0.012	1.37	0.006
1419404_s_at	seven in absentia 1A /// seven in absentia 1B	Siah1a /// Siah1b	1.15	0.559	1.31	0.078	1.32	0.231	-1.11	0.296	1.37	0.032
1421275_s_at	suppressor of cytokine signaling 4	Socs4	-1	0.579	1.2	0.796	1.14	0.224	1.16	0.219	1.37	0.045
1451596_a_at	sphingosine kinase 1	Sphk1	1.07	0.348	1.33	0.015	1.19	0.192	1.27	0.000	1.37	0.022
1443619_at	transmembrane protein 30A	Tmem30a	1.14	0.182	1.23	0.211	-1.09	0.609	-1.02	0.886	1.37	0.029
1424849_at	WD repeat domain 62	Wdr62	2.79	0.606	3.08	0.693	1.21	0.125	1.01	0.927	1.37	0.023
1421711_at	zinc finger protein 109	Zfp109	-1.07	0.503	1.09	0.704	1	0.797	1.08	0.535	1.37	0.037
1436150_at	RIKEN cDNA 1700066J24 gene	1700066J24Rik	-1.31	0.250	-1.12	0.400	-1.13	0.274	-1	0.694	1.38	0.013
1419074_at	RIKEN cDNA 2510006C20 gene	2510006C20Rik	1.11	0.163	1.39	0.015	1.25	0.036	1.14	0.010	1.38	0.042

1432425_at	RIKEN cDNA 4930418G15 gene	4930418G15Rik	2.15	0.462	2.55	0.330	1.34	0.405	-1.03	0.638	1.38	0.018
1438024_at	RIKEN cDNA 6230416A05 gene	6230416A05Rik	-1.12	0.427	1.04	0.927	1.19	0.074	1.17	0.003	1.38	0.004
1430268_at	RIKEN cDNA 9630005C17 gene	9630005C17Rik	-1.14	0.326	-1.58	0.024	1.03	0.875	2.08	0.589	1.38	0.033
1458855_at	DNA segment, Chr 11, ERATO Doi 49, expressed	D11Ertd49e	-1.15	0.344	1.3	0.424	1.1	0.907	1.33	0.616	1.38	0.034
1439531_at	RIKEN cDNA E130311K13 gene	E130311K13Rik	1.01	0.717	1.05	0.936	1.17	0.194	1.07	0.249	1.38	0.031
1449169_at	hyaluronan synthase 2	Has2	1.41	0.023	1.81	0.113	1.36	0.005	1.39	0.003	1.38	0.023
1449230_at	iduronidase, alpha-L-	Idua	1.16	0.709	1.19	0.854	-1	0.847	1.01	0.872	1.38	0.050
1456676_a_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	Pfkfb3	-1.01	0.768	1.1	0.522	1.23	0.440	1.22	0.073	1.38	0.048
1421646_a_at	protein inhibitor of activated STAT 3	Pias3	3.78	0.568	4.94	0.426	1.16	0.067	1.61	0.046	1.38	0.040
1434496_at	polo-like kinase 3 (Drosophila)	Plk3	1.11	0.903	1.3	0.253	-1.12	0.371	-1.03	0.619	1.38	0.014
1450816_at	polymerase (DNA directed), gamma 2, accessory subunit	Polg2	-1.38	0.307	-1.07	0.508	-1.12	0.692	1.23	0.084	1.38	0.043
1435057_x_at	polymerase (RNA) I polypeptide E	Polr1e	-1.01	0.702	1.34	0.371	1.13	0.055	1.23	0.049	1.38	0.028
1417972_s_at	processing of precursor 5, ribonuclease P/MRP family (S. cerevisiae)	Pop5	1.1	0.342	1.58	0.003	1.17	0.038	1.23	0.015	1.38	0.016
1430979_a_at	peroxiredoxin 2	Prdx2	1.14	0.487	1.43	0.068	1.13	0.137	1.23	0.001	1.38	0.004
1418181_at	protein tyrosine phosphatase 4a3	Ptp4a3	1.66	0.306	2.48	0.035	1.24	0.080	1.21	0.045	1.38	0.036
1426965_at	RAS related protein 2a	Rap2a	-1.03	0.529	1.23	0.019	1.22	0.040	1.17	0.048	1.38	0.008
1418640_at	sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerev	Sirt1	1.68	0.228	1.91	0.026	1.33	0.090	1.22	0.088	1.38	0.023
1457780_at	syntaxin 11	Stx11	1.13	0.938	1.72	0.170	1.44	0.301	1.16	0.507	1.38	0.041
1429194_at	tigger transposable element derived 2	Tigd2	-1.09	0.464	-1.03	0.525	1.09	0.281	1.35	0.043	1.38	0.010
1417717_a_at	tyrosinase	Tyr	-1.5	0.012	-1.14	0.365	1.17	0.740	1.02	0.964	1.38	0.047
1417088_at	zinc finger protein 346	Zfp346	-1.03	0.622	1.14	0.331	1.44	0.080	1.32	0.003	1.38	0.005
1451450_at	RIKEN cDNA 2010011I20 gene	2010011I20Rik	-1.18	0.028	-1.15	0.204	-1.27	0.039	1.14	0.247	1.39	0.003
1434175_s_at	RIKEN cDNA 2210010N04 gene	2210010N04Rik	1.15	0.072	1.15	0.267	1.14	0.520	1.05	0.879	1.39	0.038
1429073_at	RIKEN cDNA 2210015D19 gene	2210015D19Rik	-1	0.730	1.24	0.640	1.05	0.876	1.02	0.938	1.39	0.020
1455850_at	RIKEN cDNA 2310003H01 gene	2310003H01Rik	1.16	0.444	1.61	0.075	1.08	0.869	1.26	0.016	1.39	0.031
1432509_at	RIKEN cDNA 5033430I15 gene	5033430I15Rik	1.23	0.217	1.32	0.211	1.21	0.137	1.28	0.040	1.39	0.025
1431847_at	RIKEN cDNA 5330439K02 gene	5330439K02Rik	1.15	0.579	1.25	0.294	1.1	0.577	1.29	0.735	1.39	0.042
1456181_at	RIKEN cDNA 9530020G05 gene	9530020G05Rik	-1.11	0.280	1.48	0.020	1.16	0.791	1.28	0.148	1.39	0.042
1429394_at	RIKEN cDNA A130010J15 gene	A130010J15Rik	1.04	0.566	1.27	0.052	1.03	0.870	1.02	0.986	1.39	0.004
1448199_at	ankyrin repeat domain 10	Ankrd10	-1.06	0.126	1.55	0.005	1.45	0.019	1.24	0.040	1.39	0.049
1450624_at	betaine-homocysteine methyltransferase	Bhmt	-1.01	0.362	-1.66	0.147	3.04	0.201	1.15	0.555	1.39	0.049
1437210_a_at	bromodomain containing 2	Brd2	-1.06	0.299	1.16	0.120	1.07	0.706	1.34	0.002	1.39	0.039
1456609_at	calcium/calmodulin-dependent protein kinase II inhibitor 1	Camk2n1	-1.12	0.293	1.06	0.573	1.2	0.140	1.04	0.308	1.39	0.047
1422535_at	cyclin E2	Ccne2	1.07	0.667	1.54	0.097	1.26	0.060	1.38	0.043	1.39	0.029
1427088_at	cyclin T2	Ccnt2	-1.22	0.057	1.07	0.979	1.22	0.048	1.57	0.014	1.39	0.024
1437399_at	claudin domain containing 1	Cldnd1	-1.35	0.348	-1.2	0.411	1.51	0.274	-1.17	0.108	1.39	0.017
1417441_at	DnaJ (Hsp40) homolog, subfamily C, member 12	Dnajc12	-1.02	0.796	-1.01	0.994	1.44	0.047	-1.03	0.586	1.39	0.039
1435631_x_at	exocyst complex component 6	Exoc6	-1.11	0.423	1.18	0.525	1.19	0.707	1.05	0.951	1.39	0.043
1437284_at	frizzled homolog 1 (Drosophila)	Fzd1	1.03	0.393	1.27	0.017	1.34	0.060	1.23	0.012	1.39	0.042
1433622_at	gem (nuclear organelle) associated protein 4	Gemin4	1.82	0.236	2.11	0.013	1.24	0.013	1.35	0.009	1.39	0.005
1442614_at	interleukin 1 receptor accessory protein	Il1rap	1.14	0.490	1.38	0.025	1.24	0.584	-1.43	0.199	1.39	0.012
1459983_at	inositol (myo)-1(or 4)-monophosphatase 2	Impa2	1.02	0.983	-1.68	0.167	1.32	0.204	1.12	0.801	1.39	0.040
1415972_at	myristoylated alanine rich protein kinase C substrate	Marcks	1.1	0.408	1.31	0.043	1.35	0.106	1.11	0.184	1.39	0.034
1418464_at	matrilin 4	Matn4	1.76	0.639	1.16	0.595	1.32	0.929	1.37	0.836	1.39	0.012
1455787_x_at	multiple inositol polyphosphate histidine phosphatase 1	Minpp1	-1.3	0.354	-1.13	0.500	1.08	0.631	-1.11	0.307	1.39	0.018
1426950_at	poly (ADP-ribose) polymerase family, member 16	Parp16	1.18	0.831	1.68	0.254	1.69	0.266	1.34	0.142	1.39	0.047
1450259_a_at	signal transducer and activator of transcription 5A	Stat5a	1.67	0.404	1.83	0.044	1.23	0.147	1.22	0.085	1.39	0.004
1438952_x_at	TAR (HIV) RNA binding protein 2	Tarbp2	-1.35	0.313	1.02	0.549	1.04	0.891	1.26	0.383	1.39	0.033
1433530_at	RIKEN cDNA 2210411K19 gene	2210411K19Rik	-1.15	0.430	1.07	0.662	1.17	0.656	-1.02	0.639	1.4	0.031
1439387_x_at	RIKEN cDNA 2310061F22 gene	2310061F22Rik	-1.22	0.414	-1.03	0.567	1.14	0.204	1.07	0.449	1.4	0.002
1451568_at	RIKEN cDNA A630054L15 gene	A630054L15Rik	-1.23	0.296	-1.53	0.064	-1.38	0.034	1.03	0.988	1.4	0.025
1427081_at	RIKEN cDNA A630072M18 gene	A630072M18Rik	1.37	0.028	1.72	0.008	1.41	0.185	1.17	0.040	1.4	0.031
1417208_at	alpha-methylacyl-CoA racemase	Amacr	-1.01	0.593	1.21	0.900	1.26	0.101	1.1	0.012	1.4	0.005
1417419_at	cyclin D1	Ccnd1	-1.01	0.676	1.06	0.322	1.07	0.181	-1	0.937	1.4	0.036
1418585_at	cyclin H	Ccnh	1.28	0.019	1.26	0.143	1.24	0.037	1.16	0.189	1.4	0.048
1421373_at	cytochrome c oxidase subunit IV isoform 2	Cox4i2	-1.05	0.612	-1.46	0.057	1.07	0.759	1.02	0.842	1.4	0.006
1434747_at	chymotrypsin C (caldecrin)	Ctrc	-1.61	0.198	-1.19	0.172	-1.18	0.232	1.62	0.471	1.4	0.020
1452796_at	differentially expressed in FDCP 6	Def6	1.45	0.151	1.87	0.024	1.22	0.002	1.24	0.012	1.4	0.012

1454219_at	DnaJ (Hsp40) homolog, subfamily C, member 2	Dnajc2	1.21	0.505	1.29	0.725	1.36	0.681	1.19	0.398	1.4	0.036
1452388_at	heat shock protein 1A	Hspa1a	1.05	0.910	1.24	0.662	1.17	0.147	1.17	0.214	1.4	0.008
1459292_at	Mitogen activated protein kinase kinase 6	Map2k6	-1.24	0.379	1.62	0.810	1.88	0.903	1.54	0.354	1.4	0.017
1428712_at	MON1 homolog b (yeast)	Mon1b	-1.01	0.653	1.06	0.724	1.26	0.873	1.61	0.380	1.4	0.014
1416915_at	mutS homolog 6 (E. coli)	Msh6	1.1	0.060	2.15	0.000	1.51	0.047	1.47	0.029	1.4	0.023
1437834_s_at	protein kinase C and casein kinase substrate in neurons 3	Pacsin3	-1.03	0.510	1.01	0.554	1.22	0.025	1.14	0.201	1.4	0.008
1417169_at	ubiquitin specific peptidase 2	Usp2	1.2	0.876	1.24	0.954	1.33	0.095	1.49	0.014	1.4	0.029
1421478_a_at	zinc finger protein 318	Zfp318	-1.83	0.090	1.05	0.736	1.11	0.252	1.54	0.015	1.4	0.048
1454258_at	RIKEN cDNA 1110008E08 gene	1110008E08Rik	-1.14	0.373	-1.81	0.093	-1.12	0.523	1.1	0.592	1.41	0.018
1428550_at	RIKEN cDNA 1810015A11 gene	1810015A11Rik	1.06	0.364	1.27	0.025	1.34	0.004	1.43	0.017	1.41	0.040
1448552_s_at	RIKEN cDNA 2310028N02 gene	2310028N02Rik	-1.1	0.302	1.16	0.369	-1.04	0.503	1.12	0.246	1.41	0.007
1454736_at	ankyrin repeat domain 57	Ankrd57	1.06	0.862	1.27	0.133	1.22	0.081	1.35	0.001	1.41	0.017
1418653_at	cytochrome P450, family 2. subfamily c, polypeptide 37 /// cytochrome P45	Cyp2c37 /// Cyp2c	1.48	0.982	2.15	0.336	2.09	0.263	-1	0.481	1.41	0.041
1425937_a_at	hexamethylene bis-acetamide inducible 1	Hexim1	1.05	0.729	1.52	0.009	1.39	0.015	1.49	0.002	1.41	0.015
1425322_at	interferon zeta /// similar to interferon zeta /// similar to interferon zeta /// si	Ifnz /// LOC435791	-1.09	0.518	1.41	0.163	1.43	0.015	1.25	0.056	1.41	0.016
1428532_at	integrator complex subunit 7	Ints7	1.37	0.386	1.42	0.049	1.49	0.045	1.11	0.424	1.41	0.030
1451199_at	queuine tRNA-ribosyltransferase domain containing 1	Qtrtd1	-1.25	0.321	1.08	0.960	1.3	0.032	1.13	0.035	1.41	0.005
1422629_s_at	shroom family member 3	Shroom3	-1.12	0.416	-1.13	0.333	1.23	0.592	-1.07	0.311	1.41	0.000
1437190_at	serine/threonine/tyrosine kinase 1	Styk1	1.33	0.135	1.36	0.204	1.32	0.916	1.26	0.578	1.41	0.007
1420043_s_at	THO complex 1	Thoc1	-1.14	0.370	1.29	0.591	1.22	0.264	-1.22	0.020	1.41	0.020
1451268_at	translocation associated membrane protein 1-like 1	Tram1l1	1.21	0.752	1.81	0.059	1.38	0.012	1.26	0.180	1.41	0.027
1423923_a_at	WD repeat domain 8	Wdr8	-1.02	0.584	1.27	0.907	1.14	0.238	1.12	0.112	1.41	0.005
1449391_at	zinc finger protein 37	Zfp37	1.6	0.298	1.66	0.042	1.51	0.276	1.34	0.002	1.41	0.024
1424261_at	zinc finger protein 672	Zfp672	1.64	0.729	1.81	0.117	1.17	0.052	1.29	0.004	1.41	0.026
1451189_at	zinc finger, SWIM domain containing 1	Zswim1	1.12	0.522	1.45	0.012	1.12	0.044	1.35	0.015	1.41	0.045
1455581_x_at	hypothetical protein 9530028C05	9530028C05	-1.18	0.423	-1.15	0.392	1.09	0.400	1.26	0.313	1.42	0.031
1442007_at	RIKEN cDNA 9830124H08 gene	9830124H08Rik	1.03	0.648	1.18	0.866	1.17	0.080	1.33	0.042	1.42	0.046
1451123_at	RIKEN cDNA C330016O10 gene	C330016O10Rik	1.66	0.234	-1.36	0.401	-1.46	0.305	1.4	0.910	1.42	0.033
1436034_at	centrosomal protein 68	Cep68	-1.06	0.565	1.01	0.995	1.14	0.451	1.26	0.024	1.42	0.003
1430520_at	copine VIII	Cpne8	1.71	0.304	1.66	0.036	1.17	0.516	1.01	0.927	1.42	0.019
1439429_x_at	deltex 2 homolog (Drosophila)	Dtx2	1.02	0.595	1.18	0.781	1.27	0.214	1.11	0.381	1.42	0.015
1457730_at	Fanconi anemia, complementation group M	Fancm	1.01	0.609	1.24	0.761	-1.18	0.429	1.19	0.212	1.42	0.032
1435176_a_at	inhibitor of DNA binding 2	Id2	-1.06	0.725	1.12	0.673	1.31	0.184	1.17	0.032	1.42	0.007
1423229_at	inositol polyphosphate-5-phosphatase E	Inpp5e	3.39	0.335	3.83	0.019	1.17	0.549	1.41	0.061	1.42	0.002
1417973_at	inter-alpha trypsin inhibitor, heavy chain 1	Itih1	-1.03	0.663	1.05	0.817	1.26	0.450	1.26	0.571	1.42	0.010
1451219_at	ORM1-like 1 (S. cerevisiae)	Ormdl1	1.05	0.799	1.26	0.219	1.1	0.436	1.09	0.565	1.42	0.000
1428037_at	otoancorin	Otoa	-1.13	0.503	-1.01	0.858	-1.06	0.434	1.39	0.954	1.42	0.006
1416206_at	signal-induced proliferation associated gene 1	Sipa1	1.35	0.412	1.59	0.219	1.15	0.545	1.08	0.856	1.42	0.046
1452789_at	stannin	Snn	1.05	0.805	1.5	0.010	1.2	0.229	1.28	0.002	1.42	0.012
1451339_at	sulfite oxidase	Suox	5.26	0.543	8.31	0.070	1.38	0.039	1.26	0.024	1.42	0.004
1459510_at	transmembrane protease, serine 2	Tmprss2	1.04	0.863	1.59	0.193	1.61	0.290	1.25	0.370	1.42	0.015
1453141_at	RIKEN cDNA 0610009L18 gene	0610009L18Rik	-1.09	0.469	1.26	0.889	1.13	0.884	1.2	0.235	1.43	0.017
1434532_at	cDNA sequence BC035295	BC035295	-1.07	0.499	1.44	0.752	1.31	0.000	1.37	0.013	1.43	0.002
1446516_at	B-cell CLL/lymphoma 7C	Bcl7c	-1.1	0.701	-1.26	0.065	1.13	0.784	-1.15	0.105	1.43	0.005
1438317_a_at	endonuclease G	Endog	-1.1	0.435	1.03	0.493	1.04	0.675	1.05	0.538	1.43	0.027
1416969_at	G two S phase expressed protein 1	Gtse1	1.23	0.069	1.83	0.000	1.19	0.188	1.17	0.038	1.43	0.030
1452798_s_at	mitogen activated protein kinase 1 interacting protein 1	Mapk1ip1	-1.1	0.447	-1.02	0.617	1.2	0.413	1.11	0.800	1.43	0.008
1436309_at	neuropilin (NRP) and tolloid (TLL)-like 2	Neto2	1.5	0.058	1.59	0.321	1.28	0.586	1.35	0.453	1.43	0.027
1448815_at	8-oxoguanine DNA-glycosylase 1	Ogg1	1.21	0.152	1.37	0.312	1.05	0.834	1.14	0.103	1.43	0.026
1447810_x_at	pleckstrin homology domain containing, family B (evectins) member 2	Plekhb2	1.05	0.471	-1.28	0.319	1.3	0.792	1.61	0.970	1.43	0.039
1448369_at	polymerase (DNA directed), alpha 2	Pola2	1.51	0.175	1.51	0.024	1.47	0.007	1.39	0.160	1.43	0.030
1456729_x_at	regulator of telomere elongation helicase 1	Rtel1	1	0.535	1.72	0.974	-1.67	0.057	1.06	0.850	1.43	0.023
1435936_at	Solute carrier family 13 (sodium-dependent citrate transporter), member 5	Slc13a5	-1.14	0.433	-1.26	0.263	1.23	0.148	-1.09	0.396	1.43	0.030
1450681_at	zinc finger protein 143	Zfp143	1.86	0.233	1.74	0.116	1.42	0.582	1.1	0.179	1.43	0.044
1455633_at	zinc finger protein 647	Zfp647	-1.08	0.542	1.08	0.927	1.15	0.038	1.28	0.017	1.43	0.049
1441876_x_at	Zinc finger protein 93	Zfp93	1.1	0.674	1.81	0.150	1.06	0.686	1.03	0.856	1.43	0.042
1428832_at	RIKEN cDNA 1600002H07 gene	1600002H07Rik	1.07	0.550	1.53	0.024	1.37	0.141	1.18	0.330	1.44	0.039
1459992_x_at	ceroid-lipofuscinosis, neuronal 8	Cln8	-1.3	0.168	1.18	0.309	-1.07	0.631	1.09	0.638	1.44	0.003

1459757_x_at	CCR4-NOT transcription complex, subunit 10	Cnot10	-1.36	0.348	-1.68	0.207	1.19	0.031	-1.02	0.730	1.44	0.043
1452792_at	DAZ interacting protein 1	Dzip1	1.16	0.692	1.41	0.121	1.6	0.024	1.09	0.231	1.44	0.041
1417383_at	ectonucleoside triphosphate diphosphohydrolase 5	Entpd5	1.47	0.859	1.43	0.928	1.17	0.404	1.18	0.683	1.44	0.020
1454078_a_at	galactose-3-O-sulfotransferase 1	Gal3st1	-1.16	0.437	-1.01	0.617	1.04	0.805	-1.13	0.261	1.44	0.014
1453995_a_at	HpaII tiny fragments locus 9c	Htf9c	1.55	0.115	1.78	0.054	1.23	0.425	1.47	0.042	1.44	0.036
1427719_s_at	keratin complex 2, basic, pseudogene 1 /// keratin 82	Krt2-ps1 /// Krt82	1.1	0.727	2.42	0.143	1.32	0.854	1.29	0.117	1.44	0.044
1417572_at	N-methylpurine-DNA glycosylase	Mpg	1.86	0.655	2.7	0.008	1.51	0.101	1.15	0.062	1.44	0.043
1451106_at	RNA binding motif protein 21	Rbm21	1.18	0.165	1.55	0.028	1.17	0.242	1.35	0.014	1.44	0.023
1436804_s_at	SCY1-like 1 (S. cerevisiae)	Scyl1	-1.05	0.542	1.04	0.505	1.42	0.272	1.01	0.960	1.44	0.049
1455863_at	spermatogenesis associated 5-like 1	Spata5l1	-1.12	0.296	1.06	0.778	1.33	0.577	1.2	0.162	1.44	0.039
1454649_at	steroid 5 alpha-reductase 1	Srd5a1	-1.11	0.283	-1.37	0.087	-1.03	0.675	2.08	0.044	1.44	0.001
1457968_at	Transmembrane protein 23	Tmem23	1.26	0.669	1.86	0.055	-1.39	0.329	-1.04	0.564	1.44	0.014
1429896_at	RIKEN cDNA 5830408B19 gene	5830408B19Rik	1.47	0.217	1.43	0.539	1.05	0.929	1.24	0.057	1.45	0.040
1435685_x_at	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	Abcc5	1.27	0.592	-1.29	0.715	1.85	0.264	-1.1	0.049	1.45	0.024
1419011_at	crystallin, beta A2	Cryba2	1.19	0.771	1.05	0.621	1.06	0.854	1.06	0.998	1.45	0.027
1454737_at	dual specificity phosphatase 9	Dusp9	1.03	0.928	1.58	0.049	1.37	0.022	1.24	0.014	1.45	0.045
1437356_at	Epstein-Barr virus induced gene 2	Ebi2	1.65	0.671	1.74	0.755	-1.03	0.588	1.64	0.413	1.45	0.037
1455877_a_at	nanos homolog 1 (Drosophila)	Nanos1	-1.09	0.434	1.42	0.682	1.48	0.048	1.25	0.163	1.45	0.043
1427929_a_at	pyridoxal (pyridoxine, vitamin B6) kinase	Pdxk	-1.26	0.343	-1.02	0.575	1.3	0.010	1.19	0.064	1.45	0.024
1453739_at	transmembrane protein 126B	Tmem126b	1.8	0.254	2.22	0.048	1.41	0.038	1.44	0.298	1.45	0.035
1449367_at	three prime repair exonuclease 2	Trex2	1.33	0.932	-1.06	0.477	1.39	0.876	-1.32	0.363	1.45	0.048
1419239_at	zinc finger protein 54	Zfp54	1.23	0.753	1.56	0.228	1.23	0.133	1.24	0.134	1.45	0.028
1429074_at	RIKEN cDNA 1700026D08 gene	1700026D08Rik	1.06	0.822	1.56	0.226	1.13	0.999	1.03	0.956	1.46	0.047
1454355_at	RIKEN cDNA 1810021M19 gene	1810021M19Rik	-1.31	0.115	-1.59	0.080	1.37	0.090	-1.09	0.459	1.46	0.035
1432402_at	RIKEN cDNA 4930402F11 gene	4930402F11Rik	1.33	0.745	1.2	0.596	-1.11	0.524	2.42	0.540	1.46	0.013
1438125_at	RIKEN cDNA C230085N15 gene	C230085N15Rik	1.22	0.727	1.94	0.268	1.21	0.556	1.25	0.794	1.46	0.011
1441465_at	CCR4-NOT transcription complex, subunit 3	Cnot3	1.37	0.171	1.28	0.547	1.21	0.394	1.1	0.239	1.46	0.026
1433044_at	chondroitin sulfate proteoglycan 2	Cspg2	-1.06	0.783	2.18	0.101	1.05	0.874	-1.1	0.568	1.46	0.001
1437512_x_at	EBNA1 binding protein 2	Ebna1bp2	1.23	0.656	-1.15	0.171	1.03	0.913	1.09	0.975	1.46	0.018
1436270_at	gene model 740, (NCBI)	Gm740	1.12	0.105	1.31	0.024	1.22	0.188	1.13	0.018	1.46	0.004
1451021_a_at	Kruppel-like factor 5	Klf5	1.84	0.399	2.3	0.093	1.21	0.120	1.27	0.033	1.46	0.001
1447739_x_at	kelch domain containing 4 /// hypothetical gene supported by NM_145605	Klhdc4 /// LOC384	-1.02	0.414	-1.02	0.484	1.46	0.564	1.03	0.934	1.46	0.044
1424906_at	PQ loop repeat containing	Pqlc3	2.88	0.360	4.08	0.081	1.43	0.145	1.37	0.021	1.46	0.018
1426444_at	rhomboid domain containing 2	Rhbdd2	2.06	0.196	1.34	0.914	-1.2	0.205	1.1	0.697	1.46	0.000
1449946_a_at	zinc finger protein 593	Zfp593	-1.16	0.204	1.13	0.706	1.05	0.952	1.35	0.089	1.46	0.013
1424692_at	RIKEN cDNA 2810055F11 gene	2810055F11Rik	1.53	0.251	1.83	0.018	1.25	0.007	1.3	0.039	1.47	0.008
1452236_at	ATP-binding cassette, sub-family F (GCN20), member 1	Abcf1	-1.23	0.347	1.04	0.705	-1.12	0.443	-1.1	0.209	1.47	0.016
1441387_at	cDNA sequence BC030343	BC030343	1.02	0.728	1.06	0.622	1.05	0.987	1.17	0.957	1.47	0.046
1447984_at	DNA segment, Chr 1, ERATO Doi 75, expressed	D1Ertd75e	-1.48	0.164	-2.28	0.061	1.42	0.959	1.16	0.119	1.47	0.039
1449701_at	DNA segment, Chr 6, ERATO Doi 109, expressed	D6Ertd109e	1.69	0.441	1.69	0.456	-1.03	0.603	-1.11	0.479	1.47	0.044
1424171_a_at	hydroxyacyl glutathione hydrolase	Hagh	-1.1	0.395	1.08	0.788	-1	0.784	1.11	0.722	1.47	0.021
1424859_at	homer homolog 3 (Drosophila)	Homer3	1.23	0.646	1.43	0.396	1.63	0.130	1.33	0.266	1.47	0.040
1418300_a_at	MAP kinase-interacting serine/threonine kinase 2	Mknk2	-1.05	0.558	1.27	0.104	1.19	0.057	1.25	0.007	1.47	0.020
1418500_at	nucleosome assembly protein 1-like 3	Nap1l3	2.53	0.207	2.74	0.054	1.37	0.953	1.23	0.172	1.47	0.025
1449249_at	protocadherin 7	Pcdh7	1.98	0.186	2.87	0.138	1.27	0.067	1.07	0.182	1.47	0.004
1452458_s_at	peptidylprolyl isomerase (cyclophilin) like 5	Ppil5	-1.02	0.688	1.23	0.771	1.56	0.028	1.35	0.073	1.47	0.019
1426046_a_at	Rab geranylgeranyl transferase, a subunit	Rabggta	1.17	0.546	1.25	0.161	-1.01	0.875	1.1	0.274	1.47	0.034
1453278_a_at	restin-like 2	Rsnl2	1.01	0.824	-1.23	0.122	1.62	0.346	1.27	0.751	1.47	0.004
1455511_at	selenophosphate synthetase 1	Sephs1	1.09	0.608	1.47	0.128	1.87	0.074	1.32	0.001	1.47	0.038
1435278_at	SFT2 domain containing 3	Sft2d3	1.07	0.453	-1.36	0.138	-1.01	0.887	1.02	0.816	1.47	0.004
1428093_at	TraB domain containing	Trabd	-1.01	0.640	-1.05	0.539	1	0.867	1.2	0.081	1.47	0.038
1422532_at	xeroderma pigmentosum, complementation group C	Xpc	1.33	0.130	1.42	0.018	1.1	0.101	1.23	0.191	1.47	0.047
1424892_at	zinc finger protein 95	Zfp95	1.17	0.399	1.53	0.031	1.25	0.032	1.2	0.031	1.47	0.023
1434240_at	RIKEN cDNA 4632434I11 gene	4632434I11Rik	1.32	0.450	2.03	0.140	1.64	0.019	1.45	0.051	1.48	0.005
1453591_at	RIKEN cDNA 5730437N04 gene	5730437N04Rik	1.09	0.795	1.12	0.836	-1.08	0.378	-1.12	0.202	1.48	0.001
1436422_at	cDNA sequence BC026590	BC026590	1.33	0.507	1.82	0.058	1.35	0.019	1.29	0.003	1.48	0.005
1448659_at	caspase 7	Casp7	1.43	0.666	1.93	0.138	1.41	0.078	1.09	0.202	1.48	0.002
1421986_at	eukaryotic translation initiation factor 4E member 2	Eif4e2	-1.45	0.190	1.08	0.902	-1.16	0.262	1.04	0.947	1.48	0.044

1421969_a_at	fatty acid amide hydrolase	Faah	1.32	0.776	-1.32	0.310	-1.34	0.189	1.26	0.468	1.48	0.042
1448679_at	hyaluronoglucosaminidase 2	Hyal2	-1.15	0.045	1.08	0.095	1.08	0.744	1.22	0.045	1.48	0.016
1426988_at	kelch domain containing 5	Klhdc5	3.69	0.376	3.44	0.015	1.28	0.000	1.25	0.134	1.48	0.012
1424336_at	phosphopantothenoylcysteine decarboxylase	Ppcdc	1.43	0.628	-1.01	0.267	1.08	0.756	1.39	0.042	1.48	0.011
1430527_a_at	ring finger protein 167	Rnf167	3.51	0.621	6.62	0.221	1.51	0.097	1.13	0.549	1.48	0.015
1425277_at	slit homolog 1 (Drosophila)	Slit1	-1.45	0.192	1.49	0.956	1.8	0.229	1.17	0.678	1.48	0.023
1421528_a_at	surfeit gene 5	Surf5	1.03	0.625	1.42	0.007	1.34	0.007	1.3	0.009	1.48	0.025
1431112_at	unc-51-like kinase 3 (C. elegans)	Ulk3	-1.14	0.432	-1.08	0.359	1.08	0.399	1.07	0.614	1.48	0.036
1421131_a_at	zinc finger protein 111	Zfp111	1.07	0.795	1.79	0.002	1.13	0.235	1.08	0.939	1.48	0.035
1433583_at	zinc finger protein 365 /// similar to zinc finger protein 365	Zfp365 /// LOC674	2.05	0.133	3.74	0.010	1.29	0.261	1.15	0.054	1.48	0.028
1454825_at	RIKEN cDNA 1110014N23 gene	1110014N23Rik	-1.14	0.383	1.01	0.650	1.15	0.047	1.01	0.711	1.49	0.018
1459327_at	RIKEN cDNA 4931406I20 gene	4931406I20Rik	-1.23	0.164	-1	0.865	-1.03	0.702	1.25	0.302	1.49	0.025
1442168_at	RIKEN cDNA A230071A22 gene	A230071A22Rik	1.01	0.602	-1.13	0.478	1.04	0.615	-1.04	0.272	1.49	0.024
1447897_x_at	Anaphase promoting complex subunit 11 homolog (yeast)	Anapc11	-1.14	0.435	-1.07	0.460	1.16	0.954	1.15	0.483	1.49	0.028
1458174_at	coiled-coil domain containing 52	Ccdc52	2.78	0.191	2.53	0.234	2.11	0.021	2.11	0.962	1.49	0.046
1449954_at	hyaluronoglucosaminidase 1 /// N-acetyltransferase 6	Hyal1 /// Nat6	1.09	0.581	1.06	0.558	1.53	0.306	1.05	0.615	1.49	0.002
1421364_at	leucine rich repeat and fibronectin type III domain containing 1	Lrfn1	-1.34	0.170	-1.24	0.281	1.3	0.357	-1.37	0.090	1.49	0.006
1435666_at	microtubule associated serine/threonine kinase 3	Mast3	1.08	0.321	1.26	0.057	1.08	0.177	1.21	0.138	1.49	0.037
1459921_at	neurexophilin 1	Nxph1	-1.04	0.418	1.17	0.340	1.89	0.232	2.72	0.138	1.49	0.019
1442237_at	Sequestosome 1	Sqstm1	-1.34	0.093	-1.24	0.044	-1.13	0.464	-1.05	0.499	1.49	0.029
1458667_at	RIKEN cDNA 4930519N13 gene	4930519N13Rik	-1.17	0.353	1.17	0.678	1.43	0.003	1.02	0.898	1.5	0.048
1432433_at	RIKEN cDNA 4930524N10 gene	4930524N10Rik	-1.06	0.512	-1.12	0.482	-1.5	0.340	1.4	0.391	1.5	0.007
1440480_at	cDNA sequence AB182283	AB182283	1.19	0.713	-1.08	0.439	-1.25	0.267	1.23	0.080	1.5	0.020
1419233_x_at	apolipoprotein A-I	Apoa1	1.22	0.490	-1.06	0.358	-1.14	0.141	1.2	0.863	1.5	0.024
1457490_at	RIKEN cDNA B230218L05 gene	B230218L05Rik	-1.3	0.360	-1.34	0.344	2.2	0.674	1.16	0.393	1.5	0.012
1447965_at	expressed sequence C80012	C80012	1.24	0.762	1.25	0.447	-1.04	0.673	-1.16	0.266	1.5	0.017
1436619_at	RIKEN cDNA D630045M09 gene	D630045M09Rik	1.68	0.781	2.11	0.069	1.14	0.896	1.12	0.036	1.5	0.022
1451270_at	dual specificity phosphatase 18	Dusp18	1.92	0.619	1.85	0.252	1.38	0.147	1.47	0.186	1.5	0.020
1438167_x_at	Folliculin	Flcn	-1.37	0.305	1.01	0.670	1.08	0.141	1.11	0.245	1.5	0.010
1453102_at	fibronectin leucine rich transmembrane protein 3	Flrt3	1.6	0.437	2.79	0.025	1.33	0.001	1.31	0.032	1.5	0.013
1459689_at	Glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	1.39	0.788	1.1	0.775	2.19	0.249	2.18	0.332	1.5	0.048
1428800_a_at	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	Pus7l	-1.1	0.449	1.21	0.785	1.24	0.262	1.28	0.013	1.5	0.043
1419061_at	ras homolog gene family, member D	Rhod	1.33	0.344	2.09	0.012	1.26	0.021	1.21	0.049	1.5	0.005
1435728_at	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	Tyw3	-1.05	0.732	1.41	0.203	-1.23	0.256	1.17	0.733	1.5	0.012
1456641_at	RIKEN cDNA 1190007F08 gene	1190007F08Rik	1.21	0.200	1.41	0.214	1.22	0.750	1.06	0.748	1.51	0.034
1436345_at	RIKEN cDNA 5730559C18 gene	5730559C18Rik	-1.12	0.539	1.33	0.092	1.44	0.141	1.25	0.060	1.51	0.004
1448471_a_at	cytotoxic T lymphocyte-associated protein 2 alpha	Ctla2a	-1.32	0.344	-1.2	0.606	1.31	0.932	-1.02	0.796	1.51	0.020
1418780_at	cytochrome P450, family 39, subfamily a, polypeptide 1	Cyp39a1	-1.2	0.350	-1.65	0.150	1.24	0.605	1.58	0.154	1.51	0.048
1450549_s_at	ELK4, member of ETS oncogene family	Elk4	1.45	0.922	1.26	0.630	-1	0.468	1.68	0.342	1.51	0.022
1451589_at	opposite strand transcription unit to Stag3	Gats	-1.13	0.408	-1.43	0.188	2.4	0.199	1.17	0.276	1.51	0.014
1416968_a_at	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomeras	Hsd3b7	1.15	0.078	1.24	0.132	1.26	0.062	1.15	0.045	1.51	0.039
1460312_at	olfactory receptor 157	Olfr157	1.03	0.896	1.05	0.655	1.16	0.979	1.14	0.893	1.51	0.047
1421696_at	polycystic kidney and hepatic disease 1-like 1	Pkhd1l1	1.46	0.533	-1.86	0.074	2.13	0.013	2.67	0.150	1.51	0.025
1448757_at	promyelocytic leukemia	Pml	1.31	0.373	2.28	0.012	1.23	0.074	1.33	0.090	1.51	0.006
1418423_s_at	serine (or cysteine) peptidase inhibitor, clade B, member 9f /// serine (or cy	Serpinb9f /// Serpir	2.83	0.335	2.41	0.072	1.27	0.813	1.06	0.824	1.51	0.045
1427737_a_at	RIKEN cDNA 1200011M11 gene	1200011M11Rik	-1.06	0.480	1.19	0.283	1.25	0.086	1.07	0.599	1.52	0.001
1452747_at	ATPase type 13A2 /// similar to ATPase type 13A2	Atp13a2 /// LOC67	1.03	0.662	-1.31	0.276	2.21	0.848	-1.22	0.382	1.52	0.050
1451273_x_at	cDNA sequence BC025546	BC025546	1.02	0.475	1.46	0.060	1.26	0.107	1.18	0.110	1.52	0.005
1440886_at	cell division cycle 37 homolog (S. cerevisiae)-like 1	Cdc37l1	1.07	0.879	1.44	0.141	1.7	0.043	1.58	0.024	1.52	0.007
1449037_at	cAMP responsive element modulator	Crem	1.25	0.126	1.6	0.053	1.35	0.001	1.24	0.053	1.52	0.005
1426594_at	FERM domain containing 4B	Frmd4b	1.85	0.734	1.58	0.309	-2.17	0.035	-1.36	0.199	1.52	0.031
1451043_at	NIMA (never in mitosis gene a)-related expressed kinase 6	Nek6	1.22	0.384	1.41	0.320	1.5	0.246	1.42	0.757	1.52	0.018
1428615_at	purinergic receptor P2Y, G-protein coupled, 5	P2ry5	1.24	0.018	1.7	0.043	1.44	0.019	1.35	0.009	1.52	0.011
1421265_a_at	RNA binding motif protein 38	Rbm38	1.33	0.594	1.9	0.045	1.36	0.540	1.1	0.323	1.52	0.044
1436869_at	sonic hedgehog	Shh	1.03	0.594	1.41	0.959	1.43	0.938	1.73	0.856	1.52	0.018
1449011_at	solute carrier family 12, member 7	Slc12a7	1.42	0.200	1.49	0.203	1.18	0.675	1.09	0.961	1.52	0.036
1428805_at	solute carrier family 35, member E3	Slc35e3	1.93	0.233	3.11	0.012	1.18	0.069	1.35	0.006	1.52	0.003
1433705_at	zinc finger protein 213	Zfp213	1.04	0.972	1.39	0.007	1.3	0.020	1.31	0.007	1.52	0.023

1429484_at	RIKEN cDNA 1110002L01 gene	1110002L01Rik	1.07	0.465	1.22	0.201	1.17	0.094	1.12	0.092	1.53	0.006
1433877_at	RIKEN cDNA 4732473B16 gene	4732473B16Rik	2.16	0.396	2.96	0.019	1.17	0.106	1.19	0.216	1.53	0.025
1423100_at	FBJ osteosarcoma oncogene	Fos	-1.01	0.953	1.62	0.005	1.36	0.029	1.46	0.003	1.53	0.003
1428014_at	histone 1, H4h	Hist1h4h	1.88	0.081	2.05	0.044	1.17	0.339	1.03	0.856	1.53	0.018
1421332_at	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	Hs3st3b1	-1.09	0.910	1.37	0.346	-1.3	0.217	1.15	0.797	1.53	0.039
1457938_at	Nuclear receptor co-repressor 1	Ncor1	-1.12	0.293	1.03	0.717	2.31	0.164	1.34	0.457	1.53	0.044
1421321_a_at	neuroepithelial cell transforming gene 1	Net1	1.8	0.415	2.62	0.108	1.1	0.423	1.26	0.024	1.53	0.015
1457252_x_at	phospholipase D2	Pld2	1.06	0.642	1.49	0.738	1.27	0.111	1.22	0.289	1.53	0.047
1417676_a_at	protein tyrosine phosphatase, receptor type, O	Ptpro	-1.93	0.065	-1.29	0.456	-1.29	0.397	1.07	0.817	1.53	0.015
1418535_at	ral guanine nucleotide dissociation stimulator,-like 1	Rgl1	-1.01	0.743	-1.02	0.657	1.15	0.941	-1.01	0.610	1.53	0.006
1455867_at	SRY-box containing gene 4	Sox4	1.01	0.719	1.17	0.375	1.23	0.172	1.2	0.225	1.53	0.020
1432752_at	RIKEN cDNA 4930403O18 gene	4930403O18Rik	-1.73	0.038	-1.11	0.746	1.31	0.534	-1.3	0.197	1.54	0.006
1446309_at	RIKEN cDNA 5830483C08 gene	5830483C08Rik	-1.3	0.319	1.61	0.593	1.98	0.076	-2.01	0.165	1.54	0.044
1435571_at	RIKEN cDNA A530065I17 gene	A530065I17Rik	1.22	0.759	1.41	0.814	1.24	0.233	1.31	0.974	1.54	0.031
1437455_a_at	B-cell translocation gene 1, anti-proliferative	Btg1	-1.21	0.180	1.1	0.674	1.26	0.042	1.03	0.948	1.54	0.005
1423287_at	cerebellin 1 precursor protein	Cbln1	-1.06	0.525	-1.57	0.325	1.1	0.515	2.64	0.584	1.54	0.016
1416363_at	FK506 binding protein 4	Fkbp4	1.03	0.577	1.19	0.982	1.69	0.950	1.43	0.536	1.54	0.043
1430038_at	gephyrin	Gphn	1.02	0.888	1.25	0.024	1.11	0.465	1.23	0.406	1.54	0.046
1459274_at	G protein-coupled receptor 135	Gpr135	1.39	0.373	1.74	0.248	1.13	0.438	1.34	0.204	1.54	0.009
1421569_at	glutamate receptor, ionotropic, delta 1	Grid1	1.54	0.869	-1.16	0.423	1.15	0.772	1.2	0.977	1.54	0.029
1453466_at	ribosomal protein S6	Rps6	1.24	0.389	-1.1	0.356	1.43	0.223	-1.1	0.651	1.54	0.009
1450033_a_at	signal transducer and activator of transcription 1	Stat1	1.92	0.548	1.4	0.534	1.27	0.516	1.16	0.221	1.54	0.026
1452273_at	expressed sequence AA409316	AA409316	1.23	0.209	1.58	0.035	1.42	0.014	1.3	0.012	1.55	0.033
1438211_s_at	D site albumin promoter binding protein	Dbp	-1.04	0.577	1.24	0.490	1.11	0.993	-1.21	0.003	1.55	0.032
1442869_at	docking protein 7	Dok7	1.49	0.886	1.05	0.344	1.27	0.945	2.04	0.061	1.55	0.047
1418862_at	enoyl Coenzyme A hydratase domain containing 3	Echdc3	-1.49	0.180	-1.47	0.315	1.16	0.421	-1.17	0.188	1.55	0.006
1426938_at	neuro-oncological ventral antigen 1 /// similar to neuro-oncological ventral	Nova1 /// LOC6648	3.15	0.204	1.54	0.708	2.27	0.449	-1.06	0.774	1.55	0.011
1449468_at	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactos	St6galnac5	1.04	0.965	1.3	0.460	-1.2	0.316	-1.18	0.230	1.55	0.003
1422202_at	thyroid hormone receptor beta	Thrb	-1.24	0.261	-1.13	0.022	1.42	0.541	-1.05	0.694	1.55	0.043
1441842_s_at	zinc finger protein 707	Zfp707	1	0.921	1.31	0.227	-1.4	0.000	1.25	0.271	1.55	0.010
1431616_at	RIKEN cDNA 1700067C01 gene	1700067C01Rik	1.76	0.483	1.39	0.867	1.5	0.537	-1.01	0.829	1.56	0.028
1429812_at	RIKEN cDNA 2610002D18 gene	2610002D18Rik	1.01	0.946	1.38	0.034	1.42	0.060	1.27	0.186	1.56	0.040
1421134_at	amphiregulin	Areg	1.62	0.661	2.26	0.067	1.95	0.195	1.25	0.263	1.56	0.017
1437486_at	G protein-coupled receptor, family C, group 5, member A	Gprc5a	2.81	0.187	4.18	0.050	1.55	0.007	1.18	0.031	1.56	0.007
1421016_at	immunoglobulin mu binding protein 2	Ighmbp2	2.18	0.639	2.2	0.537	1.74	0.090	1.16	0.178	1.56	0.033
1433575_at	similar to Transcription factor SOX-4	LOC672274	1.53	0.189	2.22	0.048	1.45	0.012	1.39	0.011	1.56	0.000
1458299_s_at	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor	Nfkbie	-1.31	0.212	1.44	0.928	4.17	0.114	1.4	0.117	1.56	0.050
1416505_at	nuclear receptor subfamily 4, group A, member 1	Nr4a1	1.34	0.031	2.01	0.033	1.48	0.004	1.38	0.001	1.56	0.010
1455894_at	peptidyl-tRNA hydrolase 2	Ptrh2	1.57	0.223	2.77	0.009	1.65	0.003	1.8	0.019	1.56	0.012
1419342_at	translocating chain-associating membrane protein 2	Tram2	1.35	0.664	1.06	0.724	1.65	0.780	2.01	0.386	1.56	0.022
1428564_at	zinc finger protein 579	Zfp579	-1.13	0.371	-1.05	0.583	1.13	0.833	1.25	0.075	1.56	0.022
1432268_at	RIKEN cDNA 2310068J16 gene	2310068J16Rik	-1.37	0.306	1.01	0.591	-1.05	0.564	1.21	0.130	1.57	0.001
1453006_at	RIKEN cDNA 2610306H15 gene	2610306H15Rik	1.09	0.348	1.57	0.040	1.44	0.036	1.26	0.000	1.57	0.006
1451426_at	DNA segment, Chr 11, Lothar Hennighausen 2, expressed	D11Lgp2e	-1.29	0.354	1.02	0.522	-1.1	0.503	1.04	0.931	1.57	0.021
1431019_at	leucine rich repeat containing 28	Lrrc28	1.38	0.427	1.49	0.466	-1.02	0.804	1.11	0.692	1.57	0.004
1427520_a_at	myosin, heavy polypeptide 1, skeletal muscle, adult	Myh1	-1.34	0.273	1.17	0.748	1.32	0.217	-1.67	0.200	1.57	0.041
1446405_at	MYST histone acetyltransferase (monocytic leukemia) 3	Myst3	-1.44	0.204	-1.72	0.207	-1.32	0.188	-1.21	0.380	1.57	0.008
1420406_at	paternally expressed 12	Peg12	-1.25	0.323	1.35	0.538	1.39	0.434	-1.17	0.121	1.57	0.016
1456106_x_at	serologically defined colon cancer antigen 3	Sdccag3	1.02	0.559	-1.1	0.466	-1.01	0.864	1.09	0.208	1.57	0.018
1434015_at	solute carrier family 2 (facilitated glucose transporter), member 6	Slc2a6	1.73	0.222	-1.34	0.238	1.91	0.798	1.22	0.399	1.57	0.043
1450644_at	zinc finger protein 36, C3H type-like 1	Zfp36l1	-1.03	0.752	1.4	0.022	1.55	0.030	1.33	0.016	1.57	0.000
1417158_at	ZXD family zinc finger C	Zxdc	-1.04	0.651	1.22	0.016	-1.01	0.927	-1.14	0.191	1.57	0.027
1457158_at	RIKEN cDNA 0610039J04 gene	0610039J04Rik	1.54	0.632	-1.33	0.276	3.35	0.025	2.8	0.075	1.58	0.003
1432541_at	RIKEN cDNA 4930408O17 gene	4930408O17Rik	-1.57	0.071	-1.08	0.638	1.16	0.483	1.18	0.311	1.58	0.005
1452700_s_at	kelch repeat and BTB (POZ) domain containing 7	Kbtbd7	-1.03	0.673	1.55	0.008	1.52	0.005	1.29	0.083	1.58	0.025
1439960_at	RNA pseudouridylate synthase domain containing 2	Rpusd2	-1.03	0.616	1.41	0.403	1.61	0.167	1.13	0.213	1.58	0.037
1427284_a_at	tocopherol (alpha) transfer protein	Ttpa	1.35	0.822	1.4	0.852	1.76	0.241	-1.5	0.107	1.58	0.030
1418362_at	zinc finger protein 42	Zfp42	1.65	0.500	1.97	0.305	2.38	0.456	1.41	0.146	1.58	0.011

1450410_a_at	RIKEN cDNA 4930570C03 gene	4930570C03Rik	1.3	0.411	1.37	0.196	1.08	0.042	1.33	0.029	1.59	0.037
1439499_at	expressed sequence AA415398	AA415398	1.6	0.674	-1.32	0.308	1.36	0.678	1.54	0.620	1.59	0.044
1460710_at	adenosine A2a receptor	Adora2a	-1.06	0.426	1.21	0.867	-1.13	0.424	1.66	0.092	1.59	0.049
1435714_x_at	interleukin 17D	Il17d	-1.27	0.077	1.15	0.319	1.12	0.204	1.2	0.416	1.59	0.000
1428186_at	potassium channel tetramerisation domain containing 6	Kctd6	-1.12	0.307	1.14	0.846	1.44	0.069	1.12	0.086	1.59	0.012
1418924_at	Ras association (RalGDS/AF-6) domain family 7	Rassf7	-1.09	0.482	1.17	0.470	1.11	0.356	1.11	0.281	1.59	0.024
1450417_a_at	ribosomal protein S20 /// similar to 40S ribosomal protein S20 /// similar to	Rps20 /// LOC2456	1.35	0.045	1.55	0.049	1.9	0.449	1.25	0.412	1.59	0.016
1446528_at	SCY1-like 2 (S. cerevisiae)	Scyl2	1.34	0.767	-1.66	0.175	-1.01	0.697	1.21	0.747	1.59	0.015
1444275_at	Uronyl-2-sulfotransferase	Ust	1.45	0.656	1.24	0.325	1.01	0.975	1.02	0.572	1.59	0.011
1445937_at	RIKEN cDNA A630001G21 gene	A630001G21Rik	1.07	0.805	1.23	0.523	3.25	0.487	-1.1	0.609	1.6	0.031
1428669_at	brain expressed myelocytomatosis oncogene	Bmyc	-1.02	0.607	1.04	0.871	1.16	0.569	1.19	0.104	1.6	0.004
1423166_at	CD36 antigen	Cd36	1.2	0.976	1.09	0.989	-1.19	0.251	-1.03	0.858	1.6	0.048
1459683_at	similar to spermatogenic cell-specific gene 2	LOC218695	2.52	0.807	2.89	0.054	1.55	0.123	-1.19	0.547	1.6	0.047
1444419_at	prolylcarboxypeptidase (angiotensinase C)	Prcp	-1.23	0.317	1.01	0.714	1.46	0.280	1.12	0.815	1.6	0.044
1450956_at	stearoyl-coenzyme A desaturase 3	Scd3	1.14	0.196	-1.92	0.146	1.9	0.505	1.28	0.116	1.6	0.002
1419083_at	tumor necrosis factor (ligand) superfamily, member 11	Tnfsf11	2.87	0.270	1.67	0.427	1.73	0.016	1.68	0.187	1.6	0.030
1456857_at	RIKEN cDNA 1500011B03 gene	1500011B03Rik	1.11	0.995	1.24	0.243	-1.2	0.340	1.44	0.283	1.61	0.019
1438340_at	RIKEN cDNA A930006D11Rik gene	A930006D11Rik	-1.32	0.260	1.02	0.752	-1.08	0.657	-1.25	0.106	1.61	0.003
1419483_at	complement component 3a receptor 1	C3ar1	1.78	0.634	1.79	0.209	1.37	0.015	1.34	0.188	1.61	0.007
1453500_at	cytochrome P450, family 2, subfamily u, polypeptide 1	Cyp2u1	2.51	0.305	3.85	0.038	1.05	0.805	1.57	0.095	1.61	0.030
1417115_at	mitogen activated protein kinase kinase kinase 12	Map3k12	1.03	0.764	1.2	0.856	1.15	0.393	1.27	0.024	1.61	0.047
1451190_a_at	SH3-binding kinase 1	Sbk1	-1.29	0.317	1.43	0.673	1.82	0.072	1.3	0.005	1.61	0.024
1451323_at	zinc finger protein 7	Zfp7	1.25	0.645	1.71	0.062	1.52	0.002	1.49	0.006	1.61	0.046
1454218_at	RIKEN cDNA 4930405D01 gene	4930405D01Rik	1.08	0.646	-1.26	0.224	-1.2	0.268	-1.03	0.530	1.62	0.035
1424506_at	cDNA sequence BC026432	BC026432	2.75	0.714	3.01	0.079	1.08	0.505	1.02	0.224	1.62	0.043
1456005_a_at	BCL2-like 11 (apoptosis facilitator)	Bcl2l11	-1.36	0.329	1.22	0.785	1.19	0.108	1.32	0.087	1.62	0.013
1420941_at	regulator of G-protein signaling 5	Rgs5	1.16	0.934	1.24	0.399	1.24	0.913	1.18	0.090	1.62	0.028
1434560_at	WD and tetratricopeptide repeats 1	Wdtc1	1.44	0.829	-1.43	0.241	1.27	0.310	-1.24	0.018	1.62	0.010
1419612_at	RIKEN cDNA 4632415L05 gene	4632415L05Rik	1.46	0.085	1.58	0.089	1.45	0.048	1.22	0.277	1.63	0.011
1453324_at	RIKEN cDNA 6330509M23 gene	6330509M23Rik	1.04	0.869	1.2	0.279	1.36	0.008	1.18	0.151	1.63	0.033
1427985_at	RIKEN cDNA 9630042H07 gene	9630042H07Rik	1.06	0.755	1.36	0.032	1.39	0.145	1.44	0.016	1.63	0.002
1422526_at	acyl-CoA synthetase long-chain family member 1	Acsl1	-1.04	0.549	1.54	0.988	2.51	0.462	1.2	0.966	1.63	0.033
1460415_a_at	CD40 antigen	Cd40	-1.21	0.113	-1.07	0.688	1.59	0.278	1.1	0.464	1.63	0.028
1420604_at	homeo box gene expressed in ES cells	Hesx1	-1.07	0.477	1.05	0.997	1.31	0.591	2.63	0.533	1.63	0.020
1460347_at	keratin 14	Krt14	-1.05	0.705	-1.31	0.367	1.03	0.643	1.15	0.506	1.63	0.005
1449423_at	microtubule associated serine/threonine kinase 1	Mast1	2.04	0.342	2.52	0.455	-1.05	0.493	-1.14	0.187	1.63	0.007
1424544_at	nuclear receptor binding protein 2	Nrbp2	1.08	0.900	1.24	0.439	1.14	0.557	-1.09	0.089	1.63	0.039
1434530_at	odd Oz/ten-m homolog 4 (Drosophila)	Odz4	1.79	0.412	-1.01	0.727	-1.07	0.524	1.27	0.892	1.63	0.039
1451624_a_at	phosphatase, orphan 2	Phospho2	1.03	0.988	1.39	0.251	1.22	0.020	1.35	0.028	1.63	0.029
1450261_a_at	solute carrier family 10 (sodium/bile acid cotransporter family), member 1	Slc10a1	1.6	0.818	1.24	0.420	2.79	0.007	1.05	0.727	1.63	0.041
1430259_at	tumor necrosis factor receptor superfamily, member 11a	Tnfrsf11a	1.12	0.918	-1.07	0.443	-1.16	0.536	1.12	0.465	1.63	0.005
1423176_at	transducer of ErbB-2.1	Tob1	1.01	0.995	1.32	0.013	1.56	0.016	1.22	0.039	1.63	0.000
1439352_at	tripartite motif protein 7	Trim7	1.08	0.732	1.62	0.490	1.44	0.150	-1.03	0.923	1.63	0.019
1430938_at	zinc finger protein 64	Zfp64	2.54	0.198	1.99	0.200	1.15	0.917	2.26	0.953	1.63	0.046
1449074_at	RIKEN cDNA 1700019N12 gene	1700019N12Rik	1.27	0.600	1.2	0.610	-1.29	0.392	-1.81	0.075	1.64	0.040
1437265_at	RIKEN cDNA 5330438D12 gene	5330438D12Rik	-1.01	0.567	1.18	0.847	-1.11	0.143	1.13	0.900	1.64	0.025
1441792_at	RIKEN cDNA A630033E08 gene	A630033E08Rik	-1.01	0.782	-1.3	0.331	1.13	0.779	1.13	0.775	1.64	0.048
1449065_at	acyl-CoA thioesterase 1	Acot1	1.09	0.742	1.44	0.178	1.82	0.113	1.02	0.661	1.64	0.015
1420935_a_at	serine/arginine repetitive matrix 1	Srrm1	1.09	0.670	1.46	0.023	-1.25	0.176	1.03	0.941	1.64	0.037
1443978_at	ankyrin repeat domain 41	Ankrd41	1.76	0.579	-1.19	0.306	1.2	0.321	1.16	0.436	1.65	0.006
1429176_at	leucine rich repeat and sterile alpha motif containing 1	Lrsam1	1.98	0.183	1.68	0.138	1.25	0.577	1.21	0.009	1.65	0.034
1420530_at	neuronal d4 domain family member	Neud4	1.31	0.749	1.56	0.428	1.17	0.275	1.24	0.000	1.65	0.020
1433619_at	expressed sequence AI894139	AI894139	-1.21	0.142	1.38	0.148	1.69	0.002	1.25	0.293	1.66	0.023
1458656_at	expressed sequence AW050198	AW050198	-1.04	0.494	1.23	0.748	1.09	0.658	-1	0.963	1.66	0.014
1443421_s_at	protocadherin beta 15	Pcdhb15	-1.03	0.710	-1.03	0.932	2.08	0.065	-1.05	0.686	1.66	0.012
1438949_at	resistance to inhibitors of cholinesterase 8 homolog (C. elegans)	Ric8	-1.16	0.402	2.08	0.469	1.57	0.853	3.03	0.306	1.66	0.008
1450577_at	somatostatin receptor 3	Sstr3	1.88	0.564	3.04	0.204	1.49	0.288	1.22	0.622	1.66	0.035
1453479_at	RIKEN cDNA 1700086P04 gene	1700086P04Rik	-1.65	0.098	1.06	0.547	2.81	0.928	1.32	0.797	1.67	0.017

1453081_at	RIKEN cDNA 2410022M11 gene	2410022M11Rik	-1.19	0.397	-1.11	0.458	1.01	0.920	1.31	0.026	1.67	0.002
1431514_at	RIKEN cDNA 5730453C05 gene	5730453C05Rik	-1.35	0.310	-1.2	0.385	1.37	0.786	2.05	0.244	1.67	0.012
1436627_at	DNA segment, Chr 17, ERATO Doi 663, expressed	D17Ertd663e	2.3	0.228	1.39	0.957	-1.26	0.161	-1.02	0.850	1.67	0.007
1432181_s_at	endothelial cell growth factor 1 (platelet-derived)	Ecgf1	1.17	0.185	1.72	0.003	1.5	0.155	1.5	0.006	1.67	0.016
1435192_at	similar to SRY (sex determining region Y)-box 3	LOC631901	2.63	0.341	2.38	0.438	1.16	0.739	1.06	0.899	1.67	0.043
1455099_at	monoacylglycerol O-acyltransferase 2	Mogat2	1.08	0.676	-1.01	0.873	-1.19	0.467	1.04	0.932	1.67	0.010
1443922_at	REST corepressor 3	Rcor3	1.51	0.531	1.76	0.153	1.4	0.585	-1.03	0.930	1.67	0.003
1450093_s_at	zinc finger and BTB domain containing 7a	Zbtb7a	-1.17	0.351	-1.15	0.438	-1.15	0.428	-1.03	0.765	1.67	0.043
1453671_at	RIKEN cDNA 9430041J12 gene	9430041J12Rik	-1.93	0.065	1.33	0.470	1.88	0.764	1.41	0.390	1.68	0.034
1434962_x_at	chemokine (C-C motif) ligand 27	Ccl27	-1.2	0.312	-1.11	0.530	1.07	0.984	-1.01	0.632	1.68	0.042
1431026_at	N-acetyltransferase 12	Nat12	-1.17	0.434	1.21	0.886	1.25	0.237	1.35	0.005	1.68	0.037
1459068_at	Transmembrane protein 109	Tmem109	-1.29	0.415	-1.11	0.470	-1.22	0.199	1.26	0.666	1.68	0.021
1443737_at	Exportin 6	Xpo6	-1.09	0.699	-1.06	0.574	1.58	0.157	-1.18	0.401	1.68	0.020
1436219_at	RIKEN cDNA 4933403F05 gene	4933403F05Rik	1.4	0.038	2.63	0.005	1.56	0.008	1.75	0.002	1.69	0.008
1451263_a_at	fatty acid binding protein 4, adipocyte	Fabp4	-1.51	0.205	-1.04	0.663	-1.09	0.336	-1.29	0.023	1.69	0.021
1455948_x_at	matrilin 3	Matn3	-1.01	0.438	1.1	0.576	1.69	0.612	1.96	0.361	1.69	0.030
1434209_at	protein arginine N-methyltransferase 6	Prmt6	1.74	0.125	1.66	0.086	1.47	0.062	1.46	0.263	1.69	0.022
1424865_at	peptide YY	Pyy	-1.33	0.339	1.38	0.613	2	0.724	-1.65	0.199	1.69	0.019
1430032_at	RNA binding motif protein 4B	Rbm4b	-1.02	0.754	1.26	0.330	1.53	0.058	1.54	0.001	1.69	0.006
1416926_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.12	0.621	2.52	0.002	1.79	0.000	1.45	0.047	1.69	0.003
1433328_at	RIKEN cDNA 1700095A21 gene	1700095A21Rik	1.2	0.858	-1.18	0.226	1.25	0.618	1.19	0.948	1.7	0.021
1426734_at	cDNA sequence BC022623	BC022623	3.84	0.469	3.79	0.002	1.24	0.172	1.47	0.066	1.7	0.024
1446952_at	DNA segment, Chr 11, ERATO Doi 506, expressed	D11Ertd506e	-1.21	0.183	-1.16	0.403	2.26	0.079	-1.01	0.354	1.7	0.030
1446948_at	Density-regulated protein	Denr	-1.06	0.620	-1.16	0.401	1.09	0.820	1.59	0.388	1.7	0.004
1424794_at	ring finger protein 186	Rnf186	1.05	0.866	-1.09	0.649	1.79	0.083	1.5	0.584	1.7	0.014
1427523_at	sine oculis-related homeobox 3 homolog (Drosophila) /// RIKEN cDNA E13	Six3 /// E130112M	-1.08	0.416	-1.05	0.468	-1.04	0.471	1.75	0.684	1.7	0.044
1439540_at	membrane-associated ring finger (C3HC4) 2	2-Mar	2.05	0.194	2.21	0.308	1.36	0.549	1.91	0.335	1.71	0.038
1453089_at	RIKEN cDNA 3110079O15 gene	3110079O15Rik	1.02	0.813	1.76	0.999	1.73	0.656	1.15	0.262	1.71	0.042
1454617_at	arrestin domain containing 3	Arrdc3	-1.05	0.719	1.4	0.142	1.58	0.007	1.35	0.021	1.71	0.025
1456761_at	RIKEN cDNA D630030B22 gene	D630030B22Rik	1.1	0.798	1.05	0.792	-1.19	0.300	-1.26	0.212	1.71	0.041
1426236_a_at	glutamate-ammonia ligase (glutamine synthetase)	Glul	-1.14	0.493	1.05	0.909	1.18	0.056	1.14	0.028	1.71	0.003
1440644_at	poly (ADP-ribose) polymerase family, member 6	Parp6	1.78	0.953	2.19	0.846	-1.26	0.386	2.81	0.229	1.71	0.025
1448209_a_at	solute carrier family 22 (organic cation transporter), member 17	Slc22a17	-1.2	0.371	1.68	0.213	1.38	0.133	1.21	0.974	1.71	0.003
1428074_at	transmembrane protein 158	Tmem158	-1.13	0.479	1.64	0.129	1.67	0.107	1.35	0.034	1.71	0.027
1427217_at	zinc finger protein 455	Zfp455	1.32	0.681	1.53	0.201	-1.03	0.535	1.41	0.245	1.71	0.037
1452610_at	zinc finger protein 99	Zfp99	1.1	0.616	1.07	0.614	-1.28	0.077	1.25	0.908	1.71	0.044
1445339_at	cyclic nucleotide gated channel alpha 4	Cnga4	1.13	0.666	1.22	0.675	2.36	0.130	2.1	0.335	1.72	0.008
1457615_at	Cytoplasmic FMR1 interacting protein 1	Cyfip1	1.32	0.482	-2.1	0.307	1.98	0.997	2.56	0.077	1.72	0.019
1425062_at	Fc receptor-like 1	Fcrl1	1.72	0.262	1.31	0.049	1.73	0.249	1.12	0.099	1.72	0.005
1437756_at	GTPase, IMAP family member 9	Gimap9	1.58	0.493	1.05	0.473	2.3	0.290	1.75	0.565	1.72	0.049
1431053_at	M-phase phosphoprotein 9	Mphosph9	1.21	0.448	1.07	0.721	1.45	0.252	1.14	0.126	1.72	0.027
1434495_at	zinc finger protein 278	Zfp278	1.93	0.263	2.46	0.069	1.14	0.736	1.35	0.021	1.72	0.007
1429985_at	RIKEN cDNA 5430439G13 gene	5430439G13Rik	1.7	0.386	2.03	0.680	-1.05	0.603	-1.07	0.918	1.73	0.034
1439649_at	arginine decarboxylase	Adc	5.72	0.299	6.19	0.732	-1.09	0.486	1.11	0.534	1.73	0.017
1447638_at	Arylformamidase	Afmid	-1.82	0.074	-2.01	0.009	2.69	0.387	1.08	0.982	1.73	0.044
1422817_at	glycoprotein 5 (platelet)	Gp5	-1.5	0.273	-1.4	0.125	1.67	0.916	1.44	0.868	1.73	0.005
1424841_s_at	ribokinase	Rbks	-1.16	0.339	1.03	0.899	1.09	0.751	-1.14	0.132	1.73	0.021
1416571_at	Tnf receptor associated factor 4	Traf4	1.39	0.041	2.03	0.000	1.36	0.110	1.08	0.484	1.73	0.048
1436593_at	RIKEN cDNA 1700016K19 gene	1700016K19Rik	1.67	0.544	3.4	0.034	2.4	0.177	1.26	0.129	1.74	0.042
1430863_at	RIKEN cDNA 4933411B09 gene	4933411B09Rik	1.47	0.643	1.95	0.989	1.4	0.197	1.3	0.343	1.74	0.005
1458550_at	myosin ID	Myo1d	-1	0.452	1.03	0.475	1.37	0.129	1.35	0.765	1.74	0.033
1457083_at	PRP31 pre-mRNA processing factor 31 homolog (yeast)	Prpf31	1.59	0.196	2.41	0.030	1.35	0.032	1.41	0.043	1.74	0.020
1443837_x_at	B-cell leukemia/lymphoma 2	Bcl2	1.47	0.499	-1.23	0.383	4.44	0.216	1.69	0.035	1.75	0.029
1442758_at	Heterogeneous nuclear ribonucleoprotein A1	Hnrpa1	1.55	0.987	-1.18	0.191	-1.34	0.332	2.59	0.460	1.75	0.042
1458428_at	potassium channel, subfamily T, member 1	Kcnt1	-1.07	0.528	-1.28	0.105	2.84	0.305	-1.83	0.131	1.75	0.037
1451885_at	metallothionein 1K	LOC574530	1.33	0.932	1.12	0.537	1.69	0.580	2.53	0.594	1.75	0.014
1430427_a_at	protocadherin 18	Pcdh18	1.7	0.016	2.49	0.021	2.08	0.133	1.7	0.129	1.75	0.029
1456646_at	peroxisome biogenesis factor 10	Pex10	1.15	0.499	1.22	0.724	2.01	0.067	1.3	0.391	1.75	0.036

1421885_at	Son of sevenless homolog 1 (Drosophila)	Sos1	-1.64	0.131	-1.34	0.366	2.19	0.689	1.25	0.757	1.75	0.013
1442105_at	RIKEN cDNA 4831416G18 gene	4831416G18Rik	-1.01	0.665	-1.27	0.378	2.59	0.234	-1.06	0.712	1.76	0.038
1418722_at	neutrophilic granule protein	Ngp	-1.25	0.414	1.14	0.599	-1.16	0.386	1.89	0.943	1.76	0.031
1460250_at	sclerostin domain containing 1	Sostdc1	1.36	0.159	-1.04	0.587	-1.43	0.220	1.2	0.917	1.76	0.021
1436004_at	ubiquitin specific peptidase 27, X chromosome	Usp27x	-1.09	0.488	1.32	0.380	1.35	0.153	1.32	0.018	1.76	0.024
1439939_at	RIKEN cDNA E030042N06 gene	E030042N06Rik	1.39	0.883	-1.21	0.154	-1.25	0.308	1.72	0.447	1.77	0.038
1426127_x_at	killer cell lectin-like receptor, subfamily A, member 18	Klra18	1.18	0.292	1.41	0.303	2.24	0.332	1.06	0.355	1.77	0.032
1458353_at	RIKEN cDNA A230063L24 gene	A230063L24Rik	1.38	0.174	1.03	0.864	1.19	0.465	1.05	0.768	1.78	0.022
1428283_at	cytochrome P450, family 2, subfamily s, polypeptide 1	Cyp2s1	-1.65	0.107	2.08	0.429	1.03	0.857	1.86	0.034	1.78	0.047
1449370_at	SRY-box containing gene 4 /// similar to Transcription factor SOX-4	Sox4 /// LOC67227	1.04	0.137	1.63	0.065	1.78	0.033	1.5	0.022	1.78	0.018
1436327_a_at	vacuolar protein sorting 53 (yeast)	Vps53	3.06	0.626	2.27	0.948	-1.05	0.097	1.26	0.271	1.78	0.028
1430347_at	RIKEN cDNA 4930524J08 gene	4930524J08Rik	1.22	0.958	1.28	0.788	1.65	0.124	-1.18	0.341	1.79	0.014
1444320_at	DDHD domain containing 2	Ddhd2	1.02	0.976	-1.11	0.640	3.15	0.185	1.18	0.299	1.79	0.012
1433335_at	RIKEN cDNA 4930405G09 gene	4930405G09Rik	1.26	0.768	1.7	0.568	2.47	0.348	-2.54	0.006	1.8	0.020
1435932_at	Hermansky-Pudlak syndrome 6	Hps6	-1.11	0.322	1.38	0.760	1.19	0.287	-1.06	0.357	1.8	0.001
1442549_at	muscleblind-like 3 (Drosophila)	Mbnl3	2.34	0.015	2.16	0.173	-1.17	0.810	-1.05	0.718	1.8	0.044
1444518_at	Acyl-Coenzyme A oxidase 1, palmitoyl	Acox1	2.87	0.739	2.06	0.864	1.81	0.472	1.21	0.665	1.81	0.030
1419744_at	histocompatibility 2, class II, locus Mb2	H2-DMb2	1.02	0.626	-1.01	0.596	1.04	0.657	1.45	0.045	1.81	0.045
1418160_at	makorin, ring finger protein, 3	Mkrn3	2.29	0.307	2.97	0.098	-1.01	0.723	-1.16	0.553	1.81	0.023
1450266_at	sodium channel, voltage-gated, type X, alpha	Scn10a	1.91	0.502	1.05	0.471	1.36	0.279	1.23	0.567	1.81	0.008
1448940_at	tripartite motif protein 21	Trim21	2.57	0.753	1.75	0.004	2.97	0.013	1.14	0.363	1.81	0.015
1417375_at	tubulin, alpha 4	Tuba4	-1.1	0.472	-1.14	0.721	1.69	0.140	1.02	0.897	1.81	0.014
1449231_at	zinc finger protein 296	Zfp296	-1.01	0.813	1.49	0.041	1.21	0.105	1.47	0.019	1.81	0.019
1433113_at	RIKEN cDNA 4921504P20 gene	4921504P20Rik	1.05	0.947	1.29	0.316	-1.19	0.101	-1.01	0.940	1.82	0.002
1427187_at	RIKEN cDNA 6030413G23 gene	6030413G23Rik	-1.22	0.040	-1.52	0.042	1.03	0.879	1.1	0.479	1.82	0.032
1445059_at	expressed sequence C80435	C80435	1.43	0.818	-1.59	0.224	-1.22	0.555	2.33	0.448	1.82	0.031
1457048_at	G protein-coupled receptor 103	Gpr103	1.19	0.650	-1.33	0.373	1.83	0.394	2.95	0.171	1.82	0.008
1437047_at	zinc finger protein 664	Zfp664	2.07	0.243	2.65	0.100	2.31	0.062	1.24	0.172	1.82	0.018
1421531_at	A kinase (PRKA) anchor protein 3	Akap3	2.51	0.245	3.31	0.075	-1.55	0.056	1.46	0.872	1.83	0.027
1450271_at	PTK6 protein tyrosine kinase 6	Ptk6	1.53	0.172	1.53	0.478	-1.49	0.259	1.59	0.531	1.83	0.042
1454857_at	ring finger protein 122	Rnf122	3	0.333	4.85	0.042	1.39	0.024	1.58	0.034	1.83	0.017
1453391_at	spermatogenesis associated glutamate (E)-rich protein 7, pseudogene 1	Speer7-ps1	1.38	0.404	2.09	0.254	2.66	0.163	2.01	0.505	1.83	0.040
1428298_at	RIKEN cDNA 1700029G01 gene	1700029G01Rik	1.35	0.488	1.18	0.554	-1.01	0.551	1.35	0.713	1.84	0.049
1455679_at	RIKEN cDNA 5830411E10 gene	5830411E10Rik	1.93	0.264	3.7	0.007	1.83	0.053	1.96	0.005	1.84	0.005
1453306_at	RIKEN cDNA 6330531I01 gene	6330531I01Rik	-1.68	0.180	-1.35	0.329	-1.3	0.220	1.13	0.739	1.84	0.017
1420557_at	Eph receptor A5	Epha5	1.29	0.181	2.19	0.107	2.47	0.343	-1.24	0.470	1.84	0.002
1425467_a_at	proteolipid protein (myelin) 1	Plp1	1	0.463	-1.27	0.355	1.85	0.291	1	0.991	1.84	0.004
1441969_at	tripartite motif-containing 36	Trim36	1.32	0.879	1.38	0.436	-1.63	0.049	-1.08	0.699	1.84	0.024
1432858_at	RIKEN cDNA D730048M19 gene	D730048M19Rik	1.27	0.683	-1.22	0.404	1.92	0.865	1.75	0.262	1.85	0.037
1438415_s_at	Yip1 domain family, member 2	Yipf2	-1.04	0.375	1.26	0.997	-1.02	0.656	1.12	0.726	1.85	0.028
1455654_at	RIKEN cDNA 6430706D22 gene	6430706D22Rik	2.15	0.500	1.59	0.226	1.49	0.167	1.14	0.734	1.86	0.014
1446915_at	DNA segment, Chr 7, ERATO Doi 316, expressed	D7Ertd316e	-1.34	0.253	1.97	0.421	-1.33	0.373	1.3	0.047	1.86	0.031
1431226_a_at	fibronectin type III domain containing 4	Fndc4	-1.03	0.684	1.21	0.494	1.25	0.433	-1.23	0.071	1.86	0.026
1459311_at	phosphodiesterase 4D, cAMP specific	Pde4d	1.4	0.412	1.65	0.635	1.71	0.524	-1.19	0.384	1.86	0.046
1425162_at	RAR-related orphan receptor beta	Rorb	1.1	0.972	-2.22	0.018	-1.35	0.280	1.01	0.840	1.86	0.025
1446369_at	armadillo repeat containing 1	Armc1	1.41	0.719	1.03	0.486	-1.01	0.533	1.08	0.920	1.87	0.033
1416072_at	CD34 antigen	Cd34	2.83	0.021	1.33	0.680	1.77	0.715	1.14	0.722	1.88	0.032
1428304_at	establishment of cohesion 1 homolog 2 (S. cerevisiae)	Esco2	1.46	0.174	1.66	0.156	1.32	0.176	1.18	0.227	1.88	0.022
1436685_at	hypothetical LOC544888	LOC544888	-1.33	0.169	1.07	0.729	-1.42	0.043	1.63	0.433	1.88	0.017
1441520_at	asp (abnormal spindle)-like, microcephaly associated (Drosophila)	Aspm	2.52	0.139	3.19	0.414	-1.15	0.131	1.14	0.594	1.89	0.034
1457749_at	coiled-coil and C2 domain containing 1B	Cc2d1b	-1.35	0.181	-1.34	0.173	1.44	0.345	-1.32	0.170	1.89	0.038
1424229_at	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3	Dyrk3	2.16	0.096	3.82	0.004	1.72	0.023	1.43	0.038	1.89	0.003
1444477_at	Leucine rich repeat transmembrane neuronal 3	Lrrtm3	-1.24	0.344	-1.7	0.143	1.42	0.641	1.45	0.454	1.9	0.014
1436615_a_at	ornithine transcarbamylase	Otc	2.68	0.704	2.76	0.840	1.41	0.400	2.05	0.877	1.9	0.044
1454298_at	RIKEN cDNA 4932430A15 gene	4932430A15Rik	1.11	0.559	1.8	0.892	1.14	0.765	1.43	0.891	1.91	0.030
1448901_at	carboxypeptidase X 1 (M14 family)	Cpxm1	-1.35	0.105	-1.26	0.323	1.72	0.873	1.13	0.259	1.91	0.022
1452409_at	glioma tumor suppressor candidate region gene 2	Gltscr2	1.28	0.307	1.26	0.313	1.95	0.432	1	0.614	1.91	0.011
1457325_at	K+ voltage-gated channel, subfamily S, 2	Kcns2	-1.07	0.489	1.18	0.618	1.22	0.463	-1.45	0.179	1.91	0.007

1419324_at	LIM homeobox protein 9	Lhx9	1.02	0.732	1.67	0.071	1.39	0.106	1.26	0.238	1.91	0.011
1437703_at	similar to F-box- and WD40-repeat-containing protein	LOC382156	1.17	0.670	-1.21	0.085	1.43	0.522	1.16	0.142	1.91	0.006
1445420_at	Myocyte enhancer factor 2C	Mef2c	1.39	0.738	1.81	0.060	-1.16	0.484	2.27	0.294	1.91	0.040
1431748_a_at	ring finger and FYVE like domain containing protein	Rffl	2.6	0.085	1.4	0.190	1.45	0.921	1.81	0.033	1.91	0.045
1437710_x_at	RIKEN cDNA 1700021P22 gene	1700021P22Rik	1.1	0.934	1.01	0.980	2.6	0.719	1.15	0.827	1.92	0.036
1431449_at	solute carrier organic anion transporter family, member 6d1	Slco6d1	-1.13	0.544	-1.77	0.048	1.25	0.603	-1.14	0.686	1.92	0.030
1450448_at	stanniocalcin 1	Stc1	1.39	0.078	1.78	0.036	1.42	0.325	1.47	0.084	1.92	0.048
1430451_at	RIKEN cDNA 4930481B07 gene	4930481B07Rik	2.62	0.726	2.87	0.475	1.87	0.190	1.17	0.387	1.93	0.013
1443318_at	RIKEN cDNA E130016E03 gene	E130016E03Rik	1.03	0.813	-1.44	0.264	1.14	0.849	1.18	0.580	1.93	0.049
1443680_at	Otx2 opposite strand transcript 1	Otx2os1	2.03	0.734	1.47	0.673	-1.24	0.403	-1.74	0.133	1.93	0.020
1445291_at	arylsulfatase A	Arsa	-1.1	0.442	1.29	0.466	1.41	0.269	-1.73	0.061	1.94	0.027
1435860_at	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	Slc5a6	1.23	0.599	2.46	0.033	1.17	0.729	1.28	0.289	1.94	0.028
1427791_a_at	a disintegrin and metallopeptidase domain 1a	Adam1a	-1.12	0.354	-1.21	0.444	2.13	0.117	1.06	0.630	1.95	0.011
1425372_at	DnaJ (Hsp40) homolog, subfamily C, member 19	Dnajc19	-1.04	0.518	-1.35	0.058	1.22	0.798	1.54	0.080	1.95	0.006
1434109_at	SH3 domain binding glutamic acid-rich protein like 2	Sh3bgrl2	1.48	0.183	1.24	0.651	1.65	0.112	-1.04	0.408	1.95	0.002
1456770_at	zinc finger protein 14	Zfp14	2.93	0.029	3	0.096	1.63	0.959	1.11	0.562	1.95	0.046
1453789_at	RIKEN cDNA 4933440N22 gene	4933440N22Rik	-1.01	0.550	-1.09	0.812	1.72	0.405	1.19	0.872	1.96	0.011
1447716_x_at	RIKEN cDNA 6330442E10 gene	6330442E10Rik	1.72	0.319	1.4	0.796	1.32	0.275	1.72	0.184	1.96	0.018
1427215_at	acyl-CoA synthetase medium-chain family member 2	Acsm2	1.01	0.544	-1.14	0.596	-1.07	0.641	-1.11	0.488	1.96	0.049
1454244_at	minichromosome maintenance deficient 10 (S. cerevisiae)	Mcm10	1.14	0.242	1.36	0.544	1.98	0.174	1.1	1.000	1.96	0.016
1455622_at	podocalyxin-like 2	Podxl2	1.29	0.417	-1.16	0.417	1.26	0.495	1.3	0.627	1.96	0.019
1446864_at	S100P binding protein	S100pbp	1.54	0.739	1.38	0.625	2.11	0.024	1.73	0.568	1.96	0.039
1432567_at	RIKEN cDNA A430105D02 gene	A430105D02Rik	1.43	0.920	-2.29	0.119	-1.15	0.487	2.97	0.636	1.97	0.047
1440916_at	RIKEN cDNA 2510049J12 gene	2510049J12Rik	-1.4	0.124	-1.01	0.649	1.46	0.333	1.99	0.240	1.98	0.009
1418037_at	complement component 4 binding protein	C4bp	1.43	0.785	1.36	0.947	1.64	0.393	1.14	0.797	1.98	0.022
1440490_at	Membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	Mpp6	2.21	0.938	-1.08	0.281	1.56	0.853	-1.23	0.431	1.98	0.038
1446389_at	Nuclear receptor interacting protein 1	Nrip1	1.55	0.860	1.6	0.457	2.46	0.241	1.72	0.606	1.98	0.023
1447271_at	non-catalytic region of tyrosine kinase adaptor protein 1	Nck1	1.34	0.326	1.2	0.569	1.31	0.726	1.74	0.724	1.99	0.015
1436721_x_at	oogenesin 3	Oog3	2.34	0.314	1.07	0.542	1.35	0.548	1.15	0.321	1.99	0.026
1447092_at	Platelet/endothelial cell adhesion molecule 1	Pecam1	1.17	0.705	1.28	0.681	1.82	0.317	2.15	0.132	1.99	0.040
1436500_at	ribosomal protein S24	Rps24	1.13	0.894	1.22	0.588	-1.11	0.539	1.03	0.569	1.99	0.020
1441584_at	Friend leukemia integration 1	Fli1	1.74	0.160	1.25	0.987	-1.05	0.525	1.02	0.930	2	0.035
1446729_at	dispatched homolog 2 (Drosophila)	Disp2	-1.57	0.045	-1.15	0.229	1.64	0.974	1.42	0.405	2.01	0.040
1430517_at	RIKEN cDNA 4930544O15 gene	4930544O15Rik	1.01	0.908	1.84	0.261	-1.97	0.020	1.26	0.556	2.02	0.003
1440676_at	RIKEN cDNA A830043J08 gene	A830043J08Rik	-1	0.637	-1.23	0.200	-1.45	0.290	1.04	0.920	2.02	0.011
1458313_at	Cell division cycle 2-like 5 (cholinesterase-related cell division controller)	Cdc2l5	1.2	0.473	1.29	0.594	1.31	0.236	1.29	0.559	2.02	0.032
1429666_at	potassium channel tetramerisation domain containing 16	Kctd16	1.88	0.009	1.39	0.309	1.33	0.201	2.47	0.159	2.02	0.039
1453533_at	RIKEN cDNA 4933403O08 gene	4933403O08Rik	1.23	0.968	1.39	0.818	-1.24	0.164	1.54	0.411	2.03	0.037
1457310_x_at	scratch homolog 2, zinc finger protein (Drosophila)	Scrt2	1.39	0.767	1.38	0.853	1.25	0.439	1.19	0.906	2.03	0.022
1439250_at	SLIT and NTRK-like family, member 3	Slitrk3	1.21	0.879	1.44	0.227	-1.02	0.573	-1.2	0.405	2.03	0.032
1456915_at	RIKEN cDNA D930005D10 gene	D930005D10Rik	1.18	0.806	1.53	0.412	-1.56	0.161	1.03	0.706	2.04	0.010
1459795_at	G protein-coupled receptor 85	Gpr85	1.17	0.244	1.15	0.643	-1.2	0.511	1.69	0.652	2.04	0.036
1420352_at	protease, serine, 22	Prss22	1.13	0.465	2.17	0.696	-1.05	0.726	-2.13	0.047	2.05	0.005
1436133_at	RIKEN cDNA 0610011N22 gene	0610011N22Rik	1.09	0.401	1.69	0.019	1.55	0.192	1.84	0.021	2.06	0.028
1451415_at	RIKEN cDNA 1810011O10 gene	1810011O10Rik	1.49	0.099	1.99	0.005	2.24	0.033	1.43	0.101	2.06	0.012
1427300_at	LIM homeobox protein 8	Lhx8	1.51	0.957	-1.02	0.994	1.96	0.413	-1	0.929	2.06	0.030
1454629_at	RIKEN cDNA A930037G23 gene	A930037G23Rik	1.5	0.521	1.55	0.188	1.09	0.961	1.32	0.063	2.07	0.040
1447496_s_at	fibronectin type 3 and ankyrin repeat domains 1	Fank1	-1.54	0.123	-1.08	0.443	1.21	0.984	1.6	0.599	2.07	0.043
1422724_at	male germ cell-associated kinase	Mak	1.06	0.533	1.75	0.161	1.2	0.924	-1.66	0.158	2.07	0.048
1459836_x_at	splicing factor 3b, subunit 2	Sf3b2	-1.1	0.487	-1.24	0.421	1.02	0.980	-1.02	0.638	2.08	0.024
1439331_at	RIKEN cDNA 4932439E07 gene	4932439E07Rik	2.62	0.355	1.12	0.644	-1.58	0.044	-1.41	0.268	2.09	0.020
1455638_at	zinc finger protein 319	Zfp319	1.2	0.888	1.35	0.982	1.88	0.128	1.58	0.113	2.09	0.024
1457976_at	RIKEN cDNA 2010002M12 gene	2010002M12Rik	1.26	0.640	1.27	0.626	1.1	0.837	1.3	0.329	2.1	0.012
1443387_at	expressed sequence BB045044	BB045044	-1.12	0.906	-1.1	0.520	1.89	0.490	1.59	0.992	2.1	0.021
1432656_at	RIKEN cDNA 3222402N08 gene	3222402N08Rik	1.52	0.221	2.01	0.041	-1.22	0.047	1.16	0.656	2.11	0.036
1436875_at	dynamin 3	Dnm3	1.19	0.798	-1.22	0.192	1.01	0.765	-1.43	0.206	2.11	0.043
1426152_a_at	kit ligand	Kitl	-1.27	0.340	-1.34	0.116	1.13	0.784	1.1	0.489	2.11	0.035
1449032_at	prolactin-like protein M	Prlpm	-1.02	0.442	1.36	0.659	1.06	0.903	2.29	0.043	2.11	0.004

1455683_a_at	TBC1 domain family, member 8	Tbc1d8	1.12	0.392	1.01	0.371	-1.03	0.913	-1.28	0.282	2.11	0.019
1423004_at	vasoactive intestinal peptide receptor 1	Vipr1	1.73	0.381	1.41	0.215	1.11	0.724	-1.09	0.640	2.11	0.039
1447572_at	RIKEN cDNA 1700052I22 gene	1700052I22Rik	1.72	0.975	1.18	0.650	1.67	0.885	1.23	0.036	2.12	0.034
1418133_at	B-cell leukemia/lymphoma 3	Bcl3	1.11	0.967	1.66	0.393	1.51	0.733	1.82	0.342	2.12	0.014
1432639_at	RIKEN cDNA 4633401L03 gene	4633401L03Rik	1.39	0.766	1.84	0.725	1.88	0.046	-1.24	0.347	2.13	0.026
1454563_at	RIKEN cDNA 4930573C08 gene	4930573C08Rik	-1.35	0.215	-1.58	0.004	1.24	0.032	-1.37	0.313	2.13	0.008
1455737_at	RIKEN cDNA C030002B11 gene	C030002B11Rik	-1.96	0.021	1.25	0.825	3.02	0.085	1.2	0.876	2.13	0.011
1425261_at	CCAAT/enhancer binding protein (C/EBP), gamma	Cebpg	-1.25	0.300	-1.37	0.296	1.22	0.530	-1.12	0.356	2.13	0.046
1448257_at	solute carrier family 29 (nucleoside transporters), member 2	Slc29a2	1.25	0.891	1.23	0.159	2.59	0.073	1.32	0.071	2.13	0.044
1430391_a_at	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	St8sia4	1.01	0.535	-2.36	0.127	-1.73	0.112	-1.31	0.239	2.13	0.046
1439472_at	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	Gcn1l1	1.51	0.833	-1.58	0.195	1.5	0.642	-2.12	0.014	2.14	0.039
1435263_at	transmembrane protein 106A	Tmem106a	1.46	0.759	1.64	0.187	1.01	0.770	1.33	0.060	2.14	0.040
1459818_x_at	zinc finger, MYM-type 3	Zmym3	1.09	0.575	1.36	0.715	2.11	0.635	-1.14	0.736	2.14	0.020
1432824_at	RIKEN cDNA 2900018N21 gene	2900018N21Rik	-1.56	0.206	-1.2	0.377	-1.09	0.151	1.07	0.740	2.15	0.016
1424774_s_at	RIKEN cDNA 3230401I01 gene	3230401I01Rik	1.21	0.845	1.45	0.499	1.21	0.692	-1.23	0.238	2.15	0.050
1445394_at	RIKEN cDNA 4933409K07 gene	4933409K07Rik	1.56	0.981	-1.34	0.169	1.34	0.704	1.45	0.343	2.15	0.048
1453798_at	coiled-coil domain containing 93	Ccdc93	-1.15	0.437	1.63	0.634	-1.24	0.522	-1.48	0.175	2.15	0.038
1443631_at	Diacylglycerol kinase, beta	Dgkb	-1.21	0.231	-1.03	0.432	2.43	0.017	1.51	0.078	2.15	0.044
1442553_at	microtubule-associated protein, RP/EB family, member 2	Mapre2	1.44	0.157	1.21	0.599	-1.18	0.373	-1.37	0.125	2.15	0.048
1453215_at	ribonuclease, RNase A family, 10 (non-active)	Rnase10	1.55	0.093	1.83	0.106	1.5	0.253	-1.29	0.172	2.15	0.006
1445697_at	Integrin beta 1 binding protein 1	Itgb1bp1	2.01	0.852	2.28	0.922	1.16	0.777	1.08	0.653	2.16	0.023
1457378_at	Mitochondrial ribosomal protein L54	Mrpl54	1.14	0.938	1.11	0.909	1.14	0.969	1.28	0.983	2.16	0.015
1447046_at	DnaJ (Hsp40) related, subfamily B, member 13	Dnajb13	-1.36	0.475	1.58	0.467	1.88	0.347	2.6	0.162	2.17	0.026
1418499_a_at	potassium voltage-gated channel, Isk-related subfamily, gene 3	Kcne3	1.27	0.685	1.59	0.812	2.34	0.306	-1.45	0.218	2.17	0.041
1420401_a_at	receptor (calcitonin) activity modifying protein 3	Ramp3	1.07	0.859	1.22	0.738	1.45	0.168	1.21	0.829	2.18	0.014
1451599_at	sestrin 2	Sesn2	5.82	0.769	7.79	0.373	1.07	0.616	2.03	0.311	2.18	0.005
1441579_at	doublesex and mab-3 related transcription factor like family A1	Dmrta1	-1.4	0.146	1.02	0.890	-1.49	0.243	2.21	0.620	2.19	0.037
1426542_at	endonuclease domain containing 1	Endod1	1.01	0.979	1.64	0.111	2.86	0.160	1.12	0.347	2.19	0.017
1445117_at	Glycosyltransferase 28 domain containing 1	Glt28d1	-1.74	0.033	-1.65	0.088	1.55	0.716	-1.38	0.308	2.19	0.037
1443582_at	similar to growth arrest-specific 2 like 2; GAS2-related protein	RP23-249K18.2	1.02	0.476	1.44	0.529	1.5	0.533	1.08	0.696	2.2	0.003
1441445_at	period homolog 3 (Drosophila)	Per3	-1.45	0.153	-1.16	0.302	1.12	0.755	-1.1	0.125	2.22	0.037
1457051_at	tripartite motif protein 27	Trim27	2.13	0.047	1.8	0.555	1.44	0.007	1.18	0.859	2.22	0.010
1424714_at	aldolase 3, C isoform	Aldoc	-1.1	0.470	2.38	0.472	-1.2	0.279	1.4	0.913	2.23	0.033
1424627_at	cystatin 12	Cst12	-2	0.065	-1.28	0.336	-1.27	0.357	1.37	0.852	2.23	0.010
1450311_at	solute carrier family 8 (sodium/calcium exchanger), member 3	Slc8a3	2.18	0.126	1.56	0.052	1.55	0.421	1.74	0.410	2.23	0.039
1430679_at	RIKEN cDNA 4933404O12 gene	4933404O12Rik	-1.05	0.371	-1.34	0.213	1.54	0.817	1.6	0.947	2.24	0.043
1437444_at	protocadherin gamma subfamily C, 3	Pcdhgc3	2.02	0.070	1.92	0.158	1.7	0.067	2.53	0.237	2.24	0.045
1428357_at	RIKEN cDNA 2610019F03 gene	2610019F03Rik	1.54	0.613	1.93	0.693	1.87	0.062	1.6	0.369	2.25	0.040
1447550_at	hypothetical protein LOC666892 /// hypothetical protein LOC671332	LOC666892 /// LO	-1.03	0.494	1.14	0.695	1.24	0.148	1.24	0.090	2.25	0.002
1450342_at	bone morphogenetic protein 8b	Bmp8b	-1.3	0.138	-1.42	0.183	1.72	0.289	-1.83	0.054	2.26	0.038
1422175_at	matrix metallopeptidase 1a (interstitial collagenase) /// similar to matrix me	Mmp1a /// LOC67	2.01	0.403	3.04	0.366	2.14	0.354	2.69	0.427	2.26	0.002
1453552_at	RIKEN cDNA 2310014F07 gene	2310014F07Rik	1.66	0.777	1.28	0.864	1.36	0.421	-1.16	0.749	2.27	0.045
1444008_at	H2A histone family, member Y2	H2afy2	2.25	0.969	2.04	0.829	1.72	0.181	1.12	0.245	2.27	0.019
1444336_at	Potassium inwardly-rectifying channel, subfamily J, member 3	Kcnj3	1.15	0.791	-1.24	0.614	1.65	0.747	2.14	0.715	2.27	0.027
1431891_at	zinc finger, SWIM domain containing 5	Zswim5	-1.04	0.630	1.03	0.911	-2.01	0.000	1.29	0.661	2.27	0.043
1438996_at	gene model 118, (NCBI)	Gm118	2.04	0.099	2.72	0.134	-1.27	0.342	-1.29	0.226	2.28	0.006
1445565_at	Histone 1, H1e	Hist1h1e	-1.24	0.384	-1.36	0.277	-1.31	0.267	1.24	0.334	2.28	0.018
1429905_at	RIKEN cDNA 3110009O07 gene	3110009O07Rik	-1.05	0.460	1.42	0.065	3.05	0.519	1.03	0.995	2.31	0.003
1444958_at	expressed sequence C79017	C79017	-1.23	0.274	1.54	0.243	-2.05	0.072	1.04	0.987	2.32	0.047
1429381_x_at	immunoglobulin heavy chain (J558 family) /// similar to immunoglobulin he	Igh-VJ558 /// LOC	1.12	0.944	-1.25	0.350	-1.46	0.036	1.43	0.216	2.32	0.011
1457722_at	killer cell lectin-like receptor subfamily B member 1F	Klrb1f	-1.33	0.283	-1.06	0.645	-1.6	0.137	-1.78	0.139	2.32	0.046
1458831_at	NAD(P) dependent steroid dehydrogenase-like	Nsdhl	1.18	0.704	1.74	0.245	-1	0.507	1.16	0.514	2.32	0.013
1423170_at	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated fact	Taf7	1.47	0.511	1.44	0.354	2.97	0.085	1.32	0.152	2.32	0.035
1439110_at	RIKEN cDNA A930012O16 gene	A930012O16Rik	-1.08	0.570	-1.44	0.181	-1.04	0.560	-1.41	0.147	2.33	0.019
1458367_at	gene model 94, (NCBI)	Gm94	1.45	0.880	1.95	0.287	-1.13	0.493	2.23	0.196	2.33	0.026
1444003_at	lung-inducible neuralized-related C3HC4 RING domain protein	Lincr	1.06	0.465	-1	0.592	1.67	0.793	1.69	0.683	2.33	0.013
1449739_at	Phosphatidylserine synthase 1	Ptdss1	-1.86	0.347	1.39	0.412	1.61	0.617	1.13	0.489	2.33	0.023
1446769_at	RIKEN cDNA 2810439F02 gene	2810439F02Rik	2.09	0.331	2.42	0.478	3.84	0.100	1.7	0.983	2.34	0.003

1422552_at	reprimo, TP53 dependent G2 arrest mediator candidate	Rprm	1.6	0.294	4.18	0.007	1.31	0.022	1.36	0.042	2.34	0.011
1457183_at	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	Slc6a1	1.24	0.997	1.7	0.412	1.22	0.537	1.08	0.859	2.34	0.015
1459100_at	expressed sequence AU015253	AU015253	1.59	0.766	1.68	0.400	1.34	0.844	-1.33	0.233	2.35	0.032
1456428_at	Chemokine (C-X-C motif) ligand 15	Cxcl15	-1.49	0.196	-1.47	0.193	-1.13	0.180	1.25	0.797	2.36	0.038
1450300_at	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1	Gabrr1	-1.08	0.558	-1.53	0.083	-1.08	0.483	1.26	0.341	2.36	0.023
1455034_at	Nuclear receptor subfamily 4, group A, member 2	Nr4a2	1.28	0.905	2.01	0.042	2.06	0.003	1.63	0.002	2.37	0.002
1427433_s_at	homeo box A3	Hoxa3	1.18	0.703	-1	0.551	2.64	0.402	-1.43	0.263	2.38	0.010
1443262_at	mitochondrial ribosomal protein S14	Mrps14	2.08	0.366	2.33	0.062	-1.11	0.465	-1.18	0.316	2.38	0.033
1434008_at	sodium channel, type IV, beta	Scn4b	1.77	0.629	-1.03	0.479	1.99	0.747	1.57	0.439	2.38	0.012
1457255_x_at	Kinesin family member 5C	Kif5c	1.57	0.839	2.25	0.294	1.35	0.662	-1.08	0.533	2.39	0.042
1443726_at	SET and MYND domain containing 1	Smyd1	2.55	0.930	3.47	0.418	-1.17	0.375	-1.21	0.152	2.39	0.001
1438280_at	RIKEN cDNA 1700023L04 gene	1700023L04Rik	1.01	0.683	-1.31	0.029	-1.65	0.066	1.73	0.560	2.4	0.043
1432930_at	RIKEN cDNA 4930453O09 gene	4930453O09Rik	1.94	0.876	2.66	0.846	1.46	0.891	-2.09	0.020	2.4	0.039
1446191_at	ABI gene family, member 3	Abi3	1.51	0.858	1.43	0.782	1.5	0.333	1.24	0.851	2.4	0.028
1458730_at	BTB and CNC homology 2	Bach2	-1.03	0.510	2.61	0.255	1.54	0.837	1.08	0.873	2.4	0.025
1425081_at	zinc finger protein 286	Zfp286	1.7	0.788	1.12	0.522	-1.39	0.243	1.35	0.176	2.4	0.022
1424961_at	TAP binding protein-like	Tapbpl	1.69	0.812	1.42	0.800	1.48	0.383	1.57	0.248	2.41	0.028
1430209_at	RIKEN cDNA 4930404H21 gene	4930404H21Rik	1.91	0.663	1.05	0.801	-2.25	0.024	-1.22	0.200	2.42	0.020
1419378_a_at	FXYD domain-containing ion transport regulator 2	Fxyd2	1.14	0.692	1.56	0.355	-1.41	0.150	-1.04	0.706	2.42	0.008
1442830_at	Nucleolar and spindle associated protein 1	Nusap1	4.27	0.164	1.23	0.130	1.15	0.494	1.84	0.654	2.42	0.019
1445326_at	sidekick homolog 1 (chicken)	Sdk1	2.07	0.846	3.82	0.154	-1.93	0.135	1.57	0.517	2.42	0.023
1439952_at	RIKEN cDNA 3110082M05 gene	3110082M05Rik	2.21	0.578	2.42	0.281	2.88	0.176	1.15	0.856	2.43	0.024
1435907_at	neurexin II	Nrxn2	1.55	0.505	1.24	0.770	2.18	0.267	2.32	0.359	2.44	0.002
1452353_at	G protein-coupled receptor 155	Gpr155	1.47	0.670	1.35	0.628	2.24	0.101	1.97	0.008	2.45	0.011
1439322_at	Protocadherin 9	Pcdh9	1.02	0.766	1.7	0.199	1.32	0.766	-1.71	0.219	2.45	0.006
1427026_at	myosin, heavy polypeptide 4, skeletal muscle	Myh4	2.05	0.221	2.11	0.140	1.27	0.792	-1.44	0.183	2.46	0.008
1453563_at	NmrA-like family domain containing 1	Nmral1	1.15	0.842	1.56	0.093	-1.15	0.618	-1.55	0.161	2.46	0.032
1422982_at	androgen receptor	Ar	1.39	0.560	1.7	0.111	-1.17	0.381	-1.03	0.711	2.47	0.025
1451942_x_at	killer cell lectin-like receptor subfamily A, member 20	Klra20	1.18	0.974	4.69	0.193	1.12	0.996	3.07	0.166	2.47	0.011
1416899_at	undifferentiated embryonic cell transcription factor 1	Utf1	1.21	0.613	2.29	0.058	-1.23	0.251	1.22	0.995	2.47	0.032
1436361_at	vestigial like 2 homolog (Drosophila)	Vgll2	1.8	0.044	1.77	0.932	1.72	0.253	3.03	0.069	2.47	0.024
1452804_at	RIKEN cDNA 1700010A17 gene	1700010A17Rik	2.33	0.360	-1.07	0.407	1.05	0.553	2.39	0.130	2.48	0.025
1437872_at	cDNA sequence AB112350	AB112350	1.03	0.831	-1.02	0.948	2.89	0.479	1.34	0.884	2.48	0.009
1444323_at	cyclin D3	Ccnd3	1.59	0.585	1.84	0.692	1.82	0.594	-1.17	0.562	2.48	0.025
1458882_at	serine (or cysteine) peptdiase inhibitor, clade B, member 8	Serpinb8	-1.38	0.343	1.29	0.758	1.93	0.261	1.91	0.124	2.49	0.038
1458556_at	Trinucleotide repeat containing 6C	Tnrc6c	1.38	0.220	1.64	0.130	-1	0.429	1.47	0.945	2.49	0.031
1439509_at	RIKEN cDNA 2900008C10 gene	2900008C10Rik	1.14	0.846	1.66	0.072	-1.1	0.593	1.08	0.619	2.5	0.017
1446975_at	Castor homolog 1, zinc finger (Drosophila)	Casz1	-1.58	0.166	-1.02	0.858	-1.3	0.338	1.02	0.792	2.5	0.000
1428963_at	RWD domain containing 2	Rwdd2	1.46	0.156	1.64	0.136	1.39	0.084	1.36	0.090	2.5	0.024
1422388_at	vomeronasal 1 receptor, C8	V1rc8	1.18	0.601	-1.05	0.534	1.67	0.814	1.16	0.651	2.5	0.015
1449038_at	hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	1.19	0.689	1.2	0.902	1.25	0.820	2.15	0.145	2.51	0.013
1421621_at	RAS protein-specific guanine nucleotide-releasing factor 2	Rasgrf2	1.22	0.545	1.59	0.734	1.66	0.285	1.2	0.278	2.52	0.028
1429312_s_at	receptor tyrosine kinase-like orphan receptor 1	Ror1	-1.06	0.670	-1.01	0.666	1.46	0.980	1.17	0.729	2.52	0.011
1453103_at	actin-binding LIM protein 1	Ablim1	-1	0.691	-1.63	0.085	1.42	0.090	1.15	0.917	2.53	0.017
1460313_at	olfactory receptor 2	Olfr2	1.04	0.649	-1.19	0.277	1.05	0.609	-2.31	0.003	2.53	0.037
1422655_at	patched homolog 2	Ptch2	1.53	0.984	1.63	0.919	-1.03	0.577	1.99	0.162	2.53	0.023
1454108_at	RIKEN cDNA 4930524O08 gene	4930524O08Rik	1.07	0.721	1.45	0.668	1.53	0.804	-1.84	0.154	2.55	0.044
1444987_at	Cathepsin B	Ctsb	3.39	0.119	1.08	0.595	1.69	0.334	1.32	0.766	2.55	0.038
1422757_at	solute carrier family 5 (neutral amino acid transporters, system A), membe	Slc5a4b	-1.59	0.198	-1.8	0.220	2.11	0.243	1.65	0.299	2.55	0.004
1417877_at	RIKEN cDNA 2310005P05 gene	2310005P05Rik	1.21	0.985	1.01	0.486	-1.03	0.447	-1.16	0.419	2.57	0.013
1451757_at	cDNA sequence BC003883	BC003883	1.64	0.255	1.57	0.997	-1.13	0.715	1.36	0.743	2.57	0.031
1438866_at	glutamate receptor ionotropic, NMDA3A	Grin3a	1.84	0.841	1.38	0.906	3.01	0.298	1.31	0.819	2.58	0.003
1457835_at	hypothetical protein C920025J10	C920025J10	1.8	0.645	1.46	0.341	1.7	0.624	1.11	0.397	2.59	0.005
1447938_at	similar to 4933409K07Rik protein	LOC545614	1.01	0.741	1.05	0.605	-1.04	0.426	1.88	0.261	2.59	0.019
1451767_at	neutrophil cytosolic factor 1	Ncf1	1.08	0.434	1.71	0.039	1.29	0.694	1.78	0.604	2.6	0.008
1430913_at	RIKEN cDNA 1810033M07 gene	1810033M07Rik	2.45	0.180	1.24	0.983	1.85	0.623	2.09	0.362	2.61	0.034
1456509_at	RIKEN cDNA 1110032F04 gene	1110032F04Rik	2.28	0.142	2.31	0.225	1.34	0.411	1.26	0.770	2.62	0.024
1430730_at	RIKEN cDNA 9430024F10 gene	9430024F10Rik	-1.69	0.188	-1.27	0.242	2.91	0.025	-1.09	0.796	2.63	0.050

1451194_at	aldolase 2, B isoform	Aldob	2.23	0.372	1.86	0.349	1.37	0.560	-1.13	0.422	2.63	0.001
1438483_at	nitric oxide synthase 1, neuronal	Nos1	1.33	0.120	2.99	0.172	1.41	0.797	1.13	0.617	2.63	0.047
1450237_at	deoxyribonuclease II beta	Dnase2b	-1.39	0.290	1.64	0.130	2.6	0.077	1.31	0.352	2.64	0.009
1425728_at	hypothetical gene Rp23-14f5.7	RP23-14F5.7	1.04	0.530	1.03	0.472	-1.18	0.321	-1.68	0.054	2.66	0.014
1443591_at	distal-less homeobox 4	Dlx4	1.3	0.592	1.68	0.823	1.53	0.095	2.14	0.233	2.67	0.040
1441524_at	cytoplasmic tyrosine kinase, Dscr28C related (Drosophila)	Tec	1.22	0.908	2.12	0.426	1.27	0.939	1.44	0.938	2.67	0.016
1458863_at	RIKEN cDNA 6330415G19 gene	6330415G19Rik	1.51	0.144	1.72	0.010	1.45	0.007	1.34	0.123	2.68	0.024
1451951_at	Hypothetical protein LOC625794	LOC625794	2.23	0.256	2.82	0.114	-1.44	0.308	1.63	0.148	2.69	0.044
1437966_at	proline-rich transmembrane protein 3	Prrt3	-1.3	0.214	1.08	0.520	-1.09	0.725	1.08	0.470	2.69	0.017
1429354_at	thioesterase superfamily member 5	Them5	2.14	0.964	1.74	0.969	1.43	0.790	-1.19	0.117	2.69	0.010
1460715_x_at	Transcription factor CP2-like 1	Tcfcp2l1	-1.14	0.308	1.02	0.357	1.2	0.861	-1.01	0.560	2.72	0.025
1460016_at	transmembrane protein 164	Tmem164	-1.23	0.195	1.08	0.732	1.9	0.506	-1.12	0.399	2.72	0.050
1447742_at	lysosomal-associated protein transmembrane 5	Laptm5	2.04	0.434	1.27	0.456	1.64	0.069	-1.96	0.184	2.73	0.042
1445504_at	similar to Nucleolar phosphoprotein p130 (Nucleolar 130 kDa protein) (140	LOC331392	2.28	0.245	3.02	0.273	1.65	0.193	1.21	0.598	2.73	0.029
1432118_at	RIKEN cDNA 2410012E07 gene	2410012E07Rik	1.35	0.488	-1.04	0.442	1.7	0.331	1.04	0.374	2.77	0.043
1452514_a_at	kit oncogene	Kit	1.43	0.694	1.19	0.506	1.68	0.385	1.62	0.072	2.77	0.006
1420065_at	Transketolase-like 1	Tktl1	1.49	0.900	-1.12	0.485	-1.07	0.528	1.81	0.842	2.77	0.033
1432246_at	RIKEN cDNA 4922502N22 gene	4922502N22Rik	-1.8	0.224	-1.43	0.267	1.02	0.586	1.48	0.396	2.78	0.047
1432244_at	RIKEN cDNA 4930507D10 gene	4930507D10Rik	-1.2	0.458	-1.4	0.166	-1.56	0.217	1.98	0.821	2.78	0.032
1445296_at	DNA segment, Chr 7, ERATO Doi 715, expressed	D7Ertd715e	1.57	0.583	1.17	0.317	1.72	0.950	1.87	0.906	2.78	0.027
1459668_at	TRAF family member-associated Nf-kappa B activator	Tank	1.73	0.606	1.43	0.872	2.24	0.575	1.39	0.181	2.78	0.034
1422387_at	vomeronasal 1 receptor, C2	V1rc2	1.91	0.617	-1.01	0.466	1.65	0.903	3.5	0.294	2.8	0.045
1453335_a_at	spermatogenesis associated 3	Spata3	-1.25	0.396	-1.66	0.213	2.35	0.699	-1.83	0.204	2.81	0.027
1447956_at	expressed sequence C76614	C76614	-1.44	0.264	-1.09	0.537	-1.39	0.237	1.23	0.792	2.83	0.033
1460528_at	RIKEN cDNA 4930413G21 gene /// hypothetical protein LOC668574 /// hy	4930413G21Rik //	1.06	0.628	1.83	0.845	-1.66	0.106	2.41	0.598	2.84	0.044
1427292_at	immunoglobulin lambda chain, variable 1	Igl-V1	-1.9	0.050	-3.15	0.016	1.08	0.664	2.86	0.435	2.85	0.005
1420706_at	P140 gene	P140	-1.42	0.417	-1.41	0.050	-1.28	0.418	-1.61	0.247	2.85	0.009
1431370_at	RIKEN cDNA 4930512B01 gene	4930512B01Rik	1.41	0.759	1.62	0.505	-1.25	0.109	1.94	0.570	2.86	0.010
1438707_at	ATPase type 13A4	Atp13a4	1.24	0.514	1.26	0.303	1.01	0.402	2.9	0.061	2.88	0.006
1460493_at	RIKEN cDNA 4921506J03 gene	4921506J03Rik	1.06	0.896	1.81	0.099	-1.1	0.444	1.51	0.659	2.93	0.046
1418797_at	membrane-spanning 4-domains, subfamily A, member 8A	Ms4a8a	-1.33	0.155	1.93	0.237	2.38	0.490	-1.18	0.304	2.94	0.013
1424303_at	DEP domain containing 7	Depdc7	1.07	0.576	1.07	0.288	3.42	0.033	1.98	0.020	2.96	0.026
1426174_s_at	Immunoglobulin heavy chain (gamma polypeptide)	Ighg	1.2	0.846	1.08	0.692	1.11	0.424	1.48	0.902	2.96	0.014
1445247_at	RIKEN cDNA C530044C16 gene	C530044C16Rik	1.08	0.603	1.41	0.628	1.02	0.566	-1.03	0.697	2.97	0.028
1437094_x_at	dynein, axonemal, intermediate chain 1	Dnaic1	1.01	0.490	-2.09	0.251	1.21	0.992	2.03	0.699	2.99	0.037
1455963_at	RIKEN cDNA 6332401O19 gene	6332401O19Rik	1.17	0.739	2.45	0.219	1.77	0.506	1.66	0.782	3.02	0.015
1431554_a_at	annexin A9	Anxa9	1.27	0.463	-1.03	0.749	-1.19	0.370	2.09	0.663	3.02	0.011
1446370_at	RAB11 family interacting protein 4 (class II)	Rab11fip4	2.25	0.396	-1.05	0.548	1.45	0.804	2.01	0.263	3.02	0.030
1442797_x_at	CKLF-like MARVEL transmembrane domain containing 2A	Cmtm2a	1.18	0.850	1.21	0.601	1.64	0.805	2.02	0.165	3.05	0.008
1451716_at	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein B (avian	Mafb	2.53	0.165	2.33	0.112	1.31	0.088	1.15	0.905	3.05	0.025
1458770_at	DNA segment, Chr 11, ERATO Doi 4, expressed	D11Ertd4e	1.36	0.770	1.16	0.429	1.85	0.761	-1.37	0.042	3.06	0.046
1449247_at	actin-related protein T2	Actrt2	-1.08	0.836	1.32	0.722	1.96	0.050	1.52	0.311	3.07	0.001
1446279_at	Neuronal growth regulator 1	Negr1	-1.34	0.151	-1.22	0.391	2.1	0.283	2.85	0.007	3.1	0.028
1459295_at	Latrophilin 3	Lphn3	1.43	0.964	1.13	0.944	1.14	0.483	2.69	0.153	3.11	0.025
1420249_s_at	chemokine (C-C motif) ligand 6	Ccl6	1.5	0.315	1.49	0.208	-1	0.656	1.45	0.001	3.12	0.042
1428960_at	RIKEN cDNA 4933434I06 gene	4933434I06Rik	2.63	0.934	1.71	0.792	1.29	0.700	1.11	0.644	3.13	0.042
1421660_at	sodium channel, voltage-gated, type IX, alpha /// similar to sodium channe	Scn9a /// LOC6718	2.97	0.673	1.47	0.723	-1.05	0.482	1.73	0.885	3.14	0.025
1452619_a_at	ATP/GTP binding protein-like 3	Agbl3	2.95	0.915	1.13	0.987	1.08	0.891	2.2	0.231	3.16	0.034
1451755_a_at	apolipoprotein B editing complex 1	Apobec1	-1.08	0.962	2.54	0.007	2.02	0.456	2.17	0.140	3.17	0.039
1455807_at	testis-specific protein, Y-encoded-like 5	Tspyl5	-1.1	0.433	1.39	0.643	1.75	0.902	2.65	0.045	3.18	0.013
1440352_at	region containing RIKEN cDNA 1700028E10 gene; hypothetical protein A6	LOC625175	1.68	0.781	1.6	0.981	-1.3	0.243	-1.98	0.005	3.2	0.022
1446993_at	Perilipin	Plin	1.92	0.634	2.03	0.457	2.76	0.063	1.03	0.934	3.2	0.031
1453168_at	RIKEN cDNA 1700029J07 gene	1700029J07Rik	1.66	0.897	1.08	0.604	1.57	0.712	1.76	0.743	3.21	0.025
1436565_at	CEA-related cell adhesion molecule 10	Ceacam10	1.01	0.891	-1	0.989	1.81	0.641	1.03	0.522	3.21	0.045
1428573_at	chimerin (chimaerin) 2	Chn2	-1.21	0.323	1.92	0.688	1.92	0.373	2.61	0.368	3.27	0.044
1439527_at	Expressed sequence BB114106	BB114106	1.71	0.281	2.18	0.145	2.19	0.769	-1.36	0.224	3.28	0.045
1418158_at	transformation related protein 63	Trp63	1.62	0.770	1.6	0.690	2.06	0.197	-1.01	0.759	3.29	0.014
1420235_at	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associate	Bphl	-1.23	0.466	-1.31	0.429	1.18	0.956	3.07	0.272	3.3	0.039

1449581_at	EMI domain containing 1	Emid1	1.4	0.055	1.74	0.100	-1.59	0.005	1.08	0.892	3.3	0.015
1438468_at	preferentially expressed antigen in melanoma like 4 /// preferentially expres	Pramel4 /// Pramel	-1.33	0.304	-1.17	0.416	1.17	0.738	1.1	0.118	3.31	0.006
1431706_at	RAN binding protein 5	Ranbp5	1.43	0.840	-1.04	0.558	-1.48	0.074	-1.13	0.236	3.32	0.022
1433237_at	RIKEN cDNA 3830422I06 gene	3830422I06Rik	1.95	0.060	-1.11	0.675	1.3	0.938	2.99	0.274	3.34	0.017
1431115_at	TGFB-induced factor 2	Tgif2	2.04	0.586	1.61	0.077	2.11	0.902	2.58	0.250	3.34	0.046
1420571_at	prolactin-like protein B	Prlpb	1.56	0.434	-1.15	0.681	2.84	0.867	1.23	0.621	3.35	0.014
1449941_at	myosin IE	Myo1e	1.13	0.746	1.85	0.755	1.58	0.753	1.81	0.796	3.36	0.005
1443313_at	RIKEN cDNA A530058N18 gene	A530058N18Rik	-1.07	0.451	-1.09	0.429	1.88	0.469	-1.06	0.700	3.38	0.017
1456595_x_at	growth hormone	Gh	1.29	0.859	-1.16	0.363	-1.49	0.103	-1.08	0.507	3.44	0.012
1429975_at	RIKEN cDNA 4931432M23 gene /// similar to plasma kallikrein-like protein	4931432M23Rik //	1.5	0.877	2.03	0.445	-1.49	0.096	2.81	0.610	3.45	0.016
1459755_x_at	RIKEN cDNA 1700082C02 gene	1700082C02Rik	-1.04	0.737	-1.41	0.291	3.35	0.327	3.3	0.224	3.48	0.027
1418930_at	chemokine (C-X-C motif) ligand 10	Cxcl10	-1.15	0.348	1.43	0.721	1.71	0.929	1.29	0.053	3.51	0.015
1431695_at	rabphilin 3A-like (without C2 domains)	Rph3al	1.32	0.686	1.24	0.389	-1.43	0.132	1.25	0.805	3.51	0.031
1445896_at	RIKEN cDNA 2810433D01 gene	2810433D01Rik	1.2	0.749	1.27	0.999	-1.5	0.238	-1.35	0.039	3.52	0.016
1441875_at	RIKEN cDNA 1700063J08 gene	1700063J08Rik	2.22	0.164	1.23	0.555	2.06	0.525	1.06	0.570	3.55	0.010
1451694_at	tubulin tyrosine ligase-like family, member 3	Ttll3	2.93	0.311	1.98	0.110	1.14	0.767	-1.57	0.103	3.6	0.022
1437880_at	ladybird homeobox 1 homolog (Drosophila) corepressor 1	Lbxcor1	1.89	0.859	1.29	0.650	-1.91	0.009	-1.33	0.278	3.61	0.020
1447884_x_at	RIKEN cDNA 1300010M03 gene	1300010M03Rik	1.26	0.498	2.33	0.145	2.1	0.234	2.19	0.150	3.62	0.019
1420930_s_at	catenin (cadherin associated protein), alpha-like 1	Ctnnal1	1.2	0.532	1.19	0.749	1.07	0.637	1.53	0.140	3.64	0.035
1433526_at	kelch-like 8 (Drosophila)	Klhl8	3.96	0.928	3.58	0.144	1.26	0.588	2.61	0.093	3.64	0.030
1452893_s_at	RIKEN cDNA 1110065P19 gene /// RIKEN cDNA 2310040A07 gene	1110065P19Rik ///	-1.35	0.129	-1.03	0.538	1.19	0.817	-1.12	0.203	3.65	0.019
1455755_at	gene model 88, (NCBI)	Gm88	-1.78	0.191	1.37	0.608	2.15	0.274	2.15	0.658	3.65	0.017
1442355_at	hypothetical LOC546100	LOC546100	-1.38	0.153	1.17	0.865	1.57	0.444	1.76	0.815	3.65	0.001
1427459_at	carboxypeptidase N, polypeptide 2	Cpn2	2.8	0.015	1.22	0.338	2.74	0.162	-1.22	0.252	3.66	0.010
1422267_at	forkhead box B2	Foxb2	1.67	0.138	1.4	0.810	2.28	0.571	1.44	0.124	3.71	0.005
1418807_at	RIKEN cDNA 3110070M22 gene	3110070M22Rik	1.04	0.700	1.08	0.710	-1.18	0.209	-1.28	0.107	3.83	0.048
1417837_at	pleckstrin homology-like domain, family A, member 2	Phlda2	1.22	0.775	1.16	0.736	1.1	0.647	1.94	0.276	3.88	0.029
1440236_at	RIKEN cDNA A830039H05 gene	A830039H05Rik	1.5	0.571	-1.57	0.268	1.91	0.145	-1.06	0.553	3.91	0.021
1443497_at	Ankyrin repeat and BTB (POZ) domain containing 2	Abtb2	-1.38	0.027	-1.06	0.895	1.5	0.772	1.32	0.443	3.96	0.004
1452552_at	neoplastic progression 2	Npn2	2.01	0.566	11.69	0.000	3.34	0.102	7.33	0.002	3.96	0.024
1442885_at	SREBP cleavage activating protein	Scap	1.08	0.863	3.33	0.354	1.94	0.127	2.04	0.497	3.98	0.025
1419876_at	RIKEN cDNA 2810449G22 gene	2810449G22Rik	-1.67	0.059	-1.83	0.171	1.96	0.383	1.28	0.461	4.05	0.014
1455835_at	Ribosomal protein S16	Rps16	-1.53	0.156	-1.67	0.131	-1.72	0.170	1.3	0.726	4.08	0.001
1418619_at	intercellular adhesion molecule 5, telencephalin	Icam5	1.55	0.730	2.6	0.144	3.75	0.034	1.61	0.517	4.1	0.014
1436561_at	suppressor of variegation 3-9 homolog 2 (Drosophila)	Suv39h2	1.35	0.692	1.66	0.881	1.84	0.938	-1.35	0.338	4.11	0.032
1430324_x_at	RIKEN cDNA 1700049E17 gene /// similar to Spetex-2C protein	1700049E17Rik ///	1.76	0.886	1.52	0.729	-1.22	0.277	1.5	0.829	4.41	0.038
1434918_at	SRY-box containing gene 6	Sox6	2.29	0.630	2.1	0.707	1.63	0.943	1.22	0.904	4.44	0.003
1432653_at	RIKEN cDNA 1700008H02 gene	1700008H02Rik	1.41	0.385	1.58	0.591	1.51	0.727	1.09	0.692	4.7	0.020
1430935_at	RIKEN cDNA 4933413G19 gene	4933413G19Rik	1.39	0.949	-1.42	0.128	2.46	0.904	1.86	0.711	4.79	0.044
1451697_a_at	Ellis van Creveld gene homolog (human)	Evc	1.36	0.385	1.34	0.266	1.66	0.499	1.69	0.463	4.79	0.035
1423542_at	kallikrein 7 (chymotryptic, stratum corneum)	Klk7	1.14	0.359	2.61	0.973	1.35	0.388	1.44	0.759	4.98	0.007

Supplemental table 6. Expression profiles of genes (red and green color indicate up- and down-regulated genes respectively) associated with over-represented biologial processes in irradiated cells and with natural aging (kidney, liver, lung and spleen) as ccopmpared to corresponding controls.

Response to DNA damage

code	Gene Title	Gene Symbo	Kidney	Liver	Lung	Spleen	WT_0.6J	WT_4J	XPA_0.6J	CSB_0.6J	DKO_0.6J
1421220_at	ankyrin repeat domain 17	Ankrd17	1.68	1.05	1.18	-1.29	2.01	3.7	1.31	-1.17	-1.13
1451417_at	breast cancer 1	Brca1	1.06	2.00	2.25	3.57	2.74	3.54	1.17	1.12	1.15
1450677_at	checkpoint kinase 1 homolog (S. pombe)	Chek1	1.03	1.07	1.02	3.08	1.68	2.07	1.17	1.05	1.19
1423877_at	chromatin assembly factor 1, subunit B (p60)	Chaf1b	1.03	-1.43	1.21	2.47	1.17	1.2	1.15	1.21	1.07
1456280_at	claspin homolog (Xenopus laevis)	Clspn	-1.40	1.18	1.01	4.50	1.25	1.58	1.11	1.08	1.16
1424638_at	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	1.25	1.01	1.01	1.11	1.16	1.69	1.25	1.21	1.29
1441595_at	Excision repair cross-compl/ting rodent repair deficiency, compl/tatio	Csb	-1.34	1.08	1.21	1.37	3.12	2.55	1.81	2.24	1.29
1418026_at	exonuclease 1	Exo1	1.36	-1.21	1.23	3.10	1.14	1.54	1.33	1.42	1.15
1421731_a_at	flap structure specific endonuclease 1	Fen1	1.52	1.47	1.92	3.31	1.18	1.56	1.28	1.25	1.27
1417572_at	N-methylpurine-DNA glycosylase	Mpg	1.30	1.09	-1.04	1.22	1.86	2.7	1.51	1.15	1.44
1417947_at	proliferating cell nuclear antigen	Pcna	-1.06	1.11	1.05	1.51	1.36	1.57	1.15	1.16	1.13
1421196_at	protein tyrosine phosphatase, non-receptor type 11	Ptpn11	1.02	-1.67	1.31	1.11	1.78	1.75	-1.03	1.09	1.05
1448414_at	RAD1 homolog (S. pombe)	Rad1	1.28	-1.06	1.24	1.55	2.25	2.25	1.24	1.22	1.07
1453623_a_at	RAD23a homolog (S. cerevisiae)	Rad23a	1.09	-1.44	1.69	1.70	2.58	2.11	1.24	1.08	1.16
1448899_s_at	RAD51 associated protein 1	Rad51ap1	1.05	1.51	1.48	3.85	1.21	1.38	1.06	1.22	1.21
1450862_at	RAD54 like (S. cerevisiae)	Rad54l	-1.07	1.72	1.44	2.89	1.49	1.51	1.04	1.28	-1.09
1452917_at	replication factor C (activator 1) 5	Rfc5	1.23	-1.01	1.69	1.67	1.17	1.35	1.2	1.16	1.2
1449578_at	suppressor of Ty 16 homolog (S. cerevisiae)	Supt16h	1.01	1.05	-1.16	1.55	3.86	2.9	1.56	1.27	1.15
1417754_at	topoisomerase I binding, arginine/serine-rich	Topors	1.18	-1.10	1.01	1.36	1.12	1.32	1	1.15	1.23
1424492_at	transient receptor potential cation channel, C2	Trpc2	1.01	-1.12	1.33	1.09	-1.03	1.41	-1.1	1.28	1.73
1415810_at	ubiquitin-like, containing PHD and RING finger domains, 1	Uhrf1	1.11	1.41	2.44	3.26	1.18	1.64	1.21	1.04	1.2
1455335_at	X-ray repair compl/ting def/tive repair in Chin. hamster cells 2	Xrcc2	1.02	1.09	-1.00	1.49	1.14	1.57	1.46	1.01	1.2

Apoptosis

code	Gene Title	Gene Symbo	Kidney	Liver	Lung	Spleen	WT_0.6J	WT_4J	XPA_0.6J	CSB_0.6J	DKO_0.6J
1431142_s_at	apoptosis-inducing factor (AIF)-like inducer of death	Amid	1.27	-1.94	1.14	1.53	2.39	2.07	1.32	1.25	1.67
1424278_a_at	baculoviral IAP repeat-containing 5	Birc5	1.36	1.22	1.62	4.85	1.04	1.17	1.04	1.1	1.19
1448525_a_at	BCL2/adenovirus E1B interacting protein 3-like	Bnip3l	1.15	-1.07	1.07	1.61	1.75	1.98	1.23	1.06	1.07
1434748_at	cytoskeleton associated protein 2	Ckap2	1.94	1.15	1.75	4.69	1.18	1.6	1.21	-1.02	1.29
1421397_a_at	leucine-rich and death domain containing	Lrdd	1.10	1.26	1.11	2.01	1.6	3.14	1.22	1.46	1.45
1448787_at	modulator of apoptosis 1	Moap1	1.08	-1.21	1.16	1.52	1.09	1.32	1.15	1.12	1.18

1416406_at	phosphoprotein enriched in astrocytes 15	Pea15	1.18	1.26	-1.43	1.06	1.02	1.13	1.15	1.06	1.18
1460642_at	Tnf receptor associated factor 4	Traf4	1.21	-1.17	1.29	1.47	1.67	2.39	1.21	1.43	1.48
1417754_at	topoisomerase I binding, arginine/serine-rich	Topors	1.18	-1.10	1.01	1.36	1.12	1.32	1	1.15	1.23
1416927_at	transformation related protein 53 inducible nuclear protein 1	Trp53inp1	1.21	-1.19	1.22	1.19	1.13	2.95	1.08	1.78	1.83
1433699_at	tumor necrosis factor, alpha-induced protein 3	Tnfaip3	1.07	1.54	1.49	-1.58	1.12	1.2	1.24	1.2	1.1

Immune responses

code	Gene Title	Gene Symbo	Kidney	Liver	Lung	Spleen	WT_0.6J/0	WT_4J/0J	PA_0.6J/0	SB_0.6J_0	DKO_0.6/0J
1431197_at	ADP-ribosylation factor-like 6 interacting protein 2	Arl6ip2	-1.07	1.01	1.45	1.73	4.23	3.95	1.07	1.16	-1.12
1453393_a_at	carbohydrate (chondroitin 6/keratan) sulfotransferase 4	Chst4	-1.50	1.20	1.40	1.10	2.49	2.35	-1.41	-1.21	2.98
1419209_at	chemokine (C-X-C motif) ligand 1	Cxcl1	1.03	14.59	1.33	-1.18	1.36	2.12	1.44	1.23	1.68
1448823_at	chemokine (C-X-C motif) ligand 12	Cxcl12	1.51	1.25	1.31	-1.26	2.32	1.81	-1.26	-1.1	1.05
1451702_at	CKLF-like MARVEL transmembrane domain containing 7	Cmtm7	1.34	1.82	1.26	-1.40	-1.07	1.29	1	1.33	1.19
1417876_at	Fc receptor, IgG, high affinity I	Fcgr1	2.23	1.71	1.26	2.21	2.38	3.06	-1.29	1.35	1.24
1424007_at	growth differentiation factor 10	Gdf10	1.82	1.32	1.07	1.05	1.38	1.46	1.35	-2.22	1.78
1422527_at	histocompatibility 2, class II, locus DMa	H2-DMa	2.10	1.41	1.95	-1.63	1.2	1.67	-1.09	1	1.37
1419455_at	interleukin 10 receptor, beta	Il10rb	1.03	1.61	1.12	-1.38	1.67	1.91	1.28	1.2	1.31
1417638_at	left right determination factor 1	Lefty1	3.15	2.35	1.18	1.69	1.45	2.38	1.11	1.14	1.26
1451767_at	neutrophil cytosolic factor 1	Ncf1	1.44	3.10	4.00	-1.57	1.08	1.71	1.29	1.78	2.6
1448966_a_at	nuclear factor of activated T-cells 5	Nfat5	1.38	2.02	1.08	1.68	3.6	2.58	-1.52	2.77	1.42
1418162_at	toll-like receptor 4	Tlr4	1.82	1.81	-1.04	1.16	1.2	1.38	1.28	1.21	1.04
1416016_at	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	Tap1	1.55	1.24	1.47	-1.43	2.37	3.46	2.76	-1.03	1.32

Somatotroph axis

code	Gene Title	Gene Symbo	Kidney	Liver	Lung	Spleen	WT_0.6J	WT_4J	XPA_0.6J	CSB_0.6J	DKO_0.6J
1426719_at	amyloid beta (A4) precursor protein-binding, family B, member 2	Apbb2	-1.13	-1.20	-1.30	-1.33	-1.01	-4.25	-2.24	-2.8	-2.92
1434310_at	bone morphogenic protein receptor, type II	Bmpr2	-1.06	1.10	-1.33	-1.15	-1.04	-1.49	-1.25	-1.18	-1.44
1427043_s_at	cytosolic ovarian carcinoma antigen 1	Cova1	-1.20	-1.10	-1.32	-1.25	-1.41	-2.99	-1.37	-1.69	-1.63
1428011_a_at	Erbb2 interacting protein	Erbb2ip	-1.13	1.08	-1.19	-1.36	-1.08	-1.21	-1.08	-1.24	-1.11
1417558_at	Fyn proto-oncogene	Fyn	-1.11	1.14	-1.02	-1.26	-1.09	-2.24	-1.93	-1.85	-2.13
1417673_at	growth factor receptor bound protein 14	Grb14	-1.13	-1.31	-1.12	-1.66	1.1	-1.21	-1.18	-1.13	-1.12
1417962_s_at	growth hormone receptor	Ghr	1.10	-1.47	-1.27	-1.15	-1.11	-2.65	-1.58	-1.65	-2.04
1453771_at	GULP, engulfment adaptor PTB domain containing 1	Gulp1	1.12	-1.82	-1.32	-1.30	1.03	-1.71	-1.19	-1.19	-1.22
1418349_at	heparin-binding EGF-like growth factor	Hbegf	-1.56	1.14	-1.33	-1.02	-1.05	-1.44	-1.22	-1.33	-1.22
1423756_s_at	insulin-like growth factor binding protein 4	Igfbp4	-1.21	-1.16	-1.05	-1.29	-1.12	-1.26	1.01	-1.08	1.01
1452108_at	insulin-like growth factor I receptor	Igf1r	-1.74	-1.50	-1.01	-1.02	-1.16	-1.73	-1.1	-1.45	-1.55

1429062_at	kinesin family member 16B	Kif16b	**-1.12**	**-1.17**	**1.10**	**-1.22**	-1.01	-2.43	1.13	-1.28	-1.91
1444285_at	Mortality factor 4 like 1	Morf4l1	**-1.69**	**1.36**	**-1.93**	**-1.48**	-1.08	-1.54	-1.91	-2.37	-2.07
1435771_at	phospholipase C, beta 4	Plcb4	**-1.03**	**1.38**	**-1.26**	**-1.54**	-1.02	-1.48	-1.22	-1.33	-1.38
1437113_s_at	phospholipase D1	Pld1	**-1.03**	**1.15**	**-1.62**	**-1.29**	-1.08	-2.05	-1.5	-1.11	1.22
1452878_at	protein kinase C, epsilon	Prkce	**-1.26**	**-1.00**	**-1.12**	**-1.20**	-1.75	-5.11	-1.19	-1.78	-1.69
1434669_at	Ral GEF with PH domain and SH3 binding motif 1	Ralgps1	**-1.20**	**-1.46**	**1.07**	**-1.39**	-1.03	-2.96	-1.05	-1.21	1.1
1422785_at	RAS p21 protein activator 2	Rasa2	**1.05**	**-1.04**	**-1.21**	**-1.98**	-1.04	-1.24	-1.23	-1.32	-1.25
1459056_at	RAS protein-specific guanine nucleotide-releasing factor 1	Rasgrf1	**-3.31**	**-1.67**	**-1.38**	**-1.01**	-1.29	-2.55	2.22	-1.58	1.02
1438030_at	RAS, guanyl releasing protein 3	Rasgrp3	**-1.07**	**-1.03**	**-1.06**	**-1.50**	1.2	-1.18	-1.01	1.09	-1.2
1446965_at	Rho guanine nucleotide exchange factor (GEF) 12	Arhgef12	**-1.21**	**-1.30**	**-1.73**	**2.03**	-1.37	-1.29	-1.12	-1.02	-1.24
1428822_a_at	sorting nexing 24	Snx24	**-1.26**	**1.11**	**-1.36**	**-1.06**	-1.09	-1.98	-1.53	-1.58	-1.83
1438470_at	suppressor of cytokine signaling 2	Socs2	**-1.07**	**-2.39**	**-1.54**	**-1.44**	1.33	-1.35	1.05	-1.21	-1.37
1457173_at	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation	Ywhae	**-1.41**	**1.42**	**-1.55**	**-1.25**	-1.02	-1.46	-1.12	1.26	-1.64
1448670_at	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	Ube2e3	**-1.08**	**-1.09**	**-1.10**	**1.55**	-1.07	-1.24	-1.02	-1.18	-1.13
1440348_at	zinc finger, FYVE domain containing 9	Zfyve9	**-1.16**	**-1.13**	**-1.23**	**-1.27**	-1.13	-1.31	-1.17	-1.29	-1.1

Lipid metabolism

code	**Gene Title**	**Gene Symbo**	**Kidney**	**Liver**	**Lung**	**Spleen**	**WT_0.6J**	**WT_4J**	**XPA_0.6J**	**CSB_0.6J**	**DKO_0.6J**
1433444_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	**-1.07**	**1.40**	**-1.06**	**-1.86**	-1.07	-1.38	-1.19	-1.06	-1.13
1433445_x_at	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	Hmgcs1	**-1.12**	**1.39**	**-1.08**	**-1.91**	-1.02	-1.27	-1.09	-1.11	-1.11
1448789_at	aldehyde dehydrogenase family 1, subfamily A3	Aldh1a3	**-2.42**	**6.72**	**-1.28**	**-1.83**	-1.04	-1.62	-1.2	-1.27	-1.17
1454918_at	alkylglycerone phosphate synthase	Agps	**-1.37**	**1.12**	**-1.34**	**-1.25**	1.02	-1.26	-1.2	-1.29	-1.42
1443546_at	High density lipoprotein (HDL) binding protein	Hdlbp	**-1.41**	**-1.30**	**-1.54**	**1.25**	-1.17	-1.51	-1.05	-1.21	1
1434418_at	longevity assurance homolog 6 (S. cerevisiae)	Lass6	**-1.05**	**1.12**	**-1.16**	**-1.36**	-1.22	-2.06	-1.58	-1.66	-1.87
1457449_at	Longevity assurance homolog 6 (S. cerevisiae)	Lass6	**-2.18**	**-1.04**	**-1.32**	**-1.07**	1.01	-1.31	-1.31	1.26	-1.65
1434451_at	NOD-derived CD11c +ve dendritic cells cDNA	---	**-1.26**	**-1.26**	**-1.16**	**-1.21**	-1.27	-5.35	-2.24	-2.68	-3.03
1429514_at	phosphatidic acid phosphatase type 2B	Ppap2b	**1.02**	**-1.01**	**-1.16**	**-1.37**	1.01	-1.45	-1.14	-1.27	-1.25
1435771_at	phospholipase C, beta 4	Plcb4	**-1.03**	**1.38**	**-1.26**	**-1.54**	-1.02	-1.48	-1.22	-1.33	-1.38
1437113_s_at	phospholipase D1	Pld1	**-1.03**	**1.15**	**-1.62**	**-1.29**	-1.08	-2.05	-1.5	-1.11	1.22
1427132_at	SET binding factor 2	Sbf2	**-1.09**	**-1.05**	**-1.15**	**-1.01**	1.57	-1.59	-1.52	-1.32	-1.48
1417696_at	sterol O-acyltransferase 1	Soat1	**-1.28**	**1.40**	**-1.11**	**-1.00**	-1.05	-1.37	-1.13	-1.18	-1.09
1436499_at	transmembrane protein 23	Tmem23	**-1.08**	**1.12**	**-1.07**	**-1.76**	-1.08	-1.53	-1.38	-1.61	-1.55
1416934_at	X-linked myotubular myopathy gene 1	Mtm1	**-1.36**	**-1.20**	**-1.00**	**1.16**	-1.06	-1.91	-1.08	-1.18	-1.24

(Oxidative) metabolism

code	**Gene Title**	**Gene Symbo**	**Kidney**	**Liver**	**Lung**	**Spleen**	**WT_0.6J**	**WT_4J**	**XPA_0.6J**	**CSB_0.6J**	**DKO_0.6J**

1435967_s_at	3-hydroxyisobutyrate dehydrogenase	Hibadh	-1.14	-1.11	1.04	-1.25	-1.18	-1.41	-1.06	-1.06	1
1437082_at	A kinase (PRKA) anchor protein (yotiao) 9	Akap9	1.10	-1.22	-1.43	-1.27	1.05	-2	-1.47	-1.23	-1.16
1426339_at	adenylate kinase 5	Ak5	1.14	-2.44	-1.87	-1.66	-1.14	-1.3	-1.07	1.06	-1.17
1457827_at	arylsulfatase J	Arsj	1.48	-1.57	-1.87	-1.68	-1.08	-1.64	-1.01	-1.12	-1.2
1455083_at	Atpase, class VI, type 11C	Atp11c	1.02	-1.05	-1.20	-1.11	1.06	-1.34	-1.23	-1.17	-1.19
1419922_s_at	attractin like 1	Atrnl1	1.06	-1.04	-1.24	-1.45	-1.14	-1.39	-1.18	-1.17	-1.32
1421422_at	cDNA sequence AF397014	AF397014	-1.12	-1.73	1.06	-2.08	-1.01	-1.4	1.02	-1.03	1.66
1426307_at	cytochrome b5 reductase 4	Cyb5r4	-1.15	-1.04	-1.03	-1.29	-1.01	-1.14	1.02	-1.03	-1.04
1429064_at	DIP2 disco-interacting protein 2 homolog C (Drosophila)	Dip2c	-1.24	-1.09	-1.51	1.21	-1.44	-3.12	-1.41	-1.55	-1.99
1458177_at	emopamil binding protein-like	Ebpl	-1.00	1.30	-2.26	-1.78	-2.14	-2.25	-2.9	1.43	-1.09
1434335_at	expressed sequence AI317237	AI317237	1.04	-1.08	-1.02	-1.49	-1.17	-1.64	-1.18	-1.5	-1.38
1417434_at	glycerol phosphate dehydrogenase 2, mitochondrial	Gpd2	-1.14	-1.55	1.14	-1.30	1.05	-1.29	-1.13	-1.12	-1.2
1450730_at	heparan sulfate 2-O-sulfotransferase 1	Hs2st1	-1.08	-1.10	-1.23	-1.08	1.03	-1.27	-1.2	-1.04	-1.27
1438726_at	microtubule associated monoxygenase 2	Mical2	-1.53	-1.30	-1.60	1.41	-1.15	-2.13	-1.82	-2.08	-1.58
1442364_at	Mitogen activated protein kinase 14	Mapk14	-1.08	-1.83	-1.53	-2.69	-1.02	-2.29	-1.12	1.91	1.51
1428667_at	monoamine oxidase A	Maoa	-1.03	-1.07	-1.16	-1.01	-1.06	-1.21	1.04	-1.07	-1.11
1423144_at	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	Pik3ca	-1.05	1.02	-1.23	-1.33	-1.12	-1.22	-1.1	-1.08	-1.1
1455204_at	phosphatidylinositol transfer protein, cytoplasmic 1	Pitpnc1	-1.18	1.11	-1.36	-1.11	-1.07	-3.71	-1.77	-2.02	-2.17
1451405_at	propionyl-Coenzyme A carboxylase, alpha polypeptide	Pcca	-1.01	-1.17	1.11	-1.23	1.04	-1.4	-1.16	-1.15	-1.28
1424488_a_at	pyrophosphatase (inorganic) 2	Ppa2	-1.08	-1.14	-1.21	-1.03	-1.04	-1.14	-1.02	-1.04	-1.03
1452703_at	RIKEN cDNA 4631427C17 gene	4631427C17F	-1.11	-1.13	-1.05	1.07	-1.18	-1.57	-1.05	-1.07	1.04
1460243_at	serine palmitoyltransferase, long chain base subunit 2	Sptlc2	-1.08	1.07	-1.06	-1.17	1.01	-1.27	-1.18	-1.11	-1.24
1425388_a_at	thiamine pyrophosphokinase	Tpk1	-1.18	-1.18	-1.09	1.12	-1.26	-2.32	-1.05	-1.38	-1.32

Ubiquitin cycle

code	Gene Title	Gene Symbo	Kidney	Liver	Lung	Spleen	WT_0.6J	WT_4J	XPA_0.6J	CSB_0.6J	DKO_0.6J
1455082_at	Casitas B-lineage lymphoma b	Cblb	1.06	-1.03	-1.10	-1.19	-1.07	-1.69	-1.41	-1.48	-1.97
1434718_at	cullin 3	Cul3	-1.19	-1.21	-1.10	-1.15	-1.06	-1.34	1.02	-1.19	-1.2
1458464_at	HECT, C2 and WW domain E3 ubiquitin protein ligase 2	Hecw2	-1.07	-1.23	-1.95	-1.84	-1.37	-1.66	-1.04	1.17	1.76
1440582_at	itchy /// RIKEN cDNA 8030492O04 gene	Itch /// 803049	-1.80	-1.52	-1.72	-1.58	-1.06	-1.75	-1.06	-1.04	-1.48
1431367_at	membrane-associated ring finger (C3HC4) 1	1-Mar	-1.30	1.38	-1.17	-1.93	-1.11	-1.88	1.01	-1.58	-1.01
1442858_at	Pam, highwire, rpm 1	Phr1	-1.17	-1.05	-1.20	-1.53	-1.23	-2.08	-1.04	-1.15	-1.7
1418695_a_at	potassium channel modulatory factor 1	Kcmf1	-1.02	-1.00	-1.13	-1.04	-1.04	-1.11	-1.08	-1.17	-1.03
1444085_at	prenyl (solanesyl) diphosphate synthase, subunit 2	Pdss2	-1.19	-1.10	-1.17	1.30	-1.39	-2.7	-1.5	-1.35	-1.18
1424134_at	ring finger and SPRY domain containing 1	Rspry1	-1.01	-1.07	-1.03	1.20	1.02	-1.25	-1.2	-1.07	-1.14
1428070_at	synovial apoptosis inhibitor 1, synoviolin	Syvn1	-1.03	-1.14	1.50	-1.08	-1.23	-1.42	-1.05	-1.03	-1.01

1434839_s_at	transducin (beta)-like 1X-linked receptor 1	Tbl1xr1	**-1.27**	**-1.13**	**-1.08**	**-1.24**	-1.1	-1.71	1.04	1.01	-1.12
1450066_at	ubiquitin protein ligase E3 component n-recognin 1	Ubr1	**-1.18**	**-1.06**	**-1.33**	**-1.30**	1.01	-1.2	-1.09	-1.05	-1.11
1434392_at	ubiquitin specific peptidase 34	Usp34	**-1.08**	**-1.09**	**-1.28**	**-1.13**	-1.07	-1.55	-1.29	-1.46	-1.65
1424358_at	ubiquitin-conjugating enzyme E2E 2 (UBC4/5 homolog, yeast)	Ube2e2	**-1.00**	**-1.05**	**-1.35**	**-2.41**	-1.34	-2.76	-1.43	-1.63	-1.7
1448670_at	ubiquitin-conjugating enzyme E2E 3, UBC4/5 homolog (yeast)	Ube2e3	**-1.08**	**-1.09**	**-1.10**	**1.55**	-1.07	-1.24	-1.02	-1.18	-1.13
1435608_at	zinc and ring finger 3 /// similar to Goliath homolog precursor	Znrf3 /// LOC6	**-1.12**	**-1.40**	**-1.17**	**-1.02**	-1.05	-1.27	-1.05	-1.3	-1.21

Supplementary table 7. Signficantly overpresented processes beween upregulated genes in cells irradiated with 4J/m2 of UV and livers of long-lived mice

Over-represented biological processes	**Relative enrichment (%)**	**p-value**
GO:0002376~immune system process	5.64%	0.00054
GO:0006954~inflammatory response	1.91%	0.00064
GO:0006119~oxidative phosphorylation	0.77%	0.00637
GO:0051276~chromosome organization and biogenesis	2.96%	0.00090
GO:0006325~maintenance of chromatin architecture	2.32%	0.00013
GO:0006350~transcription	15.52%	0.00000
GO:0006397~mRNA processing	2.23%	0.00001
GO:0006915~apoptosis	5.37%	0.00000
GO:0006950~response to stress	6.28%	0.00000
GO:0006974~response to DNA damage stimulus	2.14%	0.00069
GO:0007049~cell cycle	6.19%	0.00000
GO:0007067~mitosis	1.59%	0.00248
GO:0008219~cell death	5.78%	0.00000
GO:0019538~protein metabolic process	18.84%	0.00008

Supplementary table 8. Biological processes involved in the response to Hydrogen Peroxide treatment

Gray color: fold change: >1.2; p<0.05

Response to oxidative strress

code	Gene Title	Gene Symbo	Biological Process (GO)	wt10/wt0	p-value	wt50/wt0	p-value
1416429_a_at	catalase	Cat	6979 // response to oxidative stress	1.10	0.5674	2.50	0.0267
1421817_at	glutathione reductase 1	Gsr	6749 // glutathione metabolism	1.25	0.0266	2.46	0.0158
1416531_at	glutathione S-transferase omega 1	Gsto1	6749 // glutathione metabolism	1.03	0.5680	1.33	0.0000
1421041_s_at	glutathione S-transferase, alpha 2 (Yc2)	Gsta2	6749 // glutathione metabolism	1.60	0.0943	16.67	0.0393
1416368_at	glutathione S-transferase, alpha 4	Gsta4	6749 // glutathione metabolism	1.28	0.0082	6.48	0.0011
1448330_at	glutathione S-transferase, mu 1	Gstm1	6749 // glutathione metabolism	1.12	0.3652	2.48	0.0023
1425946_at	glutathione S-transferase, mu 7	Gstm7	6749 // glutathione metabolism	1.92	0.6486	2.02	0.0329
1448239_at	heme oxygenase (decycling) 1	Hmox1	6788 // heme oxidation	1.48	0.0776	6.48	0.0003
1423291_s_at	hypoxia up-regulated 1	Hyou1	6950 // response to stress	1.03	0.7671	1.20	0.0076
1415897_a_at	microsomal glutathione S-transferase 1	Mgst1	6749 // glutathione metabolism	1.18	0.1052	2.46	0.0197
1433866_x_at	peroxiredoxin 1	Prdx1	6979 // response to oxidative stress	1.13	0.3504	2.15	0.0053
1442001_at	protein kinase, AMP-activated	Prkab2	6950 // response to stress	-1.03	0.8018	1.38	0.0112
1440222_at	superoxide dismutase 1, soluble	Sod1	6979 // response to oxidative stress	1.41	0.4229	4.93	0.0373
1415996_at	thioredoxin interacting protein	Txnip	6979 // response to oxidative stress	-1.09	0.1306	1.88	0.0193
1460725_at	xeroderma pigmentosum, compl/tion group A	Xpa	6979 // response to oxidative stress	-1.06	0.8263	1.24	0.0032

Absence of GH/IGF1 axis attenuation

code	Gene Title	Gene Symbo	Biological Process (GO)	wt10/wt0	p-value	wt50/wt0	p-value
1451959_a_at	vascular endothelial growth factor A	Vegfa	8151 // cell growth/maintenance	-1.05	0.2503	1.94	0.0587
1420894_at	transforming growth factor, beta receptor I	Tgfbr1	6468 // protein amino acid phosph.	1.21	0.7330	1.72	0.2144
1450421_at	transforming growth factor alpha	Tgfa	8283 // cell proliferation	-1.39	0.1700	1.61	0.3562
1450226_at	prolactin receptor	Prlr	7595 // lactation	1.29	0.9512	1.11	0.7529
1450414_at	platelet derived growth factor, B polypeptide	Pdgfb	8283 // cell proliferation	-1.12	0.2970	1.53	0.2855
1418711_at	platelet derived growth factor, alpha	Pdgfa	8283 // cell proliferation	1.06	0.4172	1.72	0.0158
1438946_at	platelet derived growth factor receptor, alpha polypeptide	Pdgfra	7169 // tyrosine kinase signaling path.	-1.07	0.5182	1.36	0.2966
1438312_s_at	latent transforming growth factor beta binding protein 3	Ltbp3	7179 // TGFbeta receptor signaling path.	-1.01	0.8871	1.48	0.0169
1446232_at	Latent transforming growth factor beta binding protein 1	Ltbp1	7179 // TGFbeta receptor signaling path.	4.17	0.0401	1.82	0.0694
1458268_s_at	insulin-like growth factor binding protein 3	Igfbp3	1558 // regulation of cell growth	1.26	0.1710	2.51	0.0662
1459825_x_at	insulin-like growth factor 2, binding protein 1	Igf2bp1	1558 // regulation of cell growth	2.12	0.2886	1.51	0.3116
1424111_at	insulin-like growth factor 2 receptor	Igf2r	6810 // transport	1.08	0.4163	1.30	0.1672

1452014_a_at	insulin-like growth factor 1	Igf1	48009 // IGF receptor signaling path.	1.01	0.9103	1.02	0.9086
1423252_at	hepatoma-derived growth factor, related protein 3	Hdgfrp3	8283 // cell proliferation	-1.05	0.6903	1.31	0.0105
1421294_at	hepatoma derived growth factor-like 1	Hdgfl1	8283 // cell proliferation	1.18	0.7904	3.58	0.1768
1451501_a_at	Growth hormone receptor	Ghr	8151 // cell growth/maintenance	1.05	0.3342	1.05	0.6787
1425457_a_at	growth factor receptor bound protein 10	Grb10	48009 // IGF receptor signaling path.	-1.04	0.3803	1.66	0.8047
1427777_x_at	fibroblast growth factor receptor 4	Fgfr4	6468 // protein amino acid phosph.	2.95	0.3887	3.61	0.2401
1424050_s_at	fibroblast growth factor receptor 1	Fgfr1	6468 // protein amino acid phosph.	1.03	0.8900	1.58	0.2836
1451693_a_at	fibroblast growth factor 12	Fgf12	6468 // protein amino acid phosph.	1.56	0.7102	1.71	0.4570
1450869_at	fibroblast growth factor 1	Fgf1	6468 // protein amino acid phosph.	-1.35	0.0954	1.52	0.6407
1438924_x_at	Fibroblast growth factor intracellular binding protein	Fibp	6468 // protein amino acid phosph.	2.12	0.6817	1.76	0.6089
1422824_s_at	epidermal growth factor receptor pathway substrate 8	Eps8	6508 // proteolysis and peptidolysis	1.24	0.1430	1.88	0.1679
1437769_at	Epidermal growth factor receptor pathway substrate 15	Eps15-rs	---	1.04	0.9222	1.30	0.6014
1457563_at	epidermal growth factor receptor	Egfr	8283 // cell proliferation	2.12	0.2243	1.36	0.4156
1435541_at	betacellulin, epidermal growth factor family member	Btc	8283 // cell proliferation	1.05	0.6876	2.41	0.0171

DNA Repair

code	Gene Title	Gene Symbo	Biological Process (GO)	wt10/wt0	p-value	wt50/wt0	p-value
1430078_a_at	8-oxoguanine DNA-glycosylase 1	Ogg1	6284 // base-excision repair	1.14	0.5054	1.85	0.0384
1460725_at	xeroderma pigmentosum, complementation group A	Xpa	6289 // nucleotide-excision repair	-1.06	0.8263	1.24	0.0032
1437715_x_at	apurinic/apyrimidinic endonuclease 1	Apex1	6281 // DNA repair	1.04	0.4128	-1.32	0.0106
1440383_at	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae)	Dclre1b	6289 // nucleotide-excision repair	-1.07	0.2950	-1.53	0.0465
1450935_at	excision repair cross-complementation group 5	Ercc5	6289 // nucleotide-excision repair	1.10	0.0598	1.39	0.0040
1453169_a_at	general transcription factor II H, polypeptide 1	Gtf2h1	6289 // nucleotide-excision repair	1.09	0.4165	1.54	0.0101
1437163_x_at	general transcription factor II H, polypeptide 4	Gtf2h4	6289 // nucleotide-excision repair	-1.03	0.6086	-1.27	0.0229
1416641_at	ligase I, DNA, ATP-dependent	Lig1	6281 // DNA repair	-1.11	0.4338	-1.24	0.0295
1423419_at	ligase III, DNA, ATP-dependent	Lig3	6281 // DNA repair	1.02	0.7835	-1.23	0.0095
1421309_at	O-6-methylguanine-DNA methyltransferase	Mgmt	6281 // DNA repair	1.19	0.6353	1.35	0.0227
1427283_at	myeloid/lymphoid or mixed-lineage leukemia	Mll	6281 // DNA repair	1.00	0.9591	1.65	0.0259
1431885_a_at	MUS81 endonuclease homolog (yeast)	Mus81	6281 // DNA repair	-1.05	0.3247	-1.70	0.0477
1435368_a_at	poly (ADP-ribose) polymerase family, member 1	Parp1	6284 // base-excision repair	-1.07	0.2111	-1.96	0.0441
1448650_a_at	polymerase (DNA directed), epsilon	Pole	6281 // DNA repair	1.04	0.5677	-1.36	0.0136
1450075_at	polymerase (DNA directed), eta (RAD 30 related)	Polh	6301 // postreplication repair	1.05	0.8936	-3.26	0.0453
1449483_at	polymerase (DNA directed), kappa	Polk	6281 // DNA repair	1.08	0.1232	1.56	0.0208
1451576_at	protein kinase, DNA activated, catalytic polypeptide	Prkdc	6302 // double-strand break repair	-1.27	0.0371	-1.79	0.0151
1448762_at	RAD17 homolog (S. pombe)	Rad17	6281 // DNA repair	1.06	0.0552	1.21	0.0308
1424222_s_at	RAD23b homolog (S. cerevisiae)	Rad23b	6974 // response to DNA damage	1.01	0.6842	1.20	0.0238
1443891_at	RAD51-like 3 (S. cerevisiae)	Rad51l3	6284 // base-excision repair	1.48	0.6394	1.46	0.0362

1450862_at	RAD54 like (S. cerevisiae)	Rad54l	6281 // DNA repair	-1.06	0.8101	-1.50	0.0326
1421235_s_at	RecQ protein-like 5	Recql5	6281 // DNA repair	-1.03	0.8381	1.33	0.0284
1422624_at	REV1-like (S. cerevisiae)	Rev1l	42276 // error-prone postrep/tion repair	1.08	0.3526	1.89	0.0151
1452917_at	replication factor C (activator 1) 5	Rfc5	6281 // DNA repair	-1.01	0.9730	-1.43	0.0342
1451968_at	X-ray repair cross-complementation group 5	Xrcc5	6302 // double-strand break repair	-1.02	0.7218	-1.44	0.0259