Probe	Gene Symbol	Gene Title	DRG	Cereb.	Fold Change	BH p-value
102704_at	Aqp4	aquaporin 4	47.98	1185.84	-24.72	7.70E-08
161329_f_at	Capzb	capping protein (actin filament) r	13171.94	951.63	13.84	4.34E-07
102703_s_at	Aqp4	aquaporin 4	62.75	504.45	-8.04	6.23E-07
100332_s_at	LOC677654 /// Prdx6	peroxiredoxin 6 /// peroxiredoxir	53.18	332.94	-6.26	1.99E-06
98478_at	Ccng2	cyclin G2	151.45	860.39	-5.68	1.99E-06
100009_r_at	Sox2	SRY-box containing gene 2	89.20	1058.39	-11.86	2.14E-06
99191_at	Eid1	EP300 interacting inhibitor of diff	110.09	3041.85	-27.63	2.94E-06
160352_at	Pcbp4	poly(rC) binding protein 4	481.10	1161.43	-2.41	3.06E-06
92420_at	Ntf3	neurotrophin 3	92.18	267.16	-2.90	3.20E-06
101680_at	EG432798 /// EG665	ribosomal protein L27a /// predic	156.45	2235.86	-14.29	3.24E-06
160234_at	Usp1	ubiquitin specific peptdiase 1	28.75	234.97	-8.17	3.36E-06
95059_at	Pnrc2	proline-rich nuclear receptor coa	726.26	3707.49	-5.10	3.39E-06
94839_at	Nucb1	nucleobindin 1	6304.97	923.27	6.83	3.43E-06
93818_g_at	LOC100042343 /// Tr	transmembrane emp24 domain t	121.21	804.65	-6.64	3.43E-06
92801_at	Plp1	proteolipid protein (myelin) 1	187.93	2668.23	-14.20	3.43E-06
98564_f_at	LOC100042812 /// LC	ribosomal protein S26 /// similar	1118.75	4149.20	-3.71	3.47E-06
104516_at	Cldn5	claudin 5	189.36	996.58	-5.26	3.47E-06
94931_at	Ufm1	ubiquitin-fold modifier 1	120.81	516.07	-4.27	3.49E-06
92526_f_at	Btbd14a	BTB (POZ) domain containing 14A	7395.96	372.48	19.86	3.52E-06
98048_at	Fusip1	FUS interacting protein (serine-ar	77.43	229.60	-2.97	3.53E-06
95122_g_at	Pole4	polymerase (DNA-directed), epsil	252.26	99.07	2.55	3.54E-06
92717_at	Neurod1	neurogenic differentiation 1	46.86	962.11	-20.53	3.59E-06
94232_at	Ccnd1	cyclin D1	224.77	489.31	-2.18	3.59E-06
95726_at	Mlf2	myeloid leukemia factor 2	656.42	2229.80	-3.40	3.61E-06
162182_f_at	Kcnab2	potassium voltage-gated channel	3404.90	362.85	9.38	3.64E-06
103543_at	Sez6l	seizure related 6 homolog like	188.96	854.91	-4.52	3.66E-06
95340_at	Mt3	metallothionein 3	1705.20	3888.76	-2.28	3.69E-06
100618_f_at	EG433923 /// LOC63(	solute carrier family 25 (mitocho	406.65	2028.54	-4.99	3.70E-06
103692_at	Efnb3	ephrin B3	442.61	1048.04	-2.37	3.75E-06
103063_at	Zfp62	zinc finger protein 62	35.66	172.65	-4.84	3.75E-06
94489_at	EG667723 /// LOC10(	protein tyrosine phosphatase 4a1	416.55	4070.36	-9.77	3.76E-06
99532_at	Tob1	transducer of ErbB-2.1	276.23	1492.06	-5.40	3.79E-06
101529_g_at	Tcea1	transcription elongation factor A	182.40	680.54	-3.73	3.85E-06
93090_at	Fgfr2	fibroblast growth factor receptor	343.63	955.84	-2.78	3.95E-06
103416_at	Mapk6	mitogen-activated protein kinase	312.50	1460.82	-4.67	3.97E-06
160085_at	Tst	thiosulfate sulfurtransferase, mit	217.51	597.17	-2.75	4.17E-06
101664_at	Rps3a	ribosomal protein S3a	1614.22	11207.72	-6.94	4.30E-06
94802_at	BC060632 /// LOC10(	cDNA sequence BC060632 /// sin	227.31	1522.62	-6.70	4.30E-06
93714_f_at	EG630499	predicted gene, EG630499	3155.02	1476.57	2.14	4.36E-06
96865_at	Marcks	myristoylated alanine rich protei	256.63	4955.59	-19.31	4.49E-06
104433_at	Atp13a2	ATPase type 13A2	480.39	1241.99	-2.59	4.51E-06
93374_at	Jph3	junctophilin 3	6369.39	1861.41	3.42	4.52E-06
95471_at	Cdkn1c	cyclin-dependent kinase inhibitor	38.74	186.92	-4.82	4.56E-06
102001_at	Rrm2	ribonucleotide reductase M2	51.09	160.98	-3.15	4.62E-06
101930_at	Nfix	nuclear factor I/X	333.24	1155.84	-3.47	4.63E-06
96696_at	Prmt1	protein arginine N-methyltransfe	269.56	1204.85	-4.47	4.63E-06
98925_at	Vamp2	vesicle-associated membrane prc	85.09	251.38	-2.95	4.71E-06
161859_f_at	Sncg	synuclein, gamma	15748.89	820.95	19.18	5.15E-06
103931_at	Gpr162	G protein-coupled receptor 162	494.30	1257.27	-2.54	5.19E-06
94236_at	Nisch	nischarin	6891.31	2493.99	2.76	5.48E-06
98580_at	Ppm1a	protein phosphatase 1A, magnes	3195.71	500.82	6.38	5.53E-06
100318_at	Dnajb13	DnaJ (Hsp40) related, subfamily E	300.19	602.62	-2.01	5.55E-06

93730_at	Rps15a	ribosomal protein S15a	494.56	7498.49	-15.16	5.55E-06
96358_at	EG667423 /// LOC10(	ribosomal protein S23 /// predict	658.83	13251.66	-20.11	5.63E-06
96300_f_at	LOC100043030 /// LC	ribosomal protein S27 /// similar	1114.59	8203.25	-7.36	5.67E-06
102309_at	Zfp326	zinc finger protein 326	83.52	339.43	-4.06	5.69E-06
104179_at	Arf6	ADP-ribosylation factor 6	29.94	141.50	-4.73	5.69E-06
94876_f_at	Gorasp2	golgi reassembly stacking protein	5112.94	1628.25	3.14	5.85E-06
104249_g_at	Ssr3	signal sequence receptor, gamma	128.72	699.94	-5.44	5.90E-06
99872_s_at	EG665937 /// Ftl1 ///	ferritin light chain 1 /// ferritin lig	2237.47	5820.45	-2.60	5.91E-06
95681_f_at	Ppp1r2	protein phosphatase 1, regulator	901.47	175.23	5.14	5.91E-06
94088_at	Ptbp2	polypyrimidine tract binding prot	76.85	416.81	-5.42	6.04E-06
104186_at	Msl2l1	male-specific lethal 2-like 1 (Dros	131.67	363.56	-2.76	6.07E-06
95633_r_at	Mvk	mevalonate kinase	346.40	694.73	-2.01	6.07E-06
103800_at	Abcc5	ATP-binding cassette, sub-family	3542.75	1319.81	2.68	6.15E-06
162001_f_at	Csnk1d	casein kinase 1, delta	612.45	222.48	2.75	6.15E-06
93120_f_at	H2-K1	histocompatibility 2, K1, K region	3812.43	1153.15	3.31	6.20E-06
99575_at	Ubqln1	ubiquilin 1	164.39	1438.39	-8.75	6.22E-06
93509_at	Ube2b	ubiquitin-conjugating enzyme E2	4732.46	991.38	4.77	6.25E-06
93740_at	LOC100045189 /// Yb	Y box protein 1 /// similar to tran	4000.80	15265.46	-3.82	6.32E-06
92628_at	LOC100043718 /// LC	ribosomal protein L36 /// similar	295.43	3948.95	-13.37	6.33E-06
104608_at	Tm2d1	TM2 domain containing 1	46.79	138.89	-2.97	6.34E-06
93568_i_at	2610042L04Rik /// B9	RIKEN cDNA B930046C15 gene //	123.06	1776.90	-14.44	6.36E-06
95417_at	Mgat2	mannoside acetylglucosaminyltra	42.81	218.56	-5.11	6.40E-06
104169_at	LOC100044533 /// Zi	zinc finger protein of the cerebell	101.51	12897.92	-127.06	6.48E-06
93547_at	Cbfb	core binding factor beta	22974.17	4301.17	5.34	6.78E-06
100024_at	Shroom3	shroom family member 3	2719.16	130.32	20.87	6.96E-06
101577_at	LOC100043734 /// LC	ribosomal protein S6 /// similar t	3880.85	8771.42	-2.26	6.97E-06
96699_at	Hmgn1 /// LOC10004	high mobility group nucleosomal	2342.35	9389.00	-4.01	7.02E-06
101528_at	Tcea1	transcription elongation factor A	95.08	498.33	-5.24	7.06E-06
96002_at	Vps24	vacuolar protein sorting 24 (yeas	1753.76	571.33	3.07	7.57E-06
102234_at	1810037I17Rik	RIKEN cDNA 1810037I17 gene	275.99	840.97	-3.05	7.79E-06
94842_at	Blmh	bleomycin hydrolase	860.33	1919.45	-2.23	7.79E-06
103781_at	Stx4a	syntaxin 4A (placental)	3613.97	650.19	5.56	7.80E-06
103534_at	Hbb-b2	hemoglobin, beta adult minor ch	143.33	4855.37	-33.88	7.85E-06
100557_g_at	Eif4b	eukaryotic translation initiation f	350.92	1263.94	-3.60	7.87E-06
97722_at	Ssr1	signal sequence receptor, alpha	139.63	433.95	-3.11	8.04E-06
103080_at	Samhd1	SAM domain and HD domain, 1	476.15	144.93	3.29	8.04E-06
160588_at	LOC100040573 /// Zf	zinc finger protein 131 /// similar	146.92	355.16	-2.42	8.07E-06
100963_at	Pnkd	paroxysmal nonkinesiogenic dysk	246.20	594.62	-2.42	8.08E-06
161127_i_at	Rpl24	ribosomal protein L24	112.81	581.08	-5.15	8.10E-06
161575_f_at	Mapk10	mitogen-activated protein kinase	2389.96	298.92	8.00	8.17E-06
93519_s_at	Nedd8	neural precursor cell expressed, d	362.18	1628.30	-4.50	8.48E-06
96299_at	2900097C17Rik	RIKEN cDNA 2900097C17 gene	10458.10	3154.43	3.32	8.66E-06
95737_at	Tprgl	transformation related protein 63	3786.64	812.66	4.66	8.70E-06
97977_at	LOC672215 /// Ntn1	netrin 1 /// similar to Netrin-1 pr	295.94	649.57	-2.19	8.87E-06
92518_at	Neo1	neogenin	468.51	960.38	-2.05	8.91E-06
93721_at	Cap1	CAP, adenylate cyclase-associate	75.30	200.20	-2.66	8.96E-06
101781_f_at	EG238836 /// EG623	H3 histone, family 3A /// H3 histo	113.24	842.94	-7.44	9.00E-06
97907_at	LOC100041500 /// LC	LSM7 homolog, U6 small nuclear	229.96	919.31	-4.00	9.00E-06
100708_at	H3f3a /// H3f3b /// L	H3 histone, family 3A /// H3 histo	833.89	7160.49	-8.59	9.01E-06
100711_at	LOC100043141 /// LC	ribosomal protein L10A /// simila	442.40	3613.29	-8.17	9.02E-06
98934_at	l7Rn6	lethal, Chr 7, Rinchik 6	349.45	1545.56	-4.42	9.02E-06
98342_at	EG234703 /// LOC10(	ribosomal protein 10 /// predicte	2087.00	7637.66	-3.66	9.05E-06
100486_at	Ezh1	enhancer of zeste homolog 1 (Dr	1255.54	292.81	4.29	9.08E-06
104092_at	LOC674195 /// Usp4	ubiquitin specific peptidase 48 //	2146.64	597.11	3.60	9.08E-06
96333_g_at	Snx2	sorting nexin 2	222.34	686.76	-3.09	9.09E-06

99579_at	Atp1b3	ATPase, Na+/K+ transporting, bet	15209.88	3945.08	3.86	9.11E-06
98338_at	En2	engrailed 2	137.66	3549.12	-25.78	9.13E-06
94889_at	Vapa	vesicle-associated membrane prc	1745.38	3999.94	-2.29	9.13E-06
101869_s_at	Hbb-b1 /// Hbb-b2	hemoglobin, beta adult major cha	382.92	11807.62	-30.84	9.18E-06
95096_at	LOC100046895 /// Ql	quaking /// similar to Quaking pr	67.29	1169.95	-17.39	9.18E-06
100630_f_at	Gstm5	glutathione S-transferase, mu 5	17165.87	7265.57	2.36	9.19E-06
92216_at	Smad7	MAD homolog 7 (Drosophila)	211.58	551.66	-2.61	9.61E-06
95129_at	Ncor2	nuclear receptor co-repressor 2	2584.88	910.02	2.84	9.88E-06
161439_f_at	Ap1m1	adaptor-related protein complex	1535.13	483.25	3.18	1.00E-05
101294_g_at	G6pd2 /// G6pdx	glucose-6-phosphate dehydroger	145.15	438.00	-3.02	1.01E-05
101198_at	Cplx1	complexin 1	1084.44	2328.23	-2.15	1.04E-05
98967_at	Fabp7	fatty acid binding protein 7, brair	3426.24	13418.30	-3.92	1.04E-05
93164_at	Rnf2	ring finger protein 2	59.07	192.76	-3.26	1.04E-05
101578_f_at	Actb	actin, beta, cytoplasmic	5081.40	765.11	6.64	1.04E-05
97540_f_at	H2-D1	histocompatibility 2, D region loc	3705.43	1127.32	3.29	1.04E-05
103514_at	Tnfrsf21	tumor necrosis factor receptor su	3558.78	938.30	3.79	1.05E-05
96192_at	D130067C23Rik /// S	trans-acting transcription factor 3	59.08	1030.89	-17.45	1.05E-05
160319_at	Sparcl1	SPARC-like 1 (mast9, hevin)	154.88	4213.67	-27.21	1.06E-05
98007_at	Rps6ka2	ribosomal protein S6 kinase, poly	2584.63	492.50	5.25	1.07E-05
160207_at	Acly	ATP citrate lyase	8278.10	2096.11	3.95	1.07E-05
103886_at	Reep5	receptor accessory protein 5	7271.31	2096.20	3.47	1.13E-05
100123_f_at	Itgb1	integrin beta 1 (fibronectin recep	11763.36	3600.83	3.27	1.13E-05
100360_f_at	LOC100046359	similar to Ighg1 protein	274.34	576.22	-2.10	1.15E-05
92887_at	Ddah2	dimethylarginine dimethylaminol	1269.72	4922.43	-3.88	1.15E-05
92376_at	Rit1	Ras-like without CAAX 1	3228.68	900.57	3.59	1.16E-05
98004_at	Pkia	protein kinase inhibitor, alpha	64.48	349.77	-5.42	1.17E-05
94817_at	Serpinh1	serine (or cysteine) peptidase inh	142.96	574.46	-4.02	1.18E-05
97255_at	Cugbp2	CUG triplet repeat, RNA binding p	57.44	708.02	-12.33	1.19E-05
97329_at	Ints3	integrator complex subunit 3	1702.12	434.06	3.92	1.21E-05
160917_r_at	Mageh1	melanoma antigen, family H, 1	21.36	49.63	-2.32	1.21E-05
92180_at	H1fx	H1 histone family, member X	149.69	376.68	-2.52	1.21E-05
96801_at	Ak1	adenylate kinase 1	1281.99	456.82	2.81	1.21E-05
93592_at	Apod	apolipoprotein D	148.75	380.79	-2.56	1.22E-05
101944_at	Lypla1	lysophospholipase 1	798.55	1902.92	-2.38	1.22E-05
94321_at	Krt10	keratin 10	61.86	300.39	-4.86	1.22E-05
161214_r_at	BC037034	cDNA sequence BC037034	5522.61	1399.41	3.95	1.22E-05
101212_at	Rps7	ribosomal protein S7	383.31	9782.66	-25.52	1.23E-05
100573_f_at	Gpi1	glucose phosphate isomerase 1	3359.98	431.37	7.79	1.23E-05
160493_at	Cd63	Cd63 antigen	564.09	3056.00	-5.42	1.23E-05
160832_at	Ldlr	low density lipoprotein receptor	8946.18	591.30	15.13	1.23E-05
98302_at	Scn10a	sodium channel, voltage-gated, t	8424.97	217.38	38.76	1.23E-05
100710_at	Vcp	valosin containing protein	10807.44	2698.64	4.00	1.24E-05
101564_at	Cnot7	CCR4-NOT transcription complex,	43.10	154.95	-3.59	1.24E-05
97368_at	Akap1	A kinase (PRKA) anchor protein 1	1349.21	3758.61	-2.79	1.27E-05
99633_at	Ncdn	neurochondrin	15194.03	2433.98	6.24	1.28E-05
161482_f_at	Prph	peripherin	9885.62	321.64	30.74	1.29E-05
98631_g_at	Nsdhl	NAD(P) dependent steroid dehyd	287.30	1084.06	-3.77	1.30E-05
102137_f_at	---	---	1848.78	912.37	2.03	1.30E-05
103574_at	Ablim1	actin-binding LIM protein 1	1872.45	382.24	4.90	1.30E-05
93548_at	Sec61b	Sec61 beta subunit	147.88	969.88	-6.56	1.31E-05
104246_at	Asxl1	additional sex combs like 1 (Dros	2301.85	972.17	2.37	1.31E-05
92545_f_at	Ptgds	prostaglandin D2 synthase (brain	253.60	2690.20	-10.61	1.31E-05
162225_f_at	---	---	988.01	249.88	3.95	1.31E-05
104330_g_at	Arid1a	AT rich interactive domain 1A (Sv	101.98	220.69	-2.16	1.31E-05
104305_at	Rars2	arginyl-tRNA synthetase 2, mitoc	1744.95	708.09	2.46	1.31E-05

97960_at	Usp22	ubiquitin specific peptidase 22	52.92	453.13	-8.56	1.31E-05
94957_at	Prepl	prolyl endopeptidase-like	8412.97	1832.64	4.59	1.32E-05
103843_at	Gnao1	guanine nucleotide binding prote	17453.16	5659.26	3.08	1.32E-05
95688_at	Degs1	degenerative spermatocyte hom	5450.91	1100.60	4.95	1.32E-05
100727_at	Rpl28	ribosomal protein L28	1112.70	9887.32	-8.89	1.32E-05
160165_at	Ube2m	ubiquitin-conjugating enzyme E2	198.32	461.71	-2.33	1.32E-05
96290_f_at	EG433125 /// EG433	ribosomal protein L21 /// similar	1614.98	10065.45	-6.23	1.32E-05
103032_at	Tpst1	protein-tyrosine sulfotransferase	2123.70	526.10	4.04	1.32E-05
161318_f_at	Ctnna2	catenin (cadherin associated prot	976.68	75.93	12.86	1.32E-05
92228_at	Ctnna2	catenin (cadherin associated prot	6364.46	972.65	6.54	1.32E-05
95430_f_at	LOC100048562 /// Sp	spastic paraplegia 21 homolog (h	2719.97	380.47	7.15	1.32E-05
92880_at	Mfge8	milk fat globule-EGF factor 8 prot	1526.45	3450.54	-2.26	1.33E-05
94781_at	Hba-a1	hemoglobin alpha, adult chain 1	644.02	16008.09	-24.86	1.33E-05
92270_at	Tro	trophinin	10323.89	1377.30	7.50	1.33E-05
92932_at	Cbln1 /// LOC100046	cerebellin 1 precursor protein ///	1013.88	6287.57	-6.20	1.33E-05
94833_at	Fstl1	follistatin-like 1	5702.30	258.55	22.05	1.36E-05
95132_r_at	Ndufb2	NADH dehydrogenase (ubiquinor	1202.01	5546.92	-4.61	1.37E-05
103088_at	Chl1	cell adhesion molecule with hom	2884.15	267.75	10.77	1.38E-05
95795_at	Supt4h2	suppressor of Ty 4 homolog 2 (S.	40.30	275.46	-6.84	1.38E-05
97277_at	Triap1	TP53 regulated inhibitor of apopt	1257.09	308.00	4.08	1.38E-05
94305_at	Col1a1	collagen, type I, alpha 1	166.59	451.13	-2.71	1.39E-05
98767_at	Yy1	YY1 transcription factor	3882.20	730.28	5.32	1.40E-05
93806_at	Sh3bgrl	SH3-binding domain glutamic aci	154.15	900.71	-5.84	1.40E-05
101083_s_at	Lsm2	LSM2 homolog, U6 small nuclear	207.24	465.74	-2.25	1.40E-05
96130_at	Slk	STE20-like kinase (yeast)	1973.99	885.85	2.23	1.41E-05
95603_at	Gldc	glycine decarboxylase	185.85	380.50	-2.05	1.41E-05
92499_at	Uncx	UNC homeobox	73.56	393.99	-5.36	1.42E-05
97104_g_at	Rfk	riboflavin kinase	145.33	321.52	-2.21	1.42E-05
101593_at	Crip2	cysteine rich protein 2	7921.59	928.38	8.53	1.42E-05
100780_at	Rps4x	ribosomal protein S4, X-linked	2250.08	7874.74	-3.50	1.43E-05
93892_at	Cugbp2	CUG triplet repeat, RNA binding p	84.25	223.16	-2.65	1.46E-05
93843_at	Dhrs1	dehydrogenase/reductase (SDR f	3237.85	1553.51	2.08	1.46E-05
103908_at	Sdccag3	serologically defined colon cance	96.79	296.26	-3.06	1.50E-05
104352_at	Brd4	bromodomain containing 4	4474.81	1579.43	2.83	1.51E-05
92691_at	Ppp2r2b	protein phosphatase 2 (formerly	559.16	2087.30	-3.73	1.51E-05
95135_at	Mid1ip1	Mid1 interacting protein 1 (gastru	3591.57	869.87	4.13	1.51E-05
103094_at	Serf1	small EDRK-rich factor 1	261.77	562.67	-2.15	1.51E-05
97251_at	Mrps10	mitochondrial ribosomal protein	455.29	132.88	3.43	1.52E-05
99944_at	Hpca	hippocalcin	416.15	1066.21	-2.56	1.52E-05
102405_at	Mag	myelin-associated glycoprotein	133.16	498.83	-3.75	1.52E-05
94267_i_at	Ubl5	ubiquitin-like 5	226.15	4060.36	-17.95	1.53E-05
98610_at	Mrps28	mitochondrial ribosomal protein	95.39	242.97	-2.55	1.53E-05
100929_at	Mtmr9	myotubularin related protein 9	1623.83	198.02	8.20	1.54E-05
98972_at	Usp8	ubiquitin specific peptidase 8	2358.29	621.43	3.79	1.60E-05
93288_at	Arpc2	actin related protein 2/3 complex	7014.05	2185.06	3.21	1.60E-05
162482_at	---	---	661.19	1385.08	-2.09	1.63E-05
103436_at	Gtpbp1	GTP binding protein 1	286.18	636.77	-2.23	1.64E-05
98085_f_at	LOC100039820 /// LC	ribosomal protein S28 /// similar	3817.15	16472.92	-4.32	1.66E-05
94181_at	Scrg1	scrapie responsive gene 1	211.25	898.09	-4.25	1.67E-05
99491_at	Il10rb	interleukin 10 receptor, beta	3494.89	680.74	5.13	1.68E-05
92664_at	Zfp777	zinc finger protein 777	76.40	200.41	-2.62	1.69E-05
102732_at	Tln1	talin 1	451.73	1034.11	-2.29	1.71E-05
104586_at	Sfrs1	splicing factor, arginine/serine-ric	54.63	284.48	-5.21	1.71E-05
92947_s_at	Gria2	glutamate receptor, ionotropic, A	608.44	1709.53	-2.81	1.71E-05
94903_at	Tmed7	transmembrane emp24 protein t	594.98	2104.86	-3.54	1.72E-05

96193_at	Dmwd	dystrophia myotonica-containing	147.90	299.59	-2.03	1.72E-05
93918_at	Taf9	TAF9 RNA polymerase II, TATA bc	48.64	517.12	-10.63	1.76E-05
97318_at	Dtd1 /// LOC1000486	D-tyrosyl-tRNA deacylase 1 homc	1694.76	436.94	3.88	1.77E-05
103555_at	Chmp4b /// LOC6747	chromatin modifying protein 4B /	10574.09	4283.06	2.47	1.77E-05
95714_at	0610009D07Rik	RIKEN cDNA 0610009D07 gene	660.57	1813.62	-2.75	1.79E-05
97520_s_at	Nnat	neuronatin	84.05	1420.72	-16.90	1.79E-05
162415_f_at	Cant1	calcium activated nucleotidase 1	1709.20	827.79	2.06	1.80E-05
96912_s_at	Ctla2a /// Ctla2b	cytotoxic T lymphocyte-associate	90.18	187.21	-2.08	1.81E-05
160286_at	Dek	DEK oncogene (DNA binding)	100.14	445.07	-4.44	1.82E-05
104222_f_at	Ggps1 /// LOC100045	geranylgeranyl diphosphate syntl	171.19	366.53	-2.14	1.85E-05
100005_at	Traf4	Tnf receptor associated factor 4	460.98	997.35	-2.16	1.90E-05
160455_s_at	Zwint	ZW10 interactor	20620.25	7131.08	2.89	1.92E-05
103697_at	Lifr	leukemia inhibitory factor recept	2539.03	179.98	14.11	1.94E-05
104437_at	Zfp30	zinc finger protein 30	64.30	131.71	-2.05	1.95E-05
96167_at	Bag3	Bcl2-associated athanogene 3	4043.67	469.98	8.60	1.95E-05
96575_at	Rpl8	ribosomal protein L8	698.05	2390.49	-3.42	1.95E-05
93095_at	2810416G20Rik /// H	high mobility group box 1 /// RIK	184.09	1075.82	-5.84	1.95E-05
AFFX-GapdhMur/I	Gapdh	glyceraldehyde-3-phosphate deh	163.36	9966.85	-61.01	1.98E-05
100562_at	Rangrf	RAN guanine nucleotide release f	308.74	722.99	-2.34	1.99E-05
98571_s_at	Naca	nascent polypeptide-associated c	258.63	2611.85	-10.10	2.01E-05
101954_at	H2afz	H2A histone family, member Z	661.75	2833.08	-4.28	2.02E-05
100974_at	Ssbp4	single stranded DNA binding prot	247.81	605.51	-2.44	2.03E-05
160195_at	1200013P24Rik	RIKEN cDNA 1200013P24 gene	2604.81	1147.97	2.27	2.04E-05
95635_g_at	0610010K14Rik	RIKEN cDNA 0610010K14 gene	620.06	1494.56	-2.41	2.06E-05
160249_at	Tpd52	tumor protein D52	3660.18	485.48	7.54	2.08E-05
102870_at	Dynlt1 /// LOC10004(	dynein light chain Tctex-type 1 //	308.48	7947.01	-25.76	2.16E-05
161612_f_at	Tubb3 /// Tubb3-ps1	tubulin, beta 3 /// tubulin, beta 3	7049.60	2160.61	3.26	2.16E-05
99544_at	Dguok	deoxyguanosine kinase	808.04	297.46	2.72	2.16E-05
95079_at	Pdgfra	platelet derived growth factor re	258.83	631.41	-2.44	2.17E-05
92587_at	Fdx1	ferredoxin 1	3511.23	1038.41	3.38	2.17E-05
160875_at	Psmb1	proteasome (prosome, macropai	7221.37	3100.37	2.33	2.17E-05
97864_at	2510049I19Rik	RIKEN cDNA 2510049I19 gene	38.07	127.75	-3.36	2.17E-05
92804_at	Polr2h	polymerase (RNA) II (DNA directe	211.04	557.92	-2.64	2.18E-05
94300_f_at	Dctn2	dynactin 2	5165.45	1137.08	4.54	2.18E-05
96755_at	Etf1	eukaryotic translation terminatio	436.65	1087.68	-2.49	2.18E-05
160724_at	Med20	mediator complex subunit 20	985.10	199.05	4.95	2.18E-05
93511_at	Itm2a	integral membrane protein 2A	40.76	436.92	-10.72	2.18E-05
98549_at	Vtn	vitronectin	171.90	572.31	-3.33	2.18E-05
93312_at	Ube2g1	ubiquitin-conjugating enzyme E2(	461.08	2615.68	-5.67	2.18E-05
100628_at	Ndufc1	NADH dehydrogenase (ubiquinor	747.90	2143.94	-2.87	2.18E-05
160725_at	4930432O21Rik	RIKEN cDNA 4930432O21 gene	38.27	82.62	-2.16	2.19E-05
94034_at	Rexo2	REX2, RNA exonuclease 2 homolc	488.86	231.92	2.11	2.19E-05
160522_at	D0H4S114	DNA segment, human D4S114	1261.55	19396.11	-15.37	2.19E-05
98064_at	Aamp	angio-associated migratory prote	695.05	2171.57	-3.12	2.19E-05
93396_at	Slc4a1ap	solute carrier family 4 (anion excl	497.10	147.68	3.37	2.19E-05
99503_at	Pptc7	PTC7 protein phosphatase homol	9041.48	705.76	12.81	2.19E-05
98892_at	Lpin1	lipin 1	2163.35	182.79	11.83	2.20E-05
95696_at	Glrx3 /// LOC620016	glutaredoxin 3 /// similar to thior	7655.78	2454.77	3.12	2.20E-05
98339_at	Syt11	synaptotagmin XI	554.73	1483.00	-2.67	2.20E-05
94449_at	Pcdhga1 /// Pcdhga1(	protocadherin gamma subfamily	1731.01	4824.56	-2.79	2.21E-05
AFFX-MURINE_b1	---	---	1237.08	22081.32	-17.85	2.21E-05
100694_at	Rplp1	ribosomal protein, large, P1	3412.38	9798.83	-2.87	2.23E-05
93823_at	Ilf2	interleukin enhancer binding fact	187.50	1140.01	-6.08	2.23E-05
160393_at	Etnk1	ethanolamine kinase 1	3602.12	473.53	7.61	2.24E-05
96165_at	LOC677213 /// Uhmk	U2AF homology motif (UHM) kin	5575.65	1433.28	3.89	2.24E-05

102476_f_at	Xpo7	exportin 7	2865.71	508.07	5.64	2.27E-05
104634_at	Lims1	LIM and senescent cell antigen-lil	2616.49	549.68	4.76	2.28E-05
160313_at	Ythdc1	YTH domain containing 1	185.46	474.75	-2.56	2.34E-05
98436_s_at	Casp3	caspase 3	120.50	417.27	-3.46	2.35E-05
98884_r_at	Ndel1	nuclear distribution gene E-like h	1641.34	418.74	3.92	2.37E-05
97250_at	Nola3	nucleolar protein family A, memb	686.84	2420.44	-3.52	2.37E-05
102715_at	LOC100046044 /// Nr	nuclear receptor subfamily 2, gro	101.35	354.22	-3.50	2.38E-05
162442_r_at	---	---	531.64	195.19	2.72	2.38E-05
98477_s_at	Ank3	ankyrin 3, epithelial	1404.69	479.39	2.93	2.39E-05
160123_at	Phpt1	phosphohistidine phosphatase 1	315.88	1545.59	-4.89	2.39E-05
92262_at	Zmat3	zinc finger matrin type 3	2208.92	695.39	3.18	2.39E-05
102376_r_at	Pcp2	Purkinje cell protein 2 (L7)	1001.30	4226.91	-4.22	2.39E-05
97333_at	Dync1h1	dynein cytoplasmic 1 heavy chair	11844.40	1082.70	10.94	2.40E-05
AFFX-b-ActinMur/	Actb	actin, beta, cytoplasmic	73.78	173.59	-2.35	2.41E-05
101518_at	Ift20	intraflagellar transport 20 homol	1229.88	89.11	13.80	2.41E-05
100155_at	Ddr1	discoidin domain receptor family	284.15	672.23	-2.37	2.41E-05
93716_at	Trim46	tripartite motif-containing 46	232.31	474.70	-2.04	2.43E-05
101959_r_at	Tfdp1	transcription factor Dp 1	174.32	849.54	-4.87	2.44E-05
99938_at	Xrcc1	X-ray repair complementing defe	162.33	402.36	-2.48	2.47E-05
99000_at	Mapk7	mitogen-activated protein kinase	539.44	1136.88	-2.11	2.47E-05
104077_at	Lage3	L antigen family, member 3	186.53	548.86	-2.94	2.47E-05
160758_at	Seh1l	SEH1-like (S. cerevisiae	886.88	422.00	2.10	2.48E-05
98516_at	BC056474	cDNA sequence BC056474	619.46	1427.64	-2.30	2.48E-05
96781_at	Rrn3	RRN3 RNA polymerase I transcrip	954.78	365.49	2.61	2.48E-05
93117_at	Hnrnpa2b1	heterogeneous nuclear ribonucle	1155.77	4170.98	-3.61	2.49E-05
99661_r_at	Cox7c /// LOC100048	cytochrome c oxidase, subunit VI	2370.19	9039.38	-3.81	2.51E-05
162486_f_at	Dscr3	Down syndrome critical region ge	2084.01	462.75	4.50	2.52E-05
93924_f_at	LOC384954 /// Tuba3	tubulin, alpha 3A /// tubulin, alpl	379.24	1108.01	-2.92	2.53E-05
93076_at	Csnk1a1	casein kinase 1, alpha 1	5553.47	1963.33	2.83	2.53E-05
93922_g_at	Bat3	HLA-B-associated transcript 3	505.17	1098.75	-2.18	2.56E-05
100984_at	Atf1 /// LOC1000474	activating transcription factor 1 /	163.11	492.63	-3.02	2.56E-05
160449_at	Dr1	down-regulator of transcription 1	159.00	717.50	-4.51	2.56E-05
98981_s_at	Tcf12	transcription factor 12	234.13	1564.59	-6.68	2.59E-05
95136_at	Arl6ip4 /// LOC10004	ADP-ribosylation factor-like 6 inte	1969.55	600.40	3.28	2.61E-05
102812_i_at	Uba5	ubiquitin-like modifier activating	1516.90	341.50	4.44	2.61E-05
103771_at	Rnf208	ring finger protein 208	7706.14	3170.33	2.43	2.61E-05
102109_at	EG668182 /// LOC10(	ribosomal protein L13 /// similar	2092.78	8849.62	-4.23	2.62E-05
103020_s_at	Map3k1	mitogen-activated protein kinase	202.42	1056.74	-5.22	2.62E-05
92341_at	B3galt2	UDP-Gal:betaGlcNAc beta 1,3-gal	123.96	295.79	-2.39	2.62E-05
97422_at	Iars2	isoleucine-tRNA synthetase 2, mi	1990.64	370.67	5.37	2.67E-05
104605_at	Adipor2	adiponectin receptor 2	2303.15	656.00	3.51	2.68E-05
92525_i_at	Btbd14a	BTB (POZ) domain containing 14A	6884.62	589.37	11.68	2.70E-05
92808_f_at	Fkbp4	FK506 binding protein 4	9391.89	3663.12	2.56	2.70E-05
94455_at	Lsm3	LSM3 homolog, U6 small nuclear	386.98	1142.34	-2.95	2.71E-05
AFFX-GapdhMur/I	Gapdh	glyceraldehyde-3-phosphate deh	1740.04	11269.83	-6.48	2.73E-05
92944_at	Gria1 /// LOC100044	glutamate receptor, ionotropic, A	196.33	542.42	-2.76	2.74E-05
98434_at	Arhgef7	Rho guanine nucleotide exchange	1253.27	2557.97	-2.04	2.74E-05
102070_at	Col9a3	collagen, type IX, alpha 3	386.48	1016.74	-2.63	2.74E-05
97923_at	Herc1	hect (homologous to the E6-AP (U	5598.36	857.59	6.53	2.75E-05
96337_at	Gp1bb /// Sept5	glycoprotein Ib, beta polypeptide	1270.65	446.38	2.85	2.75E-05
93596_i_at	Atp5e	ATP synthase, H+ transporting, m	157.03	911.21	-5.80	2.75E-05
95699_f_at	Dnajc8	DnaJ (Hsp40) homolog, subfamily	7834.05	3549.66	2.21	2.75E-05
93669_f_at	Sox11	SRY-box containing gene 11	43.80	361.78	-8.26	2.75E-05
160464_s_at	Ndrg1	N-myc downstream regulated ge	4302.77	519.68	8.28	2.78E-05
95694_at	Top1	topoisomerase (DNA) I	676.45	2353.38	-3.48	2.80E-05

93727_at	Gspt1	G1 to S phase transition 1	296.07	759.09	-2.56	2.81E-05
103600_at	Epb4.9	erythrocyte protein band 4.9	2965.48	1219.33	2.43	2.81E-05
93358_at	Eif1ay	eukaryotic translation initiation f	187.86	529.18	-2.82	2.83E-05
98912_at	Larp5	La ribonucleoprotein domain fam	2024.85	401.06	5.05	2.83E-05
93546_s_at	Cbfb	core binding factor beta	8477.95	1397.74	6.07	2.84E-05
98992_at	B9d1	B9 protein domain 1	182.96	391.68	-2.14	2.84E-05
103415_at	Wrnip1	Werner helicase interacting prote	1237.14	273.89	4.52	2.85E-05
96305_at	Bud31	BUD31 homolog (yeast)	67.75	210.62	-3.11	2.85E-05
99621_s_at	Sfpq	splicing factor proline/glutamine	40.96	272.21	-6.65	2.87E-05
96093_at	0610007P14Rik	RIKEN cDNA 0610007P14 gene	647.65	1331.41	-2.06	2.88E-05
96710_at	H2afv	H2A histone family, member V	758.41	2176.97	-2.87	2.89E-05
94263_f_at	Psmb7	proteasome (prosome, macropai	699.51	2533.64	-3.62	2.92E-05
96464_at	Plxnb2	plexin B2	270.60	602.54	-2.23	2.93E-05
93975_at	Errfi1	ERBB receptor feedback inhibitor	1515.70	518.73	2.92	2.95E-05
94253_at	Eif2s1	eukaryotic translation initiation f	141.41	693.83	-4.91	2.95E-05
160538_at	Cdk4 /// LOC640611	cyclin-dependent kinase 4 /// sim	1176.91	2942.66	-2.50	2.96E-05
102126_at	LOC671641 /// LOC67	ribosomal protein S12 /// similar	1900.32	7988.21	-4.20	2.97E-05
95666_at	Cops8	COP9 (constitutive photomorpho	5828.69	730.68	7.98	2.97E-05
96232_at	Cul2	cullin 2	2205.23	945.35	2.33	2.98E-05
92428_at	Asna1	arsA (bacterial) arsenite transpor	338.74	1229.01	-3.63	2.98E-05
96917_at	2410166I05Rik	RIKEN cDNA 2410166I05 gene	1789.94	633.96	2.82	3.01E-05
101579_at	Srp9	signal recognition particle 9	4751.87	1379.40	3.44	3.02E-05
162262_f_at	Gyg	glycogenin	1434.12	178.57	8.03	3.02E-05
92227_s_at	Ctnna2	catenin (cadherin associated prot	794.26	86.38	9.20	3.03E-05
97512_at	2010107E04Rik	RIKEN cDNA 2010107E04 gene	1196.41	4405.88	-3.68	3.03E-05
103046_at	Car4	carbonic anhydrase 4	123.93	340.88	-2.75	3.10E-05
96318_at	D17Wsu104e	DNA segment, Chr 17, Wayne Sta	319.30	737.98	-2.31	3.11E-05
96158_at	Paip2b	poly(A) binding protein interactin	5371.65	946.94	5.67	3.12E-05
92477_at	LOC100046080 /// Sp	spindlin 1 /// similar to Spindlin 1	257.61	762.07	-2.96	3.12E-05
93212_at	Ptplad1	protein tyrosine phosphatase-like	65.42	166.06	-2.54	3.13E-05
103855_at	Plec1	plectin 1	2134.47	781.85	2.73	3.16E-05
93634_at	Fbxw11	F-box and WD-40 domain protein	212.03	506.65	-2.39	3.16E-05
160979_at	Ctbp2	C-terminal binding protein 2	34.85	651.22	-18.69	3.17E-05
95541_at	D6Wsu176e	DNA segment, Chr 6, Wayne Stat	1277.23	538.14	2.37	3.18E-05
161847_r_at	2210016L21Rik	RIKEN cDNA 2210016L21 gene	452.01	957.21	-2.12	3.19E-05
102743_at	Mapt	microtubule-associated protein t	5037.78	1911.34	2.64	3.21E-05
98087_at	Tbk1	TANK-binding kinase 1	1112.04	297.69	3.74	3.29E-05
93999_at	EG666609 /// Snrpg	small nuclear ribonucleoprotein p	309.09	1319.03	-4.27	3.37E-05
93019_at	H2afx	H2A histone family, member X	430.68	1526.49	-3.54	3.37E-05
160963_at	9630050M13Rik	RIKEN cDNA 9630050M13 gene	3830.74	781.95	4.90	3.37E-05
99087_at	Zwint	ZW10 interactor	14662.02	5832.82	2.51	3.38E-05
96302_at	Sfrs7	splicing factor, arginine/serine-ric	77.14	230.43	-2.99	3.38E-05
101484_at	Nbr1	neighbor of Brca1 gene 1	4014.71	1517.85	2.64	3.38E-05
161337_f_at	LOC100046672 /// W	tryptophanyl-tRNA synthetase //,	1182.15	447.76	2.64	3.39E-05
160529_r_at	Vdac2	voltage-dependent anion channe	2992.59	1301.84	2.30	3.41E-05
98483_at	Cacnb3	calcium channel, voltage-depend	2343.37	639.73	3.66	3.42E-05
AFFX-b-ActinMur/	Actb	actin, beta, cytoplasmic	925.06	9182.70	-9.93	3.42E-05
93651_r_at	Prp2	proline rich protein 2	793.34	1705.49	-2.15	3.46E-05
101137_at	Rps3	ribosomal protein S3	3236.87	8323.31	-2.57	3.46E-05
104280_at	Sncg	synuclein, gamma	3249.97	168.82	19.25	3.47E-05
92625_at	Dscaml1 /// LOC6656	non-metastatic cells 2, protein (N	841.44	2685.37	-3.19	3.54E-05
92200_at	Adcyap1	adenylate cyclase activating poly	8493.56	168.32	50.46	3.55E-05
98629_f_at	Hif1a	hypoxia inducible factor 1, alpha	1072.43	3764.93	-3.51	3.55E-05
99128_at	Atp5o /// EG432676	ATP synthase, H+ transporting, m	2016.90	6903.42	-3.42	3.56E-05
94979_at	BC018507	cDNA sequence BC018507	2722.87	689.66	3.95	3.58E-05

99596_f_at	Gnai2	guanine nucleotide binding prote	18748.52	8265.54	2.27	3.58E-05
96084_at	Hnrpdl	heterogeneous nuclear ribonucle	251.86	1099.95	-4.37	3.60E-05
95440_at	2810432L12Rik	RIKEN cDNA 2810432L12 gene	3359.51	810.22	4.15	3.61E-05
97874_at	1500032D16Rik	RIKEN cDNA 1500032D16 gene	164.70	950.17	-5.77	3.63E-05
160326_at	Cdv3	carnitine deficiency-associated ge	1283.09	374.80	3.42	3.64E-05
162118_f_at	Btbd14a	BTB (POZ) domain containing 14A	529.18	239.16	2.21	3.65E-05
100982_at	Kctd9	potassium channel tetramerisatic	1221.44	151.09	8.08	3.65E-05
104095_at	AU040320	expressed sequence AU040320	3073.12	1457.14	2.11	3.65E-05
100213_f_at	Rpl41	ribosomal protein L41	9412.53	30930.51	-3.29	3.65E-05
160371_at	Arl6ip1	ADP-ribosylation factor-like 6 int	7873.81	2683.75	2.93	3.66E-05
160866_at	Dffa	DNA fragmentation factor, alpha	3074.06	700.72	4.39	3.66E-05
95715_at	Eif3k	eukaryotic translation initiation f	993.82	2720.36	-2.74	3.67E-05
160472_r_at	LOC100045217 /// Tr	transmembrane protein with EGF	24.27	74.30	-3.06	3.67E-05
100895_at	Lsg1	large subunit GTPase 1 homolog	258.18	108.28	2.38	3.69E-05
96185_at	Ap3d1	adaptor-related protein complex	6574.12	1840.82	3.57	3.70E-05
102878_at	Rad52	RAD52 homolog (S. cerevisiae)	129.81	274.82	-2.12	3.70E-05
96025_g_at	Ahcy	S-adenosylhomocysteine hydrola	5814.91	1489.34	3.90	3.71E-05
94019_at	Bzw1 /// LOC382722	basic leucine zipper and W2 dom	213.08	962.00	-4.51	3.75E-05
94972_at	Rbms1	RNA binding motif, single strande	3309.13	862.37	3.84	3.75E-05
104609_at	Hnrpul2	heterogeneous nuclear ribonucle	188.86	507.49	-2.69	3.76E-05
97897_at	C78339	expressed sequence C78339	2325.72	650.27	3.58	3.77E-05
104033_at	Ctage5	CTAGE family, member 5	2968.15	676.04	4.39	3.77E-05
99581_at	Hint1	histidine triad nucleotide binding	735.75	5382.89	-7.32	3.78E-05
94303_at	Hnrnpd	heterogeneous nuclear ribonucle	367.70	2313.50	-6.29	3.78E-05
101588_at	Slc16a1	solute carrier family 16 (monocar	46.77	126.89	-2.71	3.79E-05
93030_at	EG619900 /// Gm182	ubiquitin B /// ubiquitin C /// ribo	292.96	1908.52	-6.51	3.86E-05
96849_at	LOC100039343 /// LC	translocase of inner mitochondria	769.29	197.52	3.89	3.87E-05
98133_at	Calb1	calbindin-28K	261.81	3453.14	-13.19	3.88E-05
93057_at	Btf3	basic transcription factor 3	218.67	3394.48	-15.52	3.88E-05
93560_at	Acyp1	acylphosphatase 1, erythrocyte (	416.82	1993.80	-4.78	3.89E-05
102028_at	Rassf5	Ras association (RalGDS/AF-6) do	4070.35	178.14	22.85	3.89E-05
95929_at	Nhlh1	nescient helix loop helix 1	232.98	478.49	-2.05	3.89E-05
96285_at	Myadm	myeloid-associated differentiatio	5477.99	2024.44	2.71	3.89E-05
92223_at	C1qc	complement component 1, q sub	414.88	1099.07	-2.65	3.90E-05
96611_at	Ndufa11	NADH dehydrogenase (ubiquinor	167.97	1423.85	-8.48	3.90E-05
94854_g_at	Gnb1	guanine nucleotide binding prote	282.33	1779.85	-6.30	3.90E-05
98111_at	Hsph1	heat shock 105kDa/110kDa prote	5268.06	1500.53	3.51	3.90E-05
101684_r_at	Srst	simple repeat sequence-containi	1548.40	714.05	2.17	3.90E-05
99651_at	2610209M04Rik	RIKEN cDNA 2610209M04 gene	263.48	763.44	-2.90	3.90E-05
97273_at	Ars2	arsenate resistance protein 2	2123.42	898.41	2.36	3.90E-05
94896_at	Hnrpab	heterogeneous nuclear ribonucle	498.84	1075.67	-2.16	3.92E-05
96187_at	Pkp4	plakophilin 4	374.46	1836.37	-4.90	3.92E-05
96765_at	---	Transcribed locus	8102.42	1457.71	5.56	3.93E-05
102862_at	5830404H04Rik	RIKEN cDNA 5830404H04 gene	899.47	442.76	2.03	3.98E-05
102364_at	Jund	Jun proto-oncogene related gene	4372.26	13391.01	-3.06	3.98E-05
96041_at	Rbm3	RNA binding motif protein 3	813.47	3216.83	-3.95	3.99E-05
96176_at	Arih2	ariadne homolog 2 (Drosophila)	997.78	463.71	2.15	3.99E-05
160809_at	Tollip	toll interacting protein	2683.56	823.79	3.26	3.99E-05
93604_f_at	Cadm1	cell adhesion molecule 1	14672.34	2887.08	5.08	3.99E-05
94348_f_at	Pcmt1	protein-L-isoaspartate (D-asparta	7664.66	1080.05	7.10	4.00E-05
100307_at	Nfix	nuclear factor I/X	97.99	265.80	-2.71	4.01E-05
101013_at	LOC100041965 /// O	ornithine decarboxylase antizyme	2587.60	7946.32	-3.07	4.02E-05
96060_at	Serpinb6a	serine (or cysteine) peptidase inh	7275.17	291.48	24.96	4.03E-05
160270_at	Lman1	lectin, mannose-binding, 1	1080.70	342.92	3.15	4.07E-05
161077_f_at	Smarcd2	SWI/SNF related, matrix associat	6360.40	1218.20	5.22	4.07E-05

93389_at	Prom1	prominin 1	130.87	363.73	-2.78	4.07E-05
96524_at	Cdr2l	cerebellar degeneration-related p	3184.81	990.85	3.21	4.08E-05
96658_at	2900010J23Rik	RIKEN cDNA 2900010J23 gene	211.73	828.02	-3.91	4.13E-05
98628_f_at	Hif1a	hypoxia inducible factor 1, alpha	1475.38	3768.13	-2.55	4.14E-05
162284_r_at	Slc39a4	solute carrier family 39 (zinc tran	1557.34	3224.57	-2.07	4.14E-05
99127_at	Atxn10	ataxin 10	585.27	3443.58	-5.88	4.22E-05
161050_at	Nav2	neuron navigator 2	1584.74	3835.80	-2.42	4.23E-05
101042_f_at	Pepd	peptidase D	2151.10	326.36	6.59	4.24E-05
94040_at	Erh /// LOC10004277	enhancer of rudimentary homolc	68.93	1673.88	-24.28	4.25E-05
98330_at	Zic3	zinc finger protein of the cerebell	79.08	209.02	-2.64	4.26E-05
99559_at	Aldh3a2	aldehyde dehydrogenase family 3	947.96	292.27	3.24	4.26E-05
98540_g_at	Cops2	COP9 (constitutive photomorpho	90.77	189.50	-2.09	4.29E-05
96717_at	Ddx47	DEAD (Asp-Glu-Ala-Asp) box poly	2373.74	698.33	3.40	4.30E-05
98950_at	Rragc	Ras-related GTP binding C	3409.13	1330.92	2.56	4.32E-05
96061_at	Usp14	ubiquitin specific peptidase 14	1530.72	421.04	3.64	4.34E-05
102727_at	Bdnf	brain derived neurotrophic factor	1341.02	116.86	11.48	4.34E-05
96249_at	15-Sep	selenoprotein	114.10	2297.01	-20.13	4.36E-05
94466_f_at	Cebpz	CCAAT/enhancer binding protein	1337.23	544.96	2.45	4.41E-05
104408_s_at	Sox18	SRY-box containing gene 18	82.21	228.02	-2.77	4.42E-05
104082_at	Rab12	RAB12, member RAS oncogene fa	524.11	1250.59	-2.39	4.46E-05
99115_at	Uqcrh	ubiquinol-cytochrome c reductas	322.63	2427.71	-7.52	4.47E-05
93581_at	Ndufb8	NADH dehydrogenase (ubiquinor	354.40	3446.81	-9.73	4.52E-05
94225_at	Atg5	autophagy-related 5 (yeast)	605.38	247.87	2.44	4.52E-05
98965_at	Mboat5	membrane bound O-acyltransfer	866.61	317.69	2.73	4.52E-05
101957_f_at	Parp1	poly (ADP-ribose) polymerase far	1588.05	622.22	2.55	4.52E-05
98882_s_at	Ndel1	nuclear distribution gene E-like h	3378.52	1320.21	2.56	4.52E-05
97647_at	LOC100039355 /// LC	ribosomal protein S16 /// similar	485.09	9190.93	-18.95	4.53E-05
96832_at	LOC635418 /// Slc39a	solute carrier family 39 (zinc tran	244.08	653.89	-2.68	4.53E-05
96340_at	Tmem50b	transmembrane protein 50B	5658.29	1158.88	4.88	4.54E-05
93550_at	Csrp2	cysteine and glycine-rich protein	127.11	492.00	-3.87	4.57E-05
97164_at	Rnaseh2b	ribonuclease H2, subunit B	69.19	261.82	-3.78	4.60E-05
94912_at	Mrps21	mitochondrial ribosomal protein	172.49	1149.41	-6.66	4.62E-05
103234_at	Nefh	neurofilament, heavy polypeptid	8786.34	1106.50	7.94	4.62E-05
94209_g_at	LOC100046302 /// Pc	protein disulfide isomerase assoc	65.24	277.69	-4.26	4.63E-05
99149_at	LOC630539 /// Trim5	tripartite motif-containing 59 ///	61.67	184.52	-2.99	4.63E-05
102691_at	Zfp385a	zinc finger protein 385A	527.14	1161.54	-2.20	4.63E-05
160460_at	Clpb	ClpB caseinolytic peptidase B hor	904.54	358.15	2.53	4.67E-05
93013_at	Id2	inhibitor of DNA binding 2	460.39	3236.45	-7.03	4.67E-05
96876_at	Laptm4a	lysosomal-associated protein trar	2458.22	6067.05	-2.47	4.68E-05
94322_at	Sqle	squalene epoxidase	5175.58	2057.75	2.52	4.68E-05
99179_at	Cuedc2	CUE domain containing 2	2706.58	994.17	2.72	4.73E-05
103906_f_at	Nedd4l	neural precursor cell expressed, d	2298.42	742.25	3.10	4.74E-05
102046_at	Fusip1	FUS interacting protein (serine-ar	167.99	434.51	-2.59	4.74E-05
100046_at	Mthfd2	methylenetetrahydrofolate dehy	4001.94	798.69	5.01	4.75E-05
93319_at	Rasa3	RAS p21 protein activator 3	291.36	1152.39	-3.96	4.76E-05
162237_f_at	Scg3	Secretogranin III	2400.30	1104.65	2.17	4.76E-05
98958_at	Eny2	enhancer of yellow 2 homolog (D	76.51	255.31	-3.34	4.81E-05
93990_at	Hnrph1	heterogeneous nuclear ribonucle	830.45	2371.29	-2.86	4.82E-05
94077_f_at	Rpn2	ribophorin II	4670.98	1696.35	2.75	4.83E-05
94014_at	Pomp	proteasome maturation protein	269.60	659.50	-2.45	4.84E-05
96294_s_at	2410015N17Rik	RIKEN cDNA 2410015N17 gene	271.34	574.23	-2.12	4.84E-05
102827_at	Nek7	NIMA (never in mitosis gene a)-re	6119.68	537.74	11.38	4.85E-05
92361_at	Elavl4	ELAV (embryonic lethal, abnorma	1230.77	561.16	2.19	4.88E-05
95490_at	Kdelr1	KDEL (Lys-Asp-Glu-Leu) endoplas	7814.40	2768.61	2.82	4.92E-05
93102_f_at	Actg2	actin, gamma 2, smooth muscle,	391.72	869.34	-2.22	4.93E-05

93325_at	Polr2e	polymerase (RNA) II (DNA directe	52.68	367.69	-6.98	4.93E-05
94813_at	Gas1	growth arrest specific 1	283.99	1068.08	-3.76	4.94E-05
101995_at	Sqstm1	sequestosome 1	9090.17	1599.35	5.68	4.96E-05
99320_at	St8sia5	ST8 alpha-N-acetyl-neuraminide	448.46	991.83	-2.21	4.97E-05
104682_at	Tuba8	tubulin, alpha 8	723.20	1462.19	-2.02	4.98E-05
98953_at	Eif1b	eukaryotic translation initiation f	7026.03	2154.99	3.26	4.99E-05
99590_at	LOC100040123 /// Rp	ribosomal protein S17 /// similar	1323.38	3152.66	-2.38	4.99E-05
103922_f_at	Cyb5r1	cytochrome b5 reductase 1	5305.88	139.58	38.01	4.99E-05
101976_at	Cops4	COP9 (constitutive photomorpho	2930.14	1230.98	2.38	4.99E-05
92782_at	Tmpo	thymopoietin	398.70	987.09	-2.48	4.99E-05
103959_at	Phf13	PHD finger protein 13	639.88	152.69	4.19	4.99E-05
97818_at	Snx4	sorting nexin 4	3376.47	818.11	4.13	5.00E-05
103061_at	Gad1	glutamic acid decarboxylase 1	73.62	2570.87	-34.92	5.01E-05
97917_at	Bloc1s1	biogenesis of lysosome-related o	297.61	801.67	-2.69	5.01E-05
103733_at	2900006A08Rik /// T	RIKEN cDNA 2900006A08 gene //	154.29	314.82	-2.04	5.03E-05
96852_at	Prkar1a	protein kinase, cAMP dependent	8258.64	3251.31	2.54	5.03E-05
96098_at	Mrpl36	mitochondrial ribosomal protein	348.88	135.04	2.58	5.06E-05
98099_at	Nudt9	nudix (nucleoside diphosphate lir	2024.71	234.49	8.63	5.09E-05
98841_at	Acvr2a	activin receptor IIA	252.49	104.09	2.43	5.13E-05
97458_at	Gnb1	guanine nucleotide binding prote	11380.82	4530.61	2.51	5.26E-05
92577_f_at	Rpl37	ribosomal protein L37	2039.85	6825.88	-3.35	5.27E-05
96156_at	Snhg6	small nucleolar RNA host gene (n	56.41	119.65	-2.12	5.27E-05
161354_f_at	6330403K07Rik	RIKEN cDNA 6330403K07 gene	1228.52	201.75	6.09	5.27E-05
93962_at	Rap1a	RAS-related protein-1a	1337.22	327.40	4.08	5.27E-05
97462_at	Zfp706	zinc finger protein 706	215.02	934.53	-4.35	5.28E-05
160409_at	Pitpna	phosphatidylinositol transfer pro	1527.34	715.47	2.13	5.28E-05
160324_at	Rpa3	replication protein A3	81.15	191.58	-2.36	5.29E-05
95050_at	Chordc1	cysteine and histidine-rich domai	397.70	889.36	-2.24	5.33E-05
162269_at	Smyd2	SET and MYND domain containin	676.57	148.64	4.55	5.35E-05
97118_at	A630007B06Rik	RIKEN cDNA A630007B06 gene	1491.36	581.75	2.56	5.36E-05
92847_s_at	M6pr /// M6pr-ps	mannose-6-phosphate receptor,	748.14	227.19	3.29	5.38E-05
103654_at	Nsbp1	nucleosome binding protein 1	445.83	934.23	-2.10	5.42E-05
100915_at	Myh9	myosin, heavy polypeptide 9, nor	5928.51	900.22	6.59	5.43E-05
96293_at	2410015N17Rik	RIKEN cDNA 2410015N17 gene	445.34	965.40	-2.17	5.51E-05
160961_at	Sipa1l2	signal-induced proliferation-asso	455.43	985.23	-2.16	5.54E-05
97468_at	Cks1b	CDC28 protein kinase 1b	136.98	496.84	-3.63	5.57E-05
95034_f_at	Ipo4	importin 4	1901.81	314.95	6.04	5.57E-05
100894_at	Orc5l	origin recognition complex, subu	701.90	229.97	3.05	5.59E-05
103674_f_at	Eif2s3y	eukaryotic translation initiation f	38.17	166.09	-4.35	5.59E-05
97770_s_at	D6Wsu176e	DNA segment, Chr 6, Wayne Stat	4076.72	882.53	4.62	5.60E-05
98623_g_at	Igf2	insulin-like growth factor 2	1259.30	6859.62	-5.45	5.61E-05
102850_at	Tnk2	tyrosine kinase, non-receptor, 2	1508.12	462.21	3.26	5.61E-05
160696_at	Tia1	cytotoxic granule-associated RNA	175.20	415.97	-2.37	5.61E-05
104751_at	Prph	peripherin	3347.92	59.34	56.42	5.67E-05
161596_f_at	Akap8	A kinase (PRKA) anchor protein 8	220.56	470.70	-2.13	5.67E-05
AFFX-PyruCarbMu	Pcx	pyruvate carboxylase	205.04	463.60	-2.26	5.69E-05
160530_at	Ghitm	growth hormone inducible transr	2165.28	610.34	3.55	5.75E-05
94206_at	Grcc10	gene rich cluster, C10 gene	1077.46	4614.71	-4.28	5.76E-05
102128_f_at	Mrps25	mitochondrial ribosomal protein	2207.38	475.21	4.65	5.76E-05
98029_at	3110056O03Rik	RIKEN cDNA 3110056O03 gene	318.19	639.36	-2.01	5.83E-05
98464_at	Ankrd40	ankyrin repeat domain 40	1827.93	504.97	3.62	5.84E-05
93569_f_at	2610042L04Rik /// B9	RIKEN cDNA B930046C15 gene //	82.09	917.42	-11.18	5.84E-05
104453_at	LOC100044471 /// Sa	SAP30-like /// similar to SAP30-lil	1850.30	295.10	6.27	5.84E-05
95025_at	D16H22S680E	DNA segment, Chr 16, human D2	2542.00	434.88	5.85	5.84E-05
103930_at	N4bp1	NEDD4 binding protein 1	771.86	317.28	2.43	5.84E-05

104315_at	Arhgap1	Rho GTPase activating protein 1	968.50	207.15	4.68	5.84E-05
103793_at	Mvp	major vault protein	978.74	315.51	3.10	5.85E-05
99024_at	Mxd4	Max dimerization protein 4	533.30	1843.41	-3.46	5.85E-05
96840_at	Gabarapl2	gamma-aminobutyric acid (GABA	1620.59	4158.23	-2.57	5.86E-05
95095_at	Flot1	flotillin 1	8133.08	1507.05	5.40	5.86E-05
100878_at	LOC100047794	similar to SG2NA beta	121.95	693.59	-5.69	5.86E-05
95522_i_at	Zfp68	zinc finger protein 68	153.56	560.19	-3.65	5.87E-05
93648_at	Prkcc	protein kinase C, gamma	328.33	791.15	-2.41	5.87E-05
161444_f_at	Ints5	integrator complex subunit 5	1428.78	466.92	3.06	5.91E-05
98876_at	Mrpl11	mitochondrial ribosomal protein	172.29	558.53	-3.24	5.91E-05
93014_at	Atp5l /// LOC100040	ATP synthase, H+ transporting, m	398.92	6745.45	-16.91	5.91E-05
93360_at	Pmm1	phosphomannomutase 1	2208.80	575.06	3.84	5.92E-05
102677_at	Arhgdig	Rho GDP dissociation inhibitor (G	568.01	115.07	4.94	5.92E-05
100729_at	LOC100034726	ribosomal protein L26 pseudoger	2218.36	5928.59	-2.67	5.97E-05
102382_at	Arntl	aryl hydrocarbon receptor nuclea	131.33	390.98	-2.98	5.97E-05
101973_at	Cited2	Cbp/p300-interacting transactiva	361.42	1512.19	-4.18	5.98E-05
102933_at	Plxna3	plexin A3	426.09	872.18	-2.05	5.98E-05
94242_at	Txndc17	thioredoxin domain containing 1	948.32	458.86	2.07	6.00E-05
98602_at	Rangap1	RAN GTPase activating protein 1	8931.23	988.35	9.04	6.01E-05
94875_at	Mrpl20	mitochondrial ribosomal protein	195.21	490.06	-2.51	6.01E-05
101525_at	Ndufb10	NADH dehydrogenase (ubiquinor	385.42	1603.81	-4.16	6.03E-05
94259_at	LOC100043508 /// LC	prostaglandin E synthase 3 (cytos	4656.52	1191.14	3.91	6.05E-05
100446_r_at	Sprr1b	small proline-rich protein 1B	4056.04	8637.63	-2.13	6.08E-05
94882_at	Tmem30a	transmembrane protein 30A	3881.79	995.85	3.90	6.08E-05
93320_at	Cpt1a	carnitine palmitoyltransferase 1a	2807.22	690.41	4.07	6.09E-05
102103_f_at	Glrx3	glutaredoxin 3	8787.51	3481.05	2.52	6.14E-05
160857_at	Efnb2	ephrin B2	176.33	640.82	-3.63	6.14E-05
103220_at	Ndnl2	necdin-like 2	528.27	197.81	2.67	6.14E-05
98915_at	Rnf149	ring finger protein 149	472.80	234.25	2.02	6.15E-05
101420_at	Slc32a1	solute carrier family 32 (GABA ve	86.38	1184.14	-13.71	6.15E-05
95614_at	Cbx5	chromobox homolog 5 (Drosophi	153.72	408.21	-2.66	6.15E-05
93799_at	Tmem199	transmembrane protein 199	1265.27	465.31	2.72	6.16E-05
98015_at	Scamp3	secretory carrier membrane prot	2455.48	903.64	2.72	6.17E-05
160757_at	Rnf38	ring finger protein 38	1793.61	844.08	2.12	6.19E-05
100951_at	Pkd2	polycystic kidney disease 2	69.62	185.58	-2.67	6.19E-05
101509_at	Vbp1	von Hippel-Lindau binding protei	417.36	2864.46	-6.86	6.19E-05
92798_at	Atp5c1	ATP synthase, H+ transporting, m	1487.30	3493.14	-2.35	6.20E-05
94831_at	Ctsb	cathepsin B	6093.30	2180.26	2.79	6.20E-05
160289_s_at	Dlst	dihydrolipoamide S-succinyltrans	148.53	403.59	-2.72	6.20E-05
102105_f_at	Ptgds	prostaglandin D2 synthase (brain	1312.35	8755.12	-6.67	6.20E-05
93255_at	Ralbp1	ralA binding protein 1	3269.07	1103.41	2.96	6.20E-05
103438_at	Dio2	deiodinase, iodothyronine, type I	125.83	313.90	-2.49	6.20E-05
93252_at	Bcap31	B-cell receptor-associated protei	3989.88	1525.69	2.62	6.20E-05
161965_r_at	Smarcd2	SWI/SNF related, matrix associat	671.22	1534.87	-2.29	6.21E-05
95142_s_at	Capzb	capping protein (actin filament) r	5580.78	1757.26	3.18	6.30E-05
93773_f_at	Zranb2	zinc finger, RAN-binding domain	3646.06	1642.48	2.22	6.35E-05
162481_f_at	Arrb1	arrestin, beta 1	3981.74	866.56	4.59	6.35E-05
95436_at	Sst	somatostatin	239.71	552.30	-2.30	6.38E-05
161054_at	Spock1	sparc/osteonectin, cwcv and kaza	276.53	592.18	-2.14	6.39E-05
160395_at	Nudcd2	NudC domain containing 2	132.16	475.66	-3.60	6.44E-05
97385_at	Nagk	N-acetylglucosamine kinase	1349.28	465.87	2.90	6.48E-05
94256_at	Clic4	chloride intracellular channel 4 (r	511.49	2051.54	-4.01	6.49E-05
95456_r_at	Shfm1	split hand/foot malformation (ec	449.37	1215.40	-2.70	6.50E-05
96664_at	Huwe1	HECT, UBA and WWE domain cor	2136.90	501.21	4.26	6.50E-05
92893_at	Nfia	nuclear factor I/A	155.80	569.39	-3.65	6.56E-05

103010_at	6820431F20Rik	RIKEN cDNA 6820431F20 gene	1674.96	387.56	4.32	6.59E-05
92623_at	Csde1	cold shock domain containing E1,	10340.14	4324.73	2.39	6.59E-05
100899_s_at	Zbtb22	zinc finger and BTB domain conta	1790.86	790.79	2.26	6.60E-05
93104_at	Btg1 /// LOC1000473	B-cell translocation gene 1, anti-p	287.35	1228.74	-4.28	6.60E-05
160450_at	Maea	macrophage erythroblast attache	4865.08	1466.17	3.32	6.60E-05
97463_g_at	Zfp706	zinc finger protein 706	987.91	2563.55	-2.59	6.65E-05
98946_at	Wsb1	WD repeat and SOCS box-contair	81.57	293.70	-3.60	6.65E-05
98446_s_at	Cct3	chaperonin subunit 3 (gamma)	210.93	1261.33	-5.98	6.67E-05
104209_at	Cyhr1	cysteine and histidine rich 1	985.84	371.93	2.65	6.67E-05
103251_at	Cdadc1	cytidine and dCMP deaminase dc	822.64	198.85	4.14	6.72E-05
161997_f_at	---	---	572.52	66.11	8.66	6.72E-05
161524_r_at	Gpi1	glucose phosphate isomerase 1	201.52	423.90	-2.10	6.72E-05
99668_at	Bin1	bridging integrator 1	8456.11	2228.29	3.79	6.73E-05
160448_at	Pdcd2l	programmed cell death 2-like	603.93	1408.65	-2.33	6.73E-05
93724_at	Ror2	receptor tyrosine kinase-like orpl	472.03	91.67	5.15	6.73E-05
98104_at	Atp6v0b	ATPase, H+ transporting, lysosom	290.84	2851.43	-9.80	6.73E-05
92636_f_at	LOC100042561 /// LC	SEC61, gamma subunit /// similar	115.84	1554.61	-13.42	6.75E-05
96359_at	Hdlbp	high density lipoprotein (HDL) bir	4432.60	1728.54	2.56	6.81E-05
94296_s_at	Gtf2i	general transcription factor II I	308.55	910.65	-2.95	6.82E-05
93711_at	Sec23a	SEC23A (S. cerevisiae)	96.49	288.67	-2.99	6.88E-05
95040_at	Pdcd6ip	programmed cell death 6 interac	660.16	160.02	4.13	6.90E-05
104738_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily	2050.22	513.69	3.99	6.99E-05
104059_at	Chd8	chromodomain helicase DNA bin	1468.75	269.80	5.44	6.99E-05
104275_g_at	Trp53	transformation related protein 53	256.85	514.35	-2.00	7.04E-05
161980_f_at	Bag3	Bcl2-associated athanogene 3	5657.45	40.09	141.12	7.06E-05
93021_at	Bex4 /// LOC1000432	brain expressed gene 4 /// simila	590.53	2170.10	-3.67	7.06E-05
101017_at	Cdk4	cyclin-dependent kinase 4	86.28	312.40	-3.62	7.10E-05
103430_at	Dbn1	drebrin 1	1120.81	183.31	6.11	7.11E-05
98037_at	Hbxip	hepatitis B virus x interacting pro	219.67	744.49	-3.39	7.17E-05
100472_at	Enah	enabled homolog (Drosophila)	2163.23	338.69	6.39	7.22E-05
99599_s_at	Ptov1	prostate tumor over expressed g	9945.93	2119.86	4.69	7.22E-05
94908_r_at	1110001J03Rik	RIKEN cDNA 1110001J03 gene	340.53	1850.81	-5.44	7.23E-05
93011_at	Gabarapl1	gamma-aminobutyric acid (GABA	8566.36	1914.43	4.47	7.23E-05
100758_at	LOC100040426 /// LC	ribosomal protein S28 /// similar	508.04	9455.29	-18.61	7.24E-05
96298_f_at	Dynll1	dynein light chain LC8-type 1	3410.56	7891.36	-2.31	7.24E-05
96113_at	Txnl4a	thioredoxin-like 4A	4886.63	1470.54	3.32	7.31E-05
96767_at	Mbc2	membrane bound C2 domain cor	3571.34	677.84	5.27	7.35E-05
160630_at	LOC671878 /// Sms	spermine synthase /// similar to s	1421.58	412.89	3.44	7.36E-05
161109_at	1810013L24Rik	RIKEN cDNA 1810013L24 gene	491.68	174.44	2.82	7.38E-05
96306_at	Polr2i	polymerase (RNA) II (DNA directe	246.72	637.48	-2.58	7.39E-05
100948_at	Ank	progressive ankylosis	2473.96	951.91	2.60	7.41E-05
161698_f_at	Mtap7d1	microtubule-associated protein 7	5669.14	2080.26	2.73	7.42E-05
102936_at	B4galt6 /// LOC6757(	UDP-Gal:betaGlcNAc beta 1,4-gal	1628.06	385.59	4.22	7.42E-05
92802_s_at	Plp1	proteolipid protein (myelin) 1	778.05	8659.60	-11.13	7.42E-05
103956_at	Azi1	5-azacytidine induced gene 1	928.20	398.80	2.33	7.42E-05
160531_at	Emg1	EMG1 nucleolar protein homolog	193.69	706.80	-3.65	7.53E-05
101367_at	Dctn1	dynactin 1	766.40	1547.76	-2.02	7.56E-05
95657_f_at	D13Wsu177e	DNA segment, Chr 13, Wayne Sta	2798.46	702.95	3.98	7.56E-05
94109_at	Zfp281	zinc finger protein 281	253.73	853.57	-3.36	7.59E-05
100979_at	Rnf138	ring finger protein 138	53.16	392.49	-7.38	7.60E-05
96885_at	Nt5dc2	5'-nucleotidase domain containir	211.41	1686.83	-7.98	7.67E-05
160394_at	Ttc15	tetratricopeptide repeat domain	1352.09	254.52	5.31	7.69E-05
102402_at	Gbas	glioblastoma amplified sequence	4093.78	1967.98	2.08	7.69E-05
104713_at	Prpf38a	PRP38 pre-mRNA processing fact	274.09	585.97	-2.14	7.69E-05
161808_f_at	Evl /// LOC10004733	Ena-vasodilator stimulated phosp	1759.69	531.77	3.31	7.69E-05

97058_f_at	Rab33b	RAB33B, member of RAS oncoge	2894.98	812.94	3.56	7.70E-05
100910_at	Surf2	surfeit gene 2	2449.60	1219.55	2.01	7.70E-05
100130_at	Jun	Jun oncogene	1816.15	562.66	3.23	7.72E-05
160973_at	C330027C09Rik	RIKEN cDNA C330027C09 gene	33.43	112.38	-3.36	7.76E-05
AFFX-b-ActinMur/	Actb	actin, beta, cytoplasmic	419.25	10772.16	-25.69	7.77E-05
96329_at	Puf60	poly-U binding splicing factor 60	343.27	1016.61	-2.96	7.83E-05
96746_at	Dlat	dihydrolipoamide S-acetyltransfe	755.40	321.48	2.35	7.84E-05
162260_at	6330407G11Rik	RIKEN cDNA 6330407G11 gene	714.86	308.51	2.32	7.93E-05
93092_at	H2-DMa	histocompatibility 2, class II, locu	1447.64	694.72	2.08	7.97E-05
104735_at	Kctd12	potassium channel tetramerisatic	41.58	1376.92	-33.11	7.99E-05
104474_s_at	Oprl1	opioid receptor-like 1	192.28	391.31	-2.04	7.99E-05
100124_r_at	Itgb1	integrin beta 1 (fibronectin recep	2311.68	937.34	2.47	8.00E-05
100547_at	Rbm4b	RNA binding motif protein 4B	504.90	1037.87	-2.06	8.10E-05
160170_at	Stmn3	stathmin-like 3	3830.24	1910.16	2.01	8.10E-05
95049_at	Snrpd2	small nuclear ribonucleoprotein I	446.44	3435.34	-7.70	8.10E-05
162457_f_at	Hba-a1 /// Hba-a2	hemoglobin alpha, adult chain 1 /	925.61	5141.77	-5.56	8.15E-05
94805_f_at	Hist1h2ab /// Hist1h2	tripartite motif-containing 17 ///	544.33	7043.65	-12.94	8.19E-05
161891_r_at	---	---	100.33	219.99	-2.19	8.21E-05
95571_at	Slc30a4	solute carrier family 30 (zinc tran	183.32	495.74	-2.70	8.21E-05
96682_at	St6galnac4	ST6 (alpha-N-acetyl-neuraminyl-2	579.47	1267.62	-2.19	8.24E-05
100465_i_at	Gm1673	gene model 1673, (NCBI)	1240.62	3999.56	-3.22	8.24E-05
104122_at	D330001F17Rik	RIKEN cDNA D330001F17 gene	1884.31	838.96	2.25	8.24E-05
101971_at	Rnf181	ring finger protein 181	3425.78	1225.25	2.80	8.25E-05
160240_at	1110003E01Rik	RIKEN cDNA 1110003E01 gene	3985.89	865.61	4.60	8.25E-05
93277_at	Hspd1	heat shock protein 1 (chaperonin	6689.37	2391.53	2.80	8.25E-05
99466_at	Zfp444	zinc finger protein 444	128.93	280.18	-2.17	8.39E-05
160287_at	Map1lc3b	microtubule-associated protein 1	275.91	710.22	-2.57	8.41E-05
103441_at	Csnk2a1 /// LOC1000	casein kinase 2, alpha 1 polypept	1517.56	558.06	2.72	8.43E-05
100928_at	Fbln2	fibulin 2	1726.85	235.14	7.34	8.43E-05
160750_at	Prpsap2	phosphoribosyl pyrophosphate s	128.26	423.74	-3.30	8.45E-05
99618_at	Uqcr	ubiquinol-cytochrome c reductas	331.36	3543.20	-10.69	8.46E-05
96858_at	Aifm1	apoptosis-inducing factor, mitoch	3203.39	858.83	3.73	8.46E-05
94068_at	Rps19	ribosomal protein S19	680.12	1720.34	-2.53	8.46E-05
99546_at	Fkbp2	FK506 binding protein 2	458.35	2177.91	-4.75	8.46E-05
94853_at	Gnb1	guanine nucleotide binding prote	378.12	1094.86	-2.90	8.48E-05
96874_g_at	Tax1bp1	Tax1 (human T-cell leukemia viru	7001.45	2475.49	2.83	8.51E-05
102307_at	Dcx	doublecortin	227.98	2322.48	-10.19	8.52E-05
97865_g_at	2510049I19Rik	RIKEN cDNA 2510049I19 gene	276.52	842.55	-3.05	8.55E-05
96962_at	Rpl6	ribosomal protein L6	3239.88	8014.94	-2.47	8.55E-05
92673_at	Sh3gl2	SH3-domain GRB2-like 2	65.02	245.60	-3.78	8.59E-05
96861_at	Mrpl50	mitochondrial ribosomal protein	114.47	280.88	-2.45	8.61E-05
102946_r_at	Gapdhs	glyceraldehyde-3-phosphate deh	939.70	2367.90	-2.52	8.64E-05
95482_at	Usp7	ubiquitin specific peptidase 7	2295.81	630.85	3.64	8.71E-05
104404_at	Nat12	N-acetyltransferase 12	53.33	145.21	-2.72	8.71E-05
97197_r_at	AI506816	expressed sequence AI506816	44.27	392.52	-8.87	8.71E-05
162081_f_at	---	---	3282.10	1091.59	3.01	8.71E-05
104208_at	Pi4ka	phosphatidylinositol 4-kinase, cat	3353.42	751.33	4.46	8.71E-05
94260_at	Larp1	La ribonucleoprotein domain fam	3388.62	1027.84	3.30	8.72E-05
101085_at	Mrps24	mitochondrial ribosomal protein	270.97	584.33	-2.16	8.72E-05
103891_i_at	Ell2	elongation factor RNA polymeras	1166.98	273.67	4.26	8.72E-05
99119_at	Cfl1	cofilin 1, non-muscle	964.82	4095.26	-4.24	8.73E-05
104432_at	Rnd2	Rho family GTPase 2	212.35	1631.49	-7.68	8.74E-05
161696_f_at	C77080	expressed sequence C77080	1425.49	143.59	9.93	8.82E-05
94393_r_at	Elovl2	elongation of very long chain fatt	64.47	250.62	-3.89	8.82E-05
93023_f_at	Hist1h3a /// Hist1h3b	histone cluster 2, H3c1 /// histon	230.65	483.86	-2.10	8.88E-05

101527_at	Tcea1	transcription elongation factor A	576.87	1330.00	-2.31	8.91E-05
160558_at	Akt2 /// LOC1000481	thymoma viral proto-oncogene 2	672.29	1379.12	-2.05	8.91E-05
95730_at	Mrps34	mitochondrial ribosomal protein	202.83	465.88	-2.30	8.93E-05
160402_at	Tceb2	transcription elongation factor B	356.24	6707.30	-18.83	8.94E-05
97868_at	Dnaja3	DnaJ (Hsp40) homolog, subfamily	3021.72	1239.44	2.44	8.99E-05
96909_at	Ndufab1	NADH dehydrogenase (ubiquinor	305.70	1944.46	-6.36	8.99E-05
94768_at	Rad21	RAD21 homolog (S. pombe)	669.71	1908.01	-2.85	9.00E-05
103247_at	Mpp3	membrane protein, palmitoylate	452.96	1326.43	-2.93	9.00E-05
94207_at	Pdia6	protein disulfide isomerase assoc	1653.65	352.12	4.70	9.00E-05
93635_at	Kif3c	kinesin family member 3C	2111.29	544.06	3.88	9.01E-05
160899_at	Pcp4	Purkinje cell protein 4	1120.54	5742.20	-5.12	9.02E-05
98587_at	Nap1l1	nucleosome assembly protein 1-l	439.62	922.67	-2.10	9.02E-05
94564_at	Sult4a1	sulfotransferase family 4A, memb	397.94	1077.16	-2.71	9.03E-05
104557_at	Pitpnb	phosphatidylinositol transfer pro	184.99	657.01	-3.55	9.04E-05
96628_at	Eprs	glutamyl-prolyl-tRNA synthetase	2226.83	448.22	4.97	9.06E-05
160114_at	Gdi2	guanosine diphosphate (GDP) dis	4641.98	1947.86	2.38	9.09E-05
102813_f_at	Uba5	ubiquitin-like modifier activating	906.27	280.02	3.24	9.09E-05
93273_at	Snca	synuclein, alpha	221.73	723.78	-3.26	9.15E-05
95801_s_at	Zfp260	zinc finger protein 260	46.80	108.20	-2.31	9.29E-05
93284_at	Cirbp	cold inducible RNA binding prote	501.49	1529.30	-3.05	9.31E-05
103364_f_at	5730494M16Rik	RIKEN cDNA 5730494M16 gene	4585.36	1705.47	2.69	9.37E-05
96596_at	Ndrg1	N-myc downstream regulated ge	4849.37	462.52	10.48	9.51E-05
95512_at	Pcmt1	protein-L-isoaspartate (D-asparta	1184.94	257.14	4.61	9.51E-05
92794_f_at	Nme1	non-metastatic cells 1, protein (N	1829.05	454.09	4.03	9.55E-05
95718_f_at	Usmg5	upregulated during skeletal musc	2281.65	8309.76	-3.64	9.56E-05
96913_at	Hadhb	hydroxyacyl-Coenzyme A dehydr	2407.09	738.26	3.26	9.58E-05
92806_at	Pdrg1	p53 and DNA damage regulated 1	2252.86	792.25	2.84	9.58E-05
160764_at	Fbxw11	F-box and WD-40 domain protein	2785.27	1103.77	2.52	9.58E-05
161948_f_at	---	---	365.59	128.66	2.84	9.58E-05
102967_at	Gdap1	ganglioside-induced differentiatio	4096.32	1053.02	3.89	9.58E-05
95117_at	Igf2r	insulin-like growth factor 2 recep	2032.71	736.35	2.76	9.59E-05
102056_f_at	2610002J02Rik	RIKEN cDNA 2610002J02 gene	6175.35	728.63	8.48	9.62E-05
160988_r_at	Fubp1	far upstream element (FUSE) bin	55.78	116.02	-2.08	9.71E-05
101770_i_at	LOC634282 /// Pcdha	protocadherin alpha 4 /// protoc	169.58	80.63	2.10	9.74E-05
96132_at	Apcdd1	adenomatosis polyposis coli dow	141.98	663.87	-4.68	9.75E-05
95634_at	0610010K14Rik	RIKEN cDNA 0610010K14 gene	83.52	280.23	-3.36	9.75E-05
160561_at	Mdk	midkine	458.84	1596.89	-3.48	9.86E-05
96496_g_at	Myt1l	myelin transcription factor 1-like	2133.17	537.00	3.97	9.87E-05
93875_at	Hspa1a	heat shock protein 1A	1715.51	353.54	4.85	9.87E-05
94550_at	Snx1	sorting nexin 1	2089.45	934.60	2.24	9.87E-05
162032_f_at	LOC625174 /// Pkm2	pyruvate kinase, muscle /// simila	4996.56	2423.79	2.06	9.93E-05
103303_at	Chd7	chromodomain helicase DNA bin	109.08	500.18	-4.59	9.93E-05
93571_at	Spnb2	spectrin beta 2	7150.41	3173.38	2.25	9.93E-05
98081_at	LOC100039220 /// Rp	RNA polymerase 1-3 /// similar to	93.94	258.27	-2.75	9.94E-05
100600_at	Cd24a /// EG621324	CD24a antigen /// predicted gene	9566.85	2791.73	3.43	9.94E-05
100133_at	Fyn	Fyn proto-oncogene	559.68	2077.02	-3.71	0.00010007
99604_at	5-Mar	membrane-associated ring finger	2884.55	729.52	3.95	0.00010016
95670_at	Stmn2	stathmin-like 2	9519.99	4415.76	2.16	0.00010029
103557_at	Vps37c	vacuolar protein sorting 37C (yea	2423.51	582.17	4.16	0.00010049
93427_at	Myo1d	myosin ID	349.27	109.75	3.18	0.00010151
96297_at	Ebna1bp2	EBNA1 binding protein 2	69.16	157.70	-2.28	0.00010158
98575_at	Fasn	fatty acid synthase	4671.29	1608.84	2.90	0.00010183
99335_at	Hk1	hexokinase 1	492.13	1747.68	-3.55	0.00010188
95358_at	Pip4k2a	phosphatidylinositol-5-phosphate	2032.35	469.10	4.33	0.00010202
96016_at	2700094K13Rik	RIKEN cDNA 2700094K13 gene	545.39	2742.48	-5.03	0.00010236

100560_at	Pafah1b1	platelet-activating factor acetylhy	5848.69	2170.19	2.70	0.00010236
100927_at	Pltp	phospholipid transfer protein	204.52	886.99	-4.34	0.00010245
103001_at	Vegfb	vascular endothelial growth factc	1808.65	810.06	2.23	0.000103
94915_at	Ppib	peptidylprolyl isomerase B	990.63	2271.73	-2.29	0.00010308
160794_at	Smyd2	SET and MYND domain containin	1781.00	546.07	3.26	0.00010309
100470_at	Mapk10	mitogen-activated protein kinase	3657.44	1010.66	3.62	0.00010315
104343_f_at	Pla2g12a	phospholipase A2, group XIIA	9340.42	818.36	11.41	0.00010315
102780_at	Srxn1	sulfiredoxin 1 homolog (S. cerevis	3355.16	252.22	13.30	0.0001032
99578_at	Top2a	topoisomerase (DNA) II alpha	90.11	220.19	-2.44	0.00010454
104532_at	Tomm34	translocase of outer mitochondri	5038.76	2400.88	2.10	0.00010567
92546_r_at	Ptgds	prostaglandin D2 synthase (brain	340.26	3638.06	-10.69	0.00010571
97262_at	Csnk1d	casein kinase 1, delta	5891.99	1379.90	4.27	0.00010572
95472_f_at	Uqcrb	ubiquinol-cytochrome c reductas	700.61	3310.81	-4.73	0.00010586
160556_at	1810020G14Rik	RIKEN cDNA 1810020G14 gene	261.44	547.28	-2.09	0.00010609
102338_at	Pde9a	phosphodiesterase 9A	60.22	159.31	-2.65	0.00010633
93281_at	Rcn2	reticulocalbin 2	113.14	526.80	-4.66	0.00010649
95064_at	Acaa2	acetyl-Coenzyme A acyltransferas	5440.24	1313.24	4.14	0.00010701
98909_at	Lias	lipoic acid synthetase	1603.56	521.12	3.08	0.00010743
92379_f_at	Ptprz1	protein tyrosine phosphatase, re	85.00	883.27	-10.39	0.00010754
160511_at	Cxcl12	chemokine (C-X-C motif) ligand 1	28.24	145.86	-5.17	0.00010754
101082_at	Me1	malic enzyme 1, NADP(+)-depenc	2526.51	380.65	6.64	0.00010797
100958_at	Spata13	spermatogenesis associated 13	3314.14	851.33	3.89	0.00010822
160079_i_at	LOC100044766 /// W	WW domain containing adaptor	544.62	198.84	2.74	0.00010907
98905_at	7-Sep	septin 7	570.60	4420.76	-7.75	0.00010952
161400_f_at	Rpn1	ribophorin I	2241.95	1035.87	2.16	0.00010959
97705_at	Snapc3	small nuclear RNA activating com	112.79	254.56	-2.26	0.00011026
103248_at	Fkbp1b	FK506 binding protein 1b	11135.94	2470.10	4.51	0.00011087
103842_at	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box poly	33.63	176.26	-5.24	0.00011112
100457_at	Glg1	golgi apparatus protein 1	2383.31	490.67	4.86	0.00011114
104229_at	Nkain1	Na+/K+ transporting ATPase inter	144.64	1091.28	-7.54	0.0001112
101997_at	Atg12	autophagy-related 12 (yeast)	4012.19	1043.40	3.85	0.0001112
92265_f_at	Trove2	TROVE domain family, member 2	936.65	249.21	3.76	0.00011127
160860_at	Gdf10	growth differentiation factor 10	127.19	1257.50	-9.89	0.00011163
94345_at	Il6st	interleukin 6 signal transducer	1321.38	210.08	6.29	0.00011176
161294_f_at	Clu	clusterin	2331.20	962.47	2.42	0.00011181
96311_at	Mbp	myelin basic protein	1204.72	6326.72	-5.25	0.00011196
160933_at	Igtp	interferon gamma induced GTPas	360.53	96.08	3.75	0.000112
101030_at	Rhob	ras homolog gene family, membe	936.04	2878.32	-3.08	0.00011212
160183_f_at	Tmed7	transmembrane emp24 protein t	960.37	3812.27	-3.97	0.00011236
94432_at	St6gal1	beta galactoside alpha 2,6 sialyltr	1090.21	257.61	4.23	0.00011281
102752_at	Cyfip1	cytoplasmic FMR1 interacting prc	2318.10	711.17	3.26	0.00011292
101467_at	S100b	S100 protein, beta polypeptide, r	2231.79	409.59	5.45	0.00011296
104279_at	Polr2f	polymerase (RNA) II (DNA directe	527.36	1615.87	-3.06	0.00011297
93967_at	Anapc11	anaphase promoting complex sul	4643.16	1700.40	2.73	0.00011309
104260_at	AW112037 /// Lpgat1	expressed sequence AW112037 /	2291.92	793.75	2.89	0.00011363
102059_at	Nicn1	nicolin 1	2726.29	847.44	3.22	0.00011379
162499_f_at	Ube2d2	ubiquitin-conjugating enzyme E2	1319.07	351.83	3.75	0.00011382
100976_at	Ptpn9	protein tyrosine phosphatase, no	5458.74	1360.15	4.01	0.00011388
160683_at	Slc25a36	solute carrier family 25, member	3257.33	1393.11	2.34	0.00011402
93983_at	Derl1	Der1-like domain family, membe	1466.37	609.66	2.41	0.00011478
103362_at	Ptger4	prostaglandin E receptor 4 (subty	1533.38	150.99	10.16	0.00011499
97535_at	Ywhah	tyrosine 3-monooxygenase/trypt	6588.06	2756.99	2.39	0.00011509
96797_s_at	Fbxw5	F-box and WD-40 domain protein	2310.80	1116.25	2.07	0.00011544
103899_at	Atp11a	ATPase, class VI, type 11A	2001.69	172.94	11.57	0.00011568
95076_at	1500032L24Rik	RIKEN cDNA 1500032L24 gene	1574.50	3609.83	-2.29	0.00011572

103611_at	Cd47	CD47 antigen (Rh-related antiger	8959.80	3913.12	2.29	0.00011573
100527_at	Ccdc56	coiled-coil domain containing 56	689.43	1597.43	-2.32	0.00011592
160925_at	Nras	neuroblastoma ras oncogene	2097.99	334.16	6.28	0.00011663
98451_at	Dnajb10	DnaJ (Hsp40) homolog, subfamily	1454.36	230.88	6.30	0.00011672
95707_at	2900010M23Rik	RIKEN cDNA 2900010M23 gene	447.50	1453.28	-3.25	0.00011674
95419_at	H1f0	H1 histone family, member 0	1852.68	4486.82	-2.42	0.00011699
100042_at	Hagh	hydroxyacyl glutathione hydrolas	1527.95	600.48	2.54	0.00011766
99161_at	Grina	glutamate receptor, ionotropic, N	8863.24	3677.67	2.41	0.00011772
97254_at	Rbm8a	RNA binding motif protein 8a	468.63	1396.00	-2.98	0.00011775
92271_at	Pax6	paired box gene 6	49.86	317.46	-6.37	0.00011857
160164_at	Ube2v1	ubiquitin-conjugating enzyme E2	5159.75	1624.05	3.18	0.00011967
161139_f_at	Ddef1	development and differentiation	3286.24	411.24	7.99	0.00012001
94667_at	AA408396	expressed sequence AA408396	204.51	437.21	-2.14	0.00012025
103708_at	Eif1a	eukaryotic translation initiation f	877.30	312.86	2.80	0.00012033
96691_at	Taf11	TAF11 RNA polymerase II, TATA b	1697.68	776.35	2.19	0.00012079
160379_at	Epb4.1	erythrocyte protein band 4.1	165.94	586.71	-3.54	0.00012082
92580_at	Hars	histidyl-tRNA synthetase	4857.81	256.26	18.96	0.00012131
97967_at	Plxnd1	plexin D1	2229.47	541.24	4.12	0.00012132
104419_at	Fndc3a	fibronectin type III domain conta	43.94	102.79	-2.34	0.00012169
92949_at	Pacsin1	protein kinase C and casein kinas	2481.10	1214.98	2.04	0.00012235
101887_at	Agt	angiotensinogen (serpin peptidas	642.12	2372.63	-3.69	0.00012244
103688_at	Ankrd43	ankyrin repeat domain 43	64.44	204.53	-3.17	0.00012245
95448_at	Psmc2	proteasome (prosome, macropai	5749.38	1048.34	5.48	0.00012248
104237_at	Pcbd2	pterin 4 alpha carbinolamine deh	1529.87	602.99	2.54	0.00012279
92452_at	Pik3ca	phosphatidylinositol 3-kinase, cat	720.91	162.20	4.44	0.00012327
101523_at	Hnrpa3 /// LOC10004	heterogeneous nuclear ribonucle	1002.43	2996.23	-2.99	0.00012355
95565_at	Mad2l1bp	MAD2L1 binding protein	2125.24	413.59	5.14	0.00012357
160424_f_at	Fdps	farnesyl diphosphate synthetase	4793.22	1706.43	2.81	0.00012386
103665_at	Elovl6	ELOVL family member 6, elongati	2896.47	842.15	3.44	0.00012418
94832_at	Hnrph2	heterogeneous nuclear ribonucle	34.80	134.29	-3.86	0.00012418
160872_f_at	2310008H09Rik	RIKEN cDNA 2310008H09 gene	482.95	94.41	5.12	0.00012625
103216_f_at	Ikbkg	inhibitor of kappaB kinase gamm	1149.13	484.09	2.37	0.00012625
160302_at	1200003C05Rik	RIKEN cDNA 1200003C05 gene	2197.76	887.59	2.48	0.00012635
104091_at	Tspan9	tetraspanin 9	1273.10	2668.51	-2.10	0.00012651
100101_at	Snrpa	small nuclear ribonucleoprotein p	640.48	1677.17	-2.62	0.00012687
96258_at	Mgst3	microsomal glutathione S-transfe	1485.05	6806.41	-4.58	0.00012698
94331_at	Stat6	signal transducer and activator of	372.64	121.08	3.08	0.0001272
92839_f_at	Snrpb2	U2 small nuclear ribonucleoprote	1045.83	238.50	4.39	0.00012736
162249_f_at	Nkain1	Na+/K+ transporting ATPase inter	396.90	1539.91	-3.88	0.00012736
160189_at	Nudt4	nudix (nucleoside diphosphate lir	196.52	444.03	-2.26	0.00012789
98562_at	C1qa	complement component 1, q sub	168.74	478.79	-2.84	0.00012806
95435_at	Arl8b	ADP-ribosylation factor-like 8B	1962.39	315.14	6.23	0.00012808
99655_at	Sec11a	SEC11 homolog A (S. cerevisiae)	2710.59	1192.04	2.27	0.00012816
103021_r_at	Map3k1	mitogen-activated protein kinase	32.21	216.39	-6.72	0.0001283
94022_at	Gltscr2	glioma tumor suppressor candida	1682.42	651.41	2.58	0.00012995
97848_at	Rbmx	RNA binding motif protein, X chro	66.75	160.25	-2.40	0.00013024
93333_at	Tbca	tubulin cofactor a	120.59	305.63	-2.53	0.00013054
160874_r_at	Ruvbl1	RuvB-like protein 1	1474.86	3193.85	-2.17	0.00013056
160991_at	Nkiras1	NFKB inhibitor interacting Ras-lik	3121.96	911.98	3.42	0.00013061
100044_at	Cldn11	claudin 11	49.31	683.37	-13.86	0.00013062
97934_at	Galnt1	UDP-N-acetyl-alpha-D-galactosan	2277.68	906.85	2.51	0.00013065
102965_at	Znfx1	zinc finger, NFX1-type containing	760.67	177.45	4.29	0.00013109
100509_at	Rnf19a	ring finger protein 19A	3172.53	428.21	7.41	0.0001312
92374_at	Adora1	adenosine A1 receptor	1703.67	182.79	9.32	0.0001319
99057_at	Thy1	thymus cell antigen 1, theta	9063.95	1306.11	6.94	0.00013194

97448_at	4933439C20Rik /// LC	RIKEN cDNA 4933439C20 gene //	2576.84	463.67	5.56	0.00013196
95347_at	Myt1	myelin transcription factor 1	5381.17	1993.18	2.70	0.00013197
95114_s_at	Cuta	cutA divalent cation tolerance ho	501.79	1181.60	-2.35	0.00013217
93119_at	Cox5b	cytochrome c oxidase, subunit Vb	535.68	2202.95	-4.11	0.00013224
99123_s_at	Fxc1	fractured callus expressed transc	224.09	451.26	-2.01	0.00013234
93347_at	Rab24	RAB24, member RAS oncogene fa	2012.77	495.72	4.06	0.00013241
161763_r_at	Pip4k2c	phosphatidylinositol-5-phosphate	231.92	723.43	-3.12	0.00013369
96320_at	2310044H10Rik	RIKEN cDNA 2310044H10 gene	5725.53	1436.21	3.99	0.00013398
100380_at	EG544973 /// EG623	H3 histone, family 3A /// H3 histo	851.89	3401.47	-3.99	0.00013412
101993_at	Tnc	tenascin C	131.34	559.16	-4.26	0.00013415
93382_at	Pde1b	phosphodiesterase 1B, Ca2+-caln	476.35	1018.89	-2.14	0.00013429
93356_at	Mcm7	minichromosome maintenance d	316.57	732.66	-2.31	0.00013486
93988_at	Psma7	proteasome (prosome, macropai	645.13	1936.71	-3.00	0.00013541
93309_at	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) bo	42.92	165.80	-3.86	0.00013595
104348_at	Bre	brain and reproductive organ-exp	1847.59	705.94	2.62	0.00013604
102319_at	Snx12	sorting nexin 12	62.58	146.01	-2.33	0.00013614
96117_r_at	H13	histocompatibility 13	1284.84	563.86	2.28	0.00013709
94047_at	0610031J06Rik	RIKEN cDNA 0610031J06 gene	2740.06	1225.81	2.24	0.0001374
103763_at	Ash1l	ash1 (absent, small, or homeotic)	1042.07	459.84	2.27	0.00013782
103456_at	Ece1	endothelin converting enzyme 1	1803.28	628.35	2.87	0.00013792
160255_at	Ahnak	AHNAK nucleoprotein (desmoyok	6259.24	306.47	20.42	0.00013803
160308_at	Msn	moesin	3618.01	910.33	3.97	0.00013806
94301_at	Atp6v0e	ATPase, H+ transporting, lysosom	285.86	748.96	-2.62	0.00013807
160678_at	Tspan12	tetraspanin 12	32.35	94.44	-2.92	0.00013822
104314_r_at	1110032A03Rik	RIKEN cDNA 1110032A03 gene	886.68	338.52	2.62	0.00013902
98059_s_at	Lmna	lamin A	4462.17	402.38	11.09	0.00013908
160742_at	Plod3	procollagen-lysine, 2-oxoglutarat	1231.29	585.26	2.10	0.00013925
92210_at	Angpt2	angiopoietin 2	360.35	98.27	3.67	0.00013994
103370_at	Lin7c	lin-7 homolog C (C. elegans)	287.02	1852.61	-6.45	0.00014095
98356_at	Adcy9	adenylate cyclase 9	1641.69	345.81	4.75	0.000141
161951_f_at	Mcart1	mitochondrial carrier triple repea	919.74	287.43	3.20	0.00014132
160271_at	0610007C21Rik	RIKEN cDNA 0610007C21 gene	332.20	967.27	-2.91	0.00014133
96919_at	Atp6v0c /// Atp6v0c-	ATPase, H+ transporting, lysosom	3546.77	10572.08	-2.98	0.00014141
160635_at	Stx18	syntaxin 18	911.43	428.42	2.13	0.00014303
93971_f_at	Psmd12	proteasome (prosome, macropai	2672.52	747.23	3.58	0.00014349
160680_at	Cpeb1	cytoplasmic polyadenylation elen	347.24	92.69	3.75	0.00014366
96343_at	Actn4	actinin alpha 4	1250.26	619.66	2.02	0.00014437
97916_at	5730494N06Rik	RIKEN cDNA 5730494N06 gene	3100.79	1216.16	2.55	0.00014444
160776_at	Wdr42a	WD repeat domain 42A	836.41	317.69	2.63	0.00014452
97394_at	Smarca5	SWI/SNF related, matrix associat	124.01	277.33	-2.24	0.00014454
104627_at	Cds2	CDP-diacylglycerol synthase (pho	7621.00	331.68	22.98	0.00014455
101589_at	Hmgn2 /// LOC10003	high mobility group nucleosomal	259.10	1876.43	-7.24	0.00014456
93861_f_at	EG622147	predicted gene, EG622147	130.35	323.62	-2.48	0.00014478
101424_at	Nmi	N-myc (and STAT) interactor	176.43	87.34	2.02	0.00014523
99342_at	Gabrd	gamma-aminobutyric acid (GABA	143.29	347.89	-2.43	0.00014557
94450_at	Nsun2	NOL1/NOP2/Sun domain family 2	1158.94	129.57	8.94	0.00014568
92378_at	Ptprz1	protein tyrosine phosphatase, re	98.47	297.54	-3.02	0.00014576
97398_at	Pck2	phosphoenolpyruvate carboxykir	1133.53	285.61	3.97	0.00014602
93764_at	Ndufa13	NADH dehydrogenase (ubiquinor	619.22	1452.72	-2.35	0.00014645
97924_at	Gne	glucosamine	1535.23	546.13	2.81	0.00014656
100088_at	LOC100044953 /// Pp	protein phosphatase 1, catalytic s	259.70	2409.58	-9.28	0.00014691
102014_at	Homer3	homer homolog 3 (Drosophila)	251.58	561.17	-2.23	0.00014698
93476_at	Prkdc	protein kinase, DNA activated, ca	1215.66	243.43	4.99	0.00014702
97847_at	Rbmx	RNA binding motif protein, X chro	304.57	643.49	-2.11	0.00014702
99178_at	Gpm6b	glycoprotein m6b	618.69	1444.73	-2.34	0.00014733

93728_at	Tsc22d1	TSC22 domain family, member 1	205.62	1229.94	-5.98	0.00014746
92946_f_at	Gria2	glutamate receptor, ionotropic, A	59.44	228.59	-3.85	0.00014753
102335_at	Kcnk1	potassium channel, subfamily K,	545.00	2013.94	-3.70	0.00014772
95395_at	Ythdf3	YTH domain family 3	83.76	527.35	-6.30	0.0001486
104102_at	Htra2	HtrA serine peptidase 2	1498.11	316.61	4.73	0.00014872
93693_at	Hmbox1	homeobox containing 1	1975.66	771.75	2.56	0.00014883
101834_at	Mapk3	mitogen-activated protein kinase	995.35	374.04	2.66	0.00014883
93593_f_at	Emp3	epithelial membrane protein 3	3325.42	1234.09	2.69	0.00014889
95158_at	H2-Ke2	H2-K region expressed gene 2	622.54	1612.43	-2.59	0.0001491
98083_at	Klf6	Kruppel-like factor 6	1473.03	481.73	3.06	0.00014911
97541_f_at	H2-D1 /// H2-K1 /// L	histocompatibility 2, D region loc	3573.30	114.81	31.12	0.00014916
161754_f_at	Glb1	galactosidase, beta 1	407.40	138.94	2.93	0.00014956
99445_at	Slc44a2	solute carrier family 44, member	749.82	126.27	5.94	0.00015037
94001_at	Elavl1	ELAV (embryonic lethal, abnorma	116.70	427.91	-3.67	0.00015059
94048_at	Cdc34 /// LOC100046	cell division cycle 34 homolog (S.	622.62	278.90	2.23	0.000151
160479_at	Cat	catalase	1298.10	323.99	4.01	0.00015176
162134_r_at	2010111I01Rik	RIKEN cDNA 2010111I01 gene	1842.13	4408.41	-2.39	0.00015277
162049_f_at	Gdpd5	glycerophosphodiester phosphoc	685.05	192.52	3.56	0.00015285
162092_f_at	Ihpk1	inositol hexaphosphate kinase 1	299.57	111.28	2.69	0.0001536
103818_at	Slc7a7	solute carrier family 7 (cationic a	3225.08	230.48	13.99	0.00015382
160082_s_at	Arf4	ADP-ribosylation factor 4	521.80	1313.78	-2.52	0.00015384
95682_at	Ddb1	damage specific DNA binding pro	8310.69	3919.78	2.12	0.00015388
160599_r_at	Rsph1	radial spoke head 1 homolog (Ch	1002.53	2367.44	-2.36	0.0001539
97296_at	Mrpl44	mitochondrial ribosomal protein	421.24	133.68	3.15	0.00015438
92678_at	Ddx25	DEAD (Asp-Glu-Ala-Asp) box poly	88.11	251.14	-2.85	0.00015455
103911_at	Sumf1	sulfatase modifying factor 1	1282.53	203.32	6.31	0.00015462
160930_at	Sacm1l	SAC1 (suppressor of actin mutati	1224.65	290.31	4.22	0.00015464
161962_f_at	Mfap4	microfibrillar-associated protein	149.51	448.45	-3.00	0.000155
160291_at	Sec61a1	Sec61 alpha 1 subunit (S. cerevisi	4502.70	1302.26	3.46	0.00015648
103449_at	Lsm14b	LSM14 homolog B (SCD6, S. cere	4000.00	1869.67	2.14	0.00015857
160417_at	Kif5b	kinesin family member 5B	54.35	219.12	-4.03	0.00015897
101453_at	Mia1	melanoma inhibitory activity 1	178.81	1392.81	-7.79	0.00015904
96357_at	Arpc1b /// EG434782	actin related protein 2/3 comple	2750.41	1077.18	2.55	0.00015936
96708_at	Tmed3	transmembrane emp24 domain c	957.62	356.72	2.68	0.0001596
160536_at	Hras1	Harvey rat sarcoma virus oncoge	3569.50	1335.25	2.67	0.00015961
161474_r_at	Dpep3	dipeptidase 3	555.12	1315.80	-2.37	0.00015963
94514_s_at	Arcn1	archain 1	1424.93	528.42	2.70	0.00016105
99917_at	Ezh2	enhancer of zeste homolog 2 (Dr	221.09	464.31	-2.10	0.0001614
AFFX-b-ActinMur/	Actb	actin, beta, cytoplasmic	10780.67	25071.17	-2.33	0.00016146
93017_at	Sdcbp	syndecan binding protein	2212.85	158.29	13.98	0.00016148
160125_at	Cdkn2aipnl	CDKN2A interacting protein N-te	448.03	218.91	2.05	0.0001617
100225_f_at	Psmc3	proteasome (prosome, macropai	2813.43	842.11	3.34	0.00016176
97824_at	Nola2	nucleolar protein family A, memb	556.78	1217.96	-2.19	0.00016181
104677_at	Man1b1	mannosidase, alpha, class 1B, me	1942.78	394.49	4.92	0.00016184
162452_at	Pcp2	Purkinje cell protein 2 (L7)	401.65	1230.43	-3.06	0.00016187
95791_s_at	Sfrs2	splicing factor, arginine/serine-ric	102.95	660.45	-6.42	0.0001619
94042_f_at	Gng5 /// LOC100043	guanine nucleotide binding prote	1696.18	4132.53	-2.44	0.00016284
95474_at	F2r	coagulation factor II (thrombin) r	6528.88	1998.58	3.27	0.00016291
94499_at	Mgea5	meningioma expressed antigen 5	3819.44	1691.37	2.26	0.00016296
96079_at	0610010K06Rik	RIKEN cDNA 0610010K06 gene	6019.48	1427.35	4.22	0.00016297
95897_at	Atp2c1 /// LOC10004	ATPase, Ca++-sequestering /// hy	4720.12	1011.21	4.67	0.00016344
161058_f_at	R74862	expressed sequence R74862	57.52	123.67	-2.15	0.00016363
94214_at	Fabp3	fatty acid binding protein 3, musc	259.36	613.22	-2.36	0.00016404
103608_at	Fars2	phenylalanine-tRNA synthetase 2	896.83	363.37	2.47	0.00016423
95652_at	Ndufa7	NADH dehydrogenase (ubiquinor	1181.32	4280.63	-3.62	0.00016466

92597_s_at	Atp6v1b2	ATPase, H+ transporting, lysosom	52.20	212.90	-4.08	0.00016539
104030_at	Ptch1	patched homolog 1	282.38	675.22	-2.39	0.00016551
160486_at	Ccdc28b	coiled coil domain containing 28E	183.47	846.57	-4.61	0.00016613
92747_at	Nkx2-2	NK2 transcription factor related,	58.53	184.01	-3.14	0.00016618
96609_at	Sfrs11	splicing factor, arginine/serine-ric	366.75	1484.15	-4.05	0.00016634
101837_g_at	LOC100048520 /// LC	protein phosphatase 1B, magnes	167.85	438.48	-2.61	0.00016706
160982_at	Map3k7ip3	mitogen-activated protein kinase	729.46	176.45	4.13	0.00016741
103451_at	Ptk2b	PTK2 protein tyrosine kinase 2 be	991.60	286.17	3.47	0.00016773
103429_i_at	Adi1	acireductone dioxygenase 1	60.13	200.91	-3.34	0.00016781
102924_at	Dtx1	deltex 1 homolog (Drosophila)	377.06	774.51	-2.05	0.00016809
160139_at	Hspb8	heat shock protein 8	4419.49	614.45	7.19	0.00017022
160345_at	Mrpl34	mitochondrial ribosomal protein	245.78	828.07	-3.37	0.00017023
161070_at	Spred2	sprouty-related, EVH1 domain co	1485.02	525.24	2.83	0.00017084
101447_at	Apc	adenomatosis polyposis coli	114.47	289.99	-2.53	0.0001712
162462_r_at	Pck2	phosphoenolpyruvate carboxykir	351.05	167.41	2.10	0.00017166
96723_f_at	Ssx2ip	synovial sarcoma, X breakpoint 2	3817.64	1740.78	2.19	0.00017254
161897_f_at	AU021838 /// Mipol1	phosphoribosyl pyrophosphate s	61.14	125.76	-2.06	0.00017256
99619_at	Tmem41b	transmembrane protein 41B	6107.99	2516.57	2.43	0.00017259
104482_at	Stx2	syntaxin 2	3747.32	1416.23	2.65	0.00017263
161497_f_at	Itga7	integrin alpha 7	1451.71	664.69	2.18	0.00017401
92539_at	S100a10	S100 calcium binding protein A1(	4722.53	408.95	11.55	0.00017419
99120_f_at	Chd4	chromodomain helicase DNA bin	9131.48	3140.32	2.91	0.00017426
93217_at	Fbxo45	F-box protein 45	2933.58	872.70	3.36	0.00017562
97239_at	D19Ertd721e	DNA segment, Chr 19, ERATO Do	695.69	107.53	6.47	0.00017621
160297_at	Ccdc58	coiled-coil domain containing 58	53.59	111.11	-2.07	0.00017854
98441_at	Fmr1	fragile X mental retardation synd	49.40	383.45	-7.76	0.00017862
95609_at	Ppp1r15b	protein phosphatase 1, regulator	1211.65	463.68	2.61	0.00017913
97518_at	Fdft1	farnesyl diphosphate farnesyl tra	4416.36	1735.56	2.54	0.00017964
97429_at	Snrk	SNF related kinase	892.79	249.87	3.57	0.00018026
95517_i_at	BC004004	cDNA sequence BC004004	4495.53	1486.03	3.03	0.00018032
102726_at	Tac1	tachykinin 1	5837.31	59.23	98.56	0.00018082
93966_at	Ube4b	ubiquitination factor E4B, UFD2 h	2458.89	966.27	2.54	0.00018125
92358_at	Nell2	NEL-like 2 (chicken)	135.87	406.41	-2.99	0.00018132
160227_s_at	Bysl	bystin-like	2613.78	869.26	3.01	0.00018289
101524_at	Hnrpa3	heterogeneous nuclear ribonucle	35.78	140.69	-3.93	0.00018441
98049_at	1300018I05Rik	RIKEN cDNA 1300018I05 gene	1279.09	373.27	3.43	0.0001847
93844_at	Uqcrq	ubiquinol-cytochrome c reductas	2698.42	10371.84	-3.84	0.00018492
101836_at	Ppm1b	protein phosphatase 1B, magnes	197.50	42.28	4.67	0.0001851
102410_at	Hs3st1	heparan sulfate (glucosamine) 3-	101.05	335.34	-3.32	0.00018514
95483_at	Psmd1	proteasome (prosome, macropai	3081.87	1333.21	2.31	0.00018561
103484_at	Popdc3	popeye domain containing 3	1177.14	172.36	6.83	0.00018593
97473_at	Tspan4	tetraspanin 4	1145.34	2618.76	-2.29	0.000186
97527_at	Cks2 /// LOC1000394	CDC28 protein kinase regulatory	77.33	490.44	-6.34	0.00018735
160475_at	Yipf4	Yip1 domain family, member 4	293.35	880.69	-3.00	0.00018753
99085_at	Usp3	ubiquitin specific peptidase 3	228.61	497.97	-2.18	0.00018762
95232_at	Hnrnpl	heterogeneous nuclear ribonucle	155.51	452.77	-2.91	0.00018886
100720_at	Pabpc1	poly A binding protein, cytoplasm	2123.72	4421.26	-2.08	0.0001891
96259_at	Npepps	aminopeptidase puromycin sensi	4426.43	1431.94	3.09	0.00019029
95447_at	1810034K20Rik	RIKEN cDNA 1810034K20 gene	232.61	474.78	-2.04	0.00019043
161036_at	Slc6a15	solute carrier family 6 (neurotran	2299.14	789.04	2.91	0.00019131
93820_at	Cox7a2	cytochrome c oxidase, subunit VI	534.69	6450.48	-12.06	0.00019137
96561_at	Nfatc2ip	nuclear factor of activated T-cells	57.17	134.36	-2.35	0.00019138
96771_at	Erbb3	v-erb-b2 erythroblastic leukemia	791.24	224.07	3.53	0.00019196
160187_at	Pafah1b2	platelet-activating factor acetylhy	3406.59	1021.65	3.33	0.00019286
96207_at	Rbms1	RNA binding motif, single strande	1259.56	278.53	4.52	0.00019291

160159_at	Ccnb1 /// Ccnb1-rs1	cyclin B1, related sequence 1 ///	40.22	182.14	-4.53	0.00019325
102875_at	Rps6kc1	ribosomal protein S6 kinase polyl	635.88	186.24	3.41	0.00019562
97110_at	Chst2	Carbohydrate sulfotransferase 2	190.46	1082.45	-5.68	0.00019565
94422_at	Dnajc13	DnaJ (Hsp40) homolog, subfamily	1695.85	128.78	13.17	0.00019662
104501_at	Vapb	vesicle-associated membrane prc	3638.69	861.52	4.22	0.00019691
160335_at	Gclm	glutamate-cysteine ligase , modif	2352.81	250.20	9.40	0.00019697
95406_at	1810037I17Rik	RIKEN cDNA 1810037I17 gene	1068.25	3578.03	-3.35	0.00019702
96275_f_at	Tm9sf3	transmembrane 9 superfamily m	559.80	148.61	3.77	0.00019703
96495_at	Myt1l	myelin transcription factor 1-like	3746.81	956.74	3.92	0.00019781
161364_f_at	Faf1	Fas-associated factor 1	871.94	235.80	3.70	0.00019791
92770_at	S100a6	S100 calcium binding protein A6	1158.49	286.06	4.05	0.00019793
160885_at	Nucks1	nuclear casein kinase and cyclin-c	570.12	1234.06	-2.16	0.00019797
94910_at	Nde1	nuclear distribution gene E homc	76.83	248.81	-3.24	0.00019812
160726_at	Qk	quaking	85.93	883.93	-10.29	0.00019895
94508_at	Tmem126a	transmembrane protein 126A	176.81	735.96	-4.16	0.00019922
104595_at	Stag2	stromal antigen 2	77.23	262.72	-3.40	0.00019977
102058_at	Mrpl9	mitochondrial ribosomal protein	1079.13	251.73	4.29	0.00019978
100877_at	1810058I24Rik	RIKEN cDNA 1810058I24 gene	2347.09	650.33	3.61	0.00020003
97859_at	Inpp5a	inositol polyphosphate-5-phosph	227.59	1683.14	-7.40	0.00020014
161449_f_at	Cwf19l1	CWF19-like 1, cell cycle control (S	110.18	45.62	2.42	0.00020052
99593_at	BC002163 /// Ndufs5	cDNA sequence BC002163 /// NA	827.86	3725.92	-4.50	0.00020221
95010_at	Traf3	Tnf receptor-associated factor 3	1859.44	511.83	3.63	0.00020313
99166_at	0610012G03Rik	RIKEN cDNA 0610012G03 gene	459.59	1619.25	-3.52	0.00020314
94505_at	Peli1	pellino 1	269.41	598.72	-2.22	0.00020345
93987_f_at	LOC100042049 /// Rp	ribosomal protein L22 like 1 /// si	805.58	3428.38	-4.26	0.00020366
161401_f_at	Aldh3a2	aldehyde dehydrogenase family 3	930.47	219.25	4.24	0.00020395
161000_i_at	Nusap1	nucleolar and spindle associated	104.31	407.05	-3.90	0.00020468
96042_at	Sod2	superoxide dismutase 2, mitocho	1662.53	437.99	3.80	0.00020509
95913_at	Sfrs17b	splicing factor, arginine/serine-ric	1078.12	181.97	5.92	0.00020587
103668_at	Supt6h	suppressor of Ty 6 homolog (S. ce	2678.40	940.49	2.85	0.00020697
93615_at	Pbx3	pre B-cell leukemia transcription	1005.38	325.13	3.09	0.00020699
103932_at	Wdsof1	WD repeats and SOF domain con	657.06	263.00	2.50	0.00020723
92527_at	Adcy9	adenylate cyclase 9	1004.14	245.52	4.09	0.00020808
102308_at	Tulp3	tubby-like protein 3	1982.87	821.53	2.41	0.00020811
95745_g_at	Atp6v1a	ATPase, H+ transporting, lysosom	2879.94	805.90	3.57	0.00021007
103672_at	Phf23	PHD finger protein 23	2035.62	568.36	3.58	0.0002101
103467_g_at	Cyhr1	cysteine and histidine rich 1	2855.30	567.89	5.03	0.00021028
92615_at	Ndufb6	NADH dehydrogenase (ubiquinor	163.63	2379.02	-14.54	0.00021037
101889_s_at	Rora	RAR-related orphan receptor alpl	46.42	205.14	-4.42	0.00021084
94239_at	Pnn	pinin	56.35	115.89	-2.06	0.00021128
92339_at	Taf1a	TATA box binding protein (Tbp)-a	940.97	242.39	3.88	0.00021169
103312_f_at	Esf1	ESF1, nucleolar pre-rRNA process	652.46	228.34	2.86	0.00021218
104080_at	Pdap1	PDGFA associated protein 1	2435.93	889.21	2.74	0.00021261
94827_at	Fxyd2	FXYD domain-containing ion tran	5842.66	274.63	21.27	0.00021262
95620_at	Dhrs7	dehydrogenase/reductase (SDR f	1675.14	404.30	4.14	0.00021264
94958_at	1110013L07Rik	RIKEN cDNA 1110013L07 gene	756.34	166.58	4.54	0.00021386
99336_at	Rps5	ribosomal protein S5	3818.99	11033.25	-2.89	0.0002139
100066_at	Gart	phosphoribosylglycinamide form	2183.62	326.82	6.68	0.000214
161359_s_at	Apoa1bp	apolipoprotein A-I binding protei	6532.02	2802.67	2.33	0.00021414
103569_at	Sh3glb1	SH3-domain GRB2-like B1 (endop	187.87	423.49	-2.25	0.00021424
98521_at	Vamp3	vesicle-associated membrane prc	47.53	134.69	-2.83	0.00021431
102781_at	Ccnl2	cyclin L2	335.86	896.98	-2.67	0.00021493
100536_at	Mobp	myelin-associated oligodendrocy	131.64	1811.19	-13.76	0.00021496
97292_at	2810407C02Rik	RIKEN cDNA 2810407C02 gene	5643.02	2740.92	2.06	0.00021504
96573_at	Actg1	actin, gamma, cytoplasmic 1	4841.07	10288.42	-2.13	0.00021509

102561_at	Atp5k /// LOC100040	ATP synthase, H+ transporting, m	243.50	656.46	-2.70	0.00021602
92971_at	9130213B05Rik	RIKEN cDNA 9130213B05 gene	2809.95	202.01	13.91	0.0002161
99158_at	Ostf1	osteoclast stimulating factor 1	2951.54	404.96	7.29	0.00021689
98129_at	LOC100043712 /// LC	thymosin, beta 10 /// similar to t	1077.41	12595.44	-11.69	0.00021784
102409_at	Lsm8	LSM8 homolog, U6 small nuclear	309.02	767.30	-2.48	0.00021795
102852_at	Cdh2 /// LOC100044	cadherin 2 /// similar to N-cadhe	378.73	967.44	-2.55	0.00022077
160366_at	BC031181	cDNA sequence BC031181	307.39	2080.20	-6.77	0.00022084
98920_g_at	Tm2d2	TM2 domain containing 2	107.88	377.48	-3.50	0.00022093
103987_at	Mog	myelin oligodendrocyte glycopro	48.20	593.49	-12.31	0.00022106
96577_i_at	Ubap2l	ubiquitin associated protein 2-lik	1319.46	306.49	4.31	0.00022162
100459_at	Rad50	RAD50 homolog (S. cerevisiae)	968.71	409.17	2.37	0.00022227
95703_at	Sae1	SUMO1 activating enzyme subun	1595.30	655.09	2.44	0.00022244
103334_at	Crcp	calcitonin gene-related peptide-r	789.71	226.84	3.48	0.00022245
99674_at	Mrpl43	mitochondrial ribosomal protein	1988.47	852.61	2.33	0.00022269
94967_at	Ermp1	endoplasmic reticulum metallope	2593.30	419.62	6.18	0.00022275
97836_at	Rnf7	ring finger protein 7	2232.81	997.84	2.24	0.0002228
99163_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	214.75	441.86	-2.06	0.00022314
95102_at	Shisa5	shisa homolog 5 (Xenopus laevis)	1705.61	676.19	2.52	0.00022535
92850_at	Rrbp1	ribosome binding protein 1	782.80	291.44	2.69	0.00022597
104422_at	Ptprn	protein tyrosine phosphatase, re	3555.59	1051.81	3.38	0.00022605
160349_at	Cndp2	CNDP dipeptidase 2 (metallopept	1113.66	427.71	2.60	0.00022635
96569_at	Fignl1	fidgetin-like 1	1253.47	2533.80	-2.02	0.00022779
103727_at	Hrb	HIV-1 Rev binding protein	1303.44	478.16	2.73	0.00022957
92708_at	Ddx19b	DEAD (Asp-Glu-Ala-Asp) box poly	1223.80	395.61	3.09	0.00023046
100538_at	Sod1	superoxide dismutase 1, soluble	5648.45	1363.80	4.14	0.0002305
93054_at	Ankrd46	ankyrin repeat domain 46	5636.99	1618.31	3.48	0.00023057
101105_at	Banf1	barrier to autointegration factor	945.54	3594.25	-3.80	0.00023084
104645_at	Klf7	Kruppel-like factor 7 (ubiquitous)	4270.62	427.79	9.98	0.00023096
97477_at	Timm8b	translocase of inner mitochondri	225.96	843.68	-3.73	0.00023176
101853_f_at	Cfh /// LOC10004801	complement component factor h	45.75	92.54	-2.02	0.00023179
98603_s_at	Rangap1	RAN GTPase activating protein 1	230.01	601.43	-2.61	0.00023323
101573_f_at	EG432798 /// EG546(	ribosomal protein L27a /// predic	1511.81	3896.57	-2.58	0.00023329
162228_f_at	Stard3	START domain containing 3	466.14	188.97	2.47	0.00023333
104578_f_at	Actn1	actinin, alpha 1	1912.47	382.90	4.99	0.00023343
97867_at	Hsd11b1	hydroxysteroid 11-beta dehydrog	214.03	592.43	-2.77	0.0002338
96024_at	Ahcy	S-adenosylhomocysteine hydrola	1251.25	506.81	2.47	0.00023388
104078_g_at	Lage3	L antigen family, member 3	124.01	407.62	-3.29	0.00023388
93829_at	Rod1	ROD1 regulator of differentiation	507.83	139.50	3.64	0.00023391
160908_r_at	Ttc30b	tetratricopeptide repeat domain	183.39	390.18	-2.13	0.00023396
97387_at	Chpf	chondroitin polymerizing factor	3195.88	1440.17	2.22	0.00023432
96331_at	Snx2	sorting nexin 2	966.47	371.35	2.60	0.00023561
104717_at	Zfp644	zinc finger protein 644	477.27	1330.47	-2.79	0.00023662
160265_at	Eif5	eukaryotic translation initiation f	2583.77	1114.57	2.32	0.0002387
101430_at	Sox4	SRY-box containing gene 4	262.91	907.38	-3.45	0.00023875
100065_r_at	Gja1	gap junction protein, alpha 1	65.86	297.90	-4.52	0.00023916
92542_at	D4Wsu53e	DNA segment, Chr 4, Wayne Stat	4014.35	1502.36	2.67	0.00023953
97369_g_at	Akap1	A kinase (PRKA) anchor protein 1	108.79	291.84	-2.68	0.00023981
102374_at	Rcan3	regulator of calcineurin 3	5583.14	670.56	8.33	0.00023983
103081_at	Baz1b	bromodomain adjacent to zinc fi	4346.87	1621.13	2.68	0.00023989
102235_at	Mycl1	v-myc myelocytomatosis viral on	273.84	702.43	-2.57	0.00024
160803_at	Ubxd6	UBX domain containing 6	511.28	175.70	2.91	0.00024156
161796_r_at	Kcnq1	potassium voltage-gated channel	633.36	1313.00	-2.07	0.00024165
97248_at	Dbi	diazepam binding inhibitor	139.76	3078.18	-22.03	0.00024177
104492_at	Ebf3	early B-cell factor 3	178.08	519.15	-2.92	0.00024192
103647_at	Glb1	galactosidase, beta 1	869.50	334.46	2.60	0.00024287

93958_at	Rnf14	ring finger protein 14	147.37	331.17	-2.25	0.00024446
161147_f_at	---	---	2224.30	712.87	3.12	0.00024493
96590_f_at	Otud7b	OTU domain containing 7B	971.00	325.34	2.98	0.00024499
94481_at	Ugp2	UDP-glucose pyrophosphorylase	1503.22	431.05	3.49	0.00024579
93501_f_at	Sucla2	succinate-Coenzyme A ligase, AD	5081.85	1428.31	3.56	0.00024596
160236_at	Slain1	SLAIN motif family, member 1	33.65	192.99	-5.73	0.00024599
95092_at	Ppp3ca	protein phosphatase 3, catalytic	4925.61	1927.44	2.56	0.00024646
95097_at	Actr10	ARP10 actin-related protein 10 h	3126.67	1004.69	3.11	0.00024694
160539_at	LOC100048559 /// Sf	splicing factor, arginine/serine-ric	25.08	246.53	-9.83	0.00024702
92565_at	1110005A23Rik /// E	RIKEN cDNA 1110005A23 gene //	184.53	383.11	-2.08	0.00024742
160563_at	Serf2	small EDRK-rich factor 2	803.18	210.58	3.81	0.00024807
97271_at	Lsmd1	LSM domain containing 1	223.84	589.06	-2.63	0.00024853
103493_at	Nmb	neuromedin B	827.74	79.07	10.47	0.00024872
102009_at	Cyfip2	cytoplasmic FMR1 interacting prc	6276.72	512.50	12.25	0.00024878
103835_f_at	Hpcal1	hippocalcin-like 1	2333.90	5987.63	-2.57	0.00024883
93574_at	Serpinf1	serine (or cysteine) peptidase inh	687.66	173.39	3.97	0.00025105
104345_at	Exoc7	exocyst complex component 7	1023.56	503.52	2.03	0.00025241
160321_at	LOC100047896 /// Zf	zinc finger, AN1-type domain 5 //	1862.90	5172.18	-2.78	0.00025247
160585_at	Bxdc1	brix domain containing 1	384.61	100.97	3.81	0.00025302
98293_g_at	Gsbs	G substrate	69.52	263.38	-3.79	0.00025421
96354_at	Mbnl1	muscleblind-like 1 (Drosophila)	1759.40	810.36	2.17	0.00025587
102108_f_at	Myh9	myosin, heavy polypeptide 9, nor	1189.25	304.08	3.91	0.00025708
92958_at	Foxo3a	forkhead box O3a	976.73	431.42	2.26	0.00025805
101061_at	Ssr2	signal sequence receptor, beta	600.31	1270.81	-2.12	0.00025847
94366_at	2310079N02Rik	RIKEN cDNA 2310079N02 gene	928.89	422.72	2.20	0.0002595
92484_at	Hivep2	human immunodeficiency virus t	38.98	230.66	-5.92	0.00025962
160573_at	Hccs	holocytochrome c synthetase	691.35	323.47	2.14	0.00025965
99100_at	Stat3	signal transducer and activator o	2157.16	518.91	4.16	0.00025975
101568_at	Prosc	proline synthetase co-transcribec	836.93	323.63	2.59	0.00026105
94352_at	Mbtd1	mbt domain containing 1	103.59	314.53	-3.04	0.0002613
160640_at	Galnt11	UDP-N-acetyl-alpha-D-galactosar	810.47	386.90	2.09	0.00026181
95701_at	Cxxc5	CXXC finger 5	436.67	1136.42	-2.60	0.00026212
96774_at	Fermt2	fermitin family homolog 2 (Droso	484.74	166.80	2.91	0.00026256
96261_at	2310028O11Rik	RIKEN cDNA 2310028O11 gene	164.03	692.50	-4.22	0.00026284
95016_at	Nrp1	neuropilin 1	6733.78	281.96	23.88	0.00026369
104449_at	Glrb	glycine receptor, beta subunit	413.05	1457.99	-3.53	0.00026373
160626_at	Myef2	myelin basic protein expression f	214.51	930.24	-4.34	0.0002639
162358_i_at	Slc25a1	solute carrier family 25 (mitocho	1580.27	605.94	2.61	0.00026652
102249_at	Avil	advillin	10347.81	486.24	21.28	0.00027032
104444_at	Ocel1	occludin/ELL domain containing 1	1109.42	322.51	3.44	0.00027069
97490_at	Bcl7b	B-cell CLL/lymphoma 7B	507.03	193.21	2.62	0.00027126
102099_f_at	Kctd17	potassium channel tetramerisatic	2654.17	1049.58	2.53	0.00027221
104651_at	Snx14	sorting nexin 14	1161.19	337.67	3.44	0.0002727
104761_at	Antxr2	anthrax toxin receptor 2	1332.30	94.94	14.03	0.00027346
94801_at	Pgrmc2	progesterone receptor membran	1435.58	222.15	6.46	0.00027376
99617_at	Sec24c	SEC24 related gene family, memb	2163.67	949.03	2.28	0.00027433
93582_at	Coq7	demethyl-Q 7	824.57	190.79	4.32	0.00027484
94452_g_at	Nsun2	NOL1/NOP2/Sun domain family 2	1565.22	301.81	5.19	0.00027518
103504_at	Ssbp2	single-stranded DNA binding prot	3816.24	1002.27	3.81	0.00027657
104378_at	Pon2	paraoxonase 2	373.53	154.23	2.42	0.00027782
93798_at	Atp1a1	ATPase, Na+/K+ transporting, alp	10203.35	1613.60	6.32	0.00027786
97957_at	Slc27a4	solute carrier family 27 (fatty acic	1332.00	418.56	3.18	0.00027805
94759_at	Mcart6	mitochondrial carrier triple repea	2916.81	702.40	4.15	0.00027922
104680_at	Ramp1	receptor (calcitonin) activity mod	234.43	1117.29	-4.77	0.00027943
160900_at	Gkap1	G kinase anchoring protein 1	588.93	131.40	4.48	0.0002806

160462_f_at	Tubb3	tubulin, beta 3	9851.91	4721.01	2.09	0.00028071
103630_at	Lars	leucyl-tRNA synthetase	1531.13	400.06	3.83	0.00028081
160818_at	Lrrfip2	leucine rich repeat (in FLII) intera	1316.77	615.28	2.14	0.00028205
93342_at	Mki67ip	Mki67 (FHA domain) interacting r	815.28	146.30	5.57	0.00028226
98119_at	EG625281 /// EG664	ribosomal protein L30 /// predict	3624.69	9050.55	-2.50	0.00028314
160971_at	Kazald1	Kazal-type serine peptidase inhib	449.58	131.10	3.43	0.00028438
95386_at	Lycat	lysocardiolipin acyltransferase	2933.05	339.19	8.65	0.00028441
104135_at	Arl3	ADP-ribosylation factor-like 3	302.06	823.08	-2.72	0.00028485
101516_at	Cd59a	CD59a antigen	4584.40	387.18	11.84	0.00028667
92460_at	Sema4f	sema domain, immunoglobulin d	4335.47	1456.78	2.98	0.00028681
103852_at	Ttc33	tetratricopeptide repeat domain	1380.91	516.01	2.68	0.00028686
102224_at	Igf1r	insulin-like growth factor I recept	2116.63	843.31	2.51	0.00028704
160562_at	Cct7	chaperonin subunit 7 (eta)	6450.02	2170.83	2.97	0.00028719
99093_at	Rps10	ribosomal protein S10	1751.17	3626.80	-2.07	0.00028732
161814_f_at	Rnf19a	Ring finger protein 19A	1367.81	334.40	4.09	0.00028739
95591_at	Extl3	exostoses (multiple)-like 3	3114.10	1064.51	2.93	0.00028956
97914_at	Hspa9	heat shock protein 9	7005.31	859.78	8.15	0.00028961
93752_at	Iars	isoleucine-tRNA synthetase	1432.05	461.97	3.10	0.00028965
95608_at	Ctsb	cathepsin B	2356.27	242.53	9.72	0.00028993
95785_s_at	Rab7	RAB7, member RAS oncogene far	70.25	554.60	-7.89	0.00029008
101734_at	Grid2	glutamate receptor, ionotropic, d	409.79	873.57	-2.13	0.00029029
101631_at	Sox11	SRY-box containing gene 11	336.91	1024.00	-3.04	0.00029233
96068_at	Immp1l	IMP1 inner mitochondrial membı	98.54	384.19	-3.90	0.00029317
162332_f_at	Mapre3	microtubule-associated protein, I	1281.21	348.03	3.68	0.00029409
93605_r_at	Cadm1	cell adhesion molecule 1	415.31	187.34	2.22	0.00029425
95021_at	Arglu1	arginine and glutamate rich 1	2200.26	835.07	2.63	0.00029525
100576_at	Pafah1b3	platelet-activating factor acetylhy	397.54	966.63	-2.43	0.00029652
160127_at	Ccng1	cyclin G1	703.79	224.69	3.13	0.00029711
94304_at	Anxa6	annexin A6	2856.43	868.30	3.29	0.00029713
93496_at	Elovl5	ELOVL family member 5, elongati	5173.14	1666.58	3.10	0.00029741
100751_at	Adam10	a disintegrin and metallopeptidas	102.76	312.92	-3.05	0.00030196
101963_at	Ctsl	cathepsin L	4402.87	1147.10	3.84	0.00030332
160256_at	Tomm7	translocase of outer mitochondri	842.44	2507.62	-2.98	0.00030346
102873_at	Tap2	transporter 2, ATP-binding casset	698.70	285.29	2.45	0.00030388
94932_at	Pdgfa	platelet derived growth factor, al	2373.49	507.64	4.68	0.00030398
104036_at	Dpp7	dipeptidylpeptidase 7	2214.24	436.27	5.08	0.00030505
95462_at	Bzw2	basic leucine zipper and W2 dom	560.77	1553.80	-2.77	0.00030536
100917_at	Wdr55	WD repeat domain 55	593.73	270.75	2.19	0.00030551
97594_r_at	Flii	flightless I homolog (Drosophila)	11200.55	2374.22	4.72	0.00030554
161059_at	Slc6a1	solute carrier family 6 (neurotran	125.35	849.70	-6.78	0.00030555
162263_f_at	Lamb1-1	laminin B1 subunit 1	805.94	367.33	2.19	0.00030591
98904_at	Mrpl35	mitochondrial ribosomal protein	1062.88	461.59	2.30	0.00030593
101078_at	Bsg	basigin	1326.99	3223.81	-2.43	0.00030634
98025_at	Evi2a	ecotropic viral integration site 2a	37.03	76.52	-2.07	0.00030641
98346_at	Tsku	tsukushin	140.66	315.54	-2.24	0.00030668
92555_at	Tspan6	tetraspanin 6	202.58	455.34	-2.25	0.00030733
102773_at	Car8 /// LOC676792	carbonic anhydrase 8 /// similar t	29.40	382.23	-13.00	0.00030759
96272_at	Ptprf	protein tyrosine phosphatase, re	2495.17	614.23	4.06	0.0003077
94017_s_at	LOC100043293 /// Sf	splicing factor, arginine/serine-ric	2323.35	6254.36	-2.69	0.00030985
100539_at	Acot7	acyl-CoA thioesterase 7	5925.41	2439.38	2.43	0.00031007
96614_at	4933426M11Rik	RIKEN cDNA 4933426M11 gene	1919.17	416.03	4.61	0.00031011
100027_s_at	Pex14	peroxisomal biogenesis factor 14	4610.30	1841.64	2.50	0.00031015
102980_at	LOC100045684	similar to N-myristoyltransferase	2164.67	362.66	5.97	0.00031055
92349_at	Igfbpl1	insulin-like growth factor binding	219.72	644.30	-2.93	0.00031164
97485_at	Pcyox1	prenylcysteine oxidase 1	4371.22	884.98	4.94	0.00031243

160385_at	Gcsh	glycine cleavage system protein H	1860.72	846.51	2.20	0.00031267
98626_at	Trappc2l	trafficking protein particle compl	309.41	1555.16	-5.03	0.00031289
92817_at	Imp3	IMP3, U3 small nucleolar ribonuc	431.56	1043.60	-2.42	0.00031306
93261_at	Lgmn	legumain	3877.46	474.22	8.18	0.00031378
100128_at	Cdc2a	cell division cycle 2 homolog A (S	243.36	715.01	-2.94	0.00031641
99529_f_at	Rnf138	ring finger protein 138	36.82	88.64	-2.41	0.00031745
97841_at	Chmp2a	chromatin modifying protein 2A	361.69	1241.61	-3.43	0.00032031
160693_at	Pip4k2c	phosphatidylinositol-5-phosphate	751.57	287.72	2.61	0.00032198
94030_at	Commd2	COMM domain containing 2	296.53	649.75	-2.19	0.00032204
99608_at	Prdx2	peroxiredoxin 2	994.55	349.10	2.85	0.00032223
104350_at	Shc1	src homology 2 domain-containir	1278.37	206.72	6.18	0.00032268
102197_at	Nucb2	nucleobindin 2	234.03	81.45	2.87	0.00032275
103671_at	Htatip2	HIV-1 tat interactive protein 2, ho	1593.70	122.74	12.98	0.00032316
99048_g_at	Mobp	myelin-associated oligodendrocy	79.42	459.61	-5.79	0.00032341
104116_at	Stbd1	starch binding domain 1	1726.79	80.95	21.33	0.00032443
103311_at	Osbpl5	oxysterol binding protein-like 5	4270.01	894.40	4.77	0.00032551
103712_at	R3hdm1	R3H domain 1 (binds single-stran	1680.33	621.08	2.71	0.00032555
101503_at	Dpysl3	dihydropyrimidinase-like 3	320.26	738.99	-2.31	0.00032659
94228_at	Xpo1	exportin 1, CRM1 homolog (yeast	1382.01	593.68	2.33	0.00032685
102123_at	Lipa	lysosomal acid lipase A	889.32	321.79	2.76	0.00032861
103656_at	Lancl1	LanC (bacterial lantibiotic synthet	4576.15	1417.42	3.23	0.00032913
104461_at	Pik3ca	phosphatidylinositol 3-kinase, cat	1114.38	465.67	2.39	0.00032923
161882_f_at	Rdh13	Retinol dehydrogenase 13 (all-tra	467.22	204.38	2.29	0.00033184
102927_s_at	Htt	huntingtin	1951.59	731.82	2.67	0.00033311
93094_at	Cdr2	cerebellar degeneration-related 2	1024.99	143.69	7.13	0.00033324
97863_at	Hgsnat	heparan-alpha-glucosaminide N-a	2541.02	763.79	3.33	0.00033486
102412_at	Nup107	nucleoporin 107	1982.95	913.36	2.17	0.00033525
93559_at	Apex1	apurinic/apyrimidinic endonuclea	473.92	957.98	-2.02	0.00033615
97421_at	Smc2	structural maintenance of chrom	111.49	349.42	-3.13	0.0003371
92511_at	Aanat	arylalkylamine N-acetyltransferas	179.22	373.28	-2.08	0.00033755
101958_f_at	Tfdp1	transcription factor Dp 1	271.91	550.83	-2.03	0.00033772
103711_at	Casp9	caspase 9	575.25	239.05	2.41	0.00033825
93589_at	Entpd4 /// LOC10004	ectonucleoside triphosphate diph	4467.47	1420.42	3.15	0.00034186
96613_at	5730536A07Rik	RIKEN cDNA 5730536A07 gene	223.28	557.02	-2.49	0.0003442
103717_at	Wwp2	WW domain containing E3 ubiqu	3534.91	378.79	9.33	0.00034431
104446_f_at	4933428G09Rik	RIKEN cDNA 4933428G09 gene	422.40	160.74	2.63	0.00034501
160949_at	Parg	poly (ADP-ribose) glycohydrolase	1306.92	332.04	3.94	0.00034579
102360_at	Mthfr	5,10-methylenetetrahydrofolate	839.90	248.24	3.38	0.00034741
96806_at	Lpin2	lipin 2	824.41	380.45	2.17	0.00034802
161616_f_at	Rprm	reprimo, TP53 dependent G2 arre	2092.84	222.97	9.39	0.00034808
97434_at	Nsun4	NOL1/NOP2/Sun domain family,	425.21	101.17	4.20	0.00034821
103260_at	Dock5	dedicator of cytokinesis 5	1978.18	320.37	6.17	0.00034936
101058_at	Amy1	amylase 1, salivary	309.89	81.32	3.81	0.00034943
101966_s_at	Rnf13	ring finger protein 13	120.35	531.64	-4.42	0.00034946
93083_at	Anxa5	annexin A5	4260.51	974.25	4.37	0.00034971
96667_at	Vps41	vacuolar protein sorting 41 (yeas	2599.61	985.85	2.64	0.00035158
99366_at	Pqlc3	PQ loop repeat containing	2666.51	107.52	24.80	0.00035198
102794_at	Cxcr4	chemokine (C-X-C motif) recepto	46.57	114.31	-2.45	0.00035492
95586_at	P2rx4	purinergic receptor P2X, ligand-g	2510.39	257.61	9.75	0.00035499
160239_at	Psmd6	proteasome (prosome, macropai	1063.19	2237.96	-2.10	0.00035507
104374_at	Serpina3n	serine (or cysteine) peptidase inh	3841.37	1015.03	3.78	0.00035535
96065_at	Lxn	latexin	1186.53	412.48	2.88	0.00035561
101560_at	Emb	embigin	3234.65	335.61	9.64	0.00035585
162341_r_at	Akr1b3	aldo-keto reductase family 1, me	1836.33	3788.77	-2.06	0.00035641
162034_r_at	Antxr2	Anthrax toxin receptor 2	153.20	55.57	2.76	0.00035679

94208_at	LOC100046302 /// Pc	protein disulfide isomerase assoc	191.36	926.51	-4.84	0.00035694
93111_at	Kpnb1	karyopherin (importin) beta 1	3807.74	1256.23	3.03	0.00035717
97486_at	U2af1	U2 small nuclear ribonucleoprote	288.57	855.99	-2.97	0.00035788
93493_at	Ddx5	DEAD (Asp-Glu-Ala-Asp) box poly	505.19	1864.38	-3.69	0.00035816
96738_at	Adam9	a disintegrin and metallopeptidas	755.95	175.37	4.31	0.00035854
95632_f_at	LOC637711 /// Mvk	mevalonate kinase /// similar to r	1588.11	387.95	4.09	0.00035862
160846_at	Nek6	NIMA (never in mitosis gene a)-re	707.51	335.06	2.11	0.00035927
98005_at	Pkia	protein kinase inhibitor, alpha	254.03	721.53	-2.84	0.00036003
102389_s_at	Gap43	growth associated protein 43	7702.72	3052.68	2.52	0.00036011
98766_at	Sh3bp5	SH3-domain binding protein 5 (B	94.72	220.40	-2.33	0.00036271
99186_at	Ccna2	cyclin A2	742.66	1643.74	-2.21	0.0003628
98531_g_at	Gas5	growth arrest specific 5	1190.63	391.25	3.04	0.00036282
96578_r_at	Ubap2l	ubiquitin associated protein 2-lik	871.00	376.35	2.31	0.00036298
160484_at	Rtn4	reticulon 4	7207.87	2943.38	2.45	0.00036301
103023_at	Lcat	lecithin cholesterol acyltransferas	205.55	878.32	-4.27	0.00036584
160916_at	Eepd1	endonuclease/exonuclease/phos	609.61	177.19	3.44	0.00036777
94492_at	Dstn	destrin	10366.63	4783.65	2.17	0.00036796
94384_at	Ier3	immediate early response 3	148.83	300.98	-2.02	0.00036821
102819_at	Nap1l2	nucleosome assembly protein 1-l	335.04	764.89	-2.28	0.00037055
93020_at	Bex1	brain expressed gene 1	114.27	301.26	-2.64	0.00037109
103667_at	Atp13a3	ATPase type 13A3	915.37	362.59	2.52	0.00037234
97415_at	Rab3d	RAB3D, member RAS oncogene f	2995.55	589.76	5.08	0.00037293
92585_at	Map2k1	mitogen-activated protein kinase	1700.31	611.49	2.78	0.00037396
161389_f_at	Asnsd1 /// LOC67449	asparagine synthetase domain cc	508.79	174.30	2.92	0.00037586
101069_g_at	Mkrn1	makorin, ring finger protein, 1	212.45	584.75	-2.75	0.00037601
101890_f_at	Dnajc2	DnaJ (Hsp40) homolog, subfamily	1537.34	619.43	2.48	0.00037609
161084_at	Zfp612	zinc finger protein 612	583.46	62.77	9.29	0.00037757
102029_at	Il16	interleukin 16	218.02	622.05	-2.85	0.00037888
95139_at	Wipi2	WD repeat domain, phosphoinos	729.18	314.59	2.32	0.00037917
96271_at	Tmem123	transmembrane protein 123	171.19	414.33	-2.42	0.00038001
97890_at	Sgk1	serum/glucocorticoid regulated k	263.41	930.79	-3.53	0.00038006
96791_at	1500005K14Rik	RIKEN cDNA 1500005K14 gene	3133.87	1156.42	2.71	0.0003802
161519_f_at	---	---	2271.35	1031.27	2.20	0.00038091
102767_at	Gng12	guanine nucleotide binding prote	519.83	1055.80	-2.03	0.00038238
161817_f_at	Spsb1	splA/ryanodine receptor domain	836.98	324.79	2.58	0.0003824
99102_at	Usp9x	ubiquitin specific peptidase 9, X c	443.97	199.44	2.23	0.00038449
160156_at	0910001A06Rik	RIKEN cDNA 0910001A06 gene	156.37	404.17	-2.58	0.00038891
103767_f_at	Rrm2b	ribonucleotide reductase M2 B (T	1321.86	524.24	2.52	0.00038957
94694_at	Pcsk1	proprotein convertase subtilisin/	450.63	92.55	4.87	0.00038968
103345_at	Spna2	spectrin alpha 2	4352.81	1380.75	3.15	0.00039046
93372_at	Anp32a	acidic (leucine-rich) nuclear phos	57.88	170.28	-2.94	0.00039081
97937_at	Klf5	Kruppel-like factor 5	322.27	126.84	2.54	0.00039138
160356_at	Cmpk1	cytidine monophosphate (UMP-C	2358.20	1111.33	2.12	0.00039175
96338_at	Egln2	EGL nine homolog 2 (C. elegans)	6718.52	2715.85	2.47	0.00039203
93324_at	Zfp36l1	zinc finger protein 36, C3H type-l	258.24	833.75	-3.23	0.00039209
97124_at	LOC14210	hypothetical LOC14210	46.34	457.09	-9.86	0.00039253
94056_at	Scd1	stearoyl-Coenzyme A desaturase	8102.10	2157.43	3.76	0.00039393
95529_at	Dbnl	drebrin-like	3043.10	790.05	3.85	0.00039424
99632_at	Mad2l1	MAD2 (mitotic arrest deficient, h	230.00	467.53	-2.03	0.00039464
160876_at	Bcap29	B-cell receptor-associated protei	1442.01	243.22	5.93	0.00039503
103497_at	BC025546	cDNA sequence BC025546	378.82	87.17	4.35	0.00039537
160582_at	Mybpc3	myosin binding protein C, cardiac	438.30	1942.32	-4.43	0.00039551
102063_at	Pdpk1	3-phosphoinositide dependent pr	848.82	168.93	5.02	0.00039591
101062_at	Hmox2	heme oxygenase (decycling) 2	505.39	238.30	2.12	0.00039624
96677_at	Setd8	SET domain containing (lysine me	1732.78	545.07	3.18	0.00039659

160623_at	Cdkl2	cyclin-dependent kinase-like 2 (C	492.43	101.65	4.84	0.00039755
102012_at	Skap2	src family associated phosphoprc	714.99	355.69	2.01	0.00039761
97593_f_at	Flii	flightless I homolog (Drosophila)	5667.06	866.80	6.54	0.00039822
92277_at	Myo1e	myosin IE	233.14	72.32	3.22	0.00039848
99845_at	Slc1a6	solute carrier family 1 (high affini	473.10	2700.31	-5.71	0.00039864
160905_s_at	A030009H04Rik	RIKEN cDNA A030009H04 gene	105.28	467.44	-4.44	0.00040015
103006_at	Atf5	activating transcription factor 5	658.65	245.97	2.68	0.00040039
104747_at	Slc1a1	solute carrier family 1 (neuronal/	61.92	128.73	-2.08	0.00040186
100116_at	2810417H13Rik	RIKEN cDNA 2810417H13 gene	77.56	292.52	-3.77	0.00040485
97267_at	6330407G11Rik	RIKEN cDNA 6330407G11 gene	2002.39	890.31	2.25	0.00040543
160281_at	Lsm14a	LSM14 homolog A (SCD6, S. cere	445.31	952.87	-2.14	0.00040598
99603_g_at	Klf10	Kruppel-like factor 10	1439.58	503.14	2.86	0.00040761
103326_at	Tbcel	tubulin folding cofactor E-like	1193.02	375.51	3.18	0.00040852
93748_at	Grinl1a	glutamate receptor, ionotropic, N	3791.78	1708.02	2.22	0.00040864
98843_at	Zic2	zinc finger protein of the cerebell	88.02	192.84	-2.19	0.00040908
98335_at	Rfc1	replication factor C (activator 1) 1	989.61	321.25	3.08	0.00040926
102983_at	Smad1	MAD homolog 1 (Drosophila)	2227.65	635.62	3.50	0.00040938
99047_at	Mobp	myelin-associated oligodendrocy	155.74	1217.07	-7.81	0.00040968
94338_g_at	Gas2	growth arrest specific 2	613.99	130.02	4.72	0.00041035
94464_at	Clcn3	chloride channel 3	1703.43	353.94	4.81	0.00041498
103756_at	BC023829 /// LOC10(	cDNA sequence BC023829 /// sin	2408.03	1096.74	2.20	0.00041606
100139_at	Pcsk1n	proprotein convertase subtilisin/	4566.79	1117.08	4.09	0.00041921
99095_at	LOC100048299 /// M	Max protein /// similar to Myn pr	177.96	663.58	-3.73	0.00041992
104071_at	Tnpo2	transportin 2 (importin 3, karyop	4695.17	1937.15	2.42	0.00042194
95119_at	1110038D17Rik	RIKEN cDNA 1110038D17 gene	1337.31	399.34	3.35	0.00042216
96829_at	D19Wsu162e	DNA segment, Chr 19, Wayne Sta	2500.02	728.29	3.43	0.0004238
93984_at	Atpif1	ATPase inhibitory factor 1	1956.22	4356.11	-2.23	0.00042381
160171_f_at	Acot9	acyl-CoA thioesterase 9	1460.65	426.58	3.42	0.00042664
103027_at	1810030O07Rik	RIKEN cDNA 1810030O07 gene	1083.87	373.06	2.91	0.00042754
101055_at	Ctsa	cathepsin A	1811.87	812.25	2.23	0.00043056
100990_g_at	Itgb1bp1	integrin beta 1 binding protein 1	105.28	537.10	-5.10	0.00043087
100635_at	Sar1a	SAR1 gene homolog A (S. cerevisi	4769.77	1618.40	2.95	0.00043199
161119_at	Epha5	Eph receptor A5	283.50	64.29	4.41	0.0004325
95526_at	Xpo7	exportin 7	1220.45	543.82	2.24	0.00043277
161613_at	Chmp7	CHMP family, member 7	1275.45	454.14	2.81	0.00043415
103748_at	4933407C03Rik	RIKEN cDNA 4933407C03 gene	5046.28	625.37	8.07	0.00043429
101502_at	Tgif1	TG interacting factor 1	104.57	230.45	-2.20	0.00043531
96653_at	Gm1604 /// LOC1000	ribonuclease T2B /// gene model	387.68	1916.38	-4.94	0.00043535
96208_at	Grlf1	glucocorticoid receptor DNA binc	1197.28	561.32	2.13	0.0004356
102047_at	LOC100045684 /// N	N-myristoyltransferase 1 /// simi	2447.51	585.11	4.18	0.00043566
97325_at	LOC100044756 /// Px	PX domain containing serine/thre	1658.28	465.81	3.56	0.00043636
99645_at	4921506J03Rik	RIKEN cDNA 4921506J03 gene	1084.96	2197.38	-2.03	0.00043658
100912_at	Dph5	DPH5 homolog (S. cerevisiae)	378.94	168.61	2.25	0.00043731
98544_at	Guk1	guanylate kinase 1	2603.54	768.30	3.39	0.00043805
94005_at	Pmpcb	peptidase (mitochondrial process	636.64	251.92	2.53	0.00043836
97311_at	6720456B07Rik	RIKEN cDNA 6720456B07 gene	10456.69	4649.72	2.25	0.00043859
97160_at	Sparc	secreted acidic cysteine rich glyc	469.70	1291.09	-2.75	0.00044025
94870_f_at	Sar1b	SAR1 gene homolog B (S. cerevisi	369.01	895.70	-2.43	0.00044042
161221_f_at	Asns	asparagine synthetase	750.61	246.63	3.04	0.0004405
92872_at	Necap1	NECAP endocytosis associated 1	4528.35	1530.33	2.96	0.00044392
103532_at	Eomes	eomesodermin homolog (Xenopu	25.91	56.60	-2.18	0.00044392
104709_at	Sec23a	SEC23A (S. cerevisiae)	1764.19	685.38	2.57	0.00044408
92633_at	Ctsz	cathepsin Z	692.93	113.63	6.10	0.00044815
97474_r_at	Ptn	pleiotrophin	52.23	290.86	-5.57	0.00044826
97203_at	Marcksl1	MARCKS-like 1	195.18	3813.73	-19.54	0.00044889

94895_at	Ythdf2	YTH domain family 2	107.02	371.46	-3.47	0.00044907
102144_f_at	---	---	74.07	311.49	-4.21	0.00045095
100690_at	Th	tyrosine hydroxylase	1619.87	352.12	4.60	0.00045142
160105_r_at	Pigk	phosphatidylinositol glycan anch	494.02	144.32	3.42	0.0004528
93747_at	Ptplad1	protein tyrosine phosphatase-like	9476.94	3961.85	2.39	0.0004529
98418_at	Dvl1	dishevelled, dsh homolog 1 (Dros	2942.56	1397.49	2.11	0.00045312
161006_at	Slco3a1	solute carrier organic anion trans	2688.50	364.42	7.38	0.00045385
101591_at	Xpnpep1	X-prolyl aminopeptidase (aminop	272.42	658.77	-2.42	0.00045393
160540_at	Bag1	Bcl2-associated athanogene 1	1254.74	574.20	2.19	0.00045394
94739_at	Trpc1	transient receptor potential catio	66.58	144.21	-2.17	0.00045633
101977_at	LOC100047647 /// Nu	nudix (nucleotide diphosphate lir	7629.01	2642.69	2.89	0.00045658
101992_at	Psmb6	proteasome (prosome, macropai	664.00	1426.92	-2.15	0.00045699
100621_at	Rnh1	ribonuclease/angiogenin inhibito	2093.34	764.43	2.74	0.000457
93250_r_at	Hmgb2 /// LOC66635	high mobility group box 2 /// sim	30.12	236.05	-7.84	0.00045717
97526_at	Ap3m1	adaptor-related protein complex	1526.04	464.55	3.28	0.0004574
102395_at	Pmp22	peripheral myelin protein	3362.30	236.16	14.24	0.0004576
101892_f_at	Aktip	thymoma viral proto-oncogene 1	1146.70	201.99	5.68	0.00046048
95752_at	Sbds	Shwachman-Bodian-Diamond syr	4191.31	1324.88	3.16	0.00046053
93536_at	Bax	Bcl2-associated X protein	177.24	697.05	-3.93	0.00046068
97884_at	Mrps11	mitochondrial ribosomal protein	198.72	486.92	-2.45	0.00046349
160836_at	Sema4d	sema domain, immunoglobulin d	2060.01	789.13	2.61	0.00046454
94374_at	Wdr13	WD repeat domain 13	1565.46	717.25	2.18	0.00046511
98084_at	Arl2bp	ADP-ribosylation factor-like 2 bin	1477.26	3189.66	-2.16	0.00046512
97352_f_at	Cox6b2	cytochrome c oxidase subunit VIb	108.71	242.81	-2.23	0.00046524
94469_at	Mat2b	methionine adenosyltransferase	2603.99	1134.46	2.30	0.00046534
95698_at	Ndufb7	NADH dehydrogenase (ubiquinor	1254.07	3106.38	-2.48	0.00046652
161765_f_at	Rgs10	regulator of G-protein signalling 1	2631.15	669.61	3.93	0.00046677
162145_r_at	Pgs1	phosphatidylglycerophosphate sy	905.37	376.18	2.41	0.00047053
95061_at	Bcas2	breast carcinoma amplified sequ	182.86	70.23	2.60	0.00047387
161171_at	Dusp8	dual specificity phosphatase 8	758.37	333.37	2.27	0.00047668
102984_g_at	Smad1	MAD homolog 1 (Drosophila)	3737.58	1343.39	2.78	0.00047846
101934_at	Fez2	fasciculation and elongation prot	1286.83	511.57	2.52	0.00047954
101932_at	Ptpre	protein tyrosine phosphatase, re	1725.63	423.54	4.07	0.00048007
99046_at	Mobp	myelin-associated oligodendrocy	26.61	280.52	-10.54	0.00048437
101060_at	Pdia3	protein disulfide isomerase assoc	321.24	840.12	-2.62	0.00048528
103406_at	Gpn1	GPN-loop GTPase 1	5260.89	865.98	6.08	0.0004855
104334_at	2310004I24Rik	RIKEN cDNA 2310004I24 gene	1586.73	648.45	2.45	0.00048935
104212_at	Lrpprc	leucine-rich PPR-motif containing	3192.57	617.51	5.17	0.00048999
98077_at	Snrpd3	small nuclear ribonucleoprotein I	114.55	265.80	-2.32	0.00049051
93188_at	Dkk3	dickkopf homolog 3 (Xenopus lae	688.98	293.23	2.35	0.0004913
92408_at	D1Ertd53e	DNA segment, Chr 1, ERATO Doi 5	82.04	191.57	-2.34	0.00049147
104302_f_at	Commd9	COMM domain containing 9	1337.55	280.89	4.76	0.00049165
93159_at	Syt2	synaptotagmin II	6329.40	2431.25	2.60	0.00049214
94954_at	Anapc4	anaphase promoting complex sul	2850.15	753.65	3.78	0.00049448
93682_at	Ldb2	LIM domain binding 2	4889.52	937.87	5.21	0.00050296
160547_s_at	Txnip	thioredoxin interacting protein	637.40	1356.83	-2.13	0.00050479
96110_at	Cbr1	carbonyl reductase 1	1266.88	556.97	2.27	0.00050703
103298_at	Speg	SPEG complex locus	269.54	114.37	2.36	0.0005103
93203_f_at	Foxn2	forkhead box N2	34.66	110.33	-3.18	0.00051167
97834_g_at	Pfkp	phosphofructokinase, platelet	5618.29	241.43	23.27	0.00051267
103531_f_at	Ero1lb	ERO1-like beta (S. cerevisiae)	1120.24	157.72	7.10	0.0005169
101580_at	Cox7b	cytochrome c oxidase subunit VII	767.97	1917.81	-2.50	0.00051824
160328_at	Lonp1	lon peptidase 1, mitochondrial	1625.11	717.12	2.27	0.00051841
100089_at	Ppic	peptidylprolyl isomerase C	167.36	571.07	-3.41	0.00051852
104285_at	Hmgcr	3-hydroxy-3-methylglutaryl-Coen	1452.70	587.97	2.47	0.00051881

98094_f_at	Amfr /// LOC1000462	autocrine motility factor recepto	2831.54	1114.40	2.54	0.0005236
97915_at	Plekhb2	pleckstrin homology domain cont	6160.49	2427.76	2.54	0.00052416
96269_at	Idi1	isopentenyl-diphosphate delta is	2783.51	1224.71	2.27	0.00052466
93697_at	Cbx4	chromobox homolog 4 (Drosophi	347.50	853.26	-2.46	0.00052807
94501_at	Sgpp1	sphingosine-1-phosphate phosph	577.82	216.21	2.67	0.00053293
96283_at	Itm2c	integral membrane protein 2C	4557.62	2064.07	2.21	0.00053431
96890_at	Lonp2	lon peptidase 2, peroxisomal	2384.93	751.09	3.18	0.00053729
101913_at	Clcn5	chloride channel 5	2100.17	285.45	7.36	0.0005374
161617_f_at	---	---	60.55	29.67	2.04	0.00053788
101088_f_at	Cnbp	cellular nucleic acid binding prote	932.90	1980.29	-2.12	0.00053845
94485_at	Peci	peroxisomal delta3, delta2-enoyl	1659.01	592.35	2.80	0.00053852
95111_i_at	Ppil2	peptidylprolyl isomerase (cyclopl	141.81	42.58	3.33	0.00053853
94144_g_at	Gfap	glial fibrillary acidic protein	259.75	940.76	-3.62	0.00053864
161806_r_at	Atp6ap1	ATPase, H+ transporting, lysosom	464.19	190.02	2.44	0.00053865
93565_at	Klc1	kinesin light chain 1	5698.01	2537.71	2.25	0.00053867
99577_at	Kitl	kit ligand	428.75	989.45	-2.31	0.00053868
92515_at	Isl1	ISL1 transcription factor, LIM/hor	327.52	158.69	2.06	0.00054186
97227_at	Gna12	guanine nucleotide binding prote	47.69	113.78	-2.39	0.00054251
96112_at	Etfa	electron transferring flavoprotein	1296.67	546.78	2.37	0.0005466
98982_at	Tmpo	thymopoietin	404.71	995.25	-2.46	0.00055152
93414_at	Abcb1b	ATP-binding cassette, sub-family	51.59	25.42	2.03	0.00055325
104161_at	Cpsf2	cleavage and polyadenylation spe	731.76	247.42	2.96	0.00055371
101437_at	Slk	STE20-like kinase (yeast)	257.61	125.28	2.06	0.00055458
98300_at	Cacna2d3	calcium channel, voltage-depend	528.88	1068.14	-2.02	0.00056039
102305_at	Gpr37l1	G protein-coupled receptor 37-lik	882.38	2949.42	-3.34	0.00056328
94944_at	Prkar1b	protein kinase, cAMP dependent	6028.14	2615.04	2.31	0.00056401
93909_f_at	Ccrn4l /// ENSMUSG(	CCR4 carbon catabolite repressio	271.86	1167.31	-4.29	0.00056656
96605_at	Tmem176a	transmembrane protein 176A	1591.85	266.88	5.96	0.00056704
102141_f_at	4933434E20Rik	RIKEN cDNA 4933434E20 gene	809.44	322.30	2.51	0.00057308
104316_at	Gna13	guanine nucleotide binding prote	329.87	135.54	2.43	0.00057332
98127_at	Capza2	capping protein (actin filament) r	4842.42	1561.97	3.10	0.0005766
160307_at	Pi4k2a	phosphatidylinositol 4-kinase typ	2269.39	909.04	2.50	0.00057673
92610_at	Rdbp	RD RNA-binding protein	1263.78	429.51	2.94	0.00057682
98944_at	LOC100048726 /// Se	SEC23B (S. cerevisiae) /// similar	2445.52	1125.01	2.17	0.00058014
95345_at	Tpbg	trophoblast glycoprotein	112.85	243.12	-2.15	0.00058023
103527_at	Slc35e4	solute carrier family 35, member	1767.42	651.51	2.71	0.00058045
104139_at	P4ha1	procollagen-proline, 2-oxoglutara	759.67	260.35	2.92	0.00058055
98808_at	Neurod2	neurogenic differentiation 2	786.69	1918.40	-2.44	0.00058058
160929_at	Mettl3	methyltransferase-like 3	323.42	157.19	2.06	0.00058075
104288_at	Cul4a	cullin 4A	1329.70	503.91	2.64	0.0005811
96719_i_at	Pvalb	parvalbumin	5201.35	16479.27	-3.17	0.00058122
97737_f_at	Nlrx1	NLR family member X1	1186.19	282.42	4.20	0.00058279
103309_at	Frap1	FK506 binding protein 12-rapamy	2124.94	557.67	3.81	0.00058499
100718_at	EG625801 /// LOC10(	prothymosin alpha /// predicted	2526.11	5934.09	-2.35	0.00058515
103738_at	BC037034	cDNA sequence BC037034	4676.64	2190.58	2.13	0.00058528
93836_at	Bnip3	BCL2/adenovirus E1B interacting	1404.67	475.24	2.96	0.00058685
102320_at	Snx12	sorting nexin 12	2187.34	599.02	3.65	0.00058823
101362_at	Mapk9	mitogen-activated protein kinase	196.05	416.39	-2.12	0.0005884
98872_at	Ugt8a	UDP galactosyltransferase 8A	41.44	154.55	-3.73	0.0005893
97451_at	Mcfd2	multiple coagulation factor defici	2306.61	480.27	4.80	0.00059348
102090_f_at	Smyd5	SET and MYND domain containin	503.20	199.61	2.52	0.00059605
96252_at	Pdcd6ip	programmed cell death 6 interac	1365.75	652.66	2.09	0.00059872
94312_at	Pdxdc1	pyridoxal-dependent decarboxyla	174.37	418.94	-2.40	0.00059958
97829_at	Cdipt	CDP-diacylglycerol--inositol 3-phc	4083.81	2027.76	2.01	0.00060181
95508_at	Nckap1	NCK-associated protein 1	8317.07	3667.28	2.27	0.00060286

94194_s_at	Hcn2	hyperpolarization-activated, cycli	282.14	108.33	2.60	0.00060717
AFFX-DapX-3_at	---	---	957.85	45.34	21.13	0.00061126
93411_at	Sema7a	sema domain, immunoglobulin d	76.46	250.12	-3.27	0.00061186
160922_at	Ogfod2	2-oxoglutarate and iron-depende	597.34	219.53	2.72	0.0006119
103414_at	Skiv2l	superkiller viralicidic activity 2-lik	1021.74	462.91	2.21	0.00061694
102299_at	Prkca	protein kinase C, alpha	1148.64	356.88	3.22	0.00061915
103536_at	Tmeff2	transmembrane protein with EGF	1154.28	269.32	4.29	0.00061962
98121_at	Fnta /// LOC1000469	farnesyltransferase, CAAX box, al	1983.21	972.82	2.04	0.00062011
103584_at	5830471E12Rik	RIKEN cDNA 5830471E12 gene	5636.64	1997.96	2.82	0.00062376
95939_i_at	BC052328	cDNA sequence BC052328	487.79	237.55	2.05	0.00062568
94811_s_at	Gtf2h1 /// Ndn	general transcription factor II H, p	738.35	1935.73	-2.62	0.0006273
96319_at	Cdc20	cell division cycle 20 homolog (S.	288.31	677.21	-2.35	0.0006274
103619_at	Cyb5b	cytochrome b5 type B	2573.76	833.78	3.09	0.00062857
102791_at	Psmb8	proteasome (prosome, macropai	300.48	142.10	2.11	0.00063268
96881_at	Commd6	COMM domain containing 6	392.28	1029.90	-2.63	0.00064293
93272_at	Stk16	serine/threonine kinase 16	1335.82	467.32	2.86	0.00064368
95584_at	Dppa2	developmental pluripotency asso	435.08	87.12	4.99	0.00064375
93895_s_at	Itpr1	inositol 1,4,5-triphosphate recep	78.11	548.43	-7.02	0.00064657
103829_at	Herc2	hect (homologous to the E6-AP (I	558.17	192.52	2.90	0.00064799
160970_at	LOC100047199 /// Oc	outer dense fiber of sperm tails 2	371.93	160.48	2.32	0.00065001
98599_at	Hdgfrp2	hepatoma-derived growth factor,	643.95	210.01	3.07	0.00065362
95680_at	Ppp1r2	protein phosphatase 1, regulator	1933.95	528.66	3.66	0.00065418
100156_at	Mcm5	minichromosome maintenance d	378.45	1012.91	-2.68	0.00065495
92939_at	Gabra6	gamma-aminobutyric acid (GABA	59.73	2284.11	-38.24	0.00065588
102859_at	Reep1	receptor accessory protein 1	6201.62	1745.44	3.55	0.0006559
160223_at	Ttc27	tetratricopeptide repeat domain	255.31	86.54	2.95	0.00065692
160217_at	2310001A20Rik	RIKEN cDNA 2310001A20 gene	603.27	263.21	2.29	0.00065875
104418_at	Znrf2	zinc and ring finger 2	308.96	128.50	2.40	0.00065892
99458_i_at	Mark2	MAP/microtubule affinity-regulat	3750.46	1166.25	3.22	0.00065982
104304_r_at	Polr3k	polymerase (RNA) III (DNA direct	70.89	179.87	-2.54	0.00066265
93896_at	Ptprd	protein tyrosine phosphatase, re	603.81	250.66	2.41	0.00066389
103762_at	Gtf2f1	general transcription factor IIF, p	2128.66	570.52	3.73	0.00066701
93527_at	2310051E17Rik /// Kl	Kruppel-like factor 9 /// RIKEN cD	94.24	281.54	-2.99	0.00066745
160388_at	Sc4mol	sterol-C4-methyl oxidase-like	1813.68	492.27	3.68	0.00066761
93780_at	Them2	thioesterase superfamily membe	935.18	466.07	2.01	0.00066889
97297_at	Pcp4l1	Purkinje cell protein 4-like 1	4094.57	466.08	8.79	0.00067023
99457_at	Mki67	antigen identified by monoclonal	36.29	125.57	-3.46	0.00067173
160138_at	Mxi1	Max interacting protein 1	485.31	1160.09	-2.39	0.00067476
96864_at	Mrps26	mitochondrial ribosomal protein	720.06	326.03	2.21	0.00067552
99666_at	Cs	citrate synthase	3679.55	1721.56	2.14	0.00068246
100886_f_at	Mrpl45	mitochondrial ribosomal protein	805.77	377.38	2.14	0.00068593
94516_f_at	Penk1	preproenkephalin 1	279.93	815.50	-2.91	0.00068697
94415_at	Bach1	BTB and CNC homology 1	196.20	477.91	-2.44	0.00068703
95144_at	Arpc1a	actin related protein 2/3 comple	2360.29	702.64	3.36	0.00069101
102332_at	Ulk1	Unc-51 like kinase 1 (C. elegans)	1159.27	432.83	2.68	0.00069107
162095_f_at	Gas7	growth arrest specific 7	115.11	324.01	-2.81	0.00069116
160419_r_at	Ubac2	Ubiquitin associated domain cont	248.00	66.28	3.74	0.00069119
96887_at	Ndufb11	NADH dehydrogenase (ubiquinor	1297.73	3464.03	-2.67	0.00070151
98586_at	Nap1l1	nucleosome assembly protein 1-l	416.89	186.70	2.23	0.00070338
100733_at	Psma2	proteasome (prosome, macropai	1138.65	3013.29	-2.65	0.00070494
94054_at	Cttn	cortactin	3039.93	1416.83	2.15	0.00070589
102696_s_at	Pitpnb	phosphatidylinositol transfer pro	30.39	103.25	-3.40	0.00070855
102085_at	Insm1	insulinoma-associated 1	144.38	389.95	-2.70	0.00070875
104425_at	Inadl	InaD-like (Drosophila)	305.82	68.44	4.47	0.00070962
161133_at	Calm2	Calmodulin 2	240.29	503.86	-2.10	0.00071001

93539_at	Anapc13	anaphase promoting complex sul	299.85	716.85	-2.39	0.00071469
101031_at	Surf1	surfeit gene 1	1420.06	597.36	2.38	0.0007175
94002_at	Cul1	cullin 1	1874.13	868.75	2.16	0.00071754
96322_at	Edf1	endothelial differentiation-relate	220.81	586.83	-2.66	0.000719
101937_s_at	Clk4	CDC like kinase 4	71.51	205.25	-2.87	0.00072306
98154_at	Gtf3c2 /// Mpv17	Mpv17 transgene, kidney disease	736.70	269.64	2.73	0.00072709
104296_at	Hnrpul2	heterogeneous nuclear ribonucle	127.77	304.63	-2.38	0.00072763
100559_at	Dhx16	DEAH (Asp-Glu-Ala-His) box polyp	751.70	287.71	2.61	0.00073624
162166_f_at	Nrsn1	neurensin 1	2247.38	616.62	3.64	0.00073642
161358_r_at	Dpep3	dipeptidase 3	446.13	929.95	-2.08	0.00073666
97102_at	Yme1l1	YME1-like 1 (S. cerevisiae)	554.99	126.50	4.39	0.00073894
96191_at	Arfgef1	ADP-ribosylation factor guanine r	2686.18	1102.87	2.44	0.0007397
98461_at	Klc4	kinesin light chain 4	1261.17	549.58	2.29	0.00074271
101787_f_at	2700079J08Rik /// Cc	CCR4 carbon catabolite repressio	3611.82	1324.71	2.73	0.00074365
98491_at	Arl8b	ADP-ribosylation factor-like 8B	48.37	187.21	-3.87	0.0007458
93058_at	Eif1a	eukaryotic translation initiation f	893.04	275.62	3.24	0.00074856
98594_at	1190002N15Rik	RIKEN cDNA 1190002N15 gene	305.65	725.51	-2.37	0.0007493
102296_at	Pcsk2	proprotein convertase subtilisin/	1602.81	499.57	3.21	0.00075034
101946_at	Lypla1	lysophospholipase 1	40.15	183.75	-4.58	0.0007524
96011_at	Matr3	matrin 3	57.20	530.72	-9.28	0.00075698
100458_at	Napb	N-ethylmaleimide sensitive fusio	2729.68	447.28	6.10	0.0007616
103442_at	Dhrs7b /// LOC10004	dehydrogenase/reductase (SDR f	2114.28	742.46	2.85	0.00076168
93867_at	Abcd4	ATP-binding cassette, sub-family	343.04	104.76	3.27	0.00076454
93421_at	Pftk1	PFTAIRE protein kinase 1	3029.15	558.04	5.43	0.00076555
161757_f_at	Ipo5 /// LOC1000443	importin 5 /// hypothetical prote	742.07	342.47	2.17	0.00076745
102122_f_at	---	---	891.04	298.62	2.98	0.00076756
160098_s_at	Faf1	Fas-associated factor 1	165.00	349.96	-2.12	0.0007677
95002_at	D17Wsu92e	DNA segment, Chr 17, Wayne Sta	2845.41	969.54	2.93	0.00076808
160296_at	Wsb2	WD repeat and SOCS box-contair	2306.06	1093.73	2.11	0.00077021
97411_at	Ect2	ect2 oncogene	50.20	125.26	-2.50	0.00077146
162430_at	Tor1b	torsin family 1, member B	172.82	71.72	2.41	0.0007749
95156_g_at	Znrf1	zinc and ring finger 1	420.58	202.64	2.08	0.00077613
95940_f_at	BC052328	cDNA sequence BC052328	246.29	61.48	4.01	0.00078035
94079_at	4-Sep	septin 4	1037.15	2871.45	-2.77	0.00078474
93456_r_at	Bmp4	bone morphogenetic protein 4	24.60	59.79	-2.43	0.0007879
95431_at	Tomm70a	translocase of outer mitochondri	83.88	172.32	-2.05	0.0007896
93070_at	Ipo5	importin 5	1897.42	496.53	3.82	0.00079047
96680_at	Dnajb9	DnaJ (Hsp40) homolog, subfamily	182.02	368.90	-2.03	0.00079319
92892_at	Nrsn1	neurensin 1	1967.85	322.53	6.10	0.00079343
100579_s_at	Clta	clathrin, light polypeptide (Lca)	1081.43	509.58	2.12	0.00079574
95520_at	Tmbim1	transmembrane BAX inhibitor mo	498.67	222.11	2.25	0.00079592
97285_f_at	Ubxd1	UBX domain containing 1	1087.58	290.98	3.74	0.00079603
98470_at	Slc25a14	solute carrier family 25 (mitocho	532.70	215.66	2.47	0.00079611
96831_at	Pdia5	protein disulfide isomerase assoc	357.66	159.00	2.25	0.00079675
94241_at	Coasy	Coenzyme A synthase	425.34	132.05	3.22	0.00079734
102348_at	BC003993 /// LOC10(	cDNA sequence BC003993 /// hy	761.12	210.29	3.62	0.00079736
161013_f_at	Spsb1	splA/ryanodine receptor domain	910.31	279.34	3.26	0.00079788
96019_at	Sypl	synaptophysin-like protein	1473.58	507.60	2.90	0.0007984
104313_at	Pgm1 /// Pgm2	phosphoglucomutase 1 /// phosp	7054.04	1851.51	3.81	0.00080012
95470_at	Pak1ip1	PAK1 interacting protein 1	1132.17	256.54	4.41	0.00080136
101104_at	Dscr3	Down syndrome critical region ge	1456.57	678.01	2.15	0.00080375
93126_at	Ckb	creatine kinase, brain	4733.59	11629.86	-2.46	0.00080377
95405_at	Mesdc2	mesoderm development candida	1459.43	477.12	3.06	0.00081032
102941_at	LOC100044322 /// Ug	UDP-glucose ceramide glucosyltr	655.77	294.17	2.23	0.0008109
98128_at	Atp5j /// LOC654426	ATP synthase, H+ transporting, m	1428.48	3257.13	-2.28	0.00081096

94840_at	Hexa	hexosaminidase A	633.15	238.54	2.65	0.00081155
160230_at	Cox17	cytochrome c oxidase, subunit XV	1754.76	770.29	2.28	0.00081176
160948_at	Ppp3cc	protein phosphatase 3, catalytic s	678.06	154.50	4.39	0.00081198
93573_at	Mt1	metallothionein 1	399.47	1819.23	-4.55	0.00081509
100514_at	Gna13	guanine nucleotide binding prote	650.48	178.25	3.65	0.00081556
96086_at	1110031B06Rik	RIKEN cDNA 1110031B06 gene	3336.06	1600.95	2.08	0.00081585
93735_f_at	Psmc3	proteasome (prosome, macropai	3101.36	1255.92	2.47	0.00081844
93953_at	Prss12	protease, serine, 12 neurotrypsin	1058.61	302.77	3.50	0.0008187
97460_at	Ube2r2	ubiquitin-conjugating enzyme E2	5125.99	1892.47	2.71	0.00081886
101492_at	Pin1	protein (peptidyl-prolyl cis/trans	147.82	334.22	-2.26	0.00082052
95444_at	Tmem49	transmembrane protein 49	2673.79	1261.33	2.12	0.0008206
97989_at	Ppp3cb	protein phosphatase 3, catalytic s	138.05	359.78	-2.61	0.00082115
93810_at	Ctsd	cathepsin D	6011.35	2249.09	2.67	0.00082176
100079_at	Ndufb9	NADH dehydrogenase (ubiquinor	533.62	1352.08	-2.53	0.00082215
100026_at	Bcat1	branched chain aminotransferase	3221.95	1254.86	2.57	0.00082304
98070_at	Suds3	suppressor of defective silencing	2945.40	1314.92	2.24	0.00082425
97958_at	Prkcbp1	protein kinase C binding protein 1	417.68	197.14	2.12	0.00082529
160228_at	Cldnd1	claudin domain containing 1	180.92	380.01	-2.10	0.00083053
95149_at	Copz1	coatomer protein complex, subu	963.34	2011.15	-2.09	0.00083166
96920_at	Htra1	HtrA serine peptidase 1	3446.53	1337.97	2.58	0.00084824
100284_at	Zic4	zinc finger protein of the cerebell	60.32	165.38	-2.74	0.00085546
100086_at	Lrpap1	low density lipoprotein receptor-	3234.91	1602.97	2.02	0.00085981
96529_at	Ap1gbp1	AP1 gamma subunit binding prot	588.51	182.84	3.22	0.0008719
94024_at	Cdt1	chromatin licensing and DNA rep	349.93	703.10	-2.01	0.0008729
93499_at	Capza1	capping protein (actin filament) r	3251.66	1033.24	3.15	0.0008804
99930_s_at	Psen2	presenilin 2	2023.69	247.83	8.17	0.00088051
98136_at	LOC671878 /// Sms	spermine synthase /// similar to s	273.93	618.75	-2.26	0.00088178
93954_at	Gucy1b3	guanylate cyclase 1, soluble, beta	39.44	371.35	-9.42	0.00088197
103015_at	Bcl6	B-cell leukemia/lymphoma 6	343.52	129.87	2.65	0.00088391
104460_at	Cacna1g	calcium channel, voltage-depend	104.11	346.95	-3.33	0.0008856
103716_at	Cep350	centrosomal protein 350	1640.56	662.72	2.48	0.00089545
92934_at	Zfp90	zinc finger protein 90	673.52	183.68	3.67	0.00089582
160482_at	Acaa1a /// Acaa1b	acetyl-Coenzyme A acyltransferas	2154.90	863.81	2.49	0.00089615
102062_at	Smarcc1	SWI/SNF related, matrix associat	2731.97	419.37	6.51	0.00089626
103423_at	Cyb561	cytochrome b-561	3268.89	1327.21	2.46	0.00089943
102060_at	Golga4	golgi autoantigen, golgin subfami	1377.30	415.71	3.31	0.00090384
160185_at	Tagln3	transgelin 3	2961.55	1477.38	2.00	0.00090881
92220_s_at	Bin1	bridging integrator 1	306.16	639.39	-2.09	0.00091107
96674_at	Tnpo3	transportin 3	1716.43	536.71	3.20	0.00091664
98999_at	Adsl	adenylosuccinate lyase	1119.99	335.99	3.33	0.00091815
92558_at	Vcam1	vascular cell adhesion molecule 1	123.41	275.07	-2.23	0.00092078
160391_at	Fads1	fatty acid desaturase 1	2185.10	1087.96	2.01	0.0009229
93754_at	Ech1	enoyl coenzyme A hydratase 1, p	2407.88	794.82	3.03	0.00093005
160581_at	Atg16l1	autophagy-related 16-like 1 (yeas	1201.45	542.39	2.22	0.00093086
96526_at	D030029J20Rik	RIKEN cDNA D030029J20 gene	883.02	285.69	3.09	0.00093257
92574_at	Sdhd	succinate dehydrogenase comple	841.00	1964.71	-2.34	0.00093374
161895_s_at	Wdr81	WD repeat domain 81	4459.67	1980.96	2.25	0.00093896
93046_at	Nup50	nucleoporin 50	1902.00	476.51	3.99	0.00094501
160137_at	B3gnt2	UDP-GlcNAc:betaGal beta-1,3-N-	1328.12	339.22	3.92	0.00094573
98509_at	BC002199	cDNA sequence BC002199	4681.11	1435.07	3.26	0.00094706
97200_f_at	Snrpe	small nuclear ribonucleoprotein E	967.58	2059.70	-2.13	0.00094739
92648_at	Stxbp3a	syntaxin binding protein 3A	70.22	219.32	-3.12	0.00094753
98635_at	Ube2z	ubiquitin-conjugating enzyme E2	1659.18	614.80	2.70	0.00095676
160225_at	Gtf2b	general transcription factor IIB	2712.26	1076.24	2.52	0.00096866
96766_s_at	LOC100048488 /// Ty	TYRO3 protein tyrosine kinase 3 /	1129.56	519.10	2.18	0.00097027

160435_at	Cd99l2	Cd99 antigen-like 2	2389.41	758.65	3.15	0.00097608
95112_f_at	Ppil2	peptidylprolyl isomerase (cyclopl	686.08	316.69	2.17	0.00097757
101476_at	Pabpn1	poly(A) binding protein, nuclear 1	698.38	1579.54	-2.26	0.00097772
104163_at	Ipo8	importin 8	2172.24	655.23	3.32	0.00098452
94756_at	Hist1h3a /// Hist1h3l	histone cluster 2, H3c1 /// histon	354.24	88.14	4.02	0.0009856
98917_at	Hiatl1	hippocampus abundant transcrip	89.60	326.91	-3.65	0.0009862
101419_at	Tubb4	tubulin, beta 4	1174.85	2952.33	-2.51	0.00098669
161942_f_at	Cwf19l1	CWF19-like 1, cell cycle control (S	304.81	117.46	2.60	0.00098695
93753_at	Litaf	LPS-induced TN factor	876.58	308.37	2.84	0.00098988
99925_f_at	LOC100045019 /// Tu	tubulin, gamma 2 /// similar to Tu	772.43	307.56	2.51	0.00099358
94391_at	Gjb6	gap junction protein, beta 6	39.51	157.98	-4.00	0.00099398
103845_at	Slc31a1	solute carrier family 31, member	1698.30	469.13	3.62	0.00099415
99076_at	Nr1d2	nuclear receptor subfamily 1, gro	55.55	262.84	-4.73	0.00099575
92256_at	Ctsb	cathepsin B	1314.78	252.28	5.21	0.00099865
97199_at	Cpne1 /// Rbm12	RNA binding motif protein 12 ///	1303.97	618.14	2.11	0.0010023
92649_at	D0HXS9928E	DNA segment, human DXS9928E	1152.63	470.29	2.45	0.00101028
103466_at	Cyhr1	cysteine and histidine rich 1	797.68	318.43	2.51	0.00101433
92535_at	Ebf1	early B-cell factor 1	845.10	303.38	2.79	0.00101439
104274_at	Cpne3	copine III	4674.02	767.80	6.09	0.00101853
103699_i_at	Frat2	frequently rearranged in advance	1174.80	361.67	3.25	0.00101965
93089_at	Eif4a2	eukaryotic translation initiation f	2227.00	4604.34	-2.07	0.00101983
161270_i_at	Wnk1	WNK lysine deficient protein kina	1052.88	29.02	36.29	0.00102346
160785_at	Arhgap21	Rho GTPase activating protein 21	353.51	825.62	-2.34	0.00102853
94818_at	Ogt	O-linked N-acetylglucosamine (Gl	1343.76	607.44	2.21	0.00103038
161525_f_at	Rom1	rod outer segment membrane pr	102.04	37.65	2.71	0.00103076
104029_at	Clgn	calmegin	759.10	214.40	3.54	0.00103106
102892_at	Kcnab2	potassium voltage-gated channel	921.66	154.07	5.98	0.00103116
92722_f_at	Six1	sine oculis-related homeobox 1 h	743.83	134.33	5.54	0.00103581
102114_f_at	Angptl4	angiopoietin-like 4	910.40	390.25	2.33	0.00103591
92710_at	Rgnef	Rho-guanine nucleotide exchang	950.26	371.49	2.56	0.00103929
94288_at	Hist1h1c	histone cluster 1, H1c	2012.76	718.03	2.80	0.00104107
104213_at	Upp2	uridine phosphorylase 2	1027.02	369.87	2.78	0.00104678
103222_at	Eps8 /// LOC632638	epidermal growth factor recepto	31.87	238.33	-7.48	0.0010469
95028_r_at	LOC668030 /// RP23-	novel KRAB box and zinc finger, C	1207.93	394.28	3.06	0.00105284
98013_at	D15Ertd621e	DNA segment, Chr 15, ERATO Do	648.64	165.09	3.93	0.00105778
102196_at	Gna11	guanine nucleotide binding prote	1919.82	829.08	2.32	0.00105936
94812_at	Gtf2h1	general transcription factor II H, p	1597.27	653.83	2.44	0.00106204
160113_at	Brap	BRCA1 associated protein	1372.47	680.61	2.02	0.00107794
103556_at	Angptl2	angiopoietin-like 2	1741.14	846.17	2.06	0.00107836
160801_at	Pqlc1	PQ loop repeat containing 1	4735.93	1189.81	3.98	0.00108565
99169_at	Carm1	coactivator-associated arginine m	1307.97	588.90	2.22	0.00108655
104183_at	Tubgcp4	tubulin, gamma complex associat	996.57	406.59	2.45	0.00108757
96017_at	0610006I08Rik	RIKEN cDNA 0610006I08 gene	1454.03	3503.96	-2.41	0.00109141
103933_at	Siae	sialic acid acetylesterase	273.91	126.33	2.17	0.0010959
98508_s_at	Ppap2a	phosphatidic acid phosphatase 2a	894.65	201.85	4.43	0.00109776
93045_at	Abcd3	ATP-binding cassette, sub-family	3304.98	571.43	5.78	0.00109819
94010_g_at	LOC100045866 /// Tc	transcription elongation factor B	284.34	608.75	-2.14	0.00109976
96591_at	Reln	reelin	140.26	2218.52	-15.82	0.0010998
93040_at	Fxyd1	FXYD domain-containing ion tran	646.41	1576.14	-2.44	0.0011003
102864_at	Hoxa7	homeo box A7	701.13	304.21	2.30	0.00110282
104119_at	2610024E20Rik	RIKEN cDNA 2610024E20 gene	1971.37	524.66	3.76	0.00110744
97506_at	Rnf2	ring finger protein 2	157.97	387.29	-2.45	0.00112266
95559_at	6330403K07Rik	RIKEN cDNA 6330403K07 gene	5657.74	1030.74	5.49	0.00112273
160633_at	Thoc4	THO complex 4	324.02	677.98	-2.09	0.00112985
97211_at	Armcx2	armadillo repeat containing, X-lin	2964.68	656.75	4.51	0.00113023

99096_at	Ddx24	DEAD (Asp-Glu-Ala-Asp) box poly	1662.25	376.68	4.41	0.00113273
104556_at	4933426K21Rik /// LC	RIKEN cDNA 4933426K21 gene //	70.80	188.97	-2.67	0.00114665
161085_r_at	A4galt	alpha 1,4-galactosyltransferase	915.05	441.04	2.07	0.00115408
160620_at	Gt(ROSA)26Sor	gene trap ROSA 26, Philippe Soria	37.63	95.16	-2.53	0.00115415
92350_at	Mapre1	microtubule-associated protein, I	1761.66	468.58	3.76	0.00115696
99339_r_at	Kcnd2	potassium voltage-gated channel	30.86	665.33	-21.56	0.00115983
160546_at	Aldoc	aldolase 3, C isoform	1292.50	5293.63	-4.10	0.00116847
103567_at	Fryl	furry homolog-like (Drosophila)	1643.21	532.02	3.09	0.00117749
96733_at	Rap1gds1	RAP1, GTP-GDP dissociation stim	5693.20	1723.71	3.30	0.00119128
160103_at	7-Mar	membrane-associated ring finger	339.26	1135.38	-3.35	0.00119246
100068_at	Aldh1a1	aldehyde dehydrogenase family 1	285.19	848.11	-2.97	0.00119355
95618_at	Rab11fip5	RAB11 family interacting protein	1018.46	316.79	3.21	0.00119461
94347_i_at	Pcmt1	protein-L-isoaspartate (D-asparta	1263.75	151.94	8.32	0.00120699
100742_at	AA409749	expressed sequence AA409749	378.70	184.78	2.05	0.00120862
98811_at	Ptgir	prostaglandin I receptor (IP)	1083.16	99.16	10.92	0.0012091
95045_at	Mettl9	methyltransferase like 9	428.72	1020.29	-2.38	0.0012099
162220_r_at	Dnajb13	DnaJ (Hsp40) related, subfamily B	445.57	199.32	2.24	0.00121109
104766_at	Nola1	nucleolar protein family A, memb	2800.19	1275.52	2.20	0.00121127
103578_at	EG545878 /// Tom1	target of myb1 homolog (chicken	789.95	330.50	2.39	0.0012131
98938_at	Rnaseh2c	ribonuclease H2, subunit C	218.22	554.18	-2.54	0.00121408
160981_at	Atxn10	ataxin 10	1064.79	362.68	2.94	0.00121925
160386_at	Clptm1l	CLPTM1-like	2056.57	1012.14	2.03	0.00122031
102860_at	Serpina3g	serine (or cysteine) peptidase inh	2358.64	747.77	3.15	0.00122817
94143_at	Gfap	glial fibrillary acidic protein	125.04	263.71	-2.11	0.00122848
97756_s_at	LOC100046214 /// Pc	protocadherin alpha 4 /// protoc	2179.82	148.11	14.72	0.00122866
160795_at	Scamp1	secretory carrier membrane prot	1165.02	548.24	2.13	0.00123022
101582_at	Gnl2	guanine nucleotide binding prote	683.00	333.84	2.05	0.00123252
103494_at	Tspan8	tetraspanin 8	687.62	202.47	3.40	0.00124381
96205_at	Sh3bgr	SH3-binding domain glutamic aci	681.39	263.52	2.59	0.00124528
104529_at	Caml	calcium modulating ligand	1246.38	581.29	2.14	0.00125007
104716_at	LOC100045055 /// Rb	retinol binding protein 1, cellular	94.86	277.78	-2.93	0.00125177
160261_i_at	Lats2	large tumor suppressor 2	2139.00	847.53	2.52	0.00125817
97833_at	Pfkp	phosphofructokinase, platelet	1788.78	292.84	6.11	0.00126202
95062_at	Cast	calpastatin	1269.17	129.08	9.83	0.00126914
97947_at	Adam10	a disintegrin and metallopeptidas	272.14	769.92	-2.83	0.00126921
160727_at	2410002F23Rik	RIKEN cDNA 2410002F23 gene	504.54	1189.99	-2.36	0.00126966
102232_at	Slc39a9	solute carrier family 39 (zinc tran	594.05	280.67	2.12	0.00127064
162362_f_at	Tnc	tenascin C	36.94	108.36	-2.93	0.00129586
102885_at	Vamp7	vesicle-associated membrane prc	39.61	113.39	-2.86	0.00129666
161396_f_at	Ube2o	ubiquitin-conjugating enzyme E2	1759.66	338.24	5.20	0.00129949
160829_at	Phlda1	pleckstrin homology-like domain,	70.74	183.58	-2.60	0.00130741
95658_at	Commd1	COMM domain containing 1	379.96	153.96	2.47	0.00131282
161756_at	Rnmtl1	RNA methyltransferase like 1	464.06	222.95	2.08	0.00131288
95927_f_at	2610201A13Rik	RIKEN cDNA 2610201A13 gene	1452.94	318.39	4.56	0.00131856
100475_at	Trim25	tripartite motif-containing 25	424.45	109.44	3.88	0.00132207
100138_f_at	Rbm14	RNA binding motif protein 14	1159.39	572.38	2.03	0.00132409
102747_at	Tcte1	t-complex-associated testis expre	194.94	421.70	-2.16	0.00133388
95289_r_at	Ccdc88a	coiled coil domain containing 88A	29.82	60.37	-2.02	0.00133422
94731_at	Stac	src homology three (SH3) and cys	1598.92	239.48	6.68	0.00134396
101064_at	Plrg1	pleiotropic regulator 1, PRL1 hom	1869.49	756.01	2.47	0.00135114
103726_at	Yipf5	Yip1 domain family, member 5	141.73	336.09	-2.37	0.00135724
94071_at	Gosr2	golgi SNAP receptor complex mer	1615.82	696.77	2.32	0.00135742
92185_at	Arl4c	ADP-ribosylation factor-like 4C	1765.11	429.50	4.11	0.0013603
104215_at	Atf6	activating transcription factor 6	308.50	90.37	3.41	0.00138163
160755_at	Kif2c /// LOC631653	kinesin family member 2C /// sim	72.08	151.83	-2.11	0.00138592

94522_at	Dctn3	dynactin 3	1080.36	2386.15	-2.21	0.00138921
102384_at	Smarca2	SWI/SNF related, matrix associat	1449.82	456.35	3.18	0.00140944
97509_f_at	Fgfr1	fibroblast growth factor receptor	1599.50	338.70	4.72	0.00141456
95690_at	Samm50	sorting and assembly machinery	2215.69	839.92	2.64	0.0014161
103483_at	Ercc5	excision repair cross-complemen	387.67	178.88	2.17	0.00141713
95601_at	Ubqln1	ubiquilin 1	303.57	773.73	-2.55	0.00141974
95022_at	Akap12	A kinase (PRKA) anchor protein (g	1180.52	308.02	3.83	0.00142037
98881_at	Hdhd2	haloacid dehalogenase-like hydrc	1291.67	635.33	2.03	0.00142141
95066_at	Taldo1	transaldolase 1	2802.09	1118.96	2.50	0.00143285
102002_at	Ubqln2	ubiquilin 2	87.29	390.07	-4.47	0.00143295
96166_at	Tex261	testis expressed gene 261	2538.94	1006.84	2.52	0.0014355
93116_at	Prkacb	protein kinase, cAMP dependent,	5114.94	1849.29	2.77	0.00144376
92644_s_at	Myb	myeloblastosis oncogene	28.34	94.41	-3.33	0.00146514
160697_at	C77080	expressed sequence C77080	1940.91	905.04	2.14	0.00148853
99566_at	Tpi1	triosephosphate isomerase 1	2059.37	5236.79	-2.54	0.00148921
98333_at	LOC100039740 /// LC	ribosomal protein S18 /// predict	1639.78	3860.06	-2.35	0.00150074
162094_f_at	---	---	960.98	281.57	3.41	0.0015018
104243_r_at	6530401N04Rik /// LC	RIKEN cDNA 6530401N04 gene ///	290.60	138.49	2.10	0.0015097
96013_r_at	Matr3	matrin 3	34.12	187.60	-5.50	0.00151685
98424_at	Ptpn13	protein tyrosine phosphatase, no	826.20	308.29	2.68	0.00151823
102019_at	Mrpl13	mitochondrial ribosomal protein	317.79	777.89	-2.45	0.00152077
93859_at	Mtif2	mitochondrial translational initiat	535.97	181.58	2.95	0.00153548
96785_at	Kank3	KN motif and ankyrin repeat dom	474.76	219.07	2.17	0.00153562
99580_s_at	LOC632297 /// Ugt1a	UDP glucuronosyltransferase 1 fa	1954.60	889.98	2.20	0.00154456
104067_at	Tubgcp3	tubulin, gamma complex associat	628.43	292.76	2.15	0.00154688
160762_at	Abr	active BCR-related gene	1553.23	531.07	2.92	0.00154817
160685_at	Klhl7	Kelch-like 7 (Drosophila)	156.94	317.92	-2.03	0.00155084
96211_at	Dpp8	dipeptidylpeptidase 8	1283.55	464.10	2.77	0.00156747
93564_at	Yars	tyrosyl-tRNA synthetase	1583.64	625.72	2.53	0.00156892
161193_r_at	---	---	261.42	128.37	2.04	0.00157413
101998_at	4833420G17Rik	RIKEN cDNA 4833420G17 gene	263.59	100.72	2.62	0.00160069
93831_at	Nono	non-POU-domain-containing, oct	32.80	151.47	-4.62	0.00160243
95355_at	Agtrap	angiotensin II, type I receptor-ass	663.38	251.37	2.64	0.00160931
93191_at	Vamp4	vesicle-associated membrane prc	1879.02	583.56	3.22	0.00162067
100371_at	Hnrnpa1	heterogeneous nuclear ribonucle	35.95	75.61	-2.10	0.00162382
104294_at	Ibtk	inhibitor of Bruton agammaglobu	432.23	163.58	2.64	0.00162636
104610_at	Pprc1	peroxisome proliferative activate	169.08	65.71	2.57	0.00162835
160237_at	Ndufa6	NADH dehydrogenase (ubiquinor	227.51	641.89	-2.82	0.00163126
104407_at	Alcam	activated leukocyte cell adhesion	1243.62	119.87	10.37	0.00163348
104106_at	Sbno1	sno, strawberry notch homolog 1	503.10	72.21	6.97	0.00165565
160550_i_at	Magoh	mago-nashi homolog, proliferatic	192.99	582.79	-3.02	0.00166269
99833_at	Capn9 /// LOC639715	calpain 9 (nCL-4) /// similar to cal	649.56	283.12	2.29	0.00166612
99056_at	Pcbd1	pterin 4 alpha carbinolamine deh	882.44	294.44	3.00	0.00167641
94983_at	1810073G14Rik	RIKEN cDNA 1810073G14 gene	702.86	222.84	3.15	0.00168279
161066_at	Alg5	asparagine-linked glycosylation 5	166.40	61.97	2.69	0.00168506
162448_f_at	Hspb8	heat shock protein 8	251.07	112.20	2.24	0.00168712
101562_at	Hspa14	heat shock protein 14	365.67	150.24	2.43	0.00169406
103969_at	Mll5	myeloid/lymphoid or mixed-linea	528.49	1120.70	-2.12	0.00169813
93043_at	Nptn	neuroplastin	3772.18	1743.19	2.16	0.00170181
96135_at	3110003A17Rik	RIKEN cDNA 3110003A17 gene	298.19	623.59	-2.09	0.0017035
98989_at	Dhcr7	7-dehydrocholesterol reductase	366.28	146.27	2.50	0.00170458
160577_at	Atp9a	ATPase, class II, type 9A	7483.67	2904.94	2.58	0.00170499
93337_at	Vps4b	vacuolar protein sorting 4b (yeas	2067.60	498.76	4.15	0.00170708
95886_g_at	Crebbp	CREB binding protein	3050.20	1288.48	2.37	0.00171611
96152_at	Narg1	NMDA receptor-regulated gene 1	973.44	366.31	2.66	0.00171809

104306_at	Dpp3	dipeptidylpeptidase 3	1099.37	330.66	3.32	0.00171826
161799_r_at	Kcnj9	potassium inwardly-rectifying cha	534.10	207.12	2.58	0.00174037
103422_at	Cd1d1	CD1d1 antigen	943.17	168.62	5.59	0.00174948
160397_at	Ik	IK cytokine	904.00	270.05	3.35	0.00175685
94433_at	Slc38a2	solute carrier family 38, member	1915.10	800.08	2.39	0.00177202
98463_at	Smarca4	SWI/SNF related, matrix associat	2652.41	1267.63	2.09	0.0017768
97131_at	LOC100047492 /// St	serine/threonine kinase 11 intera	844.91	248.54	3.40	0.00180076
99180_at	Gtpbp4	GTP binding protein 4	1790.76	669.11	2.68	0.00181382
160320_at	Sorbs1	sorbin and SH3 domain containin	730.90	309.26	2.36	0.00181547
103316_at	Camsap1	calmodulin regulated spectrin-as	1008.10	465.66	2.16	0.00181862
94015_at	Th1l	TH1-like homolog (Drosophila)	1178.97	519.86	2.27	0.00183025
102571_at	Gjb6	gap junction protein, beta 6	119.84	268.67	-2.24	0.00183674
92571_at	Hspa4	heat shock protein 4	599.09	121.10	4.95	0.00184318
98918_at	Txndc5	thioredoxin domain containing 5	3820.72	1601.33	2.39	0.00184458
92848_at	Oat	ornithine aminotransferase	2187.80	624.62	3.50	0.00184523
98596_s_at	St3gal5	ST3 beta-galactoside alpha-2,3-si	3169.70	1322.13	2.40	0.00184547
100571_at	Laptm4b	lysosomal-associated protein tra	2369.41	1125.34	2.11	0.0018459
96240_at	Tmem106c	transmembrane protein 106C	1404.11	546.65	2.57	0.00185299
98410_at	Iigp2	interferon inducible GTPase 2	771.36	363.36	2.12	0.00185421
99923_at	Pcf11	cleavage and polyadenylation fac	53.03	134.74	-2.54	0.00189815
160565_at	Ckmt1	creatine kinase, mitochondrial 1,	1326.06	472.79	2.80	0.00190635
94058_r_at	Scd1	stearoyl-Coenzyme A desaturase	433.15	189.61	2.28	0.00192294
104725_at	Rhoq	ras homolog gene family, membe	866.61	329.06	2.63	0.00193213
97497_at	Notch1	Notch gene homolog 1 (Drosophi	1279.26	600.77	2.13	0.00193552
98511_at	Raly	hnRNP-associated with lethal yel	477.57	215.29	2.22	0.00194734
96703_at	Maged1	melanoma antigen, family D, 1	7870.54	2956.51	2.66	0.00195134
102922_at	Pitpnc1	phosphatidylinositol transfer pro	1774.75	703.22	2.52	0.00198526
92703_at	Pbrm1	polybromo 1	999.37	469.37	2.13	0.00198802
161081_at	Cpeb2	cytoplasmic polyadenylation elen	126.59	557.48	-4.40	0.00199249
99597_at	Gnai2	guanine nucleotide binding prote	2405.30	942.21	2.55	0.00199801
92579_at	Ssb	Sjogren syndrome antigen B	128.74	277.12	-2.15	0.00199904
92818_at	Uba3	ubiquitin-like modifier activating	653.22	270.31	2.42	0.00200453
95731_at	LOC100047324 /// Se	sestrin 1 /// similar to Sesn1 prot	386.71	820.77	-2.12	0.00200777
93151_at	Cpne6	copine VI	2824.06	787.98	3.58	0.00202277
99988_at	Dym	dymeclin	1367.94	457.77	2.99	0.00203533
96122_at	Cmbl	carboxymethylenebutenolidase-l	625.77	157.72	3.97	0.00205021
92551_at	Lig1	ligase I, DNA, ATP-dependent	797.30	391.27	2.04	0.00207001
92346_at	Nefm	neurofilament, medium polypept	1481.17	326.80	4.53	0.00207755
95123_at	Zfp821	zinc finger protein 821	737.12	300.32	2.45	0.00208735
98475_at	Matn2	matrilin 2	156.84	42.73	3.67	0.0021023
99150_at	Ict1	immature colon carcinoma trans	216.17	568.66	-2.63	0.00210318
96351_at	Btf3l4	basic transcription factor 3-like 4	196.60	490.91	-2.50	0.00210825
102926_at	Gfra3 /// LOC100045	glial cell line derived neurotrophi	3327.85	432.83	7.69	0.00210931
97330_at	Abcf1	ATP-binding cassette, sub-family	2747.42	1133.43	2.42	0.0021201
101475_at	Bmi1	Bmi1 polycomb ring finger oncog	1174.94	2374.66	-2.02	0.00212828
162030_r_at	LOC100044204 /// Se	selenium binding protein 1 /// se	708.38	271.32	2.61	0.0021506
94294_at	Ccnb2	cyclin B2	385.32	913.00	-2.37	0.00215159
92581_at	Acadm	acyl-Coenzyme A dehydrogenase	995.98	332.39	3.00	0.00215404
95094_g_at	Ccar1	cell division cycle and apoptosis r	64.99	138.57	-2.13	0.00215935
95288_i_at	Ccdc88a	coiled coil domain containing 88A	68.74	250.76	-3.65	0.0021641
94269_at	Rabac1	Rab acceptor 1 (prenylated)	3072.75	6244.45	-2.03	0.00216679
93464_at	Akap9	A kinase (PRKA) anchor protein (y	271.41	88.46	3.07	0.00216693
97433_at	Mcm3ap	minichromosome maintenance d	619.47	299.08	2.07	0.00217814
160376_at	Trp53inp2	transformation related protein 53	692.78	1630.51	-2.35	0.00221022
102316_at	Capn5	calpain 5	2007.82	322.32	6.23	0.00221982

100041_at	Slc25a39	solute carrier family 25, member	4590.49	2132.45	2.15	0.0022241
98927_at	Rab6	RAB6, member RAS oncogene far	3529.00	1224.78	2.88	0.00223027
92380_r_at	Ptprz1	protein tyrosine phosphatase, re	23.63	65.94	-2.79	0.00223917
95397_at	D430019H16Rik	RIKEN cDNA D430019H16 gene	3311.86	1163.59	2.85	0.00224277
99032_at	Rasd1	RAS, dexamethasone-induced 1	479.83	93.81	5.11	0.00225359
101921_at	Rab4a	RAB4A, member RAS oncogene f	268.89	542.28	-2.02	0.00225543
97401_at	Josd1 /// LOC100043	Josephin domain containing 1 ///	1218.29	432.38	2.82	0.00226286
95717_at	Elp3	elongation protein 3 homolog (S.	2048.99	1005.23	2.04	0.00229233
103998_at	Kif16b	kinesin family member 16B	178.00	54.76	3.25	0.00232583
103225_at	Dnase1l1	deoxyribonuclease 1-like 1	280.86	72.11	3.89	0.0023681
93270_at	Gars	glycyl-tRNA synthetase	2294.80	842.49	2.72	0.00237288
92202_g_at	Zbtb16	zinc finger and BTB domain conta	54.66	151.16	-2.77	0.00237556
100440_f_at	Ank1	ankyrin 1, erythroid	11935.79	3590.47	3.32	0.00239217
97930_f_at	Cd151	CD151 antigen	3029.54	743.09	4.08	0.0023977
92423_at	Pard6a	par-6 (partitioning defective 6,) h	307.32	875.22	-2.85	0.00241598
98863_at	Grik2	glutamate receptor, ionotropic, k	51.91	107.27	-2.07	0.00241841
160173_at	Meg3	maternally expressed 3	242.66	544.77	-2.24	0.00241995
162011_f_at	Rhou	ras homolog gene family, membe	1938.83	847.45	2.29	0.00242166
92513_at	Stag2	stromal antigen 2	558.39	1257.80	-2.25	0.0024233
101650_at	LOC100046214 /// Pc	protocadherin alpha 4 /// protoc	5522.16	2097.88	2.63	0.0024298
96902_at	Ccdc53	coiled-coil domain containing 53	245.16	117.15	2.09	0.00243021
97312_at	Cd164	CD164 antigen	2157.95	715.20	3.02	0.00244257
97871_at	Ero1l	ERO1-like (S. cerevisiae)	1237.76	503.63	2.46	0.00244488
95626_at	Xpc	xeroderma pigmentosum, compl	393.30	190.37	2.07	0.00246388
92671_f_at	Rgl1	ral guanine nucleotide dissociatic	216.91	68.16	3.18	0.00246748
102993_at	Ggta1	glycoprotein galactosyltransferas	1178.30	399.24	2.95	0.00249828
96822_at	Eif2b5	eukaryotic translation initiation f	995.82	311.55	3.20	0.00250721
94977_at	Itpr1	inositol 1,4,5-triphosphate recep	100.57	1129.31	-11.23	0.0025075
96572_at	Azi2	5-azacytidine induced gene 2	1274.35	417.41	3.05	0.0025146
99440_at	Nfib	nuclear factor I/B	287.83	962.39	-3.34	0.0025261
160625_f_at	Mettl8	methyltransferase like 8	1309.28	535.76	2.44	0.00256689
96735_at	Stard10	START domain containing 10	1502.01	646.87	2.32	0.00257968
101070_at	Mkrn1	makorin, ring finger protein, 1	401.77	805.50	-2.00	0.00260242
100033_at	Msh2	mutS homolog 2 (E. coli)	1853.90	601.77	3.08	0.00260811
103011_at	Sin3a	transcriptional regulator, SIN3A (	2718.71	1222.09	2.22	0.00262216
92355_at	Zfpm2	zinc finger protein, multitype 2	74.00	205.40	-2.78	0.00263127
104242_f_at	6530401N04Rik /// L	RIKEN cDNA 6530401N04 gene /,	1249.67	567.45	2.20	0.00263267
95978_at	Atp13a3	ATPase type 13A3	319.18	147.08	2.17	0.00265066
101876_s_at	H2-T10 /// H2-T17 //,	histocompatibility 2, T region loc	598.54	201.61	2.97	0.00265301
95479_at	C1d	nuclear DNA binding protein	92.47	201.65	-2.18	0.00266277
161750_f_at	Ncam1	neural cell adhesion molecule 1	1146.34	344.16	3.33	0.00266875
95128_at	Anapc2	anaphase promoting complex sul	1844.84	687.64	2.68	0.00272325
101074_at	Ddost	dolichyl-di-phosphooligosacchari	1217.40	461.96	2.64	0.00273503
97489_at	Pygb	brain glycogen phosphorylase	1729.20	341.70	5.06	0.0027424
101421_at	Rnf5	ring finger protein 5	704.05	1680.03	-2.39	0.00274267
94925_at	Dnajc19	DnaJ (Hsp40) homolog, subfamily	62.02	148.13	-2.39	0.00274754
100953_at	Timeless	timeless homolog (Drosophila)	4304.86	758.41	5.68	0.00275649
162444_r_at	Tinf2	Terf1 (TRF1)-interacting nuclear f	74.06	165.83	-2.24	0.00275649
104189_at	Traf6	Tnf receptor-associated factor 6	668.44	243.23	2.75	0.00275768
95756_at	Ftsj3	FtsJ homolog 3 (E. coli)	345.56	57.68	5.99	0.00276885
99345_at	Mphosph9	M-phase phosphoprotein 9	1124.93	390.50	2.88	0.00278187
97713_at	Pdxdc1	pyridoxal-dependent decarboxyla	2401.18	342.60	7.01	0.00278309
160739_at	Wnk1	WNK lysine deficient protein kina	825.39	133.74	6.17	0.00281901
98409_at	Myo1b	myosin IB	1040.23	477.16	2.18	0.0028482
101581_at	Ube3a	ubiquitin protein ligase E3A	305.60	106.76	2.86	0.00286997

101000_at	Oaz2	ornithine decarboxylase antizyme	2865.73	1266.78	2.26	0.0028935
93951_at	Golga3	golgi autoantigen, golgin subfami	1213.51	468.64	2.59	0.00291994
100902_at	2610019F03Rik	RIKEN cDNA 2610019F03 gene	708.70	249.24	2.84	0.002954
99832_at	Kcnmb1	potassium large conductance cal	917.42	122.50	7.49	0.00295482
96623_at	Ugcg	UDP-glucose ceramide glucosyltr	2742.72	779.88	3.52	0.00295573
94289_r_at	LOC100046560 /// M	melanoma antigen, family D, 2 //	1670.58	728.42	2.29	0.00297697
104155_f_at	Atf3	activating transcription factor 3	399.83	182.73	2.19	0.0029857
93055_at	Ankrd46	ankyrin repeat domain 46	322.27	751.82	-2.33	0.00299759
104661_at	D730040F13Rik	RIKEN cDNA D730040F13 gene	218.33	109.00	2.00	0.00301141
94009_at	LOC100045866 /// Tc	transcription elongation factor B	255.56	705.94	-2.76	0.00305197
93626_at	Abcg2	ATP-binding cassette, sub-family	1821.17	172.42	10.56	0.00306536
97484_at	Zmynd11	zinc finger, MYND domain contai	2746.21	1240.61	2.21	0.00307497
103926_at	Eif4g1	eukaryotic translation initiation f	946.96	205.55	4.61	0.00308018
100931_at	Arsa	arylsulfatase A	570.82	269.36	2.12	0.00308182
104117_at	Wdr20a	WD repeat domain 20a	95.98	293.87	-3.06	0.00310289
98819_at	Hoxd1	homeo box D1	578.18	171.54	3.37	0.00313148
103501_at	LOC100045958 /// Pu	purine rich element binding prote	1791.77	683.34	2.62	0.00313376
95368_at	Plxna2	plexin A2	759.54	356.76	2.13	0.00313716
95035_at	Ipo4	importin 4	2484.40	744.67	3.34	0.00317533
95796_g_at	Supt4h1 /// Supt4h2	suppressor of Ty 4 homolog 1 (S.	218.50	801.49	-3.67	0.00318601
100569_at	Anxa2	annexin A2	9909.43	731.66	13.54	0.00318818
161111_f_at	Dhh	desert hedgehog	1879.62	664.78	2.83	0.00321316
99592_f_at	Rdh11	retinol dehydrogenase 11	4312.07	2061.11	2.09	0.00321996
96199_at	Mtm1	X-linked myotubular myopathy g	506.16	168.86	3.00	0.00324382
93246_at	Narg1	NMDA receptor-regulated gene 1	440.90	87.06	5.06	0.00324447
93145_at	Gatad2a	GATA zinc finger domain containi	298.01	146.84	2.03	0.0032484
100597_at	Gyg	glycogenin	355.01	134.50	2.64	0.00325219
96198_at	Prkcz	protein kinase C, zeta	1531.94	749.08	2.05	0.0032749
93512_f_at	Adk	adenosine kinase	1807.89	451.99	4.00	0.00329126
99113_at	Cops3	COP9 (constitutive photomorpho	1635.08	606.54	2.70	0.00331082
104403_at	2700078E11Rik	RIKEN cDNA 2700078E11 gene	699.06	209.05	3.34	0.00332314
94406_at	Phtf1	putative homeodomain transcrip	1265.31	534.74	2.37	0.00348867
98503_at	Evi5	ecotropic viral integration site 5	1944.10	368.60	5.27	0.00352136
95501_at	2410001C21Rik	RIKEN cDNA 2410001C21 gene	1078.34	277.02	3.89	0.00354716
104011_at	Aox1	aldehyde oxidase 1	1003.53	282.92	3.55	0.00356258
94027_at	---	Transcribed locus /// CDNA clone	302.26	713.70	-2.36	0.00357635
160517_at	Lmnb1	lamin B1	189.04	441.25	-2.33	0.00357983
96266_at	Hnrpm	heterogeneous nuclear ribonucle	3819.50	1322.17	2.89	0.00360732
100516_at	Chka	choline kinase alpha	1108.81	485.67	2.28	0.00361452
94278_at	Lcp1	lymphocyte cytosolic protein 1	1709.55	461.40	3.71	0.00367235
100513_at	Ddef1	development and differentiation	1973.98	627.81	3.14	0.00368741
101084_f_at	Dpm3	dolichyl-phosphate mannosyltrar	469.02	1047.51	-2.23	0.00368846
97456_at	Acsl5	acyl-CoA synthetase long-chain fa	926.51	118.75	7.80	0.00372991
161086_at	Lin7c	lin-7 homolog C (C. elegans)	47.85	121.39	-2.54	0.00375702
96836_r_at	Zfp161	zinc finger protein 161	99.63	46.42	2.15	0.00378664
97760_at	A730034C02 /// Mta	microtubule-associated protein 2	112.77	259.60	-2.30	0.003807
100324_g_at	Amd-ps3 /// Amd1 //	S-adenosylmethionine decarboxy	32.18	65.05	-2.02	0.00382927
100013_at	Ifi35	interferon-induced protein 35	655.76	247.90	2.65	0.00385579
92208_at	Caprin2	caprin family member 2	1671.26	272.71	6.13	0.00386477
96186_at	Lrp10	low-density lipoprotein receptor-	741.30	355.29	2.09	0.00387127
96284_at	Csnk1g2	casein kinase 1, gamma 2	3141.05	1492.33	2.10	0.00387773
AFFX-18SRNAMur	---	---	1998.43	115.46	17.31	0.00387965
160458_at	Mcam	melanoma cell adhesion molecul	1748.03	634.03	2.76	0.00389737
95705_s_at	Actb	actin, beta, cytoplasmic	194.81	705.89	-3.62	0.0039116
94872_at	Smpdl3a	sphingomyelin phosphodiesteras	421.05	159.70	2.64	0.00391913

100388_at	Gnao1	guanine nucleotide binding prote	200.20	421.89	-2.11	0.00395244
96650_at	Auh	AU RNA binding protein/enoyl-cc	1648.44	671.46	2.46	0.00395632
101356_at	Tk2	thymidine kinase 2, mitochondria	271.11	122.74	2.21	0.00395709
103799_at	Mtmr9	myotubularin related protein 9	698.65	183.49	3.81	0.00398486
102225_at	Rabgap1l	RAB GTPase activating protein 1-	180.38	376.89	-2.09	0.00399046
93330_at	Aqp1	aquaporin 1	1466.67	258.59	5.67	0.00400373
99045_at	Eno2	enolase 2, gamma neuronal	4575.25	1825.50	2.51	0.00404202
102853_at	Smc3	structural maintenace of chromo	96.58	239.47	-2.48	0.00405202
101040_at	Capn2	calpain 2	1480.24	198.89	7.44	0.00406038
160264_s_at	Pcp4l1	Purkinje cell protein 4-like 1	1719.70	167.21	10.28	0.00410819
103836_at	Wbp4	WW domain binding protein 4	1309.92	417.95	3.13	0.0041205
92940_s_at	Gabra6	gamma-aminobutyric acid (GABA	117.95	2424.27	-20.55	0.00414133
160629_at	Rgs10	regulator of G-protein signalling 1	1155.47	465.66	2.48	0.0041589
96803_at	Gbe1	glucan (1,4-alpha-), branching en	134.98	63.97	2.11	0.00417846
101990_at	Ldhb	lactate dehydrogenase B	1557.63	674.36	2.31	0.00422439
99955_at	Numb	numb gene homolog (Drosophila	151.38	74.86	2.02	0.00428925
94963_at	Vcl	vinculin	1305.50	377.89	3.45	0.00430214
92938_at	Gabra1	gamma-aminobutyric acid (GABA	44.28	239.94	-5.42	0.00437317
98535_at	Comt	catechol-O-methyltransferase	1135.71	402.15	2.82	0.00445428
162255_s_at	Scn1a	sodium channel, voltage-gated, t	1382.78	408.62	3.38	0.00448127
100494_at	Fgf1	fibroblast growth factor 1	1935.86	332.27	5.83	0.00454002
99475_at	Socs2	suppressor of cytokine signaling 2	2075.59	830.80	2.50	0.00456552
98894_at	Pbrm1	polybromo 1	489.99	238.98	2.05	0.00456624
93807_at	2310016E02Rik	RIKEN cDNA 2310016E02 gene	520.21	185.98	2.80	0.00460876
161010_r_at	Cdkn1b	cyclin-dependent kinase inhibitor	29.08	72.25	-2.48	0.00468405
101587_at	Ephx1	epoxide hydrolase 1, microsomal	2596.55	639.48	4.06	0.00468867
97844_at	Rgs2	regulator of G-protein signaling 2	888.56	397.95	2.23	0.00472162
160698_s_at	Prkcd	protein kinase C, delta	2333.72	1002.14	2.33	0.00475484
104015_at	Metap1	methionyl aminopeptidase 1	3114.85	771.02	4.04	0.00476106
161075_at	D9Ertd280e	DNA segment, Chr 9, ERATO Doi 2	529.61	96.06	5.51	0.00476143
99672_at	Clcn4-2	chloride channel 4-2	2351.91	374.56	6.28	0.0048888
92456_at	Taf1c	TATA box binding protein (Tbp)-a	870.93	418.50	2.08	0.00491616
94940_at	Mccc1	methylcrotonoyl-Coenzyme A car	541.40	226.57	2.39	0.00494735
93001_at	Six4	sine oculis-related homeobox 4 h	107.98	41.22	2.62	0.00503591
103443_at	Aim1	absent in melanoma 1	474.51	224.40	2.11	0.00504332
162037_f_at	Npy2r	neuropeptide Y receptor Y2	3483.32	614.71	5.67	0.00507511
103017_at	Gpr137b-ps	G protein-coupled receptor 137B	824.54	359.63	2.29	0.0051087
99080_at	Ccdc6	coiled-coil domain containing 6	1137.65	290.49	3.92	0.00513876
93908_f_at	Ccrn4l /// ENSMUSG(	CCR4 carbon catabolite repressio	130.32	644.97	-4.95	0.00516852
94790_at	Agl	amylo-1,6-glucosidase, 4-alpha-g	179.40	52.68	3.41	0.00516932
94363_at	Bms1	BMS1 homolog, ribosome assem	268.19	130.16	2.06	0.00518245
160682_at	6430706D22Rik	RIKEN cDNA 6430706D22 gene	858.75	391.75	2.19	0.00521765
95036_at	Calb2	calbindin 2	465.55	1165.05	-2.50	0.00527973
92995_at	Vsnl1	visinin-like 1	786.43	1665.10	-2.12	0.00527999
93299_at	LOC633695 /// Msh6	mutS homolog 6 (E. coli) /// simil	125.22	270.31	-2.16	0.00530844
101053_at	Prpf6	PRP6 pre-mRNA splicing factor 6	2253.10	1037.50	2.17	0.00534419
99007_at	Flot2	flotillin 2	1589.79	717.82	2.21	0.00534435
99669_at	Lgals1	lectin, galactose binding, soluble	1342.23	638.95	2.10	0.0053463
98820_g_at	Hoxd1	homeo box D1	571.93	29.25	19.55	0.00541436
95432_f_at	Tomm70a	translocase of outer mitochondri	7510.01	2468.10	3.04	0.00542364
95393_at	Btbd3	BTB (POZ) domain containing 3	299.17	1011.68	-3.38	0.00549181
99042_s_at	Shox2	short stature homeobox 2	505.48	169.14	2.99	0.00552048
94250_at	Eif3s10	eukaryotic translation initiation f	238.69	483.56	-2.03	0.00552278
92252_at	Cckar	cholecystokinin A receptor	1016.23	141.06	7.20	0.00560415
160399_r_at	H2afy	H2A histone family, member Y	251.08	514.02	-2.05	0.00561535

98490_at	Arl8b	ADP-ribosylation factor-like 8B	48.31	107.82	-2.23	0.00562326
99365_at	Coq3	coenzyme Q3 homolog, methyltr	652.58	314.00	2.08	0.00564228
96222_at	BC003993	cDNA sequence BC003993	193.48	83.26	2.32	0.00564565
98924_at	Art3	ADP-ribosyltransferase 3	222.70	76.23	2.92	0.00565865
93346_at	Pgk1	phosphoglycerate kinase 1	4179.96	2044.54	2.04	0.00567918
103789_at	Brd4	bromodomain containing 4	1707.25	306.02	5.58	0.00570802
160610_at	LOC100046214 /// Pc	protocadherin alpha 4 /// protoc	3735.50	847.55	4.41	0.0057388
92795_at	Mtap4	microtubule-associated protein 4	1483.09	519.54	2.85	0.00582564
95594_at	Mfn1	mitofusin 1	1052.85	508.45	2.07	0.00585769
97446_at	Dhx30	DEAH (Asp-Glu-Ala-His) box polyp	2121.42	992.37	2.14	0.00593906
93005_at	Syt1	synaptotagmin I	56.46	554.29	-9.82	0.00595194
92239_at	Elavl3	ELAV (embryonic lethal, abnorma	642.44	305.88	2.10	0.0060437
94865_at	Ublcp1	ubiquitin-like domain containing	1299.76	404.42	3.21	0.0060754
104254_at	Ralgps2	Ral GEF with PH domain and SH3	389.86	165.66	2.35	0.0060807
94712_at	Vegfc	vascular endothelial growth factc	53.51	137.25	-2.56	0.00608073
AFFX-18SRNAMur	---	---	1608.32	724.46	2.22	0.00610947
101099_at	Nsg1	neuron specific gene family mem	304.02	644.25	-2.12	0.00611808
160772_i_at	Slu7	SLU7 splicing factor homolog (S. c	859.93	350.15	2.46	0.00616728
160859_s_at	Nfib	nuclear factor I/B	248.86	1049.38	-4.22	0.00641608
160843_at	LOC100046080 /// Sp	spindlin 1 /// similar to Spindlin 1	71.81	189.57	-2.64	0.00644115
96610_at	Atp6v1h	ATPase, H+ transporting, lysosom	2719.94	1114.94	2.44	0.00667948
94809_at	Tsg101	tumor susceptibility gene 101	459.87	181.32	2.54	0.00675387
103913_at	Sec61a2	Sec61, alpha subunit 2 (S. cerevis	2370.55	972.41	2.44	0.00685783
94060_at	Kctd10	potassium channel tetramerisatic	2942.98	729.62	4.03	0.00692238
99067_at	Gas6	growth arrest specific 6	1645.36	667.95	2.46	0.00708643
103433_at	Pscd3	pleckstrin homology, Sec7 and co	1047.30	520.43	2.01	0.00710633
96879_at	Ogdh	oxoglutarate dehydrogenase (lipc	3196.59	1517.81	2.11	0.00712109
98539_at	Cops2	COP9 (constitutive photomorpho	76.99	210.29	-2.73	0.00726766
97853_at	Psip1	PC4 and SFRS1 interacting protei	151.57	313.94	-2.07	0.00727755
104327_at	9030612M13Rik	RIKEN cDNA 9030612M13 gene	166.94	370.52	-2.22	0.00731531
103492_at	Cpxm1	carboxypeptidase X 1 (M14 famil	298.91	121.96	2.45	0.00736773
92989_f_at	Cadps	Ca2+-dependent secretion activa	4651.22	2276.32	2.04	0.00751463
161959_f_at	Lrrn1	leucine rich repeat protein 1, neu	86.60	31.61	2.74	0.00753001
104337_f_at	Pkp2	plakophilin 2	784.00	155.64	5.04	0.00770328
99350_at	Sec63	SEC63-like (S. cerevisiae)	257.11	104.13	2.47	0.00775682
94484_at	Hbs1l	Hbs1-like (S. cerevisiae)	1675.70	824.56	2.03	0.00780518
100464_at	3110043O21Rik	RIKEN cDNA 3110043O21 gene	1088.92	317.14	3.43	0.00798886
AFFX-PheX-3_at	---	---	581.69	205.56	2.83	0.00804573
93534_at	Dcn	decorin	4343.36	821.73	5.29	0.00822545
104018_at	Lct	lactase	174.12	79.87	2.18	0.00831844
99364_at	Rbbp6	retinoblastoma binding protein 6	42.61	98.88	-2.32	0.00850596
160812_at	Gga2	golgi associated, gamma adaptin	1644.24	579.97	2.84	0.00854057
100056_at	Fbxw2	F-box and WD-40 domain protein	1779.93	883.46	2.01	0.0085562
AFFX-ThrX-3_at	---	---	681.55	109.96	6.20	0.00880106
96545_s_at	Pcid2	PCI domain containing 2	206.48	94.52	2.18	0.00888187
98984_f_at	Gpd2	glycerol phosphate dehydrogena	1063.79	516.90	2.06	0.00889077
103459_at	Slc39a6	solute carrier family 39 (metal ior	1730.30	578.63	2.99	0.00903138
95433_at	Ddx54	DEAD (Asp-Glu-Ala-Asp) box poly	725.65	270.79	2.68	0.0091002
160906_i_at	---	---	151.64	38.69	3.92	0.00913133
97317_at	Enpp2	ectonucleotide pyrophosphatase	310.97	2508.52	-8.07	0.00940243
99489_at	Hspa4l	heat shock protein 4 like	979.40	469.80	2.08	0.00940666
101561_at	Mt2	metallothionein 2	935.57	2327.18	-2.49	0.00946029
160167_at	Nup62	nucleoporin 62	1466.54	691.29	2.12	0.00950681
96747_at	Rhou	ras homolog gene family, membe	1604.29	528.00	3.04	0.00957993
94006_at	Azi2	5-azacytidine induced gene 2	263.21	96.45	2.73	0.00963317

96656_at	Wdr48	WD repeat domain 48	173.38	348.36	-2.01	0.0096476
98336_s_at	Rfc1	replication factor C (activator 1) 1	347.83	162.50	2.14	0.00995621