Supplementary Table 5. Gene expression across all subjects for the genes in Figure 2f comparing microfluidic isolation with Ficoll-dextran isolation.

				Log$_2$ Expression for Bulk Ficoll-Dextran Isolated Neutrophils (B) and Microfluidic Isolation Neutrophils (M) for subjects 1-5									
Probe Set	**Gene Symbol**	**Gene Title**	**qvalue(FDR)**	*B1*	*M1*	*B2*	*M2*	*B3*	*M3*	*B4*	*M4*	*B5*	*M5*
1558365_at	---	---	0.275045	7.05	3.21	6.12	6.42	6.37	4.33	6.79	4.08	7.03	4.07
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)	0.329638	6.12	3.56	4.29	6.52	7.18	3.95	8.59	4.39	7.9	4.64
232307_at	---	---	0.329638	8.68	6.4	6.47	6.87	7.6	6.1	8.1	4.54	8.17	5.92
228180_at	---	---	0.329638	6.6	5.6	5.85	6.01	6.38	5.57	7.78	3.88	6.61	5
215958_at	---	---	0.363087	6.81	4.24	7.49	6.56	5.97	3.22	7.7	5.99	7.36	3.75
210479_s_at	RORA	RAR-related orphan receptor A	0.42141	6.64	3.61	3.93	4.23	6.05	3.51	7.61	3.84	5.26	4.07
244719_at	---	---	0.42141	9.14	3.35	7.65	3.33	4.47	3.92	7.14	3.56	7.28	3.12
228486_at	SLC44A1	solute carrier family 44, member 1	0.42141	5.99	7.03	4.35	5.65	5.97	7.9	6.32	8.42	5.16	5.17
223092_at	ANKH	ankylosis, progressive homolog (mouse)	0.42141	6.56	5.06	3.84	6.11	6.4	3.68	6.04	3.61	5.78	4.17
227868_at	LOC154761	hypothetical LOC154761	0.42141	6.69	5.37	6.94	7.71	7.2	5.55	7.97	5.47	6.81	4.33
1560342_at	---	---	0.42141	6.41	3.04	3.98	4.28	4.72	4.36	6.26	3.81	6.46	4.6
243329_at	---	---	0.42141	6.27	6.07	4.84	5.44	5.31	3.36	6.64	3.18	5.85	4.51
235324_at	SFRS3	splicing factor, arginine/serine-rich 3	0.42141	5.89	3.7	6.98	6.54	6.08	4.73	5.82	4.9	5.49	4.15
236595_at	---	---	0.42141	6.05	4.56	6.47	5.96	4.46	4.26	6.05	4.36	7.16	5.5
213539_at	CD3D	CD3d molecule, delta (CD3-TCR complex)	0.423946	6.16	5.42	5.09	5.43	8.15	5.61	8.92	5.37	6.31	5.43
202206_at	ARL4C	ADP-ribosylation factor-like 4C	0.423946	6.37	4.98	7.05	6.99	6.04	5.55	7.53	3.62	5.88	5.15
204890_s_at	LCK	lymphocyte-specific protein tyrosine kinase	0.423946	5.39	3.93	4	5.12	6.76	4.71	6.92	3.98	6.29	4.61
224356_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.423946	6.61	7.53	8.72	8.66	7.58	9.87	8.78	9.49	7.3	8.08
235680_at	---	---	0.423946	8.84	8.22	7.5	8.05	8.16	6.83	8.15	6.43	9.1	5.98
210116_at	SH2D1A	SH2 domain protein 1A	0.426971	5.85	3.83	5.02	6.34	7.11	4.51	8.16	5.24	7.02	4.57
205758_at	CD8A	CD8a molecule	0.454482	6.49	3.99	4.44	6.08	5.72	3.98	8.52	3.37	5.55	3.55
1558691_a_at	DOCK4	dedicator of cytokinesis 4	0.454482	8.15	2.5	7.89	8.5	5.96	3.37	8.21	3.79	8.1	4.43
210426_x_at	RORA	RAR-related orphan receptor A	0.454482	6.33	4.65	4.15	4.28	6.33	3.89	7.72	4.28	4.9	3.66
210972_x_at	TRA@ /// TRAC /// TRAJ17 /// TRAV20	T cell receptor alpha locus /// T cell receptor alpha constant /// T cell recept	0.454482	6.6	5.02	5.59	7	7.87	6.62	9.53	5.64	7.85	6.07
206804_at	CD3G	CD3g molecule, gamma (CD3-TCR complex)	0.454482	6.24	4.21	4.57	6.17	6.84	5.11	8.51	4	5.65	5.73
230464_at	S1PR5	sphingosine-1-phosphate receptor 5	0.454482	6.36	4.57	5.61	5.48	7.37	4.44	7.51	4.78	7.19	5.32
236510_at	---	---	0.454482	7.68	4.45	4.64	7.29	6.65	3.1	7.71	5.2	8.57	2.95
221558_s_at	LEF1	lymphoid enhancer-binding factor 1	0.454482	5.08	3.76	3.65	6.44	7.43	4.96	7.73	3.81	6.61	5.61
212224_at	ALDH1A1	aldehyde dehydrogenase 1 family, member A1	0.454482	4.5	5.74	4.78	6.5	6.67	9.1	6.94	7.18	5.25	6.94
201506_at	TGFBI	transforming growth factor, beta-induced, 68kDa	0.454482	5.24	6.61	5.62	6.54	7.32	9.5	7.85	8.92	6.35	6.7
244061_at	---	---	0.454482	7.3	5.69	5	7.1	6.94	4.6	7.57	4	7.2	2.98
234778_at	---	---	0.454482	8.7	6.59	6.49	7.86	7.43	3.67	8.79	5.66	7.81	5.25
226018_at	C7orf41	chromosome 7 open reading frame 41	0.454482	6.49	6.65	5.64	6.77	6.58	9.58	7.31	8.56	6.73	7.37
1569477_at	---	---	0.454482	9.37	7.28	8.96	8.65	7.34	6.93	8.89	7.18	9.18	6.83
229483_at	---	---	0.454482	6.79	6.07	4.56	6.34	5.85	3.43	5.16	4.64	6.5	3.52
209671_x_at	TRA@ /// TRAC	T cell receptor alpha locus /// T cell receptor alpha constant	0.454482	6.71	5.73	5.7	6.66	7.61	6.46	9.1	5.72	7.35	6.01

233289_at	---	---	0.454482	6.66	4.54	5.61	6.6	6.38	4.33	7.26	4.73	6.53	3.83
211902_x_at	TRA@	T cell receptor alpha locus	0.454482	6.46	5.85	5.96	6.75	7.52	6.39	9.18	6.06	7.57	6.03
223527_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	0.454482	8.05	6.71	8.44	7.96	7.74	5.81	7.53	5.63	7.46	5.08
240344_x_at	LYRM7	Lyrm7 homolog (mouse)	0.454482	7.93	7.47	7.07	7.14	8.5	5.84	8.17	5.26	7.67	7.9
1569077_x_at	ZNF836	zinc finger protein 836	0.454482	7.59	4.69	6.4	5.73	7.15	4.55	6.66	3.87	6.76	3.76
227686_at	OXNAD1	oxidoreductase NAD-binding domain containing 1	0.454482	6.79	5.36	5.71	6.87	6.92	4.54	8.57	6.82	7.95	6.42
232344_at	---	---	0.454482	9.42	8.06	7.43	8.92	7.99	6.54	9.27	7.57	9.2	4.72
210843_s_at	MFAP3L	microfibrillar-associated protein 3-like	0.454482	5.31	6.13	5.53	6.39	5.24	9.07	6.92	6.85	4.62	5.56
228433_at	NFYA	nuclear transcription factor Y, alpha	0.454482	8.05	7.6	6.11	7.07	7.24	4.58	8.12	5.93	7.77	4.54
225187_at	KIAA1967	KIAA1967	0.454482	8.19	5.97	6.82	6.87	7.02	5.14	6.85	4.89	7.93	3.41
228211_at	C9orf102	chromosome 9 open reading frame 102	0.454482	6.99	6.29	5.23	5.36	6.73	4.15	6.47	3.55	7.46	3.62
220570_at	RETN	resistin	0.454482	4.86	5.51	5.97	5.98	5.92	7.79	6.66	8.84	5.5	7.75
239829_at	---	---	0.454482	7.43	5.7	4.29	5.36	6.64	3.37	6.66	4.86	6.12	4.85
200824_at	GSTP1	glutathione S-transferase pi 1	0.454482	6.13	6.79	7.47	6.16	6.82	8.7	7.14	8.21	6.31	9.37
214469_at	HIST1H2AE	histone cluster 1, H2ae	0.454482	7.89	8.8	9.23	8.56	8.62	11.71	8.29	10.38	8.67	10.37
239571_at	---	---	0.454482	7.82	6.03	6.53	6.47	7.52	5.05	7.42	4.63	8.08	7.1
218117_at	RBX1	ring-box 1	0.454482	6.41	6.83	6.57	7.05	6.84	9.96	7.11	8.02	7.04	8.97
239504_at	---	---	0.454482	6.09	5.2	5.09	5.07	6.38	4.25	7.68	4.7	7.2	5.02
202944_at	NAGA	N-acetylgalactosaminidase, alpha-	0.454482	4.94	6.49	4.31	5.44	5.92	7.11	6.87	8.09	5.95	6.14
231211_s_at	YIF1B	Yip1 interacting factor homolog B (S. cerevisiae)	0.454482	4.45	5.76	6.37	5.61	5.84	8.13	5.27	6.74	4.69	6.17
213073_at	ZFYVE26	zinc finger, FYVE domain containing 26	0.454482	6.34	6.37	6.89	4.9	6.32	6.69	7.31	4.68	7.68	4.86
210621_s_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.454482	7.37	5.89	5.27	6.31	5.88	4.65	6.89	5.67	7.54	4.8
232354_at	---	---	0.454482	7.28	4.94	6.16	6.39	6.11	5.35	6.57	4.28	6.68	4.16
200736_s_at	GPX1	glutathione peroxidase 1	0.454951	6.72	7.52	7.01	8.04	8.17	10.27	8.29	8.95	7.93	8.46
229541_at	---	---	0.455667	6.71	7.04	5.49	6	6.46	4.08	6.3	5.77	7.03	4.33
39248_at	AQP3	aquaporin 3 (Gill blood group)	0.459351	8.45	5.03	3.52	6.46	10.3	4.88	11.25	7.07	8.74	5.82
202988_s_at	RGS1	regulator of G-protein signaling 1	0.459351	6.66	5.9	5.72	6.68	7.95	6.55	6.55	5.04	7.77	4.53
236266_at	RORA	RAR-related orphan receptor A	0.463297	5.75	4.63	4.38	5.94	6.17	4.25	6.89	3.45	6.34	4.1
234044_at	---	---	0.463297	10.5	7.99	7.17	8.76	8.22	7.09	9.95	7.47	10.18	6.24
228097_at	MYLIP	myosin regulatory light chain interacting protein	0.463687	7.08	5.02	6.81	7.43	5.57	3.78	5.53	3.84	5.77	3.16
242659_at	---	---	0.463687	7.91	5.73	7.22	7.75	6.77	6.84	7.18	4.79	7.09	5.01
223754_at	C2orf88	chromosome 2 open reading frame 88	0.479569	3.9	3.63	4.69	5.96	4.58	9.51	5.46	6.98	5.08	6.43
210254_at	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	0.479569	7.11	8.4	6.17	7.86	9.14	10.25	9.24	11.74	8.13	10.97
208078_s_at	SIK1	salt-inducible kinase 1	0.479569	9.8	5.92	9.22	9.49	7.86	5.38	8.83	5.34	8.8	6.24
230550_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.479569	6.13	6.59	6.24	7.09	6.69	9.46	8.07	7.84	6.81	8.2
203645_s_at	CD163	CD163 molecule	0.479569	5.18	7.1	5.22	6.26	7.14	7.93	8.23	7.84	5.44	6.51
1554615_at	---	---	0.479569	7.75	6.61	5.33	5.77	5.89	3.04	6.02	4.61	7.11	4.63
244423_at	---	---	0.479569	8.32	6.75	7.08	7.7	7.51	6.25	8.98	5.82	8.72	5.65
232356_at	---	---	0.479569	8.15	4.81	6.45	5.59	5.04	6.26	5.74	6.23	7.6	3.77
1557551_at	---	---	0.479569	6.53	5.14	4.89	5.69	6.74	6.95	6.52	3.64	6.57	5.59
232789_at	---	---	0.479569	7.18	5.29	7.16	7.42	5.99	5.04	6.45	3.84	7.06	3.52
1556735_at	---	---	0.479569	6.25	4.31	5.38	6.7	6.49	3.64	7.3	4.66	5.24	4.3

213653_at	METTL3	methyltransferase like 3	0.479569	7.96	7.44	6.37	7.26	8.02	6.46	7.91	4.99	8.32	6.58
238243_at	---	---	0.479569	7.7	5.25	6.02	7.59	6.07	4.45	7.09	6	6.94	4.96
240721_at	---	---	0.481145	9.23	6.35	3.71	7.96	6.49	4.2	8.47	4.24	7.15	3.3
205653_at	CTSG	cathepsin G	0.481145	4.91	6.84	5.74	5.1	6.48	8.37	6.58	10.9	5.57	10.73
1554892_a_at	MS4A3	membrane-spanning 4-domains, subfamily A, member 3 (hematopoietic cell-specific)	0.481145	2.68	4.52	4.53	3.74	4.84	7.35	5.36	8.37	4.51	6.08
210031_at	CD247	CD247 molecule	0.481145	5.8	4.6	5.25	6.25	6.95	4.97	8.22	4.87	7.14	5.76
212289_at	ANKRD12	ankyrin repeat domain 12	0.481145	9.62	9.71	8.88	9.3	9.07	5.04	9.56	6.03	8.72	7.41
204838_s_at	MLH3	mutL homolog 3 (E. coli)	0.481145	5.01	4.14	5.75	6.99	5.95	10.3	6.74	7.76	5.36	7.26
234033_at	---	---	0.481145	6.61	2.88	3.53	5.34	4.33	4.43	6.54	3.15	7.44	4.47
242320_at	---	---	0.481145	8.95	7.12	7.65	8.54	7.34	7.96	9.38	6.08	9.73	6.65
215049_x_at	CD163	CD163 molecule	0.481145	5.73	7.17	4.45	5.94	7.22	7.83	8.28	7.72	5.25	6.72
230048_at	---	---	0.481145	10.01	8.65	8.2	9.03	9.1	6.77	9.92	7.6	8.98	6.77
239152_at	---	---	0.481145	11.15	8.31	9.81	10.45	9.85	6.84	10.89	8.16	10.75	6.91
235739_at	---	---	0.481145	8.53	5.01	8.51	5.36	7.4	4.97	7.58	7.82	8.81	3.97
202207_at	ARL4C	ADP-ribosylation factor-like 4C	0.481145	6.24	5.61	5.58	7.08	6.61	5.99	7.72	4.16	6.69	4.45
242898_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	0.481145	6.93	7.4	6.44	8.11	7.17	5.03	7.01	5.69	7.83	4.83
205557_at	BPI	bactericidal/permeability-increasing protein	0.481145	5.09	6.09	6.02	6.3	6.85	8.54	7.02	9.09	5.5	8.1
244840_x_at	DOCK4	dedicator of cytokinesis 4	0.481145	6.89	4.7	7.37	7.18	4.86	5.09	6.42	4.24	6.33	6.09
208553_at	HIST1H1E	histone cluster 1, H1e	0.481145	7.25	9.17	7.31	7.07	8.33	10.79	7.92	9.82	7.67	10.38
233647_s_at	CDADC1	cytidine and dCMP deaminase domain containing 1	0.481145	8.24	7.07	7.82	8.63	7.31	5.8	8.17	5.33	8.38	6.03
234196_at	---	---	0.481145	8.94	6.21	6.23	7.89	7.89	5.27	8.42	6.08	8.03	5.39
224598_at	MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, iso	0.481145	5.12	6.07	2.94	6.23	5.09	7.54	5.37	5.92	5.49	6.45
209772_s_at	CD24	CD24 molecule	0.481145	5.08	6.27	6.63	5.4	6.55	7.12	6.23	8.89	5.98	9.46
239045_at	---	---	0.481145	9.46	7.68	9.9	8.69	8.84	6.25	9.62	8.27	9.39	6.1
1563259_at	---	---	0.481145	7.47	5.4	5.25	7.23	6.54	4.05	7.26	4.53	6.52	4.71
243182_at	---	---	0.481145	8.14	7.18	6.89	8.45	6.89	4.86	7.09	6.32	8	5.52
205967_at	HIST1H4C	histone cluster 1, H4c	0.481145	7.27	8.54	7.59	7.42	8	10.3	7.96	9.81	8.13	10.13
232478_at	---	---	0.481145	6.21	5.75	7.57	5.65	4.27	4.83	6.37	4.55	6.44	4.73
1568640_at	ASPRV1	Aspartic peptidase, retroviral-like 1	0.481145	7.06	5.2	4.84	5.52	5.32	4.67	6.45	4.58	7.49	4.87
235102_x_at	---	---	0.482511	5.27	6.63	7.75	8.12	6.32	10.83	7.94	9.48	7.94	8.41
243857_at	MORF4L2	Mortality factor 4 like 2	0.483408	6.63	3.55	5.7	4.73	4.3	2.85	5.54	6.01	6.29	2.69
214771_x_at	MPRIP	myosin phosphatase Rho interacting protein	0.489841	6.53	7.35	5.36	6.55	7.96	4.49	7.16	4.65	6.86	5.59
206488_s_at	CD36	CD36 molecule (thrombospondin receptor)	0.490832	4.29	6.26	5.4	6.65	7.24	9.86	9.18	9.38	7.46	7.46
202768_at	FOSB	FBJ murine osteosarcoma viral oncogene homolog B	0.490832	11.92	5.8	11.93	11.74	8.86	7.65	11.85	8.67	11.57	7.93
239453_at	---	---	0.490832	7.13	7.43	5.06	7.32	6.82	3.96	7.31	5.02	7.69	5.61
206655_s_at	GP1BB /// SEPT5	glycoprotein Ib (platelet), beta polypeptide /// septin 5	0.490832	5.77	5.51	6.01	6.49	6.75	10.24	6.99	8.4	6.17	8.25
213294_at	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	0.490832	6.29	6.56	4.67	6.89	6.87	3.71	6.54	5.61	6.97	4.91
1557799_at	C11orf31	chromosome 11 open reading frame 31	0.490832	6.45	7.16	7.12	6.2	6.74	5.65	5.77	3.41	6.57	6.76
222326_at	---	---	0.490832	8.86	6.97	8.65	9.24	8.11	5.67	8.92	6.73	9.02	6
231292_at	EID3	EP300 interacting inhibitor of differentiation 3	0.490832	6.69	3.93	6.58	6.02	4.18	4.24	4.86	4.29	5.72	4.05

221618_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0.490832	8.83	8.03	7.42	8.93	8.79	6.24	9.41	7.54	9.49	8.3
200602_at	APP	amyloid beta (A4) precursor protein	0.491013	5.47	7.17	4.66	7.16	6.99	10.06	8.16	9.02	5.67	7
219872_at	C4orf18	chromosome 4 open reading frame 18	0.491013	3.74	5.33	3.82	4.06	6	6.94	6.56	6.87	4.55	3.96
217591_at	SKIL	SKI-like oncogene	0.491013	10.19	5.43	10.39	9.69	7.37	7.35	8.12	6.38	9.01	6.79
216550_x_at	ANKRD12	ankyrin repeat domain 12	0.491013	10.27	10.18	7.14	9.72	10.17	7.61	10.37	8.16	10.38	7.76
208601_s_at	TUBB1	tubulin, beta 1	0.491013	4.96	5.68	6.12	6.53	6.12	9.52	7.86	8.54	6.57	8.22
219099_at	C12orf5	chromosome 12 open reading frame 5	0.491013	6.35	5.77	3.52	5.8	5.7	6.6	4.48	4.92	5.57	7
233694_at	HSPA1L	Heat shock 70kDa protein 1-like	0.491819	4.75	7.35	5.43	5.94	5.69	7.14	4.63	5.56	5.06	8.47
219321_at	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	0.492997	7.97	7.07	4.51	6.3	6.56	5.1	7.16	3.54	7.64	5.19
207269_at	DEFA4	defensin, alpha 4, corticostatin	0.493509	4.21	6.54	7.29	6.02	7.32	9.74	7.68	10.87	6.86	11.54
210321_at	GZMH	granzyme H (cathepsin G-like 2, protein h-CCPX)	0.493509	6.4	5.15	5.7	6.74	6.61	5.28	8.89	5.23	6.32	5.15
203949_at	MPO	myeloperoxidase	0.493509	5.01	6.7	5.77	6.26	5.45	7.52	7.22	9.94	6.39	10.16
215889_at	SKIL	SKI-like oncogene	0.493509	10.18	5.48	10.28	10.32	7.99	6.37	9.52	7.6	9.33	7.66
241020_at	---	---	0.493509	7.38	4.55	3.89	6.1	5.41	4.05	6.84	3.77	5.74	5.49
201163_s_at	IGFBP7	insulin-like growth factor binding protein 7	0.493509	5.79	5.46	5.05	5.89	6.99	7.45	5.74	7.81	6.7	9.96
204081_at	NRGN	neurogranin (protein kinase C substrate, RC3)	0.493509	5.75	5.05	5.51	6.01	6.54	9.78	7.36	8.59	6.15	7.08
208690_s_at	PDLIM1	PDZ and LIM domain 1	0.493509	5.01	5.94	6.11	6.16	7.38	8.67	6.72	8.98	6.7	7.63
207808_s_at	PROS1	protein S (alpha)	0.493509	4.72	4.7	5.06	5.08	5.93	7.81	6.19	7.27	4.51	5.17
209189_at	FOS	v-fos FBJ murine osteosarcoma viral oncogene homolog	0.493509	12	10.31	10.77	10.59	11.3	9.23	12.17	11.76	12.02	8.8
243842_at	---	---	0.493509	7.86	4.44	4.55	6.36	5.95	4.36	5.5	5.18	6.13	5.59
230740_at	---	---	0.493509	4.77	5.54	7.48	6.59	4.52	8.1	6.43	7.73	5.9	6.81
239163_at	UBE2B	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.493509	9.85	7.19	7.73	9.22	8.58	8.34	9.43	6.64	9.72	7.5
211842_s_at	SLC24A1	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	0.496258	6.08	3.89	4.29	4.31	5.29	4.08	6.96	3.57	6.9	4.4
202436_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.496258	4.5	7.28	7.72	6.89	6.82	9.26	8.23	8.54	7.3	7.38
234326_at	---	---	0.496258	9	6.98	7.78	8.71	7.11	5.77	8.09	7	7.82	4.43
235500_at	HNRNPC	heterogeneous nuclear ribonucleoprotein C (C1/C2)	0.496258	8.02	4.79	7.01	7.12	5.07	5.29	6.99	4.03	6.51	4.28
214923_at	ATP6V1D	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	0.496258	7.91	6.51	4.76	6.64	7.75	5.14	8.81	6.08	6.71	4.5
210244_at	CAMP	cathelicidin antimicrobial peptide	0.496258	7.84	8.48	8.62	8.54	9.17	10.54	9.24	11.23	8.08	10.41
1558877_at	---	---	0.496258	7.34	6.05	5.44	6.99	5.49	3.68	6.05	4.39	7.04	4.65
201058_s_at	MYL9	myosin, light chain 9, regulatory	0.496258	7.22	5.66	6.18	7.09	6.11	10.59	8.52	9.29	6.81	8.54
201105_at	LGALS1	lectin, galactoside-binding, soluble, 1	0.496258	5.98	6.34	6.98	7.18	6.84	9.22	8.1	8.77	6.53	7.22
1557519_at	---	---	0.496258	7.99	5.67	7.34	8.41	6.23	5.25	7.25	6.99	7.29	7.84
232174_at	---	---	0.496258	6.95	4.55	6.38	5.36	5.3	4.25	7.86	6.51	6.04	4.16
222122_s_at	THOC2	THO complex 2	0.496258	6.99	6.92	4.48	5.58	7.22	5.8	7.19	4.97	7.22	4.4
201004_at	SSR4	signal sequence receptor, delta (translocon-associated protein delta)	0.496258	6.67	6.67	7.03	6.79	6.99	9.34	7.69	8.54	6.37	8.49
233097_x_at	---	---	0.496258	6.51	4.35	4.82	5.13	6.12	4.92	6.47	3.62	5.09	3.7
240013_at	---	---	0.498419	7.54	6.34	6.41	6.48	6.25	2.77	7.69	5.51	6.1	7.3

229447_x_at	NBPF10 /// NBPF11 /// NBPF8 /// RP11-94I2.2	neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family,	0.498419	8.36	8.53	6.64	7.54	7.87	6.16	8.52	6.75	8.85	5.87
235716_at	---	---	0.498419	8.15	6.69	5.39	6.59	7.57	5.33	7.53	4.64	6.68	7.38
202241_at	TRIB1	tribbles homolog 1 (Drosophila)	0.498419	11.17	9.4	11.41	11.42	11.09	9.56	11.12	9.14	11.48	8.86
232001_at	LOC439949	hypothetical protein LOC439949	0.498769	3.85	3.33	3.33	4.91	6.63	4.3	8.56	3.36	6.35	4.56
213193_x_at	TRBC1	T cell receptor beta constant 1	0.498769	7.53	5.95	2.99	6.86	8.48	5.42	9.89	5.46	7.43	5.16
217414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.498769	9.52	10.39	5.04	10.56	10.2	12.36	8.91	11.46	6.37	9.75
204018_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.498769	9.68	10.56	5.56	10.66	10.25	12.44	8.95	11.37	6.52	9.82
211745_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.498769	10.05	10.96	5.7	10.96	10.67	12.72	9.32	11.73	7.03	10.31
204620_s_at	VCAN	versican	0.498769	3.85	6.22	3.74	7.24	5.7	9.08	8.31	7.7	5.82	4.15
202437_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.498769	4.19	4.66	3.97	4.88	5.25	7.27	6.66	7.43	5.36	4.95
212402_at	ZC3H13	zinc finger CCCH-type containing 13	0.498769	7.84	7.18	4.84	7.02	7.53	3.88	7.21	6.86	7.42	3.75
1556783_a_at	---	---	0.498769	6.63	4.98	6.23	6.33	5.6	3.14	6.12	4.08	6.25	2.58
1555680_a_at	SMOX	spermine oxidase	0.498769	5.14	5.38	4.5	5.79	4.9	9.01	5.38	6.9	4.98	6.98
1554036_at	ZBTB24	zinc finger and BTB domain containing 24	0.498769	7.21	6.42	7.03	6.29	7.61	5.92	8.56	4.52	8.74	4.48
227432_s_at	---	---	0.498769	6.4	5.35	4.6	6.13	6.13	7.63	6.65	6.76	7.79	8.93
214516_at	HIST1H4B	histone cluster 1, H4b	0.498769	6.46	8.15	6.31	5.52	5.66	8.98	8.06	9.48	7.34	9.39
208791_at	CLU	clusterin	0.498769	5.03	5.28	5.22	5.96	6.35	9.49	7.46	7.65	5.64	7.05
208576_s_at	HIST1H3B	histone cluster 1, H3b	0.498769	4.66	4.52	5.38	4.36	4.64	7.03	4.86	7.93	4.54	7.15
201104_x_at	NBPF10 /// NBPF11 /// NBPF12 /// NBPF14 /// NBPF15 /// NBPF16 /// NBPF8 /// RP11-94I2.2	neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family,	0.498769	8.65	8.03	6.8	7.57	7.14	5.79	8.01	5.49	7.82	5.98
213612_x_at	NBPF10 /// NBPF12 /// NBPF15 /// NBPF16 /// NBPF8 /// NBPF9	neuroblastoma breakpoint family, member 10 /// neuroblastoma breakpoint family,	0.498769	10.05	10.17	8.13	9	9.48	8.05	10.08	8.07	10.63	7.81
215378_at	---	---	0.498769	7.61	6.09	6.49	8.32	7.47	6.04	7.37	7.57	8.09	4.19
216563_at	ANKRD12	Ankyrin repeat domain 12	0.498769	11.83	11.65	8.92	11.01	11.34	9.59	11.39	9.8	11.42	8.98
215096_s_at	ESD	esterase D/formylglutathione hydrolase	0.498769	5.81	6.69	5.93	6.73	6.71	8.76	7.64	8.81	6.86	7.76
216667_at	LOC643332 /// RNASE2	similar to Nonsecretory ribonuclease precursor (Ribonuclease US) (Eosinophil-der	0.498769	5.37	5.15	5.19	5.13	5.28	6.75	5.24	8.79	5.07	6.62
218986_s_at	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	0.499128	5.37	5.42	6.3	6.97	6.91	3.91	6.26	5.63	7.01	4.06
209458_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.499469	9.94	10.84	5.46	10.95	10.56	12.65	9.25	11.64	6.45	10.17
206390_x_at	PF4	platelet factor 4	0.500361	6	6.86	9.01	8.32	7.97	12.27	9.38	10.46	8.43	10.46
1564052_at	TREML4	triggering receptor expressed on myeloid cells-like 4	0.500788	9.47	7.35	7.7	8.92	6.34	5.47	8.58	6.22	9.38	5.87
224685_at	MLLT4	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); tran	0.501109	6.52	5.51	4.11	5.13	6.45	4.25	6.97	5.57	7.35	4.5
1557071_s_at	NUB1	negative regulator of ubiquitin-like proteins 1	0.50163	6.32	6.81	5.43	6.56	6.17	4.97	7.24	6.18	7.51	3.94
211699_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.502371	9.63	10.48	5.09	10.64	10.27	12.36	8.9	11.39	6.13	9.73
201731_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.502577	9.8	9.77	7.12	9.07	9.44	7.03	9.11	7.29	9.27	5.58
219208_at	FBXO11	F-box protein 11	0.502577	6.5	3.51	6.75	6.42	6.29	5.28	6.47	5.5	6.48	3.91
239494_at	---	---	0.504777	8.54	6.63	7.05	7.8	7.66	5.61	8.28	7.33	8.2	5.09
203485_at	RTN1	reticulon 1	0.504785	6.88	7.12	3.53	7.44	8.13	8.21	7.31	8.13	8.39	7.79

232125_at	---	---	0.504785	6.12	4.92	3.6	5.42	6.08	5.91	5.71	4.13	6.8	3.36
210985_s_at	SP100	SP100 nuclear antigen	0.504839	8.49	8.29	4.46	8.11	8.46	5.33	7.68	5.81	8.18	6.49
1559507_at	LOC100130357	similar to hCG2038897	0.504839	6.97	5.4	7.33	7.47	7.41	4.17	7.44	4.93	6.74	4.72
231644_at	---	---	0.504839	7.26	4.32	8.26	6.14	6.93	6.91	8.15	4.78	8.24	5.55
213982_s_at	RABGAP1L	RAB GTPase activating protein 1-like	0.504839	6.65	7.55	6.6	8.15	6.99	9.18	8.47	9.82	7.57	8.02
238659_at	KIAA0141	KIAA0141	0.504839	7.77	6.84	7.35	6.74	7.03	4.17	7.77	6.37	8.71	6.33
227152_at	C12orf35	chromosome 12 open reading frame 35	0.505086	11.88	11.8	9.86	11.83	11.67	9.76	11.76	10.59	11.85	8.61
244415_at	---	---	0.505103	8.22	7.15	5.93	7.9	6.57	3.85	7.15	6.71	7.9	4.85
219691_at	SAMD9	sterile alpha motif domain containing 9	0.505103	7.87	7.5	6.76	8.16	7.15	5.36	7.48	6.74	7.03	5.06
219505_at	CECR1	cat eye syndrome chromosome region, candidate 1	0.506451	6.38	6.74	6.67	7.28	7.07	10.37	8.43	9.47	7.89	7.09
210915_x_at	TRBC1	T cell receptor beta constant 1	0.50749	7.63	6.23	3.44	6.88	8.5	6.3	9.78	6.12	7.53	6.02
211734_s_at	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	0.50749	5.13	6.82	4.48	6.29	6.56	6.56	6.56	6.94	5.01	4.26
1568845_at	---	---	0.50749	8	5.86	4.99	5.36	6.39	6.64	7.27	3.49	6.75	5.67
244578_at	LCP2	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa	0.50749	7.55	4.94	4.76	7.75	7.58	5.36	6.19	4.68	7.1	5.71
203715_at	TBCE	tubulin folding cofactor E	0.508414	4.67	8.3	6.29	7.22	7.03	5.2	3.95	7.29	6	6.87
223725_at	C3orf42	chromosome 3 open reading frame 42	0.508414	7.44	8.73	7.34	7.33	6.71	5.7	7.38	5.93	8.83	6.97
232784_at	---	---	0.508414	6.76	4.32	7.71	4.47	5.21	4.08	7.44	5.78	7.17	4.14
239886_at	---	---	0.508414	9.67	8.85	6.56	8.42	8.6	6.19	8.71	5.08	9.45	7.71
201416_at	SOX4	SRY (sex determining region Y)-box 4	0.508414	3.97	5.61	4.33	5.15	5.41	7.03	5.91	7.59	4.8	8.23
235060_at	LOC100190986	hypothetical LOC100190986	0.508414	7.66	7.51	5.9	6.43	6.39	5.5	7.02	5.24	7.24	4.2
1556055_at	---	---	0.510348	8.45	8.36	5.38	7.92	6.86	4.34	8.2	7.2	8.39	4.4
225579_at	PQLC3	PQ loop repeat containing 3	0.510348	5.63	6.32	3.44	5.67	7.4	8.45	6.98	7.11	6.62	7.05
239245_at	---	---	0.510348	6.68	5.36	4.1	6.74	5.19	3.31	6.63	4.88	6.43	5.47
223111_x_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	0.510672	10.38	10.2	7.92	9.84	9.98	7.05	9.21	8.26	9.79	5.46
220577_at	GVIN1	GTPase, very large interferon inducible 1	0.511217	6.53	7.16	4.01	6.73	6.82	4.17	7.07	5.72	6.55	4.59
244356_at	---	---	0.511662	8.3	6.86	7.4	8.49	6.09	5.73	7.72	6.23	8.34	6.75
214525_x_at	MLH3	mutL homolog 3 (E. coli)	0.5118	5.21	4.17	6.34	6.83	6.2	10.25	7.2	7.54	6.77	7.64
206110_at	---	---	0.5118	5.42	4.87	6.3	6.4	7.41	10.86	7.63	8.98	5.6	7.49
230086_at	FNBP1	formin binding protein 1	0.5118	8.14	6.83	6.97	8.09	5.6	5.21	7.36	6.6	7.78	6.07
224983_at	SCARB2	scavenger receptor class B, member 2	0.5118	4.05	5	5.31	5.18	6.98	7.67	5.42	6.47	4.69	6.63
239758_at	---	---	0.5118	6.01	5.85	3.34	4.27	5.95	3.59	6.14	4.24	7.41	5
212980_at	USP34	ubiquitin specific peptidase 34	0.5118	6.75	6.87	5.48	5.65	6.7	4.84	4.84	6.45	6.83	3.8
212820_at	DMXL2	Dmx-like 2	0.5118	7.99	7.51	8.1	8.02	7.78	6.69	7.67	6.94	8.43	4.98
214442_s_at	PIAS2	protein inhibitor of activated STAT, 2	0.5118	4.78	3.01	6.19	5.35	4.48	3.65	6.91	5.05	6.01	4.89
205221_at	HGD	homogentisate 1,2-dioxygenase (homogentisate oxidase)	0.5118	5.57	5.62	6.01	5.76	5.63	8.51	6.74	7.74	5.77	5.79
208174_x_at	ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	0.5118	8.94	9.83	7.72	7.82	8.47	6.72	8.73	7.66	7.99	6.48
228967_at	EIF1	Eukaryotic translation initiation factor 1	0.5118	9.85	8.16	10.3	9.26	8.15	8.56	9.5	8.84	10.46	7.37
243361_at	SFRS12	splicing factor, arginine/serine-rich 12	0.512163	6.87	4.28	3.29	3.74	3.97	4.04	6.09	3.33	6.64	3.79
1562468_at	---	---	0.512409	10.42	7.71	9.03	9.32	8.22	7.07	9.65	8.91	9.87	8.13

235597_s_at	RGPD1 /// RGPD2	RANBP2-like and GRIP domain containing 1 /// RANBP2-like and GRIP domain contain	0.512409	6.04	7.21	6.24	6.93	4.83	4.54	6.3	5.67	7.57	4.83
209839_at	DNM3	dynamin 3	0.512409	4.28	4.18	3.53	6.32	5.76	8.38	6.26	6.6	4.83	4.8
218102_at	DERA	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)	0.512409	6.29	6.62	4.83	5.81	6.93	8.03	5.87	7.67	6.13	7.84
223204_at	C4orf18	chromosome 4 open reading frame 18	0.512946	2.36	4.01	3.58	3.4	5.79	7.02	6.38	6.9	3.04	3.04
230014_at	---	---	0.512946	10.7	7.89	10.17	8.24	8.13	8.03	9.66	9.25	9.98	8.39
228617_at	XAF1	XIAP associated factor 1	0.513225	7.69	7.62	6.71	9.41	8.51	6.09	7.17	3.17	8.9	5.66
238183_at	---	---	0.513225	5.7	4.48	5.62	8.15	4.55	9.25	6.52	9.1	7.21	4.99
211005_at	LAT /// SPNS1	linker for activation of T cells /// spinster homolog 1 (Drosophila)	0.513225	6.86	4.97	5.7	7.37	8.29	6.73	9.86	7.99	8.22	7.97
1555225_at	C1orf43	chromosome 1 open reading frame 43	0.513225	8.32	8.23	9.12	7.38	7.76	4.56	7.75	4.44	8.83	7.41
212286_at	ANKRD12	ankyrin repeat domain 12	0.513913	9.96	8.75	6.1	8.89	8.82	6.17	8.9	7.12	8.79	7.83
214509_at	HIST1H3I	histone cluster 1, H3i	0.513913	4.1	4.69	4.46	5.58	5.04	8.7	6	7.29	5.2	7.62
205178_s_at	RBBP6	retinoblastoma binding protein 6	0.513913	9.01	8.22	5.38	8.37	8.85	5.11	8.44	7.37	8.45	6.06
209045_at	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	0.513913	3.69	5.69	3.86	4.47	4.87	7.57	6.61	5.91	4.16	6.32
223236_at	CCDC55	coiled-coil domain containing 55	0.513913	7.54	7.75	6.76	7.46	7.71	5.01	6.74	6.56	7.06	4.85
242182_x_at	---	---	0.513913	8.18	7.62	5.49	5.93	6.97	5.01	7.76	6.34	7.42	4.96
213918_s_at	NIPBL	Nipped-B homolog (Drosophila)	0.513913	9.41	9.28	8.43	9.14	9.03	6.9	9.68	8.31	9.04	6.26
205010_at	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	0.513913	6.37	5.25	6.46	5.83	5.19	4.99	7.64	4.5	6.64	4.51
227062_at	NCRNA00084	non-protein coding RNA 84	0.51407	10.07	8.29	9.33	9.71	7.93	7.21	9.18	8.19	10.99	7.34
205033_s_at	DEFA1 /// DEFA3 /// LOC728358	defensin, alpha 1 /// defensin, alpha 3, neutrophil-specific /// defensin, alpha	0.514132	9.69	12.14	12.09	11.54	12.61	13.7	12.77	13.96	12.11	14.06
215779_s_at	HIST1H2BG	histone cluster 1, H2bg	0.514132	5.74	6.55	6.9	5.99	6.82	9	6.57	8	6.14	7.65
226370_at	KLHL15	kelch-like 15 (Drosophila)	0.514132	8.05	7.54	7.77	8.05	7.42	4.66	8.16	6.57	7.14	6.4
208994_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	0.514256	10.45	10.46	8.31	9.67	10.08	8.57	9.63	9.32	9.68	6.64
225775_at	TSPAN33	tetraspanin 33	0.51519	6.42	7.21	6.32	7.03	7.38	10.64	8.3	9.4	7	8.01
225694_at	CRKRS	Cdc2-related kinase, arginine/serine-rich	0.515455	8	7.61	7.05	8.34	7.7	6.24	7.9	6.26	9.14	5.33
1569538_at	---	---	0.516648	6.46	7.7	5.44	5.35	5.79	4.56	6.04	4	6.12	5.61
223106_at	TMEM14C	transmembrane protein 14C	0.51739	4	6.05	6.63	5.6	7.06	7.89	6.85	7.4	6.97	7.63
243772_at	SDCCAG8	serologically defined colon cancer antigen 8	0.517512	5.1	5.01	6.01	5.9	6.04	6.32	3.92	5.95	5.44	8.21
1557049_at	LOC149478	Hypothetical protein LOC149478	0.518344	6.88	4.11	5.86	6.53	5.47	4.15	6.81	4.07	7.07	3.97
244433_at	---	---	0.519125	6.6	6.58	6.02	6.93	5.67	4.11	6.5	3.12	5.9	7.49
236002_at	---	---	0.519702	7.14	6.47	4.58	5.88	6.59	4.81	6.65	4.86	7.15	4.79
1556107_at	---	---	0.521203	6.57	4.73	6.39	7.24	4.79	5.04	5.93	5.21	5.02	2.91
242853_at	---	---	0.521499	7.85	5.8	6.04	6.65	7.21	6.95	8.81	6.77	8.18	5.32
223117_s_at	USP47	ubiquitin specific peptidase 47	0.521499	6.72	5.85	5.37	5.98	7.68	4.47	6.96	7.53	6.72	4.01
229935_s_at	MLL	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	0.521499	5.01	5.35	3.36	4.61	6.73	4.95	6.2	4.58	6.22	3.33
226740_x_at	NBPF1	Neuroblastoma breakpoint family, member 1	0.521499	10.08	10.27	7.63	9.29	9.57	8.09	10.05	8.05	10.49	8.11
211571_s_at	VCAN	versican	0.522724	5.6	8.03	5.81	8.12	7.92	9.39	10.14	9.69	7.6	5.71
218166_s_at	RSF1	remodeling and spacing factor 1	0.522724	7.26	7.08	4.42	6.7	7.01	4.58	6.8	6.44	7.17	4.16

208792_s_at	CLU	clusterin	0.522927	5.86	5.63	6.07	6.56	6.8	9.77	7.73	7.64	6.27	7.53
1566981_at	---	---	0.522927	6.15	4.82	5.43	5.67	5.4	4.73	6.28	6.97	7.9	4.5
226603_at	SAMD9L	sterile alpha motif domain containing 9-like	0.5234	7.46	7.23	8.48	9.08	7.72	5.78	6.53	6.37	8.22	7.74
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	0.523487	4.36	3.46	2.99	3.95	3.2	8.3	6.05	6.58	3.69	5.59
211796_s_at	TRBC1 /// TRBC2	T cell receptor beta constant 1 /// T cell receptor beta constant 2	0.523782	8.58	7.47	3.93	7.93	9.57	7.23	11	7.04	8.61	6.19
208450_at	LGALS2	lectin, galactoside-binding, soluble, 2	0.523782	5.94	7.61	5.95	5.66	6.64	6.82	9.92	10.2	5.96	6.53
217216_x_at	MLH3	mutL homolog 3 (E. coli)	0.523782	4.08	3.71	6.43	6.69	6.14	10.01	7.16	7.61	6.86	7.46
206851_at	RNASE3	ribonuclease, RNase A family, 3 (eosinophil cationic protein)	0.523782	6.04	6.69	4.91	4.6	6.67	7.46	5.82	9.86	6.27	8.61
214670_at	ZKSCAN1	zinc finger with KRAB and SCAN domains 1	0.523782	6.91	7.16	4.84	6.27	5.88	2.93	6.62	6.47	6.48	4
212672_at	ATM	ataxia telangiectasia mutated	0.523782	7.73	8.01	6.64	6.57	6.61	4.25	8.66	6.65	7.82	4.42
1556597_a_at	LOC284513	hypothetical protein LOC284513	0.523782	7.88	6.34	6	4.05	6.38	4.38	7.2	6.86	7.95	5.06
225522_at	AAK1	AP2 associated kinase 1	0.523782	8.61	8.72	5.48	8.83	9.05	7.33	9.81	8.27	9.15	7.05
244811_at	PHIP	pleckstrin homology domain interacting protein	0.523782	7.36	6.75	5.67	6.21	5.54	3.71	6.13	5.24	6.11	3.88
201251_at	PKM2	pyruvate kinase, muscle	0.523782	6.63	6.96	6.76	7.08	7.6	10.03	7.81	8.75	6.99	8.04
1557384_at	ZNF131	Zinc finger protein 131	0.523782	7.22	6.26	5.06	6.04	6.29	4.31	6.93	6.88	8.01	5.06
238490_at	KIAA2026	KIAA2026	0.523782	7.25	7.92	6.12	6.87	6.48	5.88	7.27	5.35	6.41	3.66
231038_s_at	---	---	0.523782	10.84	10.72	10.01	9.74	10.2	9.07	10.51	10.24	11.03	7.04
238978_at	---	---	0.523782	6	5.67	5.25	6.61	4.86	7.85	3.94	5.68	6.53	8.41
233674_at	---	---	0.523782	7.22	6.07	5.05	5.63	5.14	4.31	6.14	4.02	7.16	4.43
232569_at	---	---	0.523782	6.69	7.34	6.19	6.11	7.08	5.8	5.54	3.6	7.21	5.93
233656_s_at	VPS54	vacuolar protein sorting 54 homolog (S. cerevisiae)	0.523782	4.48	7.55	5.14	6.09	4.87	6.96	4.84	4.08	5.08	6.07
207815_at	PF4V1	platelet factor 4 variant 1	0.5242	3.51	3.39	2.13	4.21	4.48	8.89	5.91	7.93	5.97	6.86
204619_s_at	VCAN	versican	0.5242	3.42	4.98	3.76	4.24	4.97	7.32	7.97	6.63	5.23	4.09
207017_at	RAB27B	RAB27B, member RAS oncogene family	0.5242	5.07	5.46	6.06	6.64	6.85	10.61	7.12	8.59	7.6	7.19
218332_at	BEX1	brain expressed, X-linked 1	0.5242	6	6.03	5	5.08	6.22	7.96	4.87	8.86	4.77	8.52
218666_s_at	STX17	syntaxin 17	0.5242	7.21	6.65	7.33	6.55	7.58	3.43	5.41	7.4	6.92	7.61
237949_at	---	---	0.5242	8.04	7.02	9.31	6.3	6.2	7.39	8.11	8.12	7.57	5.19
230407_at	---	---	0.5242	7.71	8.16	7.62	6.28	6.57	5.13	6.66	6.69	6.57	4.14
203791_at	DMXL1	Dmx-like 1	0.5242	6.6	6.78	6.51	6.77	7.68	4.29	7.24	6.52	6.92	4.68
36552_at	C2CD3	C2 calcium-dependent domain containing 3	0.5242	7.48	7.6	6.27	5.59	7	5.56	7.66	4.91	7.61	6.08
217294_s_at	ENO1	enolase 1, (alpha)	0.5242	5.72	6.76	5.12	7.14	5.94	8	7.6	7.12	4.52	5.3
221230_s_at	ARID4B	AT rich interactive domain 4B (RBP1-like)	0.5242	10.64	10.57	9.46	10.46	10.29	7.74	10.01	9.58	10.13	7.34
232601_at	---	---	0.5242	9.89	8.6	6.25	7.82	8.77	6.92	8.73	7.95	8.94	7.32
226111_s_at	ZNF385A	zinc finger protein 385A	0.5242	4.62	4.45	4.43	5.43	4.8	7.61	6.18	6.39	4.63	4.07
228999_at	CHD2	chromodomain helicase DNA binding protein 2	0.5242	8.13	6.65	7.32	8.18	6.82	6.43	6.92	4.5	7.51	5.73
208591_s_at	PDE3B	phosphodiesterase 3B, cGMP-inhibited	0.5242	8.79	8.94	8.16	8.98	9.31	7.32	8.44	7	9.66	6.72
1553626_a_at	C17orf57	chromosome 17 open reading frame 57	0.525149	4.89	4.14	3.8	5.11	6.52	9.88	6.4	10.29	7.14	9.84
215193_x_at	HLA-DRB1 /// HLA-DRB3 /// HLA-DRB4	major histocompatibility complex, class II, DR beta 1 /// major histocompatibili	0.525383	6	8.98	8.2	8.51	8.38	10.45	9.07	9.71	7.2	7.83
243469_at	---	---	0.525383	7.87	6.7	5.98	7.81	6.24	6.14	6.62	5.69	8.86	5.54
235376_at	---	---	0.525383	10.25	9.45	7.68	9.37	9.16	7.51	9.7	8.86	10.45	7.49
209555_s_at	CD36	CD36 molecule (thrombospondin receptor)	0.52627	3.21	4.98	6.14	4.1	6.28	9.39	7.81	8.96	3.6	3.56

213957_s_at	CEP350	centrosomal protein 350kDa	0.52627	7.57	8.19	5.95	7.5	6.15	4.42	7.34	5.66	7.47	4.98
223548_at	C1orf26	chromosome 1 open reading frame 26	0.526638	6.92	6.03	4.61	6.75	6.32	4.67	7.44	4.59	6.55	4.84
233490_at	DCTN4	dynactin 4 (p62)	0.527274	6.03	4.32	4.9	6.34	5.08	5.81	7.53	5.32	6.52	3.1
234574_at	---	---	0.527918	8.84	7.95	6.61	8.11	8.05	5.93	6.85	5.91	7.65	5.52
223777_at	MGC13005	hypothetical LOC84771	0.527918	4.16	4.24	4.17	4.87	3.53	8.45	6.41	6.54	5.09	5.97
212566_at	MAP4	microtubule-associated protein 4	0.527918	6.07	6.85	7.39	4.79	7.72	5.63	7.96	6.77	7.06	5.54
212783_at	RBBP6	retinoblastoma binding protein 6	0.528088	8.65	7.33	5.11	8.15	7.9	4.99	7.97	5.92	8.59	6.38
202842_s_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.528088	10.7	8.17	11.02	11.06	10.55	8.44	10.65	7.97	10.38	8.25
217534_at	FAM49B	family with sequence similarity 49, member B	0.528088	7.16	6.2	3.94	6.5	5.9	4.5	6.34	5.93	6.58	4.94
219864_s_at	RCAN3	RCAN family member 3	0.528907	6.19	4.89	3.27	6.91	7.13	7.03	8.77	8.16	7.63	3.59
221731_x_at	VCAN	versican	0.528907	4.66	6.32	3.92	7.32	5.6	9.43	8.74	8.05	6.01	3.09
212197_x_at	MPRIP	myosin phosphatase Rho interacting protein	0.528907	7.27	8.04	5.58	7.18	8.59	6.49	7.86	5.39	8.24	6.37
241786_at	---	---	0.529126	8.15	7.15	7.27	7.37	6.95	7.52	8.92	7.66	8.44	5.08
203582_s_at	RAB4A	RAB4A, member RAS oncogene family	0.529552	6.46	6.72	4.92	6.45	6.78	8.96	6.99	7.69	5.49	9.54
221118_at	PKD2L2	polycystic kidney disease 2-like 2	0.529552	7.94	8.18	7.73	8.05	7.64	6.99	7.89	7.88	8.04	4.57
209301_at	CA2	carbonic anhydrase II	0.530198	4.86	5.21	5.42	5.8	5.87	8.64	6.44	7.42	5.03	6.05
217535_at	FAM49B	Family with sequence similarity 49, member B	0.531166	9.83	8.94	6.69	9.08	8.11	7.14	8.57	8.67	9.07	7.11
242904_x_at	---	---	0.531734	10.1	8.61	9.8	8.76	6.04	6.23	9.22	8.94	9.3	9.41
234284_at	GNG8	guanine nucleotide binding protein (G protein), gamma 8	0.531734	6.3	6.04	6.67	6.33	6.18	9.51	6.37	6.32	6.27	6.59
214808_at	---	---	0.532312	9.31	9.88	5.36	9	9.14	7.02	8.89	6.51	9.99	5.84
242106_at	---	---	0.532312	6.76	5.44	7.05	6.45	5.43	3.39	4.72	5.34	7.02	4.93
209312_x_at	HLA-DRB1 /// HLA-DRB4 /// HLA-DRB5	major histocompatibility complex, class II, DR beta 1 /// major histocompatibili	0.532312	6.51	10	9.03	9.12	9.27	11.28	10.07	10.57	8.27	9.02
204622_x_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.532312	8.51	4.01	7.64	8.52	6.61	5.33	7.79	4.82	8.65	4.83
214673_s_at	HUWE1	HECT, UBA and WWE domain containing 1	0.532312	7.92	8.16	6.37	6.53	8.32	4.09	7.64	6.19	6.81	5.02
212764_at	ZEB1	zinc finger E-box binding homeobox 1	0.532312	8.01	8.2	6.12	8.2	7.46	4.38	7.48	6.75	7.61	6.06
201121_s_at	PGRMC1	progesterone receptor membrane component 1	0.533444	7.8	7.35	6.91	8.3	8.59	10.85	9.66	10.65	8.52	9.57
1555691_a_at	KLRK1	killer cell lectin-like receptor subfamily K, member 1	0.533697	8.25	5.33	4.18	7.12	7.41	5.55	9.98	4.55	6.74	6.13
214523_at	CEBPE	CCAAT/enhancer binding protein (C/EBP), epsilon	0.533968	6.34	6.53	6.15	6.36	7.46	8.91	6.17	8.39	6.74	8.05
223717_s_at	ACRBP	acrosin binding protein	0.534445	6.54	5.75	6.53	7.67	7.47	11.2	8.78	9.77	7.4	7.75
204550_x_at	GSTM1	glutathione S-transferase mu 1	0.534445	5.44	6.78	4.68	5.54	6.67	7.65	6.21	8.16	6.34	6.92
207802_at	CRISP3	cysteine-rich secretory protein 3	0.535072	5.71	6.46	8.1	7	6.86	7.78	6.03	8.49	3.85	5.69
215175_at	PCNX	pecanex homolog (Drosophila)	0.535072	6.96	4.97	6.1	7.36	5.49	6.09	6.46	6.47	7.7	4.46
200762_at	DPYSL2	dihydropyrimidinase-like 2	0.535129	5.73	6.45	6.88	6.83	7.75	9.71	8.97	9.45	7.21	6.38
219777_at	GIMAP6	GTPase, IMAP family member 6	0.536068	5.17	5.5	4	3.99	5.95	6.21	7.35	6.52	6.53	5.34
1555446_s_at	TRAPPC10	trafficking protein particle complex 10	0.536068	7.26	5.84	5.47	6.42	6.18	5.17	6.31	4.23	7.39	4.19
244235_at	IVNS1ABP	influenza virus NS1A binding protein	0.536108	9.41	6.88	7.97	8.94	8.59	6.41	9.91	7.2	9.36	6.02
218370_s_at	S100PBP	S100P binding protein	0.536342	6.07	4.02	3.36	5.15	7	4.9	6.09	6.26	5.75	3.89
1559756_at	DKFZp667F0711	hypothetical protein DKFZp667F0711	0.53819	7.76	6.6	4.92	6.6	6.27	5.25	6.74	6.03	6.41	3.23
1570552_at	C18orf50	chromosome 18 open reading frame 50	0.538855	6.39	4.34	3.82	5.72	6.43	5.3	8.12	6.33	4.61	6.53
205488_at	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	0.538855	7.75	6.3	4.94	7.89	8.88	6.5	10.39	6.6	8.11	6.66
216248_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.538855	7.52	3.09	6.91	7.65	5.27	4.75	6.37	3.52	7.44	3.18

208073_x_at	TTC3	tetratricopeptide repeat domain 3	0.538855	6.48	6.81	4.18	6.41	6.17	5.05	8.19	5.36	6.35	3.11
1562056_at	---	---	0.538855	6.38	4.63	5.82	6.99	6.05	2.68	4.91	5.74	6.51	6.41
213566_at	RNASE6	ribonuclease, RNase A family, k6	0.538855	10.07	10.29	9.49	9.15	9.64	11.34	8.41	9.54	7.16	6.8
230833_at	ACRBP	acrosin binding protein	0.538855	5.28	5.47	5.7	6.23	6.1	10.14	7.33	7.87	6.18	6.4
1562865_at	---	---	0.538855	7.62	6.52	5.06	5.68	5.73	3.95	6.91	4.25	6.72	4.49
1563327_a_at	CXorf31	chromosome X open reading frame 31	0.538855	6.47	5.57	8.43	6.38	5.18	5.5	5.83	7.05	6.64	4.96
1555409_a_at	BAGE2 /// BAGE3 /// BAGE5 /// MLL3	B melanoma antigen family, member 2 /// B melanoma antigen family, member 3 ///	0.538855	7.7	6.39	3.89	6.15	6.62	4.6	6.92	5.31	6.22	3.52
237497_at	---	---	0.538855	7.61	6.31	6.88	8.09	6.83	4.57	8.39	7.77	8.29	7.47
222061_at	CD58	CD58 molecule	0.538855	7.69	6.64	5.21	7.38	6.21	4.83	6.78	5.21	7.18	5.8
225114_at	AGPS	alkylglycerone phosphate synthase	0.538855	4.95	6.46	3.68	5.22	6.59	6.28	5.94	7.5	6.24	7.23
217362_x_at	HLA-DRB6	major histocompatibility complex, class II, DR beta 6 (pseudogene)	0.538855	5.63	7.94	7.56	7.98	7.68	9.38	8.4	8.88	7.11	7.66
208753_s_at	NAP1L1	nucleosome assembly protein 1-like 1	0.538855	5.57	6.25	5.78	6.47	6.36	8.98	7.4	8.15	6.74	7.48
203357_s_at	CAPN7	calpain 7	0.539484	7.93	7.99	8.05	7.61	6.96	5.6	7.51	5.24	7.79	6.39
234759_at	---	---	0.539845	7.06	6.49	3.65	4.91	4.96	4.62	6.44	4.08	5.75	2.88
220657_at	KLHL11	kelch-like 11 (Drosophila)	0.539845	6.76	5.8	7.42	5.31	6.23	5.42	4.71	6.88	7.29	4.41
200965_s_at	ABLIM1	actin binding LIM protein 1	0.540106	6.23	4.87	3.39	5.9	7.69	6.63	8.34	5.63	6.61	4.94
227565_at	---	---	0.540106	8.36	7.49	5.21	7.39	6.78	3.39	6.29	6.77	7.17	3.56
204621_s_at	NR4A2	nuclear receptor subfamily 4, group A, member 2	0.540106	8.75	4.16	8.44	8.54	6.52	4.07	8.06	4.74	8.22	5.54
213524_s_at	G0S2	G0/G1switch 2	0.541649	12.77	9.49	12.79	12.29	12.59	9.03	13	11.41	12.87	8.93
226040_at	---	---	0.541993	7.71	7.79	3.92	5.83	7.95	4.62	7.54	7.85	8.12	3.76
1565656_x_at	---	---	0.541993	6.61	4.34	6.51	6.35	4.73	3.64	4.7	3.9	6.05	2.97
241817_at	C3orf62	chromosome 3 open reading frame 62	0.541993	8.18	9.08	7.77	7.98	8.24	6.03	8.02	8.42	8.45	6
201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	0.543369	5.78	8.07	4.99	6.51	8.3	10.66	8.8	9.28	8.44	8.13
211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.54387	4.61	7.13	4.92	5.92	7.21	9.11	7.48	7.66	6.07	6.15
212998_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.543983	8.23	9.04	8.25	8.98	6.62	10.03	8.39	9.81	6.93	5.79
209795_at	CD69	CD69 molecule	0.545368	8.67	4.79	7.27	7.86	8.56	4.43	9.48	5.49	9.46	5.9
1564932_at	---	---	0.545503	7.05	8.24	5.31	5.82	5.77	5.52	6.75	5.8	6.76	4.24
226588_at	CWC22	CWC22 spliceosome-associated protein homolog (S. cerevisiae)	0.545503	9.74	9.77	8.75	9.06	9.54	8.69	9.28	9.75	9.62	6.28
238762_at	MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	0.545709	4.7	3.3	3.76	3.97	5.67	7.17	6.04	4.4	4.44	6.55
1556003_a_at	---	---	0.547638	6.79	5.57	6.1	6.17	4.07	4.25	6.18	3.62	7.99	4
1558569_at	UNQ6228	Hypothetical LOC100131541	0.548307	6.56	5.93	4.8	6.24	6.35	3.96	6.85	5.63	6.88	7.44
233393_at	---	---	0.548307	7.34	5.27	3.99	5.22	5.06	6.93	6.91	5.88	6.76	3.86
1552318_at	GIMAP1	GTPase, IMAP family member 1	0.549512	4.14	4.08	3.23	5.19	6	6.69	7.04	6.3	5.22	3.42
1560306_at	---	---	0.549512	7.31	5.02	5.3	5.46	6.32	4.7	6.06	5.5	6.96	3.44
226218_at	IL7R	interleukin 7 receptor	0.550524	7.71	5.71	5.51	7.53	8.25	6.23	9.58	5.38	6.89	5.82
214349_at	---	---	0.550818	6.66	6.36	6.49	6.04	6.64	10.58	8.11	10.38	7.58	7.94
239331_at	---	---	0.550818	6.93	6.24	6.5	7.52	6.16	7.93	7.41	5.48	7.96	4.66
240481_at	---	---	0.550943	7.83	5.44	7.17	7.51	6.49	4.98	6.69	5.23	6.76	3.41
223380_s_at	LATS2	LATS, large tumor suppressor, homolog 2 (Drosophila)	0.551038	6.6	7.17	7.45	8.58	6.14	4.76	6.36	6.57	6.92	7.82
235482_at	LOC400960	hypothetical gene supported by BC040598	0.552255	7.35	7.84	5.49	6.16	5.07	4.51	5.96	4.49	7.72	5.46

206116_s_at	TPM1	tropomyosin 1 (alpha)	0.553743	7.73	8.28	8.5	8.35	7.41	10.62	9.62	10.35	7.73	8.08
203305_at	F13A1	coagulation factor XIII, A1 polypeptide	0.553977	4.99	4.76	4.67	6.98	5.76	9.35	8.37	8.54	6.85	7.34
213649_at	SFRS7	splicing factor, arginine/serine-rich 7, 35kDa	0.554419	7.38	4.39	5.57	6.36	4.83	6.63	6.22	4.4	7.78	4.56
205249_at	EGR2	early growth response 2	0.555036	7.96	6.13	6.88	7.23	7.57	6.1	9.03	6.54	9.68	5.58
221342_at	C6orf25	chromosome 6 open reading frame 25	0.555304	4.72	4.98	5.58	5.36	5.86	8.55	6.57	7.38	5.07	5.66
207474_at	SNRK	SNF related kinase	0.555936	7.41	4.25	3.86	5.41	4.96	5.87	6.68	3.9	7.5	5.85
208861_s_at	ATRX	alpha thalassemia/mental retardation syndrome X-linked (RAD54 homolog, S. cerevi	0.555936	8.16	8.36	6.4	8.09	8.42	4.37	7.79	6.62	8.54	6.07
201604_s_at	PPP1R12A	protein phosphatase 1, regulatory (inhibitor) subunit 12A	0.556563	8.8	8.83	6.77	9.03	8.51	6.88	9.1	8	8.53	5.88
229710_at	---	---	0.556563	6.73	7.13	5.56	5.49	6.93	5.07	7.26	4.97	6.89	4.58
208939_at	SEPHS1	selenophosphate synthetase 1	0.556619	5.17	4.63	5.97	4.1	6.65	6.2	6.56	7.32	5.31	4.82
242607_at	---	---	0.55854	5.83	5.62	7.87	6.12	3.44	4.56	5.26	6.99	5.69	6.58
243395_at	---	---	0.55854	9.81	6.94	7.65	8.39	8.37	6.71	9.8	9.01	8.28	6.03
208306_x_at	---	---	0.55854	7.19	10.18	9.46	9.72	9.97	11.09	10.54	10.73	9.14	9.67
204670_x_at	HLA-DRB1 /// HLA-DRB4	major histocompatibility complex, class II, DR beta 1 /// major histocompatibili	0.558695	7.4	10.08	9.32	9.16	9.41	10.98	10.23	10.61	9.07	9.29
203893_at	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	0.558938	6	6.97	5.04	6.53	6.78	6.07	6.06	7.73	4.56	7.75
227917_at	FAM85A	family with sequence similarity 85, member A	0.558951	6.82	4.98	4.35	6.02	9.04	6.83	5.55	5.54	5.84	4.51
243841_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.558978	8.93	8.68	4.78	7.62	6.71	3.36	7.67	5.99	8.46	6.01
204466_s_at	SNCA	synuclein, alpha (non A4 component of amyloid precursor)	0.558978	6.61	5.43	3.48	6.17	5.16	8.22	6.29	7.33	4.22	5.05
1557418_at	---	---	0.558978	8.12	7.38	9.73	8.22	7.55	5.04	7.25	6.34	8.75	5.65
1569020_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	0.558978	7.27	5.52	6.54	6.12	6.19	4.67	6.61	5.78	7.42	4.35
204373_s_at	CEP350	centrosomal protein 350kDa	0.558978	7.82	8.4	6.15	7.91	8.1	7.14	7.34	7.2	7.67	3.42
1566242_at	---	---	0.558978	7.05	4.64	4.73	5.51	6.77	5.31	5.82	6.06	7.47	4.65
235427_at	---	---	0.558978	8.72	8.57	6.11	8.64	8.19	6.35	8.58	7.95	8.62	6.1
232392_at	SFRS3	Splicing factor, arginine/serine-rich 3	0.558978	9.07	7.77	8.72	8.75	7.79	6.73	8.65	5.5	8.46	8.13
228446_at	KIAA2026	KIAA2026	0.560161	9.52	9.64	7.49	9.2	9.74	8.23	9.44	7.63	9.39	6.08
241924_at	---	---	0.560325	6.68	5.35	3.65	5.91	6.83	4.5	6.17	5.02	7.34	5.01
202710_at	BET1	blocked early in transport 1 homolog (S. cerevisiae)	0.560915	4.95	5.56	3.38	4.07	6	7.37	6.27	6.98	4.87	6.35
203545_at	ALG8	asparagine-linked glycosylation 8, alpha-1,3-glucosyltransferase homolog (S. cer	0.561101	4.7	4.88	7.46	5.16	5.19	6.56	4.48	6.82	5.33	6.95
202435_s_at	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	0.561148	4	3.88	4	5.56	4.22	7.45	6.53	7.18	6.26	5.68
202887_s_at	DDIT4	DNA-damage-inducible transcript 4	0.561498	11.99	9.04	11.9	11.11	11.65	6.68	12.45	9.21	11.49	7.31
225106_s_at	OGFOD1	2-oxoglutarate and iron-dependent oxygenase domain containing 1	0.56162	6.08	3.76	6.13	6.21	7.34	4.28	6.05	4.57	5.93	4.24
1554786_at	CASS4	Cas scaffolding protein family member 4	0.561903	9.35	8.34	6.7	8.67	8.23	6.33	7.97	5.04	9.34	7.5
238412_at	LOC100131998	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	0.561908	7.1	6.67	6.5	6.82	6.53	4.06	6.82	5.38	7.44	4.74
210928_at	LOC100131613	PRO1454	0.562164	7.85	7.14	6.13	7.04	6.08	6.55	7.91	7.47	6.68	3.97
1557158_s_at	MLL3	myeloid/lymphoid or mixed-lineage leukemia 3	0.562771	10.88	10.02	8.02	10.04	9.71	9.21	10.15	9.06	10.2	6.94

241191_at	---	---	0.562868	7.89	5.88	4.48	7.25	4.92	3.44	6.34	4.65	6.66	4.64
241462_at	---	---	0.564438	4.64	4.87	5.96	3.83	4	6.93	3.88	6.31	4.57	6.05
213275_x_at	CTSB	cathepsin B	0.564947	7.92	7.66	4.73	7.5	7.72	8.96	8.98	8.22	8.58	7.99
235009_at	BOD1L	biorientation of chromosomes in cell division 1-like	0.566784	12.4	12.2	8.33	11.79	11.92	8.86	11.99	10.49	12.27	9.36
209997_x_at	PCM1	pericentriolar material 1	0.566784	6.75	7.21	4.16	6.04	6.37	4.89	6.63	5.95	6.73	4.51
224879_at	C9orf123	chromosome 9 open reading frame 123	0.566784	4.75	5.72	6.64	5.21	6.95	7.57	7.03	7.16	5.13	8.67
213876_x_at	ZRSR2	zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	0.566784	8.71	9.91	7.58	7.69	8.39	6.67	8.55	8.09	7.76	6.29
244315_at	PLSCR1	phospholipid scramblase 1	0.566932	6.57	5.07	6.42	7.47	5.47	4.46	6.44	4.68	7.05	5.99
229155_at	---	---	0.56706	8.01	9.92	9.53	7.11	7.24	5.63	7.71	5.41	6.87	8.3
1556332_at	---	---	0.56706	7.46	7.53	5.51	7.58	6.54	4.55	5.8	5.75	7.12	4.69
241341_at	---	---	0.56706	6.66	6.01	6.07	6.62	6.71	4.41	7.31	4.72	7.24	7.38
202859_x_at	IL8	interleukin 8	0.567276	12.57	10.26	12.77	12.8	12.02	10.82	12.29	10.41	12.85	10.61
218711_s_at	SDPR	serum deprivation response (phosphatidylserine binding protein)	0.567647	6.49	5.65	6.39	7.58	7.03	10.19	8.79	9.73	7.42	7.18
204115_at	GNG11	guanine nucleotide binding protein (G protein), gamma 11	0.567853	5.87	4.68	6.6	6.58	6.95	11.23	8.17	9.32	6.56	7.48
221616_s_at	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0.56801	6.41	4.97	5.06	5.86	6.05	4.24	5.93	6.28	5.33	8.03
214414_x_at	HBA1 /// HBA2	hemoglobin, alpha 1 /// hemoglobin, alpha 2	0.568087	13.03	13.22	7.79	13.08	13.03	13.68	12.43	13.56	9.55	12.68
237241_at	ECT2	Epithelial cell transforming sequence 2 oncogene	0.568087	4.32	4.93	3.46	6.16	4.83	6.29	5.4	6.39	6.42	5.95
240695_at	---	---	0.568087	8.45	7.9	7.36	8.6	7.53	5.15	7.6	6.23	8.82	5.7
202806_at	DBN1	drebrin 1	0.568087	4.8	3.9	6.62	6.05	4.67	4.57	6.74	3.98	7.16	4.24
211406_at	IER3IP1	immediate early response 3 interacting protein 1	0.568087	4.85	7.52	4.47	5.85	5.84	7.29	6.36	6.37	6.13	7.43
211323_s_at	ITPR1	inositol 1,4,5-triphosphate receptor, type 1	0.56811	7.2	7.3	4.71	7.01	5.74	7.14	7.82	4.45	8.03	4.98
225821_s_at	BOD1L	biorientation of chromosomes in cell division 1-like	0.56811	10.02	9.82	7.59	9.85	9.53	6.61	9.02	7.14	9.36	7.47
226732_at	RBM33	RNA binding motif protein 33	0.569371	8.97	8.29	7.74	8.84	8.69	7.57	8.84	5.84	9.48	7.05
206532_at	---	---	0.569371	4.81	5.86	3.42	6.42	6.35	6.67	6.27	7.34	7.15	6.13
241275_at	CAPZA1	Capping protein (actin filament) muscle Z-line, alpha 1	0.569409	8.73	8.23	7.53	8.52	7.09	4.67	7.83	6.86	8.07	6.91
224304_x_at	NIN	ninein (GSK3B interacting protein)	0.569476	10.53	10.36	8.43	9.66	9.58	8.2	9.62	9.41	9.72	6.81
216379_x_at	CD24	CD24 molecule	0.569935	4.7	6.25	6.8	6.6	7.9	8.33	7.27	9.66	7.4	8.53
33323_r_at	SFN	stratifin	0.570102	8.43	8.19	5.7	8.37	7.73	3.6	7.06	3.88	9.02	3.92
203569_s_at	OFD1	oral-facial-digital syndrome 1	0.570451	7.16	6.48	6.27	7.24	6.95	4.06	6.64	5.41	7.48	7.82
218805_at	GIMAP5	GTPase, IMAP family member 5	0.570685	6.01	5.31	5.25	5.69	7.69	7.39	8.29	6.69	7.35	6.81
215646_s_at	VCAN	versican	0.570854	5.04	6.93	4.35	7.85	7.94	9.27	9.96	9.25	7.05	3.45
217232_x_at	HBB	hemoglobin, beta	0.571014	12.81	13.18	8.21	12.95	12.67	13.42	11.9	13.37	9.65	12.07
206171_at	ADORA3	adenosine A3 receptor	0.571014	5.77	6	6.1	6.29	7.79	9.47	5.49	6.75	6.39	8.38
1552787_at	HELB	helicase (DNA) B	0.571679	6.8	7	3.35	3.94	5.66	3.72	6.66	4.07	6.58	5.43
1558561_at	HM13	histocompatibility (minor) 13	0.572457	7.23	6.51	4.91	5	4.73	3.61	3.84	3.88	7.22	4.02
202079_s_at	TRAK1	trafficking protein, kinesin binding 1	0.573249	6.22	6.14	7.08	6.55	6.24	4.53	5.79	5.81	5.63	3.44
228151_at	---	---	0.573274	7.21	7.95	3.37	6.53	7.42	8.07	7.85	5.9	7.52	6.86
1559990_at	---	---	0.573982	9.92	10.38	11.42	11.24	10.25	7.92	9.79	10.02	9.79	7.23
236527_at	---	---	0.57438	6.03	8.07	7.31	6.62	6.05	5.37	6.8	8.15	6.06	8.15
211696_x_at	HBB	hemoglobin, beta	0.574996	13.09	13.33	8.72	13.25	12.97	13.64	12.32	13.58	10.02	12.65

216191_s_at	TRA@ /// TRD@	T cell receptor alpha locus /// T cell receptor delta locus	0.575597	4.89	3.11	2.85	5.11	7.29	5.5	7.07	2.79	6.78	4.95
230656_s_at	CIRH1A	cirrhosis, autosomal recessive 1A (cirhin)	0.575597	5.66	5.76	5.6	6.69	4.86	7.08	5.96	5.21	3.69	8.51
238669_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxyge	0.575597	8.02	7.95	6.17	8.46	8.72	10.68	9.84	10.44	8.64	8.8
238159_at	---	---	0.575597	6.09	5.04	3.67	5.02	5.09	4.47	6.35	4.52	6.94	6.46
214054_at	DOK2	docking protein 2, 56kDa	0.575597	5.5	6.37	5.86	5.86	6.83	9.74	6.83	7.61	6.42	8.42
225585_at	RAP2A	RAP2A, member of RAS oncogene family	0.575597	6.71	6.56	6.27	8.33	7.95	9.29	8.8	8.69	7.02	9.22
230703_at	---	---	0.575597	8.95	6.74	8.29	8.06	6.56	7.73	7.64	4.98	8.24	8.08
242945_at	FAM20A	family with sequence similarity 20, member A	0.576007	8.08	7.87	6.8	8.81	7.45	5.23	7.47	5.47	7.93	7.39
201567_s_at	GOLGA4	golgi autoantigen, golgin subfamily a, 4	0.576567	6.4	7.21	6.15	5.26	6.18	3.14	5.9	4.46	6.11	4.86
224303_x_at	NIN	ninein (GSK3B interacting protein)	0.57665	10.84	10.85	8.89	10.16	10.22	8.56	10.11	9.77	10.14	7.46
213117_at	KLHL9	kelch-like 9 (Drosophila)	0.580278	5.22	5.09	6.42	5.45	5.3	6.68	5.31	5.75	5.47	8.41
230535_s_at	---	---	0.580477	5.97	4.47	5.28	7.28	6.47	10.67	8.21	8.89	6.2	8.3
200869_at	RPL18A /// RPL18AP3	ribosomal protein L18a /// ribosomal protein L18a pseudogene 3	0.580795	6.83	8.42	7.41	7.81	9.01	11.53	9.27	9.58	7.99	9.43
1554929_at	KIAA0999	KIAA0999 protein	0.581904	5.71	4.33	3.58	6.03	6.32	3.82	4.64	5.51	6.02	4.28
235434_at	---	---	0.582182	6.2	3.51	5.68	6.07	5.73	5.69	6.07	3.48	4.47	3.56
209116_x_at	HBB	hemoglobin, beta	0.582225	13.13	13.39	8.59	13.26	12.96	13.62	12.37	13.58	10.02	12.44
214000_s_at	RGS10	Regulator of G-protein signaling 10	0.582225	6	5.44	5.48	6.74	6.08	9.76	7.94	7.67	6.72	7.47
1566557_at	FLJ90757	hypothetical LOC440465	0.582225	7.15	7.36	6.86	5.67	6.72	4.81	7.19	4.62	5.41	4.86
202136_at	ZMYND11	zinc finger, MYND domain containing 11	0.582225	5.18	5.04	4.06	4.96	7.99	6.31	6.28	4.84	6.48	5.83
204527_at	MYO5A	myosin VA (heavy chain 12, myoxin)	0.582345	6.05	5.68	3.33	6.73	6.21	3.78	5.79	4.03	6.55	3.64
219844_at	C10orf118	chromosome 10 open reading frame 118	0.582938	8.74	8.59	7.31	8.43	8.38	6.04	8.25	7.52	7.8	4.6
243088_at	---	---	0.582938	7.26	6.32	5.64	5.78	5.62	6.37	7.64	6.03	7.51	3.77
219819_s_at	MRPS28	mitochondrial ribosomal protein S28	0.583074	6.4	5.99	3.59	5.35	6.17	6.6	6.33	7.32	5.52	6.49
206676_at	CEACAM8	carcinoembryonic antigen-related cell adhesion molecule 8	0.583193	5.95	7.02	7.98	7.27	8.56	9.54	8.66	10.98	7.97	9.59
212768_s_at	OLFM4	olfactomedin 4	0.583679	5.51	6.1	6.76	6.15	7.27	9.28	8.16	10.74	5.88	8.34
228528_at	---	---	0.583679	8.86	8.22	5.58	7.29	6.9	5.73	8.18	6.41	8.19	7.95
200790_at	ODC1	ornithine decarboxylase 1	0.583679	6.79	7.92	4.76	7.21	6.61	9.53	8.02	8.52	6.09	6.77
222186_at	ZFAND6	Zinc finger, AN1-type domain 6	0.583679	6.18	3.27	3.61	6.17	4.63	3.38	5.55	5.82	4.85	6.61
202960_s_at	MUT	methylmalonyl Coenzyme A mutase	0.584313	5.99	6.8	4.17	5.54	5.66	7.87	6.12	7.64	5.81	6.89
229419_at	FBXW7	F-box and WD repeat domain containing 7	0.584348	8.11	8.27	7.21	7.83	8.31	5.92	8.18	8.25	8.58	4.22
225147_at	CYTH3	cytohesin 3	0.584348	6.57	5.41	5.52	5.15	7.27	4.99	8.28	6.94	6.83	7
204798_at	MYB	v-myb myeloblastosis viral oncogene homolog (avian)	0.584627	6.48	7.74	5.8	6.94	9.01	9.28	7.66	10.15	8.11	9.73
244860_at	---	---	0.585489	8.72	5.99	4.23	6.52	4.63	4.91	7.7	4.72	8.32	6.23
209771_x_at	CD24	CD24 molecule	0.585502	4.93	6.6	7.31	6.79	8.17	8.73	7.48	9.98	7.72	8.86
208651_x_at	CD24	CD24 molecule	0.586043	5.06	7.14	7.8	6.69	7.79	8.57	7.1	9.6	7.94	9.03
1561167_at	---	---	0.586107	6.81	5.52	5	5.69	4.87	3.43	6.94	5.37	6.95	7.08
208010_s_at	PTPN22	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	0.58613	7.3	7.48	10.1	8.37	8.3	8.06	6.71	8.3	7.34	9.8
1563975_at	RNF130	Ring finger protein 130	0.586175	8.62	8.56	5.02	7.25	7.17	5.45	7.9	6.25	8.64	4.94
204057_at	IRF8	interferon regulatory factor 8	0.586248	4.85	7.11	3.98	5.55	6.18	8.08	7.22	6.94	6.03	4.71

218422_s_at	RBM26	RNA binding motif protein 26	0.586248	7.45	7.22	4.78	6.63	7.82	4.52	7.74	6.64	7.57	6.29
202728_s_at	LTBP1	latent transforming growth factor beta binding protein 1	0.586248	6.15	5.63	5.54	5.92	6.59	8.63	7.46	7.96	6.75	7.23
230690_at	TUBB1	tubulin, beta 1	0.586675	6.7	5.86	6.19	8.17	7.24	11.38	9.18	10.23	7.89	8.49
214146_s_at	PPBP	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	0.588219	7.53	6.07	8.87	10.5	9.49	13.1	11.37	12.27	10.09	11.71
201730_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.588219	10.31	10.09	6.37	9.94	9.54	7.33	9.76	8.12	9.71	7.1
1569607_s_at	ANKRD20A1 /// ANKRD20A2 /// ANKRD20A3 /// ANKRD20A4 /// C21orf81 /// LOC100132733 /// LOC284232 /// LOC643187 /// LOC647595 /// LOC653436 /// LOC727770 /// LOC728783	ankyrin repeat domain 20 family, member A1 /// ankyrin repeat domain 20 family,	0.588219	4.43	2.89	2.65	2.81	6.42	7.08	4.37	3.07	6.4	2.87
212620_at	ZNF609	zinc finger protein 609	0.588219	6.6	6.82	5.81	6.23	6.11	6.5	7.81	4.5	7.59	4.3
239379_at	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	0.588335	9.37	8.14	6.95	7.88	7.04	6.12	9.09	7.23	8.85	6.95
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxyge	0.588878	12.03	10.63	11.65	11.83	12.11	9.31	12.68	10.55	13.02	10.11
213515_x_at	HBG1 /// HBG2	hemoglobin, gamma A /// hemoglobin, gamma G	0.589359	8.84	9.45	4.71	8.77	8.22	9.58	8.12	8.6	5.8	7.81
216621_at	---	---	0.589359	7.35	5.75	3.67	6.78	6.19	4.72	7.66	4.91	7.34	4.17
232045_at	PHACTR1	phosphatase and actin regulator 1	0.589844	6.74	4.78	7.74	5.82	5.77	6.23	6.02	5.7	6.51	4.03
1554534_at	DPYD	dihydropyrimidine dehydrogenase	0.589844	5.91	6.12	7.07	5.81	6.85	4.9	5.26	3.62	6.22	6.56
227109_at	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	0.589844	6.13	6.86	4.36	5.6	5.23	4.13	5.8	4.72	6.44	3.65
1566477_at	---	---	0.589844	7.88	7.88	5.31	6.32	6.3	5.39	6.35	5.76	6.7	4.97
215220_s_at	TPR	translocated promoter region (to activated MET oncogene)	0.591918	10.64	10.68	6.39	9.83	10.23	7.76	10.1	8.42	10.13	6.26
204028_s_at	RABGAP1	RAB GTPase activating protein 1	0.59341	8.77	9.33	8.18	8	8.62	8.82	9.17	9.53	9.47	6.02
238468_at	TNRC6B	trinucleotide repeat containing 6B	0.593433	9.16	9.55	7.72	9.16	9.3	6.47	8.89	7.88	9.34	7.08
239288_at	TNIK	TRAF2 and NCK interacting kinase	0.594544	5.28	4.01	4.65	6.45	6.53	7.35	6.57	4.48	6.82	5.02
226025_at	ANKRD28	ankyrin repeat domain 28	0.595959	5.35	5.28	5.79	7.13	6.71	8.26	8.12	7.82	7.31	6.98
212531_at	LCN2	lipocalin 2	0.596382	5.28	6.97	5.71	6.62	9.23	10.9	9.22	11.51	6.16	9
202761_s_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.596382	8.43	8.32	2.72	6.1	6.85	2.99	6.79	3.11	7.93	4.66
1555408_at	BAGE2 /// BAGE4	B melanoma antigen family, member 2 /// B melanoma antigen family, member 4	0.597392	9.1	8.48	6.34	8.05	7.89	5.99	7.86	6.7	8.25	4.13
233461_x_at	ZNF226	zinc finger protein 226	0.597486	7.07	8.96	5.87	6.03	7.71	5.74	7.14	5.97	6.8	5.78
206874_s_at	---	---	0.597486	7.7	6.61	4.88	7.79	6.67	4.96	7.11	5.88	7.99	4.99
206951_at	HIST1H4B	Histone cluster 1, H4b	0.597486	9.07	10.3	9.5	8.74	10.1	11.22	10.76	11.77	9.71	11.48
204661_at	CD52	CD52 molecule	0.597639	7.48	8.49	8.37	8.16	9.43	11.27	9.08	8.8	8.78	10.3

215009_s_at	SEC31A	SEC31 homolog A (S. cerevisiae)	0.598031	8.83	5.65	8.31	6.07	7.15	4.38	7.37	7.1	8.98	6.96
1569192_at	---	---	0.598135	5.78	5.54	3.42	5.2	3.84	4.29	6.65	4.07	6.25	6.43
209146_at	SC4MOL	sterol-C4-methyl oxidase-like	0.598138	5.02	4.79	8.04	5.97	4.8	6.02	5.46	7.4	4.96	5.65
238048_at	CLASP2	Cytoplasmic linker associated protein 2	0.598138	5.71	5.8	3.59	5.47	6.22	6.72	6.35	6.28	5.87	8.81
232379_at	SKIL	SKI-like oncogene	0.599322	9.4	7.15	9.91	9.08	8.37	5.58	8.35	6.25	7.75	6.42
1557257_at	BCL10	B-cell CLL/lymphoma 10	0.599322	7.28	6.73	7.33	6.81	6.97	5.26	7.51	5.87	5.32	4.3
234640_x_at	---	---	0.599504	9.32	9.15	5.23	8.78	8.49	3.82	6.83	4.12	8.57	4.03
214153_at	ELOVL5	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo	0.599504	8.87	8.14	7.42	7.64	6.69	5.28	6.89	6.06	7.58	5.86
223862_at	GHRL	ghrelin/obestatin prepropeptide	0.600254	7.68	6.9	8.77	7.58	7.38	7.39	7.09	3.9	7.4	6.88
214617_at	PRF1	perforin 1 (pore forming protein)	0.60079	7.03	5.48	3.86	8.02	9.13	7.8	9.39	4.51	9.11	7.09
34210_at	CD52	CD52 molecule	0.6009	8.45	9.42	9.2	8.97	10.38	12.15	10.25	10.01	9.76	11.28
37986_at	EPOR	erythropoietin receptor	0.601911	6.12	6.1	6.55	6.96	5.72	8	5.76	6.42	6.82	9.03
1560109_s_at	---	---	0.601969	8.21	8.38	6.07	6.93	6.1	5.5	7.13	5.25	7.74	8.12
218937_at	ZNF434	zinc finger protein 434	0.601969	6.36	6.38	4.12	5.19	5.94	3.84	7.28	5.53	5.92	5.73
233020_at	---	---	0.605156	6.9	4.7	5.58	6.98	5.69	3.73	6.99	3.07	6.41	3.97
202018_s_at	LTF	lactotransferrin	0.605156	8.03	8.82	7.77	8.06	10.98	12.02	10.66	12.49	8.47	10.85
230970_at	---	---	0.605156	7.3	7.04	6.78	7.22	6.16	3.67	6.66	3.83	7.5	5.59
201663_s_at	SMC4	structural maintenance of chromosomes 4	0.605185	7.56	6.1	6.39	6.8	6.27	6.86	7.05	3.69	6.52	3.55
220306_at	FAM46C	family with sequence similarity 46, member C	0.605185	7.08	6.89	7.73	8.16	7.69	9.14	8.23	5.91	7.69	5.41
238829_at	---	---	0.605185	7.19	5.29	5.26	6.44	6.62	3.99	7.33	4.7	6.38	5.18
201250_s_at	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	0.605452	6.72	6.39	7.71	7.81	6.65	7.75	7.69	8.35	6.6	4.79
1569380_a_at	---	---	0.605452	6.93	4.96	7.76	6.39	5.29	5.08	5.91	4.76	5.56	4.65
203496_s_at	MED1	mediator complex subunit 1	0.605868	6.97	7.32	3.75	6.07	6.26	4.73	7.24	6.14	6.83	3.74
229315_at	---	---	0.605868	7.47	6.88	4.97	6.44	6.6	3.73	7.59	4.32	6.94	4.42
203532_x_at	CUL5	cullin 5	0.605868	6	7.84	4.45	5.67	4.12	7.23	5.32	5.08	5.56	5.7
226300_at	MED19	mediator complex subunit 19	0.605868	5.61	3.82	4.64	6.82	6.36	5.19	6.36	6.05	7.05	6.62
226869_at	MEGF6	multiple EGF-like-domains 6	0.605868	6.26	5.28	4.04	5.28	6.33	3.54	6.17	3.85	5.98	5.87
221211_s_at	C21orf7	chromosome 21 open reading frame 7	0.606036	5.06	2.68	6.61	7.31	7.3	11.39	8.9	9.53	6.51	7.92
206111_at	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	0.606036	8.21	9.75	7.39	5.83	9.66	10.15	8.41	10.53	9.29	10.4
232150_at	---	---	0.606036	6.53	5.03	7.01	7.26	7.3	5.06	5.66	5.2	7.66	6.6
212785_s_at	LARP7	La ribonucleoprotein domain family, member 7	0.60614	8.6	8.66	5.37	7.99	8.42	5.86	7.96	6.37	8.19	5.73
215038_s_at	SETD2	SET domain containing 2	0.606507	8.25	7.92	5.75	7.42	6.99	5.22	7.63	5.98	7.64	6.1
218407_x_at	NENF	neuron derived neurotrophic factor	0.607425	5.26	6.36	6.12	5.98	7.15	9.55	6.93	7.58	7.38	7.42
222729_at	FBXW7	F-box and WD repeat domain containing 7	0.608267	8.73	7.42	7.35	8.47	8.67	6.3	8.01	7.1	8.54	4.84
217951_s_at	PHF3	PHD finger protein 3	0.608267	10.44	10.32	7.95	10.23	10.25	8.94	9.81	8.47	10.29	8.11
231862_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	0.608384	6.74	7.67	4.46	3.19	7.43	3.38	8.32	6.15	6.48	3.38
235232_at	GMEB1	glucocorticoid modulatory element binding protein 1	0.608462	7.18	7.45	4.5	6.49	7.03	4.71	7.53	6.2	7.05	3.72
202677_at	RASA1	RAS p21 protein activator (GTPase activating protein) 1	0.608481	8.78	6.55	4.98	7.7	7.43	7.53	8.24	6.96	8.82	7.23
208146_s_at	CPVL	carboxypeptidase, vitellogenic-like	0.608662	4.27	6.43	5.68	6.26	7.17	8.57	9.1	9.31	5.74	4.19
207018_s_at	RAB27B	RAB27B, member RAS oncogene family	0.608662	3.9	3.62	4.74	5.53	5.06	9.82	6.27	7.97	6.55	6.18

228571_at	RBAK	RB-associated KRAB zinc finger	0.608662	5.32	5.82	3.36	5.64	6.27	3.58	5.92	6.33	7.69	3.65
214016_s_at	SFPQ	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein ass	0.608662	10.27	10.28	7.15	8.31	9.41	8.94	8.98	7.39	9.78	8.65
208995_s_at	PPIG	peptidylprolyl isomerase G (cyclophilin G)	0.608662	9.41	9.44	6.24	9.26	9.19	5.76	8.54	7.59	9.02	7.73
205871_at	PLGLB1 /// PLGLB2	plasminogen-like B1 /// plasminogen-like B2	0.608662	6.58	4.05	4.21	6.42	3.91	4.08	4.82	5.57	6.87	5.42
218769_s_at	ANKRA2	ankyrin repeat, family A (RFXANK-like), 2	0.609208	6.86	6.6	6.02	7.24	7.5	4.52	6.87	5.64	6.55	4.31
219666_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	0.609476	6.19	5.8	7.58	7.56	7.87	9.92	8.6	8.26	7.48	7.71
231205_at	---	---	0.609476	6.11	3.62	6.31	5.94	3.81	5.09	7.17	4.51	6.26	7.71
202555_s_at	MYLK	myosin light chain kinase	0.609476	5.89	5.12	6.38	6.43	5.38	9.72	7.6	8.05	6.44	6.89
203414_at	MMD	monocyte to macrophage differentiation-associated	0.609792	6.97	6.5	7.11	9.03	8.86	12.06	10.66	11.48	9.02	10.07
235307_at	LMTK2	lemur tyrosine kinase 2	0.609792	9.5	9.47	9.15	8.17	8.35	7.07	9.32	7.27	8.19	6.86
221768_at	SFPQ	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein ass	0.609806	7.73	6.67	7.4	7.15	6.91	3.27	7.17	4.66	7.43	8.36
212828_at	SYNJ2	synaptojanin 2	0.610603	6.23	6.12	5.08	3.61	5.11	3.76	6.41	7.74	5.37	5.93
1554306_at	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	0.610603	7.16	5.48	3.32	5.59	6.85	4.72	6.25	3.83	6.24	4.27
233228_at	---	---	0.610603	5.59	2.36	5.11	6.36	5.59	3.5	6.54	3.42	7.66	7.12
37145_at	GNLY	granulysin	0.610707	6.91	7.46	4.89	7.26	7.14	5.37	8.24	6.4	8.08	6.47
228514_at	GFER	Growth factor, augmenter of liver regeneration	0.61114	4.34	5.23	4.34	5.78	5.34	7.13	6.16	4.86	4.67	8.29
1565566_a_at	---	---	0.611175	6.08	7.63	6.81	7.19	5.42	7.78	5.75	6	6.46	8.9
213546_at	DKFZP586I1420	hypothetical protein DKFZp586I1420	0.611361	7.28	6.28	4.99	6.32	6.74	3.76	6.79	5.78	6.2	5.24
239897_at	BCLAF1	BCL2-associated transcription factor 1	0.611953	7.55	7.9	5.57	7.77	7.17	5.99	6.89	3.19	7.79	6.53
1555659_a_at	TREML1	triggering receptor expressed on myeloid cells-like 1	0.611953	6.03	5.55	5.86	5.87	5.89	9.33	7.18	7.28	6.03	6.3
230444_at	---	---	0.611953	6.39	7.38	5.88	6.47	8.02	5.06	7.48	5.92	7.55	4.94
228394_at	STK10	serine/threonine kinase 10	0.611953	8.92	9.42	8.85	8.9	9.27	7.08	8.47	8.15	8.24	5.47
224082_at	---	---	0.612324	7.11	7.53	5.49	6.31	5.97	4.66	7.53	4.8	7.02	6.2
1555372_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.612471	6.48	6.27	3.21	6.24	5.57	7.23	5.36	4.22	6.11	3.79
1569105_at	SETD5	SET domain containing 5	0.612471	7.48	6.02	4.8	6.62	5.86	4.73	4.51	5.08	7.53	5.61
233705_at	---	---	0.61315	6.69	4.09	5.96	7.23	4.69	3.43	6.3	3.72	5.94	6.34
218026_at	CCDC56	coiled-coil domain containing 56	0.61315	5.64	6.23	4.43	5.79	6	7.52	6.28	7.92	5.45	6.87
227792_at	ITPRIPL2	inositol 1,4,5-triphosphate receptor interacting protein-like 2	0.613925	5	4.54	4.39	4.41	5.14	7.98	6.97	7.24	5.16	4.86
218406_x_at	NENF	neuron derived neurotrophic factor	0.613925	5.31	6.33	5.11	5.25	6.78	8.65	6.31	6.66	6.77	6.32
235603_at	HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.613989	6.08	4.6	4.26	5.81	6.09	5.67	6.39	5.72	6.71	3.16
208894_at	HLA-DRA	major histocompatibility complex, class II, DR alpha	0.61415	7.45	9.87	9.32	9.16	9.21	11.42	9.94	10.48	9.58	9.73
242794_at	MAML3	mastermind-like 3 (Drosophila)	0.614456	8.08	8.77	6.95	8.54	7.49	6.5	8.32	7.1	8.3	5.56
218435_at	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	0.615513	5.95	6.78	4.96	6.78	7.42	8.94	7.92	7.45	5.98	8.3
235276_at	EPSTI1	Epithelial stromal interaction 1 (breast)	0.61618	4.66	4.35	6.84	7.47	7.09	5.67	6.01	5	6.7	4.69
225354_s_at	SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	0.616424	4.2	3.35	4.69	5.2	5.26	8.22	6.41	7.23	4.61	3.83
60794_f_at	ZNF814	zinc finger protein 814	0.617401	8.35	7.48	6.96	7.92	7.38	4.57	6.61	6.16	8.28	6.37
243233_at	---	---	0.617794	7.85	5.35	4.84	6.43	6.68	6.26	6.91	4.95	8.4	6.47
206698_at	XK	X-linked Kx blood group (McLeod syndrome)	0.617985	4.96	5.23	4	4.34	5.88	7.35	5.62	7.26	6.22	7.45
209895_at	PTPN11	protein tyrosine phosphatase, non-receptor type 11	0.61814	7.61	7.36	6.52	7.05	7.01	5.68	7.17	4.32	5.89	5.04

212493_s_at	SETD2	SET domain containing 2	0.618806	8.57	8.15	6.46	8.42	7.29	6.43	7.46	6.05	8.71	4.06
201024_x_at	EIF5B	eukaryotic translation initiation factor 5B	0.619124	8.86	8.85	4.39	8.23	9.52	6.87	9.56	7.94	8.85	4.66
1557261_at	WHAMML1 /// WHAMML2	WAS protein homolog associated with actin, golgi membranes and microtubules-like	0.619124	3.47	3.48	3.48	5.12	3.63	7.39	6.31	7.3	3.36	3.64
231418_at	---	---	0.619124	4.03	7.95	3.19	4.5	4.94	6.02	5.38	5.23	6.02	4.67
200002_at	RPL35	ribosomal protein L35	0.619723	7.62	8.92	8.17	8.33	8.93	11.1	9.95	9.36	8.59	10.62
207181_s_at	CASP7	caspase 7, apoptosis-related cysteine peptidase	0.620077	5.09	6.13	3.94	4.92	5.72	7.31	5.92	6.9	4.48	4.3
229069_at	SARNP	SAP domain containing ribonucleoprotein	0.620138	7.15	7.06	7.11	6.63	6.66	5.93	7.2	4.09	7.37	8.75
204628_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.620138	6.28	5.93	6.9	7.32	7.01	10.24	9.08	9.66	7.99	8.56
1556551_s_at	SLC39A6	solute carrier family 39 (zinc transporter), member 6	0.620138	6.51	6.42	5.52	7.48	7.4	4.99	6.71	6.43	6.65	4.15
212671_s_at	HLA-DQA1 /// HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibil	0.621349	5.05	8.29	4.06	6.33	7.83	9.35	8.06	8.14	6.3	6.39
225621_at	ALG2	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cer	0.621977	5.56	7.3	4.41	5.9	6.65	7.14	6.59	7.22	5.77	4.87
201847_at	LIPA	lipase A, lysosomal acid, cholesterol esterase	0.62224	4.62	5.45	5.22	5.25	6.56	7.91	7.5	7.32	6.11	5.94
224906_at	ANO6	anoctamin 6	0.622242	5.16	4.92	4.75	5.44	6.88	7.28	6.95	7.28	5.5	6.68
236889_at	---	---	0.622242	7.5	5.29	5.99	6.7	5.32	5.05	7.37	4.98	7.21	4.55
243819_at	---	---	0.62269	8.4	4.92	7.7	7.31	5.41	6.24	7.68	7.31	7.7	5.78
220735_s_at	SENP7	SUMO1/sentrin specific peptidase 7	0.62269	6.88	6.79	6.87	6.5	6.91	5.07	6.9	3.93	6.11	4.54
212813_at	JAM3 /// LOC100133502	junctional adhesion molecule 3 /// hypothetical protein LOC100133502	0.622784	4.13	3.71	4.92	4.96	4.02	7.92	6.29	7.2	5.41	4.05
216867_s_at	PDGFA	platelet-derived growth factor alpha polypeptide	0.624871	4.38	3.57	5.4	5.31	5.9	8.22	7.46	7.69	6.16	6.84
222717_at	SDPR	serum deprivation response (phosphatidylserine binding protein)	0.624924	4.11	2.32	4.29	6.45	6.11	9.65	8.26	8.98	6.29	6.66
220305_at	MAVS	mitochondrial antiviral signaling protein	0.624924	6.43	7.48	5.35	5.58	5.96	4.75	7.5	5.86	6.41	4.42
224823_at	MYLK	myosin light chain kinase	0.625063	4.26	4.29	4.98	4.85	5.66	8.44	6.65	6.7	4.9	5.38
211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.625539	4.3	8.82	8.3	7.09	8.12	10.72	9.02	8.98	6.3	4.47
215111_s_at	TSC22D1	TSC22 domain family, member 1	0.625539	5.64	4.67	6.16	6.78	7.51	10.46	8.15	8.82	6.52	6.69
241003_at	---	---	0.625539	6.76	7.18	8.83	6.59	5.54	6.12	5.36	7.56	7.16	9.06
217771_at	GOLM1	golgi membrane protein 1	0.625775	5.13	6.3	5.26	6.13	5.77	7.29	7.33	8.41	6	4.26
244677_at	---	---	0.626062	8.44	4.5	8.1	5.23	5.88	5.92	6.84	7.33	8.41	6.25
201996_s_at	SPEN	spen homolog, transcriptional regulator (Drosophila)	0.626062	9.68	9	7.46	8.89	8.6	6.9	8.31	7.86	9.4	6.34
223850_at	---	---	0.626542	7.28	4.47	7.26	6.86	5.91	5.11	3.86	5.75	6.32	5.84
235810_at	ZNF182	zinc finger protein 182	0.626945	6.64	6.47	4.04	5.48	7.17	4.27	6.74	5.94	6.73	4.36
243701_at	---	---	0.627178	3.41	4.2	5.68	6.07	4.93	7.03	4.05	6.43	4.3	7.84
238502_at	---	---	0.627178	7.47	4.46	5.8	5	5.46	4.74	5.62	6.27	6.53	4.09
1569076_a_at	ZNF836	zinc finger protein 836	0.62765	6.27	7.33	3.55	5.31	7.28	6.23	7.22	5.51	6.05	5.87
204626_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.627967	5.81	5.07	6.56	7.36	6.82	10.86	9.04	10.4	8.48	9.12
222139_at	KIAA1466	KIAA1466 gene	0.627967	6.73	5.85	3.28	6.19	4.37	2.75	6.78	3.48	4.08	2.77
212723_at	JMJD6	jumonji domain containing 6	0.627967	9.68	8.26	9.98	9.72	8.04	7.56	8.47	6.61	8.4	6.4
221802_s_at	KIAA1598	KIAA1598	0.628857	3.43	5.69	2.93	3.68	5.59	6.74	7.74	7.44	4.43	3.43
220094_s_at	CCDC90A	coiled-coil domain containing 90A	0.628857	4.54	5.25	3.53	4.55	6.61	8.63	6.95	7.82	6.27	4.05

1558710_at	---	---	0.629545	6.3	3.64	6.19	6.65	3.54	3.51	4.48	3.65	4.64	4.91
240798_at	---	---	0.629651	6.12	5.74	4.04	6.39	6.82	4.31	5.72	5.59	4.94	3.7
209306_s_at	SWAP70	SWAP-70 protein	0.629818	6.96	8.13	4.2	5.63	6.96	6.97	6	7.82	6.38	6.36
1557236_at	APOL6	apolipoprotein L, 6	0.629876	7.5	7.52	8.58	9.76	7.98	6.3	6.85	6.72	8.69	7.45
229531_at	---	---	0.630445	7.53	7.71	5.01	6.69	8.48	5.14	7.13	5.72	6.68	5.51
213074_at	PHIP	pleckstrin homology domain interacting protein	0.630581	7.9	7.35	4.8	7.26	8.13	6.11	8.45	6.77	7.59	6.69
206115_at	EGR3	early growth response 3	0.630939	9.05	3.65	8.04	8.72	7.18	5.43	9.24	6.75	9.84	3.23
242323_at	PLA2G12A	phospholipase A2, group XIIA	0.63123	4.37	4.04	4.46	4.63	5.3	7.03	6.91	6.09	5.14	6.65
234632_x_at	---	---	0.631503	9.6	9.63	3.53	9.37	8.53	3.32	6.6	3.07	9.12	3.64
205798_at	IL7R	interleukin 7 receptor	0.631831	6.66	3.75	4.36	6.76	6.72	4.42	8.3	4.01	6.02	5.98
218622_at	NUP37	nucleoporin 37kDa	0.631831	5.18	6.48	3.98	3.89	5.88	6.17	5.49	6.61	3.97	5.53
206493_at	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	0.632348	6.95	7.17	7.41	7.16	8.49	11.19	9.76	11.05	8.59	9.18
213673_x_at	NENF	Neuron derived neurotrophic factor	0.632835	4.7	5.82	4.11	4.8	6.59	8.48	6.13	6.41	6.34	6.41
217963_s_at	NGFRAP1	nerve growth factor receptor (TNFRSF16) associated protein 1	0.632903	5.33	5	4.66	6.09	5.68	9.64	8.21	9.03	5.91	7.81
217952_x_at	PHF3	PHD finger protein 3	0.632903	10.43	10.58	6.93	9.83	9.83	8.5	10	9.03	9.87	7.08
209259_s_at	SMC3	structural maintenance of chromosomes 3	0.632903	8.23	8.89	5.94	7.64	8.7	7.2	8.06	7.17	7.96	5.68
212058_at	SR140	U2-associated SR140 protein	0.632903	7.55	7.23	7.94	7.56	6.86	6.79	6.45	5.96	7.93	4.56
207630_s_at	CREM	cAMP responsive element modulator	0.632954	7.7	6.29	7.11	7.71	6.05	4.8	7.78	6	7.76	5.72
244523_at	MMD	monocyte to macrophage differentiation-associated	0.632954	3.88	3.06	3.65	3.77	2.73	6.56	6.22	6.73	3.27	5.93
1557081_at	RBM25	RNA binding motif protein 25	0.632954	7.49	7.11	3.93	5.68	5.86	4.44	7.41	5.47	7.58	5.57
202642_s_at	TRRAP	transformation/transcription domain-associated protein	0.632954	5.83	6.68	3.78	5.79	6.34	3.53	6.13	5.93	5.64	4.88
1559822_s_at	LOC644215 /// MTDH	hypothetical LOC644215 /// metadherin	0.632954	6.11	6.62	4.94	5.93	6.07	4.43	7.63	6.69	5.79	3.34
200834_s_at	RPS21	ribosomal protein S21	0.632954	7.72	8.27	8.94	8.71	9.05	11.12	9.72	10.4	8.61	10.49
201143_s_at	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	0.633672	6.52	5.68	5	6.71	6.67	6.05	6.89	8.28	6.12	8.27
1554512_a_at	CCDC123	coiled-coil domain containing 123	0.63386	3.83	6.18	3.91	4.08	5.85	4.02	6.03	5.1	5.61	7.12
266_s_at	CD24	CD24 molecule	0.634162	3.42	4.85	6.02	5.35	6.97	7.74	6.5	9.21	6.26	7.6
1555351_s_at	PPHLN1	periphilin 1	0.634162	7.68	7.39	4.76	7.18	7.83	3.57	6.28	7.88	7.18	6.48
202546_at	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	0.634162	7	7.78	6.92	7.07	8.46	10.19	9.4	9.75	6.8	8.19
1562894_at	---	---	0.634162	7.22	6.12	4.44	6.58	5.53	4.97	6.41	3.33	5.95	6.13
1554057_at	LOC645676	hypothetical LOC645676	0.634162	7.1	5.93	7.63	5.73	4.4	4.69	6.29	3.29	6.49	6.66
239314_at	NHLRC3	NHL repeat containing 3	0.634162	5.5	4.73	4.39	5.13	6.01	7.4	6.94	6.4	3.91	5.39
239393_at	---	---	0.634162	6.79	6.5	5.5	5.84	5.02	3.99	5.81	3.75	6.83	5.16
243164_s_at	---	---	0.634708	7.46	5.98	5.42	6.96	5.22	3.47	7.43	6.13	7.15	4.18
243934_at	ODF3B	Outer dense fiber of sperm tails 3B	0.635106	6.06	5.57	8.17	6.98	4.75	7.6	6.01	8.29	8.04	8.32
211747_s_at	LSM5	LSM5 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0.635106	6.2	6.11	4.41	5.25	5.99	7.35	7.41	7.83	5.27	7.91
239490_at	C7orf44	chromosome 7 open reading frame 44	0.635106	7.4	5.92	7.11	6.16	4.92	4.17	6.06	4.52	5.3	5.87
1554049_s_at	WDR42A	WD repeat domain 42A	0.635106	5.06	4.17	4.37	4.91	6.35	3.44	4.12	6.18	6.54	4.47
214970_s_at	ST6GAL1	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	0.635409	5.75	6.8	4.48	5.32	4.86	4.03	5	6.63	5.21	7.06
234260_at	---	---	0.636316	6.59	5.55	6.26	6.31	5.32	4.38	4.95	2.47	4.77	4.67

231688_at	MMP8	matrix metallopeptidase 8 (neutrophil collagenase)	0.636551	5.12	5.22	6.04	4.39	7.22	8.05	7.18	9.65	4.67	6.04
205382_s_at	CFD	complement factor D (adipsin)	0.63671	10.12	10.39	8.51	8.24	10.74	11.13	7.05	7.87	7.63	9.05
211684_s_at	DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2	0.63671	4.39	5.66	2.81	5.53	6.35	7.11	7.34	7.16	5.47	6.57
215109_at	---	---	0.63671	7.62	5.79	6.49	7.38	5.45	3.78	6.17	7.54	7.08	7.76
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxyge	0.63671	10.69	8.6	10.68	10.51	10.78	8.56	11.68	8.86	11.97	7.99
206697_s_at	HP /// HPR	haptoglobin /// haptoglobin-related protein	0.63671	6.96	7.02	6.79	6.21	8.06	8.77	8.31	9.62	5.8	6.92
201406_at	HNRNPH2 /// RPL36A /// RPL36AP37	heterogeneous nuclear ribonucleoprotein H2 (H') /// ribosomal protein L36a /// r	0.63671	8.42	9.23	9.41	9.73	9.91	12.28	9.79	9.85	8.71	10.06
238465_at	C5orf35	chromosome 5 open reading frame 35	0.636748	4.6	4.67	7.15	6.11	6.67	7.52	5.73	5.2	4.82	5.91
236985_at	---	---	0.637402	7.1	5.93	7.28	4.96	4.69	4.05	5.81	7.38	5.7	4.12
224345_x_at	FAM162A	family with sequence similarity 162, member A	0.637402	5.69	5.51	5.33	4.72	4.64	7.79	5.91	6.65	5.92	7.33
236488_s_at	---	---	0.637505	7.41	7.33	6.68	6.83	8.55	10.8	9.16	9.69	7.36	7.1
235786_at	---	---	0.637746	6.33	4.69	3.96	7.01	5.48	3.61	6.34	4.64	6.99	3.65
204512_at	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1	0.637803	7.76	7.27	4.44	7.02	6.7	4.92	7.23	5	7.73	6.41
205081_at	CRIP1	cysteine-rich protein 1 (intestinal)	0.637803	5.47	5.25	6.05	6.21	7.43	8.72	7.87	8.25	6.21	7.17
1552719_at	CASC4	cancer susceptibility candidate 4	0.637803	7.75	7.28	4.51	5.64	5.89	4.94	6.44	4.56	6.31	5.6
217847_s_at	THRAP3	thyroid hormone receptor associated protein 3	0.638591	8.6	8.43	7.18	8.36	8.92	6.17	7.75	7.93	9.31	6.41
208276_at	---	---	0.638833	7.21	4.5	6.29	7.22	6.27	6.53	7.17	8.24	7.85	7.2
1553510_s_at	RQCD1	RCD1 required for cell differentiation1 homolog (S. pombe)	0.639024	5.1	6.08	4.91	6.51	7.66	5.2	6.09	5.34	5.93	8.73
202276_at	SHFM1	split hand/foot malformation (ectrodactyly) type 1	0.639045	8.38	9.07	7.51	8.12	9.58	10.4	10.24	10.57	8.74	9.54
1554577_a_at	PSMD10	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	0.639193	6.42	7.64	4.88	7.49	7.99	5.71	6.02	7.58	6.05	8.13
204319_s_at	RGS10	regulator of G-protein signaling 10	0.639343	6.8	5.88	6.4	7	6.71	9.92	8.03	8.04	7.32	7.7
213825_at	OLIG2	oligodendrocyte lineage transcription factor 2	0.639755	3.77	5.64	3.67	3.32	6.3	6.1	3.57	6.1	5.36	5.95
205128_x_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxyge	0.639755	7.71	7.94	6.17	7.66	7.95	10.12	8.99	9.61	7.99	8.26
226765_at	SPTBN1	Spectrin, beta, non-erythrocytic 1	0.639755	6.12	6.09	4.99	6.43	7.62	7.36	8.14	6.75	6.83	5.22
1569609_at	---	---	0.639911	7.52	7.59	7.6	7.12	6.94	5.99	7.28	5.26	6.67	3.3
229025_s_at	IMMP1L	IMP1 inner mitochondrial membrane peptidase-like (S. cerevisiae)	0.639964	4.52	4.4	5.02	3.99	7.61	4.36	7.65	7.19	5.18	7.24
1553906_s_at	FGD2	FYVE, RhoGEF and PH domain containing 2	0.639964	5.47	9.03	8.25	7.07	8.71	10.15	8.62	6.97	7.65	6.18
1558392_at	SYNE2	spectrin repeat containing, nuclear envelope 2	0.64021	8.62	8.59	4.57	7.1	6.34	2.8	6.74	7.4	8.39	6.29
1559614_at	FLJ38773	hypothetical protein FLJ38773	0.641068	7.39	7.28	5.47	6.44	5.6	3.49	5.79	3.42	6.2	5.46
227087_at	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	0.64111	8.49	8.53	6.71	7.38	8.01	6.62	7.64	8.23	7.39	3.2
60815_at	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	0.641223	7.8	7.47	4.52	6.44	7.68	5.24	7.07	4.25	7.74	5.63
213846_at	COX7C	cytochrome c oxidase subunit VIIc	0.641365	6.24	7.48	7.24	5.91	7.17	8.87	7.67	8.5	6.96	8.78
239234_at	---	---	0.641654	7.49	7.19	6.94	7.55	6.17	5.28	5.05	5.54	7.79	6.75
229514_at	C14orf118	chromosome 14 open reading frame 118	0.642176	8.09	8.29	4.03	7.07	7.95	4.12	7.08	4.64	7.65	7.01
226866_at	ESCO1	establishment of cohesion 1 homolog 1 (S. cerevisiae)	0.642176	7.68	8.76	7.06	7.79	7.84	6.89	7.55	6.47	7.66	4.04
203096_s_at	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	0.642691	8.83	8.54	8.49	8.74	8.32	7.56	8.75	7.29	8.77	5.5

1565567_at	---	---	0.643031	6.44	8.21	7.24	7.46	5.85	8.2	5.72	6.65	6.79	9.13
236678_at	---	---	0.643965	7.55	4.74	7.25	5.55	5.61	3.51	5.56	7.19	4.76	6.14
200749_at	RAN	RAN, member RAS oncogene family	0.644481	5.22	5.19	3.14	5.12	5.33	7.1	6.23	3.78	4.71	6.91
225054_x_at	LOC651250	hypothetical LOC651250	0.645036	8	6.83	5.13	7.33	7.22	5.31	5.85	5.2	7.42	7.13
243328_at	---	---	0.645037	7.15	5.97	7.45	8.45	5.22	3.64	5.55	5.4	6.04	3.97
208363_s_at	INPP4A	inositol polyphosphate-4-phosphatase, type I, 107kDa	0.645148	7.3	7.98	5.66	6.87	7.13	8.64	6.24	7.18	6.19	4.64
235175_at	GBP4	guanylate binding protein 4	0.645853	6.98	8.01	8.74	8.87	7.36	7.23	7.36	4.18	8.14	7.64
235580_at	ZNF141	zinc finger protein 141	0.646026	7.34	6.78	4.49	5.75	7.62	5.6	5.17	6.71	6.91	4.92
231528_at	---	---	0.646091	5.66	6.88	6.04	6.99	6.85	4.41	6.78	5.95	5.3	3.72
214195_at	TPP1	tripeptidyl peptidase I	0.647054	6.67	4.54	7.78	5.86	6.38	6.62	4.42	5.01	5.95	6.51
223661_at	NUCKS1	Nuclear casein kinase and cyclin-dependent kinase substrate 1	0.647907	5.26	6.36	6.52	4.91	5.06	6.84	7.3	7.64	5.83	4.52
1560636_a_at	---	---	0.648354	8.57	4.73	9.38	7.95	7.56	9.06	7.65	8.16	8.68	8.73
217422_s_at	CD22	CD22 molecule	0.648897	4.16	6.94	4.53	4.76	5.81	5.55	6.14	6.87	3.41	4.21
204671_s_at	ANKRD6	ankyrin repeat domain 6	0.648897	6.16	6.05	5.42	5.41	6.19	3.06	5.56	6.36	5.28	3.73
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	0.649003	3.71	6.94	3.85	5.66	3.19	3.6	6.98	7.3	3.49	3.34
203819_s_at	IGF2BP3	insulin-like growth factor 2 mRNA binding protein 3	0.649073	6.43	6.03	6.47	7.06	6.04	8.84	6.54	8.19	5.64	5.39
1554153_a_at	PHF21A	PHD finger protein 21A	0.649559	9.51	9.63	7.11	9.72	9.14	6.73	8.8	7.64	8.76	6.37
1567213_at	PNN	pinin, desmosome associated protein	0.649612	8.63	7.71	4.34	6.7	7.73	6.86	8.53	8.36	7.92	5.4
200872_at	S100A10	S100 calcium binding protein A10	0.650497	6.11	5.79	4.55	6.65	7.8	8.95	8.61	9	6.81	6.99
210427_x_at	ANXA2	annexin A2	0.65058	5.87	6.7	6.77	6.98	8.33	10.53	9.14	9.68	6.82	6.27
220496_at	CLEC1B	C-type lectin domain family 1, member B	0.65058	4.67	3.86	5.13	5.67	6.23	8.76	6.86	7.62	6.15	6.44
225207_at	PDK4	pyruvate dehydrogenase kinase, isozyme 4	0.651033	5.67	5	5.29	4.99	8.25	7.3	6.57	7.01	8.75	7.42
201302_at	ANXA4	annexin A4	0.651389	4.99	5.05	6.51	5.38	6.45	8.1	6.05	5.84	4.57	6.52
244187_at	---	---	0.651462	4.78	6.52	4.87	7.15	6.85	7.66	7.56	7.65	7.43	7.24
236379_at	---	---	0.651738	7.99	7.37	5.57	7.21	7.04	5.65	7.66	7.33	8.17	4.93
1554010_at	NDST1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	0.652405	6.48	4.73	6.96	5.87	4.58	5.32	7.72	4.94	7.36	7.09
208161_s_at	ABCC3	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	0.6537	4.95	4.6	4.89	3.93	4.69	7.77	6.87	7.42	4.78	4.74
238149_at	ZNF818P	zinc finger protein 818 pseudogene	0.653769	5.16	5.68	4.75	6.36	6	3.66	6.05	4.11	6.28	3.42
240547_at	---	---	0.653847	6.69	6.08	5.06	6.47	6.66	5.6	6.97	5.44	8.05	4.7
229297_at	---	---	0.654716	5.57	6.98	4.94	6.76	6.05	3.83	6.38	5.09	5.27	3.26
1556896_at	LOC284751	hypothetical LOC284751	0.654923	7.29	7.03	6.59	5.22	6.73	3.95	4.02	3.92	7.01	4.59
212827_at	IGHM	immunoglobulin heavy constant mu	0.655206	5.61	8.98	4.27	5.49	6.18	6.72	6.49	7.62	6.21	6.56
201016_at	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	0.655976	6	7.09	2.76	4.55	5.42	7.38	6.51	6.91	5.8	5.56
203497_at	MED1	mediator complex subunit 1	0.655976	9.23	8.73	5.68	8.54	8.46	7.7	8.64	8.19	9.2	7.11
220969_s_at	---	---	0.656945	4.1	4.97	5.65	4.86	4.12	7.5	4.86	6.34	5.33	8.21
208923_at	CYFIP1	cytoplasmic FMR1 interacting protein 1	0.656945	6.36	5.52	5.09	5.25	6.08	7.52	7.28	7.51	6.27	4.59
214073_at	CTTN	cortactin	0.657124	3.86	3.08	5.1	4.72	6.94	10.52	6.91	9.92	5.41	3.12
221253_s_at	TXNDC5	thioredoxin domain containing 5 (endoplasmic reticulum)	0.657124	5.28	5.81	2.62	4.99	5.6	6.97	6.59	7.21	5.27	5.33
238413_at	LOC100131998	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae) pseudogene	0.657124	6.77	6.37	5.76	6.25	5.99	3.87	6.63	4.82	6.79	4.18

229966_at	EWSR1	Ewing sarcoma breakpoint region 1	0.657124	8.19	7.87	7.07	7.35	7.6	4.6	7.08	6.59	7.85	6.28
1552316_a_at	GIMAP1	GTPase, IMAP family member 1	0.657534	5.37	6.85	3.34	6.01	8.31	9.18	8.69	9.02	7.46	6.51
224926_at	EXOC4	exocyst complex component 4	0.657804	4.95	6.68	7.44	6.02	6.66	4.76	6.06	5.07	5.5	4.01
222720_x_at	C1orf27	chromosome 1 open reading frame 27	0.657838	8.37	8.74	5.57	7.59	8.25	5.71	8.82	7.79	7.65	5.48
1553117_a_at	STK38	serine/threonine kinase 38	0.658925	8.27	8.41	9.28	8.45	8.37	6.17	7.26	7.44	7.79	6.19
227796_at	ZFP62	zinc finger protein 62 homolog (mouse)	0.660597	6.62	8.46	4.27	5.11	8.2	4.44	7.13	5.24	6.53	8.15
236823_at	---	---	0.660597	7.12	5.94	6.34	5.91	4.91	7.82	5.58	4.1	7.3	6.82
232500_at	C20orf74	chromosome 20 open reading frame 74	0.660597	8.39	6.73	6.02	7.22	6.55	5.35	7.71	6.11	7.69	8.36
1552552_s_at	CLEC4C	C-type lectin domain family 4, member C	0.660877	2.7	3.21	7.13	7.1	8.16	7.94	6.05	7.46	6.71	6.76
1554001_at	TRIM37	tripartite motif-containing 37	0.660877	6.56	5.84	7.31	6.93	5.41	6.89	3.7	5.18	5.37	8.28
223292_s_at	MRPS15	mitochondrial ribosomal protein S15	0.661122	7.58	4.37	8.23	3.2	6.4	6.25	7.93	7.25	6.61	5.18
215813_s_at	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxyge	0.661122	7.93	7.83	5.33	7.73	8.14	10.26	9.06	9.73	8.02	8.5
1566202_at	---	---	0.661295	7.55	5.22	4.69	7.17	4.85	4.69	7.27	6.92	7.66	4.64
206881_s_at	LILRA3	leukocyte immunoglobulin-like receptor, subfamily A (without TM domain), member	0.661295	10.43	10.55	8.83	9.35	10.21	9.94	9.53	10.56	7.38	7.31
204411_at	KIF21B	kinesin family member 21B	0.661295	7.69	7.84	5.93	7.68	8.2	6.1	7.81	5.99	8.21	5.57
203740_at	MPHOSPH6	M-phase phosphoprotein 6	0.661356	5.52	5.18	3.79	4.75	6.55	7.36	6.81	6.46	5.92	6.76
201528_at	RPA1	replication protein A1, 70kDa	0.661406	7.07	5.33	6.38	6.61	7.08	9.58	7.12	8.63	6.27	7.28
1558740_s_at	---	---	0.661473	6.74	6.65	5.58	6.97	4.71	7.02	7.23	3.7	7.17	6.46
213503_x_at	ANXA2	annexin A2	0.662492	5.86	6.75	6.76	6.87	8.13	10.55	9.09	9.49	6.93	6.01
217529_at	ORAI2	ORAI calcium release-activated calcium modulator 2	0.662492	9.08	8.57	8.08	9.11	8.78	6	7.8	6.76	7.57	5.11
213277_at	ZFP36L1	zinc finger protein 36, C3H type-like 1	0.662652	5.8	5.96	8.58	6.71	5.84	7.34	5.73	6.54	6.27	8.04
201938_at	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	0.662707	8.16	8.43	8.71	8.28	9.58	11.12	10.11	10.5	8.83	8.7
223006_s_at	C9orf5	chromosome 9 open reading frame 5	0.663269	4.26	5.93	6.28	4.41	6.79	6.21	7.73	5.01	4.87	4.66
236545_at	---	---	0.66347	7.09	5.93	6.33	6.69	6.89	7.56	5.6	5.29	6.14	3.9
235134_at	---	---	0.663845	4.19	6.62	4.11	4.21	3.7	6.47	4.42	4.22	4.22	7.2
212826_s_at	SLC25A6	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator	0.663887	8.27	9.33	8.21	9.18	10.11	11.72	10.81	10.76	9.94	10.39
209447_at	SYNE1	spectrin repeat containing, nuclear envelope 1	0.664014	6.44	6.7	3.74	6.25	7.57	8.49	7.92	5.91	7.54	3.86
242121_at	---	---	0.664014	6.31	6.65	4.57	7.06	6.72	3.95	6.48	3.94	5.91	5.94
215513_at	HYMAI	hydatidiform mole associated and imprinted (non-protein coding)	0.664621	6.59	4.39	4.45	6.79	4.09	3.85	4.09	3.49	6.26	3.41
223797_at	PRO2852	hypothetical protein PRO2852	0.665434	9.08	8.28	4.85	8.39	8.35	6.45	8.83	6.42	9.13	7.03
206214_at	PLA2G7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.665556	4.26	4.17	4.24	4.68	4.72	7.25	6.33	6.81	3.94	4.45
1553266_at	CNOT6L	CCR4-NOT transcription complex, subunit 6-like	0.666142	7.49	5.4	3.65	6.04	6.4	7.77	6.18	4.28	7.08	7.76
211310_at	EZH1	enhancer of zeste homolog 1 (Drosophila)	0.666318	5.24	5.55	5.19	5.55	4.93	5.05	6.79	7.25	7.61	8.71
215310_at	APC	adenomatous polyposis coli	0.667077	6.15	4.61	4.37	6.74	5.01	3.94	5.94	4.29	6.05	4
200873_s_at	CCT8	chaperonin containing TCP1, subunit 8 (theta)	0.667252	7.61	7.62	5.08	7.13	7.62	9.41	8.77	8.63	7.86	7.07
1559018_at	PTPRE	protein tyrosine phosphatase, receptor type, E	0.667426	7.51	6.12	6.15	7.43	5.88	3.37	7.72	5.2	8.08	4.78
242438_at	ASXL1	additional sex combs like 1 (Drosophila)	0.667426	6.77	5.34	4.76	5.25	4.53	5.71	5.72	4.7	7.75	6.31
209727_at	GM2A	GM2 ganglioside activator	0.668113	5.49	6.33	10.17	9.95	6.96	7.6	8.78	9.41	5.41	7.74
1565716_at	FUS	fusion (involved in t(12;16) in malignant liposarcoma)	0.668113	7.11	7.67	8.53	7.7	7.92	5.88	7.8	4.85	9.48	9.4

220220_at	LRRC37A4	leucine rich repeat containing 37, member A4 (pseudogene)	0.668378	7.91	7.99	4.46	6.19	7.77	4.76	6.54	6.48	7.85	4.91
1567214_a_at	PNN	pinin, desmosome associated protein	0.668697	9.46	8.21	4.8	7.94	8.5	7.44	9.11	8.66	8.81	6.29
226103_at	NEXN	nexilin (F actin binding protein)	0.668747	4.99	5.07	4.29	4.67	6.05	6.59	6.48	7.25	4.94	4.22
223193_x_at	FAM162A	family with sequence similarity 162, member A	0.669322	6.03	5.69	5.01	4.41	4.67	8.15	5.71	6.63	6.25	7.13
1554171_at	ZMYM3	zinc finger, MYM-type 3	0.669322	4.94	5.27	6.16	5.01	7.35	5.42	6.76	4.9	5.55	7.53
228053_s_at	TOMM5	translocase of outer mitochondrial membrane 5 homolog (yeast)	0.6698	5.79	6.64	3.19	5.93	6.29	7.66	7.33	6.42	6.75	6.26
235217_at	LOC100216546	hypothetical LOC100216546	0.669848	7.46	6.55	5.24	7.52	5.28	4.94	6.75	6.72	6.57	4.94
205513_at	TCN1	transcobalamin I (vitamin B12 binding protein, R binder family)	0.670204	4.78	5.21	6.47	5.23	7.02	7.68	6.69	8.47	6.09	6.72
213403_at	MFSD9	Major facilitator superfamily domain containing 9	0.670336	7.96	8.62	5.75	5.02	6.66	5.44	7.19	6.22	5.64	4.69
230139_at	---	---	0.671923	4.58	3.99	7.26	7.3	6.9	5.59	4.17	3.76	5.18	5.62
242263_at	TMED5	Transmembrane emp24 protein transport domain containing 5	0.672379	6.07	4.81	3.92	5.08	5.92	3.52	6.2	7.18	6.2	7.13
235242_at	---	---	0.672563	8.04	7.54	7.33	7.99	7.42	5.4	8.19	6.44	7.89	5.27
213165_at	CEP350	centrosomal protein 350kDa	0.673466	7.85	8.47	5.96	7.76	8.07	5.85	6.07	5.36	7.3	6.02
216555_at	C22orf30	chromosome 22 open reading frame 30	0.673466	8.39	7.79	7.33	7.97	7.44	7.9	7.74	8.07	8.33	3.87
200665_s_at	SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	0.673752	5.52	3.58	5.74	7.19	7.17	10.87	9.17	9.99	6.82	7.65
1554331_a_at	LRRC18	leucine rich repeat containing 18	0.674446	7.56	7.33	4.04	4.82	6.88	4.87	5.85	3.62	6.97	5.53
208998_at	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	0.674957	7.41	7.28	8.61	8.69	9.23	10.63	10.03	10.37	8.84	8.72
1560255_at	C10orf31	chromosome 10 open reading frame 31	0.675756	6.24	4.63	6.28	6.61	5.48	4	5.62	4.76	6.66	4.05
231860_at	BRWD1	bromodomain and WD repeat domain containing 1	0.675778	6.5	6.17	4.16	3.98	5.12	4.3	4.42	5.07	6.19	6.61
1569110_x_at	LOC728613	programmed cell death 6 pseudogene	0.676448	5.1	5.51	3.49	6.19	6.98	3.7	7.36	8.44	6.48	3.2
231839_at	PDE12	phosphodiesterase 12	0.676476	7.03	6.22	4.82	5.96	6.97	5.67	8.22	5.11	7.06	4.71
219199_at	AFF4	AF4/FMR2 family, member 4	0.676692	7.52	7.72	5.73	7.96	7.16	5.35	7.43	7.01	7.41	4.04
214480_at	ETV3	ets variant 3	0.67708	7.39	6.56	8.5	7.58	6.76	8.63	6.43	6.5	6.32	5.33
208680_at	PRDX1	peroxiredoxin 1	0.677925	5.48	7.02	4.58	5.08	6.93	7.97	7.7	7.48	6.02	5.68
1558560_s_at	BLZF1	basic leucine zipper nuclear factor 1	0.678369	6.07	6.58	4.51	5.92	6.7	4.23	6.72	5.92	6.76	4.16
208794_s_at	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subf	0.678643	8.72	7.74	5.38	8.08	8.38	8.88	9.18	9.21	8.47	6.46
211037_s_at	MBOAT7	membrane bound O-acyltransferase domain containing 7	0.678643	7.88	6.75	6.59	7.26	6.53	5.05	6.66	4.82	7.28	4.09
201005_at	CD9	CD9 molecule	0.678643	6.22	5.46	7.75	8.31	7.27	9.89	7.52	7.53	6.91	8.64
229521_at	FLJ36031	hypothetical protein FLJ36031	0.679444	8.06	6.24	9.48	8.76	9.22	8.01	8.15	7.63	8.11	6.34
1569867_at	EME2	essential meiotic endonuclease 1 homolog 2 (S. pombe)	0.679693	5.26	6.67	4.68	5.06	4.71	3.73	3.37	6.1	3.27	6.11
209654_at	KIAA0947	KIAA0947 protein	0.680415	7.12	7.79	3.76	6.47	6.04	5.93	6.48	6.56	6.67	4.35
1568830_at	IRAK3	interleukin-1 receptor-associated kinase 3	0.680445	6.93	4.96	7.24	7.53	6.35	3.67	6.73	5.78	6.9	6.4
201590_x_at	ANXA2	annexin A2	0.68048	5.83	6.72	6.76	6.97	8.3	10.54	9.18	9.65	6.9	5.44
1555749_at	SF1	splicing factor 1	0.681035	8.09	7.7	7.23	7.52	7.57	4.77	6.05	6.93	8.4	6.22
215555_at	---	---	0.681035	5.14	4.78	4.66	6.25	4.8	6.96	6.1	3.62	6.23	6.05
242433_at	ZBTB11	zinc finger and BTB domain containing 11	0.681035	7.01	7.16	4.47	5.72	7.27	4.32	6.73	4.41	6.97	5.15
215751_at	RBM26	RNA binding motif protein 26	0.681357	6.16	5.59	2.65	4.88	5.34	7.36	5.39	6.88	5.74	8.26

1561489_at	---	---	0.682479	7.3	6.91	5.12	6.53	6.07	3.94	6.75	6.18	7	6.44
225767_at	LOC284801	hypothetical protein LOC284801	0.682749	6.46	6.73	5.94	6.94	7.27	8.93	7.81	7.93	6.73	9.13
1555892_s_at	LOC253039	hypothetical LOC253039	0.682837	6	6.67	7.32	5.19	4.39	4.51	4.21	3.99	6.36	5.37
243826_at	---	---	0.683121	6.87	7.31	3.97	6.27	5.7	4.01	7.24	4.14	6.78	3.78
219628_at	ZMAT3	zinc finger, matrin type 3	0.683354	6.28	5.17	3.01	4.71	6.6	6.19	5.16	5.92	5.99	9.62
1556049_at	RTN4	reticulon 4	0.683464	8.59	6.53	7.9	8.27	7.28	5.75	6.74	7.34	8.05	9.03
228179_at	HAS3	hyaluronan synthase 3	0.684033	7.46	8.3	5.58	7.46	4.86	6.92	8.88	7.93	8.51	9.11
224741_x_at	GAS5	growth arrest-specific 5 (non-protein coding)	0.684033	8.77	8.51	6.75	7.63	8.88	10.01	9.99	8.96	8.48	7.8
218781_at	SMC6	structural maintenance of chromosomes 6	0.684371	5.02	6.72	3.68	5.48	6.04	3.91	7.63	4.89	7.04	5.84
214058_at	MYCL1	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	0.684646	6.03	5.87	5.67	5.01	6.06	8.47	6.04	7.22	5.38	5.26
202843_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.685695	8.49	5.32	8.75	8.23	7.96	4.71	7.59	5.85	7.94	4.76
225795_at	C22orf32	chromosome 22 open reading frame 32	0.685722	4.8	5.93	4.98	4.95	6.52	8.37	8.38	8.17	5.97	6.11
211951_at	NOLC1	nucleolar and coiled-body phosphoprotein 1	0.685843	5.96	5.8	4.19	5.87	7.44	6.66	7.36	6.74	6.68	3.93
1564207_at	FLJ35390	hypothetical LOC255031	0.68619	8.65	5.9	6.81	7.66	8.16	8.36	6.52	5.31	7.88	5.02
213357_at	GTF2H5	general transcription factor IIH, polypeptide 5	0.68619	6.27	5.77	3.96	4.98	6.52	7.65	6.15	6.27	5.17	6.17
224705_s_at	TNRC6A	trinucleotide repeat containing 6A	0.686198	7.2	7.4	5.5	6.31	7.26	4.02	6.99	5.58	6.37	7.95
1558807_at	ATAD2B	ATPase family, AAA domain containing 2B	0.686198	7.13	7.27	5.02	7.05	7.14	3.35	6.2	6.4	6.59	4.52
1552299_at	AKD2	adenylate kinase domain containing 2	0.686857	6.61	6.79	5.18	5.4	7.52	4.57	5.71	6.41	7.86	4.29
224508_at	MGC12916	hypothetical protein MGC12916	0.686919	6.29	4.08	6.44	5.45	4.27	4.63	6.82	4.29	4.42	4.01
201825_s_at	SCCPDH	saccharopine dehydrogenase (putative)	0.686919	5.82	5.53	3.36	5.25	5.9	7.06	5.82	6.16	5.57	7.29
230141_at	ARID4A	AT rich interactive domain 4A (RBP1-like)	0.68741	6.45	6.69	4.37	6.75	6.28	3.98	5.55	4.38	6.4	2.98
209377_s_at	HMGN3	high mobility group nucleosomal binding domain 3	0.687564	5.37	5	4.42	5.39	6.52	8.48	7.56	8.19	5.3	5.41
214214_s_at	C1QBP	complement component 1, q subcomponent binding protein	0.687641	3.92	5.76	4.52	5.75	6.05	6.98	6.46	7.2	5.87	6.59
244313_at	CR1	complement component (3b/4b) receptor 1 (Knops blood group)	0.687641	9.36	9.37	7.55	9.18	9.16	6.79	9.7	9.11	9.07	6.81
206237_s_at	NRG1	neuregulin 1	0.687906	4.95	5.41	5.56	5.4	5.32	6.89	7.51	8.84	5.34	6.49
1568894_at	---	---	0.688045	9.91	6.63	8.14	8.49	7.33	5.83	7.54	8.73	9.94	4.04
1556601_a_at	SPATA13	Spermatogenesis associated 13	0.688268	5.6	4.37	7.68	6.2	3.96	3.19	3.64	6.17	6.61	3.4
210164_at	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	0.688282	3.4	3.56	3.29	5.14	7.25	3.09	7.38	3.7	7.52	4.89
225285_at	BCAT1	branched chain aminotransferase 1, cytosolic	0.688282	7.33	6.8	5.76	7.75	5	6.25	5.34	6.2	7.8	8.12
204184_s_at	ADRBK2	adrenergic, beta, receptor kinase 2	0.688282	6	7.23	5.3	6.47	8.11	8.43	7.5	8.51	7.01	6.51
1558732_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	0.688618	7.22	6.25	7.72	7.13	5.43	7.15	7.41	5.23	7.38	4.48
229497_at	ANKDD1A	ankyrin repeat and death domain containing 1A	0.688618	7.98	6.85	7.89	7.78	6.16	6.5	6.98	4.21	7.99	8.28
206209_s_at	CA4	carbonic anhydrase IV	0.688618	8.12	7.74	6.94	7.74	8.07	8.11	7.22	8.23	6.35	4.9
1561538_at	---	---	0.689052	7.91	5.23	6.59	7.43	5.43	4.52	6.43	5.7	6.49	6.07
227605_at	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	0.68921	6.57	7.14	5.08	4.8	5.95	3.96	7.02	6	6.27	4.19
215375_x_at	LRRFIP1	Leucine rich repeat (in FLII) interacting protein 1	0.689326	6.71	7.29	5.32	6.46	4.91	4.79	7.46	5.21	6.21	4.98
1562364_at	---	---	0.689326	4.44	6.6	4.85	6.09	5.57	4.47	4.85	3.64	7.3	4.98
213065_at	ZFC3H1	zinc finger, C3H1-type containing	0.689326	7.17	6.32	4.9	7.16	5.8	4.18	6.39	5.11	7.33	7.05

226015_at	ZNF12	zinc finger protein 12	0.689746	5.47	7.53	4.84	4.64	7.41	4.96	4.54	5.53	4.96	6.13
200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15	0.689788	6.02	6.28	5.36	5.96	6.15	7.98	8.02	7.88	6.22	5.65
241614_at	---	---	0.689796	6.87	6.59	6.59	3.85	6.46	8.38	8.33	7.16	8.7	7.42
208442_s_at	ATM	ataxia telangiectasia mutated	0.690019	8.55	9.77	6.63	7.55	7.94	6.02	9.42	8.78	8.47	6.81
244355_at	AVL9	AVL9 homolog (S. cerevisiase)	0.690316	7.91	7.56	7.5	7	6.67	8.52	6.75	5.3	7.59	8.92
226630_at	C14orf106	chromosome 14 open reading frame 106	0.690415	7.15	7.57	4.25	6.1	7.46	5.28	6.33	5.63	7.18	3.37
217408_at	MRPS18B	mitochondrial ribosomal protein S18B	0.691643	5.41	7.92	4.88	5.18	7.83	7.98	7.76	8.62	7.47	8.42
1556669_a_at	---	---	0.691824	7.28	3.42	7.3	7.14	4.79	5.79	7.61	6.14	7.75	4.85
243366_s_at	---	---	0.691824	5.68	6.51	3.61	4.75	6.04	6.49	6.71	5.06	6	3.18
1560116_a_at	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	0.691824	4.14	4.72	3.34	4.93	4.55	6.93	5.88	7.39	6.38	6.69
239926_at	---	---	0.691824	4.93	5.87	3.71	4.96	6.05	6.71	7.08	4.16	6.03	3.79
213239_at	PIBF1	progesterone immunomodulatory binding factor 1	0.691824	5.42	3.49	6.06	6.34	5.18	4.28	5.13	4.04	6.56	6.25
225115_at	HIPK2	homeodomain interacting protein kinase 2	0.692198	6.99	7.39	7	6.44	7.79	3.75	6.39	8.5	7.1	5.5
243611_at	MICALCL	MICAL C-terminal like	0.692198	8.46	7.98	5.91	7.97	6.69	5.28	7.49	6.07	7.57	5.4
230990_at	KIF13A	kinesin family member 13A	0.692793	6.98	6.6	7.61	7.3	7.13	4.43	6.62	5.24	6.64	5.68
226485_at	FLJ20674	hypothetical protein FLJ20674	0.692837	2.71	2.45	6.11	4.73	2.49	6.5	2.63	2.71	2.86	7.05
223334_at	TMEM126A	transmembrane protein 126A	0.692837	6.51	5.97	3.41	6.27	7.14	8.94	6.35	5.85	4.81	7.03
228346_at	ZNF844	zinc finger protein 844	0.693445	8.43	8.49	5.87	5.05	7.16	4.24	7.71	5.96	6.45	6.41
219806_s_at	C11orf75	chromosome 11 open reading frame 75	0.693509	8.23	8.28	8.61	8.53	6.68	7.07	6.8	7.55	6.26	5.8
1553055_a_at	SLFN5	schlafen family member 5	0.693805	5.67	4.35	3.7	6.08	6.2	3.87	6.79	5.08	5.53	3.75
223974_at	MGC11082	hypothetical LOC84777	0.694159	6.63	6.33	8.07	7.05	4.9	5.15	6.56	4.68	7.01	5.5
230170_at	OSM	oncostatin M	0.694823	10.38	8.13	10.45	9.97	9.67	6.24	10.22	8.33	10.33	6.4
236432_at	---	---	0.694823	6.5	6.24	6.44	6.62	5.52	5.07	6.13	3.3	6.76	6.81
228105_at	---	---	0.694823	7.15	5.35	4.77	5.19	4.58	4.81	6.38	5.24	6.51	7.3
212062_at	ATP9A	ATPase, class II, type 9A	0.694823	7.05	6.67	6.17	6.86	7.76	9.31	8.2	8	6.75	5.92
201975_at	CLIP1	CAP-GLY domain containing linker protein 1	0.694823	7.06	6.88	6.13	7.85	7.22	5.48	7.75	6.66	7.68	4.66
236404_at	---	---	0.694928	7.53	6.94	4.37	7.27	7.37	5.28	7.27	6.86	7.21	6.85
1553608_a_at	C21orf109	chromosome 21 open reading frame 109	0.694979	8.38	7.95	6.48	7.4	7.11	7.28	5.18	6.01	7.48	8.29
216056_at	CD44	CD44 molecule (Indian blood group)	0.695577	8.46	5.54	7.79	8.39	6.4	4	7.66	6.31	6.1	3.4
207332_s_at	TFRC	transferrin receptor (p90, CD71)	0.697797	7.12	6.52	7.81	7.4	5.98	4.92	5.37	3.36	7.28	7.13
225884_s_at	GZF1	GDNF-inducible zinc finger protein 1	0.697797	7.27	6.27	7.93	7.11	6.45	4.44	7.11	6.33	5.45	4.34
206379_at	EYA3	eyes absent homolog 3 (Drosophila)	0.697841	6.92	7.15	9.03	6.34	7.49	8.53	7.9	6.7	7.03	5.25
220701_at	---	---	0.698224	8	8.19	7.77	7.63	5.55	5.11	7.59	6.42	7.58	7.25
1554465_s_at	ZNF673 /// ZNF674	zinc finger family member 673 /// zinc finger family member 674	0.698307	7.89	8.22	7.87	7.81	7.58	8.1	7.29	5.45	7.46	5.55
238451_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	0.698798	6.63	6.27	5.37	6.56	7.39	5.04	8.45	8.28	7.09	6.01
230318_at	SERPINA1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), membe	0.699131	7.91	5.91	8.5	8.12	7.38	7.59	6.99	5.71	6.55	5.86
229303_at	---	---	0.700213	7.64	8.11	5.37	8.23	7.93	4.09	7.51	7.43	7.53	5.14
215053_at	SRCAP	Snf2-related CREBBP activator protein	0.700717	6.29	4.64	4.38	4.62	4.44	3.7	6.2	7.12	5.3	4.69
242258_at	---	---	0.700886	6.03	6.62	3.87	6.22	6.92	5.42	4.59	4.4	4.42	2.78
227609_at	EPSTI1	epithelial stromal interaction 1 (breast)	0.700886	4.34	5.68	7.25	7.76	7.9	6.46	6.17	4.45	7.23	5.84

221823_at	C5orf30	chromosome 5 open reading frame 30	0.700886	5.1	5.51	5.14	5.75	6.2	7.61	5.13	7.25	4.81	4.73
230352_at	PRPS2	Phosphoribosyl pyrophosphate synthetase 2	0.701013	3.68	3.49	4.17	5.7	5.84	6.61	5.23	6.31	5.81	7.17
230871_at	DHX30	DEAH (Asp-Glu-Ala-His) box polypeptide 30	0.701608	3.8	6.61	6.69	4.36	6.18	6.74	3.57	4.25	4.47	3.48
228071_at	GIMAP7	GTPase, IMAP family member 7	0.701901	5.58	6.84	3.76	6.01	8.13	9.53	9.15	8.96	7.15	6.64
220814_at	---	---	0.70333	9.09	8.91	5.89	8.03	6.17	7.09	7.16	6.85	8.01	4.65
243827_at	---	---	0.703767	7.07	5.13	5	6.22	3.83	3.94	6.48	4.31	6.95	4.79
1554494_at	MTHFSD	methenyltetrahydrofolate synthetase domain containing	0.703926	6.84	6.1	3.39	7.2	6.78	4.75	5.66	8.43	6.7	7.49
1554462_a_at	DNAJB9	DnaJ (Hsp40) homolog, subfamily B, member 9	0.704138	8.11	5.91	9.1	8.96	7.51	7.69	7.22	4.71	7.9	6.68
217776_at	RDH11	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	0.704138	4.19	6.55	3.8	4.81	6.73	7.1	6.43	7.35	5.92	6.23
201419_at	BAP1	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	0.704409	5.87	5.61	6.44	5.71	5.42	5.91	5.87	10.22	6.95	5.74
216033_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.704504	5.18	4.84	4.19	5.96	5.51	6.44	8.02	7.16	5.87	5.34
214452_at	BCAT1	branched chain aminotransferase 1, cytosolic	0.704507	6.22	6.32	4.29	6.86	3.22	3.82	4.63	6.75	6	6.67
209728_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	0.70515	5.07	6.8	9.87	9.22	7.88	10.28	8.58	9.38	6.63	6.4
232931_at	SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)	0.70515	5.35	4.42	7.2	6.74	4.54	6.32	4.84	8.01	5.74	8.09
230075_at	RAB39B	RAB39B, member RAS oncogene family	0.70515	5.63	6.92	7.46	4.71	6.17	5.6	7.51	6.28	5.19	4.34
216062_at	---	---	0.705928	8.7	6.48	8.07	8.93	6.62	5.28	8.18	6.78	6.71	4.07
227701_at	C10orf118	chromosome 10 open reading frame 118	0.705928	7.32	7.41	4.17	6.49	7.47	5.36	6.63	6.44	5.73	3.58
229327_s_at	---	---	0.706697	6.01	5.51	3.76	6.69	7.22	7.34	7.7	5.44	4.29	4.48
212690_at	DDHD2	DDHD domain containing 2	0.706728	3.64	5.08	2.34	3.04	6.25	3.87	6.62	4.01	4.37	6.64
1562307_at	---	---	0.707805	8.5	6.92	5.2	6.91	6.63	5.74	7.45	5.83	6.01	5.39
205733_at	BLM	Bloom syndrome, RecQ helicase-like	0.708249	5.31	5.26	6.26	6.15	6.3	8.42	5.85	6.35	6.49	9.08
209629_s_at	NXT2	nuclear transport factor 2-like export factor 2	0.708274	6.8	4.82	6.2	6.48	7.15	8.37	6.5	7.87	5.84	5.4
213956_at	CEP350	centrosomal protein 350kDa	0.708318	7.16	7.68	4.37	6.66	6.19	4.12	5.69	4.79	6.84	5.98
228570_at	BTBD11	BTB (POZ) domain containing 11	0.708434	6.16	6.17	3.45	4.93	5.23	3.87	5.58	3.05	6.55	6.18
200855_at	C20orf191 /// LOC100133918 /// NCOR1	chromosome 20 open reading frame 191 /// similar to nuclear receptor co-represso	0.708593	7.32	6.93	4.76	7.02	7.43	5.82	7.28	8.52	7.85	4.24
217828_at	SLTM	SAFB-like, transcription modulator	0.708593	7.92	8.08	5.19	7.36	8.12	5.76	7.63	7.15	7.59	5.92
208003_s_at	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	0.708593	6.07	5.54	6.08	7.34	5.83	6.5	6	3.19	7.11	5.87
226170_at	EYA3	eyes absent homolog 3 (Drosophila)	0.708714	7.74	7.99	7.32	6.72	7.16	6.86	7.58	6.76	7.54	3.91
243559_at	---	---	0.708714	6.27	6.14	4.55	4.88	3.97	4.28	6.04	3.61	6.09	6.37
1557719_at	PIKFYVE	phosphoinositide kinase, FYVE finger containing	0.708982	7.58	6.73	5.7	6.64	6.47	6.33	6.16	5.42	8.01	4.25
205239_at	AREG	amphiregulin	0.709904	5.23	3.16	6.4	6.23	5.18	2.34	3.66	3.68	6.41	3.2
214042_s_at	RPL22	ribosomal protein L22	0.709966	8.3	9.43	7.04	8.62	9.31	11.56	10.68	10.57	9.36	9.62
1564637_a_at	FAM98B	family with sequence similarity 98, member B	0.710482	5.26	4.99	2.51	4.79	5.3	6.66	7.47	6.05	5.28	2.56
204440_at	CD83	CD83 molecule	0.711726	8.61	5.96	7.71	8.3	7.46	4.49	7.5	6.22	8.29	4.28
211657_at	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross re	0.711726	4.21	4.1	4.35	4.08	7.19	6.51	5.57	9.23	5.22	7.56
215669_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4	0.712032	3.26	4	7.1	6.42	3.91	6.16	5.81	5.77	4.26	4
244137_at	KIAA0317	KIAA0317	0.713086	5.96	4.32	4.18	6.17	4.35	3.85	5.45	4.3	6.34	6.22
214314_s_at	EIF5B	eukaryotic translation initiation factor 5B	0.713521	6.48	6.78	3.3	6.64	7.85	6.58	6.76	7.01	7.09	3.61

215533_s_at	UBE4B	ubiquitination factor E4B (UFD2 homolog, yeast)	0.714171	7.31	7.84	6.11	6.7	7.61	6.16	7.38	7.48	6.72	4.41
240941_at	ITSN2	Intersectin 2	0.714291	9.52	8.59	6.33	8.29	8.54	9.12	9.08	9.23	9.64	7.51
243751_at	---	---	0.714418	5.94	5.16	6.84	6.52	5.18	4.17	4.07	3.73	7.11	4.11
1560154_a_at	---	---	0.71492	5.69	6.66	3.42	5.71	6.25	3.93	6.91	4.28	4.56	4.06
205367_at	SH2B2	SH2B adaptor protein 2	0.714972	7.75	7.42	9.24	7.98	7.43	4.43	7.22	7.01	7.61	5.17
211986_at	AHNAK	AHNAK nucleoprotein	0.715196	7.04	7.41	6.94	7.34	8.18	8.3	10.34	9.1	7.48	6.21
212929_s_at	FAM21A /// FAM21B /// FAM21C /// FAM21D	family with sequence similarity 21, member A /// family with sequence similarity	0.715343	8.76	9.66	5.78	8.75	10.02	8.74	9.64	10.1	9.67	6.86
241891_at	---	---	0.715736	7.34	6.2	4.3	6.78	5.07	3.64	5.38	4.75	6.28	6.34
1554665_at	ZNF586	zinc finger protein 586	0.715903	7.08	6.86	4.72	6.95	5.79	4.08	6.27	5.17	5.98	5.15
212009_s_at	STIP1	stress-induced-phosphoprotein 1	0.717042	7.58	8.87	7.42	7.36	7.34	7.15	9.39	7.4	7.74	5.34
209849_s_at	RAD51C	RAD51 homolog C (S. cerevisiae)	0.717922	6.09	7.46	5.66	4.72	5.61	6.12	6.85	7.13	4.18	5.58
240050_s_at	---	---	0.718089	5.52	8.09	3.71	5.05	7.78	7.27	6.56	6.34	7.19	3.57
205101_at	CIITA	class II, major histocompatibility complex, transactivator	0.718089	5.29	8.24	3.7	5.64	7.52	7.27	7.48	5.93	8	7.78
1565868_at	CD44	CD44 molecule (Indian blood group)	0.718218	8.06	5.92	7.44	8.45	6.21	5.67	7.39	6.4	5.92	5.28
221274_s_at	LMAN2L	lectin, mannose-binding 2-like	0.718218	5.5	6.82	6.39	5.84	6.73	8.84	5.3	7.48	5.81	7.28
236384_at	---	---	0.718218	6.37	7.48	7.37	5.92	6.27	4.89	5.68	4.82	6.17	4.49
212707_s_at	LOC100133005 /// LOC100134722 /// RASA4 /// RASA4B /// RASA4P	RAS p21 protein activator 4 pseudogene /// similar to HSPC047 protein /// RAS p2	0.718218	8.4	8.8	6.11	6.14	7.18	9.05	7.91	7.4	6.64	6.34
228271_at	---	---	0.718407	7.91	7.24	5.56	7.86	6.68	5.14	6.47	5.22	7.03	4.72
208536_s_at	BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.718462	8.84	7.61	8.64	8.15	8.48	5.08	7.44	8.62	7.38	7.91
201948_at	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	0.718545	7.29	6.16	6.87	6.75	7.34	8.32	8.27	6.29	7.24	4.46
236506_at	---	---	0.718856	7.6	8.1	4.24	7.23	6.81	4.58	6.53	4.55	7.28	5.87
241249_at	LOC253039	hypothetical LOC253039	0.718962	7.95	7.8	6.83	6.78	7.11	5.46	4.81	5.43	7.29	6.7
1552485_at	LACTB	lactamase, beta	0.719202	6.19	5.03	7.69	7.04	5.5	5.1	7.81	5.76	6.58	5.33
224841_x_at	GAS5	growth arrest-specific 5 (non-protein coding)	0.719206	8.38	8.41	6.36	7.53	8.62	10.02	9.97	8.82	8.36	7.82
241331_at	SKAP2	Src kinase associated phosphoprotein 2	0.719443	6.06	6.22	7.6	5.69	4.68	6.16	4.11	4.82	5.1	6.85
243931_at	---	---	0.719897	6.8	5.47	6.24	7.11	5.5	5.35	4.95	3.65	6.91	6.18
209271_at	BPTF	bromodomain PHD finger transcription factor	0.719977	6.46	6.55	3.96	6.14	6.58	4.01	5.66	5.57	6.71	4.5
229810_at	---	---	0.720156	6.18	6.69	4.39	7.27	6.65	4.86	4.83	6.02	7.39	4.49
202890_at	MAP7	microtubule-associated protein 7	0.720456	7.5	7.93	3.67	5.61	7.38	7.68	7	6.82	8.49	8.73
218558_s_at	MRPL39	mitochondrial ribosomal protein L39	0.722011	5.62	6.64	6	5.28	7.18	4.97	7.78	4.83	5.93	3.55
211517_s_at	IL5RA	interleukin 5 receptor, alpha	0.722011	6.68	7.04	6.89	7.33	9.29	9.4	7.64	9.2	8.7	8.99
1553103_at	NFX1	nuclear transcription factor, X-box binding 1	0.722011	6.57	5.9	3.32	4.76	5.47	5.86	5.4	6.46	6.29	3.45
228416_at	ACVR2A	activin A receptor, type IIA	0.722011	6.25	5.61	4.03	6.12	6.59	3	5.92	7.18	5.57	4.37
207315_at	CD226	CD226 molecule	0.722512	4.58	3.51	4.63	6.22	6.41	9.19	7.39	7.69	6.93	6.91
204148_s_at	POMZP3 /// ZP3	POM (POM121 homolog, rat) and ZP3 fusion /// zona pellucida glycoprotein 3 (sper	0.722512	5.92	6.9	7.03	6.46	4.27	4.01	6.32	6.98	5.01	4.07
233587_s_at	SIPA1L2	signal-induced proliferation-associated 1 like 2	0.722512	8.48	8.81	7.93	9.16	8.57	6.1	8.11	7.69	8.66	6.42
206548_at	---	---	0.722915	8.43	8.23	3.45	5.99	7.06	8.12	7.93	3.83	7.84	6.22

224989_at	---	---	0.722915	5.8	4.93	5.55	7.47	5.55	5.93	7.01	6.59	6.02	3.97
204075_s_at	KIAA0562	KIAA0562	0.723454	6.69	7.17	4.63	5.87	7.8	5.74	5.81	4.97	6.63	5.21
225260_s_at	MRPL32	mitochondrial ribosomal protein L32	0.723631	4.78	5.33	4.01	4.16	5.3	6.92	6.11	7.47	4.67	5.6
216574_s_at	hCG_2024410 /// RPE	rcRPE /// ribulose-5-phosphate-3-epimerase	0.723766	6.13	6.54	5.08	6.83	7.36	7.48	7.73	9.53	7.28	8.67
223404_s_at	C1orf25	chromosome 1 open reading frame 25	0.723832	6.49	6.97	5.05	6.28	7.59	7.12	6.42	7.09	5.25	8.54
205763_s_at	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	0.723942	8.13	6.39	5.23	7.14	6.97	8.1	7.86	5.87	8.78	6.35
225925_s_at	USP48	ubiquitin specific peptidase 48	0.724064	7.29	6.67	5.47	7.16	7.21	5.16	5.75	4.31	5.87	7.59
220942_x_at	FAM162A	family with sequence similarity 162, member A	0.724309	5.64	5.72	5.14	4.65	4.92	7.64	5.86	6.47	6.79	7.37
242752_at	---	---	0.725312	5.4	7.69	3.77	5.11	7.37	7	6.69	6.34	6.98	4.45
218400_at	OAS3	2'-5'-oligoadenylate synthetase 3, 100kDa	0.725312	7.22	6.92	6.67	8.51	8.87	7.78	6.88	4.94	8.9	6.84
241590_at	---	---	0.725312	6.49	6.82	2.67	6.2	6.28	5.74	5.92	5.69	6.72	5.74
242878_at	---	---	0.725312	6.36	5.97	7.59	7.7	6.53	6.24	5.31	4.47	5.79	7.39
242482_at	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extin	0.725372	8.48	7.1	8.01	9.11	7.61	5.83	7.95	6.45	8.14	8.73
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	0.72602	8	7.13	8.58	9.4	8.47	5.72	7.87	5.9	8.61	5.58
239597_at	---	---	0.726108	6.95	4.88	5.13	5.52	5.52	8.65	5.48	4.92	7.69	6.48
212737_at	GM2A	GM2 ganglioside activator	0.726377	6.84	8.03	9.2	9.94	7.17	7.74	9.28	9.05	6.49	6.36
202605_at	GUSB	glucuronidase, beta	0.72646	8.95	9.36	6.92	6.98	9.92	8.79	8.31	9.78	9.01	10.18
210732_s_at	LGALS8	lectin, galactoside-binding, soluble, 8	0.726483	7.38	7.24	8.79	8.78	7.49	5.32	5.35	4.31	6.91	7.3
1555193_a_at	ZNF277	zinc finger protein 277	0.726852	5.92	4.97	8.87	6.38	5.33	5.95	6.81	6.08	6.39	5.33
235618_at	ZNF507	zinc finger protein 507	0.727066	6.64	5.46	3.5	4.44	6.99	4.79	6.26	6.24	5.85	5.64
212609_s_at	AKT3	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	0.727586	6.97	7.4	5.2	5.86	8.43	4.88	7.38	7.51	6.4	6.2
202566_s_at	SVIL	supervillin	0.727848	8.87	8.6	5.84	8.03	7.76	7.67	7.36	7.1	8.19	5.35
207594_s_at	SYNJ1	synaptojanin 1	0.728055	7.15	7.01	8.18	7	6.33	5.73	5.08	4.64	5.71	5.09
221830_at	RAP2A	RAP2A, member of RAS oncogene family	0.728073	4.91	4.79	4.91	5.98	5.9	5.93	6.95	8.29	6.15	5.29
216933_x_at	APC	adenomatous polyposis coli	0.72865	9.17	9.21	8.41	9.28	9.22	5.76	9.91	8.21	10.51	9.6
239811_at	---	---	0.728759	5.42	6.22	4.64	5.47	4.98	5.56	5.49	4.16	6.36	9.24
230077_at	LOC220729 /// SDHA /// SDHALP1 /// SDHALP2	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene /// succinat	0.729643	5.95	6.05	5.24	5.65	5.77	7.5	7.08	7.95	6.23	8.19
210105_s_at	FYN	FYN oncogene related to SRC, FGR, YES	0.730412	4.54	5.11	4.86	5.43	6.12	7.05	8.33	7.81	5.09	6.49
35820_at	GM2A	GM2 ganglioside activator	0.730849	6.4	7.39	8.87	9.44	7.02	7.32	8.86	8.58	5.86	5.98
1554447_at	LOC554203	alanyl-tRNA synthetase domain containing 1 pseudogene	0.730914	7.27	8.4	4.28	6.51	8.12	6.04	8.04	5.55	7.57	4.34
1565598_at	---	---	0.731012	6.72	4.98	4.85	6.84	5.55	5.1	7.04	4.36	7.08	5.27
203814_s_at	NQO2	NAD(P)H dehydrogenase, quinone 2	0.731096	7.43	7.4	9.23	9.18	9.45	10.15	7.45	7.56	9.31	9.54
209037_s_at	EHD1	EH-domain containing 1	0.73116	7.62	7.22	9.82	8.25	7.92	7.03	7.63	5.83	8.63	5.99
201540_at	FHL1	four and a half LIM domains 1	0.73116	3.25	2.13	2.99	4.48	3.73	7.54	7.02	7.96	4.24	2.66
53202_at	C7orf25	chromosome 7 open reading frame 25	0.73116	5.96	7.15	4.83	5.51	7.51	8.16	7.57	7.99	7.16	6.58
228826_at	---	---	0.73116	4.94	5.07	5.35	5.99	6.4	7.99	4.3	7.43	7.3	7.32
235858_at	CREBBP	CREB binding protein	0.73116	8.48	7.99	7.5	7.91	7.01	5.46	7.98	7.09	7.89	5.63
212722_s_at	JMJD6	jumonji domain containing 6	0.731454	9.22	7.79	8.76	8.95	7.22	6.99	7.93	6.1	7.46	5.71
201030_x_at	LDHB	lactate dehydrogenase B	0.731613	7.71	7.32	5.47	7.62	9.4	9.58	10.62	8.82	8.42	8
241968_at	---	---	0.732032	7.3	7.92	3.53	5.52	7.36	7.23	7.16	5.15	6.79	5.03

218237_s_at	SLC38A1	solute carrier family 38, member 1	0.732278	5.99	7.17	4.27	6.48	6.34	7.24	6.81	3.97	7.1	6.16
220934_s_at	TMEM223	transmembrane protein 223	0.732278	4.12	6.99	4.39	4.44	4.31	6.13	4.4	3.77	3.69	6.19
233515_at	---	---	0.733082	6.74	6.6	6.73	7.81	6.39	6.63	5.17	4.18	7	6.98
202198_s_at	MTMR3	myotubularin related protein 3	0.733194	8.6	8.39	7.7	8.49	7.96	7.31	8.45	10.12	7.73	6.18
240983_s_at	CARS	cysteinyl-tRNA synthetase	0.733847	7.74	6.77	7.99	6.94	6.53	4.71	7.48	8.04	6.98	5.82
227527_at	MLL2	myeloid/lymphoid or mixed-lineage leukemia 2	0.734095	9.83	9.29	8.67	9.42	9.48	8.81	9.63	9.27	10.19	6.49
225010_at	CCDC6	coiled-coil domain containing 6	0.734161	4.86	6.48	3.12	4.57	6.01	7.14	7.1	6.63	6	5.56
1552398_a_at	CLEC12A /// CLEC12B	C-type lectin domain family 12, member A /// C-type lectin domain family 12, mem	0.734921	7.4	8.14	6.64	7.19	12.7	12.33	11.86	12.12	11.33	11.6
209662_at	CETN3	centrin, EF-hand protein, 3 (CDC31 homolog, yeast)	0.734921	5.26	6.56	5.35	6.04	7.52	6.98	7.74	8.49	6.78	8.48
237137_at	SCARNA2	small Cajal body-specific RNA 2	0.734921	7.93	7.88	11.34	8.7	8.38	9.47	8.77	8.6	8.71	9.61
234843_s_at	KREMEN1	kringle containing transmembrane protein 1	0.734921	7.67	7.09	8.33	8.45	7.89	6	6.87	6.72	6.65	5.11
222881_at	HPSE	heparanase	0.73512	5.28	5.99	6.92	7.42	6.78	6.78	7.96	8.82	7.18	5.81
237753_at	---	---	0.73567	7.13	7.42	4.14	7.32	7.19	7.81	8.4	6.82	6.7	4.78
237442_at	---	---	0.735726	8.8	8.39	6.09	7.85	8.3	6.85	8.71	6.63	8.47	4.73
235000_at	---	---	0.735726	6.9	7.16	5.23	6.94	6.22	4.22	6.54	7.02	7.56	5.18
235764_at	---	---	0.735777	7.37	7.92	7.13	7.19	8.51	5.68	7.05	7.55	5.95	8.93
227761_at	MYO5A	myosin VA (heavy chain 12, myoxin)	0.735971	7.44	7.15	4.27	6.88	6.95	5.46	6.55	5.1	7.06	4.11
45653_at	KCTD13	potassium channel tetramerisation domain containing 13	0.736192	6.36	7.09	7.14	6.86	6.88	7.45	6.01	5.66	7.39	9.43
235350_at	C4orf19	chromosome 4 open reading frame 19	0.736442	6.3	3.13	3.19	3.98	5.61	8.16	6.13	4.05	6.55	4.47
225741_at	THUMPD3	THUMP domain containing 3	0.736511	6.9	6.5	4.24	7.36	7.52	5.32	8.13	4.76	7.71	7.29
240544_at	---	---	0.736723	6.17	5.43	2.64	6.18	2.97	2.85	6.07	4.42	6.5	4.31
201033_x_at	RPLP0	ribosomal protein, large, P0	0.736736	6.61	7.89	4.44	6.85	8.15	9.86	9.41	8.72	7.07	8.4
205001_s_at	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	0.73711	6.12	5.45	5.86	5.61	8.8	7.97	8.76	7.69	9.3	7.64
219014_at	PLAC8	placenta-specific 8	0.73711	6.99	8.45	8.41	7.07	8.44	9.41	9.26	10.37	7.79	8.71
201028_s_at	CD99	CD99 molecule	0.73711	6.36	6.34	5.3	6.49	7.06	9.03	8	8.07	5.97	6.23
1557078_at	SLFN5	schlafen family member 5	0.737612	6.22	6.08	4.13	6.17	6.62	5.58	6.95	4.11	5.79	4.21
214948_s_at	TMF1	TATA element modulatory factor 1	0.737612	5.22	4.66	3.61	4.37	4.12	7.07	4.72	6.03	4.68	6.05
204627_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.738268	6.39	4.63	6.17	8.33	8.74	12.15	11.03	11.94	9.98	10.58
243358_at	IGF1R	insulin-like growth factor 1 receptor	0.738268	6.32	6.28	6.39	6.9	4.64	4.16	5.14	4	6.3	6.24
215177_s_at	ITGA6	integrin, alpha 6	0.73838	7.02	7.65	4.4	7.08	8.51	8.22	8.1	7.07	7.89	5.54
1556865_at	---	---	0.738423	8.7	6.91	8.02	8.08	4.57	5.25	6.79	4.32	7.12	7.67
1555387_at	UBA1	ubiquitin-like modifier activating enzyme 1	0.73854	4.86	3.08	7.88	5.3	4.35	8.18	3.89	8.27	4.6	5.11
216112_at	---	---	0.73854	7.52	6.67	4.68	6.65	5.41	5.26	5.5	5.88	8.01	4.95
222417_s_at	SNX5	sorting nexin 5	0.73907	6.32	6.68	2.96	6.04	7.18	8.16	5.96	6.85	7.64	6.75
215343_at	CCDC88C	coiled-coil domain containing 88C	0.739496	4.01	6.27	5.28	4.15	3.65	7.81	4.16	6.51	3.58	4.2
1563118_at	---	---	0.740397	5.31	5.64	5.45	6.64	6.6	3.84	5.35	4.46	6.35	3.45
1557100_s_at	HECTD1	HECT domain containing 1	0.740397	7.59	6.58	3.72	5.9	5.66	6.41	6.01	5.66	5.66	4.22
204938_s_at	PLN	phospholamban	0.740542	5.92	3.56	3.28	5.83	6.16	6.42	6.88	4.09	6.6	4.04
218649_x_at	SDCCAG1	serologically defined colon cancer antigen 1	0.740678	7.92	8.39	5.79	7.3	7.72	8.48	8.16	5.28	7.78	6.14
1559911_at	---	---	0.740872	7.76	5.32	6.18	6.33	5.12	6.28	6.69	5.27	7.52	3.91
207389_at	GP1BA	glycoprotein Ib (platelet), alpha polypeptide	0.740972	6.32	5.99	6.74	5.96	7.63	9.29	7.63	8.61	7.86	8.28

235281_x_at	AHNAK	AHNAK nucleoprotein	0.741209	7	7.43	5.31	6.99	7.69	7.59	9.63	8.64	7.83	5.37
232366_at	KIAA0232	KIAA0232	0.741357	5.14	4.39	6.92	6.16	4.97	2.57	4.41	2.33	5	6.18
222023_at	AKAP13	A kinase (PRKA) anchor protein 13	0.741357	7.37	5.44	6.5	6.26	4.93	4.34	6.08	4.38	4.72	4.49
214048_at	MBD4	methyl-CpG binding domain protein 4	0.742084	7.39	5.47	4.75	6.62	6.13	3.62	3.85	4.26	5.77	6.61
219108_x_at	DDX27 /// SS18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 /// synovial sarcoma translocation, ch	0.74285	8.64	8.27	5.19	7.39	8.32	7.62	7.71	8.27	8.46	6.74
208962_s_at	FADS1	fatty acid desaturase 1	0.742869	4.16	4.3	4.7	4.93	5.28	7.02	7.27	5.49	6.03	4.08
1553162_x_at	C19orf55	chromosome 19 open reading frame 55	0.743237	8.95	8.85	8.39	9.23	9.42	8.15	7.72	7.76	8.7	5.53
227080_at	ZNF697	zinc finger protein 697	0.743947	6.32	6.1	3.85	3.79	5.43	6.86	5.02	5.77	4.39	2.94
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0.744199	8.2	4.94	9.21	9.5	7.34	5.78	8.26	6.31	8.34	7.82
200788_s_at	PEA15	phosphoprotein enriched in astrocytes 15	0.744199	6.54	7.96	6.71	6.79	8.47	9.87	9.52	10.06	7.46	7.03
1557820_at	AFG3L2	AFG3 ATPase family gene 3-like 2 (yeast)	0.744221	5.76	7.07	4.46	4.5	6.29	7.54	4.96	7.58	4.77	4.93
223681_s_at	INADL	InaD-like (Drosophila)	0.744722	2.99	4.28	2.88	4.2	6	2.58	5.61	8.13	4.04	6.04
215361_at	---	---	0.744722	9.04	8.78	5.01	7.83	7.94	5.32	8.44	6.1	8.89	6.42
212780_at	SOS1	son of sevenless homolog 1 (Drosophila)	0.744722	6.43	7.15	3.54	5.37	5.61	3.75	6.1	5.55	5.44	3.79
238190_at	TUFM	Tu translation elongation factor, mitochondrial	0.744722	4.84	6.69	4.43	5.47	4.65	4.4	7.32	4.32	6.17	4.25
1558882_at	LOC401233	similar to HIV TAT specific factor 1; cofactor required for Tat activation of HI	0.744835	7.35	6.54	6.18	7.88	6.46	5.45	3.74	5.25	5.58	5.1
211972_x_at	RPLP0	ribosomal protein, large, P0	0.745149	6.8	7.9	4.46	6.85	8.46	10.08	9.4	8.84	7.09	8.36
243319_at	---	---	0.745752	5.53	3.39	6.61	4.16	5.97	3.95	2.9	7.56	4.61	6.38
242706_s_at	MED23	mediator complex subunit 23	0.745752	6.92	5.67	3.65	6.03	6.32	7.54	5.35	5.4	6.07	4.81
201294_s_at	WSB1	WD repeat and SOCS box-containing 1	0.745752	8	8.68	9.51	8.76	7.46	7.53	6.49	6.7	8.58	9.16
1568836_at	CLK4	CDC-like kinase 4	0.745887	6.19	7.44	8.45	7.72	5.68	7.55	6.29	7.86	6.95	9.05
221919_at	HNRNPA1 /// LOC728844	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC728844	0.747876	7.53	8.03	5.05	5.52	4.65	5.7	6.4	7.01	4.83	7.68
211720_x_at	RPLP0	ribosomal protein, large, P0	0.748355	6.79	7.85	4.68	6.94	8.11	9.72	9.33	8.51	7.04	8.37
1563560_at	AHNAK	AHNAK nucleoprotein	0.748616	7.16	7.93	6.33	7.63	8.53	8.97	10.21	9.18	8.07	3.56
1570151_at	---	---	0.748668	7.32	7.1	7.3	7.36	6.91	4.66	5.48	4.52	7.62	7.03
1559881_s_at	ZNF12	zinc finger protein 12	0.748668	7.9	8.12	5.13	6.28	6.72	6.94	6.06	7.69	6.98	5.25
217388_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	0.749017	3.48	5.54	4.34	3.39	5.83	6.59	7.63	8.04	4.54	4.15
1565000_a_at	TCP11L2	T-complex 11 (mouse)-like 2	0.749017	8.8	8.1	9.82	8.13	7.57	6.31	7.54	7.73	7.28	10.18
238343_x_at	---	---	0.749354	6.88	4.18	6.71	7.19	4.4	5.84	5.22	5.08	6.27	4.51
236937_at	VPS8	Vacuolar protein sorting 8 homolog (S. cerevisiae)	0.75063	5.82	4.9	6.43	6.78	4.72	6.96	5.64	3.82	4.24	7.44
1568012_at	CLIP1	CAP-GLY domain containing linker protein 1	0.75063	7.01	7.11	4.65	6.58	6.68	4.78	6.33	5.47	5.54	2.32
241073_at	---	---	0.750799	6.26	5.72	6.42	5.19	4.62	4.67	5.13	7.47	6.92	4.38
1556204_a_at	ZNF814	Zinc finger protein 814	0.751267	7.46	6.89	3.9	7.36	6.48	4.73	7.09	6.31	7.34	3.69
220960_x_at	RPL22	ribosomal protein L22	0.751267	10.09	11.29	9.13	10.35	11.59	12.5	12.18	12.02	11.71	11.53
1555241_at	C8orf59	chromosome 8 open reading frame 59	0.751467	4.41	3.81	4.42	6.09	4.24	5.37	6.5	6.54	6.03	6.76
1554311_a_at	SUPT6H	suppressor of Ty 6 homolog (S. cerevisiae)	0.752202	8.72	9.08	6.72	8.44	8.54	6.3	8.44	8.53	8.88	9.77
209258_s_at	SMC3	structural maintenance of chromosomes 3	0.752305	10.8	10.97	7.19	9.63	10.96	10.11	10.81	10.36	10.42	9
238439_at	ANKRD22	ankyrin repeat domain 22	0.752462	4.89	5.42	8.17	8.06	6.53	5.06	7.05	7.37	4.99	6.81
236899_at	LOC729397	hypothetical LOC729397	0.752476	3.92	4.03	6.82	5.12	4.42	5.1	7.38	4.01	5.23	6.83

239761_at	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltran	0.752645	5.94	7.03	6.7	5.19	8.26	5.81	7.01	8.03	6.87	8.73
217760_at	TRIM44	tripartite motif-containing 44	0.752951	4.33	5.32	4.1	4.35	4.5	7.01	6.17	7.2	4.48	5.28
214749_s_at	ARMCX6 /// LOC653354	armadillo repeat containing, X-linked 6 /// hypothetical LOC653354	0.753176	5.98	6.75	3.38	7.24	8.59	10.3	7.74	8.96	7.85	3.34
241940_at	---	---	0.753925	7.44	7.67	5.44	7.71	6.99	6.78	7.41	6.63	7.59	4.03
222040_at	HNRNPA1 /// LOC728844	heterogeneous nuclear ribonucleoprotein A1 /// hypothetical LOC728844	0.754572	8.83	9.24	7.08	6.07	7.58	7.17	5.52	6.26	6.52	7.59
233375_at	EFCAB2	EF-hand calcium binding domain 2	0.754572	5.86	4.52	7.91	6.56	5.22	6.87	4.01	5.37	6.44	3.57
1560854_s_at	ZNF107	zinc finger protein 107	0.754572	8.85	8.53	5.59	7.35	7.14	6.17	6.39	6.24	8.12	6.75
216328_at	SIGLEC8	sialic acid binding Ig-like lectin 8	0.754572	5.58	8.64	6.3	4.82	7.3	7.49	5.66	5.77	5.94	5.81
239052_at	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1	0.754572	7.28	6.61	6.15	6.61	5.61	3.04	5.82	6.27	5.45	5.5
208913_at	GGA2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	0.754691	6.35	8.56	5.86	7.17	8.43	8.72	8.11	8.96	8.1	8.25
242974_at	CD47	CD47 molecule	0.75496	5.21	4.91	5.18	4.04	5.66	7.03	4.76	4.38	6.42	7.53
217457_s_at	RAP1GDS1	RAP1, GTP-GDP dissociation stimulator 1	0.755069	4.06	7.53	4.42	4.88	6.25	7.5	6.65	6.67	6	5.99
225622_at	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	0.755207	8.29	8.06	7.87	8.6	7.06	4.13	8.44	8.28	7.38	6.68
238677_at	WDR36	WD repeat domain 36	0.755366	5.16	4.42	3.53	5	6.22	5.82	6.09	5.93	6.27	7.74
242713_at	---	---	0.755409	6.82	6.32	7.37	8.51	5.72	4.32	5.9	5.15	6.19	7.71
239188_at	PPP2R3C	protein phosphatase 2 (formerly 2A), regulatory subunit B'', gamma	0.755527	6.13	4.95	5.07	7.37	4.68	4.45	6.14	7.24	6.38	5.79
205000_at	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	0.75567	3.98	3.94	3.76	3.57	8.2	6.68	8.42	6.71	8.92	6.69
208856_x_at	RPLP0	ribosomal protein, large, P0	0.755781	6.77	7.89	5.07	6.76	8.19	9.78	9.27	8.71	7.02	8.31
208697_s_at	EIF3E	eukaryotic translation initiation factor 3, subunit E	0.757124	7.55	8.81	7.6	8.23	9.23	10.57	10.18	9.87	8.93	9.22
201348_at	GPX3	glutathione peroxidase 3 (plasma)	0.757478	10.2	9.03	8.01	10.36	9.37	8.99	8.13	6.53	9.19	8.21
203080_s_at	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	0.757658	8.94	7.65	7.15	8.99	8.18	7.25	7.84	4.88	8.77	8.66
211698_at	EID1	EP300 interacting inhibitor of differentiation 1	0.757716	5.63	6.54	3.95	4.94	7.47	7.21	7.84	7.36	5.7	8.41
215046_at	C2orf67	chromosome 2 open reading frame 67	0.75785	6.79	8.07	4	6.92	7.57	4.75	6.56	6.01	5.78	4.33
241774_at	---	---	0.75785	8.42	8.58	5.79	8.07	8.18	4.9	7.75	7.74	8.15	8.05
218306_s_at	HERC1	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-	0.75785	7.38	7.96	5.36	6.7	7.07	7.09	6.37	6.64	7.78	4.47
203629_s_at	COG5	component of oligomeric golgi complex 5	0.75785	6.12	6.07	2.88	5.67	4.72	5.27	6.44	4.82	5.42	5.85
1563075_s_at	---	---	0.757906	6.51	6.19	3.54	7.12	6.85	4.26	4.82	4.38	6.34	4.91
220696_at	---	---	0.757906	6.4	6.2	6.54	6.57	6.17	6.29	6.51	6.44	6.49	9.97
218754_at	NOL9	nucleolar protein 9	0.758243	6.63	7.58	3.94	4.57	6.51	6.52	6.32	6.4	5.79	4.7
242161_at	---	---	0.75851	6.67	6.87	4.36	6.27	5.88	4.92	5.23	3.45	4.86	6.98
221775_x_at	RPL22	ribosomal protein L22	0.758709	9.99	11.28	9.33	10.44	11.53	12.66	12.41	12.17	11.81	11.46
1556285_s_at	PPA2	pyrophosphatase (inorganic) 2	0.75898	5.6	5.24	7.82	5.79	5.9	7.85	5.41	7.43	5.61	6.04
233700_at	---	---	0.75904	7.26	7.24	6.21	5.99	5.8	5.43	7.34	7.01	7.55	4.02
202581_at	HSPA1A /// HSPA1B	heat shock 70kDa protein 1A /// heat shock 70kDa protein 1B	0.759705	9.16	9.83	8.13	8.82	11.67	11.07	10.08	10.32	9.26	7.42
210112_at	HPS1	Hermansky-Pudlak syndrome 1	0.759705	5.73	5.11	6.12	6.24	6.5	4.64	6.95	4.39	6.26	8.41

243514_at	---	---	0.759725	7.59	7.77	5.23	7.75	6.97	4.62	7.6	5.11	7.2	5.35
233655_s_at	HAUS6	HAUS augmin-like complex, subunit 6	0.759725	7.41	7.33	5.13	4.88	7.54	6.51	7.36	6.36	5.63	7.13
229221_at	CD44	CD44 molecule (Indian blood group)	0.76021	6.9	4.39	6.17	7.5	6.29	4.2	7.2	6.42	5.4	3.79
206978_at	CCR2	chemokine (C-C motif) receptor 2	0.76021	4.51	5.64	3.82	3.79	5.85	8.65	7.58	9.06	5.62	4
207075_at	NLRP3	NLR family, pyrin domain containing 3	0.76021	5.57	5.67	6.45	7.27	6.87	6.98	7.19	8.18	8.33	9.11
242590_at	---	---	0.76021	6.7	7.93	3.5	4.56	6.08	6.63	5.59	6.86	4.03	7.71
220369_at	SMEK1	SMEK homolog 1, suppressor of mek1 (Dictyostelium)	0.76021	6.83	7.22	4.6	7.07	7.27	6.45	6.37	4.64	6.4	5.45
225238_at	MSI2	musashi homolog 2 (Drosophila)	0.76021	6.06	7.33	4.52	6.26	6.77	4.66	7.19	6.37	7.49	7.28
1566113_at	---	---	0.761113	6.84	6.19	4.5	4.91	4.46	6.37	6.13	4.44	7.51	5.04
212999_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.761363	7.25	8.61	7.92	7.78	4.9	5.29	7.86	8.26	4.61	3.69
33646_g_at	GM2A	GM2 ganglioside activator	0.761404	5.71	5.83	10.21	9.47	5.69	6.92	8.51	9.49	5.42	5.65
228592_at	MS4A1	membrane-spanning 4-domains, subfamily A, member 1	0.761924	2.8	7.05	2.87	2.21	5.93	6.27	5.71	6.36	3.39	4.29
230389_at	FNBP1	formin binding protein 1	0.762397	5.83	5.74	4.8	6.62	5.31	6.78	5.89	3.83	6.57	8.03
218140_x_at	SRPRB	signal recognition particle receptor, B subunit	0.762732	4.86	4.87	3.97	5.66	6.39	7.64	7.25	6.39	6.11	5.14
230779_at	TNRC6B	trinucleotide repeat containing 6B	0.762732	7.21	7.14	5.72	8.03	6.74	6.55	6.25	5.09	7.83	5.18
226264_at	SUSD1	sushi domain containing 1	0.762732	5.05	6.6	4.75	5.89	7.63	7.7	5.7	6.74	4.77	4.56
1552334_at	TRIOBP	TRIO and F-actin binding protein	0.762796	6.1	6.47	4.18	4.65	6.47	7.28	6.16	4.63	5.26	7.11
214322_at	CAMK2G	calcium/calmodulin-dependent protein kinase II gamma	0.762796	6.39	4.95	3.93	3.96	5.45	3.81	5.51	6.29	6.36	5.06
213638_at	PHACTR1	phosphatase and actin regulator 1	0.762879	8.35	6.89	10.8	10.79	8.6	5.85	8.13	8.06	9.28	7.74
209620_s_at	ABCB7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	0.762879	5.35	5.43	3.66	4.51	6.69	6.45	4.5	6.39	5.89	8.15
201029_s_at	CD99	CD99 molecule	0.762966	6.66	4.67	6.1	6.79	7.22	9.66	8.8	9.23	6.88	8.26
205898_at	CX3CR1	chemokine (C-X3-C motif) receptor 1	0.763128	6.1	6.63	4.55	7.39	7.53	9.09	8.47	7.77	7.32	7.01
1570566_at	---	---	0.763153	5.92	5.6	2.98	6.98	7.2	4.51	5.63	6.07	5.77	2.79
219293_s_at	OLA1	Obg-like ATPase 1	0.76324	5.65	4.96	4.35	5.71	5.31	7.33	7.17	6.46	4.02	6.81
212216_at	PREPL	prolyl endopeptidase-like	0.76324	4.89	5.93	3.3	4.8	6.14	4.92	6.02	7.07	5.25	5.38
201957_at	PPP1R12B	protein phosphatase 1, regulatory (inhibitor) subunit 12B	0.76328	8.08	7.86	6.25	7.54	7.5	3.9	5.93	6.46	7.29	4.77
240288_at	KCNRG	potassium channel regulator	0.76328	7.85	8.44	5.06	8.01	6.75	6.03	7.96	7.26	7.98	7.24
201908_at	DVL3	dishevelled, dsh homolog 3 (Drosophila)	0.763486	6.64	7.42	6.44	5.92	7.29	4.04	5.3	6.4	7.02	4.07
222047_s_at	SRRT	serrate RNA effector molecule homolog (Arabidopsis)	0.763648	7.35	7.33	6.1	6.25	5.83	4.49	7.3	7.2	7.12	5.26
200982_s_at	ANXA6	annexin A6	0.763664	5.91	6.24	4.2	5.21	7.1	6.76	6.39	7.59	5.19	5.54
1552423_at	ETV3	ets variant 3	0.763772	6.89	5.64	7.76	5.01	5.12	4.65	4.89	5.37	6.59	4.68
216605_s_at	CEACAM21	carcinoembryonic antigen-related cell adhesion molecule 21	0.763986	3.6	4.64	6.85	6.5	6.13	6.92	4.39	3.71	5.95	7.94
1562028_at	CCND3	Cyclin D3	0.763986	6.29	5.42	4.83	5.24	3.54	4.06	3.9	4.25	7.11	7.87
206059_at	ZNF91	zinc finger protein 91	0.764022	6.58	6.58	3.62	5.56	5.88	7.36	7.03	6.07	4.24	2.25
208768_x_at	RPL22	ribosomal protein L22	0.76434	9.98	11.18	9.19	10.32	11.43	12.58	12.35	12.06	11.76	11.47
208691_at	TFRC	transferrin receptor (p90, CD71)	0.764344	5.23	4.5	7.98	7.27	7.14	5.84	5.7	6.84	7.51	4.4
223168_at	RHOU	ras homolog gene family, member U	0.764631	5.12	6.26	3.13	4.27	5.6	6.58	6.05	6.92	4.31	6.68
213064_at	ZC3H14	zinc finger CCCH-type containing 14	0.764631	6.31	4.98	2.89	6.39	7.55	6.98	6.71	6.6	6.56	4.14
219551_at	EAF2	ELL associated factor 2	0.764631	6.43	5.32	7.89	7.03	7.39	5.18	6.24	7.13	5.81	8.32

231968_at	UGCGL1	UDP-glucose ceramide glucosyltransferase-like 1	0.764944	7.61	7.47	4.31	7.01	8.32	5.21	6.6	6.54	7.3	5.48
222407_s_at	ZFP106	zinc finger protein 106 homolog (mouse)	0.764953	10.44	11.19	7.68	9.52	9.91	8.35	10.04	9.69	9.94	9.1
205218_at	POLR3F	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	0.76514	5.91	5.59	3.8	5.9	6.44	7.4	6.16	8.16	6.74	5.94
214167_s_at	RPLP0 /// RPLP0P6	ribosomal protein, large, P0 /// ribosomal protein, large, P0 pseudogene 6	0.765619	5.35	6.56	4.63	5.56	7.09	8.7	8	7.73	5.86	6.82
240656_at	---	---	0.765982	6.68	3.62	5.27	6.37	4.48	4.72	5.07	9.38	5.84	7.02
224629_at	LMAN1	lectin, mannose-binding, 1	0.766278	5.99	3.8	3.74	4.07	5.74	5.71	7	6.51	6.55	5.35
205483_s_at	ISG15	ISG15 ubiquitin-like modifier	0.766475	7.94	7.81	9.48	9.13	9.26	9.73	7.21	7.75	9	10.3
1570507_at	SFRS2IP	Splicing factor, arginine/serine-rich 2, interacting protein	0.766475	6.23	5.87	3.53	6.16	4.9	4.91	5.15	4.92	6.48	7.2
231907_at	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2 (arg, Abelson-related gen	0.766489	6.29	7.31	3.87	6.16	6.74	4.48	6.69	4.93	5.45	3.97
224038_at	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	0.766523	6.27	7.48	6.62	6.83	6.73	7.8	4.32	6.56	4.66	7.46
208836_at	ATP1B3	ATPase, Na+/K+ transporting, beta 3 polypeptide	0.768242	5.49	6.18	3.98	6.34	7.62	7.74	8	8.63	6.13	5.33
219563_at	C14orf139	chromosome 14 open reading frame 139	0.768372	7.83	8.1	4.14	7.37	7.82	6.5	7.75	7.57	7.9	7.41
223392_s_at	TSHZ3	teashirt zinc finger homeobox 3	0.76869	9.75	9.36	7.36	7.93	8.87	6.72	8.21	8	8.08	5.92
213747_at	LOC100134128	similar to hCG15011	0.768934	7.93	7.82	10.31	9.67	7.73	8.82	7.07	6.95	7.89	9.3
204180_s_at	ZBTB43	zinc finger and BTB domain containing 43	0.768934	7.52	7.68	4.27	7.29	6.71	6.21	7.8	6.75	6.8	7.11
1556060_a_at	ZNF451	zinc finger protein 451	0.769098	6.5	8.08	4.54	5.85	5.41	6.37	6.66	3.77	7.21	8.23
235493_at	---	---	0.769103	6.89	6.32	4.27	6.59	5.9	6.3	4.89	4.06	6.47	4.64
225953_at	RPRD1A	regulation of nuclear pre-mRNA domain containing 1A	0.76913	3.63	4.47	4.33	4.84	5.7	6.57	6.16	6.51	4.63	6
231343_at	---	---	0.769347	6.75	7.02	7.09	8.09	8.03	4.98	7.74	7.54	8.79	4.42
1557582_at	BIN3	bridging integrator 3	0.769394	7.79	6.72	8.97	6.98	3.93	3.63	5.41	5.12	5.08	4.64
225551_at	C1orf71	chromosome 1 open reading frame 71	0.769395	5.52	5.64	6.68	6.73	6.32	9.38	6.64	6.3	6.44	6.93
213605_s_at	LOC100134401 /// LOC100272216	hypothetical protein LOC100134401 /// hypothetical LOC100272216	0.770122	8.54	7.95	7.81	9.15	7.81	5.51	8.23	8.87	8.77	6.64
1554744_at	CARD16	caspase recruitment domain family, member 16	0.770185	4.55	5.79	5.7	7.36	6.97	6.24	8.52	8.06	6.77	8.53
223400_s_at	PBRM1	polybromo 1	0.770553	5.43	6.96	4.18	4.94	5.32	5.72	6.14	6.52	5.36	2.26
201694_s_at	EGR1	early growth response 1	0.770631	8.62	8.23	9.16	9.38	10.25	8.71	11.19	10.91	12.08	6.39
230588_s_at	LOC285074	anaphase promoting complex subunit 1 pseudogene	0.770821	8.18	8.48	8.35	8.01	6.75	5.47	7.84	5.47	7.51	6.76
1567559_s_at	TREML4	triggering receptor expressed on myeloid cells-like 4	0.771342	6.8	5.29	5.41	7.17	3.96	3.77	6.58	6.86	6.37	3.4
223773_s_at	SNHG12	small nucleolar RNA host gene 12 (non-protein coding)	0.771342	5.96	6.28	4.68	4.21	4.91	5.86	5.84	4.28	6.1	7.78
222697_s_at	ABHD10	abhydrolase domain containing 10	0.771517	4.75	5.74	3.91	4.76	7.85	8.72	5.37	6.71	4.44	5.9
227404_s_at	EGR1	Early growth response 1	0.771961	9.17	8.46	10.12	10.14	10.69	9.64	11.82	11.46	12.66	6.55
244765_at	---	---	0.771961	6.69	6.52	3.93	6.96	6.8	7.04	7.8	6.56	5.88	6.64
222566_at	SUV420H1	suppressor of variegation 4-20 homolog 1 (Drosophila)	0.772404	5.17	6.79	4.67	5.62	7.08	6.09	5.49	8.33	5.82	7.41
229980_s_at	SNX5	sorting nexin 5	0.772973	6.89	6.93	2.91	5.9	8.35	9.3	7.94	8.83	7.11	8.17
1569013_s_at	LOC727914 /// LOC96610	BMS1-like, ribosome assembly protein (yeast) pseudogene /// BMS1 homolog, riboso	0.773197	7.75	7.78	6.36	8.29	7.99	6.49	7.38	7.3	5.07	3.79
244358_at	---	---	0.773364	7.16	3.2	4.5	7.06	4.83	3.21	5.6	5.28	7.85	7.92
203962_s_at	NEBL	nebulette	0.773447	7.39	7.51	3.77	4.13	3.59	3.6	7.23	7.21	4.01	4.08
1555759_a_at	CCL5	chemokine (C-C motif) ligand 5	0.773447	8.33	6.15	8.38	9.87	9.51	12.84	11.3	11.68	8.34	9.49

243032_at	---	---	0.774406	7.4	5.95	3.47	6.24	5.81	2.81	6.5	3.75	7.77	7.09
1554595_at	SYMPK	symplekin	0.774475	8.05	6.37	5.09	4.98	4.94	4.4	6.08	5.2	6.65	4.61
209711_at	SLC35D1	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual tra	0.774545	4.41	4.9	3.71	6	6.32	6.23	6.75	4.43	4.9	3.7
214351_x_at	RPL13	ribosomal protein L13	0.774576	6.75	7.55	5.63	6.73	7.88	9.01	8.66	8.34	7.11	7.87
233893_s_at	KIAA1530	KIAA1530	0.7747	6.98	5.04	6.43	7.09	5.95	5.47	5.08	3.82	7.26	5.84
208095_s_at	SRP72	signal recognition particle 72kDa	0.775832	8.22	8.41	6.28	7.85	9	8.16	8.39	9.03	7.98	5.87
209480_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.77646	8.04	8.93	8.07	8.19	2.83	2.81	7.64	7.75	2.61	3.56
231715_s_at	PYCR2	pyrroline-5-carboxylate reductase family, member 2	0.77646	4.82	4.75	6.31	5.29	6.66	6.46	5.49	8.12	5.67	8.55
242239_at	---	---	0.776771	6.88	5.46	7.59	4.32	5.84	8.3	5.65	8.55	7.43	7.29
223042_s_at	FUNDC2	FUN14 domain containing 2	0.77713	5.75	7.24	4.44	5.95	7.74	7.37	7.88	7.32	6.26	6.35
1552536_at	VTI1A	vesicle transport through interaction with t-SNAREs homolog 1A (yeast)	0.77713	6.11	3.87	4.59	4.93	4.04	5.33	4.59	4.2	7	6.51
204182_s_at	ZBTB43	zinc finger and BTB domain containing 43	0.77751	6.62	6.46	5.6	5.71	6.6	4.37	6.96	2.97	7.79	5.96
218224_at	PNMA1	paraneoplastic antigen MA1	0.77751	5.51	5.17	3.6	5.51	5.88	7.57	6.99	7.21	6.18	6.79
229041_s_at	---	---	0.77751	8.47	7.23	9.21	9.5	8.42	6.15	7.36	7.61	8.27	10.1
227631_at	---	---	0.777546	4.91	5.26	5.34	5.21	6.54	7.58	7.19	5.82	4.82	6.89
238935_at	RPS27L	ribosomal protein S27-like	0.777881	3.99	4.81	7.53	5.61	6.79	6.47	3.73	5.98	5.23	3.83
242865_at	---	---	0.777889	7.4	6.58	4.56	5.68	5.09	5.18	7.24	6.76	7.49	6.32
230225_x_at	---	---	0.777925	5.27	3.05	2.81	4.32	3.74	6.53	4.87	3.55	6.5	6.62
1563426_a_at	LOC644613	hypothetical protein LOC644613	0.778017	4.4	6.85	6.32	4.6	4.07	5.4	5.66	6.68	4.73	4.07
214097_at	RPS21	ribosomal protein S21	0.779053	7.06	7.89	5.83	6.11	7.95	9.14	8.87	9.23	6.71	7.3
228618_at	PEAR1	platelet endothelial aggregation receptor 1	0.779849	4.46	4.82	4.78	4.91	6.1	9.31	6.94	7.28	6.18	4.96
1557051_s_at	---	---	0.779849	7.4	6.52	5.97	6.04	4.28	4.8	3.24	4.17	4.27	4.4
224698_at	FAM62B	family with sequence similarity 62 (C2 domain containing) member B	0.780028	5.54	3.61	2.94	7.58	7.53	6.35	5.65	5.44	7.02	6.76
242827_x_at	---	---	0.780028	7.53	8.43	5.87	6.82	5.76	6.08	7.52	7.73	8.16	5.54
213016_at	BBX	bobby sox homolog (Drosophila)	0.780105	6.76	7.22	4.6	7.33	7.66	8.18	6.44	6.25	7.4	4.44
235622_at	---	---	0.780741	6.19	6.11	7.69	7	5.9	7.43	6.58	4.23	6.53	7.7
1569990_at	NUDT3	nudix (nucleoside diphosphate linked moiety X)-type motif 3	0.781225	6.67	6.72	3.72	5.65	4.27	4.37	3.77	4.37	6.55	4.53
209143_s_at	CLNS1A	chloride channel, nucleotide-sensitive, 1A	0.781535	4.75	6.57	4.18	5.41	6.63	7.24	7.66	7.74	5.73	6.89
231972_at	---	---	0.782098	9.63	7.87	11.83	11.68	8.32	6.93	9.96	9.09	9.56	9.07
219159_s_at	SLAMF7	SLAM family member 7	0.782129	8.28	5.51	8.94	7.77	7.84	6.91	9.73	8.75	7.46	8.82
229520_s_at	C14orf118	chromosome 14 open reading frame 118	0.782268	7.61	7.12	7.14	7.63	7.15	4.49	7.71	7.82	7.98	8.18
223995_at	SLC12A9	solute carrier family 12 (potassium/chloride transporters), member 9	0.782303	6.39	6.26	7.46	6.46	4.04	6.07	6.12	5.21	5.73	7.89
223382_s_at	ZNRF1	zinc and ring finger 1	0.782368	6.13	6.27	7.28	4.16	7.37	6.17	7.11	7.6	6.86	5.99
1557217_a_at	FANCB	Fanconi anemia, complementation group B	0.783086	3.61	5.59	7.48	6.58	7.42	6.91	8.7	2.66	4.26	5.68
228238_at	GAS5	growth arrest-specific 5 (non-protein coding)	0.783086	6.66	6.59	3.92	5.28	5.37	6.38	7.26	6.41	6.17	7.42
211786_at	TNFRSF9	tumor necrosis factor receptor superfamily, member 9	0.783105	5.69	6.15	5.69	6.24	4.16	5.11	4.79	3.49	6.8	5.16
205048_s_at	PSPH	phosphoserine phosphatase	0.783477	4.32	5.09	4.23	3.88	6.07	6.82	6.03	6.88	6.51	7.8
236475_at	MICAL2	Microtubule associated monoxygenase, calponin and LIM domain containing 2	0.783819	8.38	7.8	7.07	7.57	6.5	5.66	7.78	6.33	8.73	8.32

244482_at	---	---	0.783927	2.23	2.24	2.75	2.49	7.17	7.07	7.64	6.77	8.11	7.95
1556643_at	LOC100128718	Hypothetical protein LOC100128718	0.783946	6.68	6.83	8.52	7.72	6.24	7.15	6.24	4.39	8.24	9.72
1554835_a_at	B3GNT5	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	0.784011	8.34	6.7	8.97	9.34	7.24	7.21	7.41	7.07	7.33	5.93
1566995_at	---	---	0.784647	6.27	4.08	3.94	6.14	3.88	4.45	4.98	4.09	6.97	3.28
226397_s_at	---	---	0.784837	8.02	6.78	9.67	9.96	6.98	5.86	7.1	5.24	7.85	6.96
223169_s_at	RHOU	ras homolog gene family, member U	0.784997	4.97	5.94	4.4	4.25	5.19	5.45	6.6	7.6	4.01	6.58
202286_s_at	TACSTD2	tumor-associated calcium signal transducer 2	0.785059	4.04	5.43	6.78	5.83	5.25	4.8	6.98	8.89	4.69	3.07
235678_at	GM2A	GM2 ganglioside activator	0.785446	5.1	5.21	7.63	7.43	5.46	5.95	6.94	6.16	4.68	4.81
228812_at	---	---	0.785675	7.65	7.58	4.68	7.39	8.14	6.51	6.59	6.6	7.67	5.13
205353_s_at	PEBP1	phosphatidylethanolamine binding protein 1	0.785675	6.77	6.11	5.71	5.59	6.85	8.26	8.74	7.74	6.4	7.37
222208_s_at	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	0.785804	8.71	7.76	5.92	7.48	8.41	7.26	7.58	7.68	8.65	5.8
239917_at	VPS8	Vacuolar protein sorting 8 homolog (S. cerevisiae)	0.785941	6.39	5.33	5.9	6.29	4.47	5.33	4.29	3.85	4.34	7.33
239179_at	---	---	0.786125	8.28	8.9	6.26	6.34	8.31	6.65	8.65	8.71	8.98	7.14
202869_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	0.786313	4.77	5.59	7.04	7.1	6.72	7.15	5.56	4.58	4.22	4.89
223947_s_at	MED23	mediator complex subunit 23	0.786313	8	8.42	4.24	6.44	8.18	5.41	7.31	6.74	7.96	8.18
204351_at	S100P	S100 calcium binding protein P	0.786428	12.02	12.04	12.41	12.26	9.49	10.18	11.83	12.11	8.98	10.1
229398_at	RAB18	RAB18, member RAS oncogene family	0.78646	7.14	7.73	6.12	6.12	7.5	7.02	7.71	6.23	8.41	9.41
228585_at	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	0.78646	6.38	6.2	6.49	7.05	5.43	4.25	5.05	5.3	6.47	3.74
1561760_s_at	LOC645513	Hypothetical LOC645513	0.786677	6.7	6.86	3.9	5.78	6.83	4.86	5.33	4.23	5.36	4.01
235306_at	GIMAP8	GTPase, IMAP family member 8	0.786804	6.6	7.77	4.52	6.51	9.23	10.1	9.92	9.85	9.53	9.28
229383_at	---	---	0.786851	4.59	7.42	5.82	4.69	6.42	7.45	6.65	7.89	6.51	4.24
230098_at	PHF20L1	PHD finger protein 20-like 1	0.786851	6.84	7.36	5.21	8	7.22	5.7	8.17	6.06	6.74	5.39
225066_at	---	---	0.787447	7.73	6.59	4.86	7	7.17	5.73	6.24	6.17	6.75	8.52
202638_s_at	ICAM1	intercellular adhesion molecule 1	0.787456	8.49	7.3	8.65	9.8	7.51	6	6.64	6.35	7.23	5.95
217523_at	CD44	CD44 molecule (Indian blood group)	0.787875	6.69	6.08	5.59	7.15	5.32	5.23	6.38	5.75	4.78	3.66
228214_at	SOX6	SRY (sex determining region Y)-box 6	0.787875	4.23	5.49	8.33	5.46	5.6	7.38	5.42	8.28	5.9	8.01
211945_s_at	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes	0.787979	7.88	7.77	6.51	8.42	9.24	10.96	10.3	9.9	9.13	8.58
220410_s_at	CAMSAP1	calmodulin regulated spectrin-associated protein 1	0.788323	6.43	6.78	3.24	4.58	5.73	4.09	6.51	7.25	6.17	4.16
210663_s_at	KYNU	kynureninase (L-kynurenine hydrolase)	0.788468	4.95	5.09	5.5	3.69	5.74	5.48	7.65	8.88	6.23	4.92
227301_at	CCT6P1 /// LOC643180	chaperonin containing TCP1, subunit 6 (zeta) pseudogene 1 /// chaperonin contain	0.788591	8.02	7.9	6.61	5.23	4.57	8.62	6.92	5.07	5.19	5.32
242130_at	---	---	0.788605	5.47	4.98	4.26	6.33	5.19	4.94	4.67	4.95	6.93	7.7
219717_at	C4orf30	chromosome 4 open reading frame 30	0.789082	5.12	3.75	3.04	6.31	4.6	5.86	4.9	3.23	6.6	6.09
225545_at	EEF2K	eukaryotic elongation factor-2 kinase	0.789082	5.41	5.26	3.58	4.25	7.06	6.6	5.7	6.03	7.08	5.65
220019_s_at	ZNF224	zinc finger protein 224	0.789107	7.2	7.19	3.55	4.89	6.58	5.61	5.93	8.32	6.41	3.78
217848_s_at	PPA1	pyrophosphatase (inorganic) 1	0.789195	5.34	5.64	6.21	6.28	6.34	8.48	7.56	7.11	6.05	5.25
242961_x_at	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	0.789228	7.87	7.81	9.93	10.26	7.86	7.52	10.61	10.65	11.16	10.44
227194_at	FAM3B	family with sequence similarity 3, member B	0.789316	4.5	3.76	4.47	4.54	8.37	6.76	3.9	3.92	7.84	8.56
1560274_at	LOC100132279 /// WTAP	hypothetical protein LOC100132279 /// Wilms tumor 1 associated protein	0.789316	5.33	3.53	6.09	6.16	5.36	3.7	5.75	3.85	6.29	6.38
225527_at	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	0.789316	6.66	7.72	4.92	5.55	7.88	7.7	7.79	8.86	7.81	7.99

239633_at	---	---	0.789316	7.07	5.88	5.89	7.19	4.78	5.1	6.03	5.53	7.21	7.84
202371_at	TCEAL4	transcription elongation factor A (SII)-like 4	0.789396	6.77	6.31	5.22	4.6	5.12	6.86	7.52	7.3	5.38	3.53
237277_at	---	---	0.789449	6.31	6.22	3.67	4.94	4.47	3.33	3.83	6.24	3.96	3.35
225890_at	C20orf72	chromosome 20 open reading frame 72	0.789821	8.28	8.8	5.37	6.73	8.58	7.5	7.23	8.51	8.44	6.44
208949_s_at	LGALS3	lectin, galactoside-binding, soluble, 3	0.789877	6.2	6.5	6.73	6.95	8.3	8.67	7.75	9.64	6.49	8.47
214711_at	GATC	glutamyl-tRNA(Gln) amidotransferase, subunit C homolog (bacterial)	0.790357	5.18	6.07	3.88	5.52	5.55	3.23	3.76	6.08	5.8	7.9
238601_at	PHKB	phosphorylase kinase, beta	0.790357	5.3	6.62	5.55	6.59	7.13	8.21	6.85	7.27	6.13	3.49
213416_at	ITGA4	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	0.790866	8.59	9.1	5.12	7.89	8.8	8.48	8.97	8.11	8.52	7.43
214129_at	PDE4DIP	phosphodiesterase 4D interacting protein	0.790967	6.76	3.67	4.22	4.98	5.4	7.92	6.48	3.91	5.55	3.87
223701_s_at	USP47	ubiquitin specific peptidase 47	0.791035	4.8	5.29	8.05	6.57	5.49	6.82	6.42	4.91	4.91	3.6
201049_s_at	RPS18	ribosomal protein S18	0.791665	9.48	10	8.79	9.81	10.96	11.85	11.75	11.36	10.41	11.36
201300_s_at	PRNP	prion protein	0.792504	5.72	6.4	3.81	5.58	6.81	7.07	7.76	7.88	5.69	5.96
227505_at	---	---	0.792504	7.8	7.92	5.27	7.58	7.86	6.35	5.63	5.81	6.53	4.13
232763_at	TLN1	Talin 1	0.792504	4.64	4.22	4.12	6.61	4.98	5.28	5.19	4.08	6.71	6.65
1558794_at	LOC728190	Hypothetical LOC728190	0.792722	7.49	7.76	6.92	7.32	7.42	6.78	6.93	7.11	4.8	3.91
208787_at	MRPL3	mitochondrial ribosomal protein L3	0.792982	3.76	4.13	4.48	5.27	5.89	7.86	7	7.93	4.77	4.96
225463_x_at	GPR89A	G protein-coupled receptor 89A	0.792982	6.82	6.07	4.15	5.22	6.68	6.84	7.28	7.35	6.94	7.04
227361_at	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	0.793021	5.26	5.91	6.65	6.4	5.63	3.34	3.59	3.44	6.32	2.66
1565860_at	---	---	0.79324	5.98	5.37	3.91	5.92	3.85	4.82	6.23	5.35	6.6	6.89
216782_at	---	---	0.793995	8.05	6.11	6.01	8.12	6.07	5.81	6.77	4.85	7.34	8.45
1562481_at	---	---	0.794064	8.24	7.2	7.98	8.42	6.97	8.42	6.5	4.85	8.96	7.53
242814_at	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.79432	5.98	6.67	7.79	6.5	5.75	3.65	4.42	5.29	5.43	5.21
228945_s_at	SLC39A8	Solute carrier family 39 (zinc transporter), member 8	0.794612	4.69	4.65	5.43	5.88	5.75	5.05	7.04	6.84	5.18	7.67
215891_s_at	GM2A	GM2 ganglioside activator	0.794748	5.35	5.93	9.81	9.39	5.66	6.2	8.64	9.07	4.91	4.33
1552788_a_at	HELB	helicase (DNA) B	0.794748	7.78	7.67	4.39	6.38	7.05	6.43	7.26	5.47	7.06	7.47
227135_at	NAAA	N-acylethanolamine acid amidase	0.794748	8.38	8.43	6.02	6.65	8.16	7.8	8.15	7.18	6.35	5.34
1554309_at	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	0.794748	7.46	6.27	6.57	7.72	6.39	3.91	5.41	7.31	6.16	7.65
237895_at	---	---	0.79484	7.54	6.96	3.54	6.07	5.36	3.14	5.48	5.08	6.69	4.06
200036_s_at	RPL10A	ribosomal protein L10a	0.796023	7.79	8.2	6.69	8.09	9.21	10.59	10.36	9.67	8.07	8.95
218281_at	MRPL48	mitochondrial ribosomal protein L48	0.796067	4.13	6.09	3.66	5.38	6.32	5.72	7.09	5.12	6.09	7.05
222163_s_at	SPATA5L1	spermatogenesis associated 5-like 1	0.796272	5.23	6.49	3.39	6.58	5.15	5.19	5.8	4.31	6.56	5.79
228901_at	CDK9	Cyclin-dependent kinase 9	0.796272	6.1	6.52	7.83	5.94	5.13	4.02	4.09	5.36	6.61	5.55
244063_at	BTN2A1	butyrophilin, subfamily 2, member A1	0.796272	6.64	7.65	3.89	5.73	6.5	5.25	5.35	5.41	5.53	5.02
201913_s_at	COASY	Coenzyme A synthase	0.796404	8.29	8.23	6.41	7.97	8.55	10.02	7.93	8.61	7.75	6.68
208968_s_at	CIAPIN1	cytokine induced apoptosis inhibitor 1	0.796404	6.55	6.07	4.16	5.83	5.6	7.47	6.97	7.3	6.19	4.6
210970_s_at	IBTK	inhibitor of Bruton agammaglobulinemia tyrosine kinase	0.796502	5.47	6.41	3.64	5.24	6.92	6.72	7.14	7.54	5.95	4.84
212256_at	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase	0.796502	8.65	9.32	6.59	7.76	8.79	5.62	8.34	8.48	7.83	8.56
202948_at	IL1R1	interleukin 1 receptor, type I	0.796758	7.13	7.09	5.31	6.7	8.53	5.65	6.05	4.9	4.83	5.47

239688_at	SMC1A	structural maintenance of chromosomes 1A	0.79708	6.58	6.58	3.45	6.75	7.3	5.88	6.45	7.57	7.26	6.2
223658_at	KCNK6	potassium channel, subfamily K, member 6	0.797624	7.73	8.21	4.41	6.54	6.85	6.14	7.14	5.95	7	6.74
1552928_s_at	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	0.798002	6.56	5.98	3.43	5.72	7.25	5.21	4.46	3.98	6.13	5.44
238598_s_at	---	---	0.798002	7.34	6.04	5.03	5.9	7.11	7.85	5.53	4.45	7.2	7.8
224675_at	MESDC2	mesoderm development candidate 2	0.79852	8.29	9.06	7.79	7.47	9.12	9.57	9.88	10.04	8.88	6.97
239648_at	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae)	0.798698	6.26	4.81	7.93	7.19	7.59	6.37	5.51	7.19	5.57	5.03
1567080_s_at	CLN6	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	0.799128	9.4	9.69	8.28	7.06	7.63	4.24	8.81	8.83	7.12	6.22
207761_s_at	METTL7A	methyltransferase like 7A	0.799128	6.59	8.67	7.41	6.12	9.59	9.81	9.6	9.81	8.72	9.45
235126_at	LQK1	hypothetical LOC642946	0.799166	5.99	7.67	3.46	6.11	7.02	5.53	7.09	7.39	7.22	6.81
1562303_at	ZKSCAN3	zinc finger with KRAB and SCAN domains 3	0.799242	5.36	4.43	5.5	4.6	5.32	7.06	7.57	6.31	6.21	6.93
228662_at	SOCS7	Suppressor of cytokine signaling 7	0.799275	6.54	5.7	4.84	5.86	6.94	9.15	7.41	5.47	7.04	6.22
203344_s_at	RBBP8	retinoblastoma binding protein 8	0.799417	6.42	5.92	3.36	5.65	6.44	2.93	5.05	6.39	6.14	2.87
222623_s_at	ZNF639	zinc finger protein 639	0.799417	6.01	6.94	4.84	7.41	6.83	4.69	6.28	4.93	5.54	7.15
209419_at	THOC5	THO complex 5	0.799443	6.55	6.38	4.28	6.11	6.58	4.09	4.79	5.38	6.04	7.03
229501_s_at	USP8	ubiquitin specific peptidase 8	0.799443	6.28	7.09	4.37	7.14	5.41	5.14	5.22	4.17	5.2	5.6
238348_x_at	---	---	0.799558	8.02	5.44	7.95	8.05	5.55	6.72	6.18	5.85	7.48	5.8
243505_at	MAP3K3	Mitogen-activated protein kinase kinase kinase 3	0.799573	6.73	7.9	4.81	5.15	6.11	4.26	6.58	6.44	7.25	5.51
221215_s_at	RIPK4	receptor-interacting serine-threonine kinase 4	0.799573	7.73	7.67	5.59	5.8	7.18	6.03	6.12	5.13	5.9	4.77
220813_at	CYSLTR2	cysteinyl leukotriene receptor 2	0.800511	7.68	8.4	3.23	6.1	8.86	8.97	7.25	8.62	8.51	6.52
213564_x_at	LDHB	lactate dehydrogenase B	0.800754	7.75	7.18	2.75	7.46	9.47	9.74	10.71	8.64	8.6	7.88
242676_at	---	---	0.801154	6.38	5.82	4.86	6.11	6.98	6.65	4.86	3.27	6.02	7.76
240146_at	---	---	0.801154	7.11	6.51	7.64	7.14	6.03	7.45	5.47	4.93	7.08	8.14
217933_s_at	LAP3	leucine aminopeptidase 3	0.801225	6.64	7.67	8.72	9.06	7.97	7.83	6.96	7.46	7.16	5.35
210538_s_at	BIRC3	baculoviral IAP repeat-containing 3	0.801317	6.27	7.29	4.63	5.01	6.61	5	6.3	6.44	6.1	4.11
214557_at	PTTG2	pituitary tumor-transforming 2	0.801317	6.35	5.62	4.13	5.72	5.35	5.13	6.85	5.97	7.58	7.54
217659_at	---	---	0.801581	7.09	6.02	3.42	6.86	6.17	2.39	6.17	6.79	7.45	5.66
212296_at	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	0.801845	5.11	4.09	3.97	5.07	7.07	5.9	7.1	7.42	4.73	6.59
202003_s_at	ACAA2	acetyl-Coenzyme A acyltransferase 2	0.801885	6.87	7.41	4.56	6.18	7.7	7.6	8.09	7.34	7.6	7.45
242004_x_at	---	---	0.803153	4.43	7.6	5.36	4.03	4.4	4.24	6.1	3.81	7.71	4.04
210825_s_at	PEBP1	phosphatidylethanolamine binding protein 1	0.803556	6.51	5.65	6.51	5.98	7.04	8.27	9.19	8.26	5.95	6.96
240054_at	---	---	0.803909	7.45	7.86	6.65	5.18	3.99	6.12	4.53	7.67	6.67	4.42
237901_at	---	---	0.803909	7.32	5.81	9.07	8.65	5.9	7.52	7.69	6.65	7.74	8.76
224977_at	C6orf89	chromosome 6 open reading frame 89	0.804172	8.6	8.48	7.71	9.01	9.17	9.91	6.66	6.23	8.47	6.51
228493_at	NKAP	NFKB activating protein	0.805943	6.21	6.44	3.12	4.84	6.42	3.58	4.99	2.73	4.96	4.02
217409_at	---	---	0.806411	7.33	7.37	5.5	7.89	6.91	6.16	7.69	7.68	7.58	4.6
235540_at	GNRH1	gonadotropin-releasing hormone 1 (luteinizing-releasing hormone)	0.806444	7.65	7.15	6.84	8.72	7.16	4.4	7.15	7.71	6.93	6.28
224795_x_at	IGK@ /// IGKC	immunoglobulin kappa locus /// immunoglobulin kappa constant	0.806446	5.45	9.24	4.74	5.93	7.91	8.3	9.43	8.32	6.58	6.51
1556186_s_at	KIAA0090	KIAA0090	0.806446	6.04	5.6	3.31	4.58	3.92	5.69	6.42	4.58	6.04	3.45

235446_at	---	---	0.806493	6.74	6.32	6.2	7.51	3.69	3.92	4.23	4	3.8	3.95
240022_at	ZC3H4	Zinc finger CCCH-type containing 4	0.806815	6.47	5.97	4.42	4.33	7.87	3.77	5.72	7.89	7.5	11.17
1558103_a_at	---	---	0.806863	7.54	7.52	6.71	7.88	6.46	5.55	5.21	4.76	6.75	3.48
1552693_at	ARL11	ADP-ribosylation factor-like 11	0.807368	5.54	6.28	4.71	6.32	5.23	7.38	4.4	4.79	4.5	3.15
1557275_a_at	---	---	0.807849	8.52	6.37	5.63	6.57	6.2	4.72	5.78	5.23	5.96	4.91
1555464_at	IFIH1	interferon induced with helicase C domain 1	0.808131	5.73	6.2	6.48	6.69	4.83	5.69	4.37	3.14	6.28	6.01
240747_at	---	---	0.808651	3.25	3.5	7.6	5.27	5.52	6.67	5.72	5.69	5.48	6.82
215485_s_at	ICAM1	intercellular adhesion molecule 1	0.808719	9.3	8.2	10.49	10.11	8.06	7.58	7.33	7.48	8.03	7.44
76897_s_at	FKBP15	FK506 binding protein 15, 133kDa	0.8088	6.04	4.93	5.39	6.66	5.66	6.07	6.6	6.2	4.54	3.29
201855_s_at	ATMIN	ATM interactor	0.809163	4.76	6.11	4.51	5.56	6.83	7.56	7.32	6.53	7.18	3.75
1559812_at	---	---	0.809439	6.52	6.57	3.95	6.2	5.14	7.76	8.25	5.97	8.83	9.06
1560169_at	---	---	0.809439	6.87	8.24	4.59	6.78	7.62	5.2	6.93	4.65	7.59	7.16
227141_at	TYW3	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	0.809449	3.77	4.18	3.98	3.63	6.21	6.2	6.01	6.36	5.79	3.68
213174_at	TTC9	tetratricopeptide repeat domain 9	0.809449	10.23	10.49	8.78	8.42	8.99	7.38	8.03	6.9	8.83	8.65
224517_at	POLR2J4	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene	0.810136	6.9	6.82	4.32	5.65	6.44	4.42	5.3	4.12	6.65	6.2
214719_at	SLC46A3	solute carrier family 46, member 3	0.810286	5.8	6.08	4.48	6.78	6.21	5.83	5.6	5.48	5.52	3.15
237076_at	NCSTN	nicastrin	0.810368	7.12	8.3	5.37	7.03	7.13	7.01	6.71	8.62	7.45	5.45
1560145_at	MKLN1	Muskelin 1, intracellular mediator containing kelch motifs	0.810368	8.43	7.13	5.44	7.74	7.05	8.08	8.34	6.8	8.86	6.64
1555315_a_at	MAK	male germ cell-associated kinase	0.81065	7.04	7.27	5.79	7.04	8.18	5.88	6.54	8.12	6.54	4.34
214157_at	GNAS	GNAS complex locus	0.810946	6.9	6.52	3.61	5.96	6.41	6.22	5.12	3.37	7.52	6.33
203542_s_at	KLF9	Kruppel-like factor 9	0.810967	4.66	4.72	6.77	4.73	6.65	8.18	7.23	6.88	6.86	5.87
224744_at	IMPAD1	inositol monophosphatase domain containing 1	0.811439	5.91	5.25	3.57	5.08	4.86	5.66	6.78	8.47	6.16	4.25
1405_i_at	CCL5	chemokine (C-C motif) ligand 5	0.811449	6.07	3.11	7.19	7.21	6	9.79	10.02	9.64	7.18	7.45
237974_at	ABHD12B	abhydrolase domain containing 12B	0.811449	7.52	5.88	3.34	5.74	5.01	7.24	4.98	4.64	6.05	3.71
209861_s_at	METAP2	methionyl aminopeptidase 2	0.811527	5.52	6.53	3.58	5.4	7.09	7.65	8.29	7.42	6.07	5.4
213526_s_at	LIN37	lin-37 homolog (C. elegans)	0.811885	7.51	7.8	4.73	7.77	6.77	7.48	6.91	7.19	7.4	8.73
235188_at	---	---	0.811955	6.65	6.97	4.22	5.7	5.65	6.02	4.95	5.83	7.43	3.95
208079_s_at	AURKA	aurora kinase A	0.81196	6.26	6.52	4.5	6.28	6.19	4.68	4.66	5.68	5.43	7.77
219913_s_at	CRNKL1	crooked neck pre-mRNA splicing factor-like 1 (Drosophila)	0.812396	6.63	6.66	3.8	7.04	7.29	5.29	6.6	6.97	6.88	6.04
225961_at	KLHDC5	kelch domain containing 5	0.812614	7.33	7.57	5.14	5.8	7.43	9.08	6.66	7.44	7.78	5.54
244572_at	KY	kyphoscoliosis peptidase	0.813659	8	7.21	9.57	9.02	6.68	7.69	6.05	8.35	8.95	9
1555301_a_at	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	0.814178	3.5	4.4	5.68	7.33	6.47	7.28	5.2	7.41	5.41	6.88
222906_at	FLVCR1	feline leukemia virus subgroup C cellular receptor 1	0.814572	5.88	3.01	3.95	6.57	6.58	5.42	4.57	6.17	6.25	6.43
218374_s_at	C12orf4	chromosome 12 open reading frame 4	0.814647	4.53	4.75	6.63	6.71	6.09	8.7	6.62	5.6	6.4	8.85
225866_at	BXDC1	brix domain containing 1	0.814656	4.59	4.71	4.47	5.44	6.54	6.23	6.6	6.47	5.16	3.84
1565838_at	---	---	0.814656	3.01	2.6	2.47	3.51	2.21	3.82	6.57	2.35	6.17	8.07
226642_s_at	NUDCD2	NudC domain containing 2	0.814656	4.93	5.25	2.87	4.31	7.02	6.1	6.14	6.77	5.96	7.11
1566549_at	---	---	0.814656	4.62	3.6	3.64	4.62	3.84	5.61	6.26	6.14	6.07	4.16
213097_s_at	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	0.814805	6.58	7.37	4.06	6.11	6.54	5.2	7.74	6.31	6.21	7.26

237798_at	---	---	0.814805	7.54	6.44	5.86	6.5	7.1	6.9	6.76	4.16	6.82	8.6
1555843_at	HNRNPM	Heterogeneous nuclear ribonucleoprotein M	0.815981	5.35	9.14	4.27	4.82	7.19	3.35	3.23	7.06	6.39	3.64
200992_at	IPO7	importin 7	0.816316	5.21	5.88	3.59	5.53	6.63	6.63	6.98	7.01	5.95	5.86
234131_at	---	---	0.816775	6.56	5.82	3.92	5.63	4.46	3.99	4.39	4.4	6.19	6.25
206371_at	FOLR3	folate receptor 3 (gamma)	0.81745	7.17	7.05	7.99	8.66	8.06	7.58	11.72	12.04	6.93	6.73
225456_at	MED1	mediator complex subunit 1	0.817853	6.99	5.56	5.13	6.17	6.65	6.56	6.21	5.73	6.7	9.57
202817_s_at	SS18	synovial sarcoma translocation, chromosome 18	0.818607	5.66	5.96	4.14	5.52	6.84	7.9	6.27	6.89	5.8	5.28
244249_at	---	---	0.819083	7.98	7.86	7.22	8.03	6.92	5.88	7.03	5.12	7.31	8.44
201109_s_at	THBS1	thrombospondin 1	0.819211	4.41	3.81	4.76	5.79	6.75	7.59	6.34	6.28	6.55	6.95
211061_s_at	MGAT2	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	0.819211	6.28	5.32	9.15	7.07	7.53	8.03	6.69	5.93	6.92	6.13
224202_at	SUFU	suppressor of fused homolog (Drosophila)	0.819911	4.95	7.57	3.8	4.13	6.43	3.44	5.29	4	4.67	6.36
205552_s_at	OAS1	2',5'-oligoadenylate synthetase 1, 40/46kDa	0.820579	5.59	6.25	8.43	8.37	9.75	9.66	7.38	8.48	8.27	6.48
204103_at	CCL4	chemokine (C-C motif) ligand 4	0.820661	7.93	6.53	9.27	8.92	7.03	7.12	7.4	6.16	8.73	8.52
242019_at	LASS6	LAG1 homolog, ceramide synthase 6	0.820753	4.74	4.63	4.9	5.37	6.1	6.64	6.37	6.75	5.96	2.82
232885_at	NCRNA00081	non-protein coding RNA 81	0.820938	5.17	3.62	4.17	6.23	4.4	2.48	2.81	6.78	6.13	3.21
1558345_a_at	LOC439911	hypothetical gene supported by NM_194304	0.820938	8.27	7.94	6.65	8.36	7.83	6.77	8.1	8.43	8.28	5.2
1558028_x_at	LOC647979	hypothetical LOC647979	0.820938	5.77	5.24	5.09	5.77	7.08	7.15	7.62	6.52	6.35	4.32
239723_at	---	---	0.821543	5.06	5.42	6.69	6.44	6.77	5.32	4.79	5.85	4.88	8.15
224635_s_at	BIRC6	baculoviral IAP repeat-containing 6	0.821686	7.45	7.99	5.23	7.13	7.27	7	7.79	7.56	7.13	4.55
237424_at	---	---	0.821686	6.56	6.5	4.68	6.78	3.6	4.24	4.6	4.08	3.98	4.08
225171_at	ARHGAP18	Rho GTPase activating protein 18	0.8217	6.67	6.3	3.37	6.22	7.45	6.24	7.59	7.2	6.48	7.7
230917_at	---	---	0.821918	8.12	7.52	4.8	6.83	7.35	5.1	7.21	6.78	7.2	6.32
243312_at	ZNF107	Zinc finger protein 107	0.821957	7.5	7.34	4.66	6.01	5.38	5.28	4.44	4.73	6.07	5.32
232058_at	---	---	0.822093	6.46	7.61	4.04	6.12	6.48	7.4	6	6.09	7.55	5.92
1555760_a_at	RBM15	RNA binding motif protein 15	0.822428	7.7	7.11	8.03	6.98	7.94	6.02	7.38	9.3	7.6	5.7
202230_s_at	CHERP	calcium homeostasis endoplasmic reticulum protein	0.822428	7.63	8.08	7.73	9.18	8.16	7.29	7	5.2	8.82	8.92
206042_x_at	SNRPN /// SNURF	small nuclear ribonucleoprotein polypeptide N /// SNRPN upstream reading frame	0.822591	6.12	5.55	5.38	7.32	6.58	9.2	7.66	6.91	7.71	9.16
221842_s_at	ZNF131	zinc finger protein 131	0.822591	6.97	6.93	4.84	7.15	7.21	5.01	6.62	6.32	7.15	4.84
219543_at	PBLD	phenazine biosynthesis-like protein domain containing	0.822591	6.28	7.95	5.96	6.9	7.7	5.31	6.12	7.9	7.58	5.33
211009_s_at	ZNF271	zinc finger protein 271	0.822659	6.78	6.68	3.69	6.65	7.57	6.96	7.08	7.99	6.45	6.16
204224_s_at	GCH1	GTP cyclohydrolase 1	0.822785	7.01	6.37	8.14	8.2	8.1	8.17	8.68	8.33	6.9	5.52
1561893_at	---	---	0.822862	8.12	6.86	6.6	7.23	5.93	7.3	7.57	9.57	7.56	8.46
210293_s_at	SEC23B	Sec23 homolog B (S. cerevisiae)	0.822862	7.14	7.04	5.33	7.28	7.71	7.51	6.86	7.92	6.94	4.72
200893_at	TRA2B	transformer 2 beta homolog (Drosophila)	0.823203	7.97	7.7	6.8	7.65	8.08	7.37	8.8	7.24	7.87	5.01
224481_s_at	HECTD1	HECT domain containing 1	0.823264	7.27	7.02	3.97	7.41	6.75	6.96	6.46	7.39	7.25	6.14
235380_at	---	---	0.823465	8.18	7.95	2.91	6.9	7.77	7.22	7.69	7.04	7.71	6.54
1554661_s_at	C1orf71	chromosome 1 open reading frame 71	0.823492	5.38	4.46	5.21	5.72	5.88	7.34	6.47	6.23	5.7	3.61
235412_at	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	0.823663	6.97	6.81	3.93	5.85	5.3	6.25	6.34	6.1	5.81	7.94
224959_at	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	0.82446	6.36	5.04	3.18	4.71	6.15	6.22	6.77	6.18	6.25	4.66
209658_at	CDC16	cell division cycle 16 homolog (S. cerevisiae)	0.824481	3.99	4.23	4.17	4.37	5.15	2.49	5.63	6.13	6.3	6.36

207224_s_at	SIGLEC7	sialic acid binding Ig-like lectin 7	0.824481	7.75	8.47	7.6	7.96	7.71	7.71	7.32	6.59	8.22	4.91
205809_s_at	WASL	Wiskott-Aldrich syndrome-like	0.824495	6.28	8.09	5.02	4.94	5.24	5.17	5.55	3.86	6.13	2.97
203015_s_at	SSX2IP	synovial sarcoma, X breakpoint 2 interacting protein	0.824495	6.59	6.51	5.57	5.98	5.58	5.82	6.74	9.96	6.5	4.8
232384_s_at	---	---	0.824495	6.8	5.25	4.62	6.7	5.59	4.49	5.5	4.52	6.23	7.35
226296_s_at	MRPS15	mitochondrial ribosomal protein S15	0.824495	7.63	5.62	6.84	5.15	7.17	7.35	7.54	8.83	6.84	7.07
1569206_at	TCP11L2	t-complex 11 (mouse)-like 2	0.824503	9.98	8.02	7.07	9.64	7.55	6.48	8.16	7.56	8.87	8.86
216275_at	BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast)	0.824534	5.31	5.25	8.16	5.45	5.86	5.56	6.24	8.12	5.13	7.24
222838_at	SLAMF7	SLAM family member 7	0.824636	6.45	5.32	4.51	7.2	6.34	4.02	9.28	7.27	6.77	7.72
209198_s_at	SYT11	synaptotagmin XI	0.824636	4.98	4.85	4.37	5.65	5.51	3.86	7.27	6.71	5.53	7.8
238647_at	C14orf28	chromosome 14 open reading frame 28	0.825367	5.16	5.15	6.01	5.55	6.96	5.17	4.15	5.83	4.91	7.71
243108_at	RANBP9	RAN binding protein 9	0.82548	6.46	6.08	4.11	6.41	6.22	3.92	4.28	4.12	5.6	4.72
223071_at	IER3IP1	immediate early response 3 interacting protein 1	0.825699	4.7	6.03	6.09	4.31	5.97	7.95	5.86	5.33	6.44	6.74
1570360_s_at	DDX3Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	0.825739	3.77	3.97	4.96	4.6	6.2	5.91	7.17	6.49	5.55	7
226787_at	ZNF18	zinc finger protein 18	0.825739	7.58	7.5	4.08	6.85	6.96	6.09	5.92	5.91	8.2	7.37
1567032_s_at	ZNF160	zinc finger protein 160	0.825739	5.67	6.02	4.97	6.28	4.69	8.51	6.57	5.51	5.37	4.61
234616_at	---	---	0.825995	6.83	7.3	6.7	7.71	6.44	5.88	4.41	4.26	8.82	8.99
240271_at	---	---	0.826431	6.33	5.35	5.81	6.95	4.42	4.31	4.98	7.18	7.1	6.24
1554660_a_at	C1orf71	chromosome 1 open reading frame 71	0.826445	6.89	6.7	5.67	7.04	6.85	8.7	7.63	5.34	7.75	8.43
1559776_at	---	---	0.82724	4.14	4.67	6.8	7.36	4.96	4.22	6.18	7.09	3.63	3.77
228727_at	ANXA11	annexin A11	0.82724	6.61	6.77	4.84	6.24	5.45	5.64	5.79	4.77	5.04	3.27
208683_at	CAPN2	calpain 2, (m/II) large subunit	0.827313	4.36	4.86	2.88	5.55	6.47	7	6.7	6.58	6.25	3.02
226643_s_at	NUDCD2	NudC domain containing 2	0.827313	4.57	5.16	3.71	4.44	7.16	5.84	5.91	6.71	5.51	6.76
201326_at	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	0.827426	6.64	8	5.46	5.73	7.53	8.16	8.49	7.8	6.24	4.14
44111_at	VPS33B	vacuolar protein sorting 33 homolog B (yeast)	0.827735	6.21	3.7	4.35	6.3	5.27	5.2	6.05	4.48	3.64	7.1
242625_at	RSAD2	radical S-adenosyl methionine domain containing 2	0.828261	6.17	6.45	8.22	8.35	8.84	8.37	4.97	6.21	8.28	7.51
214677_x_at	IGL@	immunoglobulin lambda locus	0.828261	5.36	8.1	5.45	5.65	7.67	7.9	8.73	6.6	6.14	7.17
205997_at	ADAM28	ADAM metallopeptidase domain 28	0.828261	6.47	7.04	5.73	6.13	5.69	3.95	4.85	5.29	7.48	6.71
1557749_at	EHBP1L1	EH domain binding protein 1-like 1	0.8286	8.03	7.44	7.8	6.35	7.54	3.03	4.29	8.94	6.62	2.79
205703_at	---	---	0.828628	7.05	8.93	5.37	5.28	8.13	7.6	7.58	8.33	7.88	8.28
1570124_at	---	---	0.828821	6.75	4.6	6.08	5.26	5.84	4.06	4.34	4.72	4.35	7.72
209459_s_at	ABAT	4-aminobutyrate aminotransferase	0.828998	5.48	6.24	4.86	6.78	7.04	7.14	6.1	6.6	6.43	3.93
49452_at	ACACB	acetyl-Coenzyme A carboxylase beta	0.829369	6.85	8.07	4.84	4.79	6.49	6.83	8	8.03	7.54	6.79
234864_s_at	TRPM6	transient receptor potential cation channel, subfamily M, member 6	0.829692	6.69	6.52	4.55	6.07	5.43	3.87	4.96	4.13	6.33	4.33
230315_at	---	---	0.829833	8.66	6.09	8.45	8.93	6.55	7.22	5.98	7.11	7.01	8.83
238055_at	ATP8B1	ATPase, class I, type 8B, member 1	0.829833	3.87	6.32	3.44	4.5	6.24	7.19	4.71	3.88	4.82	6.8
221071_at	---	---	0.829833	8.55	8.7	6	6.85	8.41	9.69	7.96	7.49	9.13	6.96
1555011_at	ZFYVE16	zinc finger, FYVE domain containing 16	0.829833	6.63	5.7	5.19	6.75	6.3	4.49	6.06	3.96	6.61	7.67
241441_at	---	---	0.830054	6.77	4.57	3.44	6.51	6.48	5.39	6.55	6.92	5.25	4.22
224534_at	KREMEN1	kringle containing transmembrane protein 1	0.830103	6.8	7.1	8.4	7.47	7.29	5.35	6.5	6.29	4.91	3.75
1560396_at	KLHL6	kelch-like 6 (Drosophila)	0.830622	8.16	8.73	6.08	9.29	9.13	11.16	8.83	8.81	9.51	8.9
222028_at	ZNF45	zinc finger protein 45	0.830792	4.97	5.93	3.85	3.42	6.02	4.66	5.82	7.27	6.37	6.93
1562957_at	---	---	0.830864	6.44	7.47	3.02	7.14	6.53	6.08	6.38	5.11	6.53	6.48

242117_at	---	---	0.831027	8.33	8.49	4.76	7.48	8.24	6.36	8.17	6.3	8.66	8.54
1556175_at	MTSS1L	metastasis suppressor 1-like	0.83123	5.74	5.7	3.62	5.19	5.08	4.45	6.2	4.92	6.1	7.83
225250_at	STIM2	stromal interaction molecule 2	0.831329	6.87	5.67	5.53	5.77	5.47	3.35	4.15	6.48	5.16	6.4
209164_s_at	CYB561	cytochrome b-561	0.831626	7.75	8.24	6.65	7.33	6.43	6.86	6.08	6.94	8.26	9.72
1568768_s_at	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.831643	9.57	7.38	10.47	8.67	7.65	8.81	9.81	9.51	10.59	6.52
238631_at	ZNF140	Zinc finger protein 140	0.831931	6.39	5.69	3.6	5.83	3.31	6.96	4.24	4.94	7.21	5.94
214765_s_at	NAAA	N-acylethanolamine acid amidase	0.831931	9.13	9.18	7.38	6.58	8.23	7.31	7.66	8.46	6.97	6.17
225794_s_at	C22orf32	chromosome 22 open reading frame 32	0.832134	5.66	5.95	7.16	5.66	6.55	8.15	8.52	7.7	6.27	5.67
224716_at	SLC35B2	solute carrier family 35, member B2	0.832383	4.93	7.85	5.12	4.78	6.75	4.82	5.15	7.07	4.3	6.09
1561286_a_at	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	0.832756	3.53	3.75	5.58	7.24	5.99	7.04	5.14	7.35	5.34	6.67
220784_s_at	UTS2	urotensin 2	0.832835	3.16	3.37	3.56	3.24	6.95	6.69	6.47	7.86	5.69	7.21
213822_s_at	UBE3B	ubiquitin protein ligase E3B	0.832835	6.56	5.56	5.81	6.19	5.53	9.63	6.42	5.78	5.65	5.75
207216_at	TNFSF8	tumor necrosis factor (ligand) superfamily, member 8	0.832839	7.27	6.52	4.36	6.76	7.21	4.75	5.57	5.38	5.23	3.17
228919_at	---	---	0.832839	8.73	8.5	6.54	7.9	5.19	5.11	5.13	4.99	5.24	5.19
227144_at	C22orf9	chromosome 22 open reading frame 9	0.832839	6.7	7.17	5.57	5.78	6.25	7.61	7.53	7.18	5.44	4.39
1553678_a_at	ITGB1	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes	0.832865	6.33	6.15	4.26	6.28	7.12	9	8.58	7.91	6.93	5.71
241147_at	---	---	0.832895	4.24	5.74	4.14	3.96	4.27	6.35	5.47	3.12	7.69	6.87
201421_s_at	WDR77	WD repeat domain 77	0.833063	4.93	5.8	4.13	4.44	5.95	7.38	6.3	6.14	5.87	4.54
213359_at	HNRNPD	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1	0.83317	7.24	5.4	6.16	5.77	4.33	5.03	4.48	3.22	5.32	7.7
238923_at	SPOP	speckle-type POZ protein	0.833418	5.37	5.18	7.38	7.97	6.94	6.45	4.27	4.46	7.53	4.15
218239_s_at	GTPBP4	GTP binding protein 4	0.833426	4.89	6.88	4.6	3.94	5.27	3.61	6.96	7.01	5.3	4.97
205844_at	VNN1	vanin 1	0.833426	6.14	5.67	8.42	8.75	8.66	7.68	8.65	8.69	5.48	5.35
210949_s_at	EIF3C /// EIF3CL	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation	0.833426	5.01	4.4	5.41	5.61	5.82	7.71	7.01	7.26	5.4	3.57
1560679_at	LOC151438	hypothetical protein LOC151438	0.833612	8.61	8.3	7.78	8.93	7.14	5.91	6.96	7.29	6.72	6.24
217207_s_at	BTNL3	butyrophilin-like 3	0.833842	9.35	9.06	9.88	9.84	4.7	5.46	5.15	5.35	8.73	9.44
235013_at	SLC31A1	solute carrier family 31 (copper transporters), member 1	0.834398	4.87	8.07	5.84	5.92	6.09	4.8	7.67	5.66	6.47	4.81
217624_at	PDAP1	PDGFA associated protein 1	0.834509	8.15	8.44	9.8	9.26	6.85	7.36	5.86	7.59	8.37	8.75
221087_s_at	APOL3	apolipoprotein L, 3	0.8351	6.67	6.69	4.06	6.27	7.76	8.22	7.98	8.22	6.23	7.82
219799_s_at	DHRS9	dehydrogenase/reductase (SDR family) member 9	0.835592	7.97	8.96	8.69	8.62	9.88	7.33	8.9	10.06	10.59	10.01
218403_at	TRIAP1	TP53 regulated inhibitor of apoptosis 1	0.835775	5.28	5.61	6.16	5.59	6.95	7.77	8.23	7.83	7.48	6.36
227517_s_at	GAS5	growth arrest-specific 5 (non-protein coding)	0.83597	7.14	5	6.11	5.39	6.35	4.49	7.22	4.86	7.26	8.84
205449_at	SAC3D1	SAC3 domain containing 1	0.836229	4	4.15	4.12	4.11	6.64	7.49	6.7	7.96	7.1	7.36
227312_at	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	0.836538	5.28	5.58	5.29	6.1	6.31	8.33	5.81	3.8	5.54	5.11
209092_s_at	GLOD4	glyoxalase domain containing 4	0.836538	5.35	6.51	3.93	5.02	6.14	6.83	6.94	6.84	5.59	4.53
1555435_at	AFF4	AF4/FMR2 family, member 4	0.836538	7.85	5.48	8.06	7.73	4.73	6.1	6.49	6.21	7.74	8.1
205133_s_at	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	0.836725	7.02	7.74	6.32	6.56	8.65	9.48	9.73	9.12	7.83	8.07
1559227_s_at	VHL	von Hippel-Lindau tumor suppressor	0.83714	6.29	4.49	3.24	6.09	6.63	5.32	3.11	3.2	6.54	3.24

205110_s_at	FGF13	fibroblast growth factor 13	0.837178	5.39	5.26	7.78	7.87	4.93	4.17	5.26	6.71	7.85	8.85
227250_at	KREMEN1	kringle containing transmembrane protein 1	0.837178	9.5	9.33	9.47	9.92	8.4	6.78	8.96	8.78	6.65	7.32
201519_at	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	0.837595	5.28	6.09	3.14	4.43	5.68	5.73	6.83	6.2	6.11	6.87
204618_s_at	GABPB1	GA binding protein transcription factor, beta subunit 1	0.838077	8.32	8.3	4.52	7.21	8.39	6.44	7.8	5.91	6.95	9.25
203818_s_at	SF3A3	splicing factor 3a, subunit 3, 60kDa	0.838227	5.93	6.5	3.66	6.37	5.32	5.34	6.99	6.98	6.64	6.98
1552348_at	PRSS33	protease, serine, 33	0.838371	9.45	11.06	10.66	9.27	11.9	12.45	10.5	11.65	10.67	11.06
221841_s_at	KLF4	Kruppel-like factor 4 (gut)	0.838381	7.19	3.97	7.6	7.77	6.21	5.59	8.23	6.32	6.7	4.44
215783_s_at	ALPL	alkaline phosphatase, liver/bone/kidney	0.838644	10.13	10.08	11.4	11.24	10.33	9.76	11.25	11.64	9.3	8.2
228983_at	---	---	0.838701	6.84	5.4	4.75	4.75	5.13	3.89	4.81	4.75	6.55	8.09
1558214_s_at	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	0.838807	8.72	7.71	3.48	7.36	8.97	6.17	5.94	5.69	6.11	6.25
214962_s_at	NUP160	nucleoporin 160kDa	0.838807	6.95	4.3	3.84	6.05	6.91	4.65	5.25	6.21	5.28	7.35
219622_at	RAB20	RAB20, member RAS oncogene family	0.838989	8.11	7.67	9.49	9.29	6.65	6.93	8.77	8.77	6.08	4.25
204655_at	CCL5	chemokine (C-C motif) ligand 5	0.838989	7.45	5.37	7.41	8.08	8.01	10.5	10.09	9.64	7.52	8.29
212428_at	KIAA0368	KIAA0368	0.838989	6.5	5.98	4.32	5.97	6.15	4.01	5.53	6.46	5.47	3.69
218654_s_at	MRPS33	mitochondrial ribosomal protein S33	0.839017	4.24	4.57	3.6	6.49	4.5	5.5	5.8	6.1	6.04	3.55
209961_s_at	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	0.839017	5.75	6.94	5.45	6.19	9.26	7	6.51	5.73	5.9	5.84
201560_at	CLIC4	chloride intracellular channel 4	0.839669	6.21	5.49	5.97	6.16	6.86	8.57	7.57	7.09	7.59	8.35
235370_at	KREMEN1	kringle containing transmembrane protein 1	0.839669	8	7.81	8.31	8.85	7.41	6.61	7.65	7.27	5.88	5.52
238642_at	ANKRD13D	ankyrin repeat domain 13 family, member D	0.840399	7.53	7.68	8.11	8.1	7.42	6.58	7.49	6.22	8.38	9.95
210892_s_at	GTF2I	general transcription factor II, i	0.840793	7.13	8.43	6.23	6.51	8.51	8.93	8.58	9.01	8.01	7.12
1553694_a_at	PIK3C2A	phosphoinositide-3-kinase, class 2, alpha polypeptide	0.840793	8.33	8.15	5.61	6.49	7.8	5.52	6.39	6.2	6.99	7.42
220421_at	BTNL8	butyrophilin-like 8	0.841113	9.5	9.74	3.86	3.61	10.52	9.52	9.3	9.56	3.32	3.36
223393_s_at	TSHZ3	teashirt zinc finger homeobox 3	0.841213	7.64	8.05	5.86	6.03	6.67	5.47	7.11	7.69	6.35	3.75
213618_at	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	0.841215	6.32	7.34	2.94	6.77	7.42	7.23	6.98	6.55	6.54	6.32
214457_at	HOXA2	homeobox A2	0.841215	6.58	6.5	5.15	6.71	6.93	5.92	4.09	4.2	3.97	3.75
214310_s_at	ZFPL1	zinc finger protein-like 1	0.841215	5.39	4.76	7.84	5.21	5.19	6.46	4.95	5.24	5.89	7.15
1561058_at	---	---	0.841357	6.17	5.55	3.99	4.64	3.74	4.12	4.47	5.08	6.31	7.35
200988_s_at	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.841357	7.11	7.13	4.09	5.88	5.02	4.77	6.8	5.32	7.04	6.1
209425_at	C1QTNF3	C1q and tumor necrosis factor related protein 3	0.841431	3.15	4.47	3.43	4.66	5.98	3.43	6.34	7.11	6.92	3.35
1555275_a_at	KLHL6	kelch-like 6 (Drosophila)	0.841431	4.27	6.61	4.94	5.28	5.17	6.12	5.36	6.47	3.74	2.02
1552940_at	TEDDM1	transmembrane epididymal protein 1	0.841565	6.77	7.92	8.27	6.91	5.86	4.45	8.28	6.39	8.05	7.99
204972_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.841725	4.04	4.56	6.72	7.29	7.34	7.75	6.21	3.67	7.59	6.66
221570_s_at	METTL5	methyltransferase like 5	0.842008	6.24	6.79	4.14	6.48	6.84	7.02	6.99	7.77	6.11	7.94
202336_s_at	PAM	peptidylglycine alpha-amidating monooxygenase	0.84221	6.74	5.72	6.37	7.53	7.35	6.99	4.83	3.17	4.08	4.18
202760_s_at	PALM2-AKAP2	PALM2-AKAP2 readthrough transcript	0.842608	6.19	8.07	3.92	4.3	6.25	7.24	7.65	5.3	6.41	4.71
214096_s_at	SHMT2	serine hydroxymethyltransferase 2 (mitochondrial)	0.842804	6.83	7.04	5.36	6.62	8.21	9.25	8.24	8.48	6.96	5.39
235019_at	CPM	carboxypeptidase M	0.843023	3.49	2.61	2.34	3.72	5.56	5.1	6.01	6.39	6.42	3.4
240673_at	---	---	0.843023	6.61	7.35	4.17	5.05	7.24	6.06	7.06	6.65	6.86	6.26
214359_s_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	0.843236	5.4	6.48	5.44	6.38	6.6	7.98	6.04	7.23	5.79	3.73

209667_at	CES2	carboxylesterase 2 (intestine, liver)	0.843247	7.96	7.43	5.02	7.42	8.21	6.76	5.92	6.31	8.35	8.23
219158_s_at	NARG1	NMDA receptor regulated 1	0.843247	6.54	4.75	4.06	3.97	6.31	6.25	7.05	5.43	6.31	4.7
204409_s_at	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	0.843337	2.78	2.92	3.22	3.19	11.64	11.46	11.64	11.73	11.25	11.5
214901_at	ZNF8	zinc finger protein 8	0.843337	5.4	8.41	7.7	5.31	5.22	5.11	4.31	5.74	7.01	6.66
238024_at	---	---	0.843607	6.51	7.04	5.34	6.59	6.28	4.75	4.55	4.51	6.72	7.47
1570597_at	---	---	0.843607	6.48	5.46	8.89	6.29	5.51	5.69	5.75	5.94	7.73	6.53
220755_s_at	C6orf48	chromosome 6 open reading frame 48	0.843723	7.07	7.5	6.31	7.41	8.41	9.31	9.52	9.04	7.3	8.2
213915_at	NKG7	natural killer cell group 7 sequence	0.844092	6.95	6.76	5.74	7.94	8.42	8.74	9.43	8.93	7.59	8.81
234299_s_at	NIN	ninein (GSK3B interacting protein)	0.844256	8.43	7.91	5.67	8.91	7.99	8.38	8.17	6.61	8.12	6.06
205988_at	CD84	CD84 molecule	0.844469	4.92	5.27	3.71	6.07	6.79	6.95	4.97	5.42	6.54	4.96
1552349_a_at	PRSS33	protease, serine, 33	0.844544	7.16	8.48	9.15	7.09	9.57	10.1	7.93	8.75	8.54	9.83
225056_at	SIPA1L2	signal-induced proliferation-associated 1 like 2	0.844643	8.18	8.65	6.94	8.67	7.49	3.97	8.2	7.22	7.95	5.47
201909_at	RPS4Y1	ribosomal protein S4, Y-linked 1	0.844708	5.2	5.9	5.75	5.09	9.75	10.1	10.58	10.13	9.76	10.58
201108_s_at	THBS1	thrombospondin 1	0.844708	4.41	5.57	4.82	6.26	6.61	8.71	7.49	7.5	6.7	7.36
225095_at	SPTLC2	Serine palmitoyltransferase, long chain base subunit 2	0.844708	6.11	7.95	4.8	6.53	7.78	7.89	7.42	7.41	6.98	4.59
210029_at	IDO1	indoleamine 2,3-dioxygenase 1	0.844708	5.86	5.79	6.32	6.47	8.73	6.48	5.02	7.02	7.1	7.28
1558000_at	ARID5B	AT rich interactive domain 5B (MRF1-like)	0.844708	4.43	6.78	4.69	5.53	6.32	4.24	7.04	4.64	4.43	5.03
221671_x_at	IGK@ /// IGKC	immunoglobulin kappa locus /// immunoglobulin kappa constant	0.844708	5.61	8.77	6.32	5.94	7.78	8.03	9.06	8.07	6.7	6.56
1558859_at	LOC222159	hypothetical protein LOC222159	0.844708	6.39	7.67	6.27	6.41	4.69	5.19	7.41	7.69	6.56	7.64
212922_s_at	SMYD2	SET and MYND domain containing 2	0.845002	3.83	4.73	4.46	4.39	5.68	7.17	7.13	6.99	5.99	4.36
209715_at	CBX5	chromobox homolog 5 (HP1 alpha homolog, Drosophila)	0.845002	5.87	6.06	4.46	6.41	7.16	6.49	7.15	8.24	6.62	7.33
238409_x_at	OXR1	oxidation resistance 1	0.845006	5.97	6.84	3.92	4.53	5.95	6.52	6.18	4.59	6.26	3.54
237210_at	NFRKB	nuclear factor related to kappaB binding protein	0.845121	5.86	7.54	7.63	6.84	6.78	6.78	6.07	3.91	6.19	8.86
201139_s_at	SSB	Sjogren syndrome antigen B (autoantigen La)	0.845248	8.18	8.4	5.61	7.69	9.41	9.03	9.61	8.9	8.66	7.94
236399_at	---	---	0.845317	7.59	6.07	9.21	6.61	6.02	6.17	6.13	5.4	5.46	8.23
213256_at	3-Mar	membrane-associated ring finger (C3HC4) 3	0.845378	5.35	5.44	6.12	7.33	6.58	4.51	4.55	4.91	5.83	4.18
205107_s_at	EFNA4	ephrin-A4	0.845492	6.68	6.31	8.79	6.07	6.89	6.53	7.51	9.43	5.23	7.23
224253_at	EXOC5	exocyst complex component 5	0.845509	6.72	6.82	4.08	6.37	7.86	6.63	7.8	7.91	6.92	6.76
210232_at	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	0.845514	6.44	6.31	7.46	7.42	5.32	3.86	6.49	7.5	6.79	7.02
201157_s_at	NMT1	N-myristoyltransferase 1	0.84581	6.14	5.44	6.19	5.91	5.24	8.1	5.57	4.99	6.88	4.49
242431_at	---	---	0.845999	7.68	6.12	7.64	8.83	4.89	6.77	6.22	6.92	6.55	6.71
224588_at	XIST	X (inactive)-specific transcript (non-protein coding)	0.846301	6.75	7.86	8.43	7.44	3.47	3.45	3.42	3.34	3.11	3.83
219279_at	DOCK10	dedicator of cytokinesis 10	0.846837	3.34	6.13	2.67	6.11	6.08	7.07	8.24	7.01	4.87	2.89
235096_at	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	0.846837	6.58	6.95	5.36	4.51	7.11	7.83	6.82	9.32	6.84	4.26
230256_at	C1orf104	Chromosome 1 open reading frame 104	0.846837	5.01	6.82	3.62	3.45	4.74	3.61	5.33	4.46	6.39	7.3
241683_at	HECTD1	HECT domain containing 1	0.846837	6.96	7.77	5.01	6.73	7.36	7.45	5.61	7.45	6.03	4.17
212725_s_at	TUG1	taurine upregulated 1 (non-protein coding)	0.846837	6.98	6.62	7.7	7.68	7.24	7.3	6.99	4.49	7.22	8.49
1562388_at	LOC285819	hypothetical protein LOC285819	0.847054	7.62	8.36	4.83	6.92	7.15	5.99	6.55	6.14	6.19	5.72
55065_at	MARK4	MAP/microtubule affinity-regulating kinase 4	0.847094	6.72	5.07	9.39	6.51	6.56	5.1	5.47	4.8	6.07	7.29
212959_s_at	GNPTAB	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits	0.847224	4.08	5.82	3.27	4.75	6.24	5.8	6.57	5.16	6.56	5.2

219763_at	DENND1A	DENN/MADD domain containing 1A	0.84741	5.68	4.81	8.59	6.71	5.39	4.6	5.35	5.7	5.9	6.01
204410_at	EIF1AY	eukaryotic translation initiation factor 1A, Y-linked	0.847535	3.18	3.98	2.94	2.76	8.52	7.36	8	8.01	7	7.38
206055_s_at	SNRPA1	small nuclear ribonucleoprotein polypeptide A'	0.847578	5.83	6.55	2.69	4.23	6.62	7.1	7.84	7.14	6.37	4.75
229213_at	DIRC2	disrupted in renal carcinoma 2	0.847905	6.31	5.19	7.64	7.18	6.91	6.76	7.12	4.98	6.42	9.12
200691_s_at	HSPA9	heat shock 70kDa protein 9 (mortalin)	0.848208	6.81	6.31	4.33	6.38	6.44	5.72	7.28	7.05	5.95	4.01
221923_s_at	NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0.848565	6.26	6.05	4.39	5.11	7.01	7.83	8.08	7.69	5.79	6.14
202284_s_at	CDKN1A	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	0.848619	6.81	6.22	6.25	7.22	7.1	9.43	8.35	9.2	6.55	4.6
47571_at	ZNF236	zinc finger protein 236	0.848619	3.98	5.21	6.22	5.61	4.03	7.77	4.49	4.38	7.21	4
235789_at	KDM4B	lysine (K)-specific demethylase 4B	0.848619	7.62	7.03	4.76	7.06	4.91	4.98	6.04	4.38	7.42	6.72
203335_at	PHYH	phytanoyl-CoA 2-hydroxylase	0.848656	4.25	3.36	2.96	3.74	6.52	5.91	6.3	7.35	3.71	3.66
202847_at	PCK2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	0.84869	6.43	6.59	6.65	6.64	6.22	8.82	7.47	6.54	6	4.89
201559_s_at	CLIC4	chloride intracellular channel 4	0.849442	4.86	5.62	3.53	5.57	4.59	7.33	6.92	6.36	5.9	4.08
211623_s_at	FBL	fibrillarin	0.849442	6.63	7.77	5.35	6.41	8.34	8.69	9.27	8.78	8.06	7.3
235516_at	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.849442	4.81	7.18	4.52	4.08	7.63	6.45	7.2	5.46	6.46	9.23
1557910_at	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	0.849671	7.88	7.39	5.24	7.07	6.74	7.58	8.1	8.36	6.82	5.36
239654_at	CHD9	Chromodomain helicase DNA binding protein 9	0.850155	5.82	7.81	3.97	5.44	5.98	7.13	8.96	3.6	6.58	6.24
209875_s_at	SPP1	secreted phosphoprotein 1	0.850409	6.51	6.79	4.06	4.52	7.18	6.45	3.92	3.95	6.2	5.97
1570243_at	LOC440731	Similar to hCG1817424	0.850595	7.52	6.34	4.5	5.55	6.72	7.01	5.35	4.18	4.23	4.53
1556357_s_at	ERICH1	glutamate-rich 1	0.850655	4.93	3.35	6.11	7.06	6.46	4.67	5.37	8.21	6.43	7.96
217630_at	ANGEL2	angel homolog 2 (Drosophila)	0.85079	4.51	7.05	6.91	5.54	6	5.5	3.74	6.99	7.05	6.61
225583_at	UXS1	UDP-glucuronate decarboxylase 1	0.851	5.7	5.43	3.67	4.74	7.43	7.38	7.31	7.61	5.68	6.41
235922_at	---	---	0.851	7.6	3.85	6.8	5.92	4.87	7.6	6.59	5.98	7.94	5.57
1556035_s_at	ZNF207	zinc finger protein 207	0.851118	6.82	4	4.38	6.5	5.06	3.93	5.24	4.98	6.35	6.94
228822_s_at	USP16	ubiquitin specific peptidase 16	0.851192	6.25	6.38	2.88	6.38	6.36	5.49	6.36	4.78	6.73	5.39
207902_at	IL5RA	interleukin 5 receptor, alpha	0.851462	5.61	5.93	8.64	6.23	7.86	8.42	5.65	6.67	6.36	6.16
213797_at	RSAD2	radical S-adenosyl methionine domain containing 2	0.851518	7.67	8.7	9.34	9.84	10.49	10.62	7.35	7.77	10.13	10.22
205511_at	FLJ10038	hypothetical protein FLJ10038	0.851518	4.85	4.56	7.83	6.91	5.29	5.36	5.27	4.94	6.32	5.63
216591_s_at	hCG_1776980 /// SDHC	hCG1776980 /// succinate dehydrogenase complex, subunit C, integral membrane pro	0.851643	7.24	6.27	8.15	7.96	7.79	9.58	7.78	9.15	7.54	6.74
202742_s_at	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	0.852112	4.89	5.66	3.38	4.87	6.31	8.21	6.93	6.38	5.55	5.01
1555392_at	LOC100128868	testin-related protein TRG	0.852112	8.15	8.82	9.58	8.29	6.35	5.16	6.86	9.49	7.41	9.25
240103_at	---	---	0.852288	7.38	7.69	5.42	8.03	7.73	7.47	5.17	4.18	6.45	7.44
204894_s_at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)	0.852425	6.36	6.95	3.16	5.8	5.4	3.78	5.96	5.33	6.02	4.26
209426_s_at	AMACR /// C1QTNF3	alpha-methylacyl-CoA racemase /// C1q and tumor necrosis factor related protein	0.852529	6.78	7.44	6.87	5.92	9.06	9.11	8.09	8.61	8.28	8.58
203466_at	MPV17	MpV17 mitochondrial inner membrane protein	0.852723	5.94	4.46	4.68	4.84	7.38	6.69	7.85	5.76	5.35	6.31
227220_at	NFXL1	nuclear transcription factor, X-box binding-like 1	0.852776	6	5.69	8.53	9.35	8.95	7.96	6.96	6.53	8.85	8.39
200986_at	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	0.852924	6.28	6.38	8.66	8.73	6.57	5.93	6	6.63	6.88	6.71
205654_at	C4BPA	complement component 4 binding protein, alpha	0.852949	5.71	6.18	8.74	9.36	5.6	5.84	8.13	8.2	8.49	8.44

226431_at	FAM117B	family with sequence similarity 117, member B	0.852949	5.37	6.9	3.67	4.97	6.69	5	5.98	5.84	7.49	6.45
39729_at	PRDX2	peroxiredoxin 2	0.852949	5.29	5.82	4.36	5.13	6.73	8.28	7.02	6.53	6.52	6.61
222968_at	---	---	0.852949	6.98	7.41	6.51	7.19	8.4	9.34	9.31	8.7	7.11	7.85
218005_at	ZNF22	zinc finger protein 22 (KOX 15)	0.852969	5.14	5.32	4.27	3.81	5.75	6.81	6.02	7.24	5.77	4.24
1569401_at	CLEC12A	C-type lectin domain family 12, member A	0.853382	2.71	3.12	4.27	2.98	7.49	6.85	5.42	6.52	6.06	4.04
237590_at	---	---	0.85339	3.85	4.03	5.37	6.41	4.08	7.93	6.07	7.98	5.92	3.87
239690_at	---	---	0.85339	7.58	7.24	4.09	4.83	5.58	5.77	4.63	5.07	6.61	5.99
237510_at	MYNN	Myoneurin	0.853937	6.62	3.85	8.17	6.67	5.34	7.49	4.64	4.17	7.95	5.86
212089_at	LMNA	lamin A/C	0.854205	6.15	5.37	6.95	6.28	6.24	8.99	7.71	7.8	7.43	6.19
207111_at	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	0.854252	6.33	7.03	5.19	7.29	8.67	9.73	7.98	8.17	8.36	8.48
240017_at	ASPRV1	Aspartic peptidase, retroviral-like 1	0.854272	7.31	10.89	6.39	7.47	7.28	5.43	4.29	4.17	6.52	5.23
239085_at	JDP2	Jun dimerization protein 2	0.854435	7.54	7.59	5.05	6.58	5.94	4.52	6.08	6.22	7.33	5.94
1554794_a_at	UBE3C	ubiquitin protein ligase E3C	0.854762	5.34	6	6.05	4.98	5.28	5.52	4.76	3.62	6.44	3.23
239957_at	---	---	0.85504	6.28	6.8	3.93	5.41	6.17	3.96	4.16	4.73	6.27	7.82
227784_s_at	COG1	component of oligomeric golgi complex 1	0.855158	5.92	5.05	5.27	5.93	5.58	5.94	6.6	6.26	6.68	8.94
230542_at	ZNF597	zinc finger protein 597	0.855182	6.33	5.97	4.25	5.34	6.22	4.38	5.98	7.26	7.08	4.81
221516_s_at	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	0.855182	5.75	6.43	5.97	3.85	4.73	7.99	5.89	6.51	5.81	5.29
238064_at	---	---	0.855264	7.32	6.2	5.38	6.61	5.89	8.68	7.39	6.19	8.24	7.87
226146_at	---	---	0.855264	6.81	7.37	5.1	5.86	7.38	7.03	7.21	7.21	6.93	4.29
230403_at	---	---	0.855264	5.89	5.85	4.1	5.1	6.36	7.04	6.01	7.13	6.65	8.15
228927_at	ZNF397	zinc finger protein 397	0.855272	6.26	7.23	7.04	5.26	5.3	4.17	5.09	4.6	6.16	7.01
238778_at	MPP7	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	0.855335	4.7	4.68	4.54	5.68	7.17	6.54	7.08	6.75	6.27	6.22
227075_at	ELP3	elongation protein 3 homolog (S. cerevisiae)	0.855348	6.41	6.7	3.96	5.27	7.21	9.03	7.2	6.7	6.48	4.16
238408_at	---	---	0.855348	7.26	7.22	4.79	6.02	7.26	7.8	6.79	5.78	6.69	4.25
219387_at	CCDC88A	coiled-coil domain containing 88A	0.85545	7.12	7.37	4.39	7.67	7.6	6.78	8.34	7.06	7.4	6.69
243604_at	---	---	0.855646	5.1	5.74	7.57	6.07	4.51	5.08	5.58	5.29	7.07	4.6
1559754_at	LTB	Lymphotoxin beta (TNF superfamily, member 3)	0.855658	6.67	6.98	9.17	8.14	7.29	5.16	6.01	5.72	8.64	8.42
209104_s_at	NHP2	NHP2 ribonucleoprotein homolog (yeast)	0.855857	5.93	7.38	5.11	4.67	7.14	7.47	7.15	8.71	5.92	3.08
209136_s_at	USP10	ubiquitin specific peptidase 10	0.855857	6.38	7.79	2.95	5.28	5.57	4.18	6.59	6.58	5.62	5.24
210117_at	SPAG1	sperm associated antigen 1	0.855857	7.09	7.14	3.38	5.88	7.84	5.51	6.04	6.15	6.22	6.04
237556_at	LOC728804	Hypothetical LOC728804	0.85615	6.81	6.32	3.64	6.1	4.26	5.83	6.02	6	6.62	7.6
213188_s_at	MINA	MYC induced nuclear antigen	0.85615	4.97	5.68	4.89	4.66	5.52	7.55	7.06	6.34	4.51	4.08
1561870_at	---	---	0.856212	5.48	6.42	3.74	6.31	5.1	2.21	5.63	6.55	6.24	2.83
1558700_s_at	ZNF260	zinc finger protein 260	0.856404	4.92	6.06	3.56	3.09	6.49	5.79	5.11	6.64	3.63	4.32
218464_s_at	C17orf63	chromosome 17 open reading frame 63	0.856404	5.99	5.46	6.18	5.82	4.83	6.96	4.1	3.9	6.29	6.38
201501_s_at	GRSF1	G-rich RNA sequence binding factor 1	0.856774	5.68	5.51	4.24	5.57	6.1	8.08	6.66	6.04	5.65	4.68
228607_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.856986	4.34	3.83	5.08	5.44	6.2	7.21	5.19	4.34	6.61	7.04
221651_x_at	IGK@ /// IGKC	immunoglobulin kappa locus /// immunoglobulin kappa constant	0.85741	6.07	8.9	6.23	5.76	7.69	8	9.06	8.03	6.6	5.87
1562611_at	---	---	0.857585	7.13	6.39	3.43	7.07	5.66	6.69	6.07	7.32	7.34	6.94
236007_at	AKAP10	A kinase (PRKA) anchor protein 10	0.857585	6.48	6.41	6.44	6.46	7.68	8.49	6.15	7.78	7.8	4.25

238114_at	PCMTD1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	0.857943	8.27	7.36	6.48	7.22	7.01	6.05	5.08	4.91	6.73	7.51
1555851_s_at	SEPW1	selenoprotein W, 1	0.857976	6.59	8.85	6.66	5.44	8.55	8.72	8.55	8.06	7.34	8.26
1558549_s_at	VNN1	vanin 1	0.858045	7.22	6.13	9.48	9.37	8.61	8.01	8.75	8.8	6.66	5.31
203147_s_at	TRIM14	tripartite motif-containing 14	0.858279	6.67	6.78	4.03	6.21	7.37	8.5	7.61	7	7.25	5.09