Sorted by Plate ID

Image Clone ID	UniGene Cluster	UniGene Title	Calibrated Ratios																				
			BRCA1s							BRCA2s								Sporadics					
			1996	1822	1714	1224	1252	1510	1905	1900	1787	1721	1486	1816	1616	1063	1936	1572	1324	1649	1320	1542	1281	1321
21652	Hs.178452	catenin (cadherin-associated protein), alpha 1 (102kD)	0.15	0.22	0.30	0.26	1.22	0.44	0.38	0.35	1.10	1.07	1.46	0.73	0.63	0.77	0.66	0.36	0.57	0.31	0.48	0.40	0.25	0.44
25725	Hs.48876	farnesyl-diphosphate farnesyltransferase 1	1.84	1.56	0.85	0.94	0.98	1.10	1.41	0.68	0.91	0.44	0.49	1.50	0.86	1.16	1.57	0.81	1.97	2.68	1.92	1.38	0.99	0.87
26184	Hs.99910	phosphofructokinase, platelet	0.82	1.20	0.74	1.08	0.73	1.27	1.13	0.64	0.41	0.47	0.68	0.33	0.33	0.74	0.17	0.57	0.12	0.37	0.31	0.51	0.87	0.61
22012	Hs.119177	ADP-ribosylation factor 3	1.54	1.27	0.76	0.85	1.27	0.64	0.61	0.90	0.64	0.78	0.55	0.71	0.30	0.62	1.00	1.02	0.39	1.39	0.83	1.02	0.61	1.53
22293	Hs.75593	uroporphyrinogen III synthase (congenital erythropoietic porphyria)	1.72	1.57	2.13	1.09	1.98	0.74	2.43	1.71	1.16	1.33	1.46	1.71	1.26	1.41	3.00	0.83	1.13	1.46	2.24	1.18	1.34	1.14
22493	Hs.91379	ribosomal protein L26	0.71	1.24	1.69	2.23	1.16	0.82	2.08	1.44	2.03	3.60	1.20	3.24	2.41	1.56	2.56	1.72	1.75	0.93	1.09	0.67	1.23	1.06
23019	Hs.113368	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1	0.94	1.53	1.87	1.19	1.16	1.54	1.01	1.05	0.91	0.85	1.22	3.25	2.20	1.09	1.29	1.29	0.74	0.87	1.05	0.62	1.34	1.08
23132	Hs.21729	splicing factor 3a, subunit 1, 120kD	0.80	0.95	1.53	1.37	1.02	1.22	1.09	0.78	0.96	0.65	1.02	0.66	1.40	1.32	1.13	1.22	0.74	0.84	0.56	0.93	0.94	0.84
24145	Hs.104125	adenylyl cyclase-associated protein	0.78	0.81	1.42	0.97	1.04	1.12	0.56	1.04	0.97	0.88	1.11	1.57	0.47	0.97	1.36	1.32	0.64	0.67	0.77	1.24	1.36	0.91
25584	Hs.173554	ubiquinol-cytochrome c reductase core protein II	0.27	0.35	0.87	0.88	0.51	0.45	0.39	0.35	0.42	0.28	0.34	0.21	0.34	0.49	0.32	0.47	0.38	0.43	0.44	0.36	0.68	0.38
26922	Hs.79064	deoxyhypusine synthase	1.78	0.71	0.77	0.69	0.54	0.70	0.53	0.55	0.96	0.95	1.07	1.47	1.76	2.12	0.80	0.67	0.76	0.77	1.02	0.62	0.47	0.31
30664	Hs.207776	aspartylglucosaminidase	1.31	3.23	1.56	2.06	2.28	1.91	1.15	1.33	1.47	1.41	1.96	1.23	1.21	0.78	2.27	1.24	1.39	1.40	1.66	1.19	2.07	1.89
31143	Hs.73742	ribosomal protein, large, P0	0.29	0.71	0.60	1.11	0.42	0.41	0.96	0.44	0.33	0.24	1.28	1.27	1.57	0.35	0.69	0.37	0.50	0.54	0.45	0.39	0.36	0.55
31169	Hs.75546	capping protein (actin filament) muscle Z-line, alpha 2	0.66	1.11	1.35	1.05	1.38	1.11	0.63	1.07	0.96	0.86	1.26	0.65	0.99	0.60	0.77	1.95	0.57	0.97	0.59	0.86	2.21	0.97
27549	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	0.59	1.08	1.16	0.70	0.76	0.52	1.12	0.62	0.41	0.43	0.57	0.68	0.29	0.35	0.69	0.52	0.41	1.02	1.00	0.64	0.69	0.82
27624	Hs.75887	coatomer protein complex, subunit alpha	2.17	1.22	1.64	1.79	0.92	1.65	3.35	1.32	1.44	1.29	1.25	1.27	1.15	2.24	1.42	1.62	1.38	0.93	1.37	1.71	1.07	1.85
27848	Hs.166160	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	0.62	0.73	1.05	0.71	0.62	0.54	0.69	0.60	0.38	0.43	0.65	1.37	0.92	0.67	1.05	0.55	0.76	0.79	0.82	0.52	0.78	0.77
28309	Hs.171625	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	1.05	0.92	1.58	0.97	0.80	0.73	2.60	0.97	1.10	1.55	0.80	2.21	1.75	2.03	1.84	0.90	1.20	1.43	1.39	1.46	0.74	0.65
28410	Hs.82927	adenosine monophosphate deaminase 2 (isoform L)	1.69	1.48	1.93	1.88	1.40	1.58	1.82	1.89	1.70	1.15	2.22	1.65	1.31	1.31	3.62	1.14	0.97	1.45	1.23	0.92	1.50	1.48
28985	Hs.75372	N-acetylgalactosaminidase, alpha-	1.12	1.06	1.57	1.32	1.52	1.31	0.83	1.13	1.51	1.15	1.38	2.22	2.09	3.01	1.95	1.44	1.57	1.13	1.33	1.53	0.61	1.03
29054	Hs.153961	ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha)	0.87	1.08	0.81	1.54	1.45	0.97	1.09	1.63	1.48	1.45	1.57	1.79	1.81	1.31	1.68	1.42	0.86	0.82	1.10	1.00	1.71	1.01
30272	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amil	0.70	0.72	1.17	0.78	0.90	0.68	0.56	0.85	0.59	0.63	1.52	1.72	0.80	1.54	1.69	0.91	1.14	0.82	0.83	0.99	0.60	0.71
34945	Hs.12084	Tu translation elongation factor, mitochondrial	0.52	0.97	0.87	0.80	0.75	0.50	0.72	0.74	0.60	0.67	0.68	0.37	0.78	0.99	0.74	0.72	0.59	0.85	0.77	0.68	0.77	0.74
32875	Hs.159627	death associated protein 3	1.43	2.47	0.84	2.10	1.68	2.12	4.02	1.52	1.18	1.54	1.58	1.47	1.25	1.40	1.83	1.32	1.57	1.44	2.09	1.28	1.68	2.44
32898	Hs.76394	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0.67	1.08	2.77	1.26	2.29	1.16	1.58	1.40	1.45	1.34	1.70	1.93	1.18	1.24	1.13	2.13	0.69	0.59	0.97	0.84	1.09	0.68
33525	Hs.2186	eukaryotic translation elongation factor 1 gamma	0.51	1.14	0.88	0.77	1.11	0.69	1.03	0.65	0.47	0.47	0.81	1.46	1.17	1.11	1.07	0.74	0.63	1.05	0.52	0.91	0.84	0.98
33632	Hs.597	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	1.05	1.33	2.30	2.80	1.41	2.77	2.63	1.42	2.70	2.81	2.40	1.60	0.95	0.86	1.76	2.14	1.12	1.28	1.59	1.04	0.95	1.99
34255	Hs.240013	catechol-O-methyltransferase	1.53	0.71	0.84	0.71	0.79	0.70	1.54	0.80	0.65	0.46	0.89	1.00	0.65	1.09	0.90	0.73	1.21	1.62	1.63	1.57	1.05	0.82
34357	Hs.180952	actin, beta	0.99	1.43	1.65	0.84	1.05	0.83	0.95	0.73	0.81	0.89	0.86	3.47	2.15	1.10	1.11	1.21	1.14	0.89	0.89	0.88	0.78	0.93
34355	Hs.182278	calmodulin 2 (phosphorylase kinase, delta)	2.87	1.43	1.56	2.16	1.32	1.66	1.88	1.13	1.25	0.93	1.19	1.44	1.15	0.90	1.47	1.34	1.75	1.57	2.05	1.96	1.43	1.33
34396	Hs.74335	heat shock 90kD protein 1, beta	0.72	1.73	1.29	0.99	1.03	0.95	1.17	0.85	1.05	1.23	1.71	1.28	1.58	0.84	1.00	1.44	1.01	0.89	1.13	1.29	1.02	1.31
39285	Hs.77508	glutamate dehydrogenase 1	0.54	0.60	0.37	0.74	0.69	0.38	0.41	0.74	0.75	0.51	0.53	0.38	0.82	0.35	0.61	0.65	0.85	1.42	0.99	0.90	0.66	0.87
39796	Hs.831	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	0.81	0.53	0.80	0.62	0.61	0.89	0.93	0.56	1.06	1.29	0.64	1.11	1.08	0.88	1.44	0.58	1.08	1.07	0.98	0.85	0.62	0.62
37196	Hs.181373	accessory proteins BAP31/BAP29	1.23	1.08	0.65	0.46	0.73	0.98	0.91	1.09	0.85	0.80	1.23	1.06	1.23	1.06	1.05	1.26	0.94	0.67	0.84	1.26	0.91	0.85
37366	Hs.179661	Homo sapiens clone 24703 beta-tubulin mRNA, complete cds	1.34	0.69	1.81	1.01	1.16	2.58	2.77	0.49	2.07	3.13	1.16	3.15	0.71	0.85	1.53	1.38	2.24	1.94	2.17	1.33	1.00	1.90
37904	Hs.78802	glycogen synthase kinase 3 beta	1.73	0.61	1.54	0.91	0.64	0.93	1.12	0.67	1.11	1.16	0.93	1.56	0.75	1.15	1.19	1.12	1.52	1.22	1.17	1.74	0.88	0.80
38471	Hs.82380	menage a trois 1 (CAK assembly factor)	1.34	1.17	0.76	0.86	1.09	0.81	0.57	1.66	1.49	1.74	0.94	1.79	3.23	2.07	1.70	1.45	1.11	1.08	1.29	1.15	1.46	0.73
39993	Hs.75428	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	0.93	0.61	0.84	0.71	0.56	0.52	0.96	0.63	0.76	1.32	0.98	2.16	0.75	0.99	1.35	0.68	1.05	0.62	0.99	0.43	0.86	0.90
42214	Hs.74101	spleen tyrosine kinase	4.57	2.20	1.77	2.73	3.40	4.33	1.52	2.03	2.65	2.91	0.73	2.57	1.85	2.11	2.04	1.01	1.66	2.60	2.59	2.22	1.76	2.84
42352	Hs.164280	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6	0.39	0.61	1.17	0.25	0.54	0.63	0.78	0.81	0.33	0.52	0.80	1.58	0.99	0.73	0.72	0.57	0.45	0.56	0.44	0.34	0.65	0.54
40304	Hs.469	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.68	0.73	2.33	1.32	1.06	0.86	0.69	0.95	1.52	0.87	1.00	0.64	0.70	0.75	1.08	1.08	0.92	1.15	0.98	1.46	0.78	0.90
40360	Hs.2437	eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)	2.37	2.05	1.22	1.21	1.88	1.21	1.60	1.88	1.35	2.10	1.48	2.41	1.50	1.33	2.64	1.06	1.86	1.53	2.29	1.40	1.40	1.45
41199	Hs.75238	chromatin assembly factor 1, subunit B (p60)	2.05	0.72	2.05	1.57	0.99	0.66	1.88	1.36	1.85	2.38	1.54	1.40	1.16	1.01	1.33	0.69	1.10	1.14	1.65	1.06	0.93	1.67
41452	Hs.28491	spermidine/spermine N1-acetyltransferase	0.36	0.97	1.38	0.58	1.02	0.47	0.34	0.81	0.69	0.83	0.90	1.02	0.29	0.50	0.76	0.64	0.33	0.49	0.53	1.17	1.85	0.60
41511	Hs.12163	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	0.91	0.69	0.85	0.76	0.79	0.62	0.84	0.58	0.54	0.72	0.79	0.43	0.31	0.42	0.63	0.51	0.48	0.38	0.53	0.69	1.53	0.78
42059	Hs.74635	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-	0.67	0.89	0.74	0.93	0.91	0.90	0.47	0.62	0.46	0.29	0.70	0.55	0.49	0.54	0.85	0.53	0.37	0.75	0.55	0.71	1.23	0.85
42096	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	1.09	2.03	0.75	1.47	1.03	1.04	2.89	1.15	0.61	0.78	1.17	0.73	0.54	0.72	1.41	1.10	0.68	0.72	1.25	1.04	1.01	1.20
44180	Hs.74561	alpha-2-macroglobulin	4.80	12.92	10.07	7.12	10.28	8.27	19.54	8.02	11.16	10.24	8.84	10.68	5.41	2.03	7.53	5.75	9.13	5.90	13.97	3.64	4.47	5.65
44255	Hs.79086	ribosomal protein, mitochondrial, L3	1.42	0.79	0.87	1.08	0.93	0.89	1.49	0.92	1.05	0.86	0.60	1.44	0.78	0.76	0.55	0.84	0.90	1.01	1.25	1.27	0.63	1.10
44307	Hs.2178	H2B histone family, member Q	0.56	1.20	1.24	0.58	0.87	0.62	0.56	0.62	0.63	0.57	0.61	0.45	0.36	0.51	0.65	1.19	0.58	0.92	0.50	0.67	0.87	0.83
43021	Hs.239817	histidyl-tRNA synthetase	0.56	0.82	0.53	0.92	0.97	0.52	0.76	0.92	0.75	1.18	0.75	0.88	0.70	1.19	1.08	0.81	0.80	0.75	1.02	0.66	0.92	0.93
43129	Hs.317	phospholipase C, gamma 1 (formerly subtype 148)	0.60	0.72	0.74	1.02	0.74	0.47	0.88	0.77	0.70	0.89	0.84	0.78	0.59	0.81	0.65	0.64	0.73	0.69	0.78	0.88	0.91	0.48
43231	Hs.74619	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	1.89	1.36	1.08	1.19	1.28	1.03	1.54	1.05	1.43	1.36	0.99	1.02	1.36	0.85	1.24	1.16	1.19	0.84	0.91	0.99	1.07	1.82
43338	Hs.182447	heterogeneous nuclear ribonucleoprotein C (C1/C2)	0.87	1.46	1.06	1.22	0.66	0.93	1.05	0.76	0.77	0.83	0.91	0.74	0.95	0.90	1.18	0.93	0.77	0.85	1.09	1.01	0.68	0.73
43241	Hs.173912	eukaryotic translation initiation factor 4A, isoform 2	2.45	1.89	1.14	1.39	1.68	1.03	1.02	1.56	1.03	1.18	1.57	1.00	1.29	0.66	1.49	1.23	1.50	1.42	1.47	0.98	1.26	1.80
43550	Hs.2795	lactate dehydrogenase A	0.29	0.57	0.94	0.34	0.36	0.18	0.55	0.59	0.29	0.29	0.68	0.43	0.73	0.73	0.58	0.25	0.25	0.45	0.47	0.93	0.56	0.64
43563	Hs.82568	cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthoma	3.76	7.81	1.66	2.46	5.38	5.84	10.42	3.58	3.73	5.09	2.89	10.22	4.09	4.41	8.57	2.95	5.79	4.10	4.67	0.96	1.99	3.45
43622	Hs.89582	glutamate receptor, ionotropic, AMPA 2	3.62	1.03	0.82	1.27	1.06	0.68	2.43	1.23	1.30	2.36	4.53	1.89	0.54	1.56	1.68	0.83	1.33	3.89	9.58	1.20	0.51	1.17
44537	Hs.83753	small nuclear ribonucleoprotein polypeptides B and B1	0.69	1.03	0.87	0.84	0.69	0.85	1.29	0.86	0.66	0.83	0.98	1.38	1.28	1.11	0.84	2.02	0.76	0.53	1.00	0.92	1.53	0.66
50359	Hs.75694	mannose phosphate isomerase	1.04	1.45	1.25	1.20	1.49	1.21	1.43	1.62	1.42	2.10	1.26	1.73	0.95	1.05	1.28	0.64	1.58	1.88	1.91	1.27	1.71	1.18
50666	Hs.89674	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	0.72	0.68	0.92	0.83	0.52	0.85	0.63	0.51	0.62	0.40	0.74	0.72	0.79	1.19	0.95	0.91	0.65	0.55	0.53	1.29	0.58	0.68
50941	Hs.63984	cadherin 13, H-cadherin (heart)	0.56	0.86	0.56	0.51	0.89	1.23	0.26	0.66	0.64	1.16	0.49	3.52	0.48	0.71	0.75	0.33	0.46	0.60	0.59	0.50	0.99	0.59
45233	Hs.82916	chaperonin containing TCP1, subunit 6A (zeta 1)	1.46	1.34	1.16	1.78	1.40	1.63	1.21	1.11	0.90	0.97	1.71	0.69	0.76	0.75	0.91	0.77	0.85	1.01	1.20	1.69	2.42	1.70
45941	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.71	1.91	2.14	2.71	1.40	1.86	3.51	0.89	2.10	2.53	1.29	2.36	1.82	1.39	1.56	1.43	0.97	1.52	2.97	1.36	0.73	1.48
45941	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.71	1.91	2.14	2.71	1.40	1.86	3.51	0.89	2.10	2.53	1.29	2.36	1.82	1.39	1.56	1.43	0.97	1.52	2.97	1.36	0.73	1.48
46171	Hs.129673	eukaryotic translation initiation factor 4A, isoform 1	0.75	0.86	1.69	0.89	1.33	0.76	0.96	1.01	0.68	0.60	0.96	1.20	1.06	0.97	0.76	1.00	0.60	0.88	0.82	0.82	0.97	0.99
47202	Hs.74571	ADP-ribosylation factor 1	2.03	1.74	1.62	1.46	1.50	1.52	1.56	1.44	1.46	0.78	1.58	3.46	2.62	1.31	1.61	2.04	0.88	0.99	1.46	1.57	1.74	1.42
47833	Hs.248323	Tubulin, alpha, brain-specific	1.25	1.12	1.86	1.72	0.78	1.18	1.33	0.84	1.09	1.03	1.79	1.34	2.55	1.38	1.24	1.27	1.34	0.99	1.11	1.48	0.81	1.00
49888	Hs.183153	ADP-ribosylation factor 4-like	0.58	0.61	0.43	0.36	0.57	0.36	0.48	0.45	0.61	0.46	0.52	0.53	0.33	0.36	0.44	0.28	0.82	0.45	0.58	0.80	1.12	0.36
50117	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	0.26	0.69	1.23	0.60	0.47	0.43	0.97	0.40	0.34	0.59	0.46	1.02	1.83	1.12	0.81	0.35	0.40	0.28	0.52	0.29	0.55	0.91
51293	Hs.79	aminoacylase 1	1.09	2.11	1.42	1.21	1.76	0.60	1.12	0.94	1.25	2.02	0.73	2.11	1.11	0.67	0.64	1.12	0.74	0.96	1.19	0.82	1.59	0.93
51666	Hs.77929	excision repair cross-complementing rodent repair deficiency, complementation group 3 (x	1.01	1.80	0.93	1.18	1.39	1.23	1.90	0.99	1.15	1.59	1.08	1.60	1.75	1.14	1.27	1.01	1.45	1.65	1.18	1.05	1.16	1.75
51740	Hs.146812	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzy	0.62	1.11	0.60	0.70	0.58	0.78	0.60	0.34	0.80	0.76	0.33	0.87	0.49	0.88	0.82	0.64	0.81	0.74	0.45	0.79	0.46	0.52
53316	Hs.75375	malate dehydrogenase 1, NAD (soluble)	1.24	0.53	0.92	1.34	0.62	0.87	0.65	0.48	0.83	0.49	0.52	0.35	0.36	0.73	0.56	0.56	0.67	0.60	0.60	0.63	1.50	0.77
752652	Hs.154485	transcription factor 7-like 2 (T-cell specific, HMG-box)	2.20	3.88	2.94	2.52	3.06	1.58	6.84	2.07	2.02	1.31	3.00	0.98	0.97	1.49	2.58	2.33	0.42	1.64	1.14	0.96	2.08	1.78
770192	Hs.81337	lectin, galactoside-binding, soluble, 9 (galectin 9)	4.04	11.50	7.92	5.78	5.98	4.50	3.04	7.56	21.27	4.72	6.99	9.09	3.87	6.06	5.08	3.51	3.65	3.33	4.23	3.04	4.95	2.66

129865	Hs.48915	serine/threonine kinase 15	2.41	1.75	1.92	1.54	1.41	1.97	2.27	2.00	1.02	2.25	2.73	0.81	1.33	1.18	1.18	0.44	1.75	0.73	1.91	1.71	1.79	1.50
109221	Hs.14912	KIAA0286 protein	1.86	3.26	3.02	3.31	1.64	1.57	2.79	3.15	2.21	2.26	2.21	1.34	0.69	0.92	1.04	1.28	2.26	1.54	2.90	1.72	1.50	2.17
754479	Hs.75470	hypothetical protein, expressed in osteoblast	3.11	2.72	5.53	5.00	1.84	2.89	3.14	5.63	7.40	3.47	4.40	3.97	1.15	2.91	4.61	2.96	3.67	1.71	3.83	1.47	2.67	2.29
123980	Hs.147189	HYA22 protein	1.37	2.10	1.62	3.03	1.73	1.29	1.35	1.21	1.28	1.36	1.59	3.47	2.77	1.48	2.73	1.67	0.81	1.59	0.90	0.84	1.33	1.12
37491	Hs.73999	thyroid receptor interacting protein 10 (CDC42-interacting protein)	0.61	0.76	0.50	1.23	0.72	0.58	0.58	0.54	0.52	0.48	0.61	0.52	0.28	0.67	0.60	0.70	0.34	0.34	0.45	0.56	0.57	0.54
129146	Hs.30888	cytochrome c oxidase subunit VIIa polypeptide 2 like	0.99	0.84	0.84	1.43	1.21	1.04	1.49	1.06	0.85	0.76	1.11	0.47	0.83	0.85	0.95	1.03	1.22	1.24	0.78	1.35	1.57	1.13
300590	Hs.153884	ATP binding protein associated with cell differentiation	1.15	0.51	1.20	0.79	0.33	0.60	1.57	0.41	1.18	0.95	0.63	0.71	0.69	0.80	0.87	2.08	0.98	0.70	0.60	0.92	0.51	1.27
770910	Hs.166096	E74-like factor 3 (ets domain transcription factor)	0.48	0.60	0.11	0.21	0.59	0.70	0.23	0.32	0.40	0.37	0.38	1.99	1.27	0.44	1.53	0.33	0.64	0.45	0.33	0.58	1.12	0.45
380394	Hs.155103	eukaryotic translation initiation factor 1A, Y chromosome	1.42	1.31	1.90	0.99	1.76	0.88	1.81	1.09	0.62	2.44	1.01	3.27	5.55	1.46	3.13	0.84	1.55	1.24	1.99	1.07	1.00	1.11
144932	Hs.3436	deleted in oral cancer (mouse, homolog) 1	1.44	2.77	1.37	3.14	1.76	0.90	3.62	1.32	1.97	1.39	0.79	0.67	0.58	0.77	0.62	1.51	1.32	1.15	1.14	1.49	2.32	2.24
165857	Hs.153687	inositol polyphosphate-4-phosphatase, type II, 105kD	0.24	1.25	0.72	0.70	1.16	0.64	0.13	1.33	0.95	0.93	2.31	1.60	0.79	0.33	1.31	1.38	1.11	0.51	0.69	0.47	1.03	0.91
359395	Hs.60415	N-ethylmaleimide-sensitive factor attachment protein, gamma	1.75	4.07	3.28	2.31	3.15	2.27	1.04	1.56	2.55	1.76	1.98	2.93	1.97	1.62	1.91	1.21	1.65	1.32	0.85	1.21	2.42	1.98
129644	Hs.24752	spectrin SH3 domain binding protein 1	0.94	0.78	1.08	1.29	1.10	1.18	1.54	0.60	0.98	1.00	1.15	1.23	0.76	0.89	0.99	0.94	1.00	1.00	0.78	1.07	0.63	1.00
137836	Hs.28866	programmed cell death 10	2.05	2.97	0.86	1.39	2.02	1.80	1.32	1.34	1.76	1.58	1.31	0.95	0.74	0.51	0.84	0.95	1.80	1.22	1.63	1.39	1.11	1.60
823691	Hs.79069	cyclin G2	0.39	1.19	0.60	0.51	1.13	0.79	0.39	1.85	0.97	0.55	2.27	0.65	0.64	0.44	1.41	0.87	0.58	1.07	0.88	0.71	0.95	0.55
248371	Hs.75887	coatomer protein complex, subunit alpha	1.68	1.14	1.81	0.48	3.16	1.98	2.24	0.73	2.38	0.95	1.34	1.59	1.43	1.86	1.53	2.51	2.05	0.94	1.33	1.46	2.19	2.39
813171	Hs.20237	DKFZP566C134 protein	2.44	5.43	2.94	2.38	4.05	2.02	2.62	2.58	2.56	3.51	2.02	1.47	1.05	1.11	0.92	0.99	2.18	1.84	3.30	1.28	2.49	1.51
150314	Hs.12540	lysophospholipase I	0.84	1.64	0.88	1.10	1.72	0.80	0.89	1.10	1.09	1.74	1.29	0.69	0.99	0.56	0.81	0.98	0.82	1.36	1.13	2.04	1.13	1.19
187266	Hs.170001	eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD)	1.29	5.29	1.28	3.31	6.76	2.21	1.69	3.46	4.71	5.75	4.66	3.75	1.13	4.04	3.35	2.87	1.69	4.63	3.78	2.28	3.77	1.39
823679	Hs.153498	chromosome 18 open reading frame 1	2.43	8.01	9.35	15.68	5.95	4.17	3.16	5.16	12.19	5.02	3.69	5.59	4.15	3.37	9.69	3.13	6.16	3.54	8.66	1.28	2.06	2.64
246524	Hs.20295	CHK1 (checkpoint, S.pombe) homolog	1.77	3.48	3.10	2.93	2.41	1.74	2.98	1.54	1.72	2.55	1.52	1.37	0.54	0.92	0.90	0.57	1.01	1.21	1.12	1.28	2.09	1.61
243343	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)	1.11	0.73	1.84	0.47	0.53	0.41	2.45	0.55	1.33	10.38	0.37	3.10	1.19	1.68	2.20	0.32	1.99	1.48	1.99	1.41	0.58	0.98
470930	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)	2.08	5.99	2.31	2.91	2.94	1.55	3.78	1.96	1.32	2.59	1.75	2.44	2.07	2.31	1.79	1.57	2.12	1.18	1.76	1.08	1.72	2.76
377152	Hs.10758	NADH dehydroqenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase	0.54	0.42	0.46	0.36	0.63	0.22	0.72	0.59	0.58	0.48	0.63	0.29	0.39	0.58	0.79	0.43	0.62	0.64	0.82	0.40	0.61	0.20
283301	Hs.177664	KIAA0914 gene product	0.65	0.94	1.59	0.67	1.64	0.37	0.43	1.07	0.37	0.37	0.72	0.93	0.22	0.52	0.85	0.30	0.35	0.83	0.57	0.37	2.26	1.02
755416	Hs.37501	MAD (mothers against decapentaplegic, Drosophila) homolog 5	2.03	2.60	2.07	2.17	2.77	0.73	1.01	4.87	0.63	1.84	2.48	1.42	1.16	0.89	1.19	0.59	1.79	2.12	1.29	1.28	2.25	1.24
347373	Hs.184693	transcription elongation factor B (SIII), polypeptide 1 (15kD, elongin C)	1.98	2.01	1.15	1.13	1.33	0.66	1.27	1.59	0.83	1.63	1.54	0.65	0.97	0.95	1.19	0.68	1.03	1.12	1.15	1.38	1.68	1.03
42118	Hs.9610	purinergic receptor P2X, ligand-gated ion channel, 4	1.90	1.21	1.67	2.25	1.14	1.35	9.56	1.02	3.28	2.56	2.31	9.09	6.74	5.69	8.70	1.59	4.25	2.54	4.04	1.41	0.93	1.26
359982	Hs.79428	BCL2/adenovirus E1B 19kD-interacting protein 3	0.80	0.96	1.53	1.54	1.07	0.55	1.88	2.02	0.78	0.53	3.24	1.11	0.77	0.75	0.92	0.71	0.89	1.18	1.19	1.50	1.45	1.22
813591	Hs.69575	peroxisomal acyl-CoA thioesterase	1.35	1.01	0.97	0.75	1.80	1.55	0.83	1.85	0.93	1.37	1.53	1.50	1.53	1.07	1.00	1.20	0.76	0.93	1.15	0.55	1.55	1.09
198917	Hs.83086	Homo sapiens GT212 mRNA	1.03	1.88	0.85	1.52	1.67	1.51	1.89	1.38	2.02	2.33	1.54	1.49	1.46	1.46	2.53	1.52	1.79	1.36	1.99	0.89	1.50	1.29
771084	Hs.12272	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	0.77	1.56	1.72	0.81	1.39	0.89	0.95	1.06	1.48	2.44	0.99	0.89	0.84	0.81	1.40	0.65	1.84	1.26	2.10	0.80	1.30	0.99
813714	Hs.195175	CASP8 and FADD-like apoptosis regulator	1.48	0.85	1.95	1.67	0.92	1.08	2.47	0.95	2.20	3.24	1.49	1.44	0.72	1.52	1.22	1.92	1.55	1.93	0.94	1.07	0.74	1.29
30502	Hs.250500	delta-like 1 (mouse) homolog	0.69	1.08	0.47	0.69	0.70	0.59	0.49	0.70	1.18	0.80	1.03	1.04	1.36	1.00	1.33	0.93	0.83	0.52	1.39	0.82	0.74	0.94
358850	Hs.74137	transmembrane trafficking protein	0.91	0.74	1.15	1.02	0.62	0.58	0.50	0.62	0.73	0.57	0.88	0.76	1.20	0.90	1.05	0.90	0.91	1.12	0.76	1.48	0.80	0.35
138991	Hs.80988	collagen, type VI, alpha 3	5.65	11.25	18.29	12.06	15.06	8.72	24.01	6.60	4.32	18.27	18.33	23.65	6.35	3.99	15.97	7.79	8.41	6.25	12.19	4.02	7.09	5.20
139573	Hs.75875	ubiquitin-conjugating enzyme E2 variant 1	0.94	1.15	0.54	0.67	1.31	0.65	0.59	0.99	1.23	1.17	0.85	0.95	1.03	1.01	1.11	0.83	1.07	0.74	1.72	1.20	1.25	0.97
811842	Hs.237825	signal recognition particle 72kD	1.36	3.83	1.45	1.58	1.45	1.76	0.96	1.25	1.54	0.94	1.61	0.94	0.75	0.56	1.05	1.06	1.19	0.80	1.16	1.23	2.37	2.32
243580	Hs.36787	chromodomain helicase DNA binding protein 2	2.77	3.67	1.51	2.28	2.76	1.49	1.88	2.43	1.67	2.52	1.90	1.14	0.47	0.70	0.74	1.03	2.74	1.74	1.46	1.07	2.40	1.90
262996	Hs.22670	chromodomain helicase DNA binding protein 1	1.28	4.15	1.41	2.22	3.19	1.47	1.07	1.84	2.09	1.49	2.01	3.21	1.50	1.63	3.39	0.90	1.01	1.78	2.00	0.90	1.73	1.63
130820	Hs.173854	PAX transcription activation domain interacting protein 1 like	2.02	2.81	1.36	1.78	1.99	1.25	1.84	1.80	2.02	3.36	1.76	2.86	1.04	0.99	1.49	0.79	1.23	1.93	2.73	0.96	2.37	1.73
203351	Hs.23103	Golgi vesicular membrane trafficking protein p18	1.08	1.62	1.22	1.37	1.90	1.35	1.22	1.03	1.50	0.95	1.71	1.46	0.94	0.99	1.44	1.04	1.02	1.09	1.28	1.10	1.50	1.22
340558	Hs.82425	actin related protein 2/3 complex, subunit 5 (16 kD)	1.33	0.92	1.42	0.97	1.00	0.88	0.52	0.64	1.04	0.49	0.75	0.91	0.87	0.77	1.01	1.04	0.66	0.47	0.71	0.85	0.98	1.33
202904	Hs.184167	splicing factor, arginine/serine-rich 7 (35kD)	1.67	3.54	1.74	3.78	1.71	1.65	2.83	1.45	0.93	1.71	1.39	2.88	1.44	2.02	2.36	1.27	2.31	1.96	2.29	1.49	1.55	1.04
150623	Hs.120980	nuclear receptor co-repressor 2	1.08	1.62	0.99	1.15	1.63	1.06	0.92	1.36	1.65	1.15	1.17	3.29	1.96	1.60	0.45	1.77	1.43	1.27	1.03	0.89	1.03	1.24
327350	Hs.75598	heterogeneous nuclear ribonucleoprotein A2/B1	1.26	1.19	1.23	1.40	1.24	1.12	1.51	1.40	1.17	1.12	0.96	1.24	0.64	0.63	1.08	0.76	1.21	1.21	1.93	1.35	1.11	0.86
767828	Hs.83951	Hermansky-Pudlak syndrome	1.35	1.91	0.77	1.63	1.99	1.46	1.24	2.13	1.64	0.87	1.30	1.99	1.55	1.44	1.19	1.55	1.00	1.68	2.02	1.18	1.00	1.74
363103	Hs.80684	high-mobility group (nonhistone chromosomal) protein 2	2.14	5.51	4.58	2.96	3.00	1.89	3.09	2.68	1.51	4.86	2.52	1.30	0.93	0.67	0.99	0.84	2.30	1.91	2.86	1.72	1.97	1.85
129506	Hs.79162	structure specific recognition protein 1	1.12	4.16	2.06	1.66	2.47	1.69	1.21	1.47	1.57	2.96	1.42	1.42	1.56	2.78	2.47	1.24	1.07	1.25	0.70	0.88	1.41	1.67
211780	Hs.51043	hexosaminidase B (beta polypeptide)	1.44	1.08	0.88	1.37	1.72	1.17	0.70	1.16	1.79	0.87	1.20	0.76	0.71	0.73	0.72	1.20	1.06	1.71	1.45	1.20	1.46	1.09
23185	Hs.204133	hexabrachion (tenascin C, cytotactin)	0.77	1.08	1.09	0.89	1.28	1.55	0.70	1.64	1.95	1.82	1.18	0.92	0.81	1.01	1.25	1.11	0.98	1.41	1.02	1.70	0.72	0.82
153411	Hs.76807	Human HLA-DR alpha-chain mRNA	5.80	48.41	21.72	14.13	21.85	11.63	14.60	10.19	8.91	14.91	22.17	11.34	11.34	1.97	13.36	8.76	3.97	6.71	15.24	4.01	7.79	7.36
256664	Hs.147097	H2A histone family, member X	3.67	3.22	2.60	1.78	1.04	1.62	3.35	1.81	1.26	1.87	2.63	1.22	1.19	1.24	1.30	1.56	0.93	0.99	1.96	1.10	1.70	0.88
66317	Hs.7644	H1 histone family, member 2	4.19	5.07	6.83	1.47	1.44	3.30	5.56	3.30	1.86	5.40	5.36	1.20	2.85	1.20	7.08	1.90	1.85	0.96	8.87	1.04	1.54	3.41
811827	Hs.20894	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1.89	1.71	0.85	2.06	1.48	1.76	1.17	1.05	1.72	1.44	1.73	1.60	2.77	1.60	1.50	1.01	2.04	2.84	1.37	1.54	2.58	1.78
124824	Hs.252574	ribosomal protein L10a	0.70	0.57	0.64	0.65	0.62	0.39	1.10	0.59	0.30	0.25	0.67	0.34	0.42	0.44	0.59	0.63	0.44	0.86	0.77	0.67	0.60	0.45
770066	Hs.13421	KIAA0056 protein	3.92	2.85	1.90	2.55	2.13	1.51	2.76	1.69	1.05	1.78	1.88	0.92	0.78	0.87	0.98	1.70	1.11	1.80	1.78	1.67	3.20	1.58
121621	Hs.103804	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	1.15	1.24	1.11	1.69	0.83	1.40	1.61	0.81	0.99	0.39	0.91	2.40	1.66	1.52	1.91	1.25	0.88	1.07	1.31	1.09	0.91	1.09
295729	Hs.18426	translational inhibitor protein p14.5	0.85	1.97	1.25	1.51	1.96	0.76	0.92	1.20	0.89	1.42	1.86	1.89	1.78	0.77	1.73	0.72	1.00	1.17	0.97	1.09	1.73	1.59
301849	Hs.25732	eukaryotic translation initiation factor 4 gamma, 3	1.07	1.26	1.18	1.07	1.40	1.29	1.18	1.23	1.25	1.28	1.50	2.21	0.92	1.15	2.74	0.82	1.32	1.55	1.44	1.53	1.72	1.24
823901	Hs.13137	UV radiation resistance associated gene	2.92	2.38	0.75	1.31	2.98	1.66	2.56	1.45	1.95	1.73	2.10	2.94	1.61	2.13	2.89	1.54	2.26	2.44	2.12	1.35	1.90	2.34
301018	Hs.50905	serine/threonine kinase 9	1.44	1.31	2.65	1.99	1.41	0.89	3.44	1.57	2.31	2.10	4.71	2.21	0.80	1.48	4.28	1.32	2.30	1.60	3.07	1.08	0.61	1.19
108667	Hs.21729	splicing factor 3a, subunit 1, 120kD	0.82	1.47	1.34	1.33	1.29	1.16	1.40	0.82	1.49	1.40	1.42	1.19	1.33	1.54	1.37	1.04	1.03	1.23	1.17	0.48	0.64	0.75
589433	Hs.27076	RNA 3'-terminal phosphate cyclase	1.51	2.05	0.98	1.27	1.26	1.70	1.11	0.87	0.95	1.24	0.95	1.58	0.79	0.85	1.34	0.80	0.96	1.33	1.14	1.30	1.39	1.19
210862	Hs.167835	acyl-Coenzyme A oxidase	2.28	2.37	1.46	1.68	2.66	2.85	2.90	1.35	1.90	1.35	1.75	1.59	1.21	1.71	1.51	2.00	1.78	1.78	1.64	1.97	1.27	1.70
27548	Hs.211608	nucleoporin 153kD	1.36	2.47	1.68	1.92	1.53	2.33	1.24	1.10	1.25	0.93	1.62	1.05	1.32	0.83	1.43	1.27	1.31	1.65	1.26	0.78	1.95	1.93
668442	Hs.71891	discoidin domain receptor family, member 2	2.47	5.44	8.11	6.72	7.06	3.61	13.25	6.31	10.95	6.79	3.67	6.31	1.23	2.75	6.49	2.42	5.05	5.39	7.83	2.18	3.64	3.45
295798	Hs.90061	progesterone binding protein	2.26	2.53	1.79	1.98	1.98	1.55	1.26	1.10	2.03	2.09	1.86	2.42	1.45	1.49	1.77	1.64	1.08	1.45	1.67	1.46	0.83	1.03
813854	Hs.29117	H.sapiens mRNA for pur alpha extended 3'untranslated region	0.86	1.35	1.11	0.75	1.05	0.82	0.86	1.09	1.50	1.58	1.23	0.88	0.64	1.05	1.27	0.68	1.34	1.43	1.91	1.16	0.43	0.61
234011	Hs.25051	plakophilin 2	0.72	1.67	0.44	0.94	0.88	1.93	0.76	0.73	0.70	0.62	0.72	0.46	0.19	0.54	0.46	0.33	0.82	0.78	0.66	0.65	1.32	2.14
813536	Hs.32971	phosphoinositide-3-kinase, class 3	0.98	1.61	1.38	1.06	1.75	1.66	0.65	1.04	1.09	1.16	1.11	0.79	0.32	1.33	0.68	0.61	0.75	1.03	1.33	0.98	0.62	0.67
234562	Hs.51957	SC35-interacting protein 1	1.03	1.27	1.62	1.98	1.47	1.76	0.99	1.24	1.58	2.23	1.09	1.49	1.35	0.93	1.16	0.57	1.33	1.42	0.95	1.15	0.91	1.22
810791	Hs.82380	menage a trois 1 (CAK assembly factor)	1.19	1.19	1.27	0.90	1.24	0.75	0.84	0.88	1.11	1.04	1.00	3.11	1.73	0.76	2.13	0.68	0.96	0.92	1.38	0.81	1.32	0.86
547058	Hs.79101	cyclin G1	0.17	0.28	0.16	0.32	0.35	0.29	0.20	0.20	0.22	0.15	0.22	0.15	0.25	0.18	0.23	0.21	0.21	0.42	0.31	0.38	0.29	0.32
134476	Hs.24167	synaptobrevin-like 1	1.67	2.74	1.10	1.53	2.02	0.61	0.86	1.22	2.09	1.07	1.17	1.17	1.39	0.83	0.73	1.28	1.46	1.15	1.16	1.34	1.53	1.30
809353	Hs.75254	interferon regulatory factor 3	0.81	1.35	0.74	0.72	1.34	0.68	0.97	1.04	0.84	1.00	0.67	1.35	0.77	0.72	1.14	0.86	1.27	0.87	1.59	0.72	0.87	0.60
525518	Hs.78683	ubiquitin specific protease 7 (herpes virus-associated)	0.63	1.22	0.68	0.91	1.12	1.04	1.19	1.00	0.93	0.93	1.11	0.83	1.26	0.86	0.87	1.02	1.26	1.13	0.75	0.92	0.80	0.98
243741	Hs.44532	diubiquitin	2.02	31.90	4.61	11.21	5.02	7.73	2.84	10.64	104.36	0.95	7.43	11.87	1.41	3.69	1.18	4.39	7.59	4.78	5.25	1.10	3.00	5.06
752732	Hs.78943	bleomycin hydrolase	1.30	2.83	2.96	2.24	1.88	1.35	2.88	2.05	2.83	3.50	1.67	1.11	0.86	1.07	3.58	1.16	2.41	1.71	2.68	1.25	1.97	1.41
469686	Hs.96038	Ric (Drosophila)-like, expressed in many tissues	1.20	1.75	1.57	2.17	2.69	1.39	2.26	2.02	1.90	1.31	1.59	0.77	0.52	0.98	1.21	1.00	1.26	0.88	1.21	0.84	1.73	1.42
234237	Hs.38842	Pirin	2.05	1.18	2.32	1.34	2.66	0.88	2.18	0.95	1.33	1.97	1.51	1.03	0.87	1.01	2.40	1.27	2.12	0.66	0.66	0.42	1.25	1.56

177621	Hs.79372	retinoid X receptor, beta	1.59	1.72	1.28	1.04	1.59	0.81	1.06	1.59	1.15	1.45	1.06	1.13	1.38	1.22	1.83	0.83	1.17	1.52	1.68	0.66	1.69	1.62
154465	Hs.184552	biphenylhydrolase-like (serine hydrolase; breast epithelial mucin-associated antigen)	1.58	2.08	1.86	1.51	2.14	1.70	1.55	1.85	1.37	2.25	2.13	1.11	1.69	0.89	1.73	1.44	1.84	1.98	2.05	1.66	3.05	1.51
132012	Hs.132243	aminopeptidase puromycin sensitive	0.73	0.73	0.68	1.10	0.62	0.58	0.63	0.51	0.95	0.90	0.58	0.42	0.74	0.66	0.79	0.56	0.60	0.78	0.88	0.31	0.83	0.34
194214	Hs.90077	TG-interacting factor (TALE family homeobox)	1.70	1.00	0.69	0.57	1.09	0.82	0.84	0.97	1.11	0.96	1.05	0.91	0.74	0.83	1.29	0.82	1.23	0.99	1.42	1.17	0.84	0.71
823930	Hs.90370	actin related protein 2/3 complex, subunit 1A (41 kD)	0.82	1.01	0.80	0.73	0.67	0.42	0.82	0.52	0.40	0.65	0.64	0.63	0.24	0.44	0.68	0.41	0.27	0.47	0.70	0.67	0.62	0.35
366558	Hs.183800	Ran GTPase activating protein 1	2.59	1.93	1.39	1.78	2.10	2.57	1.74	1.90	1.52	2.03	1.62	1.82	2.89	2.21	1.76	1.64	1.36	1.62	2.02	1.72	2.01	1.64
365060	Hs.75618	RAB11A, member RAS oncogene family	1.11	1.09	0.49	0.97	0.80	0.82	0.94	0.72	1.43	0.92	0.89	2.06	0.61	1.13	1.47	0.70	0.75	0.87	1.46	1.07	0.64	0.57
813158	Hs.78582	developmentally regulated GTP-binding protein 2	0.91	1.35	1.29	0.92	1.57	1.38	1.58	1.28	0.92	1.35	1.79	1.67	1.83	1.27	2.32	1.06	1.54	1.18	1.22	0.81	1.66	1.28
299154	Hs.62187	phosphatidylinositol glycan, class K	1.64	0.75	1.42	2.42	0.96	0.96	0.70	0.84	1.42	1.63	0.79	1.21	1.16	1.19	1.29	0.92	0.82	1.77	1.87	1.25	0.55	0.91
770216	Hs.75196	ankyrin repeat-containing protein	1.34	5.84	2.18	2.44	3.99	2.12	3.34	3.11	2.07	2.27	3.20	1.94	2.77	1.77	3.19	2.25	1.86	1.74	2.71	1.33	3.64	3.27
812251	Hs.75074	mitogen-activated protein kinase-activated protein kinase 2	2.25	3.14	1.39	1.93	3.23	1.48	2.20	1.96	2.57	3.99	1.85	1.55	1.51	1.27	1.96	2.08	2.28	1.55	3.75	1.09	2.11	2.02
727292	Hs.74076	CD163 antigen	2.50	2.81	4.11	3.67	2.71	3.27	3.30	3.09	6.00	3.12	5.36	9.85	2.50	4.24	3.95	2.44	3.40	3.00	4.45	1.41	0.87	2.23
21738	Hs.7153	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	2.38	1.45	1.28	1.50	2.21	1.93	1.57	1.12	1.16	1.08	1.88	4.62	2.42	1.72	6.13	1.42	0.94	1.26	1.81	1.22	1.80	1.39
72050	Hs.84974	chloride channel, nucleotide-sensitive, 1A	1.30	1.10	0.61	0.91	0.98	0.77	1.00	0.85	0.93	0.95	1.45	0.83	0.56	0.64	0.94	0.77	0.92	0.93	0.79	0.77	0.63	0.89
754046	Hs.18212	DNA segment on chromosome X (unique) 9879 expressed sequence	3.39	6.15	1.50	2.06	2.51	1.76	2.77	4.21	2.79	2.27	4.15	2.74	4.45	1.47	4.35	2.70	2.25	1.55	2.18	1.50	3.26	1.47
810040	Hs.23119	ITBA1 gene	1.99	3.12	2.49	2.15	2.03	1.08	2.76	1.75	1.99	1.97	3.71	2.22	1.94	1.22	0.89	1.26	1.49	1.53	3.25	1.05	0.72	0.74
154749	Hs.26433	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1	2.48	1.87	0.86	1.33	1.91	1.33	1.61	1.12	1.23	1.16	1.74	1.01	0.83	1.34	1.43	1.30	1.67	1.83	1.37	1.49	2.36	1.15
813751	Hs.75268	sialyltransferase 4C (beta-galactosidase alpha-2,3-sialytransferase)	1.31	1.47	1.87	1.87	1.78	0.61	2.47	1.23	1.16	1.41	1.88	0.67	0.67	0.96	0.72	0.96	0.72	0.59	0.46	1.06	0.77	1.15
251019	Hs.194657	cadherin 1, E-cadherin (epithelial)	1.39	0.71	0.12	0.41	0.50	0.55	1.01	0.57	1.36	1.12	0.59	1.42	0.84	0.60	1.24	0.80	1.22	0.67	1.27	1.01	0.60	0.71
184365	Hs.182907	ESTs	2.33	2.30	1.15	1.46	2.01	1.40	1.30	1.90	2.05	2.57	1.71	1.61	0.93	1.55	1.63	1.51	1.38	1.87	2.31	1.20	1.35	0.78
210317	Hs.115279	RAB11B, member RAS oncogene family	1.60	2.08	0.98	1.77	1.95	3.34	2.50	1.45	2.40	1.32	1.66	1.32	3.65	1.82	2.03	2.04	1.70	1.88	1.30	1.38	1.83	1.95
471266	Hs.153910	DiGeorge syndrome critical region 6	2.03	3.17	2.54	1.74	2.47	2.04	2.53	2.74	2.37	3.64	2.31	2.95	2.76	1.78	2.23	2.58	2.33	1.85	2.47	1.68	3.84	2.19
755239	Hs.42957	methyltransferase-like 1	0.60	1.31	0.74	1.09	0.52	0.62	2.48	1.61	0.86	0.74	1.47	0.78	0.51	0.79	1.13	0.86	0.64	0.89	1.06	1.42	0.69	0.95
341246	Hs.74362	ClpP (caseinolytic protease, ATP-dependent, proteolytic subunit, E. coli) homolog	1.20	1.06	0.44	0.42	0.79	1.03	1.11	0.83	0.65	0.90	1.24	0.78	1.30	0.87	0.91	0.96	1.16	1.05	1.40	0.80	0.96	1.09
26711	Hs.240770	nuclear cap binding protein subunit 2, 20kD	2.20	2.01	1.29	1.39	1.55	1.28	1.17	1.73	1.56	1.40	2.08	1.08	1.66	0.71	1.51	1.03	1.43	1.14	1.12	1.16	0.77	1.30
254321	Hs.15164	nuclear DNA-binding protein	1.57	1.46	1.01	1.94	1.59	1.57	0.94	1.13	1.35	1.10	0.95	0.81	0.67	0.69	1.12	0.99	1.68	1.39	1.50	1.22	1.43	1.22
809992	Hs.74619	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	2.02	1.52	0.95	1.06	1.30	1.25	1.43	1.08	1.42	1.56	0.95	0.93	0.95	0.76	1.05	1.18	1.08	0.90	1.11	1.26	0.63	1.36
275871	Hs.179662	nucleosome assembly protein 1-like 1	0.67	0.57	0.92	0.99	0.80	0.65	0.94	0.56	0.70	0.41	0.70	0.51	0.63	0.37	0.77	0.58	0.82	1.05	0.83	0.57	0.86	0.69
470175	Hs.3548	mature T-cell proliferation 1	1.36	3.82	1.54	0.94	1.77	0.89	1.20	0.96	1.36	2.80	0.80	1.89	0.77	0.54	0.83	0.80	0.92	1.09	1.43	0.81	0.98	0.52
41591	Hs.79085	meningioma (disrupted in balanced translocation) 1	1.09	4.41	2.49	1.84	2.94	2.06	1.10	2.41	4.04	1.74	1.97	2.43	1.48	2.15	4.06	1.19	1.64	1.86	1.89	0.95	1.67	1.44
549146	Hs.68054	stimulated trans-acting factor (50 kDa)	0.93	1.95	0.42	1.26	1.25	1.25	0.31	1.42	1.51	0.61	1.10	1.31	0.30	0.67	0.71	1.28	0.85	1.03	0.87	0.84	0.82	0.72
241880	Hs.155986	angiotensin receptor-like 2	0.89	3.48	1.54	1.96	2.96	1.11	1.16	1.14	1.11	6.50	1.18	1.24	1.28	0.92	1.00	1.10	1.01	1.11	0.82	0.81	1.04	0.84
810813	Hs.38991	S100 calcium-binding protein A2	0.30	0.13	0.10	0.06	0.18	0.11	0.21	0.17	0.16	0.12	0.12	0.09	0.01	0.03	0.05	0.13	0.27	0.22	0.34	0.31	0.18	0.08
177737	Hs.25180	purine-rich element binding protein A	0.92	1.59	0.87	0.65	1.38	0.78	0.88	1.13	1.36	1.41	0.98	1.26	0.62	0.62	1.31	0.86	1.22	1.30	1.93	0.87	0.90	0.78
511066	Hs.49007	poly(A) polymerase	1.26	1.75	0.87	1.79	1.58	2.04	1.07	0.93	1.26	0.94	1.70	2.36	2.03	1.26	1.83	0.86	1.30	1.79	1.06	1.37	1.21	0.55
194182	Hs.23581	Homo sapiens mRNA for leptin receptor gene-related protein	1.26	1.05	0.46	0.77	0.83	0.87	0.63	0.64	1.44	0.99	0.70	0.89	0.45	0.62	0.98	0.84	0.76	1.13	0.75	1.12	0.81	0.68
768299	Hs.85155	butyrate response factor 1 (EGF-response factor 1)	0.79	0.96	1.71	0.83	1.69	0.53	0.73	0.84	0.75	0.38	0.75	1.25	0.27	0.53	1.28	0.74	0.50	1.26	0.96	0.77	1.81	0.63
144834	Hs.146388	microtubule-associated protein 7	3.81	2.71	0.74	2.56	2.45	3.00	2.61	1.65	2.32	3.69	1.34	2.93	0.70	1.76	2.22	1.21	2.65	1.59	1.59	1.88	3.28	1.49
755037	Hs.250911	interleukin 13 receptor, alpha 1	2.32	1.51	1.89	1.50	2.42	1.55	0.72	2.49	2.78	1.82	1.73	1.26	1.69	1.34	1.97	1.60	1.94	1.83	1.10	2.58	2.73	1.22
33690	Hs.64542	pre-mRNA cleavage factor Im (68kD)	1.52	1.47	0.97	1.24	1.26	1.08	0.98	1.34	1.08	0.70	0.98	0.65	1.55	1.04	1.22	0.69	0.75	1.15	0.94	1.07	1.51	1.15
810986	Hs.82887	protein phosphatase 1, regulatory (inhibitor) subunit 11	0.97	1.07	1.04	0.98	1.34	1.03	1.21	1.13	1.61	1.11	1.15	0.92	1.52	1.48	1.76	1.11	1.00	0.87	1.20	0.91	1.53	1.21
50506	Hs.75465	mitogen-activated protein kinase 6	1.37	0.87	0.88	1.28	1.08	1.03	0.77	0.70	1.02	0.46	0.89	0.45	0.34	0.81	0.50	0.55	0.42	0.53	0.66	1.21	1.06	1.19
308041	Hs.3847	peanut (Drosophila)-like 1	4.49	6.27	5.43	6.10	7.29	3.03	0.94	5.22	6.74	12.70	7.03	4.09	7.42	3.68	6.55	2.78	6.32	3.47	5.56	2.19	4.09	3.36
563444	Hs.155591	forkhead box F1	1.30	1.63	1.94	1.43	1.34	1.31	1.56	1.56	1.34	1.20	1.50	1.09	1.07	0.91	0.94	1.13	2.44	1.15	1.26	1.26	1.71	1.36
71606	Hs.10306	natural killer cell group 7 sequence	3.14	10.81	3.20	2.58	3.19	6.16	1.81	3.81	3.82	2.48	3.49	23.35	4.54	7.11	6.30	3.15	4.49	1.60	2.58	1.54	2.17	3.90
276449	Hs.183868	glucuronidase, beta	2.39	2.45	1.52	1.61	2.00	2.18	1.07	1.36	1.97	1.59	1.78	3.79	2.94	2.55	2.55	1.55	1.74	1.76	2.19	1.25	2.35	1.58
245920	Hs.82614	glycogen synthase 2 (liver)	1.21	4.25	1.40	1.01	2.60	5.18	3.11	2.73	2.38	6.98	2.59	2.92	1.00	1.14	1.64	0.35	2.49	1.54	2.32	0.49	1.83	1.78
45632	Hs.772	glycogen synthase 1 (muscle)	0.28	0.59	0.76	0.49	0.56	0.72	0.40	0.52	0.46	0.79	0.91	0.52	0.89	0.42	0.41	0.86	0.43	0.35	0.46	0.46	0.45	0.53
248261	Hs.27	glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system	1.61	3.50	1.18	3.90	3.87	1.22	2.31	2.99	4.48	2.82	2.04	2.69	4.25	1.68	1.04	0.76	7.10	1.49	2.48	1.35	2.18	1.90
136235	Hs.226795	glutathione S-transferase pi	0.75	0.30	0.65	0.74	0.34	0.58	0.92	0.38	0.28	0.10	0.36	0.17	0.08	0.74	0.10	0.25	5.38	0.28	0.22	1.11	0.83	0.55
811792	Hs.82327	glutathione synthetase	0.95	0.59	0.53	0.51	0.89	0.56	0.69	0.84	0.82	1.00	0.82	1.11	0.43	0.59	0.76	0.76	0.60	0.70	0.83	0.83	2.10	0.67
823928	Hs.1581	glutathione S-transferase theta 2	0.39	0.95	0.45	1.00	1.60	0.34	0.69	0.55	0.38	0.63	0.89	0.79	1.03	0.49	0.55	1.01	0.35	0.72	0.72	0.70	1.38	0.33
713922	Hs.247510	glutathione S-transferase M1	2.37	7.03	6.71	2.50	3.94	3.88	3.15	2.67	3.92	1.85	2.21	3.26	5.74	1.73	2.38	1.68	2.55	4.71	6.98	1.35	2.00	2.07
753775	Hs.1435	guanosine monophosphate reductase	0.49	2.23	0.97	0.42	1.04	0.45	1.18	1.06	1.13	0.95	0.79	0.94	0.38	0.55	0.63	1.10	1.67	1.60	0.83	0.92	0.73	0.60
35185	Hs.89768	gamma-aminobutyric acid (GABA) A receptor, beta 1	0.36	0.62	0.52	0.52	0.51	0.36	0.76	0.40	0.45	0.43	0.24	0.78	1.23	0.85	0.71	0.69	0.55	0.77	0.62	0.54	0.59	0.78
197888	Hs.5662	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	0.88	1.68	0.40	2.08	1.15	0.75	1.20	1.17	2.49	0.85	0.76	0.87	0.37	0.46	0.74	0.69	0.84	1.18	1.28	0.90	0.85	0.92
122636	Hs.242	glucose-6-phosphatase, catalytic (glycogen storage disease type I, von Gierke disease)	0.71	2.01	0.69	0.79	0.95	1.44	1.09	0.76	0.62	0.77	0.75	1.59	0.85	1.84	1.12	0.60	0.86	0.61	1.20	0.90	1.26	0.92
741474	Hs.944	glucose phosphate isomerase	0.77	1.71	0.74	0.68	0.80	1.49	1.61	0.67	0.59	0.83	0.65	0.92	0.52	1.03	0.60	0.49	0.84	0.43	1.23	0.94	1.24	0.93
127509	Hs.1691	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease	0.42	0.62	0.32	0.38	0.67	0.34	0.25	0.50	0.54	0.33	0.46	0.43	0.18	0.26	0.33	0.36	0.34	0.49	0.57	0.42	0.66	0.41
51362	Hs.258561	general transcription factor IIB	0.95	1.61	0.64	0.86	1.23	1.00	0.69	0.78	2.02	0.85	0.90	0.89	0.54	1.09	1.05	0.83	0.66	0.79	0.70	0.75	0.80	0.73
823859	Hs.81795	ESTs	0.85	2.78	4.05	2.23	2.68	0.70	1.41	5.13	8.15	2.66	3.00	2.10	0.80	1.67	1.34	3.47	0.61	1.43	3.55	0.98	1.15	0.91
230218	Hs.94672	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 1	1.90	1.04	1.57	0.91	1.35	0.99	1.12	2.37	1.58	1.98	2.05	1.43	0.89	1.16	1.63	1.31	1.09	1.10	2.04	0.66	1.90	0.91
562927	Hs.239894	leucine rich repeat (in FLII) interacting protein 1	1.12	1.23	1.31	1.31	1.48	1.51	0.61	0.99	1.23	0.68	1.25	0.70	0.74	1.35	0.91	1.03	0.52	0.97	0.54	1.12	1.14	1.29
214068	Hs.169946	GATA-binding protein 3	1.37	3.17	0.25	0.46	3.11	2.19	1.10	6.28	6.91	4.36	8.13	5.58	5.11	0.91	7.60	4.69	4.28	4.50	7.12	1.02	1.44	2.02
756480	Hs.111039	N-myristoyltransferase 1	1.09	1.09	0.57	0.79	0.94	1.13	0.84	0.92	1.10	0.89	0.73	0.47	0.68	0.67	0.92	0.70	0.90	1.02	0.89	0.68	1.31	0.99
134748	Hs.77631	glycine cleavage system protein H (aminomethyl carrier)	0.82	0.92	0.72	0.75	0.95	0.67	1.34	0.48	0.56	0.60	0.64	0.59	0.44	0.55	0.61	0.43	0.51	0.42	0.86	0.48	0.71	0.86
768443	Hs.790	microsomal glutathione S-transferase 1	0.47	0.17	0.34	0.25	0.62	0.64	0.33	0.27	0.07	0.08	0.17	0.49	0.05	0.49	0.49	0.20	0.26	0.19	0.39	0.33	0.82	0.62
173228	Hs.151413	glia maturation factor, beta	1.50	0.61	1.21	1.07	1.02	0.76	0.63	0.77	0.92	0.45	0.64	0.47	0.57	0.43	0.81	0.38	0.80	0.93	0.81	0.93	1.45	0.57
214990	Hs.80562	gelsolin (amyloidosis, Finnish type)	2.99	0.80	1.22	1.62	1.74	0.89	0.97	1.10	1.95	1.34	1.37	1.61	0.55	1.99	2.41	1.45	0.70	1.48	0.86	1.05	1.16	0.93
131839	Hs.73769	folate receptor 1 (adult)	4.24	2.74	5.04	2.26	4.17	0.90	0.76	2.19	1.82	1.70	2.14	2.78	1.42	2.22	2.35	1.22	0.72	1.59	0.56	0.88	1.83	1.85
221092	Hs.78915	GA-binding protein transcription factor, beta subunit 2 (47kD)	1.44	2.10	1.51	1.89	2.58	2.26	1.89	2.01	1.83	1.80	1.89	2.45	1.73	1.23	1.71	1.20	1.42	1.62	2.27	1.61	1.61	1.46
260325	Hs.78	GA-binding protein transcription factor, alpha subunit (60kD)	1.44	1.64	2.25	1.65	0.77	1.04	0.57	1.27	1.48	1.49	0.97	4.61	2.05	1.94	3.02	1.08	1.00	1.59	0.74	0.88	0.92	1.85
183200	Hs.73875	fumarylacetoacetate	0.95	1.19	1.03	1.02	1.72	0.67	0.81	1.45	1.99	1.64	2.13	1.35	1.77	2.92	2.44	1.25	1.44	2.05	2.38	0.79	1.44	1.57
469412	Hs.75653	fumarate hydratase	0.66	1.57	1.27	2.22	1.65	1.41	1.23	0.83	0.98	0.55	0.83	0.86	0.96	1.27	1.03	1.09	0.58	0.50	1.33	0.88	1.36	2.26
308437	Hs.576	fucosidase, alpha-L- 1, tissue	2.19	2.92	3.28	3.23	2.50	4.36	1.32	3.39	3.88	4.09	3.12	6.54	2.29	4.55	4.02	3.72	3.54	2.47	2.84	1.96	3.12	1.86
669419	Hs.95998	Friedreich ataxia	2.27	4.47	1.78	2.52	3.13	1.42	0.94	1.62	1.57	2.19	3.88	2.15	0.72	0.88	1.33	1.71	1.02	2.02	3.28	1.09	4.77	2.31
197525	Hs.14286	flavin containing monooxygenase 5	0.92	2.61	2.49	1.23	2.43	1.74	0.86	2.94	4.05	2.85	2.49	1.17	0.44	0.58	0.64	1.21	3.29	2.08	2.52	1.25	1.12	1.00
139009	Hs.118162	fibronectin 1	0.53	0.42	1.66	0.72	1.28	1.58	0.71	1.14	0.93	1.01	2.12	2.08	0.60	1.69	1.00	1.99	0.76	1.13	1.54	1.32	0.68	0.53
811162	Hs.230	fibromodulin	0.58	4.42	8.72	3.80	7.05	3.52	0.75	8.34	10.58	4.03	3.15	3.16	0.96	2.27	1.89	3.83	1.85	1.32	2.51	1.21	1.95	2.02
752631	Hs.1420	fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism)	2.18	4.30	2.75	2.34	4.91	1.61	4.47	5.67	9.64	12.07	3.76	6.41	9.37	4.71	5.31	1.59	3.13	2.30	2.66	1.49	6.09	2.03
767851	Hs.750	fibrillin 1 (Marfan syndrome)	1.12	0.68	1.84	1.73	2.58	1.33	0.41	1.57	5.17	1.49	1.78	2.54	0.62	1.82	2.02	2.62	1.38	1.57	1.21	1.55	1.68	0.98

66728	Hs.26	ferrochelatase (protoporphyria)	0.71	1.78	0.96	1.39	1.65	0.72	0.35	0.53	0.96	0.66	1.45	1.67	0.99	0.79	1.11	1.14	1.03	0.71	0.41	0.76	1.08	1.04
143519	Hs.227729	FK506-binding protein 2 (13kD)	0.95	1.74	0.87	0.93	1.54	0.84	1.68	1.29	1.47	1.87	1.37	2.32	0.72	1.36	1.84	1.23	1.54	0.75	1.79	1.45	1.40	0.41
302292	Hs.75334	exostoses (multiple) 2	0.76	1.77	1.76	0.66	2.43	0.74	1.24	0.83	1.58	1.19	1.03	1.28	0.63	1.32	1.10	1.17	0.81	0.85	1.13	0.79	1.36	1.54
135449	Hs.129953	Ewing sarcoma breakpoint region 1	1.41	2.68	1.40	1.27	1.83	1.13	1.55	2.15	1.93	1.72	2.05	0.96	0.65	0.81	1.18	1.24	1.46	0.89	1.82	1.84	1.68	1.25
665774	Hs.79306	eukaryotic translation initiation factor 4E	0.62	1.20	1.15	1.34	1.14	0.90	0.57	0.71	1.19	1.26	0.99	0.59	0.83	0.97	0.95	1.22	0.81	0.89	0.64	1.32	1.21	1.18
209296	Hs.189584	ESTs	1.30	3.71	2.02	1.44	1.17	1.06	1.34	2.45	1.51	3.16	1.26	1.62	0.63	0.94	1.13	0.39	1.18	1.21	1.66	0.66	1.15	0.91
34849	Hs.75309	eukaryotic translation elongation factor 2	0.33	0.63	0.48	0.54	0.47	0.36	0.64	0.35	0.49	0.41	0.24	0.76	1.25	0.69	0.80	0.68	0.56	0.69	0.60	0.52	0.51	0.73
124597	Hs.1531	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	2.42	2.29	2.09	1.88	2.29	0.89	1.32	1.60	1.87	2.24	2.23	1.54	1.20	0.79	1.20	0.86	2.07	1.14	1.25	0.16	1.28	1.30
811999	Hs.77324	eukaryotic translation termination factor 1	0.80	1.13	0.69	0.60	1.33	0.44	1.21	0.82	0.60	1.54	0.95	0.74	0.39	0.48	0.91	0.82	1.13	0.73	1.40	0.61	1.69	1.35
241412	Hs.154365	E74-like factor 1 (ets domain transcription factor)	1.41	0.95	1.27	1.52	1.44	0.91	0.74	0.74	1.58	1.04	1.09	0.82	0.75	1.40	1.23	1.32	0.63	0.92	1.53	0.93	0.84	0.78
138936	Hs.160483	erythrocyte membrane protein band 7.2 (stomatin)	4.74	1.96	0.83	2.74	2.94	1.75	0.84	1.68	3.69	16.83	2.05	3.66	0.72	1.15	2.15	2.92	1.61	3.46	1.71	1.54	1.82	1.76
366834	Hs.25482	envoplakin	2.86	2.07	0.25	0.82	2.00	1.95	1.96	1.38	1.68	3.47	2.08	2.46	1.42	2.06	2.52	1.60	0.89	1.00	1.36	0.73	2.50	1.78
809939	Hs.861	mitogen-activated protein kinase 3	1.98	1.08	0.78	0.90	1.42	1.06	0.83	1.31	1.26	1.50	1.19	0.85	1.89	1.14	1.49	1.32	1.49	1.38	1.24	0.55	1.53	0.67
813678	Hs.75379	solute carrier family 1 (glial high affinity glutamate transporter), member 3	2.75	0.91	2.69	2.85	1.45	1.67	1.14	0.94	1147.23	2.37	2.69	3.03	0.88	1.40	0.78	2.10	1.03	1.14	1.56	1.33	1.01	0.66
232612	Hs.5822	lectin, mannose-binding, 1	2.91	5.82	4.13	2.61	3.25	1.79	4.07	2.34	2.44	2.35	1.57	4.24	0.76	2.13	4.06	0.94	3.12	1.57	3.28	1.60	1.23	1.81
810156	Hs.79006	deoxythymidylate kinase	1.32	2.68	1.09	1.16	0.95	0.85	2.30	1.08	0.83	0.91	1.05	0.99	0.93	1.50	1.04	1.00	0.50	0.85	1.84	1.81	0.66	1.01
125722	Hs.77494	deoxyguanosine kinase	2.09	1.63	0.76	1.43	1.99	1.17	1.69	1.54	1.30	1.42	1.90	0.97	0.88	0.96	1.25	1.06	1.20	1.23	1.32	0.68	2.11	1.04
184175	Hs.78040	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	0.84	0.53	1.34	0.48	0.97	0.45	0.86	0.87	0.67	0.76	0.62	0.63	0.69	0.68	0.75	0.77	1.02	0.79	0.82	0.79	1.29	0.71
22411	Hs.183	Duffy blood group	1.98	0.57	0.34	0.84	1.41	0.28	4.23	0.27	1.07	0.28	0.64	4.31	5.45	2.21	1.44	0.54	1.82	1.56	7.67	2.58	0.57	0.81
753104	Hs.240217	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2)	1.02	0.41	0.27	0.45	1.27	0.18	0.65	0.38	0.85	0.30	0.44	1.61	0.19	0.74	1.42	0.42	0.46	2.16	0.69	0.79	0.45	0.27
35828	Hs.799	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)	0.58	0.62	1.58	0.72	0.94	0.44	0.83	0.42	1.81	0.95	1.00	2.56	0.51	1.10	0.72	3.26	0.69	1.64	0.71	0.70	0.76	0.65
813648	Hs.74635	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-	0.56	1.07	0.72	1.31	1.08	0.98	0.78	0.52	0.41	0.57	0.79	0.85	0.61	0.83	0.74	0.63	0.53	0.98	0.76	0.83	1.02	1.04
196992	Hs.201967	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpl	0.24	0.41	0.22	0.25	0.35	0.05	0.27	0.15	0.13	0.21	0.25	0.20	0.07	0.93	0.23	0.17	0.12	0.19	0.15	0.21	0.80	0.05
43198	Hs.709	deoxycytidine kinase	2.05	3.78	2.66	2.98	2.80	2.60	1.86	1.36	1.97	1.47	2.68	2.43	1.74	2.75	0.92	1.52	11.43	1.39	2.56	1.63	1.97	1.82
26811	Hs.150930	X-ray repair complementing defective repair in Chinese hamster cells 4	1.06	4.01	1.84	1.35	3.44	2.90	0.82	1.84	1.59	1.43	1.05	1.42	0.63	0.65	1.39	0.83	1.04	1.28	1.94	0.81	1.71	1.69
741769	Hs.180107	polymerase (DNA directed), beta	1.17	3.28	1.28	1.52	1.64	1.70	2.05	1.24	2.74	6.52	1.45	2.29	0.72	1.50	2.02	1.00	1.70	1.27	2.20	1.37	1.59	0.93
276547	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.78	4.86	1.90	2.89	2.69	3.48	3.79	1.77	1.93	2.69	1.47	2.20	2.30	1.58	1.92	1.86	1.61	1.98	3.10	1.69	2.25	2.72
45291	Hs.169488	dentatorubral-pallidoluysian atrophy (atrophin-1)	1.93	1.27	1.68	0.95	1.34	0.99	1.19	1.45	1.58	1.72	1.57	0.69	0.56	0.97	1.15	1.09	1.49	0.97	1.90	1.97	1.85	0.76
510679	Hs.250773	signal sequence receptor, alpha (translocon-associated protein alpha)	1.14	1.06	1.48	2.18	1.27	1.71	1.33	1.07	1.55	0.62	1.51	2.04	1.54	1.41	1.43	1.50	1.49	1.12	0.86	2.09	2.39	1.64
128126	Hs.1369	decay accelerating factor for complement (CD55, Cromer blood group system)	1.46	1.74	1.06	1.71	2.09	1.34	1.55	2.33	4.24	2.36	1.90	1.69	0.94	1.22	1.50	1.15	1.49	1.59	1.88	2.14	1.74	1.48
753447	Hs.77602	damage-specific DNA binding protein 2 (48kD)	0.92	0.67	0.52	0.48	0.65	0.45	0.66	0.55	0.73	0.74	1.16	1.73	0.92	1.56	1.69	0.79	0.41	0.86	0.86	0.83	0.67	0.26
33826	Hs.3446	mitogen-activated protein kinase kinase 1	0.71	0.58	0.48	0.62	0.54	0.88	0.40	0.39	0.74	0.59	0.81	0.43	0.27	0.51	0.39	0.53	0.45	0.64	0.68	0.64	0.63	0.63
810053	Hs.77768	heat shock protein, neuronal DNAJ-like 1	1.48	1.22	0.70	0.73	1.06	1.02	1.28	1.01	1.01	1.87	0.94	7.12	3.95	5.07	4.36	1.29	1.57	1.23	1.05	1.36	0.81	0.62
809916	Hs.184669	zinc finger protein 144 (Mel-18)	1.38	3.52	3.06	2.68	2.27	1.66	1.85	1.34	2.63	2.59	1.71	1.83	1.64	1.27	2.33	1.79	2.01	1.84	3.53	2.78	2.22	1.45
810057	Hs.1139	cold shock domain protein A	0.78	0.87	0.42	1.16	0.65	0.73	1.07	0.51	0.38	0.24	0.47	0.20	0.22	0.26	0.42	0.54	0.31	1.10	0.44	0.88	0.50	0.94
292463	Hs.48576	excision repair cross-complementing rodent repair deficiency, complementation group 5 (x	1.27	3.10	1.00	1.13	1.66	1.35	0.56	0.82	1.22	1.19	0.84	0.79	0.58	1.31	0.99	0.88	0.98	0.89	0.84	0.70	0.88	1.13
810321	Hs.159604	cysteinyl-tRNA synthetase	0.69	2.06	1.09	1.14	2.18	0.70	1.32	1.29	1.35	3.79	1.01	1.33	0.70	1.22	0.72	0.84	0.86	0.71	1.14	0.71	0.93	0.80
810039	Hs.82890	defender against cell death 1	1.54	1.49	1.58	0.95	1.34	0.96	1.14	1.56	1.81	1.64	1.59	0.76	0.56	0.85	1.06	1.08	1.44	0.88	1.59	1.93	1.79	0.71
160126	Hs.77513	COX10 (yeast) homolog, cytochrome c oxidase assembly protein (heme A: farnesyltrans	0.70	4.58	1.56	1.19	2.11	0.95	1.00	1.42	1.40	1.49	0.84	1.01	0.61	1.18	0.95	1.04	0.61	1.18	1.14	0.85	1.33	1.23
196189	Hs.83834	cytochrome b-5	1.38	1.48	1.13	1.25	1.87	2.18	1.04	2.56	1.83	2.74	2.14	1.48	0.74	2.64	4.68	2.33	3.36	2.08	4.13	1.77	3.09	0.92
284620	Hs.124918	ESTs	0.99	0.60	1.24	0.54	0.31	0.35	0.89	0.50	0.62	4.02	0.23	2.42	1.65	1.25	1.96	0.33	1.16	1.14	1.60	1.11	0.40	0.65
28475	Hs.83114	crystallin, zeta (quinone reductase)	2.25	1.47	0.74	2.26	1.55	2.22	1.36	1.30	1.59	1.89	1.06	0.96	1.15	0.68	2.13	1.23	0.62	1.45	2.21	0.33	1.98	1.55
245853	Hs.74626	adaptor-related protein complex 2, beta 1 subunit	0.53	1.50	0.95	1.01	1.06	0.85	0.54	1.01	1.13	0.87	1.06	0.51	1.27	0.97	0.87	1.05	1.93	0.98	0.63	2.41	0.83	0.69
264117	Hs.79572	cathepsin D (lysosomal aspartyl protease)	1.43	1.40	0.72	1.28	1.45	2.97	1.06	1.26	2.69	1.60	1.43	1.91	0.89	1.35	2.11	1.79	1.32	1.76	1.65	2.29	1.92	1.41
122091	Hs.155140	casein kinase 2, alpha 1 polypeptide	1.27	2.12	0.88	1.02	1.57	4.03	1.21	1.34	0.87	1.28	1.05	2.37	0.86	1.05	1.60	2.54	1.29	1.11	1.04	1.59	2.02	1.41
727526	Hs.75573	centromere protein E (312kD)	2.78	3.32	2.04	1.64	1.59	1.23	2.53	1.91	1.69	2.96	1.47	1.84	0.65	0.71	1.61	0.25	1.12	0.79	2.51	0.67	1.81	1.96
771196	Hs.138860	Rho GTPase activating protein 1	1.42	1.40	0.90	1.05	1.42	1.12	2.67	1.69	2.28	2.48	1.39	6.11	1.36	1.83	2.31	1.77	1.47	1.08	2.11	0.96	1.06	0.53
243202	Hs.1355	cathepsin E	1.56	2.34	2.73	2.29	1.38	2.84	1.98	2.21	12.89	4.91	1.81	2.95	1.59	2.79	3.70	3.18	3.29	2.77	2.02	1.34	1.70	1.38
46182	Hs.251871	CTP synthase	2.20	1.53	2.23	3.01	2.25	2.58	1.79	0.76	1.50	1.09	0.93	1.65	1.43	1.42	0.51	1.15	1.20	1.12	1.15	1.23	1.69	2.13
241348	Hs.99918	carboxyl ester lipase (bile salt-stimulated lipase)	2.02	2.17	1.98	2.34	1.78	1.48	0.69	1.31	1.29	1.54	1.16	1.14	2.02	1.42	1.30	0.61	2.41	1.64	0.79	1.27	1.38	1.33
51865	Hs.155097	carbonic anhydrase II	0.16	0.21	0.11	0.26	0.29	0.15	0.12	0.46	0.13	0.20	0.11	0.45	0.42	0.26	0.79	0.19	0.22	0.11	0.20	0.29	0.16	0.11
275738	Hs.23118	carbonic anhydrase I	0.27	0.40	0.15	0.29	0.50	0.17	0.17	0.62	0.13	0.32	0.12	1.17	1.07	0.58	1.45	0.18	0.27	0.20	0.30	0.35	0.29	0.14
511521	Hs.155560	calnexin	0.67	0.56	0.66	0.88	0.93	0.79	0.47	0.77	0.99	0.52	1.41	0.50	1.01	0.71	0.81	1.17	1.57	1.12	0.84	1.97	0.68	1.88
810408	Hs.169992	protein phosphatase 3 (formerly 2B), regulatory subunit B (19kD), alpha isoform (calcine	0.83	0.53	0.63	0.37	0.79	0.49	0.58	0.91	0.71	0.91	0.79	0.70	0.64	0.60	0.64	0.86	0.88	0.64	0.91	0.69	1.37	0.98
301976	Hs.75206	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gan	0.48	1.25	1.30	0.89	2.10	0.75	1.23	0.78	1.50	3.83	0.45	1.76	0.85	1.15	0.77	0.59	1.17	1.21	1.05	0.77	0.62	0.67
208001	Hs.119663	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, E	0.61	0.52	0.91	0.28	1.08	0.22	0.50	0.54	0.50	0.26	0.42	0.73	0.22	0.54	0.35	0.41	0.45	0.74	0.51	0.52	0.69	0.55
813552	Hs.82685	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	2.90	7.43	1.48	1.88	3.44	2.47	2.56	2.74	1.49	1.78	2.22	2.24	1.38	1.39	2.06	1.54	1.43	1.75	1.75	1.56	1.57	2.36
183337	Hs.77522	major histocompatibility complex, class II, DM alpha	3.32	11.18	5.35	4.93	7.06	6.36	1.46	5.40	5.84	7.33	7.42	14.32	4.61	7.61	8.92	5.22	4.63	3.94	4.89	2.76	3.15	2.72
115292	Hs.108338	ESTs, Highly similar to CAMPATH-1 ANTIGEN PRECURSOR [H.sapiens]	1.71	1.10	0.42	1.00	1.81	1.08	1.01	1.25	1.01	1.58	1.21	1.28	0.72	1.51	1.72	0.63	1.00	1.03	1.23	0.63	1.82	1.02
810899	Hs.77550	CDC28 protein kinase 1	2.54	2.40	1.28	2.63	2.23	1.64	4.16	1.62	0.99	0.86	1.44	0.61	0.80	1.10	1.26	1.35	0.87	0.59	1.81	0.80	1.10	1.69
727251	Hs.1244	CD9 antigen (p24)	1.20	0.75	0.50	1.24	1.14	1.10	1.90	1.78	1.29	1.32	1.39	0.94	1.29	0.91	1.95	1.46	1.27	1.28	0.74	0.63	1.94	1.21
771258	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.99	3.23	1.65	2.01	2.88	4.31	2.02	2.03	3.52	3.44	2.12	5.43	0.72	2.68	1.95	6.21	5.64	1.83	1.90	1.77	1.70	1.40
262231	Hs.75525	calreticulin	1.91	1.22	1.32	1.44	1.78	0.76	1.04	0.98	1.10	0.67	1.03	1.04	2.20	1.89	1.50	1.69	0.71	0.98	0.73	1.60	1.94	2.21
274638	Hs.154868	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	2.90	6.22	2.11	3.45	5.24	3.26	1.93	3.64	3.08	1.88	3.41	3.95	3.42	2.66	2.71	2.09	1.38	1.81	1.01	1.25	1.91	2.25
243816	Hs.75613	CD36 antigen (collagen type I receptor, thrombospondin receptor)	1.49	4.26	1.39	2.71	8.02	1.75	2.47	7.20	2.40	2.99	18.64	4.42	3.63	2.57	5.17	2.09	2.15	7.82	5.09	1.60	3.30	1.96
265874	Hs.184771	nuclear factor I/C (CCAAT-binding transcription factor)	3.34	2.28	0.83	1.31	5.81	1.45	1.63	1.95	1.41	1.22	0.99	2.17	3.51	2.01	3.05	2.40	2.97	2.74	3.51	0.93	2.00	0.91
123926	Hs.83942	cathepsin K (pycnodysostosis)	1.31	1.21	2.02	2.71	3.05	2.31	0.61	3.18	9.47	2.36	3.44	8.72	3.05	7.76	8.86	5.20	3.07	4.02	4.21	3.25	0.96	2.24
211548	Hs.73858	carboxypeptidase N, polypeptide 2, 83kD	1.41	1.78	1.47	2.04	1.76	1.50	1.09	1.09	1.43	0.83	1.24	4.37	2.66	3.01	2.13	1.44	0.75	0.63	0.76	1.28	1.16	1.93
241365	Hs.227152	mannan-binding lectin serine protease 1 (C4/C2 activating component of Ra-reactive fac	0.50	0.68	0.36	0.67	0.79	0.67	0.68	0.78	0.62	0.56	0.68	0.93	0.61	0.75	0.61	0.64	0.50	0.57	0.88	1.00	0.40	0.35
767753	Hs.166891	regulatory factor X, 5 (influences HLA class II expression)	1.32	4.02	1.40	2.29	2.85	2.26	2.25	3.44	1.72	1.66	2.53	2.02	1.35	1.24	1.54	0.88	1.40	1.85	2.80	0.92	1.91	3.22
132373	Hs.64025	basonuclin	0.29	0.55	0.35	0.23	0.81	0.21	0.39	0.27	0.33	0.30	0.29	0.60	0.19	0.29	0.45	0.33	0.51	0.38	0.47	0.93	0.54	0.91
756163	Hs.234799	breakpoint cluster region	1.58	5.25	1.12	1.54	3.24	2.27	5.25	2.43	2.18	2.55	2.20	3.55	3.10	3.25	4.17	1.66	1.58	1.63	2.16	2.20	3.67	4.00
753301	Hs.50964	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein)	1.40	2.93	0.78	1.37	3.80	2.12	6.14	1.09	1.19	1.16	1.60	2.24	1.03	1.69	1.21	1.15	2.64	2.99	4.14	1.71	3.57	1.67
194384	Hs.101025	basic transcription factor 3	0.57	0.40	0.54	0.54	0.65	1.86	0.88	0.82	0.55	0.56	0.71	0.43	0.41	0.41	0.77	0.57	0.51	1.02	1.32	0.62	0.72	0.67
811942	Hs.89578	general transcription factor IIH, polypeptide 1 (62kD subunit)	0.84	1.98	0.92	1.19	2.01	0.66	0.72	0.88	1.06	1.09	0.72	0.62	0.62	0.54	0.65	0.74	0.53	0.91	0.77	0.76	0.89	0.96
810444	Hs.101382	tumor necrosis factor, alpha-induced protein 2	0.71	1.54	0.24	0.54	0.71	1.24	0.44	0.56	0.62	0.45	0.51	5.71	2.62	1.71	2.62	0.73	0.71	0.70	0.63	0.53	0.53	1.37
753897	Hs.80731	autocrine motility factor receptor	1.08	1.34	0.84	0.51	1.16	1.09	0.50	0.68	2.54	2.23	1.03	1.28	0.90	0.79	0.85	1.14	2.66	1.38	1.36	1.02	1.17	0.73
682528	Hs.74520	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	0.97	3.91	3.65	1.96	3.43	1.39	1.39	2.26	4.61	2.85	2.34	1.75	0.69	1.58	0.56	1.73	1.87	2.23	2.93	1.63	2.65	1.47
755506	Hs.77840	annexin A4	0.98	0.48	0.32	0.94	0.76	1.17	0.37	0.56	0.71	0.33	0.43	0.42	0.60	0.82	0.73	0.66	0.36	0.70	0.56	0.78	0.75	0.91
208718	Hs.78225	annexin A1	0.53	0.21	0.40	0.25	0.49	0.53	0.13	0.16	0.26	0.17	0.21	0.16	0.04	0.12	0.12	0.21	0.08	0.31	0.17	0.32	0.17	0.46
563673	Hs.74294	antiquitin 1	1.05	1.29	1.05	1.22	1.30	0.40	0.69	0.55	0.72	0.60	0.74	0.65	0.74	1.07	1.13	1.04	0.53	0.84	0.89	0.57	0.58	1.20

810117	Hs.75510	annexin A11	0.62	0.50	0.29	0.50	0.58	0.66	0.36	0.64	0.71	0.32	0.69	0.52	0.69	0.48	0.60	0.73	0.35	0.40	0.40	0.27	0.46	0.52
666879	Hs.87268	annexin A8	3.41	0.17	0.09	0.43	0.29	1.00	0.26	0.42	0.36	0.17	0.12	0.22	0.08	0.23	0.12	0.11	0.06	0.30	0.39	0.19	0.41	0.31
49352	Hs.78637	annexin A7	0.84	0.71	0.68	1.31	0.86	0.96	0.61	0.76	0.84	0.44	0.98	0.58	1.82	1.18	1.48	1.20	0.63	0.82	0.63	0.72	0.87	0.82
240249	Hs.64797	amyloid beta (A4) precursor-like protein 2	1.07	0.69	0.88	1.09	1.05	1.20	0.85	0.55	0.79	0.28	0.91	0.97	3.23	1.91	1.05	1.30	0.61	0.83	0.30	0.70	0.90	0.76
122159	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	5.71	25.44	12.05	13.67	16.47	9.51	11.01	5.55	3.40	13.12	20.70	48.06	9.48	22.51	67.80	8.65	8.73	6.07	14.95	3.78	6.85	6.72
36387	Hs.2533	aldehyde dehydrogenase 9 (gamma-aminobutyraldehyde dehydrogenase, E3 isozyme)	3.11	2.33	0.79	2.49	2.63	1.60	1.99	1.53	1.63	1.53	1.86	1.13	0.86	0.99	1.61	1.27	1.80	2.11	3.23	0.98	1.34	1.80
813651	Hs.78712	aminolevulinate, delta-, synthase 1	1.23	1.91	1.52	1.75	1.35	1.66	0.84	1.19	1.27	1.45	1.71	1.65	0.88	1.43	0.68	1.38	1.36	1.15	0.70	1.30	0.70	0.96
823775	Hs.73799	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	1.57	1.66	2.05	2.23	1.19	1.32	1.76	1.46	1.33	1.17	1.59	2.01	0.80	1.42	2.02	0.80	0.75	0.59	0.84	1.34	0.75	0.91
813711	Hs.78989	alcohol dehydrogenase 5 (class III), chi polypeptide	0.79	2.13	1.72	0.96	2.31	1.10	1.21	1.26	1.73	1.64	1.27	1.75	0.61	0.66	1.04	1.08	0.89	1.29	1.09	1.02	0.85	0.96
298155	Hs.79158	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain	0.84	0.62	0.55	0.65	0.67	0.65	0.39	0.32	0.54	0.57	0.41	0.32	0.21	0.31	0.55	0.35	0.46	0.96	0.62	0.86	1.02	0.77
813280	Hs.75527	adenylosuccinate lyase	0.97	1.62	1.42	1.55	1.60	1.35	1.82	1.01	1.09	1.18	1.01	0.74	0.62	0.95	0.83	1.02	0.79	1.41	1.72	1.17	0.81	1.03
124127	Hs.83918	adenosine monophosphate deaminase (isoform E)	1.27	2.37	1.17	1.32	2.67	1.50	0.76	1.68	2.55	1.84	2.03	2.11	1.18	1.21	1.56	0.85	1.22	1.42	1.25	0.45	1.99	1.14
128243	Hs.94382	adenosine kinase	0.44	1.56	0.59	0.73	1.15	0.58	0.36	0.62	0.42	0.40	0.92	0.67	0.43	0.35	0.54	0.62	0.36	0.48	0.52	0.55	0.59	0.44
812083	Hs.75081	adenomatosis polyposis coli	0.86	1.56	0.65	1.29	1.93	1.02	0.63	1.05	1.12	1.13	1.37	1.03	0.59	0.65	0.78	0.65	0.60	1.32	1.16	1.09	1.25	1.45
222181	Hs.1526	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0.96	1.85	0.85	1.60	1.35	0.94	1.00	1.26	1.80	1.38	1.30	1.44	1.50	1.52	1.41	0.96	0.98	0.72	0.85	1.48	1.50	1.28
813712	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	0.58	0.99	0.69	0.73	0.67	0.68	0.73	1.60	0.61	0.75	1.52	0.34	0.20	0.34	0.50	0.53	0.45	0.47	0.72	0.91	0.70	1.04
51448	Hs.460	activating transcription factor 3	1.08	0.72	0.44	0.85	1.66	0.75	0.52	0.30	1.33	0.32	0.93	1.60	0.78	0.84	0.60	0.77	0.89	1.59	0.41	0.60	0.85	1.39
26617	Hs.10247	activated leucocyte cell adhesion molecule	0.14	0.41	0.15	0.24	0.28	0.32	0.24	0.22	0.48	0.35	0.61	0.60	2.19	0.90	0.53	0.41	0.35	0.46	0.46	1.07	0.49	0.40
262932	Hs.75900	aconitase 2, mitochondrial	0.55	0.53	0.51	0.67	1.11	1.10	0.61	0.50	0.75	1.10	0.59	0.58	0.65	0.62	0.72	0.96	0.77	0.88	0.97	1.16	0.94	1.16
841203	Hs.75350	vinculin	1.14	0.87	2.52	1.46	1.93	0.95	0.84	1.58	3.01	0.70	1.46	1.11	0.77	0.86	1.25	1.49	0.78	1.26	0.90	0.74	1.52	1.34
840511	Hs.2064	vimentin	1.96	7.17	2.55	4.76	5.35	3.74	3.11	4.07	4.34	2.82	5.99	7.48	4.14	5.51	2.78	4.84	1.72	2.01	1.75	1.61	3.06	3.63
701112	Hs.320	xeroderma pigmentosum, complementation group C	0.91	0.52	0.30	0.83	0.93	0.44	0.53	0.79	0.67	0.55	0.57	0.28	0.78	0.33	0.70	0.55	0.77	1.31	0.99	0.74	0.99	0.70
815816	Hs.2062	vitamin D (1,25- dihydroxyvitamin D3) receptor	1.62	1.91	1.11	1.56	2.26	0.99	0.84	1.65	2.08	1.27	2.79	4.87	1.54	2.36	2.99	1.90	0.85	1.38	1.04	0.70	1.35	1.39
760344	Hs.2057	uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-	1.68	1.77	1.09	1.81	2.54	1.72	1.20	1.79	1.13	1.83	1.79	1.06	1.25	1.61	1.26	1.28	1.31	1.26	0.97	0.87	1.57	2.00
841292	Hs.84285	ubiquitin-conjugating enzyme E2I (homologous to yeast UBC9)	1.08	1.90	0.90	1.61	1.86	1.19	1.73	1.44	1.21	1.47	1.66	1.48	0.74	1.02	1.39	1.32	1.01	0.86	1.24	1.15	1.09	1.30
826254	Hs.28505	ubiquitin-conjugating enzyme E2H (homologous to yeast UBC8)	0.99	1.21	0.83	1.11	1.33	1.48	0.84	1.46	1.36	1.37	1.36	2.27	2.37	1.19	1.92	1.39	0.85	1.22	1.00	1.17	1.66	2.28
77133	Hs.81972	SHC (Src homology 2 domain-containing) transforming protein 1	0.57	0.43	0.49	0.29	1.00	0.36	1.05	0.64	0.63	0.63	0.80	0.69	0.22	0.45	0.50	0.50	0.38	0.64	1.61	0.53	0.81	0.56
795847	Hs.198767	Jun activation domain binding protein	0.60	1.05	0.83	1.99	1.12	0.43	0.80	0.67	0.60	1.38	0.68	0.50	1.21	0.79	1.25	0.60	0.65	0.51	0.55	1.10	0.78	1.18
783729	Hs.173664	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma deri	1.28	2.08	0.55	0.50	1.31	1.77	0.78	4.38	1.92	1.60	4.59	1.63	4.41	2.57	2.98	6.08	1.96	1.56	1.54	2.01	4.42	1.46
897642	Hs.146355	v-abl Abelson murine leukemia viral oncogene homolog 1	1.05	2.45	1.21	2.09	1.51	0.95	1.22	1.75	2.23	1.99	1.30	1.60	1.05	1.41	1.08	1.14	0.86	0.94	1.28	1.26	1.28	1.14
714106	Hs.77274	plasminogen activator, urokinase	1.30	1.77	1.18	2.09	1.86	1.09	2.24	3.40	7.38	3.67	3.46	3.74	0.62	3.13	3.16	2.16	1.21	1.54	2.40	2.10	1.42	1.74
898138	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.49	1.12	0.64	0.71	1.32	0.69	1.03	1.22	0.95	1.02	1.30	3.74	1.88	1.68	2.65	1.55	0.87	0.67	1.16	0.47	0.61	1.42
841149	Hs.82028	transforming growth factor, beta receptor II (70-80kD)	0.22	0.18	0.29	0.24	0.59	0.23	0.22	0.23	0.38	0.20	0.23	0.29	0.08	0.23	0.20	0.42	0.18	0.57	0.36	0.43	0.37	0.28
486208	Hs.2025	transforming growth factor, beta 3	1.54	5.03	4.08	2.86	6.04	1.81	2.29	5.25	9.12	3.71	3.45	6.69	1.85	3.14	6.89	4.20	3.46	4.63	6.50	1.04	4.60	1.44
841703	Hs.77356	transferrin receptor (p90, CD71)	0.96	0.68	0.56	0.83	0.78	1.72	0.41	0.47	0.65	0.58	0.70	1.00	0.66	0.45	0.48	0.46	0.47	0.79	0.69	0.97	0.69	2.04
898262	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing	0.98	1.42	0.92	0.83	1.32	0.92	0.72	1.14	1.03	1.05	1.02	0.77	0.73	0.92	0.72	1.22	0.60	0.70	1.11	0.85	1.02	1.84
840325	Hs.76480	ubiquitin-like 4	2.40	3.05	1.65	1.42	2.73	1.79	1.79	1.70	2.28	2.40	1.98	3.46	1.98	1.19	1.71	1.28	1.45	1.21	2.09	1.62	1.16	1.68
782800	Hs.3712	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0.80	0.87	0.60	0.52	0.89	0.84	0.84	0.42	0.72	0.60	0.62	0.50	0.70	0.56	0.63	0.75	0.67	0.58	0.74	0.92	0.90	1.08
208161	Hs.182238	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polype	0.91	0.71	0.52	0.64	0.71	0.86	0.55	0.82	1.03	1.26	0.68	0.71	0.74	0.41	0.66	0.56	1.38	0.88	0.88	1.03	1.09	0.94
24415	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.34	4.44	1.12	1.46	2.22	1.36	1.74	2.32	2.61	1.49	1.60	1.40	0.84	1.07	1.13	2.72	0.93	1.48	0.85	0.96	2.84	4.84
712641	Hs.218791	megakaryocyte stimulating factor	1.91	2.97	1.40	2.68	2.42	1.62	1.60	2.24	1.89	1.59	1.25	2.03	1.56	1.27	2.08	0.73	1.28	1.38	2.67	0.86	2.32	1.89
789376	Hs.13046	thioredoxin reductase 1	0.60	0.76	0.57	0.50	0.70	0.46	0.59	1.02	0.38	0.70	1.15	0.39	0.64	0.93	0.42	0.49	0.97	0.40	0.56	0.60	1.10	0.70
843159	Hs.21704	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	0.96	2.08	1.52	2.43	1.94	1.60	1.15	1.55	3.11	1.11	1.56	1.13	0.95	1.17	1.16	1.12	0.94	1.64	1.25	1.05	1.41	1.71
526657	Hs.155202	transcription elongation factor B (SIII), polypeptide 3 (110kD, elongin A)	0.54	0.43	0.73	0.69	1.84	0.43	0.92	1.19	2.59	0.56	0.73	1.12	0.24	0.44	1.25	1.11	0.39	1.91	1.45	1.32	0.49	0.41
825470	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.64	4.28	1.74	1.91	1.35	1.39	1.44	3.24	1.87	2.06	2.56	1.29	0.70	1.06	1.51	0.64	1.53	1.58	2.13	1.23	2.46	1.91
842846	Hs.6441	tissue inhibitor of metalloproteinase 2	0.43	1.92	2.60	2.01	1.79	0.99	0.79	2.02	3.50	1.46	1.96	1.61	1.79	1.98	0.98	3.13	0.82	0.86	0.54	0.87	1.15	1.81
795330	Hs.211606	nuclear receptor subfamily 1, group D, member 1	0.99	2.35	0.78	0.96	2.20	0.75	1.10	2.58	1.47	1.74	1.65	1.26	0.95	0.91	1.01	0.78	1.21	1.36	1.53	1.17	2.08	1.88
840788	Hs.76293	thymosin, beta 10	1.59	1.54	0.76	0.83	1.36	1.04	1.55	1.32	0.82	0.78	1.02	1.29	0.48	1.41	1.01	0.75	0.96	0.53	0.83	1.01	1.82	0.85
840567	Hs.3337	transmembrane 4 superfamily member 1	5.56	1.05	1.12	2.48	2.72	3.70	2.71	0.68	2.16	0.14	0.25	0.84	0.34	1.97	1.17	0.41	0.46	0.98	0.69	1.33	1.06	4.05
612274	Hs.75318	tubulin, alpha 1 (testis specific)	2.07	1.01	1.45	1.49	0.98	0.80	0.84	1.20	1.02	0.60	1.44	0.49	0.63	0.91	0.65	0.81	0.75	0.62	0.70	0.98	0.97	0.61
784841	Hs.249247	heterogeneous nuclear protein similar to rat helix destabilizing protein	2.51	1.82	1.23	1.33	2.73	0.89	1.71	1.39	1.23	1.20	1.22	0.93	0.62	0.88	1.27	1.21	1.06	1.30	0.93	0.84	1.62	2.59
79898	Hs.28935	transducin-like enhancer of split 1, homolog of Drosophila E(sp1)	2.61	2.69	1.80	2.17	2.23	1.30	1.17	1.50	1.50	1.02	1.68	0.81	0.40	1.34	0.81	1.41	0.48	0.88	1.94	1.48	1.76	1.78
797016	Hs.64	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	0.92	0.49	0.49	0.72	0.73	1.11	0.65	0.77	0.59	0.68	0.62	0.33	0.58	0.74	0.60	0.75	0.75	0.79	0.76	0.97	0.95	1.45
80915	Hs.469	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.22	1.52	1.04	1.65	1.04	1.18	1.08	0.77	0.63	0.69	1.15	0.77	0.80	1.15	0.83	2.43	0.67	0.85	0.85	1.35	1.13	1.12
787857	Hs.154546	syntaxin 5A	1.35	1.96	2.29	2.98	1.79	1.89	1.71	1.56	1.84	1.29	1.85	1.96	2.60	2.56	2.27	1.87	1.63	0.90	1.11	1.56	1.58	1.40
950489	Hs.75428	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	1.00	0.93	0.75	1.27	0.82	0.70	1.09	0.99	1.20	1.69	1.19	1.12	0.73	1.04	1.24	0.98	1.49	0.82	1.30	0.56	1.33	1.54
897822	Hs.74101	spleen tyrosine kinase	4.43	7.80	5.68	6.62	6.75	4.21	1.83	4.51	21.37	5.71	5.42	2.32	0.93	1.49	1.56	3.51	2.96	2.26	3.18	1.07	3.82	4.23
898242	Hs.75730	signal recognition particle receptor ('docking protein')	2.76	1.59	1.15	1.30	1.63	1.58	2.82	1.42	1.45	1.59	1.47	1.13	0.50	1.34	0.99	1.70	1.63	1.65	2.01	1.60	2.94	1.14
950430	Hs.49346	signal recognition particle 54kD	1.78	1.61	1.49	1.40	1.39	1.13	0.81	1.25	1.97	1.36	1.47	0.98	0.81	1.09	1.01	1.06	1.57	0.95	1.26	1.41	1.96	0.97
76362	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	1.74	1.61	0.77	1.40	1.41	1.47	0.93	1.19	1.43	1.97	1.26	1.60	0.65	1.20	1.48	1.52	0.89	0.92	1.35	0.90	1.01	0.79
785574	Hs.75283	sorting nexin 1	0.89	1.04	0.87	3.18	1.39	1.44	1.13	0.98	1.70	1.53	1.01	1.96	0.77	1.51	1.30	1.28	1.18	1.47	1.98	0.83	1.14	0.91
950482	Hs.83753	small nuclear ribonucleoprotein polypeptides B and B1	0.81	1.23	0.85	1.02	0.92	0.94	1.39	1.03	0.82	1.00	1.23	1.31	1.14	1.30	0.91	2.07	0.66	0.67	1.10	1.12	2.02	0.58
74119	Hs.48375	SNRPN upstream reading frame	1.56	1.77	0.55	2.11	2.81	1.18	9.28	2.18	2.15	3.04	2.99	3.56	2.59	2.46	2.01	2.55	4.36	2.34	2.54	0.98	4.09	1.78
827156	Hs.82575	small nuclear ribonucleoprotein polypeptide B''	0.85	1.88	1.23	0.94	1.58	0.87	0.99	1.38	1.26	1.41	1.23	1.24	0.65	0.82	0.95	0.93	0.85	0.64	1.09	1.79	2.03	1.40
125183	Hs.923	single-stranded DNA-binding protein	1.04	1.50	0.98	1.23	1.40	1.05	1.44	1.12	0.97	1.34	1.15	0.78	0.36	0.58	0.65	0.75	0.61	0.95	1.44	0.88	2.09	1.32
785616	Hs.250773	signal sequence receptor, alpha (translocon-associated protein alpha)	1.21	1.47	1.54	2.09	1.38	1.82	1.08	1.04	1.37	0.63	1.82	0.96	1.35	1.79	1.25	1.80	1.34	1.12	1.24	2.02	2.28	1.60
897906	Hs.2554	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	0.60	2.22	0.79	2.30	2.03	3.16	0.70	1.21	1.17	0.59	1.92	2.12	0.85	1.92	1.75	3.00	1.03	1.11	0.39	1.27	1.64	1.91
491066	Hs.150402	activin A receptor, type I	1.10	2.78	1.56	1.24	2.46	1.01	1.68	2.10	2.91	2.26	1.45	1.25	0.42	1.53	1.25	0.73	2.31	1.79	2.24	1.74	1.33	1.57
713382	Hs.171834	PCTAIRE protein kinase 1	1.67	1.88	1.37	1.00	1.66	1.63	0.93	1.09	1.68	1.37	1.14	1.03	1.40	1.34	1.18	1.72	0.81	0.96	1.06	0.77	1.24	2.83
795241	Hs.92	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha	1.44	2.51	2.27	1.71	1.23	0.69	2.29	2.14	1.57	2.00	1.13	2.05	2.19	1.35	2.50	0.52	1.64	1.96	2.82	1.31	1.31	1.62
840636	Hs.155321	serum response factor (c-fos serum response element-binding transcription factor)	1.22	2.87	2.20	1.17	1.57	1.10	3.76	1.45	1.40	1.51	1.17	1.43	0.57	1.89	1.17	1.00	0.87	2.22	1.84	0.77	1.85	1.58
418126	Hs.59271	U2(RNU2) small nuclear RNA auxillary factor 1 (non-standard symbol)	2.45	4.32	1.82	2.10	2.60	0.91	2.04	1.57	1.52	1.93	1.65	5.04	1.50	3.11	2.93	0.99	1.90	1.85	2.38	1.32	1.85	2.25
773618	Hs.92909	SON DNA binding protein	0.93	1.38	0.94	1.19	1.35	1.06	0.66	1.28	1.40	1.21	1.10	0.80	0.85	0.83	1.00	1.21	1.09	0.94	0.93	0.65	0.96	1.17
840691	Hs.21486	signal transducer and activator of transcription 1, 91kD	2.98	12.47	1.88	5.49	3.51	5.95	3.57	4.72	5.21	3.39	6.68	4.96	4.08	4.68	4.64	4.25	6.21	2.05	2.77	2.39	2.75	3.14
950607	Hs.145279	SET translocation (myeloid leukemia-associated)	0.88	0.92	0.55	1.00	0.76	0.54	0.64	0.58	0.74	0.81	0.57	0.52	0.72	0.50	0.96	0.75	0.50	0.73	0.74	0.83	0.85	0.67
840364	Hs.172673	S-adenosylhomocysteine hydrolase	1.13	0.65	0.63	0.62	0.79	0.44	1.00	0.49	0.48	0.66	0.60	0.71	0.65	0.73	0.86	0.62	0.64	0.74	0.57	0.64	1.02	0.78
32684	Hs.169793	ribosomal protein L32	1.55	1.80	1.26	0.87	1.86	0.66	1.59	1.32	0.55	0.78	1.44	1.41	0.62	0.76	1.99	1.01	1.39	1.65	1.50	0.59	1.27	0.97
897835	Hs.151134	oxidase (cytochrome c) assembly 1-like	1.04	0.86	0.64	0.69	0.61	0.62	0.57	0.59	0.61	0.35	0.86	0.62	0.60	1.07	0.72	0.58	0.60	0.78	0.71	1.24	0.69	0.22
210887	Hs.119222	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting protein)	0.90	0.86	0.95	0.91	1.21	0.96	0.88	0.75	0.75	0.73	0.75	0.39	0.31	0.45	0.81	0.90	1.08	1.74	1.04	0.56	1.06	1.22
788511	Hs.149957	ribosomal protein S6 kinase, 90kD, polypeptide 1	1.17	0.75	0.46	0.44	0.52	0.65	0.44	0.50	0.40	0.73	0.59	0.79	0.30	0.84	0.81	0.69	0.41	0.84	1.08	0.71	0.59	0.38
66686	Hs.29797	ribosomal protein L10	0.64	1.27	0.82	0.55	0.82	0.73	1.13	0.77	0.59	0.35	0.98	0.93	1.06	0.76	1.97	0.85	0.77	1.33	0.68	1.00	0.88	0.63

208001	Hs.119663	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, E	0.87	0.49	0.72	0.26	0.75	0.16	0.57	0.33	0.40	0.19	0.31	0.40	0.19	0.27	0.31	0.35	0.43	0.65	0.54	0.24	0.41	0.67
166195	Hs.75108	ribonuclease/angiogenin inhibitor	0.77	0.46	0.77	0.86	0.58	0.43	0.71	0.25	0.93	2.82	0.60	0.81	2.13	1.15	0.96	1.89	0.54	0.81	0.73	0.58	0.35	0.77
827132	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	0.54	1.44	0.86	1.29	0.80	1.50	0.48	0.78	0.72	0.61	0.90	2.34	0.20	1.45	0.72	1.31	0.81	0.77	1.06	0.79	0.44	0.59
740554	Hs.144904	nuclear receptor co-repressor 1	2.02	1.68	0.81	1.21	1.91	1.64	1.21	0.57	0.72	0.79	1.12	4.39	1.79	1.38	2.72	1.10	0.88	1.28	0.60	0.80	1.65	3.44
784593	Hs.6838	ras homolog gene family, member E	0.57	0.46	0.50	0.39	0.42	0.28	0.54	0.21	0.37	0.43	0.20	0.28	0.40	0.27	0.12	0.26	0.15	0.54	0.17	0.55	0.35	0.32
741379	Hs.107979	small membrane protein 1	1.65	0.88	1.16	1.09	1.02	1.29	0.73	1.02	1.23	0.75	1.23	1.74	0.94	1.32	0.92	1.21	1.26	1.26	1.25	1.19	1.17	1.10
45525	Hs.142653	ret finger protein	1.30	1.95	1.48	1.44	1.42	1.34	1.81	1.42	1.61	1.14	1.29	1.67	1.99	2.20	1.50	1.38	1.25	1.26	2.02	1.36	1.46	1.60
256260	Hs.115474	replication factor C (activator 1) 3 (38kD)	2.93	3.21	0.64	1.23	2.87	1.73	2.13	1.37	0.88	1.62	1.89	4.18	2.09	1.73	2.11	1.16	1.49	0.78	2.33	1.28	1.92	1.94
841384	Hs.75562	discoidin domain receptor family, member 1	2.73	1.37	1.69	1.51	0.77	0.98	0.84	0.79	1.54	0.97	0.80	1.23	1.16	1.40	1.57	1.28	1.32	1.09	1.66	1.38	0.93	1.59
509484	Hs.106061	RD RNA-binding protein	1.60	1.23	1.88	1.32	0.96	1.36	2.35	1.10	1.50	1.96	1.31	1.30	1.86	1.90	1.51	1.66	1.53	1.23	1.94	1.22	1.19	1.45
79520	Hs.78305	RAB2, member RAS oncogene family	1.33	1.01	0.99	0.82	1.30	1.07	1.05	0.83	1.23	1.46	0.84	0.49	0.67	0.62	1.21	0.96	1.19	1.54	1.09	1.04	1.49	1.38
826077	Hs.979	pyruvate dehydrogenase (lipoamide) beta	1.09	1.02	0.92	1.01	1.38	1.10	0.97	1.45	1.39	1.46	1.03	0.91	0.78	0.53	2.18	0.94	1.41	1.41	2.22	0.96	1.45	1.53
108815	Hs.79350	RYK receptor-like tyrosine kinase	1.58	0.67	0.58	0.73	1.10	0.76	0.68	0.57	0.59	0.42	0.86	0.82	0.44	0.49	0.86	0.80	0.63	1.11	0.92	1.24	0.76	1.02
773319	Hs.86858	ribosomal protein S6 kinase, 70kD, polypeptide 1	2.38	1.50	1.68	1.76	1.14	1.03	2.55	2.90	1.20	3.40	2.61	2.11	0.84	1.36	1.38	1.06	1.49	1.49	1.98	1.34	0.93	0.83
773599	Hs.16003	retinoblastoma-binding protein 4	3.22	1.65	1.56	1.54	1.15	1.23	0.92	1.19	1.53	1.28	0.86	1.20	1.01	1.14	1.76	1.43	1.82	1.80	2.35	1.74	1.74	2.32
795888	Hs.76272	retinoblastoma-binding protein 2	1.38	3.09	2.56	2.12	1.92	1.53	4.24	2.16	1.74	2.42	1.58	1.68	0.59	0.66	1.48	1.53	1.71	1.58	1.74	1.30	1.18	1.49
525566	Hs.5947	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog	2.30	1.49	1.10	1.31	1.39	1.63	1.87	1.23	1.31	1.19	1.16	1.58	1.84	1.66	2.00	1.89	1.61	1.52	2.16	1.03	1.43	1.63
898148	Hs.1742	IQ motif containing GTPase activating protein 1	1.12	1.19	1.12	0.93	1.49	1.11	1.30	1.10	1.19	1.04	0.76	0.83	0.33	0.78	0.92	0.88	0.80	1.23	1.81	1.03	0.51	0.84
80374	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha 1	1.15	0.76	0.96	0.73	0.52	0.42	1.23	0.54	0.61	0.95	0.30	1.07	0.67	0.64	0.91	0.49	0.72	0.68	0.98	0.80	0.80	0.90
774502	Hs.62	protein tyrosine phosphatase, non-receptor type 12	1.40	2.25	1.12	1.34	1.60	1.40	1.35	0.81	1.80	2.09	0.95	1.45	0.71	1.16	1.09	0.57	0.83	1.08	1.53	1.39	0.85	0.64
588500	Hs.114366	pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase)	1.99	2.89	0.97	1.53	2.14	1.24	2.29	2.30	2.15	1.37	1.91	1.81	1.09	1.44	1.60	1.74	1.37	1.21	2.21	1.62	1.70	2.59
773215	Hs.129914	runt-related transcription factor 1 (acute myeloid leukemia 1; aml1 oncogene)	1.04	0.91	1.08	1.02	1.31	0.61	1.31	1.25	2.16	3.09	0.67	1.20	0.70	1.11	1.73	0.88	1.04	1.12	2.06	1.24	0.60	0.40
207029	Hs.182371	prothymosin, alpha (gene sequence 28)	2.65	3.31	1.66	2.42	1.90	2.12	3.26	1.46	1.49	1.17	2.52	2.24	0.83	1.35	2.14	1.82	1.66	1.86	2.91	2.33	1.19	1.94
897788	Hs.75216	protein tyrosine phosphatase, receptor type, F	2.24	3.24	0.51	1.40	1.71	1.59	2.74	1.40	1.70	1.96	1.08	3.74	2.18	2.05	3.50	1.12	1.46	1.37	1.60	1.59	1.63	1.41
824568	Hs.171995	kallikrein 3, (prostate specific antigen)	0.95	1.93	0.66	1.44	1.39	1.22	1.52	1.03	0.95	0.93	0.93	1.01	2.80	1.36	2.31	1.22	0.44	1.22	1.32	0.58	1.72	1.32
950445	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.80	0.68	0.63	0.53	0.51	0.26	0.63	0.62	0.57	0.66	0.62	0.42	0.55	0.62	0.78	0.55	0.87	0.76	0.88	0.64	0.52	0.55
756666	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	2.30	1.48	0.72	1.17	1.14	1.21	1.81	1.61	1.05	1.46	1.77	1.55	1.38	1.41	1.75	1.21	0.98	1.03	1.46	1.67	2.18	0.75
897669	Hs.1432	protein kinase C substrate 80K-H	0.74	1.06	1.15	0.98	1.17	0.96	1.11	0.71	0.86	0.86	0.79	0.97	0.99	1.12	1.00	0.99	0.83	0.92	0.88	0.80	1.06	0.62
155434	Hs.181309	proteasome (prosome, macropain) subunit, alpha type, 2	1.60	0.94	0.93	1.08	1.14	1.21	1.05	1.05	0.75	1.05	1.14	0.82	1.82	1.32	2.28	0.83	1.90	0.85	1.08	1.41	2.08	1.12
843134	Hs.80423	prostatic binding protein	1.63	1.77	0.73	1.84	0.85	1.09	1.97	0.88	1.21	1.22	0.86	1.65	1.29	0.92	1.69	1.22	1.07	0.96	1.48	1.16	1.24	0.89
785605	Hs.110613	KIAA0220 protein	1.17	2.27	1.02	1.58	1.22	1.11	1.33	1.42	0.69	1.26	0.94	2.37	1.58	1.77	1.95	1.07	2.03	2.64	2.54	1.17	1.30	1.01
789182	Hs.78996	proliferating cell nuclear antigen	1.16	0.68	0.86	0.93	0.53	0.85	0.76	0.58	0.49	0.41	0.61	0.36	0.58	0.56	0.45	0.95	0.52	0.40	0.67	1.10	1.01	0.34
42313	Hs.75323	prohibitin	0.92	1.45	0.92	1.46	0.69	0.84	1.99	2.76	1.18	0.97	2.79	0.80	1.22	1.55	1.17	1.39	0.96	0.95	1.04	1.25	0.92	1.19
838802	Hs.76768	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypept	0.50	0.90	2.96	1.19	0.92	0.39	0.94	1.40	1.17	0.68	1.82	0.62	1.29	0.61	1.07	0.86	0.52	0.99	1.08	0.57	0.79	0.58
789253	Hs.25363	presenilin 2 (Alzheimer disease 4)	1.59	1.65	0.84	1.51	2.02	1.59	1.21	1.38	1.58	1.20	1.77	2.18	2.57	1.89	2.22	1.56	2.75	1.90	2.25	0.67	1.93	1.68
740130	Hs.171880	polymerase (RNA) II (DNA directed) polypeptide A (220kD)	2.03	2.43	1.75	1.77	1.85	1.21	4.78	1.83	1.94	2.66	1.51	2.74	2.16	2.85	1.70	1.55	1.95	0.83	2.91	1.65	1.54	1.35
67654	Hs.1976	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene ho	1.41	1.15	1.66	1.26	1.36	1.42	3.30	2.27	1.62	4.67	1.71	2.81	2.47	1.68	2.27	1.68	2.30	1.63	2.51	1.46	0.94	0.84
950682	Hs.99910	phosphofructokinase, platelet	0.99	1.23	0.53	0.97	0.57	1.65	1.49	0.46	0.25	0.36	0.43	0.22	0.27	0.35	0.17	0.33	0.21	0.51	0.52	0.82	0.95	0.64
788136	Hs.188	phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E	0.88	4.21	2.06	3.70	4.21	1.79	1.99	1.81	3.41	1.08	1.83	1.94	0.45	1.10	1.50	1.81	1.23	2.83	2.20	1.83	3.45	5.92
70692	Hs.75716	plasminogen activator inhibitor, type II (arginine-serpin)	0.25	0.87	0.43	0.23	0.41	0.11	0.32	0.22	0.26	0.71	0.26	0.77	0.20	0.37	0.42	0.19	0.18	0.45	0.40	0.90	0.20	0.10
898123	Hs.82285	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phos	2.18	1.41	0.93	1.45	1.16	1.43	1.06	0.84	0.71	0.68	0.69	0.84	0.81	0.90	0.79	1.19	0.78	1.19	0.88	0.80	1.37	1.76
503097	Hs.2910	phosphoribosyl pyrophosphate synthetase 2	2.70	2.30	1.50	1.25	1.58	1.14	7.03	0.89	1.63	1.61	1.14	0.93	0.72	0.61	0.78	0.92	1.02	1.58	2.25	1.22	1.27	1.41
897673	Hs.75888	phosphogluconate dehydrogenase	1.42	0.78	0.62	0.98	1.05	2.11	0.99	0.87	0.49	0.44	1.10	0.52	1.06	1.96	1.15	1.17	1.32	0.72	0.73	1.61	1.66	1.14
842784	Hs.78713	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	0.43	0.54	0.71	0.71	0.49	0.51	0.79	0.60	0.59	0.33	0.51	0.42	0.49	0.74	0.45	0.44	0.53	0.61	0.48	0.68	0.56	0.71
897952	Hs.76913	proteasome (prosome, macropain) subunit, alpha type, 5	1.82	1.67	1.32	0.97	1.02	1.52	1.40	1.34	0.98	1.25	1.95	0.61	0.48	1.06	1.07	1.07	0.96	0.97	1.36	1.21	1.36	2.17
788518	Hs.180612	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	0.82	1.27	0.61	1.14	0.57	0.55	0.48	0.88	0.99	0.58	1.10	0.90	1.21	0.53	0.94	0.74	0.79	1.29	0.53	0.96	0.75	1.11
898198	Hs.43910	Sialomucin CD164	0.69	0.94	0.77	1.48	1.35	2.49	0.34	0.87	1.53	0.52	1.14	0.81	0.57	1.55	1.44	1.19	1.48	1.26	0.78	1.70	1.52	0.84
773254	Hs.180610	splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-associated)	1.21	1.09	1.37	1.46	1.14	1.23	0.91	0.82	0.99	0.63	0.71	2.56	2.89	1.94	3.86	1.01	1.04	1.14	1.04	1.16	1.01	1.06
79629	Hs.89414	chemokine (C-X-C motif), receptor 4 (fusin)	2.77	4.19	3.99	2.55	5.62	4.20	8.40	2.82	4.10	3.27	2.73	16.89	1.49	3.52	7.95	5.46	5.52	3.16	4.18	2.08	2.61	4.85
82991	Hs.11951	phosphodiesterase I/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen	1.91	8.49	5.23	5.38	5.35	1.56	3.29	21.08	20.96	36.48	3.40	6.95	1.71	3.57	5.28	0.61	7.58	2.77	3.79	2.61	1.53	1.53
725677	Hs.2994	PCTAIRE protein kinase 3	0.66	3.55	1.31	1.98	2.71	0.96	1.22	2.60	1.70	1.87	1.76	1.31	0.89	1.06	1.19	1.01	0.35	0.99	0.78	0.40	1.90	2.06
897646	Hs.76122	splicing factor, arginine/serine-rich 4	1.83	1.79	2.08	1.73	1.60	1.28	1.46	1.22	1.33	1.23	1.26	1.16	0.55	0.85	1.21	1.32	1.20	1.25	1.41	1.20	0.98	0.94
950092	Hs.167460	splicing factor, arginine/serine-rich 3	1.99	2.56	1.66	1.72	2.02	1.31	2.48	1.69	1.12	1.17	1.41	1.37	0.63	0.88	1.31	1.02	1.01	1.67	2.80	1.51	1.98	1.49
80399	Hs.73737	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor)	1.40	1.82	1.42	1.89	1.33	1.02	2.23	2.67	1.03	1.50	2.33	1.71	1.03	1.57	2.18	1.14	0.96	1.14	1.91	1.36	1.41	0.92
811108	Hs.119498	thyroid hormone receptor interactor 6	0.51	1.36	0.87	0.88	0.75	0.61	1.02	0.74	0.63	0.34	0.62	0.80	0.39	0.39	0.52	0.52	0.38	0.74	0.55	0.38	0.75	0.58
80549	Hs.93728	pre-B-cell leukemia transcription factor 2	1.26	1.60	1.13	1.21	1.37	0.99	1.46	1.23	1.21	1.21	1.28	2.88	1.70	2.35	2.98	1.32	0.89	1.03	1.14	0.48	1.05	0.86
192694	Hs.182237	POU domain, class 2, transcription factor 1	1.72	2.88	1.58	1.72	2.33	1.40	1.56	2.76	2.02	2.50	1.78	2.18	0.96	1.53	2.11	1.04	1.50	1.38	2.27	1.29	2.13	1.23
796646	Hs.75212	ornithine decarboxylase 1	0.41	3.11	1.73	1.37	1.45	1.10	2.57	1.19	0.57	0.45	2.46	0.91	0.35	0.83	0.63	0.99	0.86	0.83	0.53	1.10	0.72	1.33
33045	Hs.169266	neuropeptide Y receptor Y1	3.18	2.37	3.27	2.46	2.59	1.30	1.67	6.94	7.79	11.85	4.61	2.17	0.82	0.70	2.43	2.24	1.01	0.86	4.39	1.07	1.35	2.55
784876	Hs.76888	internexin neuronal intermediate filament protein, alpha	1.31	1.11	1.62	1.32	1.69	1.15	1.56	1.15	0.89	1.47	1.10	1.95	1.08	1.79	1.68	1.03	1.00	1.03	1.10	1.39	1.70	1.17
783696	Hs.75485	ornithine aminotransferase (gyrate atrophy)	0.90	1.86	0.93	1.81	2.05	1.93	1.79	1.48	1.10	1.06	1.16	0.67	1.03	0.61	1.18	1.65	0.83	1.75	1.03	0.75	1.61	2.49
81518	Hs.181060	apelin; peptide ligand for APJ receptor	1.38	1.92	1.80	1.96	1.77	0.83	1.18	1.52	1.88	2.16	1.72	2.60	2.45	1.65	2.76	1.15	1.48	0.98	1.52	1.13	0.86	0.91
40042	Hs.159971	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b,	1.42	1.63	1.16	1.10	1.65	1.20	1.26	1.50	1.57	1.56	1.80	1.68	0.96	1.18	1.61	1.02	1.56	1.36	1.33	1.85	1.84	1.89
611956	Hs.169149	karyopherin alpha 1 (importin alpha 5)	0.66	1.50	1.37	1.94	1.36	0.81	1.13	1.31	1.23	1.11	1.14	0.95	0.64	0.64	0.98	0.93	0.53	0.94	0.49	0.75	0.87	1.15
789357	Hs.83428	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	1.54	1.80	1.07	1.36	1.96	15.20	0.94	1.39	1.74	1.09	1.35	0.96	0.64	0.77	0.99	1.60	1.02	1.60	2.07	0.93	0.92	2.08
784278	Hs.77617	nuclear antigen Sp100	1.83	4.14	0.91	1.59	3.27	1.93	1.70	2.68	2.41	2.59	2.22	2.11	0.53	1.03	1.70	1.35	2.02	1.69	2.26	1.07	3.18	2.24
712683	Hs.54589	NCK adaptor protein 1	1.68	1.48	1.68	1.72	1.41	0.91	1.86	0.92	1.18	0.88	1.43	1.89	1.16	1.29	1.51	1.29	0.88	0.56	0.48	0.89	0.91	1.50
839623	Hs.69855	NRAS-related gene	0.90	1.66	1.51	1.23	1.18	1.10	1.05	0.85	1.09	0.83	0.67	1.21	0.56	0.61	1.06	0.99	0.60	0.70	0.74	1.02	1.31	1.19
774751	Hs.1565	neural precursor cell expressed, developmentally down-regulated 4	0.55	1.79	0.90	0.65	1.42	0.52	0.34	1.00	1.25	0.89	1.12	2.07	0.72	0.53	0.80	0.41	0.45	0.58	0.88	0.50	0.63	0.55
810859	Hs.943	natural killer cell transcript 4	3.97	21.34	1.85	5.91	7.57	6.06	9.62	6.30	7.40	3.64	9.39	19.67	6.57	5.68	10.41	3.10	6.76	4.69	4.34	2.06	4.52	8.15
814615	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate	1.92	2.66	0.77	2.32	1.61	1.59	1.87	1.21	1.05	1.21	1.74	1.15	0.67	1.64	1.30	0.92	1.18	0.69	1.23	2.18	2.03	1.36
701481	Hs.926	myxovirus (influenza) resistance 2, homolog of murine	4.60	12.89	7.16	7.44	6.74	3.87	4.89	7.19	10.56	6.25	5.23	15.35	8.05	8.86	10.69	3.24	5.93	2.72	2.87	1.46	4.64	5.41
815542	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine (interferon-inducible protein p78)	5.24	26.90	8.86	8.66	10.25	8.43	13.19	9.21	12.27	3.11	14.26	13.24	10.63	6.31	15.18	7.20	6.85	4.18	12.68	2.44	7.60	7.71
46916	Hs.90800	matrix metalloproteinase 16 (membrane-inserted)	1.97	10.43	13.40	14.43	3.26	1.58	7.79	5.64	0.63	31.94	2.75	15.16	1.30	2.74	4.14	0.50	3.32	2.38	5.12	1.08	1.31	2.06
824704	Hs.75694	mannose phosphate isomerase	0.98	1.14	1.55	1.25	1.35	0.79	1.35	0.95	0.68	0.96	0.65	1.12	0.87	1.55	0.86	1.06	0.82	1.02	1.22	1.63	1.58	0.73
68103	Hs.90318	myosin, light polypeptide 1, alkali; skeletal, fast	1.16	1.06	2.05	1.07	1.28	0.86	1.11	1.46	1.99	1.75	1.37	1.51	0.91	3.55	0.98	1.16	1.70	0.98	1.60	0.96	1.54	1.16
740457	Hs.431	murine leukemia viral (bmi-1) oncogene homolog	0.75	2.09	2.50	1.75	1.49	1.78	0.33	1.09	1.95	0.65	2.26	2.65	4.47	1.44	2.56	2.00	1.27	1.22	1.51	0.85	0.94	1.55
840687	Hs.89603	mucin 1, transmembrane	0.82	0.30	0.15	0.19	0.30	0.36	0.36	0.63	0.34	0.35	0.48	0.16	0.52	0.68	1.53	0.24	0.42	0.66	3.11	0.73	0.33	0.09
796994	Hs.83532	membrane cofactor protein (CD46, trophoblast-lymphocyte cross-reactive antigen)	0.59	1.78	0.46	1.36	1.84	1.12	0.56	0.99	2.20	1.24	1.03	0.79	1.97	1.19	1.75	1.10	1.49	1.20	2.08	1.55	1.45	1.84
786067	Hs.153752	cell division cycle 25B	1.32	0.76	1.74	1.22	0.89	0.75	1.39	0.99	0.57	0.61	0.63	0.57	0.47	1.18	0.51	1.00	0.51	0.83	0.90	1.65	1.78	0.45
842989	Hs.77385	myosin, light polypeptide 6, alkali, smooth muscle and non-muscle	0.77	0.75	1.84	0.74	1.11	0.77	1.12	1.70	1.48	1.06	1.62	0.97	1.13	1.44	1.28	1.24	1.32	0.86	1.28	0.73	1.33	0.60

713469	Hs.182280	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	1.18	1.48	2.27	1.84	2.27	0.76	0.79	0.90	1.34	1.05	1.60	2.42	0.86	1.50	2.37	0.86	1.15	1.14	0.69	0.93	0.93	1.01
949914	Hs.55921	glutamyl-prolyl-tRNA synthetase	1.41	2.09	1.21	1.82	2.03	1.13	2.60	1.31	1.32	1.76	1.27	1.23	0.68	0.77	1.61	1.11	0.82	0.95	2.18	1.14	1.14	2.36
815501	Hs.76084	lamin B2	1.98	3.46	1.26	2.47	3.15	2.83	1.50	3.33	2.94	2.21	3.69	1.51	0.72	1.08	0.77	2.19	1.04	0.80	1.66	1.23	2.31	2.40
774471	Hs.82124	laminin, beta 1	0.58	2.81	4.28	2.59	1.96	0.90	1.78	1.92	2.66	2.29	1.56	1.15	0.34	1.75	0.84	0.94	0.90	1.11	1.69	0.98	1.27	1.49
49710	Hs.150101	lysosomal-associated membrane protein 1	2.67	2.59	0.67	1.93	3.48	2.55	2.77	2.66	2.80	2.11	2.00	3.75	3.00	1.94	1.95	1.56	3.90	3.44	3.69	2.80	4.37	2.41
842785	Hs.75140	low density lipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin recept	0.70	0.86	0.92	0.99	0.95	0.67	0.60	1.05	0.99	1.10	1.36	0.91	1.00	1.06	1.29	1.29	0.87	0.57	0.81	0.77	0.76	0.91
82734	Hs.154890	fatty-acid-Coenzyme A ligase, long-chain 2	0.99	0.33	0.24	0.33	0.44	0.42	0.36	0.33	0.27	0.35	0.47	0.38	0.23	0.34	0.32	0.44	0.31	0.69	0.38	0.77	0.80	0.45
725266	Hs.1770	ligase I, DNA, ATP-dependent	1.73	1.96	1.50	1.12	1.63	1.11	2.37	1.46	1.29	1.43	1.14	2.39	1.16	1.08	1.46	1.69	1.89	1.11	2.30	1.48	0.96	1.55
814095	Hs.81118	leukotriene A4 hydrolase	0.59	1.07	0.64	0.81	0.97	0.94	0.94	0.84	0.57	0.82	1.01	0.95	0.39	0.50	1.12	0.79	0.85	0.90	0.85	0.56	1.21	1.13
194182	Hs.23581	Homo sapiens mRNA for leptin receptor gene-related protein	1.09	0.87	0.57	0.54	0.85	0.82	0.77	0.75	1.26	0.93	1.00	1.37	0.61	1.03	1.42	0.90	0.60	0.69	0.66	0.92	0.69	0.85
767202	Hs.83337	latent transforming growth factor beta binding protein 2	2.12	1.44	1.55	2.94	5.19	2.30	2.11	5.00	5.11	5.35	5.17	3.82	0.97	2.68	5.23	2.34	2.53	3.36	4.12	2.09	1.15	2.09
839594	Hs.2017	ribosomal protein L38	2.24	2.68	1.83	1.51	2.61	2.43	2.22	1.64	2.04	1.90	1.68	2.28	1.00	1.60	1.33	1.76	1.35	0.73	0.91	1.12	1.43	1.88
488413	Hs.149436	kinesin family member 5B	2.49	4.87	1.85	2.74	3.69	2.46	1.96	1.62	1.83	2.59	1.74	1.90	1.26	0.90	0.90	0.82	3.04	1.70	1.10	1.74	2.16	1.94
898237	Hs.243960	HLA-B associated transcript-3	1.29	2.39	1.24	1.10	1.96	1.28	1.87	1.85	1.22	1.96	1.77	1.60	1.18	1.24	1.35	1.37	1.23	1.26	2.29	1.49	2.37	1.89
897781	Hs.242463	keratin 8	0.36	0.38	0.27	0.16	0.30	0.69	0.35	1.00	1.09	0.64	2.02	1.97	3.02	0.72	1.42	1.18	0.79	0.98	0.82	0.98	0.65	0.58
592540	Hs.195850	keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	0.42	0.14	0.21	0.18	0.20	0.12	0.27	0.17	0.18	0.12	0.09	0.09	0.09	0.12	0.12	0.12	0.20	0.38	0.34	0.28	0.17	0.07
810131	Hs.182265	keratin 19	3.70	1.33	0.27	1.44	1.65	4.29	5.13	2.33	2.10	2.38	3.75	2.00	1.55	0.76	2.06	2.02	2.77	4.52	6.52	2.58	2.06	3.07
842980	Hs.115242	developmentally regulated GTP-binding protein 1	0.36	2.55	2.06	1.34	1.63	1.40	2.55	1.35	1.37	1.43	1.65	0.98	1.18	1.58	1.58	1.21	0.86	0.82	1.46	1.38	1.27	1.45
126320	Hs.2340	junction plakoglobin	0.82	0.81	0.21	0.40	0.52	0.94	0.78	0.49	1.60	1.02	0.24	0.62	1.42	0.93	0.96	0.65	0.82	0.47	0.69	0.45	0.83	0.66
740476	Hs.80645	interferon regulatory factor 1	1.74	2.84	1.51	2.29	1.86	2.21	1.01	3.17	2.48	2.28	2.57	12.86	5.79	6.77	8.96	1.26	5.28	1.92	1.45	1.66	1.89	2.04
773332	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptic	0.81	2.82	2.07	1.59	2.43	1.37	1.04	1.39	1.50	1.31	1.28	1.28	0.83	1.04	1.13	1.25	1.06	0.92	1.47	1.24	1.15	1.24
784319	Hs.202669	thiopurine S-methyltransferase	1.32	1.58	1.81	1.66	1.42	1.33	0.86	1.58	1.71	1.26	1.84	5.75	5.24	4.60	6.61	1.11	1.28	1.71	1.58	1.23	1.82	1.76
767784	Hs.2780	jun D proto-oncogene	1.46	4.15	1.40	1.51	2.17	1.52	1.77	1.71	2.24	2.89	1.73	2.60	1.59	1.56	2.33	1.73	2.25	1.72	2.59	1.60	2.04	1.62
726147	Hs.75217	mitogen-activated protein kinase kinase 4	0.74	1.86	1.36	1.02	1.54	0.85	0.94	1.31	1.30	1.94	0.88	1.32	1.19	1.11	1.41	0.92	0.90	0.92	0.59	0.78	0.96	1.06
714453	Hs.75545	interleukin 4 receptor	1.21	1.31	0.68	1.00	1.65	1.45	0.73	1.24	1.40	1.14	1.07	2.02	0.98	1.84	1.43	1.38	0.97	1.12	1.52	0.83	1.20	1.13
488019	Hs.12503	interleukin 15 receptor, alpha	1.34	1.96	0.56	0.89	1.25	1.81	1.04	1.42	2.13	0.58	1.06	3.09	1.30	2.12	2.33	1.51	2.26	1.42	1.85	1.27	0.83	1.18
84295	Hs.81134	interleukin 1 receptor antagonist	1.93	1.31	0.63	0.90	1.26	1.95	1.59	1.52	1.19	1.04	1.09	1.78	2.47	1.99	3.27	0.86	1.91	0.72	2.48	1.36	1.13	1.61
782513	Hs.179972	interferon, alpha-inducible protein (clone IFI-6-16)	2.90	8.19	4.11	3.28	3.95	2.58	3.46	4.89	5.49	6.04	5.28	4.48	2.91	3.17	5.69	3.64	4.50	2.19	5.19	2.10	4.43	2.87
753620	Hs.106283	insulin-like growth factor binding protein 6	0.52	0.33	0.44	0.29	0.38	0.16	0.46	0.25	0.22	0.30	0.26	0.53	0.17	0.35	0.25	0.31	0.33	0.72	0.40	0.59	0.27	0.12
80948	Hs.76325	Human Ig J chain gene	1.56	7.39	1.53	5.76	6.06	9.17	1.63	6.42	5.69	5.79	3.04	10.29	1.28	4.40	9.24	5.43	6.46	6.30	8.59	3.44	4.22	1.95
79712	Hs.76473	insulin-like growth factor 2 receptor	1.95	2.01	2.55	1.94	2.45	1.80	2.55	2.89	2.51	1.66	2.25	3.25	1.20	3.73	3.33	1.57	1.75	1.95	1.78	1.96	2.30	1.46
427812	Hs.89695	insulin receptor	2.81	4.32	2.38	3.25	5.04	1.91	4.35	4.20	6.06	5.05	3.39	3.76	2.75	3.20	5.19	0.96	2.72	3.97	6.01	2.69	2.20	1.82
703964	Hs.75339	inositol polyphosphate phosphatase-like 1	1.94	2.66	1.56	1.72	2.19	2.01	2.11	1.92	1.38	1.58	2.65	2.01	1.34	1.81	2.91	1.84	1.31	1.54	2.03	1.59	1.89	1.23
789369	Hs.34853	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein	2.64	1.67	2.69	4.72	3.19	2.31	2.34	2.81	2.90	1.29	3.24	1.44	0.80	1.43	1.70	1.69	2.09	2.60	1.58	1.25	2.22	1.99
214441	Hs.179543	immunoglobulin heavy constant mu	1.03	5.37	0.64	2.22	2.59	5.59	1.66	4.62	1.49	1.65	10.75	3.81	1.27	3.71	2.23	4.07	1.37	3.01	2.36	2.30	1.67	1.37
71434	Hs.129758	proline-serine-threonine phosphatase interacting protein 1	1.27	5.01	1.83	1.61	2.56	2.61	1.06	4.63	5.17	3.48	5.15	1.89	1.30	1.78	2.88	1.74	3.76	1.93	3.85	1.61	2.06	1.35
843287	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-related)	1.03	0.60	1.39	1.33	0.91	1.17	0.38	0.51	0.94	0.04	0.88	0.91	1.86	2.13	1.48	1.08	0.45	1.68	0.58	0.95	0.57	0.74
897670	Hs.84775	Human transposon-like element mRNA	1.14	1.00	1.00	1.09	0.96	0.81	0.95	0.76	1.32	1.01	0.99	0.57	0.77	0.72	0.69	0.94	0.87	0.92	0.93	1.16	0.64	0.63
814696	Hs.168075	karyopherin (importin) beta 2	1.42	2.64	1.50	1.72	2.76	1.11	1.29	1.52	1.28	1.51	2.29	2.01	0.76	1.06	1.29	1.51	1.03	1.26	1.46	1.11	1.48	2.27
75923	Hs.78765	Human zinc finger protein mRNA, complete cds	1.96	7.12	7.43	5.67	7.45	1.97	2.04	5.19	8.96	20.66	5.29	2.79	0.55	1.09	3.03	1.93	4.28	5.45	4.92	1.46	2.67	1.69
843094	Hs.81424	ubiquitin-like 1 (sentrin)	0.81	1.48	1.03	1.63	1.57	1.07	1.14	1.04	1.05	1.03	0.94	0.64	0.74	0.98	1.11	0.91	1.03	0.80	0.91	0.90	0.91	1.35
80708	Hs.181369	ubiquitin fusion degradation 1-like	0.90	1.40	1.76	1.82	1.76	0.89	1.81	1.10	1.40	1.79	1.58	1.52	0.78	1.47	0.90	1.24	1.23	0.74	1.19	1.36	1.78	1.36
77391	Hs.200526	TNF receptor-associated factor 2	2.15	5.85	1.07	2.01	3.26	3.33	1.40	3.12	1.83	3.05	2.88	7.20	3.38	2.18	4.19	1.93	2.14	2.45	4.07	0.43	2.76	2.62
897570	Hs.182366	heat shock protein 75	0.71	1.26	0.55	1.25	1.09	0.74	1.52	0.69	0.67	0.70	0.91	0.86	1.05	0.78	0.97	0.94	0.79	1.15	0.92	0.83	0.61	1.39
825585	Hs.32675	tubulin-specific chaperone e	1.02	3.10	1.01	2.41	2.02	2.09	2.39	2.57	1.63	2.29	1.98	2.48	1.19	1.33	2.46	1.31	1.72	1.33	2.26	1.24	2.06	2.25
86220	Hs.183671	tryptophan 2,3-dioxygenase	1.68	0.56	2.11	1.64	0.55	0.85	1.59	0.55	5.16	4.78	1.39	2.46	1.33	1.71	1.95	2.38	2.37	1.07	1.97	1.51	1.00	0.91
725274	Hs.7733	tetratricopeptide repeat domain 1	1.03	1.27	0.56	0.82	1.29	0.78	0.83	1.04	1.15	1.46	1.07	0.59	0.36	0.67	0.71	1.05	1.35	0.95	1.62	0.99	1.14	1.21
898109	Hs.5437	Tax1 (human T-cell leukemia virus type I) binding protein 1	1.37	1.07	0.98	1.07	1.06	1.21	0.89	1.03	1.38	1.42	0.96	1.26	0.84	0.60	0.92	0.71	1.49	1.09	1.72	1.42	1.64	0.55
81599	Hs.75981	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	1.55	1.77	1.68	1.23	1.30	1.34	1.00	0.97	1.55	1.51	1.11	0.72	0.82	0.68	1.19	1.28	1.86	1.29	2.21	1.33	1.79	1.79
897982	Hs.4835	eukaryotic translation initiation factor 3, subunit 8 (110kD)	0.85	0.74	1.43	0.93	1.38	0.33	1.34	0.84	0.70	1.21	0.89	0.53	0.37	0.75	0.41	0.89	0.55	1.22	1.29	0.58	1.23	0.82
843249	Hs.107474	NGFI-A binding protein 1 (ERG1 binding protein 1)	0.86	1.55	0.83	1.07	1.38	0.97	0.48	0.53	0.46	0.45	0.85	0.95	1.02	1.35	0.77	0.89	0.43	0.89	0.45	0.85	0.72	1.06
950574	Hs.180877	H3 histone, family 3B (H3.3B)	1.96	2.44	1.51	1.64	2.41	1.75	2.06	2.01	2.06	2.03	2.09	3.96	1.05	1.36	1.42	1.49	1.49	2.47	2.38	1.25	2.07	1.41
712840	Hs.244613	signal transducer and activator of transcription 5B	1.66	3.68	1.35	1.85	2.68	2.97	1.49	1.90	3.42	3.16	1.85	3.36	2.98	1.64	2.50	1.39	2.62	3.85	1.78	1.07	2.35	1.90
843067	Hs.154970	transcription factor CP2	1.23	2.49	1.17	1.61	2.18	1.64	1.32	1.44	1.40	1.31	1.92	1.63	0.72	1.79	1.45	1.97	1.35	1.38	1.33	1.18	1.90	1.81
770868	Hs.159223	NGFI-A binding protein 2 (ERG1 binding protein 2)	1.69	8.11	1.93	2.76	3.36	6.87	2.97	5.77	3.67	4.25	8.55	4.60	1.64	2.24	4.14	3.99	1.59	2.15	1.71	1.87	2.85	2.15
366728	Hs.247660	thymidine kinase 2, mitochondrial	1.12	1.04	1.38	0.80	0.74	0.66	0.92	0.63	1.65	2.30	1.60	1.57	0.99	0.89	2.81	1.98	1.42	1.23	1.57	1.14	0.43	0.28
757961	Hs.82240	syntaxin 3A	1.69	6.47	7.13	4.98	5.95	2.00	3.09	4.27	8.97	17.09	5.11	3.17	1.42	1.82	3.20	3.15	1.99	2.60	2.99	1.60	3.42	1.79
39593	Hs.12409	somatostatin	1.27	1.80	0.91	1.18	1.55	1.07	1.31	1.18	1.50	1.24	1.26	3.69	1.80	1.92	3.14	1.01	1.63	1.58	1.80	0.87	1.07	1.64
842894	Hs.76941	ATPase, Na+/K+ transporting, beta 3 polypeptide	1.92	0.61	0.77	0.53	0.50	0.46	0.59	0.33	0.41	0.59	0.26	0.41	0.41	0.53	0.31	0.30	0.47	0.32	0.32	0.53	0.27	0.57
823819	Hs.78050	small acidic protein	0.82	1.17	0.69	1.06	1.82	0.75	0.80	1.07	1.33	0.81	0.98	0.88	0.71	0.71	1.06	1.06	0.98	0.94	1.20	0.63	0.71	1.34
843248	Hs.66708	vesicle-associated membrane protein 3 (cellubrevin)	1.09	0.75	0.92	0.84	1.21	0.80	0.57	0.75	1.07	1.09	0.69	0.65	0.77	0.96	0.80	1.07	0.76	0.90	0.90	1.07	1.00	0.90
231355	Hs.194534	vesicle-associated membrane protein 2 (synaptobrevin 2)	1.06	2.15	1.07	1.49	1.71	1.37	1.17	1.50	1.80	1.40	0.98	1.53	1.23	1.22	1.26	1.48	1.28	1.81	1.48	0.82	1.15	1.01
712668	Hs.50640	JAK binding protein	0.75	4.29	1.04	1.55	1.76	1.53	2.11	1.18	1.24	1.00	2.04	2.87	0.84	1.81	1.21	1.61	0.91	0.82	1.31	0.83	1.33	1.39
839552	Hs.74002	nuclear receptor coactivator 1	0.84	2.72	1.56	2.31	2.03	2.35	0.45	2.10	2.06	1.71	1.92	2.73	1.59	1.46	2.01	2.03	1.36	1.15	1.74	1.04	1.64	2.39
898265	Hs.166975	splicing factor, arginine/serine-rich 5	1.18	1.34	0.92	1.38	1.66	0.96	0.60	1.67	1.00	0.94	1.02	1.18	1.03	0.63	1.10	0.93	1.06	1.96	1.74	0.93	1.18	0.81
824041	Hs.77608	splicing factor, arginine/serine-rich 9	0.78	1.10	0.82	1.10	0.64	0.66	1.57	0.95	1.27	1.64	0.74	0.88	1.00	0.54	0.80	0.94	1.01	1.04	1.14	1.06	0.89	0.89
813266	Hs.239069	four and a half LIM domains 1	1.94	0.47	1.48	1.16	0.88	0.30	2.85	0.56	1.39	1.90	0.45	1.79	0.91	1.48	3.56	0.43	2.71	3.87	3.49	1.59	0.35	1.46
841044	Hs.4437	ribosomal protein L28	0.66	0.72	0.66	0.44	0.61	0.29	1.03	0.56	0.36	0.42	2.04	0.93	0.23	0.41	0.73	0.51	0.63	0.68	0.79	0.49	0.71	0.52
949940	Hs.76064	ribosomal protein L27a	0.88	1.32	1.02	0.66	1.18	0.39	1.21	0.97	0.57	0.49	1.26	0.64	0.34	0.48	1.02	0.61	0.44	0.90	0.75	0.66	0.96	0.76
825013	Hs.84264	acidic protein rich in leucines	1.94	2.72	1.10	1.69	1.24	0.66	2.69	1.15	1.07	1.20	0.62	1.10	0.63	0.65	1.39	0.46	0.93	1.62	1.74	1.31	1.16	1.63
80772	Hs.120980	nuclear receptor co-repressor 2	0.73	1.04	0.90	1.05	0.88	0.51	1.38	0.87	1.39	1.02	0.75	1.09	0.80	0.82	0.81	1.05	0.84	0.81	0.94	0.75	0.76	0.51
826405	Hs.155939	inositol polyphosphate-5-phosphatase, 145kD	1.45	1.83	1.95	1.96	2.61	2.25	1.32	2.39	3.64	1.78	2.31	1.86	1.13	1.50	1.90	1.83	2.14	2.80	2.17	1.32	2.04	1.47
843076	Hs.153487	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	1.34	1.43	1.64	1.56	1.90	1.23	1.44	1.03	0.99	1.10	1.03	0.69	0.85	1.56	0.88	1.03	0.94	1.04	0.91	0.94	1.37	1.16
823590	Hs.107573	sialyltransferase	5.08	2.07	1.37	2.90	3.81	2.93	3.94	4.68	5530.69	7.62	2.42	5.40	4.09	2.18	6.25	1.16	4.18	1.66	4.62	2.22	3.03	2.67
592801	Hs.59403	serine palmitoyltransferase, subunit II	2.60	1.76	1.13	1.69	2.18	2.21	1.74	1.43	1.50	1.68	1.20	2.18	1.50	1.58	1.62	1.81	1.54	1.65	1.75	1.67	1.34	1.57
840702	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selenium donor protein	2.28	2.93	3.90	3.46	2.00	4.47	2.78	1.80	1.74	1.30	1.67	0.98	2.30	1.54	1.65	1.06	1.93	1.49	1.30	1.49	2.18	2.14
712577	Hs.211571	holocytochrome c synthase (cytochrome c heme-lyase)	1.30	1.20	1.06	1.41	0.94	0.41	0.88	0.71	0.95	0.82	1.19	1.60	1.01	0.56	0.55	0.69	0.95	0.87	0.69	1.40	1.41	1.58
786083	Hs.79300	ubiquitin-conjugating enzyme E2 variant 2	1.15	0.86	1.40	1.20	0.82	0.35	0.95	0.54	0.97	0.78	0.65	0.46	0.69	0.52	0.55	0.68	0.72	0.64	0.48	1.35	0.96	0.69
700699	Hs.54411	putative T1/ST2 receptor binding protein	1.39	2.03	1.15	0.99	1.85	1.04	1.36	1.23	1.16	1.29	1.75	2.55	1.40	1.12	1.78	1.29	1.14	1.03	1.66	0.96	1.14	1.09
838389	Hs.81728	unc119 (C.elegans) homolog	1.31	1.42	0.33	0.40	1.39	0.84	1.04	0.78	0.60	2.17	0.96	2.53	1.57	1.17	1.74	0.52	2.17	1.58	1.99	0.94	1.31	0.91
47853	Hs.77448	aldehyde dehydrogenase 4 (glutamate gamma-semialdehyde dehydrogenase; pyrroline-5	2.36	1.59	1.40	1.19	2.88	1.58	1.02	2.55	1.98	2.68	4.14	5.55	2.51	1.82	2.92	2.46	3.20	2.24	1.51	1.07	2.88	1.36

843426	Hs.171501	ubiquitin specific protease 11	2.53	3.08	2.02	2.12	2.36	1.73	5.14	1.80	2.24	1.55	2.09	1.44	0.87	1.64	1.80	1.66	1.38	2.25	1.28	1.18	1.52	1.56
758468	Hs.197877	Homo sapiens clone 23777 putative transmembrane GTPase mRNA, partial cds	2.89	2.42	0.98	1.57	1.52	1.94	1.02	1.54	1.26	1.76	1.39	1.43	1.45	1.88	1.08	0.82	1.21	1.44	0.93	1.03	1.68	1.76
75415	Hs.256697	histidine triad nucleotide-binding protein	0.51	0.66	0.33	0.45	0.43	0.34	0.69	0.48	0.42	0.54	0.36	0.43	0.45	0.46	0.55	0.58	0.48	0.48	0.66	0.66	0.53	0.41
712604	Hs.239138	pre-B-cell colony-enhancing factor	1.38	2.04	0.91	1.69	2.03	1.72	1.68	0.87	1.07	0.56	0.94	1.48	0.49	0.75	0.86	0.81	0.59	3.75	1.77	2.81	2.00	1.35
898328	Hs.75878	early development regulator 2 (homolog of polyhomeotic 2)	2.00	1.80	2.28	1.00	1.35	1.43	1.66	1.26	1.80	1.25	1.17	1.52	0.90	1.29	1.46	1.50	0.92	1.25	1.87	1.62	0.84	0.72
781362	Hs.79706	plectin 1, intermediate filament binding protein, 500kD	0.68	0.56	0.51	0.21	0.57	0.36	0.72	0.65	0.60	0.61	0.52	0.44	0.56	0.46	0.62	0.52	0.35	0.80	0.77	0.66	0.50	0.26
811899	Hs.168102	Human proteinase activated receptor-2 mRNA, 3'UTR	0.85	0.87	0.24	0.24	0.69	0.46	0.42	0.33	1.04	1.98	1.15	1.48	0.46	0.37	0.90	0.30	0.62	0.48	0.69	0.34	0.26	1.76
825442	Hs.82911	protein tyrosine phosphatase type IVA, member 2	1.09	1.53	1.62	1.16	1.71	1.39	1.32	1.75	1.43	1.35	1.31	1.60	0.78	0.78	2.56	1.80	1.78	1.90	2.93	1.22	1.65	1.84
796268	Hs.76780	protein phosphatase 1, regulatory (inhibitor) subunit 1A	1.82	2.03	1.45	1.74	1.77	1.57	1.17	1.46	1.58	1.07	1.58	1.78	0.86	1.49	1.55	1.72	0.86	1.60	1.51	1.31	1.92	1.39
814595	Hs.75871	protein kinase C binding protein 1	0.50	0.55	0.39	0.32	0.57	0.30	0.47	0.67	0.72	1.73	0.62	0.76	0.42	0.46	0.72	0.53	0.72	0.88	1.13	1.24	1.05	0.27
510396	Hs.211601	mitogen-activated protein kinase kinase kinase 12	1.51	2.12	1.83	1.79	2.50	1.87	1.54	2.45	2.06	2.49	2.03	2.58	1.57	1.44	2.43	2.03	2.05	2.23	2.63	1.36	2.77	1.29
897956	Hs.30743	preferentially expressed antigen in melanoma	3.74	1.99	8.57	4.69	1.35	0.38	10.69	5.74	1.03	6.82	11.15	1.68	0.65	1.05	1.80	0.62	1.60	1.92	1.99	1.29	0.25	1.74
767994	Hs.183105	nuclear autoantigen	1.23	2.05	1.25	0.90	1.65	0.62	0.89	1.36	1.94	1.55	1.12	2.55	1.63	1.81	1.97	0.61	1.23	1.13	1.53	1.99	0.95	0.61
823851	Hs.118397	AE-binding protein 1	1.27	1.48	1.62	0.71	1.44	0.59	1.55	1.64	2.07	1650.17	0.96	2.50	1.32	1.72	2.13	0.79	1.43	1.14	1.84	2.05	0.74	0.38
898062	Hs.82906	cell division cycle 20, S.cerevisiae homolog	1.71	1.72	1.57	1.39	1.32	1.31	2.57	1.18	0.58	1.27	1.52	0.53	0.42	0.60	0.59	0.59	0.51	0.59	1.97	1.24	1.20	1.34
700302	Hs.95821	osteoclast stimulating factor 1	1.60	1.40	0.85	1.45	1.22	1.21	0.58	0.86	1.58	0.59	0.83	1.80	0.61	1.08	1.26	1.41	0.73	1.16	1.04	1.19	1.16	1.17
79624	Hs.241510	interferon-induced protein 41, 30kD	2.25	4.98	1.63	2.45	3.60	2.94	1.53	3.12	3.59	2.65	4.40	3.93	1.73	3.03	4.34	3.09	2.68	1.47	2.35	1.30	5.09	2.44
785816	Hs.256583	M-phase phosphoprotein 4	2.27	2.26	1.39	3.73	2.99	1.46	2.91	1.86	0.74	0.88	1.28	2.46	0.83	0.82	1.10	0.84	0.81	2.14	0.88	0.78	1.64	1.83
416959	Hs.33287	nuclear factor I/B	2.08	2.21	1.21	3.11	2.22	1.24	2.89	1.38	0.61	2.17	0.93	1.90	0.54	0.61	0.93	0.58	0.69	2.02	0.63	0.88	0.84	1.20
949928	Hs.82210	zinc finger protein 220	1.28	2.87	1.00	1.31	1.87	1.02	1.61	1.46	1.38	4.70	1.41	1.09	1.12	1.20	1.49	1.26	1.10	1.40	1.48	1.19	2.12	1.21
814701	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like 1	1.49	1.11	1.80	1.84	1.19	1.45	3.46	1.07	0.97	1.04	1.40	0.45	0.51	0.34	0.61	0.80	0.61	0.78	0.98	1.26	0.81	1.71
51463	Hs.79019	neuronal apoptosis inhibitory protein	2.72	0.82	6.93	4.07	3.38	0.59	4.09	0.88	2.12	3.34	1.76	1.72	0.73	1.61	1.55	0.99	1.80	3.02	2.78	2.74	0.69	2.10
49630	Hs.23838	calcium channel, voltage-dependent, L type, alpha 1D subunit	0.91	0.39	0.14	0.18	0.51	0.46	0.52	0.43	0.22	0.20	0.37	0.42	0.48	0.74	0.80	0.41	1.04	2.29	1.78	0.46	0.76	0.39
841498	Hs.180224	death-associated protein 6	1.03	0.87	0.89	0.57	0.80	0.70	0.76	0.76	0.81	0.91	0.69	0.74	0.61	0.55	0.66	0.74	0.52	0.63	0.95	0.67	0.59	0.59
841308	Hs.211582	myosin, light polypeptide kinase	3.25	1.34	12.25	4.30	6.11	1.04	4.53	1.07	18.08	3.40	2.61	5.69	1.18	2.38	3.72	1.77	1.95	3.35	3.93	1.99	0.74	2.71
490306	Hs.91586	transmembrane 9 superfamily member 1	1.39	1.33	1.53	1.19	1.14	0.74	1.03	1.03	1.55	1.68	1.49	1.31	1.48	2.22	1.95	1.07	1.40	0.89	1.45	1.46	1.11	0.57
363086	Hs.153998	creatine kinase, mitochondrial 1 (ubiquitous)	0.80	0.86	0.44	0.20	1.38	0.24	0.26	0.32	0.24	0.76	0.26	0.42	0.28	0.50	0.44	0.36	0.18	0.49	0.31	0.83	0.61	0.17
824511	Hs.156000	zinc finger protein homologous to Zfp161 in mouse	1.94	1.83	0.83	1.08	2.39	1.53	0.96	1.26	1.22	1.35	1.11	1.40	2.08	1.50	2.18	1.10	1.24	1.56	1.46	1.23	1.58	2.08
263200	Hs.153445	Human mRNA for unknown product, partial cds	1.11	1.65	2.39	1.87	1.80	0.69	1.01	0.90	0.90	0.66	0.95	1.48	0.62	0.96	0.85	1.00	0.42	0.45	0.33	0.56	0.89	1.75
898305	Hs.76307	neuroblastoma candidate region, suppression of tumorigenicity 1	0.83	0.71	0.22	0.38	0.67	1.04	0.94	1.20	1.49	0.83	1.09	1.05	0.40	0.89	1.20	1.70	0.55	1.09	1.08	0.45	0.52	0.61
289818	Hs.170008	methylmalonate-semialdehyde dehydrogenase	1.56	2.19	2.33	1.89	3.19	1.24	1.13	1.66	1.26	1.40	2.91	3.17	1.12	0.83	1.79	1.86	1.67	2.50	3.49	1.14	2.51	1.86
713782	Hs.92208	a disintegrin and metalloproteinase domain 15 (metargidin)	0.91	0.75	0.18	0.36	0.64	0.39	0.70	0.61	0.27	0.44	0.59	0.52	0.25	0.77	0.54	0.49	0.32	0.46	1.02	0.97	0.62	0.25
843321	Hs.23881	keratin 7	0.32	0.19	0.11	0.13	0.30	0.41	0.37	0.29	0.15	0.10	0.31	0.20	0.12	0.45	0.24	0.29	0.10	0.29	0.36	0.59	0.44	0.32
877651	Hs.94211	rcd1 (required for cell differentiation, S.pombe) homolog 1	1.50	2.41	1.10	1.64	2.98	1.96	1.63	1.46	1.15	1.71	2.70	2.68	0.88	1.33	1.23	2.01	1.53	1.96	1.34	1.05	1.70	1.80
897563	Hs.84883	KIAA0864 protein	1.79	1.41	1.97	1.06	1.65	0.71	2.12	0.79	1.56	1.04	0.91	1.61	0.64	0.96	1.23	0.78	0.78	1.35	0.84	1.14	0.59	2.42
789204	Hs.8146	translocation protein 1	1.49	1.59	1.42	0.88	0.85	0.76	1.32	0.89	1.66	2.10	1.15	1.44	0.89	0.74	1.35	0.69	1.13	1.23	2.03	1.43	0.48	0.99
772220	Hs.76901	for protein disulfide isomerase-related	1.99	3.93	4.42	2.18	3.99	3.02	3.45	2.21	3.70	2.71	2.20	1.96	0.90	1.84	1.95	2.01	2.24	1.37	3.12	2.18	2.44	2.41
784830	Hs.82043	D123 gene product	1.07	2.46	1.54	2.46	1.13	2.17	1.82	0.86	0.73	0.92	0.79	0.56	0.49	0.51	0.62	0.97	0.98	0.92	0.82	1.15	1.84	1.93
814636	Hs.198296	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	2.31	7.15	1.10	2.01	2.32	1.02	2.16	1.58	1.76	1.36	1.26	0.94	0.34	0.46	1.68	0.88	0.68	2.74	2.63	1.23	1.50	1.63
784126	Hs.248267	thiosulfate sulfurtransferase (rhodanese)	0.89	1.67	1.15	1.28	1.55	1.30	2.01	0.83	0.80	1.44	1.28	0.84	1.19	1.15	1.02	1.43	0.77	1.03	1.56	0.83	0.94	0.81
843110	Hs.74576	GDP dissociation inhibitor 1	1.63	2.13	1.23	1.22	1.56	1.31	1.15	1.40	1.94	1.74	1.22	2.71	1.58	1.12	1.50	1.30	1.59	1.38	1.74	1.20	1.51	1.40
843352	Hs.118065	proteasome (prosome, macropain) subunit, beta type, 7	1.08	1.54	0.88	0.86	0.82	0.65	0.98	0.97	0.96	1.70	0.67	0.84	1.08	0.67	0.97	0.76	0.74	0.64	0.94	0.82	1.07	0.93
824352	Hs.178658	RAD23 (S. cerevisiae) homolog B	1.32	2.39	0.88	1.53	1.30	0.78	2.10	1.61	1.78	2.06	0.99	0.68	0.81	0.76	1.03	1.17	0.95	1.18	2.00	1.58	1.87	1.54
758662	Hs.5648	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	1.47	2.23	0.99	1.98	1.45	1.22	2.67	1.64	2.27	1.83	1.53	1.97	1.42	0.96	1.64	1.39	1.26	1.40	1.75	0.97	1.05	1.37
843028	Hs.155981	mesothelin	0.42	0.29	0.14	0.07	0.16	0.17	0.12	0.17	0.09	0.16	0.07	0.08	0.05	0.06	0.06	0.09	0.14	0.32	0.26	0.27	0.11	0.04
841617	Hs.125078	Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	0.82	1.14	0.56	0.85	0.77	1.12	0.76	1.25	1.43	1.25	1.52	1.10	1.55	1.47	1.73	1.21	1.52	0.96	1.37	0.98	0.92	0.93
840524	Hs.7844	golgi autoantigen, golgin subfamily b, macrogolgin (with transmembrane signal), 1	1.55	2.03	1.39	1.21	2.46	1.36	0.93	1.31	2.47	1.57	1.29	1.31	1.15	1.33	1.36	1.02	1.50	1.47	1.71	0.91	1.62	1.47
841620	Hs.173381	dihydropyrimidinase-like 2	0.76	0.62	0.77	1.07	1.04	0.38	1.35	0.35	0.62	0.74	0.50	0.65	0.46	1.03	0.85	0.59	0.58	0.91	0.73	0.65	0.45	0.44
760298	Hs.18069	protease, cysteine, 1 (legumain)	1.78	4.12	3.11	3.37	3.34	2.77	1.85	2.54	4.35	3.42	3.31	2.77	1.91	2.52	2.10	4.00	1.90	1.72	2.03	2.18	3.22	1.72
796757	Hs.80917	adaptor-related protein complex 3, sigma 1 subunit	0.51	1.24	0.62	0.87	1.07	0.51	0.63	0.61	0.68	0.94	0.74	0.41	0.38	0.50	0.89	0.67	0.62	0.48	0.72	0.87	0.60	0.73
824117	Hs.82771	vaccinia related kinase 2	1.75	1.23	1.41	2.68	1.38	1.31	1.04	0.87	1.56	0.94	0.83	1.24	0.83	0.87	1.46	0.70	1.13	1.20	1.19	0.46	1.12	0.85
78869	Hs.90107	cell membrane glycoprotein, 110000M(r) (surface antigen)	1.19	1.62	1.08	1.02	1.64	1.36	1.20	1.58	1.28	2.65	1.39	1.57	1.86	1.57	1.36	0.68	1.85	0.83	1.09	0.91	1.76	1.24
52646	Hs.156814	KIAA0377 gene product	0.59	0.92	0.67	1.20	0.96	0.76	0.51	0.75	0.76	1.08	0.95	0.63	0.89	0.98	1.06	0.59	0.63	0.57	0.86	0.66	0.76	0.35
724387	Hs.1063	small nuclear ribonucleoprotein polypeptide C	1.45	1.99	2.13	1.64	1.81	0.98	1.80	1.70	1.27	1.98	1.73	0.58	1.02	0.84	1.34	1.16	1.09	1.14	1.81	1.01	2.82	2.05
788832	Hs.116577	prostate differentiation factor	1.90	0.88	2.94	2.03	0.95	0.84	1.61	0.91	3.67	2.76	1.49	0.72	1.15	0.83	2.13	1.18	3.73	1.49	2.08	1.41	0.55	0.95
35191	Hs.118684	stromal cell-derived factor 2	0.94	1.04	1.12	1.07	1.00	0.65	1.82	0.73	1.40	1.38	1.17	0.55	1.11	1.42	1.00	1.01	1.25	0.69	1.16	1.27	1.15	0.75
842863	Hs.75789	N-myc downstream regulated	2.06	1.65	2.29	2.02	3.23	1.75	1.36	3.00	0.68	0.81	2.60	1.17	1.56	0.61	1.01	0.85	0.78	1.30	0.79	2.59	2.79	1.65
841689	Hs.6551	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	2.19	2.86	0.90	0.85	1.47	1.34	1.17	2.25	2.24	3.26	1.88	2.39	2.72	1.75	3.57	2.41	1.99	1.22	1.85	0.97	2.63	0.95
627541	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)	1.26	0.84	1.91	1.85	3.24	1.14	1.11	0.88	3.36	1.41	0.76	6.80	4.83	3.16	6.53	1.55	3.03	1.73	2.78	1.63	0.29	0.92
49873	Hs.25515	KIAA0362 protein	1.10	1.86	2.14	1.60	1.10	0.84	1.83	1.41	1.39	1.28	1.29	0.74	1.05	0.95	1.05	1.15	0.93	0.69	1.34	0.87	1.45	1.50
824895	Hs.154545	PDZ domain containing guanine nucleotide exchange factor(GEF)1; RA(Ras/Rap1A-associ	0.90	2.22	2.48	2.83	1.92	1.09	0.85	2.01	2.14	2.41	3.02	4.66	1.80	2.29	2.30	2.24	0.84	1.40	1.06	0.99	1.15	0.91
783681	Hs.3383	upstream regulatory element binding protein 1	1.65	1.30	0.83	0.87	1.01	1.31	1.13	1.04	0.76	1.02	1.10	0.92	0.78	0.80	0.96	1.10	0.90	1.00	1.06	0.88	1.40	2.90
502067	Hs.16950	Human mRNA for KIAA0342 gene, complete cds	2.45	1.83	1.70	1.52	0.60	0.87	1.64	0.79	2.46	2.69	1.44	2.86	1.72	1.97	2.23	1.18	2.13	1.74	2.04	1.77	0.46	1.12
773233	Hs.155313	death associated transcription factor 1	3.88	3.20	2.39	1.13	3.64	4.12	2.27	3.07	3.28	2.97	4.33	4.17	5.13	2.33	3.65	2.14	6.34	3.70	2.54	1.77	2.71	2.31
795805	Hs.7976	KIAA0332 protein	2.11	2.25	2.13	1.69	1.15	0.93	1.49	1.11	1.67	1.20	0.95	2.23	0.86	1.29	1.30	0.53	0.70	0.79	0.86	0.85	0.84	1.70
502909	Hs.6833	KIAA0326 protein	0.86	1.64	1.40	1.57	1.26	0.80	1.07	1.14	1.65	1.52	1.09	1.38	0.99	1.49	1.49	1.27	1.00	0.67	0.94	0.66	0.77	0.91
755891	Hs.20126	KIAA0317 gene product	0.97	2.12	2.36	2.39	1.71	0.93	1.20	1.45	1.30	0.95	1.08	1.78	0.94	1.71	1.58	1.08	1.06	0.61	0.92	1.02	0.90	1.23
786672	Hs.80620	guanine nucleotide exchange factor for Rap1	3.50	4.18	2.67	1.50	3.30	1.72	5.46	1.81	2.75	7.56	1.44	2.39	1.04	1.96	2.71	1.08	2.97	2.48	4.26	1.17	1.23	1.62
788203	Hs.82324	KIAA0157 protein	0.98	2.21	0.76	1.65	2.05	1.04	1.39	1.67	1.36	1.13	1.51	1.38	0.66	0.68	1.45	0.75	1.55	0.92	1.45	0.80	1.54	1.63
795989	Hs.82042	solute carrier family 23 (nucleobase transporters), member 1	1.05	1.94	1.43	1.03	2.22	0.86	1.22	0.88	1.13	1.32	1.62	1.55	1.15	1.08	1.22	1.23	0.90	1.22	1.08	0.93	1.04	0.64
591465	Hs.79077	KIAA0233 gene product	1.20	1.52	0.37	0.77	1.79	1.17	1.54	0.81	0.67	0.88	1.15	2.21	1.53	1.55	0.93	1.33	0.80	0.33	1.76	0.65	1.27	2.08
826668	Hs.10037	KIAA0274 gene product	0.83	1.47	0.58	0.98	1.66	2.33	0.57	1.13	1.28	1.06	1.22	1.26	0.54	0.78	1.17	1.21	1.42	1.22	1.10	0.83	1.55	0.81
843133	Hs.122669	KIAA0264 protein	0.74	1.16	0.48	0.84	1.08	0.84	0.75	1.13	1.03	0.93	0.95	1.28	0.78	0.52	0.76	0.93	0.58	0.99	0.92	0.92	1.24	0.92
825451	Hs.7763	vesicle docking protein p115	2.25	2.42	1.18	1.20	1.27	1.03	0.94	1.33	1.52	1.67	1.14	1.19	0.47	1.12	1.11	0.62	1.14	0.90	1.43	1.15	0.99	0.49
82976	Hs.170218	KIAA0251 protein	0.97	1.68	0.52	0.98	1.06	0.91	1.97	0.90	0.96	1.80	1.30	1.35	0.80	0.99	1.12	1.30	1.61	1.36	2.03	0.99	1.87	1.81
32231	Hs.84753	KIAA0246 protein	1.74	1.51	3.14	2.32	2.51	2.01	2.47	2.27	1.55	1.33	2.47	1.61	1.42	1.72	1.58	1.43	1.19	1.19	1.17	1.00	1.43	1.07
753321	Hs.79276	Human mRNA for KIAA0232 gene, complete cds	0.63	1.99	0.94	0.57	2.32	0.47	0.90	1.61	1.92	2.31	0.97	1.29	1.29	0.83	1.73	0.73	0.89	1.13	1.95	0.90	0.96	0.33
565379	Hs.81875	growth factor receptor-bound protein 10	2.70	4.08	3.92	8.25	4.87	1.47	5.92	2.61	5.11	4.64	2.24	3.24	2.44	1.75	2.37	2.60	6.54	2.32	3.47	1.78	1.76	1.63
815781	Hs.36927	heat shock 105kD	0.86	1.37	0.49	0.98	1.60	1.61	1.24	1.23	1.07	1.41	1.06	1.90	0.71	1.05	1.55	0.96	1.34	0.71	2.07	1.33	1.20	1.24
950369	Hs.84790	KIAA0225 protein	1.25	3.08	1.62	3.74	2.55	1.48	1.58	1.64	1.34	3.59	1.00	1.14	0.63	0.77	0.78	0.88	0.94	1.12	1.63	0.93	1.83	1.50
49404	Hs.75863	KIAA0218 gene product	1.76	3.10	2.53	2.72	2.94	1.52	1.29	2.16	1.74	2.57	1.97	1.74	1.09	1.27	1.63	2.02	2.07	1.81	1.60	1.34	1.72	1.93

824044	Hs.78851	KIAA0217 protein	0.28	0.18	0.09	0.12	0.27	0.40	0.29	0.30	0.09	0.07	0.20	0.23	0.11	0.55	0.19	0.30	0.14	0.22	0.27	0.53	0.34	0.23
781222	Hs.75822	TGFB1-induced anti-apoptotic factor 1	0.69	1.35	0.51	0.72	1.20	0.97	0.69	0.87	1.05	1.13	0.91	0.72	0.50	1.05	0.71	0.86	0.84	0.86	0.81	0.88	1.45	0.67
49117	Hs.82292	KIAA0215 gene product	2.02	2.71	2.37	1.92	2.61	4.57	1.35	2.07	7.32	4.88	1.89	2.31	2.13	1.89	2.45	1.58	2.57	1.65	2.02	0.97	1.32	2.72
703846	Hs.115740	KIAA0210 gene product	0.91	1.25	0.76	0.94	1.16	1.02	0.84	0.69	0.84	0.98	0.81	0.90	0.69	0.84	0.91	0.97	0.96	0.77	0.86	0.61	0.79	0.89
234856	Hs.174007	von Hippel-Lindau syndrome	1.88	0.93	2.16	2.23	1.51	0.88	1.67	1.74	2.16	2.71	1.68	1.32	0.80	1.46	1.69	0.91	2.03	1.77	2.02	0.86	0.84	1.36
50794	Hs.78434	zinc finger protein 133 (clone pHZ-13)	0.55	0.78	0.78	0.82	0.77	0.45	0.34	0.59	0.37	0.55	1.02	0.77	0.75	0.91	1.03	0.49	0.58	0.59	0.62	0.53	0.77	0.40
768644	Hs.250867	zona pellucida glycoprotein 3A (sperm receptor)	2.32	1.49	1.04	0.90	1.68	1.91	1.80	1.29	0.87	1.84	1.27	1.42	2.74	1.97	2.11	1.92	1.77	2.67	3.35	0.89	1.10	1.09
753430	Hs.96264	alpha thalassemia/mental retardation syndrome X-linked	1.29	1.77	1.28	1.32	2.31	0.73	1.54	1.97	1.21	1.28	0.62	0.89	0.82	0.73	1.30	0.42	1.31	1.37	2.11	0.95	1.18	1.12
324901	Hs.152213	wingless-type MMTV integration site family, member 5A	0.63	0.72	1.11	1.17	1.40	0.26	0.33	0.71	1.36	0.39	1.66	0.50	1.40	1.52	3.21	0.57	0.50	0.51	0.51	0.48	0.80	0.73
755145	Hs.155191	villin 2 (ezrin)	0.66	0.87	0.41	0.68	0.83	0.69	1.10	0.69	1.03	1.41	0.73	2.42	0.73	0.99	1.68	0.80	0.84	0.53	0.57	1.14	0.68	0.62
345839	Hs.71816	v-akt murine thymoma viral oncogene homolog 1	0.78	0.61	1.19	1.77	0.77	2.16	0.68	1.05	0.89	0.65	1.61	3.44	6.89	3.83	4.12	1.69	1.15	1.04	0.99	1.25	0.96	0.88
753418	Hs.93183	vasodilator-stimulated phosphoprotein	0.61	0.57	0.56	0.46	0.65	0.46	0.53	0.53	0.51	0.44	0.52	0.89	0.63	0.78	0.93	0.72	0.82	0.59	0.66	0.70	0.79	1.05
34778	Hs.73793	vascular endothelial growth factor	0.27	0.48	0.69	0.73	0.66	0.32	0.75	0.41	0.32	0.21	0.59	3.17	6.48	5.50	2.66	0.30	0.38	0.48	0.56	0.95	0.51	0.35
812965	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	0.54	0.85	0.44	1.68	0.55	0.63	1.22	0.24	0.33	0.34	0.34	0.13	0.77	0.35	0.60	0.27	0.27	1.80	0.38	0.75	0.17	1.59
124261	Hs.174051	small nuclear ribonucleoprotein 70kD polypeptide (RNP antigen)	1.76	1.96	1.10	1.16	1.95	1.50	1.49	1.45	1.32	1.21	1.34	2.36	2.35	1.78	2.27	0.72	2.24	2.82	1.80	1.38	1.59	1.49
292996	Hs.75544	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypep	1.94	3.25	1.83	1.94	2.04	1.95	2.82	1.94	2.76	2.85	3.12	1.30	0.72	1.11	1.74	1.19	1.57	1.81	2.36	2.32	1.74	1.93
180520	Hs.180686	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman synd	1.67	1.08	0.81	0.88	1.08	1.19	0.81	0.88	0.98	1.00	1.11	2.80	1.78	1.23	1.51	0.42	1.49	1.53	1.27	0.94	1.05	1.94
66686	Hs.29797	ribosomal protein L10	0.94	1.32	0.88	0.55	1.02	0.75	1.07	0.81	0.82	0.44	0.84	1.01	0.73	0.56	1.04	0.78	0.79	1.28	0.86	1.21	0.80	0.67
190491	Hs.90303	tuberous sclerosis 2	1.98	0.59	1.36	1.17	1.17	1.75	0.74	1.21	1.78	2.13	1.23	3.99	3.29	1.81	3.20	1.22	2.37	1.67	0.76	1.07	0.94	0.85
723986	Hs.170453	tropomodulin	1.30	0.72	1.72	1.99	0.97	1.06	1.61	1.21	2.31	3.36	0.99	3.63	2.12	2.17	3.72	0.91	1.21	0.77	2.31	1.34	0.96	1.38
306813	Hs.126700	ESTs	0.33	0.97	0.45	0.24	0.61	0.17	0.36	0.18	0.22	0.92	0.27	0.60	0.24	0.33	0.39	0.20	0.30	0.35	0.30	0.93	0.39	0.33
241530	Hs.171596	EphA2	0.35	0.26	0.11	0.10	0.26	0.29	0.24	0.16	0.25	2.81	0.19	0.11	0.06	0.17	0.18	0.25	0.10	0.32	0.24	0.26	0.17	0.13
755821	Hs.83469	nuclear factor (erythroid-derived 2)-like 1	0.56	0.49	0.56	0.41	0.47	0.33	0.73	0.51	0.60	0.71	0.37	0.73	0.26	0.85	0.76	0.39	0.61	0.49	0.96	0.37	0.73	0.46
810512	Hs.87409	thrombospondin 1	1.91	0.73	0.62	1.62	3.40	1.37	0.30	2.20	3.86	1.08	1.63	5.75	8.17	3.38	8.62	1.71	1.99	1.15	0.59	0.64	1.61	1.02
813459	Hs.145381	general transcription factor IIE, polypeptide 1 (alpha subunit, 56kD)	1.93	2.38	1.09	1.61	2.68	1.18	1.47	2.36	1.99	2.26	1.54	2.59	2.22	2.10	2.89	0.99	1.85	1.85	2.40	1.85	1.57	1.24
191603	Hs.179661	Homo sapiens clone 24703 beta-tubulin mRNA, complete cds	1.24	1.56	2.17	1.78	1.13	1.59	2.26	0.96	1.35	0.93	1.14	1.02	1.05	1.36	1.26	1.13	0.85	0.82	1.49	1.53	1.47	1.71
768370	Hs.245188	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory)	1.04	1.08	1.99	2.08	2.07	0.76	3.89	1.93	4.73	3.27	2.79	11.50	5.91	4.88	9.55	2.76	4.73	3.34	3.63	2.52	0.99	0.83
771220	Hs.75569	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light	1.16	1.74	1.27	1.56	1.32	1.38	2.45	1.54	1.64	1.85	1.56	1.39	1.00	1.54	1.63	1.05	1.25	1.18	1.41	1.60	1.04	1.08
812276	Hs.76930	synuclein, alpha (non A4 component of amyloid precursor)	2.10	3.55	1.45	1.51	1.46	1.63	3.10	2.45	1.70	2.57	1.49	2.63	0.94	1.26	1.69	0.35	2.81	1.71	2.94	1.04	1.34	1.43
126858	Hs.14553	ESTs	2.02	1.18	1.72	1.68	0.83	1.96	1.51	1.55	2.15	1.19	2.38	2.62	1.31	2.61	3.15	0.45	1.21	1.42	1.05	1.10	0.88	2.76
163174	Hs.78869	transcription elongation factor A (SII), 1	1.34	1.07	0.93	1.37	1.34	0.94	1.08	1.01	1.00	0.93	1.18	1.37	0.81	0.72	0.66	0.52	1.23	1.83	1.04	1.59	1.40	1.14
246300	Hs.182741	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	1.59	1.69	0.83	1.12	1.29	0.87	1.90	1.67	0.91	1.34	1.26	1.36	0.48	0.62	0.82	0.32	0.93	1.12	2.13	0.60	0.98	1.36
36393	Hs.4112	t-complex 1	1.12	0.79	1.30	1.08	0.70	2.02	1.40	1.34	0.99	1.31	1.37	1.00	0.53	1.20	0.78	0.39	1.24	1.04	1.14	0.97	1.06	0.70
770014	Hs.74647	T-cell receptor, alpha (V,D,J,C)	3.59	2.81	4.85	5.39	1.43	5.60	2.72	4.80	5.72	5.24	3.67	7.82	1.64	4.10	4.49	1.28	7.10	3.91	5.43	1.97	1.84	1.80
809535	Hs.73965	splicing factor, arginine/serine-rich 2	1.56	1.15	1.01	1.80	0.85	1.15	1.73	0.97	1.14	1.41	0.98	1.27	1.33	0.96	1.53	1.16	1.08	1.41	1.77	1.32	0.84	1.30
823886	Hs.2094	Smooth muscle myosin heavy chain isoform SMemb [human, umbilical cord, fetal aorta, mR	0.89	2.23	6.62	1.79	1.35	1.27	1.92	2.28	2.92	2.07	1.39	2.44	1.24	1.71	3.13	0.60	1.52	2.22	2.57	1.19	1.43	1.97
128875	Hs.76253	spinocerebellar ataxia 2 (olivopontocerebellar ataxia 2, autosomal dominant, ataxin 2)	1.06	1.88	0.94	1.42	1.10	1.08	1.03	1.15	1.93	1.27	1.02	0.70	1.08	0.81	0.56	0.76	1.13	1.32	1.15	1.20	1.34	1.13
359835	Hs.28491	spermidine/spermine N1-acetyltransferase	0.39	1.17	1.14	0.87	1.16	0.70	0.45	0.70	1.16	0.71	1.00	1.83	0.39	0.80	0.95	1.11	0.62	0.53	0.52	1.82	0.96	0.99
320763	Hs.44450	Sp3 transcription factor	1.45	1.63	1.02	2.75	1.05	1.77	0.52	0.80	1.69	0.94	1.17	2.23	3.26	1.35	1.73	0.69	1.27	1.73	0.93	1.34	1.44	1.64
205303	Hs.117816	sorcin	0.54	0.71	0.49	0.86	0.53	0.82	0.98	0.76	0.84	1.10	0.76	0.63	0.49	0.46	0.96	0.63	0.83	0.93	0.84	0.90	0.46	1.02
810873	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	0.38	0.24	0.12	0.07	0.22	0.20	0.15	0.26	0.23	0.21	0.15	0.24	0.03	0.21	0.27	0.60	0.31	0.48	0.39	0.44	0.30	0.09
812227	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amil	0.85	1.03	0.71	0.63	0.92	0.83	0.66	1.30	1.27	1.88	1.04	1.90	0.88	1.26	1.57	1.18	1.41	1.10	1.08	1.09	0.85	0.62
190732	Hs.33084	solute carrier family 2 (facilitated glucose transporter), member 5	0.83	0.85	1.07	0.97	0.72	1.00	1.28	1.37	1.15	1.54	1.05	1.76	0.94	1.11	1.29	0.72	0.49	1.09	1.22	0.65	0.47	1.26
814792	Hs.78829	ubiquitin specific protease 10	1.03	0.96	1.03	0.96	1.05	0.83	1.93	0.71	0.81	0.71	0.93	0.50	0.51	0.75	1.20	0.94	0.55	0.65	1.00	0.59	0.95	0.96
245015	Hs.8127	KIAA0144 gene product	1.54	1.92	1.30	1.68	2.01	1.60	2.01	2.00	1.33	1.41	1.38	0.94	1.43	1.55	1.48	1.33	1.01	1.22	1.66	1.02	2.01	2.13
815530	Hs.172813	PAK-interacting exchange factor beta	2.05	2.79	2.87	1.71	2.15	1.59	1.10	1.41	1.79	1.56	1.19	1.07	0.76	1.41	1.70	1.34	1.58	1.38	1.28	1.18	1.39	1.10
783698	Hs.81412	KIAA0188 protein	0.61	1.46	0.54	0.55	0.84	0.69	0.85	0.49	0.22	0.40	0.39	0.52	0.13	0.38	0.45	0.29	0.27	0.62	0.56	0.42	0.98	0.46
837905	Hs.76666	KIAA0183 protein	1.68	1.86	1.45	2.01	2.07	0.96	2.26	1.49	1.97	2.07	1.37	1.00	0.55	2.85	1.13	1.18	0.85	1.19	2.23	1.36	1.17	2.14
173309	Hs.80338	KIAA0164 gene product	2.43	2.20	0.98	1.69	2.20	1.15	1.28	1.94	1.23	1.21	0.89	1.44	0.93	0.99	1.56	0.34	1.22	2.05	1.71	1.02	1.33	1.40
180195	Hs.12303	suppressor of Ty (S.cerevisiae) 6 homolog	0.69	1.35	1.09	1.32	1.37	0.94	0.93	1.14	1.53	1.25	1.25	0.87	1.39	1.89	1.27	1.10	0.90	0.83	0.77	0.99	1.05	0.85
826137	Hs.197803	KIAA0160 protein	1.57	2.95	1.77	2.42	2.39	1.31	1.94	2.66	1.80	1.30	1.98	0.78	0.94	0.63	1.20	0.33	1.29	1.38	2.16	1.55	2.40	2.10
840620	Hs.181418	KIAA0152 gene product	0.88	1.12	0.95	1.35	1.42	0.72	2.09	0.82	1.05	1.35	1.09	0.65	1.03	0.76	1.04	0.98	0.91	1.53	1.37	1.53	1.06	0.95
898095	Hs.119	gene predicted from cDNA with a complete coding sequence	1.04	0.82	1.23	1.42	1.73	1.31	0.61	1.01	1.06	1.33	1.52	0.57	0.51	0.83	0.58	1.20	0.90	1.34	0.54	0.29	1.59	1.05
841501	Hs.77665	KIAA0102 gene product	2.25	2.45	1.84	2.68	1.56	1.52	1.16	1.24	1.84	1.56	1.54	1.25	0.79	1.28	1.66	1.27	1.71	1.30	1.29	1.32	1.54	1.25
342640	Hs.81892	KIAA0101 gene product	0.94	1.50	0.65	1.15	0.98	0.88	2.29	1.01	0.65	1.48	1.03	1.00	0.31	0.45	0.77	0.51	0.65	0.60	2.50	1.11	1.20	0.76
526184	Hs.184627	KIAA0118 protein	1.00	0.42	0.77	0.69	2.11	0.69	1.30	1.46	2.85	0.78	1.12	1.32	0.21	0.43	1.27	1.18	0.56	3.16	2.27	0.52	0.80	0.53
80504	Hs.109281	Nef-associated factor 1	0.55	0.70	1.07	2.37	0.80	0.91	0.64	0.60	0.89	0.64	0.97	0.66	0.78	0.98	0.70	1.22	0.66	0.66	0.70	0.70	0.61	0.87
562867	Hs.71827	KIAA0112 protein; homolog of yeast ribosome biogenesis regulatory protein RRS1	2.91	2.97	2.49	2.08	2.72	2.07	3.43	2.27	2.60	3.35	2.53	3.13	0.89	0.55	1.25	3.36	3.26	3.31	4.15	2.61	1.60	2.36
897983	Hs.120	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium-independent p	0.85	1.56	0.89	1.83	1.01	0.96	0.81	1.11	1.09	0.82	1.26	0.59	0.67	0.61	0.84	0.62	0.85	0.81	1.07	0.63	1.10	1.82
898032	Hs.76989	KIAA0097 gene product	1.23	1.77	0.80	1.45	1.32	1.47	2.60	0.76	1.32	1.39	1.34	1.16	1.49	1.03	1.17	1.29	1.11	0.81	1.38	0.85	1.47	1.99
84955	Hs.81964	SEC24 (S. cerevisiae) related gene family, member C	1.18	1.10	0.60	0.86	1.32	0.95	0.99	1.65	1.19	1.00	1.82	1.23	1.29	0.90	1.31	0.79	1.28	1.49	1.57	1.44	1.64	1.43
725223	Hs.75935	KIAA0077 protein	1.40	1.84	1.73	2.61	2.22	1.20	1.76	1.30	1.46	1.17	1.53	1.63	0.65	1.97	1.25	1.49	1.30	1.25	1.37	1.15	2.30	2.42
740122	Hs.51039	KIAA0076 gene product	2.14	2.59	1.65	1.42	2.78	1.51	5.89	2.17	1.98	2.95	2.14	2.46	1.96	2.08	1.82	1.39	2.32	2.49	3.50	1.37	3.38	2.18
784504	Hs.75890	site-1 protease (subtilisin-like, sterol-regulated, cleaves sterol regulatory element binding	1.27	0.77	0.77	0.51	1.10	0.73	1.17	0.95	0.80	1.03	1.08	0.97	1.16	0.76	0.88	1.14	0.88	1.10	1.41	0.63	0.99	0.95
788721	Hs.154797	KIAA0090 protein	1.43	1.64	1.39	1.22	1.47	1.25	1.62	0.73	1.01	0.74	1.07	1.23	0.97	1.17	1.48	1.09	1.16	0.86	1.05	1.26	0.85	0.94
840333	Hs.82432	KIAA0089 protein	1.76	2.64	1.10	2.30	2.56	2.67	1.60	3.52	3.53	2.29	2.96	2.90	2.11	1.31	3.31	2.46	1.66	3.82	5.67	1.29	3.17	0.91
229537	Hs.76847	KIAA0088 protein	0.92	1.50	1.17	1.04	1.85	0.93	2.07	1.04	1.47	1.23	1.44	1.25	0.76	1.20	1.32	1.42	1.06	0.80	1.30	1.10	1.54	0.97
815529	Hs.79123	KIAA0084 protein	1.34	2.14	1.29	1.52	2.65	1.70	1.53	1.51	2.59	2.71	1.75	7.82	2.65	4.65	4.85	1.88	1.16	1.43	2.73	1.41	1.67	1.46
825293	Hs.154045	KIAA0082 protein	1.69	2.73	1.74	1.55	2.63	1.33	2.10	2.11	1.89	2.93	1.73	2.04	1.64	1.85	1.72	1.39	2.20	2.02	2.84	1.98	2.88	1.53
815503	Hs.78398	KIAA0071 protein	0.48	1.33	0.87	0.97	0.95	0.55	0.55	0.46	0.67	0.55	0.54	0.60	0.61	0.51	0.66	0.57	0.46	0.59	0.75	0.56	0.55	0.53
843016	Hs.75337	nucleolar phosphoprotein p130	1.62	3.06	1.94	3.00	3.00	1.08	2.82	2.00	1.68	1.88	1.58	1.66	1.07	1.96	1.59	0.71	1.57	1.88	2.24	1.08	1.73	2.37
788444	Hs.174905	KIAA0033 protein	0.71	1.02	0.77	0.83	1.34	0.52	0.67	1.02	1.63	0.86	0.70	1.34	1.15	0.73	1.86	0.77	0.84	0.94	1.36	0.76	0.87	0.66
704697	Hs.35804	hect domain and RLD 3	0.94	1.26	0.84	0.86	1.71	0.99	0.46	0.88	1.16	0.90	0.71	2.12	0.97	1.18	1.43	0.96	0.60	1.30	1.39	0.73	1.38	0.78
842818	Hs.3100	lysyl-tRNA synthetase	1.00	0.87	0.58	0.59	1.72	0.89	1.15	0.68	0.85	0.89	0.79	0.39	0.20	0.45	0.40	0.72	0.74	0.40	0.91	0.82	1.46	1.10
897840	Hs.77257	KIAA0068 protein	0.76	1.20	0.57	1.38	1.29	1.03	0.80	0.64	1.09	0.92	0.69	0.75	0.94	1.21	0.79	1.15	0.89	0.70	0.78	0.87	0.68	1.82
79229	Hs.3094	KIAA0063 gene product	1.53	2.04	2.08	1.85	2.78	2.22	3.10	1.35	2.09	1.95	1.01	1.71	1.17	2.35	2.32	1.33	1.27	0.93	1.23	1.35	1.31	1.98
85093	Hs.89868	KIAA0062 protein	0.35	0.71	0.57	0.99	1.01	0.55	1.08	0.42	1.22	0.42	0.50	0.80	0.41	0.60	0.60	0.70	0.47	0.58	0.55	0.64	0.58	1.09
84820	Hs.153954	KIAA0057 gene product; TRAM-like protein	1.88	3.85	4.61	3.43	8.44	2.43	2.63	3.68	6.48	7.51	2.68	2.65	1.10	3.86	2.03	1.53	2.10	2.12	2.30	1.22	2.03	2.45
814054	Hs.158282	KIAA0040 gene product	0.60	2.98	0.96	1.11	2.15	2.97	1.03	2.35	4.68	3.96	1.51	6.63	1.59	1.72	4.14	2.35	1.39	2.33	6.47	1.57	1.35	0.83
825265	Hs.82502	DNA polymerase delta, subunit 3	2.98	5.27	1.62	3.62	1.35	1.78	1.15	1.87	1.78	2.25	1.70	1.51	0.97	1.85	1.63	0.70	1.66	1.53	1.66	0.74	1.56	1.56
512133	Hs.172199	adenylate cyclase 7	2.55	6.34	2.40	4.83	4.79	3.44	1.70	2.95	7.29	7.79	2.81	4.08	1.70	3.00	2.89	3.33	2.00	1.88	1.93	1.26	2.44	3.08

773188	Hs.37288	nuclear receptor subfamily 1, group D, member 2	2.20	2.44	2.36	2.72	3.26	1.60	1.13	3.04	3.51	1.78	1.54	1.12	2.34	1.08	0.23	1.05	2.22	2.19	1.19	0.81	2.09	1.71
796680	Hs.82921	solute carrier family 35 (CMP-sialic acid transporter), member 1	0.73	0.93	0.49	1.45	2.21	0.94	0.86	1.60	0.68	1.16	1.17	0.71	0.53	1.05	1.11	0.83	1.48	1.48	1.23	1.45	2.38	0.99
825271	Hs.189954	KIAA0029 protein	1.18	2.70	1.31	1.67	2.76	1.61	1.37	1.49	1.17	1.68	1.26	1.21	1.30	1.19	1.49	1.14	1.11	1.40	1.13	1.14	1.98	1.69
811930	Hs.2471	KIAA0020 gene product	2.42	6.63	1.71	2.80	2.41	1.12	5.36	1.16	1.40	1.12	1.81	1.06	0.36	0.99	1.17	0.72	0.58	1.31	1.73	0.59	0.84	1.97
840878	Hs.75616	Human mRNA for KIAA0018 gene, complete cds	0.78	0.29	0.25	0.68	0.61	1.08	0.46	0.62	1.15	1.06	0.63	1.13	0.51	0.97	1.61	0.85	0.76	1.15	1.18	1.71	1.06	0.21
713862	Hs.155287	KIAA0010 gene product	1.15	1.37	0.82	1.23	1.66	0.83	1.27	1.36	1.18	1.38	0.93	0.59	0.69	0.92	1.13	0.59	0.56	1.19	1.30	1.21	1.65	1.30
814319	Hs.170198	KIAA0009 gene product	0.67	1.18	1.75	2.21	1.40	0.89	1.04	1.12	1.09	1.21	1.05	0.40	1.04	0.87	1.02	1.05	0.86	0.99	0.92	2.54	1.00	1.67
686172	Hs.77695	KIAA0008 gene product	2.73	2.03	3.22	2.11	2.32	0.90	2.50	1.71	0.73	1.33	1.26	0.80	0.49	0.52	1.03	0.27	0.81	0.91	2.27	1.37	2.09	1.10
773922	Hs.155291	KIAA0005 gene product	0.36	0.46	0.51	0.60	0.73	0.33	0.53	0.50	0.63	1.11	0.70	0.66	0.33	0.48	0.58	0.45	1.12	0.51	1.17	0.74	0.62	0.46
825224	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	0.85	1.54	1.32	1.77	0.94	1.26	1.30	1.23	1.43	1.72	1.19	1.10	0.93	1.31	1.06	0.89	1.92	0.47	0.80	1.04	0.96	0.95
758037	Hs.306	human immunodeficiency virus type I enhancer-binding protein 1	1.28	3.93	2.76	2.70	3.44	1.89	1.18	2.01	2.45	1.90	2.65	2.12	1.17	1.79	1.91	1.52	1.49	1.28	2.00	1.27	1.27	1.85
72391	Hs.166294	sortilin-related receptor, L(DLR class) A repeats-containing	4.70	5.55	1.31	5.23	4.94	3.57	2.10	4.12	4.75	3.64	5.38	5.58	2.62	3.92	5.49	2.42	3.98	4.02	3.85	2.01	3.56	2.49
81394	Hs.6721	lysophospholipase-like	1.85	2.00	1.41	2.02	2.21	2.46	1.23	1.56	5.31	2.96	1.81	2.02	1.53	2.96	2.85	1.71	1.02	0.98	0.94	1.77	0.82	1.14
814409	Hs.240534	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, a	0.75	1.16	1.41	0.93	1.42	0.64	1.25	1.49	0.93	1.47	1.33	0.82	1.04	0.71	0.90	1.18	0.83	1.18	1.19	0.97	1.18	1.09
613126	Hs.85482	ubiquitin specific protease 13 (isopeptidase T-3)	2.59	2.44	1.96	2.00	2.54	1.53	1.78	1.83	0.72	2.58	2.10	1.35	0.40	0.42	0.68	0.92	1.06	0.99	3.20	1.99	2.14	1.79
824602	Hs.155530	interferon, gamma-inducible protein 16	0.67	4.59	1.12	2.59	2.51	2.13	0.81	1.93	3.20	1.60	2.16	1.71	0.46	1.31	1.16	1.98	1.08	1.47	1.19	1.14	1.46	2.48
814546	Hs.1050	pleckstrin homology, Sec7 and coiled/coil domains 1(cytohesin 1)	1.44	1.70	1.19	0.97	1.22	0.92	1.81	0.83	1.28	1.03	1.09	2.08	1.93	2.58	1.72	0.89	1.16	1.00	1.33	1.19	0.83	0.81
809838	Hs.75452	heat shock 70kD protein 2	1.94	2.29	1.36	1.96	1.62	1.23	1.45	1.47	1.98	2.24	1.52	2.13	2.02	0.71	3.09	0.99	1.26	1.43	1.96	1.12	2.35	2.23
52629	Hs.184402	calcium/calmodulin-dependent protein kinase I	1.81	3.40	2.41	1.93	2.87	1.69	2.41	2.07	1.99	2.97	2.92	3.39	1.35	2.51	3.34	2.31	2.42	3.54	3.67	0.86	2.36	1.78
826204	Hs.83849	flightless I (Drosophila) homolog	0.83	0.73	0.68	0.75	0.92	1.00	0.66	0.71	0.83	0.72	0.86	0.67	0.73	0.91	0.70	1.29	0.83	1.01	0.86	0.84	0.95	1.08
726236	Hs.155606	paired mesoderm homeo box 1	0.92	1.80	0.90	0.92	1.67	0.65	1.35	1.62	2.12	1.38	1.55	1.64	0.42	1.09	1.27	1.16	0.83	0.93	1.39	0.81	0.70	0.82
789091	Hs.28777	H2A histone family, member L	2.59	5.22	2.81	1.51	2.56	2.16	3.18	1.82	3.70	3.96	1.35	2.33	3.41	1.29	4.60	2.10	2.38	1.65	5.18	1.04	1.40	3.09
80924	Hs.77798	histidyl-tRNA synthetase-like	1.05	1.58	0.50	0.76	1.21	0.80	1.72	0.80	1.18	0.93	1.03	0.87	0.56	1.36	1.01	0.96	0.72	0.83	1.15	1.46	0.94	1.07
810703	Hs.177516	high density lipoprotein binding protein (vigilin)	1.59	1.58	0.57	0.78	1.63	1.17	1.75	1.12	1.18	0.97	1.09	0.87	0.49	1.23	0.89	1.36	0.85	1.15	1.49	1.61	1.71	1.66
949934	Hs.77492	heterogeneous nuclear ribonucleoprotein A0	0.75	1.60	0.91	1.34	1.15	0.65	1.01	0.90	1.20	0.99	0.96	1.03	0.93	1.38	1.30	0.94	0.90	1.47	0.98	1.40	0.95	0.87
786084	Hs.77254	chromobox homolog 1 (Drosophila HP1 beta)	1.48	2.61	1.72	3.00	2.04	1.25	3.03	1.59	2.34	2.35	1.67	1.90	0.76	1.12	1.43	0.82	2.33	1.92	3.04	2.34	2.98	2.24
71545	Hs.86575	mitogen-activated protein kinase kinase kinase kinase 1	0.90	5.90	1.31	3.11	3.28	2.48	1.09	2.44	3.02	2.08	2.76	1.90	0.54	1.28	1.43	2.05	1.41	1.86	1.77	1.33	1.71	2.42
563444	Hs.155591	forkhead box F1	1.43	1.50	1.37	1.04	1.76	1.26	1.50	1.08	1.15	1.19	0.98	0.97	1.01	0.81	0.83	0.84	2.39	1.30	1.48	1.53	1.37	1.32
131867	Hs.25155	guanine nucleotide regulatory protein (oncogene)	1.29	1.75	0.52	1.11	1.92	1.68	3.45	0.90	1.18	1.29	0.85	1.68	1.11	0.71	1.47	0.91	1.77	1.15	1.21	1.15	1.07	1.48
898218	Hs.77326	insulin-like growth factor binding protein 3	0.31	0.66	1.48	0.31	1.28	0.34	0.21	0.90	0.67	0.37	0.43	1.36	0.32	0.64	0.64	0.52	0.49	0.31	0.30	0.39	0.49	0.31
796137	Hs.183773	golgi autoantigen, golgin subfamily a, 4	1.57	1.69	0.82	1.62	1.47	1.37	1.38	1.04	1.73	0.92	0.94	0.72	0.54	0.49	0.70	0.66	0.94	0.95	1.20	1.03	1.02	0.83
774036	Hs.11465	glutathione-S-transferase like	0.99	1.33	0.53	0.76	1.58	0.89	1.42	1.20	1.17	0.97	0.95	0.83	0.50	1.07	0.82	0.99	0.70	0.98	1.26	1.30	1.24	1.05
713647	Hs.100090	tetraspan 3	0.59	1.69	1.73	0.75	0.89	0.69	0.64	0.79	0.94	1.63	0.88	0.59	0.47	0.58	1.18	0.97	0.94	1.09	0.51	1.13	1.01	1.48
684661	Hs.64639	glioma pathogenesis-related protein	1.09	2.56	2.08	1.90	2.12	1.15	1.88	1.41	2.70	1.55	1.16	1.10	0.63	1.91	0.94	0.58	1.71	1.99	1.83	1.13	1.50	0.92
812155	Hs.78948	Rab geranylgeranyltransferase, beta subunit	0.92	2.06	0.74	1.11	1.17	1.06	1.39	1.43	1.00	2.04	1.05	1.17	0.57	0.73	1.38	0.62	0.44	1.16	1.12	1.20	1.35	0.93
842806	Hs.95577	cyclin-dependent kinase 4	1.49	2.03	1.81	1.58	1.54	1.41	3.80	1.75	1.62	1.45	0.62	1.43	0.56	1.30	1.41	1.32	1.27	1.49	1.60	1.64	1.02	0.91
839682	Hs.75355	ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13)	1.68	1.44	1.43	1.33	1.73	1.30	1.72	2.22	1.81	1.89	2.63	1.49	1.24	0.92	1.37	0.78	1.48	1.17	1.04	1.36	2.29	1.80
770992	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.42	0.81	1.71	2.95	0.76	1.23	3.53	0.71	0.57	1.20	1.60	3.03	2.36	2.22	2.36	0.80	0.96	0.59	1.51	1.32	0.62	0.97
841691	Hs.78935	methionine aminopeptidase; eIF-2-associated p67	0.41	0.50	0.78	0.92	1.03	0.49	0.57	0.40	0.44	0.52	0.68	0.26	0.35	0.25	0.41	1.10	0.52	0.60	0.51	0.54	0.47	0.55
686164	Hs.89981	diacylglycerol kinase, zeta (104kD)	1.17	0.57	0.89	1.15	0.80	0.66	1.00	0.45	1.42	1.54	1.00	1.71	1.25	1.06	1.65	1.53	0.82	1.08	1.33	0.90	0.55	0.64
79353	Hs.3382	protein phosphatase 4, regulatory subunit 1	0.61	0.85	0.87	0.51	0.81	0.52	0.33	0.35	0.60	0.47	0.54	0.41	0.44	0.62	0.50	0.95	0.27	0.35	0.39	0.78	0.41	0.25
785371	Hs.111039	N-myristoyltransferase 1	1.39	1.55	0.59	0.46	3.09	1.39	1.43	1.08	1.17	0.86	4.11	1.49	1.37	1.31	1.87	3.42	1.72	1.66	1.75	1.01	0.73	2.41
843139	Hs.166887	copine I	1.08	1.09	0.91	0.79	2.16	0.99	0.95	1.12	0.91	1.72	1.42	1.07	0.94	0.91	0.69	1.31	0.84	0.93	0.79	0.53	1.59	0.99
785575	Hs.177559	interferon gamma receptor 2 (interferon gamma transducer 1)	1.92	2.19	1.24	1.35	2.45	1.54	1.33	1.79	1.36	1.37	1.77	2.86	1.62	1.64	2.63	1.54	1.56	1.44	2.60	1.88	1.90	1.66
827013	Hs.170263	tumor protein 53-binding protein, 1	1.44	0.86	1.04	0.94	3.32	0.74	0.97	0.70	1.50	1.60	0.89	1.24	0.77	1.32	1.38	1.36	1.17	0.69	1.42	0.99	0.68	0.65
774071	Hs.7885	Clathrin assembly lymphoid-myeloid leukemia gene	2.02	1.66	0.74	1.15	2.36	1.72	0.71	1.51	1.75	1.57	1.28	1.11	0.47	1.01	0.68	1.72	0.77	1.28	0.96	1.12	1.63	0.91
740344	Hs.83724	Human clone 23773 mRNA sequence	1.52	1.99	1.12	1.91	2.36	1.50	2.47	1.48	1.29	1.82	1.92	0.98	0.91	1.16	0.89	1.98	1.26	1.14	1.31	1.24	1.76	2.23
814776	Hs.83572	Human clone 23721 mRNA sequence	0.52	0.95	0.70	1.50	0.70	0.83	1.21	0.40	0.63	1.14	0.84	0.50	0.84	0.44	0.79	1.46	0.84	1.00	0.84	1.32	0.41	0.75
838716	Hs.241515	COX11 (yeast) homolog, cytochrome c oxidase assembly protein	1.09	1.14	0.66	1.35	1.43	1.15	1.32	2.93	1.50	0.95	3.17	1.01	1.00	0.95	2.04	1.15	1.23	1.65	1.44	1.43	1.85	1.55
760282	Hs.15562	Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence	0.69	2.74	0.66	1.27	1.49	0.74	1.35	0.64	0.63	1.45	0.56	1.27	0.74	0.79	1.50	1.91	0.92	0.80	1.19	0.39	1.34	0.57
40562	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated glycoprotein)	1.15	0.21	0.12	0.08	0.92	0.98	1.05	0.17	0.14	0.48	0.08	0.91	0.67	0.84	0.81	0.40	0.68	0.79	0.68	0.74	0.58	0.91
840882	Hs.74130	Human chromosome 17q12-21 mRNA, clone pOV-2, partial cds	0.95	1.33	0.49	0.75	1.30	0.91	1.03	0.99	1.08	1.13	0.94	1.19	1.04	0.75	1.39	0.74	1.26	1.23	1.64	0.50	1.23	0.85
782497	Hs.6349	Human Chromosome 16 BAC clone CIT987SK-A-362G6	0.67	1.56	1.20	1.70	1.72	0.92	1.27	1.27	1.37	1.61	1.13	1.13	0.85	0.69	2.68	1.15	2.92	1.21	3.87	0.90	1.02	2.94
826622	Hs.30909	Human Chromosome 16 BAC clone CIT987SK-A-362G6	1.13	2.03	1.63	1.49	1.99	1.13	1.59	1.30	1.78	1.91	1.38	1.75	0.98	1.17	2.10	0.88	1.67	1.79	1.93	0.98	1.02	0.91
180298	Hs.20313	protein tyrosine kinase 2 beta	0.44	0.56	0.42	0.34	0.64	0.34	0.29	0.36	0.59	0.57	0.18	0.59	0.30	0.65	0.45	0.61	0.24	0.33	0.31	0.38	0.25	0.22
785793	Hs.184270	capping protein (actin filament) muscle Z-line, alpha 1	1.24	1.17	0.68	0.91	0.86	1.18	0.56	1.37	1.00	0.58	1.85	1.48	0.65	1.28	1.49	1.06	0.61	0.75	0.88	1.02	0.91	1.97
753587	Hs.167741	butyrophilin, subfamily 3, member A3	1.80	9.37	2.65	3.74	4.28	4.41	2.72	4.45	3.77	3.41	2.77	4.67	0.93	2.86	3.50	2.57	5.07	3.01	3.62	2.23	1.83	0.91
773344	Hs.75317	solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transpor	0.46	0.57	0.83	1.02	0.96	0.39	0.66	0.86	1.17	1.17	1.29	0.42	0.79	1.63	0.77	0.97	0.57	0.72	0.50	1.47	0.57	0.91
788745	Hs.39913	novel RGD-containing protein	0.50	0.68	0.70	0.69	0.97	0.43	0.60	0.68	0.96	0.88	1.14	0.48	0.40	0.34	0.70	0.59	0.45	0.54	0.62	0.36	1.02	0.44
789232	Hs.148495	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	1.72	0.71	1.46	1.37	0.76	0.96	1.41	1.09	0.89	1.04	1.14	1.33	0.84	1.11	1.61	1.22	1.22	1.28	1.33	0.94	0.56	0.91
795543	Hs.83383	thioredoxin peroxidase (antioxidant enzyme)	1.51	0.67	2.38	0.75	1.37	0.51	1.42	0.90	0.59	1.21	1.24	0.37	0.45	0.43	0.67	0.85	0.63	0.75	0.87	0.93	1.91	2.10
839890	Hs.2853	poly(rC)-binding protein 1	1.08	0.57	2.46	0.73	0.83	0.46	1.26	0.72	0.45	0.61	1.00	0.51	0.42	0.46	0.59	1.04	0.46	0.62	0.89	0.88	0.82	1.34
713886	Hs.169718	calponin 2	2.00	0.88	1.49	0.95	2.16	1.30	1.05	1.64	2.05	1.69	1.47	1.53	0.36	1.74	3.04	1.55	1.69	2.30	2.06	1.17	1.51	0.47
768453	Hs.50740	ESTs	2.20	3.07	1.14	2.16	2.20	1.73	2.84	1.99	1.99	2.57	2.76	1.87	1.86	1.96	2.10	2.19	1.79	1.17	1.88	1.87	1.79	2.64
73381	Hs.76362	general transcription factor IIA, 1 (37kD and 19kD subunits)	0.66	1.11	0.65	1.28	1.38	1.03	1.08	0.75	1.04	1.00	2.30	0.79	0.41	1.34	0.72	1.33	0.56	0.53	1.03	0.80	0.85	1.23
841261	Hs.24644	TATA box binding protein (TBP)-associated factor, RNA polymerase II, C1, 130kD	1.53	1.72	1.13	1.07	2.74	1.41	1.13	1.29	1.01	1.24	1.72	4.05	2.16	1.96	6.01	0.90	1.37	1.29	1.38	0.83	1.32	1.91
47908	Hs.75639	Human TB1 gene mRNA, 3' end	0.75	0.75	1.45	1.10	2.40	0.69	0.46	0.54	1.10	1.63	0.82	1.39	1.60	0.87	1.04	1.61	0.52	0.99	0.58	0.84	0.53	0.89
756968	Hs.144700	ephrin-B1	0.80	0.90	1.51	0.43	0.95	0.67	0.65	0.60	0.67	0.85	1.34	1.29	1.10	0.64	1.10	1.02	0.42	0.77	0.77	0.50	0.75	0.91
841679	Hs.10803	calcium and integring binding protein (DNA-dependent protein kinase interacting protein)	0.91	1.15	0.78	0.62	1.44	0.78	1.24	1.38	0.99	0.92	1.24	1.96	0.77	2.37	1.54	1.29	1.00	1.17	2.56	1.14	0.71	0.79
825085	Hs.56937	suppression of tumorigenicity 14 (colon carcinoma)	1.27	1.34	0.31	0.66	1.04	0.69	1.19	0.81	0.73	0.46	0.90	3.78	2.64	3.42	2.74	1.32	0.58	0.54	0.55	1.43	0.87	0.62
824426	Hs.250728	PDGF associated protein	1.01	2.48	1.34	1.56	1.60	1.62	2.13	1.37	1.50	1.62	2.14	1.33	0.84	1.21	1.11	2.21	0.60	0.87	1.40	1.22	0.86	0.92
39808	Hs.6241	phosphoinositide-3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	1.88	1.26	0.61	1.97	2.34	1.98	1.20	1.22	1.09	0.68	0.83	0.84	0.37	1.57	1.33	2.81	0.53	2.56	1.26	1.96	2.06	0.91
687397	Hs.75551	Ras suppressor protein 1	2.33	2.73	1.81	1.20	1.90	1.74	3.07	0.96	1.42	1.63	1.65	1.15	0.52	0.92	0.98	1.28	1.37	1.44	1.28	1.36	1.58	2.30
711959	Hs.250745	polymerase (RNA) III (DNA directed) (62kD)	1.68	1.51	0.95	1.09	2.00	1.20	2.37	1.21	1.22	1.64	1.59	1.07	0.62	0.82	1.38	0.58	1.61	2.15	3.35	1.50	1.94	2.16
760299	Hs.4909	regulated in glioma	2.59	1.03	2.89	1.34	1.22	1.44	4.54	1.91	0.63	2.88	0.63	6.25	2.62	3.20	5.65	1.52	4.54	3.92	9.46	1.56	0.35	1.06
814378	Hs.31439	serine protease inhibitor, Kunitz type, 2	1.02	0.98	0.19	0.41	0.93	1.76	0.67	0.80	0.72	1.02	0.76	0.80	0.73	0.66	1.11	1.14	1.38	0.59	0.71	0.72	1.46	0.81
788190	Hs.76873	hyaluronoglucosaminidase 2	0.98	0.96	0.80	0.86	2.12	1.08	1.46	1.27	1.23	0.98	1.22	1.22	1.90	1.09	1.28	1.33	1.15	1.42	1.42	1.34	1.44	0.72
788566	Hs.80296	Purkinje cell protein 4	0.96	1.77	1.18	1.38	1.44	0.94	0.90	1.10	1.23	1.19	1.45	1.44	0.97	2.18	1.50	1.47	1.25	1.05	1.14	1.00	0.89	0.67
73531	Hs.9908	nitrogen fixation cluster-like	2.04	2.53	3.69	1.74	1.80	2.13	2.48	1.11	1.57	1.61	1.16	2.14	1.03	1.50	1.72	0.74	1.48	1.24	1.25	1.04	1.39	1.70
950578	Hs.83916	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)	0.66	2.06	1.42	1.78	1.75	1.27	1.55	1.04	1.48	1.63	1.02	1.15	0.86	0.95	1.16	0.83	0.85	1.13	1.68	0.67	1.12	1.64
897806	Hs.197540	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	1.31	0.72	0.73	0.61	0.91	1.08	0.31	0.57	0.99	0.43	0.75	1.29	1.12	1.38	1.11	0.74	0.51	0.56	0.40	1.72	0.72	0.83

781097	Hs.252831	reticulon 3	1.37	0.69	0.56	0.76	0.82	1.31	1.18	0.72	1.04	1.45	0.66	1.06	0.76	1.15	1.14	0.64	1.53	0.87	0.84	1.49	0.62	0.51
712049	Hs.66576	suppression of tumorigenicity 16 (melanoma differentiation)	1.51	1.24	0.61	1.13	1.44	1.74	1.13	0.99	1.25	1.38	1.48	1.75	1.08	1.43	2.08	1.19	1.97	0.70	1.05	1.68	1.03	0.91
292388	Hs.4187	Homo sapiens clone 24636 mRNA sequence	1.02	1.00	0.18	0.26	2.10	0.81	2.16	0.33	2.12	0.49	0.69	0.88	0.96	0.76	1.36	0.52	2.02	1.00	1.91	1.72	0.72	1.61
898317	Hs.183874	cullin 4A	1.83	2.77	1.34	1.44	1.58	1.77	0.82	1.05	1.33	0.82	0.94	0.79	1.00	1.20	1.49	1.10	1.83	1.10	1.26	1.13	1.54	1.60
841093	Hs.14541	cullin 1	0.80	1.08	0.81	1.00	1.19	0.77	0.98	0.80	0.90	0.73	0.92	0.52	0.46	0.59	0.81	0.74	0.75	0.76	0.84	0.59	0.77	0.98
704532	Hs.54483	N-myc (and STAT) interactor	2.29	3.88	1.83	2.88	2.96	2.38	1.36	2.43	2.83	1.82	2.31	3.91	1.51	2.69	3.08	1.66	2.56	2.70	2.31	1.41	2.58	2.23
840517	Hs.152978	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0.81	1.74	0.61	1.04	1.45	1.20	1.18	0.83	1.02	1.00	1.07	0.69	0.90	0.67	0.89	0.86	1.07	1.05	1.15	0.72	1.65	1.27
48631	Hs.154417	potassium voltage-gated channel, shaker-related subfamily, beta member 2	1.40	2.33	0.93	1.35	1.82	1.54	1.73	1.36	1.30	1.46	1.48	5.76	1.65	4.48	2.54	1.71	1.91	1.70	2.19	0.62	1.71	0.91
842906	Hs.181368	U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8p	1.55	0.92	0.63	1.39	1.24	1.67	1.86	0.87	1.20	1.12	1.32	0.67	1.54	0.97	1.37	1.24	1.51	0.92	0.98	1.23	1.85	0.75
781018	Hs.159971	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b,	1.33	2.48	1.58	1.50	1.55	1.52	2.61	1.71	1.61	1.29	2.09	1.12	1.44	1.58	1.49	1.65	0.96	1.11	1.39	1.42	2.71	1.40
711680	Hs.54452	zinc finger protein, subfamily 1A, 1 (Ikaros)	1.64	0.97	1.26	1.56	1.24	1.52	1.17	0.61	0.93	0.61	1.05	0.59	0.67	0.76	1.12	1.19	0.64	1.40	1.30	1.40	0.83	0.93
564803	Hs.239	forkhead box M1	2.63	7.69	3.22	5.02	4.06	2.59	10.29	2.33	1.44	2.30	1.93	1.60	1.99	1.14	1.62	1.36	1.65	1.56	2.82	1.29	2.88	3.51
843069	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	0.89	1.14	1.10	1.88	1.20	0.98	1.98	0.84	1.32	1.39	1.02	0.76	0.98	1.32	1.07	1.05	1.12	0.90	1.01	1.01	0.87	1.27
144777	Hs.15318	HS1 binding protein	1.03	1.55	1.13	1.40	1.59	1.09	2.75	1.15	1.11	1.30	1.31	1.24	0.84	1.45	1.39	1.32	1.40	0.54	2.13	1.19	1.09	0.89
788645	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein	1.11	1.78	0.88	1.13	1.10	1.14	0.93	1.20	0.97	0.93	1.45	0.89	0.72	0.71	1.07	1.02	1.24	1.08	1.24	1.10	1.17	1.73
79022	Hs.75678	FBJ murine osteosarcoma viral oncogene homolog B	0.93	1.39	0.78	1.03	1.74	0.95	1.46	0.89	0.91	0.83	0.95	1.24	0.55	0.70	1.20	1.07	0.78	1.58	1.26	0.82	0.86	0.75
795738	Hs.79126	guanine nucleotide binding protein 10	0.48	0.49	0.44	0.62	0.81	0.48	0.55	0.53	0.69	1.04	0.76	0.60	0.53	0.35	0.55	0.48	0.53	0.54	0.62	0.35	0.90	0.89
814117	Hs.5122	ESTs	0.84	0.96	0.77	1.88	0.93	0.77	0.99	0.77	0.70	0.41	0.75	0.57	0.95	0.48	0.67	0.65	0.45	0.75	0.51	0.77	0.71	1.25
826350	Hs.252979	G protein pathway suppressor 1	2.46	2.15	0.95	1.45	1.72	1.38	0.94	1.51	2.02	2.80	2.23	2.59	7.19	3.97	2.59	2.94	1.96	1.29	1.47	1.35	2.63	2.77
785745	Hs.264	GS2 gene	0.93	0.93	1.06	0.66	1.62	0.70	0.48	0.92	0.88	1.12	0.88	1.30	0.67	0.48	1.18	1.29	0.70	1.19	1.37	0.34	1.99	0.85
841332	Hs.83656	Rho GDP dissociation inhibitor (GDI) beta	0.72	1.63	1.41	1.69	1.83	3.19	0.53	1.47	1.83	1.18	2.34	4.32	1.16	2.84	2.81	2.28	1.31	1.44	2.13	0.98	2.27	2.43
788574	Hs.101067	GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2	1.10	2.77	1.41	1.84	1.69	1.74	1.63	1.47	1.76	1.95	1.75	2.31	3.79	1.77	2.74	1.33	1.48	1.61	1.63	0.60	0.98	1.59
739126	Hs.75801	tissue specific transplantation antigen P35B	1.40	2.40	0.49	0.72	1.84	1.64	1.04	2.04	0.80	1.17	1.56	0.86	0.83	1.27	1.89	1.52	0.48	0.73	1.57	1.42	0.93	0.51
740914	Hs.239737	C-terminal binding protein 1	1.40	1.72	0.89	1.22	1.25	0.85	0.92	1.58	1.03	1.39	1.35	1.16	1.09	1.04	1.31	1.31	1.11	1.48	1.94	1.28	1.78	1.56
788247	Hs.82919	cullin 2	1.73	3.02	1.42	2.00	1.97	1.69	1.54	1.36	1.41	1.61	1.18	0.94	0.49	0.43	0.78	0.96	1.83	2.06	2.08	1.02	2.18	2.08
815285	Hs.6430	protein with polyglutamine repeat	1.57	2.67	1.08	1.63	1.88	2.78	2.38	1.32	1.38	1.36	0.90	1.77	1.72	1.63	1.77	1.95	1.16	0.97	1.28	1.05	0.88	1.51
754538	Hs.118724	DR1-associated protein 1 (negative cofactor 2 alpha)	1.22	1.46	0.68	1.11	0.96	1.14	1.98	1.36	3.87	1.85	1.60	1.26	0.76	0.88	0.93	1.53	1.46	1.14	1.52	1.32	1.80	1.65
814465	Hs.210604	postmeiotic segregation increased 2-like 3	2.39	2.82	1.62	2.47	2.48	2.29	2.83	1.99	1.91	1.64	2.53	3.08	0.20	1.49	1.99	1.69	2.49	2.36	3.12	0.74	2.18	2.00
591907	Hs.15114	ras homolog gene family, member D	0.80	1.37	0.71	0.94	1.03	1.14	1.59	0.73	1.39	0.90	1.01	1.59	0.67	1.28	1.32	1.22	0.83	0.65	0.98	1.03	0.72	0.94
712848	Hs.82548	MAP-kinase activating death domain	1.41	2.56	0.85	1.53	2.50	1.73	1.67	2.09	2.18	3.29	2.52	3.61	1.71	2.26	2.44	2.03	1.19	2.17	2.77	1.18	3.26	2.02
843312	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	1.09	2.53	1.61	1.55	1.75	1.49	3.13	1.42	4.36	1.42	1.00	14.12	5.38	3.08	5.54	3.00	1.70	3.05	4.04	2.59	2.26	1.33
772261	Hs.79107	mitogen-activated protein kinase 14	0.70	1.29	1.45	1.17	2.36	0.84	1.06	1.16	1.32	1.57	0.85	1.03	0.88	1.08	0.88	0.86	0.87	0.77	1.06	1.10	1.06	1.14
897774	Hs.28914	adenine phosphoribosyltransferase	1.08	1.39	1.51	1.18	2.20	1.04	1.25	1.13	1.49	1.10	1.33	1.01	0.63	0.98	0.86	1.19	1.33	0.89	1.27	1.23	0.80	1.68
824382	Hs.75193	COP9 homolog	0.23	0.18	0.22	0.20	0.42	0.18	0.35	0.23	0.32	0.25	0.19	0.26	0.14	0.19	0.18	0.28	0.41	0.36	0.47	0.51	0.27	0.30
741841	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)	1.42	5.13	1.86	2.92	3.58	1.69	3.37	1.46	1.46	2.54	1.34	2.60	1.90	1.54	1.50	1.13	2.29	1.55	1.93	1.20	1.39	1.49
669435	Hs.91161	prefoldin 4	1.21	3.97	1.92	1.41	1.95	1.25	1.77	1.87	1.16	16.46	1.13	1.84	0.90	1.40	1.57	0.51	1.98	0.91	1.38	1.06	1.35	1.06
814478	Hs.227817	BCL2-related protein A1	2.54	12.27	2.44	5.07	3.81	3.09	2.95	2.58	2.87	1.88	2.44	2.55	2.35	1.81	1.95	1.76	2.99	1.85	3.61	1.78	2.21	5.57
162208	Hs.83583	actin related protein 2/3 complex, subunit 2 (34 kD)	0.77	1.42	0.76	1.05	1.00	1.04	1.63	0.87	1.50	1.06	0.85	1.25	0.44	0.97	0.98	1.22	1.15	0.74	1.04	1.18	0.77	1.18
897814	Hs.99847	peroxisome biogenesis factor 1	1.37	2.63	1.00	2.50	2.30	1.76	1.12	1.33	2.31	1.66	1.31	1.90	1.44	1.19	1.48	1.23	1.43	0.68	1.33	1.18	2.06	1.57
810552	Hs.7771	B-cell associated protein	0.45	1.11	0.47	0.88	0.51	0.84	1.18	0.64	0.64	0.55	0.62	0.50	0.96	0.82	0.78	0.76	0.57	0.67	0.43	0.45	0.50	1.20
767345	Hs.44898	ESTs, Moderately similar to cadherin 12 [H.sapiens]	1.99	2.87	1.84	3.04	4.81	1.42	1.04	3.71	2.77	2.33	2.59	5.51	1.16	1.89	1.43	0.96	2.45	3.99	6.67	1.33	3.37	0.91
897636	Hs.227949	SEC13 (S. cerevisiae)-like 1	1.40	0.93	1.58	0.89	1.36	0.84	1.49	0.95	1.01	0.92	1.08	0.72	0.50	1.77	0.81	1.49	1.44	0.71	1.04	0.90	0.78	1.13
897690	Hs.82689	tumor rejection antigen (gp96) 1	1.35	1.90	2.12	1.49	1.97	1.27	2.24	1.64	1.68	1.13	1.97	0.74	0.46	0.70	0.86	0.88	1.68	1.27	1.81	1.71	2.13	2.44
416833	Hs.7557	FK506-binding protein 5	0.18	0.27	0.28	0.15	0.18	0.12	0.20	0.13	0.12	0.06	0.15	0.05	0.11	0.08	0.14	0.14	0.08	0.33	0.39	0.22	0.34	0.32
46154	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	1.05	1.61	1.28	1.37	1.92	1.59	0.65	1.94	1.08	1.14	1.90	1.26	2.80	1.29	1.48	1.75	0.97	1.06	1.02	0.81	2.22	1.20
814306	Hs.2384	tumor protein D52	1.31	3.11	0.63	2.37	1.29	0.77	3.06	2.02	4.03	3.86	2.60	2.89	4.94	2.81	6.13	1.89	2.56	3.05	1.32	1.95	1.78	1.68
711450	Hs.1540	nuclear matrix protein p84	1.57	2.09	2.20	2.22	2.07	1.69	1.74	1.08	1.52	1.63	1.25	1.24	1.00	1.79	1.54	0.93	1.39	0.83	2.80	1.45	0.97	1.24
897594	Hs.75104	RNA-binding protein S1, serine-rich domain	1.25	1.72	0.82	1.06	1.28	1.47	1.45	0.99	0.97	1.09	0.99	0.79	1.66	1.05	1.18	1.44	1.08	1.29	0.98	0.88	1.35	1.27
826166	Hs.82508	Human (clone CTG-B43a) mRNA sequence	1.11	1.11	1.14	1.35	1.16	1.03	1.38	0.95	1.42	1.45	1.28	0.60	0.87	0.89	0.94	1.29	0.93	0.79	0.90	0.78	0.68	0.97
628955	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	0.23	0.42	0.28	0.36	0.53	0.31	0.37	0.35	0.53	0.33	0.38	0.36	0.19	0.36	0.42	0.84	0.20	0.50	0.44	0.61	0.25	0.22
712341	Hs.8297	ribonuclease 6 precursor	2.03	4.41	1.86	2.49	2.97	2.14	1.98	2.67	2.43	1.91	4.02	5.95	1.58	2.12	2.49	2.92	3.19	2.77	3.40	1.54	3.84	2.26
897632	Hs.13495	requiem, apoptosis response zinc finger gene	0.75	1.70	1.14	1.70	1.70	2.44	1.67	1.40	1.48	1.29	1.53	1.28	2.09	2.06	1.51	1.78	1.43	0.87	0.83	1.00	1.25	1.26
809648	Hs.180677	zinc finger protein 162	1.06	2.73	1.51	1.89	2.14	1.24	2.60	1.93	1.73	1.54	1.68	1.28	0.81	1.09	1.42	1.64	1.33	1.65	2.22	1.54	1.28	1.16
781704	Hs.77558	thyroid hormone receptor interactor 7	3.40	2.04	1.02	2.54	1.02	1.02	0.70	0.83	0.67	0.46	0.77	0.76	0.35	1.06	0.70	0.61	1.17	0.65	0.53	0.95	1.39	1.11
785334	Hs.116784	thyroid hormone receptor interactor 4	1.49	2.12	0.85	1.31	2.19	1.73	1.18	1.54	1.28	1.32	1.46	2.51	0.63	1.35	1.28	2.17	1.37	1.19	2.12	0.76	0.73	1.52
824906	Hs.2210	thyroid hormone receptor interactor 3	0.98	1.20	0.67	0.95	0.99	0.90	1.15	1.28	1.16	0.85	1.31	0.59	0.90	0.66	0.95	1.32	0.92	0.69	1.30	2.05	0.77	0.91
840818	Hs.81008	filamin B, beta (actin-binding protein-278)	0.27	0.34	0.30	0.68	0.58	0.41	0.40	0.59	0.56	0.51	0.60	0.33	1.17	0.22	0.82	0.61	0.65	0.78	0.93	0.43	0.26	0.89
781019	Hs.169857	paraoxonase 2	0.28	0.43	0.69	0.40	0.72	0.41	0.48	0.34	0.53	0.42	0.54	0.49	0.23	0.61	0.55	0.57	0.33	0.51	0.88	0.68	0.32	0.32
814731	Hs.75305	aryl hydrocarbon receptor-interacting protein	2.30	1.35	0.67	1.26	1.37	1.41	1.45	1.34	1.00	1.16	1.74	1.22	0.69	0.90	1.16	1.49	1.19	1.16	1.42	1.28	1.74	1.60
782692	Hs.154846	phosphatidylinositol 4-kinase, catalytic, beta polypeptide	0.62	2.57	1.10	1.57	1.82	1.83	1.40	1.11	1.08	1.00	1.18	1.41	1.37	1.22	1.38	1.24	0.75	0.75	1.41	0.87	1.09	0.75
897910	Hs.136348	osteoblast specific factor 2 (fasciclin I-like)	3.90	2.02	0.80	5.53	6.16	2.97	1.95	5.92	10.28	6.98	9.38	6.22	2.07	6.73	6.56	4.91	5.07	4.67	6.66	2.67	4.03	2.81
815534	Hs.173274	integrin cytoplasmic domain-associated protein 1	1.25	3.66	2.23	1.27	1.53	2.16	1.77	1.28	1.36	1.08	1.12	0.82	0.24	0.82	0.90	0.40	1.07	0.91	1.29	1.05	1.45	1.98
684634	Hs.180446	karyopherin (importin) beta 1	1.13	2.35	1.26	2.49	1.47	1.21	1.90	1.25	1.57	1.31	1.24	2.08	0.72	1.28	1.55	0.96	1.20	1.13	1.44	0.87	1.74	1.14
825583	Hs.74111	RNA-binding protein (autoantigenic)	1.35	1.16	0.75	0.89	1.42	1.83	0.94	1.20	0.89	1.18	1.16	1.66	1.63	1.43	1.29	0.88	1.18	1.06	0.98	1.28	1.23	1.57
784360	Hs.12451	echinoderm microtubule-associated protein-like	1.12	4.41	14.91	4.02	6.16	2.31	0.66	3.54	1831.39	1506.35	2.42	2.59	0.88	1.27	2.30	2.03	2.23	3.37	2.35	1.88	1.67	1.58
429182	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit	1.04	0.89	0.95	0.97	1.39	1.75	0.83	0.78	0.71	1.20	0.73	0.50	0.70	0.29	0.49	0.80	2.05	0.68	0.91	0.83	1.24	1.62
949932	Hs.74497	nuclease sensitive element binding protein 1	1.25	1.85	1.68	1.85	1.45	1.49	2.04	0.90	0.80	1.06	0.95	0.55	0.24	0.54	0.50	0.96	0.76	0.60	0.53	1.42	1.36	1.51
713080	Hs.73986	CDC-like kinase 2	2.33	3.16	1.51	2.51	3.59	1.76	3.14	2.17	1.73	2.23	1.66	4.67	1.82	3.26	3.36	1.35	2.02	1.45	4.19	1.23	1.91	1.82
783629	Hs.75528	ESTs, Highly similar to AUTOANTIGEN NGP-1 [H.sapiens]	2.55	1.66	4.01	2.36	2.03	1.74	2.45	1.42	1.45	2.27	1.49	1.95	1.34	1.48	1.99	1.74	1.67	1.49	2.29	2.36	2.26	1.98
626502	Hs.11538	actin related protein 2/3 complex, subunit 1B (41 kD)	0.47	1.55	0.85	0.55	1.27	0.87	0.75	1.30	0.91	0.90	1.25	0.63	0.33	0.76	0.78	1.05	0.46	0.64	0.66	0.75	1.07	0.51
789011	Hs.83347	angio-associated, migratory cell protein	1.07	2.10	0.73	1.40	1.93	1.14	2.13	2.09	1.47	2.43	1.45	1.19	1.72	1.91	2.13	1.41	1.51	1.06	1.40	0.89	1.87	1.30
788107	Hs.193163	amphiphysin-like	1.05	1.29	1.70	1.39	1.35	0.88	1.29	1.09	1.15	1.64	1.22	1.89	1.30	1.65	1.96	1.15	0.87	1.09	1.16	1.22	1.26	0.81
774082	Hs.1619	achaete-scute complex (Drosophila) homolog-like 1	1.25	1.30	1.30	1.25	1.42	0.97	1.46	1.51	1.14	1.11	1.46	2.07	1.00	0.89	1.10	1.06	1.07	1.44	1.93	1.26	1.71	1.15
711768	Hs.76057	lysophospholipase II	1.68	0.89	1.17	1.07	1.46	1.29	1.11	0.98	0.62	0.54	0.82	0.40	0.67	0.71	1.05	1.50	0.55	1.12	1.43	1.41	0.75	1.20
824591	Hs.808	heterogeneous nuclear ribonucleoprotein F	2.06	2.92	1.15	1.77	2.10	1.51	1.58	2.15	1.15	0.94	1.65	0.82	1.16	0.76	1.70	0.99	1.43	1.42	2.24	1.69	2.13	2.38
786607	Hs.95243	transcription elongation factor A (SII)-like 1	0.66	0.94	0.92	1.28	1.27	0.59	0.35	0.94	3.04	0.76	0.96	1.04	1.15	0.87	1.15	1.28	3.03	1.50	1.11	0.78	0.67	0.69
782811	Hs.139800	high-mobility group (nonhistone chromosomal) protein isoforms I and Y	0.60	2.22	0.30	0.69	2.32	0.70	0.78	0.89	0.41	0.60	1.61	0.46	0.25	0.47	0.50	1.15	0.33	0.63	0.77	0.57	0.66	1.68
840158	Hs.118625	hexokinase 1	1.07	1.17	0.84	0.71	1.25	1.07	0.93	1.06	1.02	0.72	1.17	1.43	1.26	0.75	1.42	1.17	0.71	0.97	1.02	0.72	1.51	1.27
786202	Hs.6445	Homo sapiens (clone s153) mRNA fragment	1.13	0.99	0.88	1.00	1.38	8.88	0.94	0.86	0.97	0.89	1.91	1.02	0.60	0.50	1.02	1.00	0.93	0.89	1.83	1.54	1.32	1.01
796253	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	1.04	1.92	2.87	1.42	1.59	1.21	1.99	1.45	1.21	1.35	3.23	2.14	1.28	1.19	1.50	2.07	1.09	1.02	1.78	1.45	1.08	1.00
727390	Hs.3260	presenilin 1 (Alzheimer disease 3)	1.40	1.25	1.12	1.05	1.12	0.98	0.94	1.35	0.89	1.53	2.17	1.86	1.26	1.60	2.04	1.37	0.91	1.21	1.79	0.72	1.28	1.16

783645	Hs.180789	Homo sapiens (clone S164) mRNA, 3' end of cds	1.60	2.45	1.41	2.19	1.88	1.51	1.67	1.37	1.35	0.74	3.09	5.96	3.03	1.91	3.87	0.94	1.39	2.69	2.90	1.20	1.57	1.68
79254	Hs.1845	MHC class I region ORF	2.02	2.92	1.20	1.56	2.37	1.56	1.69	1.78	1.16	1.06	2.37	2.29	1.79	1.16	3.08	1.16	1.61	1.32	2.23	1.01	1.84	2.17
236305	Hs.239817	histidyl-tRNA synthetase	0.76	1.37	0.66	1.91	1.48	0.52	1.06	0.78	0.93	1.41	1.39	1.14	0.47	1.15	1.16	1.78	0.88	1.13	1.61	0.63	0.80	1.24
26566	Hs.99654	protein-O-mannosyltransferase 1	2.82	1.28	1.07	1.00	1.46	0.73	1.04	0.56	0.93	1.63	1.15	2.41	3.05	1.92	3.34	0.76	1.46	1.79	2.34	1.54	1.48	0.91
511586	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	1.10	1.53	0.92	0.75	1.45	0.97	1.21	0.91	0.89	0.90	1.12	0.97	0.52	0.70	1.02	1.09	0.96	1.37	1.81	1.42	1.41	1.99
75009	Hs.155227	EphB4	1.18	1.88	1.38	1.53	1.82	1.79	1.78	0.90	1.10	0.78	1.43	1.31	0.74	0.89	0.73	1.82	0.60	1.27	1.46	1.48	1.02	0.91
781341	Hs.1197	heat shock 10kD protein 1 (chaperonin 10)	0.84	2.13	0.85	1.28	2.84	1.30	3.72	1.86	0.95	1.69	3.04	2.29	0.78	0.88	1.66	0.97	1.54	1.32	1.49	1.50	1.80	1.81
135083	Hs.110029	glucose regulated protein, 58kD	0.83	1.77	1.79	0.74	2.22	1.19	0.88	0.95	1.42	1.21	1.29	0.92	0.52	0.63	0.95	1.43	1.02	0.99	1.28	1.50	1.69	1.01
760231	Hs.77578	ubiquitin specific protease 9, X chromosome (Drosophila fat facets related)	1.45	1.27	1.40	0.84	1.65	1.28	0.83	0.96	1.12	1.27	0.77	1.19	0.90	1.34	1.52	0.92	0.75	1.21	1.55	1.11	1.09	1.39
48398	Hs.153752	cell division cycle 25B	0.87	1.25	1.24	1.53	1.32	1.75	0.73	0.70	0.71	0.61	1.64	1.69	2.73	2.54	1.04	2.27	0.46	0.65	0.50	1.55	1.97	0.91
275871	Hs.179662	nucleosome assembly protein 1-like 1	0.68	0.70	0.72	1.08	1.13	0.85	0.87	0.85	0.83	0.55	0.88	0.62	0.53	0.65	0.64	0.68	0.89	1.00	0.75	0.53	0.92	0.87
212165	Hs.146354	thioredoxin-dependent peroxide reductase 1 (thiol-specific antioxidant 1, natural killer-enl	1.90	1.39	0.50	1.17	2.52	1.61	1.05	0.94	0.75	1.29	1.09	0.97	1.20	0.50	0.69	0.53	0.79	0.96	1.57	1.03	0.97	1.00
814508	Hs.36587	protein phosphatase 1, regulatory subunit 7	1.39	1.86	0.58	0.90	2.94	1.57	1.27	1.04	1.19	1.17	1.69	1.59	0.66	1.42	1.49	0.88	0.83	1.13	2.06	1.30	0.89	1.66
898073	Hs.74368	transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment	0.66	1.85	1.96	1.44	1.73	1.07	1.47	1.53	2.86	1.13	1.70	1.89	1.61	3.27	1.50	2.35	1.33	0.89	0.68	1.66	1.93	2.45
770377	Hs.118855	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory pro	0.65	1.57	0.49	0.64	1.77	1.06	0.94	1.26	1.21	2.39	1.25	1.05	1.05	1.43	1.07	2.02	1.20	0.94	1.17	0.66	0.82	1.84
826459	Hs.80324	protein phosphatase 6, catalytic subunit	1.39	1.26	0.98	1.32	1.24	1.38	1.00	1.12	1.29	1.51	0.99	0.83	1.00	1.04	1.90	1.09	0.74	1.11	1.29	1.07	1.43	0.81
754358	Hs.8122	ESTs	0.94	0.90	0.32	1.46	2.17	0.47	0.98	3.49	5.63	5.30	1.52	0.67	0.14	0.40	2.64	1.49	1.12	0.90	2.44	0.63	1.76	1.48
704299	Hs.79021	tafazzin (cardiomyopathy, dilated 3A (X-linked); endocardial fibroelastosis 2; Barth syndr	1.29	1.47	0.87	0.90	1.44	1.01	0.98	1.02	0.64	0.68	0.62	1.44	2.15	1.30	1.45	1.76	0.91	1.13	1.64	0.91	0.76	0.91
565235	Hs.89718	spermine synthase	1.27	0.85	0.76	0.84	1.52	0.72	1.47	1.34	0.57	1.73	1.11	1.06	0.75	0.57	1.46	0.86	0.97	0.76	0.99	0.94	1.54	1.70
785459	Hs.149098	inositol polyphosphate 5-phosphatase	1.08	1.39	4.25	1.63	2.24	0.77	2.65	1.74	1.85	2.11	1.47	1.83	1.02	2.19	1.62	1.67	1.07	0.90	1.73	1.52	1.69	0.81
815287	Hs.169344	H.sapiens mRNA for skeletal muscle abundant protein	1.44	1.47	0.82	1.13	1.56	0.78	0.31	1.90	1.08	1.37	1.17	2.40	1.36	1.20	1.21	0.87	1.94	1.32	2.18	0.99	1.10	0.91
530814	Hs.3314	selenoprotein P, plasma, 1	2.93	1.66	7.20	4.82	6.91	2.34	1.11	2.77	5.19	2.14	2.23	5.35	4.18	2.77	6.50	3.63	2.62	4.69	4.35	1.65	3.18	0.90
840821	Hs.102135	signal sequence receptor, delta (translocon-associated protein delta)	2.31	1.37	1.01	1.24	1.69	1.42	1.06	1.83	1.14	1.35	1.39	1.53	2.48	1.91	2.50	1.19	1.55	1.28	1.75	2.67	1.85	1.31
753700	Hs.57304	Ras-related GTP-binding protein	1.27	1.73	0.97	0.96	1.52	0.68	0.96	0.72	0.95	0.73	0.76	0.59	0.62	0.43	0.94	0.95	0.56	0.98	1.31	0.61	0.62	0.80
591266	Hs.166994	FAT tumor suppressor (Drosophila) homolog	0.89	1.66	1.03	0.90	1.68	1.44	0.44	1.02	0.94	0.73	1.79	4.31	0.47	3.44	2.12	0.78	0.25	0.88	0.31	1.06	1.71	1.44
842928	Hs.75854	SULT1C sulfotransferase	1.96	1.87	0.95	1.03	1.95	1.12	3.50	1.02	1.20	1.57	1.47	1.30	1.57	0.98	2.27	1.15	1.56	1.80	1.87	1.43	1.60	1.59
877644	Hs.9629	papillary renal cell carcinoma (translocation-associated)	1.61	1.86	0.63	1.33	1.89	1.37	2.37	1.18	1.15	0.71	2.24	1.60	1.73	1.70	2.05	1.62	1.16	1.03	1.92	0.75	1.59	1.82
772951	Hs.78060	phosphorylase kinase, beta	0.59	0.76	0.59	1.24	1.08	0.65	0.52	0.50	0.60	0.82	0.76	1.49	0.29	1.00	0.62	1.51	0.78	1.09	0.82	0.61	0.76	0.91
625923	Hs.75812	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	2.48	1.97	1.09	1.40	1.89	1.78	1.55	1.73	1.38	2.34	2.16	1.57	1.78	2.52	2.13	1.19	1.81	1.97	2.18	2.09	2.08	1.28
843319	Hs.171545	HIV-1 Rev binding protein	0.59	1.42	0.60	1.06	1.67	1.48	0.96	0.46	0.83	0.63	1.60	0.48	0.48	1.43	0.60	1.93	0.75	0.85	0.66	1.85	2.51	1.24
950689	Hs.78335	microtubule-associated protein, RP/EB family, member 2	4.76	2.15	0.88	1.60	1.83	1.72	3.29	1.10	1.55	0.84	2.77	3.32	1.22	3.30	3.22	1.42	3.38	3.04	3.60	2.64	2.26	2.34
773724	Hs.86131	Fas (TNFRSF6)-associated via death domain	1.88	1.38	1.02	2.10	1.79	1.33	1.12	1.11	1.45	1.57	1.93	0.95	1.28	1.15	1.04	2.18	1.22	0.97	1.79	2.79	1.37	1.09
814765	Hs.78921	A kinase (PRKA) anchor protein 1	1.82	2.01	0.72	1.52	1.68	1.57	2.65	1.82	1.24	1.19	2.35	3.01	1.84	2.08	3.46	1.18	1.26	1.85	1.78	1.01	2.16	1.74
753381	Hs.92962	Sec23 (S. cerevisiae) homolog A	1.71	1.10	2.56	1.01	1.08	0.82	0.77	1.16	2.18	1.35	1.14	0.61	0.29	0.39	1.07	0.52	0.99	1.06	1.43	1.06	1.15	0.75
813410	Hs.150675	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)	1.24	1.29	1.69	1.87	1.72	1.57	1.12	1.58	1.54	2.43	1.81	0.95	1.48	0.90	1.57	1.61	1.81	0.93	0.84	1.76	1.68	2.17
897626	Hs.237955	RAB7, member RAS oncogene family	1.42	0.89	0.80	0.92	1.58	1.05	1.07	0.81	1.48	1.31	1.38	0.70	1.20	0.87	1.36	1.28	1.18	1.46	1.08	1.29	1.30	1.09
877613	Hs.74617	dynactin 1 (p150, Glued (Drosophila) homolog)	1.74	1.70	0.78	1.20	2.86	1.60	1.51	0.90	1.39	1.62	0.59	1.11	0.83	1.37	2.02	1.43	1.81	1.83	2.20	1.41	1.48	2.12
897971	Hs.3059	coatomer protein complex, subunit beta	1.01	0.87	0.57	0.87	1.30	1.37	0.81	0.77	1.24	0.58	1.57	0.65	0.55	0.70	0.84	1.67	0.81	1.04	1.04	1.01	0.91	1.76
796996	Hs.3631	immunoglobulin (CD79A) binding protein 1	0.81	1.36	0.77	0.44	3.11	1.19	0.58	0.64	0.65	0.73	2.71	0.37	0.26	0.32	0.62	1.19	0.43	1.02	1.35	0.63	1.09	2.08
812266	Hs.239114	mannosidase, alpha, class 1A, member 2	3.46	2.32	1.40	1.13	4.05	1.93	4.93	0.87	1.34	1.42	2.55	2.92	0.60	1.24	3.18	0.86	4.99	2.68	3.47	2.06	1.60	0.91
788493	Hs.4147	translocating chain-associating membrane protein	1.36	1.41	1.03	1.24	1.36	0.77	0.83	0.94	1.22	1.43	0.93	0.52	0.94	1.18	0.95	0.89	1.03	0.97	0.65	1.42	1.23	1.24
667883	Hs.82101	pleckstrin homology-like domain, family A, member 1	1.28	0.52	0.42	0.55	0.72	0.68	0.84	0.52	0.87	0.50	0.23	1.13	0.68	0.40	0.49	0.43	0.41	0.93	0.50	0.51	0.31	0.30
74566	Hs.79090	exportin 1 (CRM1, yeast, homolog)	1.67	0.92	1.31	1.26	1.15	1.02	0.73	0.71	1.50	1.06	0.83	1.78	1.36	1.06	1.15	0.75	0.92	1.13	0.90	1.29	0.84	1.54
843070	Hs.172108	nucleoporin 88kD	2.51	1.81	1.09	1.04	1.73	0.95	0.80	1.11	1.23	0.90	0.73	1.58	2.22	1.77	1.15	0.66	2.12	1.94	0.81	0.98	0.98	1.23
897901	Hs.168516	ESTs, Moderately similar to NuMA protein [H.sapiens]	3.13	1.32	0.71	1.03	1.36	1.13	0.42	0.85	1.10	0.85	0.79	1.86	3.14	1.61	1.67	1.28	2.16	1.64	0.50	0.88	0.90	1.93
826135	Hs.8724	serine threonine protein kinase	1.97	1.39	0.95	1.01	0.86	1.35	0.71	0.98	1.00	0.99	1.09	2.39	1.37	1.52	1.69	0.72	1.53	1.35	0.89	1.04	0.98	1.47
784744	Hs.152720	M-phase phosphoprotein 6	1.33	1.85	0.77	1.15	1.69	1.65	1.36	1.18	1.14	1.19	1.01	0.69	0.76	1.70	0.77	2.81	0.58	0.98	1.34	1.22	1.66	0.91
815294	Hs.155975	protein tyrosine phosphatase, receptor type, c polypeptide-associated protein	1.35	1.77	1.94	1.33	1.92	1.19	0.96	1.54	2.07	1.38	1.49	2.71	2.29	5.44	1.86	1.94	0.98	1.18	1.41	1.28	1.10	1.10
773192	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	1.03	1.50	1.04	0.93	2.15	1.09	1.71	0.83	0.97	0.88	1.43	0.63	0.39	0.83	1.42	0.91	0.97	0.88	1.27	1.06	3.01	1.72
814460	Hs.78354	surfeit 5	2.64	0.98	0.72	0.65	1.65	0.87	0.94	0.81	0.80	1.06	0.77	0.92	1.93	1.00	1.19	0.97	1.09	1.64	1.82	1.33	1.52	0.91
567414	Hs.84928	nuclear transcription factor Y, beta	0.97	0.94	0.63	0.82	1.27	0.77	0.92	0.66	0.79	0.95	1.01	0.39	0.92	0.51	0.75	0.62	0.61	1.14	0.86	0.63	0.80	2.11
898108	Hs.3238	adenovirus 5 E1A binding protein	1.16	0.96	1.25	2.56	0.59	1.23	3.51	1.20	1.03	2.02	1.10	0.85	0.52	0.63	1.02	1.11	1.66	1.28	1.84	0.61	0.52	0.72
840606	Hs.75441	hydroxysteroid (17-beta) dehydrogenase 4	0.80	1.07	0.62	0.67	1.27	0.41	0.56	0.64	1.25	1.65	0.86	1.02	0.36	0.89	1.57	0.79	0.79	1.13	1.71	0.75	0.97	0.87
591281	Hs.80680	lung resistance-related protein	0.27	0.38	0.28	0.28	0.36	0.42	0.41	0.55	0.67	0.36	0.39	0.80	0.62	1.31	0.94	0.64	0.33	0.37	0.38	0.38	0.32	0.13
782449	Hs.63525	poly(rC)-binding protein 2	0.78	1.18	0.93	0.96	0.94	0.80	1.22	0.81	0.99	1.21	0.98	0.57	0.79	0.73	0.89	1.25	0.90	1.23	1.05	1.09	1.05	1.12
782543	Hs.208344	ESTs	0.93	1.24	1.00	1.43	0.88	0.99	2.18	0.85	0.91	0.95	0.86	0.82	0.84	0.70	1.26	1.12	1.08	1.19	1.18	0.87	0.83	0.67
813520	Hs.2913	EphB3	3.90	2.46	2.37	2.10	3.52	1.18	0.94	1.45	1.79	1.20	2.79	2.47	0.91	1.06	1.73	2.04	1.54	3.00	1.59	1.31	1.91	2.50
786675	Hs.2719	epididymis-specific, whey-acidic protein type, four-disulfide core	0.35	0.28	0.21	0.17	0.76	0.15	0.29	0.18	0.28	0.42	0.13	0.63	0.73	0.57	2.52	0.49	1.19	0.40	0.88	0.32	0.18	0.42
825478	Hs.75471	zinc finger protein 146	1.23	1.33	1.39	1.70	2.30	1.54	1.22	0.62	1.01	0.97	0.60	1.09	1.01	1.46	1.24	1.03	1.09	0.73	0.93	1.05	0.90	1.18
825577	Hs.77628	steroidogenic acute regulatory protein related	1.56	1.65	1.12	1.03	2.49	1.44	1.63	2.15	1.82	1.27	2.47	6.48	4.95	2.76	3.16	3.28	2.02	1.55	1.98	3.53	1.92	1.98
898312	Hs.8375	TNF receptor-associated factor 4	0.41	1.03	0.77	0.69	0.66	0.53	0.74	0.69	0.83	0.67	0.65	0.77	1.03	1.81	0.78	1.35	0.68	0.40	0.66	0.97	0.77	0.45
811870	Hs.194625	dynein, cytoplasmic, light intermediate polypeptide 2	1.11	2.26	1.06	1.80	2.29	1.97	0.96	1.47	1.97	1.35	3.32	2.16	0.81	1.08	1.14	2.96	1.55	1.09	1.35	0.85	1.55	1.64
825296	Hs.82399	brefeldin A-sensitive, peripheral Golgi protein	0.80	1.57	1.08	1.33	1.24	1.00	1.73	1.25	1.20	0.76	1.08	1.41	1.13	0.87	1.42	1.64	1.10	1.00	2.43	1.28	0.87	0.75
898253	Hs.79088	reticulocalbin 2, EF-hand calcium binding domain	1.12	1.13	2.70	1.97	0.78	1.10	1.82	0.59	1.47	1.86	1.38	1.47	0.62	1.12	0.90	0.87	1.04	0.92	1.62	0.86	1.15	1.44
796341	Hs.174139	chloride channel 3	0.65	1.01	0.83	0.77	1.37	1.09	0.57	0.67	1.08	1.40	0.70	0.77	0.66	0.80	0.78	0.90	2.49	0.77	0.65	1.09	0.88	0.78
840600	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1	1.28	1.79	1.36	1.05	1.32	1.59	0.91	1.25	1.89	1.70	1.01	1.16	1.13	1.85	1.60	1.88	1.09	0.89	0.88	1.11	0.83	1.25
788654	Hs.6289	growth factor receptor-bound protein 2	2.31	1.47	1.67	1.30	1.14	0.76	1.70	1.74	2.92	1.74	3.60	2.81	3.41	2.44	2.24	2.66	2.53	1.39	1.16	1.58	0.62	0.53
415698	Hs.273	galactosylceramidase (Krabbe disease)	1.57	2.45	1.41	1.22	1.93	1.29	1.32	1.62	1.71	1.81	1.09	1.02	0.62	0.92	1.02	1.07	1.28	1.32	2.19	1.75	1.35	2.06
700527	Hs.28988	glutaredoxin (thioltransferase)	0.47	1.44	0.38	0.86	1.56	0.94	0.44	0.85	1.08	0.60	1.55	1.03	0.21	0.89	1.46	1.06	0.87	0.63	1.39	0.29	0.71	0.91
841370	Hs.170197	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	0.54	0.80	0.49	0.46	0.78	0.50	0.35	0.70	1.05	1.28	0.39	0.70	0.65	0.63	0.46	0.51	0.99	0.40	0.96	0.45	0.49	0.48
51702	Hs.597	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	0.68	1.32	0.41	1.08	1.82	1.18	0.98	0.97	0.59	0.81	0.62	0.77	0.95	0.87	0.73	1.33	0.84	0.74	1.30	1.07	0.45	0.91
711961	Hs.68257	general transcription factor IIF, polypeptide 1 (74kD subunit)	1.03	2.24	0.96	1.33	2.31	1.52	1.12	1.70	1.69	1.32	1.19	2.46	1.79	1.13	2.30	1.48	1.26	1.38	1.01	1.02	0.99	0.91
81289	Hs.77443	actin, gamma 2, smooth muscle, enteric	1.01	1.14	3.11	1.21	1.36	1.44	1.58	1.67	3.05	0.63	0.78	1.02	1.59	2.20	1.29	0.58	0.92	1.16	1.23	1.28	0.79	0.78
703479	Hs.78991	DNA segment, numerous copies, expressed probes (GS1 gene)	1.16	0.59	2.26	2.00	2.43	1.14	1.06	0.82	2.02	1.80	1.97	5.13	2.41	5.38	2.53	1.75	1.68	1.17	1.12	1.25	0.44	1.16
376875	Hs.1424	flavin containing monooxygenase 1	1.64	2.36	1.46	1.34	1.94	1.08	1.58	1.73	1.94	1.66	1.69	1.16	0.89	1.18	1.37	1.36	1.12	0.92	2.15	1.87	1.97	0.95
814526	Hs.236361	H.sapiens seb4D mRNA	3.18	1.27	2.04	2.89	2.04	2.47	4.29	0.71	1.34	2.51	3.76	4.64	2.42	3.49	2.24	2.10	4.11	1.65	1.73	1.85	0.55	1.92
795173	Hs.69743	GM2 ganglioside activator protein	0.85	0.60	0.62	0.49	0.92	0.71	0.54	0.72	0.74	0.69	0.95	1.64	0.62	1.94	1.18	1.33	0.78	0.63	0.85	0.67	0.65	0.31
789318	Hs.118442	cyclin C	0.60	0.96	0.57	1.65	1.71	1.50	0.77	0.73	0.70	1.69	1.23	0.54	0.40	0.77	0.37	0.71	0.78	0.98	0.70	1.13	1.78	1.41
840384	Hs.79295	G-rich RNA sequence binding factor 1	1.87	1.30	0.99	1.12	0.85	0.79	0.91	0.80	1.00	1.39	1.01	0.99	0.93	0.74	1.32	1.06	0.75	0.88	0.80	1.62	0.67	0.70
814260	Hs.74050	follicular lymphoma variant translocation 1	1.14	0.80	0.98	0.89	1.07	0.69	1.86	0.66	1.01	0.93	2.25	0.66	0.40	0.60	1.05	0.90	0.80	0.89	1.31	0.77	0.98	0.55
81331	Hs.153179	fatty acid binding protein 5 (psoriasis-associated)	3.34	6.97	2.99	4.53	2.99	1.88	4.74	1.76	1.54	1.67	2.22	1.93	0.70	1.49	1.72	1.63	0.77	1.41	2.23	1.01	0.68	3.44

841698	Hs.184161	exostoses (multiple) 1	0.88	1.35	0.80	0.99	3.06	2.22	0.85	0.89	0.92	0.87	2.33	0.61	0.53	0.77	1.09	1.65	0.40	0.72	0.70	1.24	1.50	4.89
139009	Hs.118162	fibronectin 1	0.69	0.29	1.22	0.68	1.19	1.62	0.88	1.66	4.25	1.96	2.31	1.86	0.93	1.43	1.01	1.85	1.01	1.18	1.91	0.77	0.39	0.43
784224	Hs.165950	fibroblast growth factor receptor 4	1.15	1.24	1.82	1.37	1.52	1.46	1.71	1.76	2.86	2.82	1.68	3.11	2.07	2.73	1.97	2.46	1.96	1.33	2.94	2.47	1.45	0.97
566887	Hs.8123	chromobox homolog 3 (Drosophila HP1 gamma)	1.19	1.64	1.44	1.64	1.07	1.63	1.52	0.68	0.95	0.83	0.63	0.79	0.68	0.69	0.83	1.31	1.14	0.74	0.99	1.13	1.09	0.67
122159	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	5.03	4.93	17.83	10.68	15.78	8.17	19.09	6.51	7.61	9.47	14.40	56.80	11.32	28.55	52.33	7.91	6.75	6.16	10.49	2.96	3.38	7.48
80410	Hs.77393	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstra	2.22	2.21	1.42	2.00	2.87	2.75	0.94	1.63	1.20	0.88	2.91	1.17	0.60	1.35	1.17	1.87	1.24	1.15	3.44	1.46	2.33	2.36
204614	Hs.239483	Human clone 23933 mRNA sequence	0.83	0.88	1.28	0.90	0.74	1.25	0.85	0.83	0.63	0.97	0.48	1.05	1.05	1.12	0.69	0.95	0.71	1.46	0.75	1.05	1.46	0.66
840944	Hs.738	early growth response 1	0.79	0.70	0.24	0.36	0.66	0.24	0.63	0.47	0.71	0.36	0.63	0.44	0.12	0.38	0.47	0.55	0.24	1.89	0.72	0.49	0.26	0.23
80500	Hs.82193	esterase D/formylglutathione hydrolase	1.22	1.88	1.20	0.79	1.94	1.01	1.29	1.05	1.13	1.90	0.70	2.22	1.13	0.77	1.02	1.16	1.03	0.91	1.50	1.04	1.58	0.64
796198	Hs.30942	ephrin-B2	0.65	0.72	0.45	0.42	0.85	0.50	0.40	0.33	0.82	0.60	0.34	0.96	0.48	2.03	1.08	0.57	0.46	0.40	0.31	0.57	0.44	0.62
704290	Hs.181406	endothelin converting enzyme 1	1.57	0.98	1.41	0.86	1.50	2.94	0.83	0.98	1.33	0.91	1.27	3.32	4.82	3.68	3.79	1.71	2.40	1.07	0.88	1.54	0.82	0.64
774409	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	4.11	4.85	2.94	3.48	2.15	2.01	6.40	2.31	2.83	1.98	1.08	3.05	0.13	0.98	1.95	2.04	3.85	5.40	4.03	2.79	2.74	1.86
71672	Hs.169919	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	0.43	0.78	0.57	0.40	0.71	1.84	0.56	0.54	0.57	0.55	1.85	0.88	0.44	1.45	0.66	1.09	0.41	0.52	0.94	1.09	0.59	0.84
815564	Hs.250801	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0.88	1.24	0.72	0.83	2.25	1.57	0.84	1.14	0.96	1.23	0.90	0.87	0.53	0.67	0.71	1.47	0.50	0.93	1.20	0.90	1.28	1.95
815555	Hs.172690	diacylglycerol kinase, alpha (80kD)	0.35	0.89	0.38	0.47	1.61	0.58	0.32	0.40	0.51	0.46	0.24	0.50	0.15	0.39	0.33	0.55	0.37	0.45	0.45	0.53	0.41	0.91
843140	Hs.118778	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	2.45	1.54	1.20	1.47	1.80	1.70	2.82	1.73	3.09	2.01	1.85	1.56	1.02	1.12	1.85	1.08	3.02	1.62	2.56	1.73	1.03	0.91
328802	Hs.183864	elastase 3B	1.26	0.84	0.95	0.61	1.97	0.81	1.43	0.67	1.27	2.41	0.36	2.63	0.92	0.91	1.62	0.60	1.14	0.96	1.41	1.04	0.48	0.94
786048	Hs.108371	E2F transcription factor 4, p107/p130-binding	0.87	1.65	0.84	1.19	1.89	1.49	0.78	0.90	1.31	1.28	0.66	0.83	0.54	0.58	0.53	0.98	0.74	0.74	1.00	0.59	0.78	0.91
950367	Hs.7957	adenosine deaminase, RNA-specific	1.93	1.60	1.67	1.64	2.14	1.89	2.77	2.15	2.34	1.82	1.39	2.80	1.96	3.27	3.09	1.59	2.13	1.21	2.78	1.27	1.32	2.05
195753	Hs.139410	dihydrolipoamide branched chain transacylase (E2 component of branched chain keto aci	1.33	1.03	1.03	0.55	2.01	1.27	1.30	0.98	1.49	1.35	0.43	1.42	0.76	1.01	1.15	0.57	1.08	1.24	1.06	1.23	0.71	0.91
767817	Hs.46405	polymerase (RNA) II (DNA directed) polypeptide F	1.70	1.99	2.14	1.37	1.78	1.76	2.57	1.42	1.04	1.70	1.29	0.91	0.46	0.83	1.16	0.92	0.99	0.77	1.70	0.74	1.45	1.34
666425	Hs.317	phospholipase C, gamma 1 (formerly subtype 148)	0.87	1.03	1.23	1.42	1.31	0.48	1.22	1.04	0.81	1.10	1.11	0.90	0.69	0.87	0.96	0.68	0.91	0.75	1.41	0.95	1.20	0.79
784777	Hs.76894	dCMP deaminase	0.98	1.05	0.66	0.83	1.14	0.75	0.58	0.85	1.01	0.89	0.68	0.53	0.93	1.04	1.00	0.90	0.79	0.98	0.94	0.53	1.47	0.87
45641	Hs.180533	mitogen-activated protein kinase kinase 3	0.55	0.89	0.88	1.14	1.09	0.80	1.55	0.67	0.86	1.10	0.88	1.12	0.76	1.77	1.09	1.03	0.77	1.04	0.58	1.31	0.96	0.73
824031	Hs.94	heat shock protein, DNAJ-like 2	1.76	2.60	1.48	1.93	2.26	0.98	2.14	1.85	1.50	1.28	1.67	0.76	0.68	0.76	1.53	0.86	1.42	1.30	1.35	1.21	1.02	2.04
810787	Hs.82646	heat shock 40kD protein 1	0.98	0.99	0.45	0.65	0.73	0.51	1.68	0.48	0.57	0.70	0.49	0.56	0.39	0.42	0.71	0.53	1.09	0.51	0.77	0.70	0.43	0.31
51666	Hs.77929	excision repair cross-complementing rodent repair deficiency, complementation group 3 (x	1.03	2.06	1.68	1.57	1.59	2.33	1.21	1.67	2.30	1.38	3.02	4.69	2.70	4.69	1.94	3.03	1.56	0.79	0.82	1.20	1.10	1.93
40017	Hs.697	cytochrome c-1	0.87	0.42	0.88	1.49	0.82	0.75	1.05	0.39	0.77	0.43	0.74	0.61	0.43	0.49	0.51	0.44	0.81	0.53	0.61	1.41	1.15	0.97
838373	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase	0.95	1.23	1.09	2.08	1.20	1.30	0.90	0.81	0.88	0.63	1.31	1.17	2.22	1.80	1.82	1.56	0.69	0.76	0.75	0.96	0.70	1.57
66564	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	2.96	3.65	0.87	1.63	2.43	1.79	0.44	1.83	1.17	1.23	2.88	1.57	3.41	0.98	1.38	1.56	2.20	1.80	2.46	0.91	2.66	2.44
666128	Hs.155597	D component of complement (adipsin)	2.73	1.86	2.28	1.45	3.46	1.21	2.65	1.44	1.77	1.10	1.72	2.35	1.17	1.92	2.25	1.44	1.15	0.91	0.92	1.10	1.00	3.66
753862	Hs.41072	protease inhibitor 6 (placental thrombin inhibitor)	1.49	0.86	1.01	1.02	1.04	0.61	1.49	1.35	0.46	0.50	1.50	0.48	0.56	0.66	0.80	0.67	0.80	1.18	0.97	0.54	0.93	0.53
842860	Hs.173936	interleukin 10 receptor, beta	2.67	1.68	2.48	1.31	3.49	1.07	2.18	1.46	2.61	1.01	1.73	2.92	1.11	2.86	2.51	1.52	1.28	1.28	1.33	1.11	0.89	3.22
739901	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha-demethylase)	1.15	2.84	1.96	1.83	1.84	4.02	1.32	2.32	4.23	2.52	3.84	4.30	2.46	3.88	2.04	2.98	1.47	1.15	1.14	1.48	1.58	1.24
898092	Hs.75511	connective tissue growth factor	0.75	0.48	0.75	0.68	1.50	0.43	1.21	1.05	2.72	0.58	0.91	0.92	0.17	0.50	1.12	1.04	0.46	2.90	2.01	1.31	0.48	0.39
782760	Hs.154654	cytochrome P450, subfamily I (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infan	1.12	1.42	6.03	3.15	4.85	2.01	1.16	2.33	1.50	2.74	1.35	1.52	0.49	1.28	1.60	1.98	1.83	0.84	1.33	0.79	2.96	1.56
949938	Hs.135084	cystatin C (amyloid angiopathy and cerebral hemorrhage)	1.67	2.30	1.55	1.25	2.27	1.87	2.19	0.77	1.44	1.27	1.32	4.59	1.71	2.79	4.52	1.19	1.58	2.82	2.11	1.11	0.68	1.31
795296	Hs.514	cyclin H	1.60	1.61	0.98	1.20	1.09	1.21	1.68	1.65	2.06	2.86	1.69	1.56	1.29	0.81	1.55	0.39	1.56	2.29	2.63	1.30	1.01	1.50
841641	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	0.73	0.53	0.36	0.58	1.10	0.44	2.48	1.93	2.75	3.23	2.73	2.45	2.60	1.25	2.77	1.10	2.31	1.65	2.20	2.46	0.51	0.39
950690	Hs.85137	cyclin A2	2.61	1.61	0.87	1.67	1.70	2.48	2.32	1.00	0.81	1.16	1.37	5.49	4.37	3.23	6.36	0.91	1.04	0.83	3.08	1.61	1.57	1.70
701751	Hs.147049	cut (Drosophila)-like 1 (CCAAT displacement protein)	0.63	2.86	1.95	2.02	2.29	1.21	1.17	1.55	3.04	1.70	2.66	1.64	1.47	1.21	1.15	1.86	0.86	0.95	0.98	1.22	1.33	1.06
839736	Hs.1940	crystallin, alpha B	4.00	1.81	3.53	2.02	8.23	0.34	4.36	0.79	0.94	0.67	0.74	0.77	0.15	0.30	0.54	0.81	0.73	1.50	0.85	0.31	1.03	4.59
85497	Hs.2253	complement component 2	1.30	8.11	3.77	2.78	3.59	2.95	1.73	3.23	14.63	0.95	3.29	3.14	1.10	2.00	2.11	2.09	2.85	1.27	2.08	1.57	1.79	1.64
839991	Hs.179573	collagen, type I, alpha 2	1.16	2.22	2.47	1.94	3.12	1.49	1.62	1.82	3.02	1.48	2.12	2.95	2.57	3.69	4.19	1.76	2.83	1.07	1.61	0.61	1.44	1.70
758148	Hs.251373	DNA segment on chromosome X (unique) 1253 expressed sequence	1.68	3.44	1.97	2.20	2.76	1.83	1.18	1.96	2.60	2.14	1.74	3.56	1.24	1.17	1.79	1.12	1.80	2.21	2.00	1.28	2.29	1.78
142788	Hs.9930	collagen-binding protein 2 (colligen 2)	2.17	2.50	3.57	3.42	4.64	1.09	2.02	3.18	5.28	2.70	2.41	2.56	0.86	2.19	2.28	2.01	2.04	1.39	2.31	1.47	1.99	1.66
810632	Hs.4217	collagen, type VI, alpha 2	1.38	3.41	2.06	1.78	2.41	1.50	1.55	2.14	2.66	0.95	1.48	2.01	1.02	1.17	1.83	1.40	1.59	1.43	1.74	1.46	1.43	1.86
714426	Hs.693	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kD	1.86	1.11	1.68	1.44	1.32	0.97	1.46	0.90	2.00	1.09	1.23	1.03	0.55	0.68	1.07	1.14	1.33	1.12	1.67	0.92	0.64	0.88
898286	Hs.184572	cell division cycle 2, G1 to S and G2 to M	3.00	1.10	2.17	2.63	2.17	1.11	1.73	2.11	0.68	1.01	1.83	0.67	1.13	0.44	1.14	0.48	0.98	0.61	2.62	1.26	1.34	1.64
687875	Hs.181301	cathepsin S	2.01	11.43	10.82	9.06	6.40	4.53	1.94	10.90	21.29	12.29	8.52	12.07	2.21	3.44	5.86	3.38	5.48	2.71	3.99	2.50	3.16	2.67
796984	Hs.88974	cytochrome b-245, beta polypeptide (chronic granulomatous disease)	3.05	5.57	5.32	5.73	6.09	6.31	2.16	4.48	6.01	2.67	6.47	10.82	4.14	3.45	4.08	3.43	5.82	6.98	6.44	3.02	2.88	2.83
724615	Hs.84746	chromosome condensation 1	1.33	1.22	0.73	1.20	1.15	1.02	1.07	0.76	0.79	0.70	1.18	1.00	0.87	1.14	1.06	1.03	0.55	0.53	0.62	0.70	0.61	1.19
756211	Hs.112028	cholinergic receptor, nicotinic, epsilon polypeptide	1.03	2.01	1.18	0.78	1.95	0.84	1.41	1.52	0.94	1.59	1.15	1.74	0.58	1.06	1.21	0.87	0.74	0.96	1.25	0.99	1.67	0.62
898258	Hs.169965	chimerin (chimaerin) 1	0.38	0.61	1.59	1.02	1.12	0.47	0.42	0.70	1.02	1.10	0.89	0.56	0.39	0.72	0.54	0.70	0.22	0.43	0.34	0.67	0.53	0.47
825335	Hs.78497	spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive)	2.33	2.42	2.15	1.86	3.47	0.99	1.87	2.45	2.23	1.91	1.71	2.61	1.23	1.49	2.30	0.90	1.73	1.70	1.45	1.24	1.66	2.05
841470	Hs.76476	cathepsin H	0.67	1.16	0.37	0.58	0.89	0.17	1.01	0.34	0.34	0.19	0.17	1.01	0.67	0.68	0.90	0.57	0.20	0.19	0.27	0.55	0.20	1.19
69672	Hs.76206	cadherin 5, VE-cadherin (vascular epithelium)	1.71	1.55	0.62	1.26	2.00	1.98	0.76	1.25	1.29	0.86	2.17	4.70	1.82	1.73	1.76	1.32	1.84	1.47	2.23	0.59	1.83	1.97
774754	Hs.171271	catenin (cadherin-associated protein), beta 1 (88kD)	3.38	2.04	2.67	2.06	2.87	2.08	6.08	1.51	3.43	1.43	1.41	1.03	0.65	0.54	1.04	2.34	2.39	2.47	2.68	1.55	1.10	1.60
795840	Hs.75360	carboxypeptidase E	0.81	1.92	1.23	1.96	1.58	0.81	1.45	1.19	1.04	1.31	2.01	1.57	0.51	1.17	0.93	1.43	0.73	0.78	1.04	1.13	0.88	0.86
511521	Hs.155560	calnexin	0.57	0.50	0.83	1.12	0.87	0.73	0.49	0.53	1.07	0.49	0.78	0.47	0.93	0.70	0.83	0.79	1.16	0.68	0.58	1.94	0.52	1.08
773301	Hs.2877	cadherin 3, P-cadherin (placental)	0.69	1.21	0.22	0.30	0.77	0.26	0.92	0.20	0.33	0.22	0.36	1.22	0.60	0.85	0.14	0.38	0.17	0.23	0.33	0.53	0.19	1.07
897655	Hs.82767	sperm specific antigen 2	1.14	1.21	0.86	1.38	2.92	0.99	2.48	1.26	0.97	2.00	1.10	1.15	0.52	0.88	0.97	1.09	1.07	1.73	2.62	1.17	1.61	1.60
838568	Hs.74649	cytochrome c oxidase subunit VIc	0.67	0.68	1.39	0.95	0.83	1.12	0.44	1.72	3.15	2.77	1.16	4.19	3.31	1.36	6.53	1.65	1.68	0.93	2.20	1.00	1.04	0.84
840894	Hs.180714	cytochrome c oxidase subunit VIa polypeptide 1	0.90	0.83	0.50	0.97	0.41	0.44	1.38	0.64	1.34	1.08	0.90	1.31	1.32	0.85	0.99	0.72	0.70	0.50	1.08	0.93	0.69	0.51
51814	Hs.695	cystatin B (stefin B)	2.20	1.96	0.73	1.46	1.55	1.71	2.22	1.30	1.07	1.15	1.27	0.99	0.50	0.96	0.62	1.05	1.28	1.02	1.46	1.56	1.62	2.44
789049	Hs.144630	nuclear receptor subfamily 2, group F, member 1	1.70	3.50	1.59	2.13	2.75	1.17	1.83	1.39	1.69	1.89	2.29	1.42	0.60	0.85	1.67	0.88	1.50	1.90	1.78	1.14	1.22	1.00
950096	Hs.33642	archain 1	2.61	2.52	1.38	1.23	1.61	1.17	2.27	1.06	1.60	1.38	1.50	1.05	0.45	1.08	0.88	1.41	1.32	1.33	1.92	1.33	1.06	1.95
77805	Hs.75724	coatomer protein complex, subunit beta 2 (beta prime)	3.67	2.05	1.20	1.40	1.66	1.28	2.92	1.53	2.05	1.94	1.60	1.24	0.48	0.85	0.94	1.46	1.80	1.22	2.28	1.80	1.92	1.71
897531	Hs.211579	melanoma adhesion molecule	0.27	0.63	0.81	0.51	0.87	1.45	0.19	0.77	2.36	0.77	0.72	2.84	5.84	4.63	1.72	1.46	0.55	0.37	0.45	0.69	0.29	0.91
713145	Hs.169610	CD44 antigen (homing function and Indian blood group system)	0.80	0.86	0.36	0.85	0.86	1.98	0.39	0.35	0.84	0.33	0.61	1.19	1.83	1.36	0.63	1.16	1.32	1.55	0.78	1.26	1.09	1.17
725454	Hs.83758	CDC28 protein kinase 2	1.52	3.41	1.58	1.93	1.55	1.11	4.08	1.68	0.56	1.63	1.25	0.99	0.62	0.51	0.64	0.66	0.57	0.80	1.79	1.20	0.87	2.13
843049	Hs.154443	minichromosome maintenance deficient (S. cerevisiae) 4	2.17	2.16	1.51	2.19	1.98	1.03	3.45	1.19	1.25	1.16	1.11	2.67	1.66	2.99	1.48	1.40	0.89	1.37	1.54	2.14	1.74	2.18
840978	Hs.54457	CD81 antigen (target of antiproliferative antibody 1)	1.14	2.37	1.85	1.49	1.54	0.93	1.07	1.81	2.31	1.50	1.67	0.91	0.89	0.75	0.68	2.04	1.04	1.70	1.05	1.26	0.98	1.15
795827	Hs.79358	testis-specific kinase 1	2.73	2.21	1.43	2.90	3.32	1.71	3.50	3.33	3.42	3.52	2.24	4.68	3.40	2.62	2.98	0.88	2.05	1.66	2.86	1.55	2.01	2.06
739183	Hs.246381	CD68 antigen	1.32	3.41	2.96	2.73	2.37	3.43	0.95	3.47	3.81	3.18	4.64	4.58	2.30	4.51	1.90	4.29	2.13	1.29	1.28	1.48	2.59	2.49
490368	Hs.75626	CD58 antigen, (lymphocyte function-associated antigen 3)	2.11	2.27	1.51	1.47	2.42	0.90	0.96	1.01	1.65	0.95	0.92	2.13	1.00	1.34	1.49	0.83	0.73	0.93	0.95	1.25	1.31	1.28
785845	Hs.75133	transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	1.59	1.45	1.59	2.36	1.82	1.42	1.92	1.61	1.50	0.93	1.74	1.42	1.13	1.04	1.32	1.22	1.02	1.60	1.38	1.19	1.58	1.97
191664	Hs.108623	thrombospondin 2	3.24	0.91	6.72	8.80	4.96	2.07	6.17	4.73	9.19	15.87	8.13	9.08	1.87	4.39	8.23	5.45	4.69	4.90	9.11	3.32	0.91	2.03
712641	Hs.218791	megakaryocyte stimulating factor	1.72	2.38	1.40	2.52	2.20	1.60	2.06	1.75	1.49	1.88	1.48	1.53	1.03	0.90	1.85	0.91	1.00	1.32	2.38	0.87	2.39	1.71
193913	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0.84	2.63	1.90	1.92	3.30	2.00	1.22	1.41	1.74	0.96	2.21	1.79	0.56	1.45	1.13	2.22	0.80	1.14	0.77	1.10	1.51	3.17
258589	Hs.44313	v-rel avian reticuloendotheliosis viral oncogene homolog	2.43	3.13	2.30	2.31	3.50	2.43	2.00	2.53	2.88	2.68	2.94	5.33	1.10	1.16	3.62	2.53	2.94	2.66	3.61	1.14	2.85	1.64

322617	Hs.181309	proteasome (prosome, macropain) subunit, alpha type, 2	0.61	0.88	0.71	0.63	1.50	1.08	0.48	1.13	1.53	0.75	1.42	0.73	0.73	0.63	1.08	1.50	0.74	0.87	0.75	1.04	1.34	0.81
267634	Hs.85181	v-raf-1 murine leukemia viral oncogene homolog 1	1.30	1.10	1.50	1.13	1.37	0.88	1.08	0.96	0.96	0.85	1.10	1.22	0.64	0.97	1.04	1.26	1.10	0.78	1.01	0.79	0.84	0.91
207618	Hs.77183	v-raf murine sarcoma 3611 viral oncogene homolog 1	1.58	1.98	1.15	1.23	2.16	1.45	1.17	2.12	1.48	1.54	2.22	1.24	1.28	1.20	2.18	1.35	1.20	1.51	1.86	1.12	2.00	2.00
760148	Hs.78601	uroporphyrinogen decarboxylase	1.21	0.57	1.56	1.23	0.77	0.48	1.42	0.95	1.31	2.26	1.27	0.69	0.56	1.12	0.99	0.57	1.16	0.92	1.47	0.83	0.58	0.62
305606	Hs.89839	EphA1	1.11	1.67	0.69	2.25	2.16	1.45	1.39	1.45	1.26	1.85	1.74	1.78	0.58	0.86	1.27	1.85	1.13	1.13	1.25	1.16	1.67	0.91
128302	Hs.171814	parathymosin	1.54	2.30	2.54	2.55	1.13	1.34	4.10	2.34	2.38	1.71	2.69	1.33	1.20	1.15	1.56	2.01	1.96	2.34	2.18	1.25	1.32	2.06
730410	Hs.1765	lymphocyte-specific protein tyrosine kinase	3.04	2.01	1.94	2.89	1.02	1.50	0.64	1.42	2.83	2.67	1.90	7.35	1.67	4.53	5.89	1.83	3.93	1.82	1.94	0.77	1.04	1.15
135083	Hs.110029	glucose regulated protein, 58kD	1.05	2.43	1.98	1.45	2.24	1.26	1.17	1.49	1.60	1.95	1.84	1.17	0.48	0.99	1.26	1.96	1.15	0.97	1.74	1.39	1.66	1.80
278808	Hs.157441	spleen focus forming virus (SFFV) proviral integration oncogene spi1	1.97	6.21	1.03	2.96	6.05	2.92	1.18	3.52	2.04	3.09	4.66	7.86	1.79	2.64	4.16	3.79	2.62	3.09	2.75	1.25	5.05	2.52
109179	Hs.77031	Sp2 transcription factor	1.45	7.43	1.36	5.11	7.16	3.59	0.65	4.21	3.76	5.37	7.02	3.18	0.58	1.20	2.29	3.81	1.91	1.45	1.47	0.68	3.34	2.68
712840	Hs.244613	signal transducer and activator of transcription 5B	2.00	2.50	0.66	1.36	3.44	1.57	0.46	1.70	1.33	1.27	2.53	5.02	0.63	3.57	3.34	1.85	1.52	1.77	1.48	0.77	2.11	1.40
711826	Hs.250759	KIAA0019 gene product	1.45	2.64	1.45	2.87	2.49	3.14	1.95	0.99	1.13	0.91	2.34	1.29	0.80	1.00	1.10	1.50	0.74	1.07	0.87	1.53	1.68	1.99
897596	Hs.180946	ribosomal protein L5	1.28	2.00	0.71	0.78	1.00	0.48	1.70	1.01	0.43	0.57	0.96	0.51	0.16	0.25	1.09	0.51	0.49	1.36	1.12	0.74	0.78	1.05
172440	Hs.5636	RAB6, member RAS oncogene family	1.57	1.16	0.76	1.80	1.46	1.36	0.53	0.69	1.46	0.73	1.21	1.36	1.47	1.21	1.56	1.35	1.38	0.95	0.50	2.30	1.20	1.44
950445	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.80	0.88	0.85	0.66	0.98	0.42	0.83	1.12	0.87	0.98	0.82	0.64	0.66	0.45	1.01	0.89	1.12	0.92	1.03	0.71	0.87	0.85
950710	Hs.80741	propionyl Coenzyme A carboxylase, alpha polypeptide	0.99	0.69	1.45	1.00	0.92	0.61	1.03	0.55	1.55	1.54	0.94	2.02	0.59	1.19	0.91	3.52	1.50	1.05	0.85	1.04	1.04	0.76
85805	Hs.76461	retinol-binding protein 4, interstitial	1.28	1.54	0.68	1.68	2.23	2.03	1.21	1.19	1.36	0.83	3.10	1.82	0.57	1.24	1.08	2.23	1.16	1.18	1.53	1.64	1.39	1.71
242578	Hs.171955	trophinin-assisting protein (tastin)	1.91	1.86	1.95	1.66	1.23	1.63	3.33	2.04	0.63	2.49	1.04	1.44	1.09	1.44	1.28	0.85	1.90	1.03	2.17	1.34	0.89	0.75
156386	Hs.184488	flotillin 2	1.91	2.37	1.84	1.60	1.94	1.54	2.56	2.15	1.56	2.26	2.44	1.41	0.84	1.43	1.34	1.42	1.83	1.61	2.35	1.66	2.49	2.36
773305	Hs.99902	opioid-binding protein/cell adhesion molecule-like	1.74	4.15	0.99	2.19	5.69	2.50	1.81	2.28	2.18	1.88	4.08	4.03	1.00	1.43	2.05	1.79	2.27	2.09	2.41	1.64	3.89	0.91
297392	Hs.94360	metallothionein 1L	3.37	0.50	0.50	0.69	1.07	0.32	1.76	0.89	0.63	0.65	0.95	0.57	0.16	0.37	0.40	0.43	0.57	1.39	1.23	1.27	0.79	0.58
80109	Hs.198253	major histocompatibility complex, class II, DQ alpha 1	3.37	5.45	3.68	8.32	10.77	9.61	4.55	8.51	10.76	5.18	12.77	15.16	5.09	5.74	3.87	6.35	8.22	6.91	10.84	2.04	5.28	4.84
789069	Hs.102267	lysyl oxidase	1.82	2.07	1.26	3.03	3.91	3.03	2.96	3.08	2.91	2.09	3.46	3.52	1.14	2.45	1.94	2.26	2.17	2.89	2.88	2.19	2.41	1.76
110788	Hs.56729	lymphocyte-specific protein 1	2.48	7.88	3.43	3.47	6.69	4.46	3.34	5.02	5.90	6.66	5.12	6.91	1.88	4.70	4.34	4.31	3.18	3.97	6.16	1.69	3.97	2.47
782513	Hs.179972	interferon, alpha-inducible protein (clone IFI-6-16)	1.52	3.99	1.52	2.05	2.74	1.85	2.50	2.82	1.85	2.29	2.46	2.45	1.28	1.29	2.66	2.38	2.02	1.79	2.66	1.65	2.61	2.15
115281	Hs.79630	CD79A antigen (immunoglobulin-associated alpha)	1.21	1.43	1.27	1.44	1.79	2.18	2.09	1.16	2.13	1.95	1.46	2.74	1.05	3.12	2.18	1.26	1.82	2.86	1.74	1.47	0.61	1.05
897880	Hs.79150	chaperonin containing TCP1, subunit 4 (delta)	0.95	0.86	0.58	1.98	0.90	1.12	0.73	0.58	0.93	0.49	0.61	0.28	0.44	0.67	0.56	0.77	0.77	0.76	0.56	0.99	1.67	1.29
781050	Hs.80686	prefoldin 5	0.89	1.42	1.11	1.08	1.18	0.86	1.07	0.80	1.47	1.18	1.09	1.02	0.64	1.49	1.25	1.03	1.36	1.28	1.56	0.95	0.90	1.19
814119	Hs.171872	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 8 (RNA helicase)	0.80	1.82	1.24	1.21	1.20	0.98	1.18	0.92	1.50	1.76	0.43	1.13	0.85	1.06	1.13	0.57	1.29	0.82	0.99	0.67	0.70	0.69
83363	Hs.79137	protein-L-isoaspartate (D-aspartate) O-methyltransferase	0.87	1.17	0.81	1.08	1.23	1.21	0.81	0.92	0.93	1.12	1.20	0.76	0.70	0.80	0.67	1.01	1.27	0.98	0.65	1.16	0.90	1.31
154093	Hs.89421	CBF1 interacting corepressor	1.20	2.72	1.60	2.46	3.26	1.95	1.38	1.89	2.40	2.37	1.93	3.76	3.26	1.54	2.38	0.86	1.86	1.82	1.70	0.82	3.12	1.94
85840	Hs.76669	nicotinamide N-methyltransferase	2.38	1.45	0.97	2.36	4.66	1.81	3.96	3.84	5.93	3.38	3.02	2.96	2.67	2.00	2.74	1.76	1.26	1.43	2.82	1.84	1.71	1.10
951117	Hs.75069	serine hydroxymethyltransferase 2 (mitochondrial)	0.91	1.68	1.04	1.04	1.29	0.73	1.75	1.80	1.02	0.90	1.29	0.89	0.48	0.88	0.81	0.96	0.59	0.61	1.07	1.11	1.20	1.51
951233	Hs.82793	proteasome (prosome, macropain) subunit, beta type, 3	1.28	2.05	1.06	1.23	1.72	1.26	1.82	1.94	2.00	1.85	1.22	1.19	1.31	0.85	1.64	1.20	1.88	1.25	1.90	1.97	2.06	1.66
797059	Hs.21365	nucleosome assembly protein 1-like 3	1.19	1.21	2.32	0.64	0.83	0.65	2.55	0.80	1.59	1.16	0.32	2.34	0.86	1.71	2.02	1.36	1.73	1.71	1.92	0.88	0.49	1.18
788486	Hs.201377	apyrase, lysosomal	0.97	1.48	1.35	1.63	1.72	1.08	0.72	1.21	1.02	1.90	1.18	1.11	0.50	1.07	1.52	1.17	0.85	0.81	1.22	0.54	1.42	1.22
239877	Hs.6975	histone deacetylase 3	0.64	0.86	0.75	1.11	1.09	0.69	0.74	0.95	1.03	1.33	1.06	0.85	1.00	1.05	1.20	0.92	0.74	0.84	0.77	0.70	1.43	0.92
842939	Hs.85302	adenosine deaminase, RNA-specific, B1 (homolog of rat RED1)	1.92	0.87	1.76	1.63	1.10	0.80	2.31	1.04	2.05	1.84	1.25	5.26	2.27	2.86	5.51	0.99	1.29	1.32	2.30	1.23	0.80	0.70
544639	Hs.95612	ESTs	1.03	0.53	1.20	1.48	1.28	0.74	1.04	0.55	0.56	1.56	0.58	0.71	0.33	0.63	0.83	0.29	0.21	0.58	0.58	0.63	1.11	1.50
155575	Hs.26395	erythrocyte membrane protein band 4.1-like 1	0.87	0.83	0.39	0.57	1.29	0.54	0.59	1.12	0.75	1.37	0.83	0.55	0.39	0.34	0.95	0.79	0.68	0.70	0.58	0.47	1.48	0.77
240505	Hs.7911	KIAA0323 protein	1.48	1.82	1.05	1.35	1.45	0.93	0.91	1.30	1.27	1.39	1.64	1.38	1.02	1.14	1.69	1.12	1.29	1.41	1.53	1.24	1.34	0.66
772111	Hs.173035	KIAA0300 protein	3.54	2.52	1.84	4.23	3.88	2.22	1.70	5.32	1167.04	2.26	2.20	2.05	1.26	1.91	2.27	0.97	1.13	1.78	3.24	2.41	2.65	1.58
510760	Hs.141296	Human mRNA for KIAA0226 gene, complete cds	1.28	0.55	1.14	0.83	0.62	0.36	0.49	0.53	0.59	0.52	0.55	0.59	0.97	0.35	0.42	0.34	0.51	0.37	0.49	0.61	0.94	0.62
785963	Hs.12413	KIAA0191 protein	0.95	1.11	1.16	1.12	1.62	0.97	0.80	0.92	0.62	0.81	0.80	0.35	0.37	0.47	0.74	0.52	0.57	1.14	0.88	0.74	1.39	0.93
758365	Hs.180669	conserved gene amplified in osteosarcoma	1.86	2.36	1.38	1.79	1.33	1.12	2.43	1.28	1.72	1.09	1.28	1.01	1.15	1.01	1.13	1.58	0.94	0.74	1.18	1.08	1.77	2.19
233581	Hs.155485	huntingtin-interacting protein 2	1.26	1.20	1.09	0.92	1.49	1.02	1.78	1.88	1.35	1.31	1.79	1.42	0.70	0.77	1.30	0.86	1.05	1.31	1.15	1.17	1.65	1.40
788421	Hs.75862	MAD (mothers against decapentaplegic, Drosophila) homolog 4	0.99	0.65	1.89	1.60	0.77	0.65	1.10	0.53	0.89	0.62	0.81	0.46	0.38	0.93	0.80	0.64	0.55	1.01	1.11	0.57	0.72	0.85
130843	Hs.228548	EST	2.84	2.40	1.41	1.94	1.97	2.74	2.12	1.52	2.48	5.98	1.22	5.26	0.77	2.16	2.70	2.83	5.12	1.78	6.74	0.93	1.58	2.78
203132	Hs.83429	tumor necrosis factor (ligand) superfamily, member 10	5.91	10.26	2.20	2.22	3.53	6.64	1.53	6.29	10.64	3.94	8.09	6.31	2.98	2.65	6.68	3.63	4.86	4.94	5.07	3.54	3.71	2.65
146577	Hs.82173	TGFB inducible early growth response	0.92	1.28	1.01	0.71	0.75	0.54	0.52	0.63	1.35	0.43	0.85	1.44	0.97	1.33	1.03	1.10	0.41	0.82	0.45	0.99	0.69	0.51
235155	Hs.743	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide	4.62	23.59	12.26	2.90	9.60	8.60	6.47	6.62	10.97	14.27	12.50	14.75	4.68	5.67	8.87	4.26	5.90	5.56	7.41	2.25	5.12	4.29
85394	Hs.173717	Phosphatidic acid phosphatase type 2b	1.07	2.70	1.87	2.25	3.81	2.11	1.36	1.68	2.63	2.49	3.00	3.05	0.70	2.56	2.31	3.23	1.00	1.75	2.10	1.77	1.87	1.53
632074	Hs.21413	Human clone 23586 mRNA sequence	1.76	3.80	1.24	2.02	3.27	2.10	1.96	1.77	1.95	1.71	3.24	2.48	0.86	1.93	1.52	2.17	1.28	2.10	2.03	1.65	2.23	2.21
358531	Hs.78465	v-jun avian sarcoma virus 17 oncogene homolog	1.35	0.82	1.27	0.93	2.03	0.37	1.00	0.69	1.28	0.82	0.98	0.92	0.33	0.66	1.34	0.74	1.01	2.33	0.96	1.01	1.14	0.67
785744	Hs.3745	milk fat globule-EGF factor 8 protein	0.75	0.95	1.71	1.69	1.96	0.60	2.60	0.61	1.18	0.63	0.46	0.55	0.28	0.73	0.50	0.85	0.30	0.82	0.58	0.61	0.45	2.25
627542	Hs.81029	biliverdin reductase A	1.29	1.45	1.13	0.83	1.86	1.19	0.89	2.01	1.66	2.13	2.13	3.07	0.60	1.46	3.26	1.26	3.26	0.68	4.14	1.71	2.86	1.05
594743	Hs.75737	pericentriolar material 1	0.81	0.87	1.19	1.47	0.90	0.72	0.57	0.59	1.24	0.87	0.82	3.06	1.01	1.10	1.70	0.79	0.83	0.75	0.79	0.44	0.96	0.47
83120	Hs.154583	RNA binding motif protein 10	1.21	2.27	1.02	1.24	1.41	1.79	1.90	1.17	0.87	1.22	1.51	2.07	1.01	1.60	1.80	1.16	0.83	1.11	1.82	1.05	1.42	1.76
294487	Hs.100407	programmed cell death 4	1.40	1.91	0.94	1.02	1.93	1.61	0.45	1.18	1.05	0.86	1.20	2.17	1.02	1.77	2.30	1.07	1.50	2.11	0.96	0.67	1.50	1.44
841282	Hs.105700	secreted frizzled-related protein 4	2.13	3.90	5.50	4.99	4.79	5.52	4.22	6.33	14.65	2.18	3.01	4.04	1.34	2.71	6.64	5.49	4.34	5.71	7.38	3.16	2.35	0.64
740914	Hs.239737	C-terminal binding protein 1	1.41	1.85	0.85	1.26	1.81	0.97	0.97	1.89	1.40	1.91	1.80	1.18	1.20	1.09	1.68	1.60	1.04	1.55	2.14	1.33	2.01	0.94
632137	Hs.112058	CD27-binding (Siva) protein	1.61	2.79	1.17	1.61	1.71	1.76	1.88	1.59	1.23	1.67	1.61	1.13	0.87	1.82	1.16	1.29	1.07	1.41	1.69	1.46	2.16	1.87
789049	Hs.144630	nuclear receptor subfamily 2, group F, member 1	1.68	2.67	1.25	2.36	2.81	1.28	2.21	2.01	1.76	2.68	2.22	0.75	0.25	0.37	1.90	0.94	1.66	1.93	2.09	0.95	3.14	1.62
207358	Hs.169902	solute carrier family 2 (facilitated glucose transporter), member 1	1.43	0.45	1.21	0.77	0.66	0.41	0.56	0.68	0.59	0.81	0.51	0.47	0.87	0.22	0.36	0.37	0.60	0.39	0.55	0.80	1.09	0.49
62277	Hs.251557	EST	1.13	1.86	1.01	1.17	1.40	0.87	1.62	1.23	1.40	2.28	0.52	1.70	0.71	1.10	0.53	0.95	1.27	1.30	1.85	1.18	1.56	1.21
788185	Hs.51233	tumor necrosis factor receptor superfamily, member 10b	0.97	2.05	1.01	1.24	1.56	1.30	0.47	0.85	1.06	7.67	0.96	1.52	0.87	1.26	1.23	1.57	0.64	0.90	0.57	0.91	1.29	1.99
814526	Hs.236361	H.sapiens seb4D mRNA	2.85	2.44	3.27	4.93	2.15	4.14	3.05	3.15	3.68	1.75	1.53	4.58	2.91	2.94	2.48	1.13	4.17	1.75	1.57	1.64	0.95	2.53
785293	Hs.37189	similar to rat HREV107	0.77	2.02	0.58	0.73	1.50	2.08	0.40	1.25	1.07	1.65	1.64	1.21	1.46	0.64	2.07	1.48	1.28	2.33	1.21	0.96	0.52	1.02
502369	Hs.166468	programmed cell death 5	1.78	3.48	1.58	1.90	2.04	2.06	2.23	1.48	1.20	1.75	1.00	0.75	0.66	1.05	1.20	0.72	1.48	1.07	1.68	0.97	2.45	2.28
745347	Hs.76507	LPS-induced TNF-alpha factor	0.96	2.58	1.69	2.00	2.48	2.65	1.52	0.70	2.94	0.93	2.51	1.51	0.76	0.97	0.83	2.96	0.76	1.16	0.54	1.18	1.92	3.65
859359	Hs.50649	quinone oxidoreductase homolog	0.71	0.98	0.55	0.57	0.93	0.44	0.69	0.96	0.72	0.77	0.54	0.69	0.35	0.41	0.54	0.50	0.52	0.78	0.79	0.73	1.09	0.36
48285	Hs.74427	p53-induced protein	1.34	0.82	1.10	0.92	0.79	0.58	0.60	0.79	0.92	0.76	0.60	0.70	0.86	0.48	0.43	0.47	0.66	0.48	0.60	0.91	0.93	0.66
275180	Hs.110613	KIAA0220 protein	1.57	1.88	1.08	1.45	1.49	1.12	1.65	1.80	1.28	1.86	1.16	1.67	1.79	1.55	1.01	0.92	2.17	1.84	2.01	1.80	1.09	0.91
589751	Hs.90753	Tat-interacting protein (30kD)	0.81	1.39	0.70	1.44	1.75	1.01	0.99	1.04	0.91	0.60	1.08	1.01	0.82	1.08	0.73	1.03	0.50	0.56	0.62	0.78	1.31	1.36
236305	Hs.239817	histidyl-tRNA synthetase	0.76	1.52	0.76	0.80	1.60	0.59	1.05	1.60	1.29	2.01	1.00	1.29	0.62	1.81	1.06	0.78	1.24	0.95	1.72	0.58	1.26	0.93
840158	Hs.118625	hexokinase 1	0.82	1.15	0.75	0.53	0.87	0.58	1.05	0.97	0.95	2.11	0.46	0.90	0.96	0.69	0.86	0.53	0.95	0.97	1.79	0.95	0.79	0.55
214162	Hs.2667	metallothionein 1H	1.18	0.50	0.52	0.44	0.92	0.49	1.41	0.41	0.30	0.32	0.84	0.68	0.38	0.56	0.49	0.53	0.64	0.89	0.98	1.01	0.93	0.58
42076	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and name)	0.85	1.19	0.91	0.71	0.99	1.14	1.67	0.40	1.17	0.70	0.62	0.34	0.51	0.74	0.58	1.14	0.83	0.57	0.68	0.87	0.60	0.85
127925	Hs.100555	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 18 (Myc-regulated)	1.41	2.21	1.46	2.08	3.04	2.07	2.65	1.13	1.31	1.22	2.55	1.22	1.70	1.04	1.45	1.34	1.41	1.70	1.27	1.49	3.26	2.51
38763	Hs.250595	S-phase response (cyclin-related)	2.86	2.06	1.58	2.03	2.49	1.40	1.92	1.72	1.14	0.77	1.55	1.08	1.09	0.71	1.18	1.37	1.46	1.76	1.57	1.37	2.12	1.81
137236	Hs.103329	KIAA0970 protein	1.38	1.66	0.75	1.56	2.22	1.72	0.36	0.99	1.11	1.14	1.42	1.60	0.83	0.78	1.18	0.94	1.24	1.16	1.43	1.23	1.35	1.49

246749	Hs.93560	ESTs, Weakly similar to trg [R.norvegicus]	0.91	1.63	1.60	1.63	1.11	1.11	1.38	0.73	1.30	1.18	0.78	0.63	0.46	0.58	0.70	1.39	0.72	0.76	0.66	0.86	1.00	0.91
129392	Hs.14337	ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-orf7 p	1.40	2.44	1.32	1.85	1.68	1.43	2.99	1.94	1.72	2.53	1.76	4.28	2.35	2.77	2.85	2.65	1.22	0.84	1.46	1.17	1.06	1.01
66953	Hs.76907	ESTs, Highly similar to HSPC002 [H.sapiens]	0.95	2.05	1.92	1.55	1.97	1.02	1.83	1.59	1.49	1.54	1.03	1.63	1.04	1.44	1.19	1.16	0.74	1.08	1.08	0.64	0.83	1.55
123614	Hs.19002	ESTs, Weakly similar to unknown [H.sapiens]	0.99	1.48	0.53	1.05	2.40	1.31	0.44	1.48	1.60	2.36	1.54	1.61	3.84	1.85	1.46	3.04	1.57	1.07	2.44	1.00	2.20	1.11
140354	Hs.206613	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.17	1.80	0.60	1.03	1.77	1.15	0.83	1.54	1.27	1.61	1.43	1.87	1.61	1.12	1.54	0.96	1.57	1.60	2.33	1.74	2.22	1.16
26566	Hs.99654	protein-O-mannosyltransferase 1	2.39	1.88	0.83	1.17	1.81	1.49	1.08	1.17	1.26	2.83	4.00	2.02	2.29	1.86	2.33	1.96	1.24	1.78	1.68	1.34	1.04	0.84
135608	Hs.24430	ESTs, Weakly similar to OXYSTEROL-BINDING PROTEIN [H.sapiens]	0.49	1.21	0.89	0.52	0.99	1.42	0.35	0.56	0.48	0.81	0.89	2.39	2.06	1.12	2.00	0.81	0.34	0.41	0.30	3.39	0.89	0.63
140100	Hs.239218	ESTs, Weakly similar to PROBABLE PEROXISOMAL ENOYL-COA HYDRATASE [M.musculus]	0.51	1.14	0.44	0.98	0.64	1.96	0.17	0.43	0.70	0.50	0.40	0.47	0.15	0.48	0.39	0.39	0.65	0.67	0.67	0.51	0.97	0.88
382773	Hs.6975	histone deacetylase 3	1.55	2.99	1.47	3.25	2.63	1.75	2.70	3.25	3.02	2.12	1.88	1.93	0.92	0.63	1.29	1.87	3.35	2.82	3.16	2.06	2.13	0.92
246035	Hs.78026	ESTs	2.10	2.05	0.73	3.88	1.12	0.47	1.29	1.12	3.02	1.70	0.92	2.90	0.68	1.12	1.56	0.61	0.67	1.02	1.60	0.86	1.05	0.99
366341	Hs.11896	ESTs, Weakly similar to similar to S. cerevisiae longevity-assurance protein 1 [C.elegans]	2.08	1.52	1.72	1.19	1.34	2.25	1.16	1.59	1.93	2.31	4.50	5.44	2.07	3.06	4.57	1.31	1.98	2.02	0.91	1.47	0.81	0.53
471196	Hs.111577	integral membrane protein 2C	1.23	0.79	2.57	0.76	2.19	1.17	0.98	1.36	1.45	1.23	1.60	0.91	0.25	0.88	0.38	1.36	0.55	0.72	0.59	0.95	2.85	1.48
565493	Hs.91448	MKP-1 like protein tyrosine phosphatase	1.15	0.66	1.22	0.69	1.73	1.05	0.82	1.41	0.92	0.86	0.79	0.97	0.47	0.88	0.62	0.96	0.49	0.92	0.59	0.85	0.93	0.58
194006	Hs.15981	ESTs, Weakly similar to line-1 protein ORF2 [H.sapiens]	0.97	1.65	0.50	0.68	1.57	0.43	1.80	1.10	1.38	1.64	0.65	1.25	0.52	0.74	0.98	0.69	1.46	1.31	1.90	0.97	0.78	0.76
246543	Hs.70617	zinc finger protein 33a (KOX 31)	1.92	6.22	3.24	2.83	4.85	2.28	1.29	2.91	8.39	0.95	1.98	3.20	1.56	1.32	2.65	0.79	1.85	1.85	2.14	0.92	1.99	2.40
137638	Hs.108642	ESTs	3.63	11.63	6.73	6.32	6.89	2.91	3.52	2.96	3.89	1.70	2.65	1.83	1.31	1.63	3.08	1.90	2.25	3.31	2.79	2.34	3.24	2.82
165921	Hs.27910	centrosome associated protein	2.01	1.02	1.03	0.80	1.09	0.86	0.77	1.03	0.47	1.57	1.17	0.90	0.49	0.62	0.80	0.75	0.79	0.94	1.06	0.61	1.82	0.87
66535	Hs.74563	Homo sapiens ornithine decarboxylase antizyme 2 (OAZ2) mRNA, complete cds	0.85	0.95	1.84	1.72	1.27	1.16	1.08	0.55	1.61	1.11	1.25	1.22	2.30	1.92	1.97	1.33	1.04	0.89	0.81	0.92	0.91	0.74
110503	Hs.4245	ESTs, Weakly similar to similar to S. cerevisiae hypothetical protein YKL166 [C.elegans]	0.81	1.12	0.44	0.62	1.27	1.80	0.84	0.79	0.44	0.97	0.91	0.81	0.25	0.72	0.61	0.62	0.52	0.73	1.06	0.49	0.94	0.99
684940	Hs.74985	TATA element modulatory factor 1	1.10	1.63	1.56	1.74	1.26	1.42	1.10	0.84	1.48	1.10	1.64	1.21	0.77	1.21	0.30	0.81	0.82	1.08	0.71	0.86	0.90	1.76
251875	Hs.44268	ESTs, Highly similar to myelin gene expression factor 2 [H.sapiens]	1.54	1.91	0.71	1.13	1.84	0.92	1.03	1.37	1.25	1.95	1.57	0.78	1.26	1.22	1.41	1.03	0.95	1.44	1.26	0.91	1.23	1.20
161950	Hs.24125	KIAA1082 protein	0.76	1.13	0.97	1.29	1.37	0.75	1.05	1.09	0.89	0.88	1.07	0.75	0.76	0.86	0.98	1.06	0.65	0.85	1.20	0.84	0.69	0.99
66774	Hs.180347	Human DNA sequence from clone 425C14 on chromosome 6q22 Contains the HSF2 gene	1.21	2.32	2.02	1.34	1.47	1.59	0.80	0.85	1.42	1.56	1.16	1.24	1.09	0.68	1.07	0.84	0.65	1.11	1.28	0.72	0.69	0.83
248649	Hs.28436	ESTs, Weakly similar to coded for by C. elegans cDNA CEESW58F [C.elegans]	2.48	2.45	0.84	1.78	1.47	1.40	1.24	1.44	1.31	1.71	1.46	2.40	1.69	1.49	2.03	0.40	2.23	1.96	1.13	1.26	2.06	1.47
137581	Hs.105509	ESTs, Weakly similar to NG22 [H.sapiens]	0.80	1.19	0.56	0.85	1.50	1.88	1.21	0.35	0.85	1.10	0.92	1.65	1.71	1.77	1.51	1.72	0.91	0.88	0.89	0.95	0.72	0.98
344672	Hs.15536	ESTs	1.39	2.67	1.00	1.71	2.21	1.21	0.94	2.94	1.65	1.79	3.13	1.36	0.51	0.80	1.16	0.65	1.77	1.37	1.93	0.82	1.50	1.38
233365	Hs.203445	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	2.84	2.14	1.91	3.14	1.89	2.68	2.14	1.72	2.28	1.77	1.54	1.23	0.98	1.15	1.55	1.54	1.57	1.81	1.84	1.64	1.08	0.88
230562	Hs.227133	KIAA0670 protein/acinus	1.43	2.07	1.19	1.15	1.10	1.05	1.22	1.34	0.99	1.79	1.02	2.17	0.90	1.29	1.20	1.28	1.67	1.56	2.48	1.58	1.57	0.92
201986	Hs.171692	ESTs	0.83	1.23	1.48	0.89	1.05	1.14	0.82	1.03	1.12	1.28	1.07	3.58	2.83	2.10	3.14	0.85	0.88	1.26	0.78	1.11	0.61	0.94
141627	Hs.28728	ESTs, Weakly similar to F55A12.9 [C.elegans]	0.78	0.66	1.64	0.46	0.76	0.45	0.72	1.15	0.54	0.51	1.50	2.92	1.96	2.21	2.26	0.74	0.63	0.73	1.14	1.06	0.44	0.57
202213	Hs.93127	Homo sapiens mRNA; cDNA DKFZp586I0523 (from clone DKFZp586I0523)	1.37	1.80	1.60	0.84	1.88	0.91	1.18	1.27	1.95	1.53	1.15	1.40	1.19	0.99	1.34	1.02	1.28	1.65	1.93	1.06	1.19	0.83
292719	Hs.16157	ESTs, Highly similar to unknown [H.sapiens]	1.10	1.25	1.23	1.24	1.10	1.01	1.12	0.75	1.11	1.18	2.47	1.37	0.63	0.88	1.40	1.19	1.16	1.02	1.33	1.10	0.64	0.65
310356	Hs.9613	ESTs, Highly similar to angiopoietin-related protein [H.sapiens]	0.48	0.67	0.71	0.42	0.98	0.13	2.19	0.42	0.17	1.54	0.39	0.63	0.36	0.75	0.47	0.18	0.28	1.32	1.24	0.84	0.50	0.19
843426	Hs.171501	ubiquitin specific protease 11	2.66	1.45	0.86	1.39	2.12	1.27	5.32	1.31	1.20	0.83	0.88	2.11	0.95	1.87	1.98	0.94	1.77	2.20	1.51	1.65	1.58	0.91
136449	Hs.22451	ESTs	1.54	3.03	6.54	1.91	4.15	1.37	2.94	2.30	3.89	5.46	1.86	4.01	2.73	2.17	2.81	1.99	2.94	3.20	3.55	1.12	2.05	0.91
199158	Hs.93796	DKFZP586D2223 protein	0.74	1.05	1.09	1.45	1.48	0.80	3.08	0.70	0.97	0.80	0.95	0.66	0.81	0.92	1.07	0.86	0.74	0.83	1.13	0.73	0.91	0.87
321605	Hs.181634	Human Chromosome 16 BAC clone CIT987SK-A-61E3	0.72	0.83	0.66	0.84	1.31	0.43	1.15	1.10	0.50	0.82	0.58	0.46	0.84	1.18	0.70	0.72	1.19	1.62	1.01	0.23	1.20	0.64
243155	Hs.184352	ESTs, Weakly similar to cDNA EST EMBL:D36107 comes from this gene [C.elegans]	2.83	2.84	1.05	1.98	2.18	1.22	2.64	1.96	1.51	2.41	1.40	1.59	2.38	1.75	2.13	1.11	1.90	1.67	1.91	1.44	1.69	2.05
66336	Hs.12953	PTPRF interacting protein, binding protein 2 (liprin beta 2)	2.82	9.15	3.05	5.96	6.05	3.25	2.96	4.43	9.88	5.76	4.71	4.41	2.17	3.41	5.58	4.40	3.44	3.75	5.31	2.77	4.06	1.72
292512	Hs.108396	ESTs, Moderately similar to ALR [H.sapiens]	1.29	4.61	1.82	1.69	2.09	1.45	1.00	1.05	1.21	1.03	1.17	1.00	1.41	0.93	0.24	1.38	0.86	1.44	1.35	1.38	1.58	1.21
144977	Hs.92384	vitamin A responsive; cytoskeleton related	0.47	1.22	0.60	1.02	0.81	0.92	0.48	0.62	1.00	0.40	0.65	0.64	0.39	0.47	0.93	0.95	0.73	0.96	0.73	0.95	0.69	0.89
202919	Hs.74626	adaptor-related protein complex 2, beta 1 subunit	2.18	1.41	1.00	1.18	1.48	1.52	1.74	1.39	0.98	1.35	1.14	1.45	1.14	1.46	2.10	1.42	0.97	1.18	1.27	1.32	1.34	1.89
346134	Hs.92198	ESTs, Highly similar to calcium-regulated heat stable protein CRHSP-24 [H.sapiens]	2.43	2.40	1.29	1.58	1.80	2.03	2.83	1.80	2.25	1.66	3.26	2.30	2.60	2.40	1.52	1.67	1.44	1.16	1.92	1.85	1.07	0.95
214731	Hs.174174	KIAA0601 protein	1.43	1.23	0.91	1.63	1.26	1.63	1.40	0.76	0.74	0.86	1.03	0.85	0.66	0.76	1.26	0.86	0.99	1.29	1.27	1.18	1.21	1.69
208531	Hs.7994	ESTs, Weakly similar to CGI-69 protein [H.sapiens]	1.14	1.59	0.74	1.47	1.14	1.27	0.86	1.10	1.96	0.80	1.46	1.52	1.77	0.96	1.55	1.74	1.35	1.07	1.29	0.69	1.00	0.86
141845	Hs.19280	KIAA0544 protein	1.39	0.95	0.63	1.07	3.67	0.99	1.42	1.34	1.42	1.72	1.51	1.30	0.80	0.44	1.73	0.93	0.86	1.76	2.74	0.83	2.14	1.39
812266	Hs.239114	mannosidase, alpha, class 1A, member 2	3.58	4.21	3.32	2.55	2.78	2.05	3.55	2.09	1.76	2.84	2.34	2.91	0.75	1.28	2.43	2.35	3.85	1.71	3.01	1.35	1.60	1.67
322794	Hs.43864	ESTs, Weakly similar to C10G11.5 [C.elegans]	1.18	1.37	1.34	1.04	1.66	1.05	1.34	1.49	1.31	1.47	1.60	1.62	0.79	0.84	1.75	1.71	1.42	1.32	1.31	1.21	1.80	0.83
66354	Hs.173684	ESTs, Highly similar to NY-REN-37 antigen [H.sapiens]	0.83	1.12	0.87	1.79	1.38	1.23	0.80	0.96	1.21	0.61	1.82	1.09	0.97	0.65	0.93	1.25	0.79	1.33	1.09	0.89	1.11	1.31
196866	Hs.117741	ESTs, Weakly similar to ORF YDL040c [S.cerevisiae]	2.49	2.28	1.70	2.44	2.41	2.16	2.36	1.83	1.62	2.03	1.88	0.90	0.40	0.32	0.62	1.29	2.12	2.31	2.15	1.88	2.75	2.78
204211	Hs.33930	ESTs	1.29	1.07	0.58	0.84	1.54	1.68	0.32	0.71	0.59	0.40	2.83	2.96	1.75	1.75	2.18	1.05	0.78	0.80	0.48	1.00	0.94	1.39
377191	Hs.23528	ESTs, Highly similar to HSPC038 protein [H.sapiens]	1.24	1.03	0.84	0.96	1.01	1.08	1.18	1.26	0.95	1.52	1.15	0.58	1.23	0.60	0.95	0.69	1.02	1.49	0.80	1.51	1.32	1.46
197791	Hs.136309	Chromosome 1 specific transcript KIAA0491	1.89	2.61	1.25	1.06	1.34	1.58	1.04	1.09	1.65	1.65	1.41	0.79	0.58	0.77	1.02	1.16	0.99	1.65	1.16	1.68	2.30	1.57
134523	Hs.24178	microtubule-associated protein like echinoderm EMAP	0.66	0.94	0.27	0.39	1.02	0.51	1.07	0.82	0.63	0.57	0.45	1.12	0.54	0.53	0.87	1.03	1.49	0.94	1.01	0.57	0.85	1.25
198312	Hs.21198	translocase of outer mitochondrial membrane 70 (yeast) homolog A	1.49	1.37	0.99	1.46	1.60	1.46	1.50	1.21	1.76	1.27	1.08	8.79	4.53	4.29	4.47	1.26	1.84	1.21	1.40	1.41	1.26	2.00
230235	Hs.215766	GTP-binding protein	1.26	4.94	1.19	3.63	1.31	3.34	3.24	1.44	1.38	1.64	1.06	1.03	0.86	0.66	0.94	1.08	1.36	0.89	1.02	1.16	1.05	1.71
310493	Hs.24550	fatty-acid-Coenzyme A ligase, long-chain 3	1.11	1.71	0.54	0.89	2.18	0.67	1.29	0.96	1.12	0.95	0.92	0.59	0.81	0.73	0.88	0.71	1.66	1.26	1.57	2.07	1.17	1.54
361485	Hs.227891	ESTs, Weakly similar to KIAA0167 protein [H.sapiens]	0.92	2.17	0.93	1.46	1.92	1.25	1.27	1.33	1.47	2.08	1.38	2.75	1.61	1.97	2.19	1.58	0.95	1.15	1.63	1.14	1.29	1.42
108658	Hs.4084	KIAA1025 protein	1.29	3.99	4.28	5.13	1.48	1.92	2.62	3.81	5.54	4.33	2.60	6.95	4.39	1.80	4.88	1.13	3.47	2.73	5.01	1.15	1.70	2.86
128351	Hs.90680	ESTs, Weakly similar to WD40 protein Ciao 1 [H.sapiens]	1.32	1.65	1.34	1.35	1.28	1.07	0.60	1.16	1.57	1.33	0.93	1.31	1.67	1.83	0.98	1.34	1.12	1.03	0.99	1.00	1.09	1.37
205049	Hs.111676	ESTs, Weakly similar to heat shock protein 27 [H.sapiens]	1.33	1.00	1.54	1.26	4.21	1.87	2.25	3.25	10.49	13.87	2.19	3.09	3.48	1.08	1.83	2.51	6.08	4.21	1.58	1.14	2.71	2.04
201274	Hs.154248	KIAA0549 protein	1.03	1.42	2.05	1.95	2.40	1.75	0.68	1.94	1.88	2.92	1.70	1.85	0.60	1.75	2.34	2.79	1.40	1.42	2.98	1.18	1.27	1.44
137353	Hs.241531	peflin	1.86	1.15	1.43	1.11	1.49	1.24	1.14	1.52	1.58	1.11	1.29	0.95	1.36	1.00	1.74	1.43	1.47	1.61	1.79	0.97	1.71	1.82
292731	Hs.120975	ESTs, Weakly similar to hypothetical protein [H.sapiens]	3.42	1.36	2.79	2.41	1.40	1.66	1.79	2.02	1.74	3.03	1.37	1.68	0.54	0.83	1.16	1.23	2.40	1.65	1.83	0.95	0.74	1.38
198509	Hs.3850	Homo sapiens clone 23596 mRNA sequence	0.92	1.05	1.57	1.01	1.55	0.82	1.22	1.05	0.99	0.80	0.64	0.91	0.66	1.07	1.39	0.86	0.62	0.81	0.90	0.63	0.67	0.92
66894	Hs.13094	ESTs, Weakly similar to ORF YGR101w [S.cerevisiae]	1.83	1.92	0.97	1.16	1.56	0.78	1.53	1.68	1.21	1.55	1.30	1.12	1.05	0.86	1.54	1.14	1.39	1.17	1.26	0.97	1.41	1.62
140289	Hs.144488	ESTs	0.91	0.96	0.87	1.18	1.38	0.88	0.98	1.36	0.89	0.91	0.82	0.63	0.48	0.57	1.21	0.74	0.87	0.82	1.22	1.01	1.20	0.69
132142	Hs.127294	ESTs, Weakly similar to GOLIATH PROTEIN [D.melanogaster]	2.21	2.66	1.64	2.59	2.47	1.73	1.21	3.26	2.71	2.96	2.05	2.16	1.58	1.70	2.91	1.17	3.28	2.64	2.15	1.17	1.97	1.97
145132	Hs.6710	mannose-P-dolichol utilitzation defect 1	0.85	1.04	0.81	0.81	1.73	0.76	1.22	1.57	0.94	1.52	1.38	1.50	1.12	1.24	1.23	1.13	1.08	1.04	1.63	0.62	1.23	0.80
199610	Hs.96657	ESTs, Weakly similar to KIAA0605 protein [H.sapiens]	0.41	0.83	0.65	2.15	1.00	0.50	0.77	0.56	0.55	0.42	0.99	0.82	0.25	0.97	0.35	1.03	0.40	0.79	0.51	0.58	0.51	0.48
290422	Hs.3776	zinc finger protein 216	1.51	1.58	1.16	1.81	2.14	1.15	0.77	1.14	1.11	1.31	1.08	2.28	1.60	1.32	0.48	1.26	1.02	1.89	1.40	1.52	2.06	1.65
124629	Hs.179817	DKFZP586F0222 protein	2.13	0.82	1.00	1.38	1.26	0.98	0.74	1.30	0.78	0.70	1.51	0.87	1.26	0.72	1.27	0.98	0.96	1.44	1.13	0.89	1.45	1.44
161992	Hs.234680	Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616)	0.46	0.32	0.31	1.27	0.54	0.31	0.24	0.32	0.93	0.32	0.40	0.25	0.43	0.24	0.37	0.74	0.42	0.70	0.53	0.30	0.27	0.27
191882	Hs.169764	ESTs	1.28	2.18	0.72	1.20	1.64	1.32	1.28	1.33	1.25	1.58	1.74	3.53	2.34	2.25	3.25	1.42	1.05	1.79	1.96	0.95	1.81	2.11
129355	Hs.239641	ESTs, Weakly similar to cDNA EST yk288h5.5 comes from this gene [C.elegans]	1.64	1.78	1.07	1.84	1.33	0.84	1.30	0.90	1.32	1.40	1.87	1.12	0.83	1.10	1.00	2.15	1.28	1.44	1.56	0.91	1.23	1.76
549016	Hs.21332	ESTs, Moderately similar to R27216_1 [H.sapiens]	1.46	1.94	1.06	1.52	1.89	1.13	1.33	1.08	1.69	1.66	1.40	1.79	0.96	1.13	1.15	1.59	1.49	1.06	1.64	1.19	1.26	1.38
122077	Hs.93832	Homo sapiens clone 24483 unknown mRNA, parital cds	1.19	1.14	0.54	1.42	0.97	1.03	1.21	0.75	1.46	1.02	0.97	0.81	0.86	0.97	1.49	1.47	1.19	0.97	1.58	0.93	0.88	1.30
299085	Hs.20993	ESTs, Highly similar to NY-REN-2 antigen [H.sapiens]	1.71	1.64	0.99	1.41	1.41	1.21	1.36	1.24	1.47	1.11	1.06	1.44	0.77	0.86	1.52	1.02	1.21	1.73	1.83	1.75	1.50	1.53
202034	Hs.107001	ESTs, Highly similar to 45kDa splicing factor [H.sapiens]	2.10	5.59	1.40	3.12	2.72	3.01	4.47	2.05	1.46	2.14	1.78	2.00	0.94	0.96	1.53	1.34	1.77	2.34	2.19	1.20	2.42	2.02
121533	Hs.27721	ESTs, Weakly similar to MMSET type I [H.sapiens]	1.43	4.23	1.38	1.50	2.57	2.08	1.55	2.43	1.92	5.06	2.36	2.36	1.22	1.02	2.07	1.54	2.33	1.54	2.13	1.14	1.64	1.54
246541	Hs.105684	cyclin-dependent kinase-like 1 (CDC2-related kinase)	1.04	1.18	1.45	1.30	1.70	1.23	1.35	0.88	0.63	1.45	0.87	0.98	0.97	1.19	1.04	1.37	1.05	1.15	1.01	0.92	1.04	1.84

120362	Hs.143601	ESTs, Moderately similar to 67A9.b [D.melanogaster]	1.55	1.30	0.68	0.71	1.13	0.82	0.47	0.88	0.67	0.92	0.60	2.77	1.87	1.90	2.39	0.61	0.57	1.03	1.30	0.96	0.98	0.99
124405	Hs.107528	ESTs, Highly similar to CGI-103 protein [H.sapiens]	1.83	1.19	0.43	0.50	1.28	1.53	0.50	0.85	0.63	0.94	0.58	1.39	0.88	0.79	1.01	0.73	1.25	0.62	0.59	0.84	0.68	0.39
144915	Hs.8148	Homo sapiens clone 24856 mRNA sequence, complete cds	1.74	1.84	1.29	1.25	2.13	1.12	2.34	1.67	1.68	2.46	1.29	6.66	1.38	2.38	2.89	0.68	1.56	2.13	2.29	1.22	1.04	1.71
232908	Hs.9601	ESTs, Highly similar to CGI-106 protein [H.sapiens]	0.49	0.66	0.61	0.74	0.54	0.59	0.75	0.76	0.47	0.86	0.75	1.38	0.90	1.35	1.32	0.53	0.52	0.60	0.65	0.36	0.45	0.88
126412	Hs.215857	ring finger protein 14	0.60	0.61	0.35	0.42	0.90	0.55	0.45	0.54	0.63	0.89	0.47	1.00	2.17	1.20	2.06	0.74	0.86	0.80	0.62	0.68	0.72	1.14
359713	Hs.221189	ESTs, Weakly similar to 15-HYDROXYPROSTAGLANDIN DEHYDROGENASE [H.sapiens]	0.75	0.70	1.11	0.84	1.27	0.45	0.68	0.69	0.50	2.11	1.00	1.20	1.17	0.79	2.14	0.81	1.16	1.00	0.95	1.28	0.77	0.36
244205	Hs.32062	ESTs	2.73	1.61	0.40	1.09	1.97	1.05	1.65	1.12	1.01	2.61	0.68	2.10	0.25	2.10	2.09	0.46	1.60	1.71	2.06	1.64	1.67	1.76
121625	Hs.188497	ESTs	2.28	0.83	0.86	1.29	3.03	1.36	1.65	1.36	1.48	2.44	1.30	2.31	1.19	1.36	1.68	1.78	1.22	1.08	1.28	1.89	0.48	1.97
66694	Hs.6127	ESTs, Weakly similar to prostate-specific transglutaminase [H.sapiens]	1.64	0.79	2.06	1.63	1.36	0.89	2.27	0.34	1.43	2.66	0.53	2.44	1.67	1.45	1.37	0.62	1.35	1.16	0.93	1.59	0.76	1.28
110519	Hs.188481	ESTs	2.98	0.73	4.95	1.53	1.10	0.45	0.89	0.56	1.74	3.45	0.47	8.68	4.15	3.51	5.40	2.10	3.61	2.27	2.31	0.91	0.54	1.57
197474	Hs.19081	ESTs	1.79	0.51	0.23	0.23	1.31	0.69	1.01	0.55	0.75	1.77	0.97	2.54	0.69	1.20	1.58	0.59	1.45	1.81	1.89	0.89	0.35	0.91
195947	Hs.188570	ESTs	1.35	0.71	0.37	0.39	2.07	0.78	2.98	3.15	1.21	1.80	0.63	2.19	0.39	1.02	1.39	0.38	2.69	1.90	3.72	2.30	1.16	0.91
344757	Hs.83513	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.58	0.70	0.40	0.65	1.79	1.33	2.98	1.11	1.18	1.93	0.84	0.14	0.04	0.05	0.06	0.40	2.11	1.67	3.80	0.96	0.85	0.91
241824	Hs.30237	ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	1.40	2.24	1.10	0.87	1.97	0.37	3.65	0.81	1.35	2.32	0.77	3.20	0.86	1.54	1.93	0.76	1.98	1.98	2.82	2.19	0.61	2.17
247233	Hs.193379	ESTs	1.43	0.62	0.26	0.26	1.16	0.58	3.30	0.46	1.29	2.09	0.74	4.96	1.64	2.11	2.98	0.34	1.94	1.70	2.26	0.97	0.40	3.32
213527	Hs.38931	ESTs	1.92	0.69	0.40	0.43	2.84	0.57	3.24	1.57	0.82	1.84	0.90	2.55	1.45	1.26	2.44	0.43	1.48	2.09	2.34	0.88	0.64	0.91
247925	Hs.178614	down-regulated in metastasis	1.65	1.04	1.83	1.23	1.66	0.80	3.19	0.47	0.63	2.65	0.54	2.43	0.88	1.30	1.76	0.53	2.45	1.10	2.27	1.28	0.42	0.81
292207	Hs.49455	EST	1.74	0.71	0.34	0.35	2.26	0.62	2.71	0.83	1.26	1.73	1.58	2.23	0.60	1.12	1.92	0.44	1.98	1.42	2.22	0.94	0.64	2.01
113488	Hs.184407	ESTs	1.29	0.66	1.43	0.55	1.81	0.52	2.04	0.73	1.66	2.49	0.61	2.96	1.02	1.21	2.28	0.43	2.06	2.01	2.32	1.22	0.26	0.94
295939	Hs.75470	hypothetical protein, expressed in osteoblast	1.04	0.81	0.31	0.64	0.88	0.47	2.00	1.24	0.85	1.19	0.51	1.72	0.33	0.86	1.26	0.79	1.19	0.46	0.73	2.17	0.89	0.81
137417	Hs.25276	ESTs, Weakly similar to putative p150 [H.sapiens]	2.11	1.51	0.39	0.90	1.53	1.04	2.16	2.09	1.46	3.89	0.79	8.49	5.50	4.64	10.86	0.55	1.33	1.80	1.83	1.64	0.49	0.84
128738	Hs.94952	ESTs, Highly similar to transcription elongation factor TFIIS.h [H.sapiens]	3.04	0.59	1.95	1.75	1.11	1.99	3.22	0.08	1.84	2.67	0.69	5.18	1.19	1.35	3.08	0.57	3.93	2.28	5.84	1.93	0.80	2.69
245585	Hs.20535	ESTs	0.94	0.59	0.46	1.16	0.94	0.94	1.92	0.96	1.32	2.37	0.37	5.10	3.31	4.34	3.48	0.85	1.79	1.53	0.85	1.13	0.38	0.91
141854	Hs.207693	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.68	1.30	0.57	0.70	1.11	0.56	2.31	1.37	1.07	1.94	0.50	1.87	0.38	1.29	1.33	0.57	3.58	0.71	1.58	1.77	1.15	1.28
208161	Hs.182238	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polype	0.68	0.49	0.69	0.79	0.66	1.02	0.73	0.50	0.84	1.23	0.71	0.72	0.92	0.56	0.68	0.95	1.41	0.61	0.69	0.90	0.75	0.95
211878	Hs.247123	ESTs	1.65	0.73	1.48	0.57	1.33	0.44	1.86	0.23	1.11	2.55	0.19	1.70	0.87	0.86	1.52	1.79	2.11	1.71	2.64	1.58	0.46	0.61
243260	Hs.174877	ESTs	2.89	1.21	3.28	3.27	1.49	2.23	1.31	1.40	2.49	2.91	0.37	1.50	1.37	1.40	1.46	0.64	2.13	0.85	0.62	1.24	0.53	1.86
208993	Hs.80857	ESTs, Weakly similar to dTDP-D-glucose 4,6-dehydratase [H.sapiens]	1.02	0.67	0.38	0.59	1.58	0.75	1.96	0.66	0.76	6.93	0.59	0.41	0.90	0.54	0.30	0.49	1.33	1.25	0.81	1.04	0.54	3.52
345128	Hs.58215	ESTs, Moderately similar to rhotekin [M.musculus]	1.60	0.53	0.74	1.01	0.86	0.72	1.09	0.27	1.13	1.28	0.95	1.02	1.54	1.51	1.51	0.83	0.87	0.82	1.01	0.61	0.27	0.97
197933	Hs.35552	ESTs	1.33	0.55	0.37	0.77	2.89	0.70	0.94	1.01	0.73	2.47	0.74	2.15	1.07	1.16	1.80	0.46	2.28	1.31	1.59	1.00	0.91	2.50
356707	Hs.111279	ESTs, Weakly similar to unnamed protein product [H.sapiens]	1.19	0.90	0.77	1.42	1.98	0.97	1.25	1.64	0.70	1.79	0.69	1.25	0.95	1.11	1.22	1.24	1.59	0.88	1.90	1.21	0.62	1.13
786048	Hs.108371	E2F transcription factor 4, p107/p130-binding	1.07	0.90	0.54	0.69	0.94	0.79	0.84	0.77	0.76	0.90	0.62	0.78	0.61	0.84	0.59	0.78	0.71	0.73	1.10	0.68	1.57	0.94
340722	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34) fusion gene [H.sapiens]	3.13	0.72	1.73	1.92	1.07	1.49	1.21	0.27	1.97	0.95	0.62	0.70	1.11	0.47	1.11	0.72	1.73	0.65	0.38	1.05	0.25	1.34
35191	Hs.118684	stromal cell-derived factor 2	1.11	0.80	0.61	0.60	1.14	0.65	1.68	1.14	0.82	2.06	0.68	1.34	1.47	1.62	1.13	0.71	1.60	1.10	1.67	1.63	0.75	1.15
194986	Hs.91065	ESTs, Moderately similar to proliferation potential-related protein [M.musculus]	1.07	0.81	0.54	0.71	1.72	0.86	1.23	0.87	1.15	1.75	0.84	3.85	1.80	1.47	2.60	1.28	0.61	0.86	1.31	0.55	0.54	1.99
739625	Hs.227489	KIAA0973 protein	1.13	0.95	2.62	2.01	1.06	2.44	1.00	1.18	2.74	3.19	2.37	5.65	2.62	5.65	9.35	3.30	1.52	0.88	0.90	1.47	0.95	1.68
366580	Hs.77735	fibrogenic lymphokine	1.22	1.40	0.72	0.99	1.10	1.72	1.01	1.44	1.62	1.73	1.51	1.75	1.47	2.65	1.34	1.73	1.22	1.40	1.32	1.07	1.14	1.75
141677	Hs.28483	pregnancy specific beta-1-glycoprotein 9	3.53	2.46	1.31	2.78	3.61	1.72	3.50	2.02	2.09	3.75	2.04	6.76	1.77	4.73	7.02	0.88	3.69	5.32	4.52	1.50	1.45	1.91
247901	Hs.187579	ESTs, Moderately similar to 17-beta-hydroxysteroid dehydrogenase type 7 [M.musculus]	1.90	0.76	0.68	0.88	2.37	1.44	1.52	1.44	1.02	1.96	0.99	4.53	2.68	2.39	4.43	1.32	2.05	1.19	2.40	1.69	1.05	1.51
240702	Hs.108665	ESTs, Weakly similar to CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA [H.sapiens]	1.19	1.68	0.88	0.68	1.37	0.77	1.52	0.90	0.89	2.85	0.77	1.73	0.61	1.85	1.37	0.76	1.30	0.92	1.49	0.85	1.18	1.25
129502	Hs.21871	ESTs, Moderately similar to ninein [M.musculus]	2.04	0.73	0.46	0.54	2.31	1.42	0.66	0.90	0.71	1.25	0.87	3.06	1.05	1.10	1.56	2.01	1.76	1.59	2.14	0.59	0.72	1.71
192481	Hs.124085	KIAA0921 protein	3.09	0.65	1.07	1.64	0.88	1.07	0.48	0.32	1.64	2.34	0.64	1.82	3.69	2.13	1.64	2.99	1.79	1.45	0.52	1.05	0.44	1.01
364840	Hs.5900	5'-3' exoribonuclease 2	0.96	0.63	0.62	0.62	0.85	0.78	0.47	0.73	0.77	0.82	0.71	0.41	0.46	0.65	0.63	1.22	0.65	1.14	1.10	0.87	1.14	1.16
137063	Hs.173880	interleukin 1 receptor accessory protein	3.23	0.55	3.26	1.14	1.13	0.42	1.78	0.20	1.96	2.84	0.37	2.52	0.82	0.93	1.71	2.31	1.66	1.53	1.86	1.64	0.61	1.83
156211	Hs.64173	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD,	1.15	0.60	0.26	0.38	1.81	0.86	1.52	0.81	0.77	1.87	1.37	2.28	0.83	1.28	1.74	0.83	1.37	1.66	1.92	1.40	0.94	0.91
194468	Hs.193228	ESTs, Moderately similar to ALANINE--GLYOXYLATE AMINOTRANSFERASE 2 PRECURSOR	1.76	0.63	0.29	0.30	2.31	0.48	2.47	0.75	1.36	2.33	0.64	1.99	0.21	0.51	1.31	0.36	1.95	1.56	2.16	0.62	0.54	2.68
361656	Hs.103267	ESTs, Moderately similar to Rabin3 [R.norvegicus]	1.31	0.68	0.27	0.30	0.88	0.46	1.10	0.35	0.61	1.61	0.25	0.77	0.26	0.53	0.32	0.33	0.96	1.12	1.12	1.04	0.43	1.30
47043	Hs.9973	ESTs	3.36	4.52	2.02	2.11	3.04	1.46	6.04	3.40	3.40	3.69	2.51	9.11	5.27	5.55	9.34	1.11	3.70	6.75	8.44	1.37	1.42	3.08
297148	Hs.220656	ESTs, Moderately similar to TRANSLATION INITIATION FACTOR EIF-2B ALPHA SUBUNIT [H	1.68	0.61	0.37	0.35	1.80	0.83	1.95	0.49	1.28	1.37	0.78	2.54	0.99	1.48	1.67	0.35	2.05	1.57	1.39	1.15	0.45	0.91
123087	Hs.118910	tumor susceptibility gene 101	0.80	0.76	0.83	0.53	1.71	0.18	0.72	0.23	1.06	2.41	0.30	1.54	0.70	0.98	0.99	0.28	0.73	0.95	0.99	0.85	0.27	0.40
240589	Hs.7510	mitogen-activated protein kinase kinase kinase 7	1.23	0.91	0.53	0.85	2.57	1.47	0.57	1.04	0.87	2.05	0.73	3.13	0.85	1.21	1.48	0.50	1.22	1.42	1.52	0.98	1.18	1.92
306484	Hs.22630	cofactor required for Sp1 transcriptional activation, subunit 6 (77kD)	1.75	1.14	1.45	1.42	1.69	1.39	1.06	0.81	1.54	2.08	0.91	1.41	0.79	0.83	1.17	1.13	1.28	1.10	0.95	1.18	0.76	0.89
122063	Hs.194693	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	2.10	0.65	2.26	0.97	1.58	2.02	1.02	1.91	1.81	2.11	0.52	4.25	1.24	2.88	2.11	2.38	3.38	2.43	3.60	0.75	0.28	0.91
292519	Hs.31731	antioxidant enzyme B166	0.46	0.45	0.47	0.30	0.47	0.37	0.74	0.55	0.41	0.79	0.35	0.53	0.21	0.60	0.39	0.42	0.58	0.50	0.65	0.56	0.44	1.11
246620	Hs.8215	ESTs, Weakly similar to double-stranded RNA-binding nuclear protein DRSBP76 [H.sapiens	0.52	0.50	0.50	0.35	0.47	0.45	0.79	0.33	0.51	1.69	0.23	0.70	0.38	0.76	0.56	0.58	0.78	0.60	0.81	0.45	0.33	0.40
235056	Hs.78019	Homo sapiens clone 24432 mRNA sequence	0.98	0.53	0.42	0.68	1.26	0.88	0.58	0.58	1.23	2.05	0.71	0.96	1.06	0.82	0.59	0.76	0.77	0.62	0.90	0.53	0.64	1.05
199995	Hs.102021	ESTs	1.44	1.02	1.00	0.90	1.17	0.61	1.30	0.71	1.20	1.61	0.40	2.05	1.17	1.34	1.29	0.54	1.60	1.39	1.66	1.09	0.79	0.92
897901	Hs.168516	ESTs, Moderately similar to NuMA protein [H.sapiens]	2.48	0.81	1.01	1.00	0.96	0.94	0.43	0.54	1.04	2.31	0.43	2.17	2.90	1.25	1.89	0.81	2.13	1.42	0.41	0.76	0.59	0.61
245426	Hs.167822	ESTs, Highly similar to Ran-binding protein 2 [H.sapiens]	2.93	0.74	20.15	2.96	1.96	2.45	4.09	3.48	2.60	2.39	1.06	7.74	4.36	4.58	7.04	2.66	4.89	4.67	5.45	2.28	0.96	2.48
321354	Hs.18349	ESTs, Weakly similar to partial CDS [C.elegans]	1.42	0.63	0.42	0.64	0.92	0.70	0.69	0.77	1.54	1.17	0.57	0.62	0.37	0.56	0.71	0.76	1.33	1.42	1.09	0.96	0.50	0.91
49591	Hs.79876	steroid sulfatase (microsomal), arylsulfatase C, isozyme S	0.52	0.60	0.70	1.15	0.65	0.82	0.67	0.65	0.74	0.37	0.71	0.46	1.38	1.09	1.23	1.12	0.64	0.80	0.65	0.69	0.90	0.60
486544	Hs.164915	small nuclear RNA activating complex, polypeptide 3, 50kD	2.33	1.91	1.75	2.28	2.05	0.84	1.32	2.24	2.35	1.59	0.81	1.01	1.93	0.92	1.77	0.34	1.67	1.59	1.73	0.98	1.58	1.44
768561	Hs.340	small inducible cytokine A2 (monocyte chemotactic protein 1, homologous to mouse Sig-i	3.86	18.78	2.58	14.53	4.19	3.32	2.07	13.69	4045.48	5362.24	9.07	14.76	4.77	2.78	12.17	1.11	4.90	5.96	3.29	1.22	3.04	2.11
49970	Hs.83715	Sjogren syndrome antigen B (autoantigen La)	0.93	1.63	1.30	1.84	1.29	1.01	1.37	1.05	0.95	1.03	1.47	0.64	0.74	0.41	0.76	0.50	0.95	1.04	1.05	0.69	2.71	1.79
754998	Hs.2943	signal recognition particle 19kD	1.60	2.05	1.34	1.77	3.45	1.01	1.06	2.24	2.32	2.08	1.71	1.09	0.87	0.98	1.30	0.57	0.93	1.37	2.38	1.43	1.16	1.48
47542	Hs.86948	small nuclear ribonucleoprotein D1 polypeptide (16kD)	1.43	1.88	1.10	0.94	1.00	1.12	1.30	0.89	0.71	0.85	0.97	0.69	0.68	0.54	0.83	0.57	0.60	0.64	1.14	0.83	0.90	1.16
135221	Hs.2962	S100 calcium-binding protein P	0.19	0.16	0.08	0.12	0.48	0.15	0.19	0.31	0.07	0.15	0.37	0.05	0.03	0.19	0.16	0.17	0.16	0.19	0.32	0.57	0.40	0.20
161456	Hs.181062	serum amyloid A1	0.73	4.92	0.24	0.84	4.16	0.80	3.06	1.52	0.76	0.85	2.24	1.12	0.40	0.75	0.99	0.61	0.38	1.76	1.25	1.08	1.67	1.12
39798	Hs.8889	serine hydroxymethyltransferase 1 (soluble)	0.57	1.07	0.81	1.56	1.34	0.71	0.47	0.83	0.76	0.66	0.74	1.13	0.62	1.28	0.70	0.84	0.55	0.60	0.57	0.68	0.93	1.01
40704	Hs.75232	SEC14 (S. cerevisiae)-like 1	1.12	2.23	1.16	1.29	1.79	1.26	0.97	1.60	1.14	1.69	1.74	1.92	2.06	1.74	0.44	1.00	1.05	1.41	0.75	0.99	1.58	1.23
149013	Hs.75744	S-adenosylmethionine decarboxylase 1	0.90	0.60	1.63	2.44	0.95	1.32	0.91	0.57	1.06	0.89	1.08	1.26	0.47	1.02	0.91	0.69	0.83	0.89	0.61	1.05	0.69	0.97
809578	Hs.76194	ribosomal protein S5	0.33	0.48	0.74	0.45	0.57	0.24	0.72	0.32	0.42	0.34	0.26	0.66	0.64	0.41	0.51	0.40	0.54	0.63	0.46	0.45	0.32	0.49
810802	Hs.31638	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	1.66	1.64	0.81	1.66	1.60	1.46	1.81	1.21	2.43	1.57	1.35	1.50	1.18	0.97	0.99	0.69	1.57	1.63	1.43	1.56	1.77	1.43
26616	Hs.79411	replication protein A2 (32kD)	2.00	1.26	1.62	1.61	1.08	1.53	0.88	0.87	1.32	1.56	0.89	2.31	1.46	1.33	1.47	1.79	1.51	1.20	1.30	1.14	0.65	0.94
204299	Hs.1608	replication protein A3 (14kD)	2.23	1.96	1.24	1.60	2.03	1.58	1.48	1.41	1.27	1.66	1.16	0.92	0.77	0.85	0.97	0.74	0.60	1.21	2.24	1.00	2.21	0.88
51981	Hs.99858	ribosomal protein L7a	1.52	0.87	0.43	0.66	0.67	0.51	0.57	0.87	0.50	0.73	1.08	0.44	0.47	0.35	0.65	0.65	0.50	1.24	1.03	0.77	2.06	0.48
322561	Hs.184014	ribosomal protein L31	1.19	1.48	0.51	0.63	0.90	0.69	1.63	0.76	0.65	0.60	0.84	0.59	0.36	0.53	0.79	0.48	0.69	1.27	1.06	0.83	0.75	1.12
810617	Hs.184108	ribosomal protein L21	0.79	1.25	0.74	1.15	1.07	0.68	1.39	0.76	0.46	0.38	0.84	0.86	0.25	0.36	1.03	0.61	0.49	1.13	1.08	0.82	0.78	0.47
549101	Hs.75879	ribosomal protein L19	0.77	1.04	0.56	0.95	1.02	0.77	1.71	1.61	0.67	0.80	1.63	0.46	0.45	0.37	1.13	1.09	0.89	1.38	1.41	1.76	1.71	0.93
203275	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.58	3.01	1.98	3.27	1.75	1.97	2.87	2.09	1.31	2.13	1.93	1.97	2.16	1.12	1.83	1.05	1.60	1.53	2.59	0.96	1.15	2.88
47559	Hs.73957	RAB5A, member RAS oncogene family	1.22	1.19	1.54	1.33	1.67	0.97	0.99	1.19	1.00	1.10	1.01	0.99	0.85	1.53	0.77	1.37	1.61	1.14	1.10	1.09	1.10	1.59

214537	Hs.166563	replication factor C (activator 1) 1 (145kD)	1.52	2.62	1.59	1.28	1.35	1.50	2.02	1.77	1.73	1.77	1.80	1.99	1.45	1.06	1.91	0.69	0.99	1.79	1.59	0.88	1.64	1.65
159118	Hs.75082	ras homolog gene family, member G (rho G)	1.10	2.10	1.32	1.46	1.62	1.25	1.37	1.68	2.22	1.48	1.61	2.11	1.23	1.90	1.36	1.79	0.85	1.02	1.30	1.14	1.00	1.19
214133	Hs.75243	female sterile homeotic-related gene 1 (mouse homolog)	1.27	3.24	2.10	2.10	1.38	1.37	1.38	2.32	2.32	2.51	2.21	2.17	1.34	1.54	1.84	2.01	1.68	0.95	2.11	1.23	1.70	3.41
280752	Hs.79362	retinoblastoma-like 2 (p130)	1.16	0.70	0.99	0.61	0.79	0.62	0.67	0.66	1.02	4.03	0.54	1.73	0.99	1.39	1.36	0.67	1.16	1.14	1.39	0.92	0.77	0.59
230205	Hs.119007	RAB4, member RAS oncogene family	0.98	0.67	0.95	1.33	1.13	0.95	0.53	0.96	0.56	0.41	1.13	0.81	0.68	0.81	1.30	0.64	0.60	0.91	0.71	0.80	1.13	0.59
770901	Hs.147663	protein tyrosine phosphatase, non-receptor type 9	1.24	1.37	1.77	1.31	1.60	1.18	1.31	1.27	1.26	1.01	1.40	1.37	0.83	1.33	1.28	1.20	0.88	1.32	1.13	0.84	1.90	1.35
150221	Hs.144137	ESTs	1.53	0.85	0.86	1.46	1.28	0.89	0.56	1.03	1.27	0.73	0.79	2.76	1.21	1.00	1.17	0.60	1.28	1.19	0.86	0.52	1.30	0.96
30093	Hs.24763	RAN binding protein 1	1.51	1.85	2.74	1.99	2.00	1.33	2.61	1.67	1.35	1.57	1.49	0.86	0.60	0.79	1.03	0.95	0.96	1.37	1.62	1.21	1.57	1.59
340630	Hs.248	mitogen-activated protein kinase kinase kinase 8	1.19	0.91	1.30	0.91	1.03	0.75	0.60	0.89	1.12	0.53	0.91	0.73	0.66	0.84	0.92	0.75	0.60	0.52	0.67	0.85	1.16	1.23
756452	Hs.75516	tyrosine kinase 2	1.26	2.42	1.79	1.91	2.10	1.76	1.78	2.07	1.56	2.65	1.10	2.55	1.31	1.71	2.07	1.11	1.40	1.12	1.81	0.97	1.37	1.20
813742	Hs.90572	PTK7 protein tyrosine kinase 7	1.20	2.59	2.37	1.49	2.76	0.73	3.17	2.77	3.87	1.36	1.57	1.86	0.80	2.35	1.61	0.67	0.71	0.89	1.36	0.83	2.37	1.61
321661	Hs.171734	protein phosphatase 2, regulatory subunit B (B56), gamma isoform	0.94	0.85	0.86	1.33	1.39	1.12	0.63	1.21	0.78	0.74	1.40	0.90	0.84	0.75	1.26	0.79	0.89	1.10	0.86	0.98	1.68	0.74
132911	Hs.21537	protein phosphatase 1, catalytic subunit, beta isoform	1.98	3.31	1.66	1.17	2.48	1.33	1.99	1.18	0.95	1.30	1.00	0.66	0.31	0.76	1.02	0.85	1.64	1.00	1.76	1.27	2.90	1.25
359184	Hs.30376	protein kinase, interferon-inducible double stranded RNA dependent	3.30	3.29	2.31	2.38	1.98	2.67	0.34	4.63	4.04	3.13	1.11	7.53	2.06	3.31	3.67	1.06	3.06	1.94	2.23	1.81	1.71	2.49
811012	Hs.1519	protein kinase, cAMP-dependent, regulatory, type I, beta	0.97	2.13	1.07	1.42	1.75	1.37	2.13	1.57	1.22	1.38	1.59	3.39	4.20	3.56	3.61	0.72	1.29	1.33	1.58	0.86	1.71	1.49
167280	Hs.107101	ESTs	1.13	2.06	1.72	1.09	1.76	1.18	1.16	1.30	1.28	1.56	1.81	2.13	0.48	2.12	2.00	0.87	1.02	1.15	1.28	1.62	1.23	1.10
134544	Hs.82159	proteasome (prosome, macropain) subunit, alpha type, 1	0.78	0.97	0.49	0.75	1.75	1.55	0.95	0.69	0.75	0.53	1.95	0.60	0.54	0.81	0.83	0.94	0.70	0.87	1.20	0.79	0.74	0.82
130541	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antigen)	2.57	3.18	5.63	6.22	3.48	3.81	3.40	3.26	8.44	5.32	4.12	6.62	2.07	3.21	5.11	3.96	4.65	4.35	5.91	2.66	1.65	1.43
40643	Hs.76144	platelet-derived growth factor receptor, beta polypeptide	2.27	2.46	6.26	3.06	3.79	2.72	2.77	3.49	6.17	5.14	3.86	4.78	2.11	2.20	3.51	2.67	2.73	2.60	4.70	2.72	2.95	1.88
529861	Hs.77060	proteasome (prosome, macropain) subunit, beta type, 6	1.09	0.92	0.87	1.37	1.43	1.06	0.69	1.14	0.83	1.00	1.17	0.96	0.76	0.78	1.18	0.72	0.93	1.22	0.95	0.98	1.72	0.76
812048	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrom	0.94	0.91	0.65	0.92	1.42	0.63	0.92	0.50	0.81	0.56	0.59	0.34	0.17	0.48	0.33	0.73	0.94	0.92	0.53	0.51	0.73	0.63
810017	Hs.179657	plasminogen activator, urokinase receptor	1.47	2.08	1.13	0.79	1.89	0.91	1.32	1.62	3.04	1.30	1.39	1.37	0.61	1.34	0.60	1.56	0.96	1.21	1.63	1.11	0.92	2.12
244307	Hs.82085	plasminogen activator inhibitor, type I	0.71	0.78	0.52	0.71	1.34	0.61	0.46	0.90	2.98	1.45	0.90	2.61	0.92	1.91	1.40	0.79	0.57	1.14	0.73	0.69	0.57	0.45
809981	Hs.2706	glutathione peroxidase 4 (phospholipid hydroperoxidase)	0.67	0.95	0.47	0.75	0.63	0.71	0.39	1.29	0.92	1.50	1.03	1.52	1.59	1.14	1.25	1.28	0.80	0.48	1.04	0.81	0.89	0.68
204897	Hs.75648	phospholipase C, gamma 2 (phosphatidylinositol-specific)	3.74	3.37	1.34	2.40	3.31	3.03	3.01	1.89	1.93	2.27	1.65	3.43	0.76	1.24	1.35	0.55	1.12	1.85	1.04	0.64	1.39	1.80
51916	Hs.245990	EST	0.96	0.79	1.57	1.05	0.69	1.04	1.61	1.16	1.26	2.67	1.04	1.51	1.34	1.56	1.85	0.86	1.36	1.70	0.89	2.37	1.58	1.30
246869	Hs.62112	zinc finger protein 207	1.53	1.19	0.87	1.14	1.21	1.00	1.25	1.20	1.19	0.91	1.11	0.50	0.77	0.71	0.85	0.72	1.23	1.29	1.47	1.56	1.39	1.29
300474	Hs.5344	adaptor-related protein complex 1, gamma 1 subunit	1.20	0.71	0.69	0.89	1.04	0.72	0.81	0.53	1.03	0.98	0.79	0.53	0.93	0.77	0.49	0.93	1.00	0.60	0.62	0.86	0.62	0.48
309894	Hs.15744	SH2-B homolog	0.85	1.03	0.56	0.83	1.36	0.73	0.96	0.89	0.74	1.10	0.59	0.78	1.13	1.27	1.29	0.93	0.88	1.29	1.41	0.56	1.05	0.69
344282	Hs.25821	Fas (TNFRSF6) associated factor 1	1.75	0.72	1.53	2.29	1.56	1.88	1.23	0.71	1.13	0.82	0.96	1.60	2.01	1.85	2.52	1.00	0.95	1.30	0.73	1.36	0.56	1.05
153743	Hs.107538	ESTs, Moderately similar to /prediction	1.69	2.13	1.23	1.97	2.37	1.62	2.69	1.83	1.36	1.45	1.50	0.96	1.06	1.55	1.64	1.70	1.41	1.32	2.03	1.16	2.21	1.97
123425	Hs.15282	ESTs, Moderately similar to RNA helicase HDB/DICE1 [H.sapiens]	2.18	1.05	1.34	2.19	1.48	1.89	1.21	0.86	1.29	1.97	1.28	1.32	0.68	0.96	1.30	0.81	0.78	1.40	1.44	0.86	0.55	0.67
297086	Hs.5233	eukaryotic translation initiation factor 4E binding protein 2	1.66	1.55	1.47	1.36	1.34	0.86	1.73	0.92	1.48	0.91	0.71	3.84	3.02	2.84	1.02	2.52	1.18	1.21	1.40	1.05	0.93	1.12
127243	Hs.19631	ESTs	2.21	2.06	1.56	2.11	1.54	1.84	1.30	1.34	2.14	1.76	1.88	2.08	1.17	1.18	0.59	2.08	1.62	1.50	2.81	1.44	1.27	1.32
66792	Hs.9552	binder of Arl Two	1.72	1.25	0.77	0.79	1.11	0.84	0.84	0.75	1.29	1.11	1.08	1.53	1.09	0.98	1.60	1.06	1.25	1.22	1.36	0.66	1.22	1.12
142259	Hs.164036	tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; H	1.04	1.40	1.37	1.81	0.73	3.10	1.29	0.87	1.84	1.62	0.88	1.29	0.59	0.79	1.05	1.43	1.55	1.39	0.85	0.90	0.86	1.30
242823	Hs.20787	ESTs	1.46	1.41	1.15	1.59	1.51	1.16	1.92	0.91	1.52	1.38	1.34	1.23	0.85	1.16	1.25	2.42	1.35	1.03	1.23	1.23	0.81	0.97
196148	Hs.14478	ESTs	1.21	1.78	0.87	1.24	3.39	1.50	0.78	1.64	1.29	1.15	1.74	1.35	0.80	1.34	1.21	1.26	1.41	2.00	0.86	2.34	2.09	0.91
130781	Hs.101414	KIAA0557 protein	1.10	1.38	1.06	1.05	1.99	1.21	2.02	1.91	1.98	1.96	2.80	2.33	2.11	1.09	2.17	2.37	2.26	1.93	2.09	1.07	1.20	1.25
124719	Hs.185030	ESTs	1.81	2.40	2.82	2.55	2.96	1.19	8.43	3.05	4.24	8.22	1.74	4.53	2.91	1.20	1.67	1.58	5.12	2.92	2.85	1.93	2.62	1.17
124090	Hs.74571	ADP-ribosylation factor 1	0.84	1.49	1.15	1.14	2.37	1.28	0.75	1.06	1.46	1.17	1.73	3.26	2.45	1.99	1.94	1.78	1.00	1.21	1.28	1.03	1.16	1.25
362742	Hs.169572	ESTs, Moderately similar to PROFILIN I [H.sapiens]	1.08	1.15	0.93	0.81	1.18	0.95	1.29	1.23	0.86	0.78	0.75	1.87	0.77	1.04	0.91	0.75	0.96	1.20	1.32	1.23	0.92	1.01
45525	Hs.142653	ret finger protein	0.95	2.23	1.84	1.87	2.15	1.48	1.38	1.26	1.97	2.14	1.27	1.48	2.03	1.61	1.63	1.51	1.37	1.39	1.98	1.59	1.84	2.19
246661	Hs.187991	DKFZP564A122 protein	1.54	2.21	4.27	2.27	2.75	1.84	2.16	2.86	2.85	2.20	1.77	4.13	2.42	2.76	3.35	1.71	1.72	2.75	1.79	2.37	2.34	1.59
239958	Hs.15832	DKFZP586P2220 protein	1.96	2.47	2.08	2.35	2.46	1.87	3.22	1.81	1.28	1.86	1.62	1.84	1.61	1.57	2.16	1.36	1.53	1.68	1.96	1.17	2.24	1.16
469704	Hs.27023	KIAA0917 protein	2.44	2.98	1.71	1.54	2.04	0.95	1.66	1.87	1.85	1.75	1.60	1.08	0.52	0.87	1.22	0.52	2.28	1.44	1.97	2.35	1.58	1.09
344251	Hs.93871	ESTs, Weakly similar to Containing ATP/GTP-binding site motif A(P-loop): Similar to C.elec	1.24	0.87	0.67	0.63	1.60	0.80	1.20	0.95	0.81	1.01	0.97	0.94	0.44	0.75	0.63	1.04	0.94	1.03	1.29	0.91	2.00	0.71
358162	Hs.23642	protein predicted by clone 23627	2.05	1.97	1.55	2.10	2.34	2.10	4.00	1.11	1.27	2.51	1.91	1.93	1.53	1.90	2.24	1.62	1.67	1.57	2.82	1.87	1.17	1.15
236055	Hs.165998	DKFZP564M2423 protein	1.84	1.92	1.20	2.24	1.07	1.92	1.84	0.62	1.03	0.75	0.98	0.73	0.56	0.95	1.22	1.04	0.91	1.40	1.14	1.36	1.19	1.71
207107	Hs.117774	ESTs, Moderately similar to CALDESMON [H.sapiens]	1.21	2.42	2.09	1.85	5.68	1.22	4.19	2.89	3.10	1.79	1.97	7.57	1.49	5.12	6.43	1.16	0.92	2.60	3.24	1.36	2.34	2.77
235164	Hs.5809	putative transmembrane protein	1.33	1.30	0.84	1.32	1.24	1.23	2.60	1.13	1.14	1.25	1.52	1.08	1.51	1.43	2.02	2.05	0.98	0.38	0.50	1.25	0.80	1.05
43878	Hs.79968	splicing factor 30, survival of motor neuron-related	1.26	1.06	0.84	1.21	1.53	0.90	1.11	1.12	0.72	0.83	0.98	0.94	0.69	0.60	0.87	1.02	0.72	1.10	0.96	0.80	1.35	1.48
347687	Hs.146409	cell division cycle 42 (GTP-binding protein, 25kD)	1.74	1.60	2.16	1.98	1.57	0.85	1.69	1.15	1.66	1.68	1.28	1.32	0.61	0.87	2.09	2.00	0.86	1.07	1.11	0.91	0.85	1.52
204111	Hs.151903	Homo sapiens clone 24706 mRNA sequence	1.37	1.78	0.59	0.78	1.64	0.95	0.64	1.32	0.76	1.66	1.59	2.21	1.17	0.65	1.21	1.20	0.94	1.28	1.25	1.04	1.51	1.40
282051	Hs.71741	ESTs, Highly similar to melanoma ubiquitous mutated protein [H.sapiens]	1.08	2.57	1.95	2.40	2.68	1.78	1.69	3.18	2.50	2.81	2.22	3.14	1.61	2.25	3.70	3.91	2.45	2.04	2.78	1.16	1.49	1.94
248256	Hs.94761	ESTs	1.07	1.35	1.52	1.97	2.20	2.18	1.76	1.23	1.91	1.33	1.51	2.18	1.31	2.02	1.32	2.22	1.16	0.77	1.01	1.88	3.52	1.52
303035	Hs.77738	KIAA0463 protein	1.99	1.80	0.63	0.93	2.07	0.95	1.09	1.49	1.19	1.86	1.30	1.72	1.04	0.99	2.10	0.43	1.04	1.19	1.49	1.17	1.81	1.36
321247	Hs.79362	retinoblastoma-like 2 (p130)	1.66	1.18	0.49	0.78	1.18	0.84	0.83	1.05	1.13	1.30	0.94	0.93	0.45	0.56	1.03	0.67	1.50	1.63	1.47	1.11	1.54	0.95
263040	Hs.5119	ATPase, H+ transporting, lysosomal (vacuolar proton pump), alpha polypeptide, 70kD, iso	1.10	0.92	0.59	0.78	0.85	0.82	0.65	0.38	0.88	0.59	0.68	0.73	0.80	0.91	0.76	0.99	1.22	0.81	0.66	0.93	0.48	0.64
50765	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (from clone DKFZp586C1723)	1.35	1.84	1.44	2.72	2.02	1.42	1.36	1.28	2.38	1.41	1.84	3.03	3.47	2.25	1.02	0.89	1.43	1.96	1.81	2.00	2.85	1.77
137535	Hs.183858	transcriptional intermediary factor 1	1.49	3.14	2.64	3.10	2.41	2.93	2.05	1.60	2.25	1.00	1.64	9.24	2.48	2.24	2.87	1.16	1.39	1.51	2.03	1.62	2.39	1.74
345055	Hs.114670	ESTs, Highly similar to NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENA	2.02	1.42	0.77	0.93	1.66	0.84	0.64	1.34	0.80	0.71	1.16	2.94	1.28	1.03	2.30	0.65	1.09	1.31	1.40	0.90	1.33	0.98
324745	Hs.183655	sec22 homolog	1.55	3.08	1.60	1.39	1.75	1.00	1.43	1.43	1.93	0.95	0.97	1.44	0.60	0.75	1.09	1.14	1.19	1.25	1.44	1.19	1.02	1.09
108422	Hs.25213	Homo sapiens mRNA; cDNA DKFZp586F1318 (from clone DKFZp586F1318)	0.54	2.10	0.60	0.83	1.16	1.03	0.54	0.39	0.35	0.49	0.27	0.53	0.49	0.67	0.99	0.38	0.50	0.78	0.81	0.76	0.44	0.80
250519	Hs.17585	KIAA0801 gene product	0.79	2.20	1.04	1.30	1.47	0.86	0.70	0.85	1.08	0.81	0.71	1.10	1.20	0.75	1.14	0.65	0.96	1.01	0.91	0.74	0.76	1.51
22711	Hs.169501	ESTs	0.70	0.87	0.69	0.77	1.92	0.79	0.53	0.96	0.89	0.89	0.91	1.77	0.61	1.31	0.93	1.39	0.90	1.01	0.98	0.95	1.90	1.29
79520	Hs.78305	RAB2, member RAS oncogene family	1.11	1.03	1.19	0.92	1.41	1.02	0.84	0.81	1.51	1.33	0.82	1.10	1.11	1.20	1.56	1.04	1.49	1.44	1.04	1.53	0.81	1.01
325102	Hs.171391	C-terminal binding protein 2	0.67	1.80	1.97	1.28	2.34	0.78	2.28	2.50	0.94	0.91	1.95	1.13	0.56	0.60	0.80	1.15	0.72	1.10	1.68	0.79	2.01	1.49
109153	Hs.75887	coatomer protein complex, subunit alpha	1.71	2.02	1.25	1.82	2.05	2.73	1.06	1.47	0.98	1.22	1.39	2.71	1.68	1.55	1.62	1.62	1.48	0.83	0.43	1.45	1.33	2.11
785816	Hs.256583	M-phase phosphoprotein 4	1.06	2.12	1.42	1.92	2.20	1.38	1.62	1.61	1.09	1.05	0.99	0.86	0.73	0.71	1.43	0.90	0.70	1.26	1.51	1.01	1.70	1.19
143039	Hs.96656	ESTs	0.77	1.25	1.04	1.86	2.14	0.91	1.25	1.67	1.17	1.65	1.05	0.85	0.52	0.84	1.06	0.95	0.98	1.06	1.85	1.14	0.94	1.05
112906	Hs.106019	protein phosphatase 1, regulatory subunit 10	1.08	1.57	1.22	1.29	1.88	1.37	1.76	3.08	1.38	1.71	1.97	2.23	1.36	1.71	0.57	1.30	0.83	1.29	2.48	1.77	2.77	1.13
243151	Hs.8366	ESTs, Highly similar to EF-9 [M.musculus]	1.46	1.96	1.85	1.51	2.30	1.30	1.57	1.70	1.02	1.59	1.85	1.52	0.68	0.79	1.36	1.27	1.59	1.24	1.90	1.20	1.97	1.38
244147	Hs.821	biglycan	4.39	4.00	9.73	2.42	8.47	5.83	11.71	5.54	8.66	8.10	7.19	25.70	8.18	8.84	22.94	6.34	5.75	5.79	8.87	3.21	3.85	2.90
144926	Hs.110695	ESTs, Weakly similar to B0495.6 [C.elegans]	3.41	2.47	1.06	1.72	1.54	1.93	1.51	1.60	1.22	1.26	1.55	0.86	0.58	1.14	0.74	1.11	0.83	0.64	0.90	1.27	1.36	0.89
245099	Hs.69855	NRAS-related gene	1.22	1.31	1.77	1.60	1.29	1.28	1.23	1.07	1.25	1.06	1.06	0.86	0.47	0.77	1.18	0.90	1.25	1.04	0.83	1.28	2.67	1.80
292515	Hs.21293	UDP-N-acteylglucosamine pyrophosphorylase 1; Sperm associated antigen 2	1.65	2.46	0.80	2.12	1.52	1.15	2.58	0.92	1.36	1.09	1.07	0.91	0.63	0.93	1.69	1.06	0.99	0.97	1.72	1.66	1.38	2.01
66952	Hs.13128	zinc finger protein 205	1.12	2.10	1.58	1.53	2.06	1.19	1.22	1.24	1.49	1.51	1.45	2.53	1.42	1.58	2.01	1.33	1.49	1.03	1.80	0.92	1.40	1.91
144951	Hs.23240	ESTs	1.24	1.78	1.08	1.20	2.73	2.26	1.20	1.68	1.40	1.39	2.33	1.13	1.06	2.69	1.40	1.80	1.98	1.29	1.59	2.02	2.41
112158	Hs.70589	ESTs, Weakly similar to neuron-restrictive silencer factor, form 2 [H.sapiens]	0.95	2.29	1.12	1.67	1.86	1.14	1.08	1.56	2.05	1.67	2.44	3.00	1.61	3.05	1.92	1.38	1.50	1.13	1.51	0.89	2.36	0.97
124116	Hs.184325	ESTs, Highly similar to CGI-76 protein [H.sapiens]	1.47	1.97	1.59	2.05	2.51	3.03	1.23	1.55	1.94	1.04	2.07	1.91	1.16	2.22	1.45	1.79	1.79	1.73	1.00	1.59	1.76	1.86

298833	Hs.11473	Homo sapiens mRNA; cDNA DKFZp586B1024 (from clone DKFZp586B1024)	1.66	1.62	1.89	1.00	2.03	1.04	0.67	1.80	1.94	1.65	1.76	1.87	1.29	0.79	1.71	1.30	1.41	1.73	1.70	0.89	1.32	0.98
141314	Hs.113029	ribosomal protein S25	2.79	5.71	2.16	4.67	6.76	3.20	3.35	5.85	7.83	3.43	3.52	3.36	1.47	3.37	3.83	5.62	2.37	2.62	5.54	1.50	2.97	3.26
307882	Hs.24930	tubulin-specific chaperone a	0.89	1.03	0.57	0.96	1.13	0.87	1.39	1.38	0.98	1.12	0.99	0.85	0.46	0.64	1.06	0.85	0.78	0.86	1.37	0.83	1.93	0.83
134172	Hs.168232	ESTs, Weakly similar to ubiquitin conjugating enzyme [H.sapiens]	1.13	1.89	0.87	1.26	1.30	1.10	1.74	1.23	1.86	1.62	1.05	1.06	0.84	1.04	1.41	1.70	1.30	1.35	1.65	1.51	1.87	1.23
129610	Hs.22026	ESTs	4.83	5.01	2.72	3.29	3.73	1.41	9.10	2.84	5.65	2.89	1.25	8.27	1.46	3.20	3.61	0.76	7.46	3.63	14.93	3.44	1.89	3.27
137387	Hs.18387	transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)	1.06	1.88	1.22	1.04	1.19	0.73	0.73	1.34	1.51	1.43	1.02	1.57	1.32	0.33	1.47	1.61	1.48	1.57	1.80	1.20	3.33	1.19
153779	Hs.183171	ESTs, Weakly similar to YCR053w, len:514 [S.cerevisiae]	1.27	2.14	1.29	1.94	2.21	1.55	1.58	1.83	1.61	1.57	1.45	2.61	1.06	1.37	1.90	1.64	1.08	0.95	1.24	1.05	1.83	1.96
122194	Hs.79150	chaperonin containing TCP1, subunit 4 (delta)	1.26	1.56	0.86	2.33	1.24	1.36	0.68	0.93	0.96	0.73	0.90	1.36	1.05	1.47	1.02	0.88	1.01	1.02	0.65	1.43	1.25	1.49
141959	Hs.223014	protease, serine, 15	0.97	2.66	1.34	1.13	1.57	0.70	0.91	3.01	3.99	6.21	1.58	3.05	6.62	1.29	6.22	0.83	3.39	2.16	3.71	1.19	1.81	1.34
248856	Hs.161040	EST	1.61	2.51	1.47	2.08	1.85	2.01	0.81	1.92	3.32	1.97	1.54	2.97	1.88	1.53	2.31	0.86	2.05	2.11	1.42	1.54	1.57	0.91
179336	Hs.469	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	2.68	1.82	1.26	1.28	1.68	1.20	1.91	1.37	1.09	1.25	0.94	1.40	1.41	0.89	1.13	1.50	1.35	1.72	1.62	1.44	1.34	1.67
308478	Hs.5855	ESTs	1.55	3.90	1.63	0.59	2.19	1.33	1.40	4.19	0.97	5.41	2.96	3.97	2.19	1.29	1.30	4.74	1.21	1.41	1.69	0.64	1.30	2.07
204737	Hs.93005	slug (chicken homolog), zinc finger protein	0.32	0.55	1.85	0.63	0.69	0.21	0.38	0.45	0.89	0.45	0.31	0.36	0.12	0.28	0.33	0.38	0.25	0.77	0.68	0.86	0.50	0.18
346299	Hs.234839	ESTs, Highly similar to vacuolar sorting protein 4 [H.sapiens]	1.04	2.17	2.04	1.43	2.04	1.08	2.24	1.24	2.90	2.24	1.33	1.17	0.54	0.81	0.89	1.43	1.01	0.71	1.02	1.12	1.10	1.73
198904	Hs.12152	ESTs, Moderately similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [M	2.37	2.07	1.47	1.67	2.87	1.07	1.49	1.95	2.24	3.13	1.18	1.36	0.64	1.09	1.43	0.92	1.96	1.13	1.71	1.53	1.87	1.16
232946	Hs.159640	serum/glucocorticoid regulated kinase	0.70	1.17	0.90	1.21	2.10	0.66	0.36	0.34	0.71	1.12	0.66	1.03	0.48	0.53	0.68	0.82	0.49	0.90	0.52	0.71	1.15	0.54
130100	Hs.206097	oncogene TC21	0.50	0.56	0.32	0.53	1.08	0.50	0.61	0.63	0.33	0.29	0.86	0.24	0.29	0.30	0.27	0.31	0.13	0.58	0.38	0.43	1.17	1.19
341269	Hs.102447	Homo sapiens mRNA for TSC-22-like protein	1.24	1.61	1.33	1.35	1.66	1.13	1.43	2.28	1.01	1.23	2.26	1.72	0.74	0.84	1.21	0.85	0.98	0.71	1.32	0.97	1.58	1.14
825470	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.20	4.00	3.22	2.46	1.71	2.13	4.48	7.85	2.23	2.67	8.76	0.56	0.84	0.48	1.02	0.53	1.66	0.84	4.38	1.14	3.50	2.44
144881	Hs.7753	calumenin	1.49	2.16	3.09	1.96	3.13	1.32	4.30	1.73	3.51	1.91	1.73	1.97	0.56	1.23	1.60	1.96	0.80	0.70	1.41	1.44	1.40	3.13
145513	Hs.1010	regulator of mitotic spindle assembly 1	2.38	2.11	1.88	1.95	2.48	1.09	2.06	3.18	3.42	2.78	1.37	2.60	1.98	2.02	3.65	0.70	2.23	2.53	2.95	2.07	1.94	1.75
321189	Hs.156764	DKFZP586H0723 protein	0.55	0.85	1.71	1.27	1.24	0.98	0.73	0.94	1.51	0.56	1.18	0.60	0.54	0.66	0.81	1.25	0.97	0.77	0.81	0.95	0.92	0.83
115111	Hs.16258	ESTs, Weakly similar to RAS-RELATED PROTEIN RAB-5A [H.sapiens]	0.78	1.41	0.65	0.91	1.57	0.85	1.12	2.46	1.36	2.34	1.84	1.92	1.13	1.38	0.62	0.98	1.47	1.14	1.75	1.34	1.74	1.04
308989	Hs.150826	ESTs, Weakly similar to RAS-RELATED PROTEIN RAB-11A [H.sapiens]	0.80	0.77	0.12	0.64	1.01	0.91	0.96	0.71	0.53	0.63	0.51	3.42	1.17	1.07	2.03	0.65	0.47	0.39	0.92	0.51	0.74	0.47
112576	Hs.171835	ESTs, Weakly similar to PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE [H.sapiens	1.78	2.16	1.01	1.07	2.61	1.31	1.42	1.96	1.23	2.18	2.51	1.81	0.75	0.84	1.76	0.79	1.09	1.26	2.60	0.88	1.57	1.48
210698	Hs.28669	ESTs, Weakly similar to PROTEIN-TYROSINE PHOSPHATASE MEG1 [H.sapiens]	1.13	1.14	0.76	2.41	1.19	0.57	0.76	0.42	0.67	0.53	0.78	1.74	0.76	1.11	0.93	0.79	0.36	1.71	0.41	0.98	0.72	1.21
358456	Hs.9950	Sec61 gamma	1.59	1.22	1.65	1.02	1.75	1.18	1.51	1.56	1.91	1.04	1.29	0.69	0.53	0.68	1.58	0.85	1.33	0.81	1.40	1.34	2.25	1.51
363569	Hs.199248	prostaglandin E receptor 4 (subtype EP4)	1.24	1.54	1.17	1.20	1.84	1.02	1.74	1.27	1.56	1.65	1.19	1.79	1.28	2.18	1.75	1.14	1.12	0.90	1.38	1.26	1.28	1.31
34689	Hs.12971	thioredoxin reductase beta	0.77	1.24	0.82	0.79	1.66	1.00	1.30	1.36	0.85	1.39	1.28	1.58	1.76	1.29	1.28	1.17	1.00	1.34	1.06	0.92	2.14	0.93
308682	Hs.153612	ATP-binding cassette, sub-family F (GCN20), member 2	0.72	1.72	1.24	1.57	1.55	1.28	1.25	0.99	1.53	1.18	1.47	1.19	1.18	1.37	1.17	1.41	0.96	0.87	0.75	1.11	1.28	1.71
67074	Hs.12797	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	1.09	2.00	1.26	1.34	1.74	1.34	1.56	1.47	1.89	1.55	1.51	1.71	1.22	1.21	1.28	1.45	1.22	1.32	2.21	1.27	1.60	1.51
130371	Hs.23255	nucleoporin 155kD	2.60	2.35	1.98	2.87	1.85	1.44	2.14	1.47	1.47	1.90	1.64	1.24	0.80	0.97	1.19	0.72	1.51	1.70	2.23	1.22	1.89	2.19
241900	Hs.182937	peptidylprolyl isomerase A (cyclophilin A)	1.66	1.60	0.84	1.03	1.46	1.65	1.70	1.32	1.18	1.34	1.32	0.95	0.71	0.73	1.01	0.90	1.81	1.26	1.89	1.60	1.73	1.27
138775	Hs.17775	ovarian granulosa cell protein (13kD)	1.19	2.04	3.22	1.62	2.34	0.29	1.73	1.02	2.94	2.34	0.62	1.11	1.19	1.02	1.77	1.51	1.74	1.03	1.20	0.53	1.51	1.61
358333	Hs.109805	Homo sapiens incomplete cDNA for a myosin class I, myh-1c	1.18	1.59	3.51	2.36	2.51	0.80	0.62	1.73	4.49	2.05	1.45	6.07	6.55	4.07	4.33	0.75	1.55	1.09	0.66	1.71	1.49	2.27
364469	Hs.19561	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (14.5kD, B14.5a)	0.63	1.43	0.43	0.68	0.62	0.72	1.67	0.93	0.81	1.83	0.77	1.18	1.59	0.75	1.02	0.91	0.71	0.77	1.24	0.75	0.75	0.62
470861	Hs.109646	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6 (17kD, B17)	1.69	1.24	0.86	1.39	1.35	0.66	0.76	1.47	1.12	1.04	0.77	0.38	0.72	0.53	0.70	0.60	0.89	0.74	1.02	0.52	1.61	1.07
144916	Hs.92287	ESTs, Highly similar to INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 [H.sapiens	1.31	1.67	1.03	1.59	2.98	2.16	0.51	2.00	2.09	2.05	2.81	4.36	1.40	2.77	4.08	1.66	2.89	2.00	2.59	0.82	1.86	1.35
290124	Hs.177559	interferon gamma receptor 2 (interferon gamma transducer 1)	1.43	0.80	1.38	1.48	1.65	0.98	1.06	0.81	1.74	1.57	1.47	1.50	1.29	2.15	1.63	1.70	1.73	1.72	2.26	1.66	0.92	1.04
244764	Hs.11953	ESTs	0.86	1.47	2.24	1.27	2.15	1.03	3.29	2.26	2.85	2.03	1.63	2.48	1.35	2.63	2.35	2.37	1.46	1.71	2.36	1.57	1.84	2.55
143306	Hs.56729	lymphocyte-specific protein 1	1.52	1.16	1.45	1.36	2.34	1.24	1.76	1.54	2.32	1.62	1.21	1.76	1.13	1.96	1.75	1.75	1.34	1.79	1.26	0.80	1.41	1.61
356992	Hs.24003	ESTs, Moderately similar to LEYDIG CELL TUMOR 10 KD PROTEIN [R.norvegicus]	1.79	1.20	1.21	1.36	1.09	1.19	1.79	0.76	0.98	1.45	1.05	1.35	1.20	0.98	1.23	1.02	0.86	0.65	1.30	0.72	0.99	0.56
154482	Hs.183583	protease inhibitor 2 (anti-elastase), monocyte/neutrophil	0.81	1.77	0.55	1.02	1.63	1.79	0.54	1.16	1.21	1.34	1.18	1.22	0.80	1.05	1.26	1.25	1.14	1.14	1.16	0.87	1.42	0.89
108395	Hs.170290	discs, large (Drosophila) homolog 5	0.29	0.33	0.34	0.40	1.23	0.22	0.76	0.72	0.44	0.55	0.69	0.28	0.32	0.21	0.75	0.36	0.34	0.44	0.89	0.38	0.46	0.16
32996	Hs.168655	Homo sapiens mRNA for H-2K binding factor-2, complete cds	1.15	1.61	1.39	1.01	1.89	1.29	0.79	1.33	1.13	1.71	1.84	1.10	1.17	1.08	1.26	1.40	0.99	1.43	1.37	1.17	1.76	1.28
129725	Hs.22073	ESTs, Highly similar to J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN [H.sapiens]	0.87	1.53	1.10	0.77	1.21	0.82	1.47	0.86	1.06	1.01	1.63	1.41	1.03	1.48	1.02	1.45	1.17	0.87	1.78	1.56	1.73	0.56
179232	Hs.184011	pyrophosphatase (inorganic)	0.43	0.39	0.29	0.59	0.36	0.41	0.55	0.28	0.26	0.14	0.42	0.34	0.52	0.40	0.55	1.75	0.34	0.38	0.39	0.66	0.59	0.52
293921	Hs.180455	RAD23 (S. cerevisiae) homolog A	1.10	1.42	1.13	1.54	1.55	0.95	1.25	1.26	1.60	1.83	1.42	3.96	2.07	2.45	3.71	3.45	1.48	1.57	2.58	1.26	0.84	1.30
342994	Hs.12273	ESTs	1.62	2.24	0.68	1.44	2.86	0.85	1.65	1.12	1.33	1.53	1.87	1.46	0.79	0.94	0.93	1.13	1.29	1.85	2.07	0.55	1.44	1.75
125788	Hs.8739	ESTs, Weakly similar to ORF YGR200c [S.cerevisiae]	1.50	1.20	2.01	1.20	0.98	0.63	1.23	0.39	1.75	2.88	0.99	2.98	1.24	1.55	3.01	5.21	1.02	1.28	3.06	1.07	0.99	0.91
295923	Hs.5862	ESTs, Highly similar to ORF is homologous to hypothetical 9.8 kD protein ZK652.3 of Cae	1.48	1.72	1.00	1.84	1.24	1.42	0.57	1.11	1.86	1.19	1.35	1.83	2.52	1.55	2.43	2.67	0.96	1.10	0.86	1.68	1.13	1.02
198960	Hs.84038	Novel gene on chromosome 20	0.96	0.87	0.44	0.68	0.59	0.96	0.91	0.75	0.65	0.95	0.49	0.64	0.86	0.59	0.58	1.36	0.56	0.67	0.85	0.86	0.43	0.25
346545	Hs.27375	ESTs, Highly similar to LAMININ BETA-1 CHAIN PRECURSOR [H.sapiens]	1.27	0.88	0.36	0.79	0.81	1.21	0.89	0.87	0.81	1.13	0.98	1.06	1.05	0.67	0.77	1.09	0.70	1.12	0.95	0.57	0.79	0.46
293977	Hs.6820	ESTs, Weakly similar to putative [C.elegans]	1.05	1.66	1.63	1.50	1.30	1.17	1.60	0.90	0.97	0.87	0.85	0.87	1.05	1.10	1.15	1.98	0.89	1.06	0.70	1.05	0.75	1.00
205993	Hs.25516	ESTs, Highly similar to ORF [H.sapiens]	0.79	0.84	0.87	0.95	0.86	0.95	0.79	0.44	1.21	2.32	1.06	1.60	1.72	1.59	1.81	0.82	1.40	0.88	0.91	0.91	0.54	0.88
121275	Hs.203656	EST	0.81	0.54	0.96	0.68	0.83	0.46	0.41	0.72	1.18	0.69	0.57	0.61	0.38	0.43	0.73	0.54	0.71	0.74	1.27	0.73	1.34	0.55
365098	Hs.3990	ESTs	0.61	0.44	0.93	0.56	0.75	0.58	0.42	0.42	1.09	0.68	0.70	0.36	0.36	0.46	0.74	0.56	0.59	0.65	0.94	0.67	0.72	0.28
125148	Hs.113052	RNA cyclase homolog	2.28	6.83	0.87	1.60	1.98	1.09	2.30	1.52	0.86	1.17	2.57	1.28	0.73	0.62	1.20	1.13	1.24	1.73	2.00	1.15	1.55	1.79
201819	Hs.5298	ESTs, Highly similar to CGI-45 protein [H.sapiens]	1.18	1.11	0.75	1.17	0.82	0.94	0.99	1.15	1.42	2.20	1.00	1.36	1.77	1.11	1.89	1.21	1.21	0.77	1.81	1.57	1.07	0.94
345423	Hs.107942	DKFZP564M112 protein	0.82	1.12	0.97	1.06	1.15	1.06	1.14	0.59	1.02	1.48	1.52	1.67	1.80	1.18	1.74	0.86	0.97	0.98	0.73	1.07	0.68	0.51
244974	Hs.234156	ESTs, Weakly similar to CGI-128 protein [H.sapiens]	1.15	1.43	0.71	2.43	1.03	1.42	1.10	1.07	1.19	1.17	1.05	1.07	0.60	0.81	1.00	0.88	0.90	0.96	1.17	0.94	1.18	1.19
307843	Hs.91604	ESTs	2.15	4.09	2.13	1.60	2.52	2.03	2.88	1.37	0.81	1.73	1.95	1.03	1.00	0.82	1.37	0.73	0.66	1.36	1.00	1.62	0.78	0.91
308633	Hs.54990	ESTs	1.71	2.23	1.54	1.26	1.21	1.39	1.90	1.16	0.88	1.83	2.18	1.42	0.74	0.59	1.04	0.65	0.81	1.37	2.99	1.05	0.40	0.55
628418	Hs.25478	glycerol-3-phosphate dehydrogenase 1 (soluble)	1.45	1.87	1.28	2.46	3.80	0.89	2.81	1.04	1.35	1.64	0.91	0.99	0.79	0.93	0.64	1.06	0.59	0.38	0.47	0.56	1.28	3.12
246722	Hs.21858	trinucleotide repeat containing 3	1.08	1.61	1.10	2.13	2.30	0.72	2.23	0.89	0.64	1.33	1.36	2.47	1.10	1.37	0.92	0.81	0.52	0.37	0.39	0.62	0.90	3.38
207255	Hs.91251	ATP-binding cassette, sub-family F (GCN20), member 3	1.78	1.92	0.74	1.54	2.25	1.53	1.86	1.55	1.25	1.92	0.71	3.22	1.96	1.62	2.27	1.40	2.04	0.97	1.78	1.14	1.22	2.17
283398	Hs.8769	Homo sapiens mRNA; cDNA DKFZp564E153 (from clone DKFZp564E153)	2.10	1.76	13.92	1.68	1.44	2.28	4.93	2.81	13.64	0.95	1.29	3.29	0.84	1.39	2.15	1.06	4.29	5.03	6.08	1.94	0.84	1.86
191978	Hs.155751	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	0.66	1.56	1.23	1.24	1.12	0.87	1.05	1.09	0.71	1.12	0.93	0.88	0.51	0.70	0.61	0.72	0.57	0.56	0.94	0.60	0.84	1.66
251250	Hs.18350	chromosome 21 open reading frame 1	3.14	2.86	3.20	2.26	2.43	1.56	2.11	2.06	3.01	3.66	1.47	2.56	0.84	1.05	1.78	2.07	3.84	2.45	3.08	1.88	1.90	2.03
842980	Hs.115242	developmentally regulated GTP-binding protein 1	0.37	1.82	2.18	1.36	1.37	1.33	2.24	1.01	1.13	1.32	1.51	0.52	0.65	1.00	1.04	1.09	0.91	0.93	1.44	1.42	1.04	1.12
470061	Hs.20191	seven in absentia (Drosophila) homolog 2	3.50	3.71	1.69	2.39	3.42	1.62	4.64	3.22	3.21	4.51	2.99	1.86	5.97	2.08	4.54	1.70	3.54	3.54	6.32	1.32	1.82	2.67
358736	Hs.59523	ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]	0.59	0.58	1.22	1.09	1.01	1.07	1.77	0.54	1.04	0.51	1.25	0.58	0.69	0.76	1.01	0.88	0.97	1.23	0.83	0.85	0.65	1.56
366570	Hs.59523	ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG [H.sapiens]	0.76	1.44	0.84	0.97	1.59	1.64	1.76	0.99	0.79	1.75	1.38	0.51	0.64	0.72	0.68	1.22	1.16	1.52	0.82	1.08	1.34	2.55
307532	Hs.173912	eukaryotic translation initiation factor 4A, isoform 2	3.21	3.06	1.95	2.54	2.50	1.83	0.80	1.53	1.54	1.31	2.21	2.85	5.78	2.91	2.11	1.97	2.56	2.18	1.65	1.33	2.15	2.10
295831	Hs.24332	ESTs, Highly similar to CGI-26 protein [H.sapiens]	0.69	0.66	0.76	0.71	0.60	0.67	0.43	0.32	0.53	0.30	0.37	0.50	0.24	0.38	0.44	3.54	0.36	0.40	0.46	0.51	0.97	0.45
327094	Hs.111460	ESTs, Highly similar to multifunctional calcium/calmodulin-dependent protein kinase II delta	1.51	1.62	1.92	1.81	1.29	1.42	0.81	0.93	1.52	1.02	1.34	2.22	1.36	2.19	2.86	2.21	0.40	1.16	0.43	1.03	0.92	1.67
289288	Hs.106778	Homo sapiens mRNA for putative Ca2+-transporting ATPase, partial	2.49	1.64	0.89	1.59	3.01	2.37	1.31	1.40	1.53	1.63	1.58	1.38	0.84	1.21	1.32	1.29	1.33	1.50	2.18	1.34	1.57	1.89
141623	Hs.182579	Homo sapiens leucine aminopeptidase mRNA, complete cds	1.51	7.52	1.09	2.84	2.93	2.96	1.10	3.13	2.44	2.04	3.96	2.47	1.20	1.47	1.97	2.75	2.03	1.81	2.00	1.84	2.16	2.29
129446	Hs.180570	Homo sapiens chromosome 19, cosmid F22329	0.87	0.38	0.21	0.19	0.28	0.19	0.24	0.14	0.08	0.35	0.18	0.56	0.53	0.33	0.13	3.28	0.11	0.25	0.20	0.64	0.74	0.04
376515	Hs.105737	ESTs, Weakly similar to gene 9306 protein [H.sapiens]	1.41	3.32	1.27	1.92	2.47	2.10	1.81	1.54	1.53	1.24	2.19	1.45	0.82	0.90	1.69	1.47	1.25	1.13	2.50	0.96	1.63	1.97
66327	Hs.89688	ESTs, Moderately similar to complement receptor 1 [H.sapiens]	1.31	2.37	3.82	2.89	1.41	1.99	1.30	1.17	6.34	6.83	3.01	5.36	3.79	3.04	4.18	3.29	1.99	1.57	2.59	1.49	1.01	1.29

292833	Hs.94953	ESTs, Highly similar to COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR [H.sapi	4.83	24.02	11.71	7.93	13.04	8.79	10.79	8.06	10.90	11.09	16.25	31.90	15.31	5.31	16.94	6.65	7.32	5.17	13.71	3.12	6.19	3.66
741841	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase)	2.28	7.03	1.60	2.98	4.68	2.05	3.99	2.09	1.21	2.15	3.03	2.15	2.23	2.11	1.84	1.57	2.94	2.07	2.72	1.31	2.20	3.02
66714	Hs.155524	peanut (Drosophila)-like 2	4.34	2.99	6.31	3.18	1.85	1.62	4.88	2.05	1.91	3.37	1.67	4.60	2.28	2.46	4.61	1.67	2.90	3.31	4.94	1.38	0.85	1.67
244911	Hs.177461	ribosomal protein L39	1.47	1.97	0.80	0.99	1.51	0.88	1.28	1.59	0.97	0.86	1.25	0.83	0.51	0.45	0.84	0.88	1.50	1.33	1.54	0.78	1.70	1.23
366389	Hs.187991	DKFZP564A122 protein	1.38	2.07	2.13	1.71	3.01	1.35	3.38	3.10	1.83	2.36	1.87	4.31	1.76	2.35	3.37	1.03	1.75	3.02	3.71	2.68	3.11	1.07
196005	Hs.234642	aquaporin 3	2.23	1.25	0.67	0.90	0.89	0.73	1.45	1.24	0.55	0.81	0.83	1.24	0.76	0.96	2.01	0.96	0.47	1.65	3.68	0.90	2.11	0.30
134948	Hs.15485	ESTs, Weakly similar to APICAL-LIKE PROTEIN [H.sapiens]	0.73	1.69	0.15	0.28	1.27	0.60	0.40	1.82	0.74	0.77	2.11	0.93	0.52	0.19	1.22	1.23	0.56	1.65	1.78	0.75	1.05	0.69
293579	Hs.49636	ESTs, Weakly similar to M130 antigen [H.sapiens]	0.90	2.13	1.88	0.70	2.38	0.74	0.96	0.67	0.88	2.22	1.11	1.55	0.86	1.94	1.22	1.33	0.72	0.83	0.64	0.85	1.97	0.44
295710	Hs.26516	ESTs, Moderately similar to CGI-98 protein [H.sapiens]	2.98	4.34	0.92	2.27	1.70	2.45	5.31	1.89	0.95	1.53	1.80	2.87	1.06	1.20	1.74	1.06	1.46	1.20	3.86	1.80	1.60	0.91
194161	Hs.182485	actinin, alpha 4	1.20	1.59	0.44	0.58	1.09	1.75	1.04	0.51	1.00	0.65	0.73	0.81	0.34	0.62	0.51	0.78	1.04	0.63	0.81	0.64	0.64	0.78
109316	Hs.234726	alpha-1-antichymotrypsin	2.12	7.25	0.61	3.19	6.66	0.63	7.11	2.04	2.87	7.77	1.96	4.54	6.30	2.15	10.21	1.55	3.61	3.62	5.98	0.91	1.73	3.60
201757	Hs.173739	3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 2	1.51	2.05	2.32	0.98	1.74	1.90	0.71	1.04	2.60	1.94	3.91	1.62	6.74	3.86	1.79	1.85	2.11	1.18	1.04	1.96	1.46	1.08
110772	Hs.109052	chromosome 14 open reading frame 2	0.45	0.79	0.79	0.78	0.64	0.42	0.68	0.72	0.64	0.62	0.55	1.00	0.56	0.59	0.82	0.27	0.43	0.44	0.79	0.47	0.39	0.46
42258	Hs.11700	ESTs	1.50	2.55	3.49	3.99	3.33	1.59	8.24	2.51	3.98	3.24	1.71	2.07	2.07	1.30	1.80	1.64	4.58	3.87	3.05	1.90	1.71	2.10
66697	Hs.75425	ESTs	1.35	2.73	1.42	1.38	1.36	1.15	1.13	1.00	0.98	0.95	1.32	1.18	1.44	0.88	1.21	0.88	1.24	1.24	1.25	1.85	1.13	1.16
66316	Hs.191117	ESTs	1.09	3.03	0.28	0.99	1.49	1.54	2.22	0.89	1.19	0.74	0.43	2.87	1.43	1.29	1.70	1.08	1.75	1.11	1.94	1.64	0.47	2.29
210646	Hs.93850	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	0.17	0.42	0.15	0.28	0.28	0.15	0.16	0.14	0.12	0.01	0.06	0.23	0.17	0.27	0.21	0.16	0.14	0.28	0.20	0.22	0.21	0.13
214565	Hs.3491	ribosomal protein S14	0.40	0.84	0.46	0.45	1.08	0.70	0.60	0.96	0.45	0.49	0.77	0.34	0.33	0.43	0.60	0.78	0.56	0.79	0.85	0.54	0.37	1.84
245531	Hs.102521	ESTs, Highly similar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR [R.norvec	0.31	0.74	0.71	0.73	0.82	0.77	0.73	0.49	0.58	1.67	0.37	0.39	0.35	0.29	0.44	0.52	0.68	0.61	0.46	0.33	1.10	0.45
128208	Hs.112423	Homo sapiens mRNA; cDNA DKFZp586I1420 (from clone DKFZp586I1420)	1.94	4.08	1.05	2.42	2.61	1.94	2.10	2.97	1.97	4.66	2.26	4.51	1.70	2.01	3.29	1.62	2.73	2.04	3.71	1.57	2.40	1.86
66815	Hs.152925	ESTs	3.36	8.94	4.84	5.61	4.69	6.41	1.79	6.61	8.48	15.29	7.37	9.08	0.81	5.42	8.19	3.33	5.69	3.10	4.76	1.99	3.08	3.92
66555	Hs.13011	ESTs, Weakly similar to putative G-protein [H.sapiens]	1.65	2.38	1.50	1.34	2.81	1.22	3.64	2.49	1.52	2.89	1.82	1.53	1.98	2.15	1.58	1.22	2.19	1.67	2.06	1.59	3.14	1.54
66582	Hs.13035	ESTs	1.94	1.89	1.17	1.37	1.48	1.33	1.80	1.37	1.40	1.07	1.27	2.01	0.97	1.38	1.58	1.57	1.46	1.78	2.04	1.29	0.71	1.15
66584	Hs.13036	DKFZP727A071 protein	1.74	2.55	0.78	1.35	3.03	1.66	0.57	1.60	0.96	1.17	3.05	3.13	0.97	1.06	2.07	1.04	1.16	1.27	1.58	1.00	1.91	2.69
66608	Hs.189762	ESTs	1.48	0.86	1.54	2.51	1.83	1.20	1.94	1.84	2.20	2.48	1.33	2.20	0.69	1.93	1.63	1.28	1.76	2.22	2.77	0.66	1.20	1.89
66975	Hs.13145	ESTs	1.87	4.41	1.42	2.88	4.85	2.11	3.45	2.95	1.57	2.58	3.89	10.11	2.98	3.36	5.74	1.51	2.30	2.26	3.47	2.13	3.16	2.35
67070	Hs.13192	ESTs	1.19	1.50	0.46	0.65	1.62	0.80	0.82	1.07	0.94	0.95	0.91	1.25	0.72	0.64	1.06	0.90	1.28	1.58	1.84	1.20	1.14	1.19
111981	Hs.179972	interferon, alpha-inducible protein (clone IFI-6-16)	3.05	2.95	1.05	1.38	2.46	1.65	0.54	1.39	1.18	1.32	0.98	1.81	1.58	0.91	2.48	0.69	1.75	1.99	1.09	1.09	0.99	2.04
242706	Hs.3576	ESTs	0.63	0.55	0.89	0.64	0.97	0.69	0.48	0.86	1.11	0.89	0.81	0.71	1.15	0.86	0.88	1.97	1.14	0.66	0.59	1.15	0.73	0.62
340840	Hs.164036	tumor necrosis factor alpha-inducible cellular protein containing leucine zipper domains; H	0.90	1.10	0.80	1.05	1.48	0.89	1.28	1.87	2.12	2.23	0.97	2.02	0.97	1.21	1.58	0.81	1.65	1.31	1.90	0.54	0.74	2.10
40721	Hs.26455	ESTs	1.61	2.01	1.27	1.80	2.20	1.63	0.85	1.62	1.69	1.42	1.42	2.25	1.80	1.01	1.85	0.87	1.21	2.01	1.81	1.02	1.57	2.06
154654	Hs.3321	ESTs, Highly similar to IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3 [M.musculus]	1.34	1.77	0.96	1.09	1.79	0.55	1.82	1.20	1.26	1.34	0.78	3.46	0.83	0.88	1.61	1.94	1.65	2.40	3.06	1.58	1.72	1.74
173878	Hs.3430	ESTs	1.90	2.15	1.00	1.18	1.65	1.33	0.87	1.49	1.30	4.47	1.29	1.25	1.11	0.65	0.98	1.18	1.23	1.33	1.46	1.21	0.89	0.67
293901	Hs.3459	ESTs	1.05	1.93	1.54	1.86	2.02	0.88	1.76	1.59	1.89	1.79	1.09	1.04	1.56	1.51	1.69	0.70	1.75	1.73	1.55	0.97	1.38	2.09
196038	Hs.87603	ESTs	1.20	2.52	2.09	3.80	2.90	1.72	1.80	1.72	2.53	3.06	1.48	1.32	0.74	1.13	1.16	1.56	1.28	1.67	1.42	1.23	1.04	0.91
740554	Hs.144904	nuclear receptor co-repressor 1	1.75	1.54	0.95	1.21	1.93	1.28	0.93	0.83	0.60	0.61	1.00	0.80	0.87	0.61	1.19	0.39	0.60	0.95	0.58	0.92	1.71	3.64
151261	Hs.237971	ESTs	0.63	0.90	0.68	1.62	1.12	0.79	1.12	0.83	0.99	0.74	0.68	0.54	1.67	1.16	0.81	1.29	1.05	0.90	0.61	0.46	0.60	1.03
67037	Hs.51615	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	2.36	1.22	3.48	1.86	2.80	1.19	0.91	3.31	2.27	2.35	1.39	3.26	0.41	1.29	2.25	1.72	2.84	2.43	3.16	0.79	2.42	0.86
290308	Hs.4095	ESTs	2.08	2.29	0.93	1.53	1.62	1.01	1.32	1.23	1.22	1.69	1.08	0.88	0.84	0.72	1.39	0.56	1.37	1.79	2.27	1.33	1.23	1.59
202901	Hs.4248	ESTs	1.60	1.37	0.73	1.47	1.21	0.57	0.95	0.86	1.54	3.03	1.18	1.49	1.24	1.29	1.65	1.47	0.77	0.96	1.13	0.98	1.18	0.55
122150	Hs.169539	ESTs	1.47	1.08	0.44	0.89	1.11	1.32	0.51	0.69	0.87	0.53	0.72	0.80	1.55	1.24	1.61	0.84	1.40	1.04	0.66	1.37	1.10	1.05
123255	Hs.238126	ESTs, Highly similar to CGI-49 protein [H.sapiens]	2.79	3.11	3.17	2.18	2.95	5.48	2.18	3.91	4.11	4.71	2.50	5.08	1.52	1.52	5.49	3.80	3.85	2.34	7.61	1.04	1.43	3.08
261587	Hs.4985	ESTs	2.52	2.21	1.27	1.60	2.63	0.99	1.31	2.72	1.94	3.38	4.23	2.56	1.24	1.04	2.35	0.51	2.42	2.07	2.24	2.15	0.93	0.91
159166	Hs.243901	KIAA1067 protein	1.91	1.34	1.29	1.69	1.36	0.95	2.21	1.28	1.83	2.63	1.02	2.25	2.60	2.89	2.72	2.19	1.24	1.33	1.80	1.11	1.08	1.72
240033	Hs.5605	ESTs	1.73	2.85	0.78	1.70	3.78	2.45	2.79	2.12	0.96	1.36	3.64	3.20	1.65	1.46	2.69	0.96	2.80	2.76	2.74	1.54	1.30	1.75
66977	Hs.107528	ESTs, Highly similar to CGI-103 protein [H.sapiens]	1.86	0.90	0.44	1.39	0.73	1.61	0.35	0.68	0.64	0.77	0.65	1.12	0.69	0.68	0.66	0.73	1.25	0.43	0.29	0.67	0.76	0.25
245485	Hs.5723	ESTs	1.75	1.44	0.96	1.08	2.44	1.07	0.92	1.72	0.96	1.28	1.07	2.57	0.53	1.28	1.85	1.13	1.78	1.78	2.27	0.63	2.17	0.91
66919	Hs.187404	ESTs	1.89	3.99	1.12	2.77	2.71	1.46	3.41	2.81	1.72	2.38	2.15	3.38	1.21	1.83	2.75	1.65	1.69	1.70	3.10	1.97	3.11	1.91
280837	Hs.5320	Human Chromosome 16 BAC clone CIT987SK-A-101F10	0.49	1.06	0.87	1.22	0.87	0.52	1.07	0.89	0.76	0.60	0.70	0.63	0.55	1.10	0.81	1.01	0.97	1.21	1.04	0.84	0.56	1.04
144894	Hs.5332	Homo sapiens clone 23967 unknown mRNA, partial cds	0.83	1.03	0.44	0.92	1.37	0.86	1.01	1.43	0.74	0.79	1.78	1.14	0.83	0.78	1.11	0.97	0.65	1.33	1.23	0.73	1.31	0.83
292232	Hs.237924	ESTs, Highly similar to CGI-69 protein [H.sapiens]	2.90	2.95	1.94	2.26	2.29	1.39	3.15	1.96	2.22	1.68	1.83	3.91	2.65	1.82	2.39	1.52	2.77	1.42	2.64	0.89	1.76	1.82
363146	Hs.167795	ESTs	1.94	2.14	0.85	1.65	2.63	1.51	1.26	1.48	1.26	1.33	1.49	2.05	1.05	0.74	1.97	1.35	1.41	1.28	1.28	1.17	1.97	1.45
211813	Hs.5476	serine proteinase inhibitor	1.15	1.25	0.62	1.88	0.88	0.54	0.66	1.09	1.05	1.44	1.71	1.58	1.15	0.88	1.19	0.72	0.66	0.99	0.82	1.01	1.01	0.82
123262	Hs.5486	ESTs	0.68	1.19	0.99	0.71	1.56	0.65	1.16	1.22	0.72	1.34	1.32	0.63	0.43	0.43	0.72	0.69	0.52	1.36	0.92	1.21	1.19	0.72
234036	Hs.5548	Homo sapiens clone 23765 mRNA sequence	1.16	1.64	1.38	1.94	1.71	1.10	0.77	1.24	2.58	2.39	1.72	1.68	1.08	1.45	1.87	1.55	1.61	1.70	1.75	1.01	1.50	0.94
357091	Hs.6363	ESTs	2.03	4.23	1.41	1.46	5.00	1.75	6.12	2.29	3.14	3.66	1.47	4.10	2.81	1.83	3.51	1.65	3.40	2.91	4.71	2.45	2.12	3.23
282378	Hs.6407	ESTs	0.50	0.79	0.37	0.36	1.76	0.41	0.69	0.60	0.51	0.92	0.64	1.09	0.33	0.44	1.13	0.35	0.41	0.80	0.60	0.88	0.68	0.74
200599	Hs.5985	Homo sapiens clone 25186 mRNA sequence	1.69	4.63	1.60	3.44	8.68	2.80	4.91	3.01	4.66	3.03	2.20	9.63	3.54	4.02	7.33	2.44	5.71	4.14	4.63	2.65	4.29	2.42
132527	Hs.6075	ESTs	1.41	1.84	1.22	1.30	1.63	0.63	1.44	0.93	1.46	1.22	0.74	1.13	0.80	0.58	1.08	1.08	0.79	1.13	1.79	0.93	0.60	1.68
203350	Hs.173864	KIAA0561 protein	1.49	2.64	0.92	1.11	1.95	1.67	1.13	1.02	1.28	1.58	2.08	2.24	0.99	1.19	1.39	1.59	1.63	1.46	1.39	1.46	0.74	1.05
246703	Hs.6483	chromosome X open reading frame 5	2.63	1.32	0.78	1.03	1.11	0.95	1.46	1.02	1.47	1.05	0.48	1.49	0.55	0.51	1.06	1.37	1.29	1.63	2.06	0.83	0.35	0.91
345090	Hs.7045	ESTs	0.92	1.60	1.05	1.13	1.62	1.00	1.20	1.09	1.07	1.49	1.17	0.77	0.73	0.94	0.81	0.51	1.21	1.62	1.32	1.40	3.54	1.91
111721	Hs.7089	Homo sapiens mRNA; cDNA DKFZp434O071 (from clone DKFZp434O071)	0.77	1.20	0.95	0.81	2.05	0.94	1.24	0.68	1.28	1.19	0.85	1.04	0.80	0.67	0.88	0.92	1.09	0.80	0.63	0.73	1.10	1.36
203544	Hs.6523	ESTs	0.64	2.43	1.62	1.07	1.27	1.20	0.85	0.85	1.02	0.88	0.81	0.74	1.44	0.61	0.91	1.03	0.94	1.40	1.16	1.09	0.97	2.11
324255	Hs.6799	ESTs	1.21	1.47	1.38	1.45	1.32	0.77	1.50	0.71	1.29	1.03	0.62	0.89	0.77	0.77	0.96	0.56	1.01	1.41	1.37	0.93	0.63	1.17
136073	Hs.169552	ESTs	2.19	3.12	1.25	2.03	2.30	2.34	3.73	1.53	1.98	2.06	1.41	2.95	1.61	1.54	2.79	1.16	1.68	1.66	2.02	1.50	1.66	2.07
201483	Hs.179882	Homo sapiens clone 24655 mRNA sequence	2.52	2.83	2.66	3.95	3.89	1.79	4.01	2.38	2.25	8.79	1.48	2.47	2.72	2.46	2.41	4.55	2.83	1.86	1.73	1.63	2.36	0.59
293191	Hs.7187	ESTs, Weakly similar to similar to glycoproteins [C.elegans]	1.17	2.41	1.92	1.45	2.10	1.04	2.31	1.75	1.15	1.89	1.49	1.44	0.60	1.56	1.50	1.72	1.84	0.88	1.55	0.72	1.15	1.43
416833	Hs.7557	FK506-binding protein 5	0.14	0.27	0.16	0.16	0.27	0.12	0.21	0.14	0.12	0.07	0.14	0.14	0.11	0.08	0.13	0.24	0.10	0.31	0.32	0.19	0.22	0.14
111492	Hs.7314	KIAA0614 protein	0.80	1.13	0.65	1.36	1.58	0.94	0.94	0.85	0.55	0.96	1.77	1.59	2.30	1.72	1.95	1.56	1.02	0.95	0.90	1.06	0.65	0.91
195051	Hs.236556	ESTs	0.94	0.95	1.00	0.48	1.19	0.52	0.63	1.24	1.01	0.96	1.10	0.52	0.65	1.03	1.21	0.50	0.63	0.82	1.02	0.80	1.42	0.91
277274	Hs.7424	Homo sapiens clone 25232 mRNA sequence	1.97	1.57	1.07	1.71	2.83	1.20	1.33	1.42	0.89	1.20	1.18	1.47	1.14	1.43	1.57	2.31	1.83	1.61	1.32	1.33	1.11	0.91
108801	Hs.27047	ESTs	1.44	2.46	1.72	1.90	1.97	1.37	1.03	3.24	1.99	1.56	2.10	1.80	0.70	0.72	1.58	0.77	1.74	1.39	1.76	1.03	2.45	1.79
144924	Hs.7446	DKFZP586G0522 protein	0.80	1.19	0.37	0.86	1.93	1.03	2.21	0.88	0.87	0.65	1.14	1.60	0.30	1.77	1.11	0.88	0.43	0.82	0.90	1.15	0.94	0.99
121252	Hs.7503	ESTs	1.26	0.50	0.82	1.06	0.69	0.71	0.54	0.40	1.09	0.75	0.98	0.61	0.87	0.74	1.06	1.05	1.03	0.65	0.45	0.49	0.42	0.63
197676	Hs.7972	KIAA0871 protein	0.63	0.66	0.70	0.53	0.62	0.57	0.75	0.63	0.75	0.72	0.44	0.57	0.40	0.70	0.59	2.67	0.61	0.64	0.67	0.71	0.54	0.52
306806	Hs.7988	ESTs	1.83	1.13	0.41	0.60	1.50	1.25	0.55	0.57	0.92	4.17	1.50	1.12	1.01	1.09	0.79	0.99	0.91	1.20	1.47	0.85	1.68	1.93
209624	Hs.250820	ESTs	0.83	1.37	0.75	2.15	1.68	1.28	1.72	1.32	1.76	1.59	1.99	2.01	1.93	1.24	1.34	1.47	1.28	0.71	0.83	1.19	0.96	1.43
247655	Hs.7740	ESTs	0.40	0.35	0.20	0.30	0.65	0.35	0.39	0.42	0.33	0.78	0.42	0.58	0.29	0.48	0.41	0.37	0.32	0.39	0.32	0.49	0.81	0.53
34302	Hs.221426	ESTs	1.14	2.01	1.67	1.51	2.33	1.37	1.34	1.70	1.69	1.62	2.77	2.37	1.98	2.16	1.70	2.26	1.48	1.13	1.01	1.27	1.89	1.91
142139	Hs.7905	ESTs, Highly similar to sorting nexin 9 [H.sapiens]	0.84	1.08	1.37	1.22	2.31	1.34	1.20	2.68	2.23	2.62	2.76	2.16	0.79	1.08	1.91	1.59	2.30	2.78	2.31	1.44	2.49	1.03

233308	Hs.7922	ESTs, Weakly similar to contains similarity to human cyclin A/CDK2-associated protein p1	1.44	0.90	1.63	1.77	0.72	1.07	1.14	0.56	4.10	4.28	1.88	2.41	0.87	1.44	1.69	2.48	2.16	2.25	2.19	1.37	0.77	0.68
113048	Hs.5459	ESTs	1.24	0.96	1.11	0.82	1.55	1.01	0.51	1.02	0.76	0.74	1.87	1.84	1.01	1.38	1.90	0.85	0.97	1.03	0.67	0.79	1.26	0.91
236129	Hs.202955	Homo sapiens mRNA; cDNA DKFZp434B1935 (from clone DKFZp434B1935)	1.57	0.95	0.82	0.92	1.01	1.29	0.99	1.97	1.53	1.52	1.20	2.05	2.18	2.15	2.03	1.43	2.26	1.56	0.94	1.35	0.53	0.72
196650	Hs.8999	ESTs	1.31	2.15	0.76	1.17	1.36	1.34	1.72	1.86	1.65	2.18	1.22	3.33	1.26	1.72	2.38	1.50	1.34	1.23	3.07	1.26	2.07	1.05
144797	Hs.8230	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif,	2.15	6.48	3.98	4.17	6.42	2.09	6.39	4.74	2.88	14.39	1.01	4.56	3.08	2.46	4.30	0.84	5.89	7.19	6.28	0.99	3.71	6.21
121577	Hs.8261	Homo sapiens clone 24921 mRNA sequence	2.16	1.83	1.13	1.53	3.26	1.41	2.36	2.38	3.28	1.27	1.88	1.77	0.68	1.11	1.23	2.01	0.70	1.14	2.02	0.97	1.03	1.76
206816	Hs.170310	ESTs	2.45	9.07	1.53	3.18	2.99	2.05	7.91	2.20	3.96	4.70	0.24	6.49	1.58	3.04	3.14	1.37	6.72	4.22	9.08	1.04	2.58	0.91
241988	Hs.8737	ESTs	1.01	1.45	0.78	1.09	1.70	1.03	1.84	2.11	0.96	1.22	0.50	2.00	2.09	1.14	1.89	1.13	1.46	1.92	2.05	1.11	1.16	0.65
295410	Hs.8854	ESTs	1.01	2.51	0.71	0.86	2.77	1.38	1.28	1.69	1.12	1.80	2.25	1.69	1.04	0.94	1.60	1.24	0.89	0.95	0.95	0.87	1.07	1.15
29063	Hs.90797	Homo sapiens clone 23620 mRNA sequence	0.43	0.71	0.38	0.36	0.94	0.76	0.35	0.75	0.72	0.99	0.83	0.63	0.46	0.40	0.83	0.59	0.59	0.49	0.26	0.56	0.19	0.91
244955	Hs.9884	spindle pole body protein	1.41	3.46	1.34	1.65	3.73	1.87	1.16	1.32	1.19	1.32	1.04	0.94	0.65	0.85	1.12	1.00	2.10	1.62	1.79	1.00	0.79	1.84
139138	Hs.168491	ESTs, Moderately similar to TRF1-interacting ankyrin-related ADP-ribose polymerase [H.sa	1.55	3.44	3.53	1.00	3.35	0.79	0.90	2.57	1.90	0.95	1.00	2.26	1.72	1.38	1.56	0.64	2.04	1.56	0.88	1.20	0.80	0.64
138929	Hs.239870	Homo sapiens mRNA; cDNA DKFZp564H0764 (from clone DKFZp564H0764)	0.99	1.79	1.53	1.42	2.02	1.01	1.50	0.93	1.58	1.19	0.90	1.30	0.34	0.63	0.80	0.95	0.77	0.90	0.81	1.04	0.74	1.24
366156	Hs.107573	sialyltransferase	1.02	1.60	1.84	1.11	1.77	0.76	1.42	2.26	2.22	3.02	1.47	3.09	1.12	1.61	1.71	0.78	2.32	1.04	1.81	1.15	1.92	1.63
143227	Hs.9645	ESTs	0.61	1.36	0.78	0.59	1.80	0.60	1.20	0.86	1.05	1.16	1.23	0.75	0.65	1.01	0.85	1.23	0.81	0.88	0.91	0.91	0.77	0.69
281114	Hs.252748	ESTs	0.66	1.30	0.95	0.74	1.47	0.46	0.74	1.09	0.94	1.13	0.68	1.26	0.60	1.02	1.17	0.46	0.97	1.17	1.34	1.06	1.26	1.38
120561	Hs.9873	ESTs	1.15	0.64	1.24	0.64	1.11	0.76	1.33	0.41	1.33	2.03	0.37	1.70	0.79	1.27	1.39	2.32	2.22	1.45	0.93	1.05	0.42	0.72
142944	Hs.10784	ESTs	0.63	0.46	1.98	0.59	1.09	0.34	0.34	0.42	0.45	0.35	0.40	0.66	0.22	0.39	0.49	0.42	0.50	0.49	0.51	0.38	0.81	0.73
66406	Hs.104859	ESTs	2.40	2.87	1.32	2.02	2.03	1.82	4.10	2.39	0.82	2.13	1.77	1.29	0.83	1.20	1.34	0.59	1.36	0.78	2.68	1.88	1.78	2.26
142076	Hs.10490	ESTs	0.97	1.24	0.84	1.22	1.59	1.54	1.61	1.01	0.95	0.78	0.93	1.35	0.68	1.22	1.59	0.98	0.48	0.88	1.16	0.88	0.99	1.75
36607	Hs.8372	ubiquinol-cytochrome c reductase (6.4kD) subunit	0.58	0.63	0.60	0.79	0.57	0.53	0.71	0.65	0.70	1.11	0.79	0.63	0.79	0.78	0.90	0.75	0.70	0.56	1.21	0.77	0.74	0.40
274529	Hs.10862	ESTs	0.31	0.88	0.48	1.55	0.83	0.93	0.24	0.46	0.61	0.48	1.29	1.74	1.30	1.37	0.79	0.69	0.57	0.31	0.20	0.30	1.11	1.03
83210	Hs.38069	complement component 8, beta polypeptide	1.06	1.48	1.03	1.13	1.24	0.94	1.00	1.82	1.60	1.36	1.77	1.02	0.68	0.93	1.05	1.35	1.10	1.52	1.44	1.26	1.49	1.38
232658	Hs.179898	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	0.68	1.00	0.99	0.86	0.82	0.81	1.17	0.76	0.83	0.81	0.85	1.00	0.62	0.65	0.93	1.67	1.01	1.30	1.04	1.04	0.55	0.64
309092	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	0.79	1.40	0.73	1.53	2.16	1.44	0.66	0.93	1.25	0.69	1.96	1.01	0.39	0.80	0.74	1.06	0.80	0.69	0.49	1.00	1.00	1.86
201301	Hs.11248	ESTs	1.45	1.86	1.05	1.39	3.02	1.18	1.87	1.76	1.41	1.57	1.37	1.72	0.29	0.83	0.86	0.81	1.04	1.35	1.31	1.51	1.05	1.41
293177	Hs.11460	ESTs	1.81	1.20	1.72	1.31	1.11	0.74	1.33	0.80	1.99	2.56	0.90	1.72	0.75	1.07	1.47	2.06	1.66	1.51	1.71	1.48	0.95	1.17
42313	Hs.75323	prohibitin	0.88	1.58	0.61	1.46	0.83	1.05	1.64	3.17	1.06	1.12	3.36	0.94	1.04	1.21	1.28	1.63	1.28	1.20	1.28	1.51	1.74	2.00
38465	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha 1	1.37	1.00	0.98	0.88	0.88	0.61	1.14	1.16	0.88	1.79	1.00	1.18	0.65	0.70	1.07	0.68	0.85	1.07	0.85	1.15	0.66	0.75
345047	Hs.11582	ESTs	1.97	4.57	1.73	1.01	2.70	1.01	4.01	2.17	1.49	3.51	0.30	2.48	0.83	1.02	1.88	0.61	2.48	2.50	2.22	0.78	1.94	0.91
144042	Hs.239720	ESTs, Weakly similar to KIAA0691 protein [H.sapiens]	1.14	1.67	1.22	1.36	1.76	1.05	1.44	1.85	2.03	1.65	0.26	1.45	0.68	0.85	1.16	1.05	1.68	1.44	2.14	1.29	1.78	0.89
47853	Hs.77448	aldehyde dehydrogenase 4 (glutamate gamma-semialdehyde dehydrogenase; pyrroline-5	2.02	1.37	1.01	0.87	1.74	1.01	0.95	1.00	1.46	2.69	1.11	4.93	1.95	1.58	2.59	1.40	2.61	2.07	1.46	0.83	0.93	0.91
66552	Hs.119021	ESTs	0.83	0.79	1.42	0.85	0.96	0.86	1.26	1.04	1.01	2.18	0.67	2.50	1.11	1.61	2.71	1.55	1.43	1.49	1.38	1.19	0.45	0.30
297102	Hs.12028	ESTs	0.83	2.18	0.86	1.46	2.04	1.37	0.92	1.04	1.21	0.95	1.21	0.89	0.77	0.71	0.94	0.88	0.97	0.90	0.86	1.12	0.62	1.41
283897	Hs.91585	protein phosphatase 1, regulatory (inhibitor) subunit 2	1.82	0.88	1.29	1.09	1.61	1.14	0.71	1.08	2.91	3.52	0.59	1.11	1.38	0.65	1.43	0.83	1.16	1.19	1.91	1.03	0.53	1.24
245195	Hs.12908	CDC42-binding protein kinase beta (DMPK-like)	0.80	1.28	0.74	0.98	3.37	1.09	0.85	1.56	1.25	1.36	1.06	1.12	0.75	0.81	1.00	1.35	1.16	1.24	1.49	0.97	0.77	1.65
234331	Hs.12030	ESTs	0.73	1.83	0.49	1.57	1.67	1.30	1.29	1.24	1.33	1.70	0.84	1.91	1.01	1.65	1.89	0.60	1.07	1.38	1.74	1.05	0.91	1.93
133820	Hs.12259	KIAA0630 protein	1.47	2.56	2.40	1.82	1.81	1.35	1.34	2.28	2.45	2.84	1.93	1.28	0.86	0.81	1.16	0.68	2.11	1.66	1.88	1.51	1.33	2.00
135561	Hs.12439	ESTs, Weakly similar to KIAA0840 protein [H.sapiens]	0.76	2.30	1.07	0.64	1.49	1.21	1.11	1.06	1.36	1.96	1.38	1.78	1.51	1.15	1.44	1.05	1.14	1.11	1.55	0.93	1.03	0.91
247818	Hs.239666	ESTs	1.50	2.06	1.72	2.23	3.43	2.07	2.55	1.69	1.14	1.00	1.01	0.88	0.58	0.67	0.83	0.62	1.46	0.83	0.73	1.23	1.58	0.91
243817	Hs.12547	ESTs	1.03	1.07	1.60	0.66	0.42	0.41	0.81	0.79	1.15	3.08	0.78	0.90	1.15	0.60	1.10	0.29	1.87	1.51	1.55	0.91	1.36	1.89
230196	Hs.13179	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.71	1.19	1.17	1.44	2.25	1.23	1.86	0.35	0.95	1.79	1.34	2.74	0.61	1.48	2.69	1.95	2.27	2.15	5.35	1.55	0.40	0.91
244847	Hs.13702	ESTs	1.10	1.28	0.40	0.54	0.58	1.40	0.73	0.38	0.62	0.62	0.44	1.82	0.64	0.61	0.98	2.76	0.44	0.76	0.48	0.92	0.55	0.52
108265	Hs.13740	ESTs	0.83	1.00	0.54	0.55	2.09	1.03	0.84	0.92	0.82	0.81	3.39	0.85	0.64	0.49	1.13	1.09	0.79	1.16	1.15	0.48	1.90	1.42
108351	Hs.13781	ESTs	2.88	2.79	0.61	1.56	5.33	2.87	4.34	2.00	1.56	1.09	2.87	2.63	4.47	2.79	4.75	3.15	5.39	4.50	5.40	2.26	2.49	0.91
110094	Hs.13785	ESTs	1.15	1.12	1.21	1.04	1.39	1.04	1.75	1.02	1.30	0.85	2.59	2.65	1.08	2.09	0.80	4.01	3.17	2.12	3.92	1.96	0.25	1.65
247803	Hs.13895	ESTs	0.99	1.16	0.62	0.71	1.03	1.42	1.27	0.43	1.08	1.20	1.23	1.47	0.86	0.72	1.30	1.76	0.93	1.06	1.20	1.08	0.41	0.83
294973	Hs.23672	low density lipoprotein receptor-related protein 6	2.18	0.64	1.11	1.07	2.03	1.76	12.71	1.96	1.40	1.29	1.86	1.90	0.85	0.69	1.79	1.98	3.24	2.54	2.12	0.88	0.73	1.40
123408	Hs.69559	KIAA1096 protein	2.23	0.86	1.82	0.68	0.94	1.49	1.56	0.94	1.64	2.61	0.32	2.80	1.00	1.27	2.47	0.61	2.31	1.58	1.25	1.36	0.26	1.38
275802	Hs.14173	ESTs	1.61	1.46	3.01	1.95	2.32	2.23	2.17	2.16	2.12	1.79	1.37	2.76	1.28	2.14	2.11	0.50	2.30	3.21	3.07	2.49	1.44	0.70
297439	Hs.14355	ESTs	1.14	1.20	0.71	1.56	2.01	1.09	1.44	0.89	0.87	1.11	1.09	0.65	0.68	1.23	1.54	1.18	1.27	0.81	1.06	1.05	0.58	0.91
144902	Hs.239938	ESTs	1.60	3.18	1.31	2.15	2.16	1.72	2.85	1.76	1.87	2.72	2.24	4.05	1.34	2.46	2.60	4.74	2.38	1.98	2.52	1.29	1.74	1.39
251461	Hs.14619	ESTs	2.49	1.96	0.36	2.42	6.66	2.85	2.95	1.05	1.75	0.72	4.84	3.08	1.87	1.41	3.08	2.12	2.11	3.12	1.17	1.31	2.85	1.61
121270	Hs.14870	ESTs	1.19	1.70	0.77	1.07	1.29	0.80	1.07	1.16	1.14	0.95	2.50	1.02	0.77	1.02	0.88	0.83	0.80	1.07	1.19	0.76	0.52	1.47
245885	Hs.15036	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	1.02	1.72	1.59	1.41	1.99	1.13	1.20	3.29	2.08	1.88	2.50	0.80	0.68	0.55	0.92	0.38	0.98	1.52	1.70	1.25	2.12	0.91
245745	Hs.14931	ESTs	1.69	3.95	1.32	2.66	4.88	0.84	5.33	2.14	1.39	1.57	1.78	1.39	0.98	1.40	2.51	1.12	0.95	2.31	2.46	1.36	1.34	0.91
139354	Hs.15093	ESTs	0.48	0.38	0.69	0.22	0.79	0.69	0.32	0.94	0.86	1.88	1.68	1.31	0.96	0.79	1.39	0.94	1.03	0.46	0.99	0.55	0.66	1.18
140171	Hs.15098	ESTs	2.24	2.31	2.31	1.42	2.26	1.59	1.39	1.33	1.79	2.08	3.33	3.38	1.90	1.99	2.63	2.67	2.25	1.76	1.84	1.74	1.47	1.61
198605	Hs.15514	ESTs	0.63	1.28	0.83	0.76	1.91	0.68	0.79	1.32	0.78	1.26	1.01	1.02	0.78	0.75	1.10	1.30	0.52	1.02	0.83	0.81	2.38	1.28
111571	Hs.15654	ESTs, Highly similar to HP1-BP74 protein [M.musculus]	3.40	2.39	0.99	2.50	3.63	2.59	0.87	1.34	1.33	0.75	2.76	6.88	5.10	2.74	5.92	1.39	2.06	2.35	1.61	2.04	1.82	0.91
295985	Hs.180059	ESTs	0.30	1.03	0.70	1.66	1.59	0.62	3.49	0.44	0.75	0.53	0.90	0.85	0.26	0.37	0.52	0.46	0.20	0.53	0.30	0.39	0.55	1.88
244154	Hs.184227	F-box protein 21	1.20	1.42	0.55	0.93	2.37	1.18	2.16	1.18	1.59	1.13	2.04	1.36	1.39	0.90	1.40	1.07	1.30	1.73	1.93	1.22	1.85	0.91
129293	Hs.15783	ESTs	0.56	1.27	0.73	0.70	1.96	0.80	0.60	0.93	0.88	0.70	1.59	1.33	1.01	0.71	1.06	1.02	0.76	0.82	0.89	0.84	0.61	0.91
111765	Hs.15797	ESTs	2.07	2.01	0.52	1.32	2.44	1.51	2.44	1.10	2.03	1.82	2.96	3.70	3.27	2.39	2.10	1.29	2.90	1.58	1.92	1.85	2.08	2.14
111391	Hs.15866	ESTs	1.65	1.57	0.46	0.62	2.32	1.28	1.30	1.22	1.10	1.34	2.85	1.79	1.65	1.17	1.42	0.91	1.76	1.71	1.76	1.07	1.25	0.91
161195	Hs.8258	DKFZP434D1335 protein	1.40	2.60	1.13	1.62	2.04	2.38	2.09	0.97	1.24	1.29	1.76	1.06	0.82	1.02	1.27	1.30	1.24	1.04	0.95	1.21	1.33	1.79
206544	Hs.238954	ESTs	3.12	1.98	1.30	2.18	1.25	1.96	3.12	0.60	1.92	1.20	1.44	5.23	1.34	2.24	3.68	3.44	3.80	3.11	2.38	1.19	0.57	0.91
130243	Hs.16740	ESTs	1.09	0.66	0.27	0.40	1.17	1.19	0.43	0.84	0.59	1.49	3.29	1.12	0.35	0.62	0.72	0.63	0.28	0.41	0.44	0.51	1.26	0.91
111006	Hs.168212	kinesin family member 3B	0.70	0.70	0.49	0.79	1.48	0.68	1.09	0.87	1.23	1.25	1.97	0.76	0.69	0.70	0.85	1.10	1.00	0.85	0.94	0.83	1.75	0.94
293569	Hs.16769	ESTs	1.00	1.17	0.38	0.65	1.59	1.42	0.59	1.43	0.93	1.16	1.02	2.43	1.16	0.53	3.47	1.08	1.50	4.03	4.23	0.91	1.18	0.91
234398	Hs.16773	ESTs	1.80	0.99	0.96	0.96	0.53	0.87	1.68	0.58	1.35	1.67	0.97	1.48	0.69	0.82	1.62	3.90	0.79	1.21	2.01	1.28	0.47	0.37
203469	Hs.12329	KIAA0697 protein	2.15	1.39	1.15	1.16	0.81	0.72	1.37	0.94	1.39	1.11	0.91	2.38	0.90	1.06	1.58	2.25	1.19	1.54	1.36	1.42	0.57	1.02
120695	Hs.31334	putative mitochondrial outer membrane protein import receptor	1.48	1.76	1.24	1.23	4.18	2.78	0.80	1.94	1.50	1.28	0.55	2.67	1.48	1.29	1.90	1.14	2.54	1.26	0.66	1.01	0.93	0.91
294881	Hs.17713	ESTs	1.14	0.81	0.72	0.42	1.04	0.51	1.65	1.55	1.18	0.95	0.19	0.95	0.79	0.86	0.87	0.26	0.61	0.89	1.38	0.66	0.18	0.55
121159	Hs.17936	Homo sapiens mRNA; cDNA DKFZp434H132 (from clone DKFZp434H132)	0.83	1.08	0.96	0.89	3.32	0.66	1.19	0.29	1.36	1.53	1.10	1.56	0.69	1.68	1.32	0.92	0.55	0.82	0.80	1.28	0.38	0.91
137793	Hs.17962	ESTs	3.26	5.74	0.55	1.97	5.33	2.16	9.12	4.37	1.38	4.31	4.66	22.76	6.82	5.54	17.86	1.24	7.58	2.96	15.06	0.64	3.00	0.91
130276	Hs.18016	Homo sapiens mRNA; cDNA DKFZp586H0324 (from clone DKFZp586H0324)	0.89	1.04	1.03	1.04	1.12	0.82	1.47	0.76	1.70	1.30	0.90	0.83	0.62	2.47	0.99	2.92	1.05	0.99	1.47	1.70	0.74	0.90
121501	Hs.220831	ESTs	1.58	1.23	1.40	1.63	0.92	0.90	2.12	0.80	1.95	1.00	0.72	2.60	0.82	1.22	1.69	3.07	2.66	1.43	2.11	1.37	1.42	0.58
214165	Hs.18046	ESTs	1.97	3.76	1.52	2.28	4.07	2.86	1.97	4.45	2.48	1.89	4.51	2.85	1.21	1.68	2.52	2.54	3.50	1.67	2.32	1.06	2.25	0.91
121459	Hs.18067	ESTs	1.56	1.11	0.75	0.57	1.18	0.82	2.05	0.35	0.67	1.71	0.54	1.94	0.87	0.67	1.21	0.98	2.48	1.36	2.18	1.09	0.92	0.91
139113	Hs.18271	ESTs, Weakly similar to Ydr372cp [S.cerevisiae]	3.22	1.89	1.06	1.34	0.99	1.39	2.11	2.22	2.20	0.95	1.20	1.51	1.31	1.50	1.54	1.08	1.28	1.77	2.02	2.25	1.48	0.44

121736	Hs.18213	EST	2.22	0.51	1.02	0.36	1.63	0.80	2.97	1.52	1.44	0.95	0.21	1.83	0.77	1.05	1.56	0.38	2.54	2.75	2.02	1.55	0.31	0.39
134525	Hs.78946	cullin 3	1.12	0.90	0.98	1.32	1.52	0.85	1.65	0.69	1.25	1.48	1.04	1.19	0.69	0.89	1.39	1.08	1.27	1.55	1.79	1.18	0.66	0.81
121994	Hs.18331	ESTs	1.49	1.88	1.03	1.78	2.11	1.08	2.03	1.30	1.45	1.83	1.50	1.06	0.80	0.83	1.54	1.13	1.80	1.97	2.03	1.37	1.93	1.48
357970	Hs.18368	DKFZP564B0769 protein	0.84	1.29	0.95	1.98	1.70	1.14	0.70	1.08	0.76	0.69	0.90	1.15	0.39	0.57	1.00	0.41	0.88	1.61	1.18	0.67	0.58	0.96
296444	Hs.18376	ESTs	0.66	1.59	0.70	1.48	4.39	0.73	2.88	2.60	1.74	3.32	1.90	2.86	1.66	0.88	2.09	0.98	3.34	1.76	1.23	0.44	1.90	1.52
122397	Hs.18616	ESTs	1.91	1.57	1.83	1.75	2.06	1.23	2.18	0.75	1.24	1.34	1.07	2.68	1.46	1.91	1.49	1.07	1.05	0.89	1.95	1.62	1.19	1.45
122295	Hs.18463	ESTs	2.11	2.99	0.73	1.20	3.32	1.29	1.84	1.94	1.61	1.97	2.57	1.88	1.52	0.73	2.54	1.13	1.21	2.24	1.76	1.54	1.91	2.40
122443	Hs.18624	KIAA1052 protein	2.16	1.86	1.52	0.97	3.38	3.43	0.94	2.89	1.93	1.56	6.44	2.38	0.98	1.29	1.56	1.48	3.32	1.86	3.53	1.17	1.48	2.21
123405	Hs.61960	ESTs, Moderately similar to HYPOTHETICAL PROTEIN KIAA0176 [H.sapiens]	0.89	1.07	0.57	0.55	1.03	0.98	1.01	0.63	0.76	0.96	0.89	1.20	0.74	0.82	0.87	1.07	1.02	0.80	0.89	1.13	0.58	0.55
244686	Hs.18800	ESTs, Weakly similar to KIAA0579 protein [H.sapiens]	2.03	1.67	1.13	1.80	3.84	2.68	1.71	2.67	4.96	4.52	2.21	1.95	0.79	0.93	1.83	1.22	3.83	2.62	2.37	1.17	1.47	0.83
123441	Hs.99858	ribosomal protein L7a	0.51	1.13	0.92	1.13	1.35	0.94	0.54	0.85	0.84	0.61	0.78	1.67	1.10	0.98	0.89	1.25	0.59	0.55	0.43	0.69	0.89	1.90
198874	Hs.19039	ESTs	1.01	1.45	0.81	1.16	2.14	0.57	1.08	1.63	0.98	1.37	1.22	1.12	0.97	0.76	1.55	0.61	1.94	2.05	1.59	1.08	1.79	1.13
244062	Hs.19054	ESTs	2.87	1.51	1.50	1.44	1.83	1.74	4.86	3.05	1.77	2.21	2.34	2.51	0.93	1.69	2.43	2.45	3.66	2.15	2.45	3.50	3.24	0.44
124179	Hs.19175	ESTs	1.82	4.35	2.51	1.41	3.28	1.48	3.38	2.70	1.66	2.28	3.18	1.72	1.06	0.81	1.60	1.50	1.46	2.10	3.36	2.13	2.52	2.13
233688	Hs.8850	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	1.87	1.36	2.95	1.82	2.95	2.57	1.19	2.11	8.22	1.85	2.77	3.74	1.11	3.57	2.25	3.02	3.00	3.23	4.33	2.86	1.45	0.91
245442	Hs.19306	sir2-like 3	1.18	1.22	0.50	0.86	1.64	0.96	1.08	1.16	1.18	0.87	1.31	0.77	0.94	0.63	1.11	1.03	1.03	2.10	1.95	0.85	0.99	1.41
128785	Hs.19479	ESTs	2.79	3.63	1.50	3.14	3.31	2.02	3.98	3.17	2.08	3.15	2.26	2.90	1.40	1.60	2.64	1.45	3.63	3.05	3.76	3.18	2.41	2.14
126221	Hs.154718	tumor protein D52-like 2	1.03	1.27	0.83	0.95	1.95	0.74	0.87	1.36	0.56	0.99	0.91	1.46	1.03	1.12	0.84	1.18	1.07	0.43	0.60	0.75	0.37	1.31
126887	Hs.183749	ESTs	1.47	1.61	0.32	0.60	2.05	1.21	1.68	0.65	1.27	1.62	0.69	1.86	0.75	0.96	1.22	1.25	1.11	1.41	1.74	1.15	1.00	0.91
126650	Hs.132959	ESTs	3.12	2.99	1.90	2.06	4.26	2.08	2.23	1.56	1.79	1.21	3.40	2.16	1.14	0.88	2.06	3.01	1.70	1.45	4.62	1.26	1.64	0.91
341821	Hs.94769	ESTs, Moderately similar to RAS-RELATED PROTEIN RAB-23 [M.musculus]	1.86	1.32	0.64	1.09	2.64	1.82	2.47	1.06	1.37	2.05	1.60	1.75	0.64	0.69	1.29	0.82	1.87	2.27	2.53	0.99	1.52	1.84
125589	Hs.163118	ESTs	1.20	1.70	0.78	0.78	2.35	1.31	1.40	1.41	1.51	1.45	1.16	1.25	0.88	1.10	1.05	1.21	1.01	1.02	1.38	1.18	1.63	1.66
210688	Hs.20196	adenylate cyclase 9	1.02	0.86	0.79	0.61	0.98	0.53	1.07	2.34	1.09	1.37	1.21	0.77	1.08	0.68	1.37	0.67	1.13	1.37	1.20	0.75	0.86	0.91
230224	Hs.124777	ESTs	1.23	1.57	1.61	2.21	3.26	1.39	1.92	0.89	1.17	2.32	1.59	1.19	0.53	0.55	1.17	0.94	1.60	1.81	1.56	0.69	1.06	1.36
127409	Hs.124244	ESTs	1.35	0.71	0.98	0.65	0.63	0.59	2.86	0.76	1.45	1.59	0.32	1.40	0.76	1.35	1.54	0.49	0.87	1.72	2.17	2.23	0.92	0.91
127099	Hs.20100	ESTs, Moderately similar to atypical PKC specific binding protein [R.norvegicus]	1.61	2.07	1.19	2.02	1.47	2.61	1.77	1.40	1.23	1.28	1.05	0.94	0.89	0.82	0.87	0.49	2.51	1.54	1.40	1.35	1.33	0.91
143759	Hs.20157	ESTs	0.67	0.90	0.34	0.68	2.15	0.64	0.50	0.55	0.62	1.02	0.69	0.56	0.40	0.40	0.57	0.71	0.58	0.59	0.66	1.06	0.58	0.91
345670	Hs.20665	ESTs	3.86	1.65	1.88	0.63	2.39	1.42	13.09	1.25	2.71	1.46	2.35	3.26	0.99	2.08	2.64	1.05	5.08	5.29	5.04	0.90	3.46	0.91
203514	Hs.21256	ESTs	1.81	0.73	1.08	0.90	0.80	0.73	1.08	0.75	1.23	1.63	0.42	1.89	1.17	1.02	1.40	0.40	1.89	2.19	1.37	0.97	0.84	1.19
130004	Hs.20854	ESTs	2.59	3.97	2.57	5.00	3.94	3.54	5.79	3.53	1.62	2.07	1.57	2.98	2.22	1.94	2.78	2.06	2.70	2.08	7.79	1.51	1.52	0.91
243291	Hs.20888	ESTs	0.97	1.20	0.94	0.86	0.97	0.57	0.73	0.95	1.62	0.94	0.58	0.76	0.55	0.59	0.76	0.34	0.70	1.39	2.14	0.82	0.61	2.13
299737	Hs.20952	Homo sapiens clone 24411 mRNA sequence	0.88	1.29	0.89	1.79	2.63	1.15	1.19	1.16	1.73	1.07	1.34	1.38	0.80	0.81	1.11	1.00	1.23	1.86	1.27	0.99	1.23	0.91
207082	Hs.251788	glucosamine-6-phosphate deaminase	1.75	1.39	1.08	1.30	1.16	1.40	1.06	1.18	0.87	1.14	1.01	1.15	1.49	1.19	1.53	1.18	0.88	0.93	1.03	0.72	1.35	2.02
770670	Hs.211600	tumor necrosis factor, alpha-induced protein 3	0.74	3.33	2.03	2.62	2.07	2.76	1.31	2.17	2.54	1.00	2.46	4.12	1.15	1.56	2.03	2.68	2.08	2.66	1.98	2.15	1.04	2.51
162211	Hs.76781	ATP-binding cassette, sub-family D (ALD), member 3	1.17	1.60	0.82	1.50	1.26	0.99	0.56	0.86	1.05	0.84	1.10	0.86	1.17	0.36	1.62	0.71	1.04	1.41	0.85	0.93	1.81	1.00
140806	Hs.83920	peptidylglycine alpha-amidating monooxygenase	0.69	0.78	0.92	0.67	1.10	0.17	1.02	0.87	1.47	0.35	0.77	0.44	0.13	0.44	0.69	0.66	0.22	0.52	0.55	0.39	0.60	0.77
45556	Hs.172766	MAP/microtubule affinity-regulating kinase 3	1.30	1.60	1.34	1.40	1.75	1.02	0.97	1.57	0.79	1.00	1.46	1.90	0.80	0.56	1.32	0.72	0.99	1.64	2.16	1.26	1.79	0.99
34773	Hs.83572	Human clone 23721 mRNA sequence	0.59	0.70	0.89	2.12	0.58	0.81	0.43	0.45	1.02	0.51	0.69	1.37	2.94	1.08	1.47	0.72	0.70	0.80	0.37	1.00	0.45	0.79
49920	Hs.77329	phosphatidylserine synthase 1	1.11	1.26	1.24	1.56	0.70	0.98	1.14	0.78	0.74	0.93	0.87	0.52	0.93	0.80	0.97	0.86	0.77	1.04	0.77	1.31	0.60	1.14
345430	Hs.85701	phosphoinositide-3-kinase, catalytic, alpha polypeptide	2.27	3.41	1.18	1.29	3.17	1.68	1.73	1.75	1.58	1.83	1.81	1.81	1.18	1.29	1.83	0.43	1.39	1.49	1.67	1.09	1.27	1.72
770027	Hs.173902	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	0.40	0.56	0.84	0.43	0.53	0.32	0.77	0.69	0.75	0.62	0.66	0.57	0.68	0.45	0.63	0.70	0.76	0.48	0.73	0.57	0.63	0.59
769657	Hs.91585	protein phosphatase 1, regulatory (inhibitor) subunit 2	2.97	2.88	1.29	2.12	2.71	2.21	0.99	2.07	2.54	2.01	2.89	1.50	2.76	1.16	1.95	1.30	1.28	1.66	2.09	1.44	1.34	2.16
509495	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	0.93	1.09	0.98	0.86	0.47	0.77	0.83	0.77	1.06	0.91	1.38	0.89	1.16	1.30	1.13	0.85	1.33	0.53	0.89	1.50	0.61	0.63
68977	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 10	1.35	2.92	0.86	1.53	3.42	2.71	0.78	2.00	2.37	1.65	3.05	3.31	1.13	2.44	3.99	2.28	2.47	0.81	1.54	0.50	1.57	1.75
194804	Hs.79709	phosphotidylinositol transfer protein	0.64	0.91	1.14	1.00	1.25	1.15	0.74	0.91	0.76	0.86	0.82	0.86	0.84	1.17	0.76	1.07	0.70	0.99	0.60	1.12	0.65	0.76
770452	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein	1.93	2.05	1.47	2.43	1.70	1.63	1.23	0.95	0.97	0.99	1.04	2.87	1.27	1.63	1.71	0.52	1.68	2.00	1.45	0.84	1.29	1.05
308281	Hs.89781	upstream binding transcription factor, RNA polymerase I	1.77	2.21	1.47	1.28	2.08	2.27	2.10	1.60	2.03	1.80	3.22	2.10	1.22	1.61	1.98	1.63	1.68	1.47	2.38	1.29	0.85	1.00
299388	Hs.151734	nuclear transport factor 2 (placental protein 15)	2.34	1.76	1.31	1.25	1.78	1.30	2.32	1.27	1.74	1.81	1.24	1.23	0.52	0.86	0.90	0.98	1.50	0.85	1.58	0.66	1.88	1.22
43884	Hs.173125	peptidylprolyl isomerase F (cyclophilin F)	0.99	1.77	1.02	1.89	1.29	1.05	2.04	1.24	0.83	0.88	1.52	1.38	5.74	1.45	1.18	1.44	0.77	1.60	1.41	1.54	1.06	1.35
162775	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)	1.29	0.74	0.78	1.30	0.78	1.23	0.36	0.81	0.95	0.39	0.99	0.70	2.87	1.70	1.06	1.08	0.89	1.17	0.75	1.61	0.94	1.19
128159	Hs.169750	translocated promoter region (to activated MET oncogene)	3.38	2.66	1.88	2.77	1.80	2.33	1.82	1.94	2.04	2.00	1.29	3.12	1.89	1.17	2.46	0.55	2.10	1.58	2.11	0.92	2.46	0.91
809627	Hs.155017	nuclear receptor interacting protein 1	0.33	0.71	0.69	0.55	1.37	0.60	0.41	0.82	1.63	2.80	0.54	1.09	1.43	1.10	1.76	0.51	1.28	0.97	2.71	0.63	0.65	1.94
725473	Hs.74085	DNA segment on chromosome 12 (unique) 2489 expressed sequence	1.12	1.47	0.96	0.82	1.38	1.09	1.46	1.21	1.20	1.90	0.86	0.71	0.44	1.18	0.95	1.07	0.83	0.98	1.41	0.63	1.36	0.88
741497	Hs.204238	lipocalin 2 (oncogene 24p3)	0.94	2.07	0.22	0.26	2.64	1.14	0.51	0.59	0.16	0.22	0.59	0.51	0.16	0.45	0.48	0.35	0.18	0.44	0.44	1.38	0.87	0.31
753457	Hs.8248	NADH dehydroqenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase	0.56	0.96	0.67	0.94	0.72	0.62	0.78	0.90	0.61	1.51	0.55	1.06	0.76	1.09	1.10	0.57	0.96	0.72	0.92	0.91	0.60	0.60
813387	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5 reductase)	0.66	0.67	0.27	0.26	1.00	0.63	0.61	1.06	0.56	0.71	0.66	0.28	0.40	0.51	0.51	0.85	1.11	0.48	0.95	0.90	1.24	0.36
813279	Hs.78223	N-acylaminoacyl-peptide hydrolase	0.58	0.68	0.37	0.46	0.67	0.68	0.72	0.65	0.44	0.69	0.99	0.56	1.34	0.48	0.58	0.66	0.73	0.75	0.98	0.78	0.66	0.26
36493	Hs.75372	N-acetylgalactosaminidase, alpha-	1.06	0.76	2.18	1.30	1.50	1.58	0.90	1.47	1.96	2.02	1.45	2.08	1.98	2.21	1.86	1.45	1.50	1.43	1.40	1.16	0.91	0.88
296880	Hs.1861	membrane protein, palmitoylated 1 (55kD)	1.39	2.83	2.32	1.87	2.60	2.09	1.03	2.43	3.99	3.10	2.28	1.92	1.16	1.82	1.48	2.41	2.27	1.80	1.82	1.10	1.84	1.25
200814	Hs.1298	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	0.24	0.23	0.49	0.27	0.35	0.04	0.14	0.19	0.18	0.05	0.45	0.10	0.04	0.14	0.15	0.14	0.08	0.36	0.21	0.14	0.20	0.09
154707	Hs.75659	MpV17 transgene, murine homolog, glomerulosclerosis	1.46	1.75	1.49	1.58	1.27	1.07	2.05	1.63	1.83	1.98	1.37	1.55	0.81	1.28	1.74	1.38	1.55	1.61	1.75	1.01	1.23	0.69
131362	Hs.170328	moesin	2.15	1.79	1.66	0.97	1.47	1.29	2.42	0.97	1.20	0.69	0.90	1.33	0.24	0.83	0.72	0.86	0.58	0.98	0.94	0.73	0.98	1.39
809557	Hs.179565	minichromosome maintenance deficient (S. cerevisiae) 3	1.43	3.11	3.71	2.98	2.04	1.73	4.70	2.07	1.16	2.01	1.99	1.06	0.96	0.39	1.60	1.29	1.03	1.42	3.40	1.45	2.10	2.25
470393	Hs.2256	matrix metalloproteinase 7 (matrilysin, uterine)	1.75	1.09	2.52	3.33	1.98	0.12	9.03	1.68	5.32	1.49	0.59	1.79	0.17	0.52	0.44	0.45	0.73	0.78	0.69	0.30	0.47	3.22
768316	Hs.35750	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	0.57	1.01	1.59	0.90	1.79	0.50	0.80	0.78	0.78	0.38	0.78	1.04	0.36	0.75	1.47	0.74	0.64	1.29	1.04	0.72	1.57	0.72
212496	Hs.32965	mannosidase, alpha, class 2A, member 1	1.40	2.91	0.91	1.77	4.52	1.35	0.97	1.63	2.33	1.52	2.05	2.00	1.14	1.10	1.12	1.16	1.49	2.35	1.81	1.74	1.51	1.82
82879	Hs.2314	mannose-binding lectin (protein C) 2, soluble (opsonic defect)	1.65	0.82	2.19	1.72	0.36	0.32	2.36	0.84	2.02	1.69	4.82	2.29	0.92	1.19	0.51	0.72	2.05	1.59	2.19	0.77	0.27	1.20
289615	Hs.8262	lysosomal-associated membrane protein 2	2.65	2.64	1.50	1.52	2.22	1.22	1.37	2.04	1.89	1.89	1.64	1.47	0.67	0.89	1.30	0.77	1.91	1.97	2.88	0.91	1.62	1.51
813823	Hs.79914	lumican	4.04	1.89	3.31	10.15	5.45	8.06	20.72	9.76	8.79	12.43	13.93	17.74	3.79	5.23	16.15	6.20	7.94	7.27	16.54	3.70	4.53	5.34
770012	Hs.188021	potassium voltage-gated channel, subfamily H (eag-related), member 2	1.93	5.26	6.19	1.48	2.95	3.99	3.91	2.56	2.87	7.59	3.08	2.99	0.90	0.98	1.39	0.66	2.10	2.32	2.45	2.81	2.62	1.43
44255	Hs.79086	ribosomal protein, mitochondrial, L3	1.69	1.19	1.13	1.44	1.54	1.25	1.38	1.31	1.63	1.54	1.35	1.53	0.77	0.82	0.98	0.70	1.47	1.46	1.97	1.55	1.55	1.89
544664	Hs.78825	matrin 3	0.95	1.59	1.13	1.27	0.94	1.06	0.96	1.12	1.11	1.00	1.29	0.75	0.64	0.58	0.86	0.78	1.28	1.00	1.49	0.97	0.67	0.87
340734	Hs.81328	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	1.02	3.51	0.77	1.21	1.38	1.23	1.51	1.57	1.42	1.19	2.39	2.70	2.25	1.27	1.77	1.49	1.08	1.38	2.26	1.50	0.70	1.35
771323	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndr	1.50	1.12	2.25	0.55	1.11	0.82	1.41	0.77	0.79	0.54	1.31	1.05	0.35	0.98	0.48	0.70	0.40	0.61	0.82	0.91	0.48	1.10
770355	Hs.93199	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1.29	1.09	0.72	1.85	1.17	1.28	1.05	0.93	1.18	1.31	0.72	1.67	1.06	0.98	0.90	0.82	1.41	0.87	1.10	0.87	0.76	0.79
42558	Hs.75335	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	3.55	4.18	5.34	4.87	2.32	6.52	1.60	2.26	5.09	2.26	2.10	4.49	3.98	3.30	12.90	0.71	3.09	4.41	3.60	3.06	2.39	1.57
153025	Hs.2250	leukemia inhibitory factor (cholinergic differentiation factor)	0.55	1.30	0.38	0.39	3.26	0.83	1.39	0.68	0.76	0.53	0.61	0.83	0.33	0.45	1.08	0.36	0.34	1.19	0.66	0.97	0.87	0.44
32609	Hs.78672	laminin, alpha 4	0.84	0.90	7.73	2.76	1.66	1.62	0.95	1.78	3.37	2.76	1.94	1.96	0.79	1.67	1.90	2.00	1.46	1.38	1.26	1.59	1.57	0.86
811900	Hs.1116	lymphotoxin beta receptor (TNFR superfamily, member 3	1.16	2.77	1.34	1.62	1.68	1.26	4.84	1.45	1.81	2.24	0.93	1.52	0.57	1.79	0.93	1.48	1.24	1.39	1.60	1.35	1.92	1.74
51447	Hs.763	Fc fragment of IgG, low affinity IIIa, receptor for (CD16)	3.06	2.27	11.49	11.43	2.70	8.49	4.85	8.72	12.48	13.44	13.73	17.23	5.81	6.00	7.60	5.76	7.19	4.55	11.18	2.18	2.16	4.29
292236	Hs.21921	ESTs	1.79	1.39	0.89	1.35	2.13	1.06	0.84	1.08	1.10	0.93	1.11	1.15	0.97	1.33	1.36	1.06	1.67	1.97	1.42	1.00	1.30	0.91

156023	Hs.21362	ESTs, Weakly similar to acid-rich protein [C.elegans]	1.04	1.22	0.49	0.60	1.19	0.88	1.09	0.80	1.03	1.33	0.60	0.95	1.25	1.16	1.74	0.99	1.27	1.22	1.63	0.81	0.95	0.91
292171	Hs.21648	ESTs	2.00	0.52	0.85	1.35	0.63	1.05	4.74	0.32	0.63	2.78	0.96	1.98	2.02	1.91	2.27	0.60	3.15	1.86	1.61	1.08	0.47	1.38
138374	Hs.21801	ESTs	1.08	0.77	1.22	1.01	1.26	0.71	0.98	0.55	1.18	1.06	0.98	0.62	0.67	0.68	0.98	1.25	0.99	1.07	0.93	0.94	0.51	0.85
138304	Hs.238272	inositol 1,4,5-triphosphate receptor, type 2	1.98	0.59	1.54	1.42	1.97	0.93	10.63	0.26	1.01	2.34	1.52	2.79	2.09	1.31	3.09	1.74	1.88	3.69	2.94	1.38	0.42	0.86
301752	Hs.167716	ESTs	1.69	0.50	0.81	0.78	0.70	0.43	3.42	0.16	1.35	2.58	0.62	3.19	1.01	1.37	1.99	0.73	2.47	1.89	2.65	1.17	0.43	0.75
129817	Hs.155972	KIAA0615 gene product	1.40	1.46	0.40	0.86	5.22	1.75	0.89	0.82	0.80	1.47	2.87	1.61	0.97	1.18	1.34	0.78	1.42	1.83	1.06	1.12	1.59	1.85
138589	Hs.12342	Homo sapiens clone 24538 mRNA sequence	1.50	1.89	1.11	1.54	2.91	1.40	1.09	1.43	1.33	1.66	2.73	2.00	0.88	0.69	1.24	1.08	1.08	1.97	2.09	1.45	2.50	1.33
128617	Hs.21999	ESTs	2.31	1.17	1.77	1.23	1.57	1.17	3.63	0.59	2.00	2.93	1.97	2.78	0.85	1.12	1.62	3.68	3.48	1.89	3.74	1.39	0.60	0.91
128679	Hs.22011	ESTs	1.30	1.96	2.01	1.48	3.84	1.49	2.32	2.41	2.95	1.67	3.39	3.09	1.46	2.51	2.76	2.96	1.91	2.71	4.81	2.48	1.35	1.67
128695	Hs.22015	ESTs	1.81	4.05	1.03	1.95	5.29	7.02	1.22	3.32	4.32	2.30	4.52	5.49	2.22	4.06	5.11	2.84	3.63	2.29	3.15	3.56	6.85	0.91
129840	Hs.91604	ESTs	2.19	0.83	0.96	0.87	1.14	0.91	2.64	0.41	0.95	2.27	0.94	2.02	1.36	0.95	2.04	0.17	0.89	1.81	1.42	1.12	0.36	0.74
137971	Hs.22937	ESTs	1.60	0.73	0.35	0.72	1.58	1.29	2.00	1.09	1.04	1.42	2.30	1.25	0.89	0.88	1.50	0.79	2.09	1.34	1.95	1.03	1.44	0.91
294496	Hs.23037	ESTs	0.93	1.15	0.23	0.58	1.13	0.89	0.85	0.63	0.70	1.05	0.75	0.32	0.35	0.43	0.65	0.61	0.65	1.58	1.01	1.50	0.95	1.53
358543	Hs.22216	ESTs	1.50	1.47	1.76	1.61	1.02	0.93	2.18	0.85	1.11	1.51	0.85	1.09	0.69	0.57	0.96	0.88	1.07	1.60	1.64	0.85	0.49	0.88
296155	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA homolog)	1.78	0.46	0.98	0.47	0.91	0.32	6.49	0.44	0.82	2.19	0.13	1.55	1.04	0.91	1.30	1.54	1.48	1.34	2.30	1.70	0.17	0.91
130057	Hs.23057	ESTs	0.46	0.98	0.68	0.90	2.10	0.46	0.70	1.08	0.83	1.19	0.93	0.88	7.11	0.58	0.84	0.88	2.43	3.40	2.79	0.75	0.74	0.91
364873	Hs.23128	ESTs	1.00	0.66	0.61	0.73	1.06	0.58	0.82	0.82	1.02	1.64	1.06	0.51	0.56	0.47	0.75	0.46	1.36	1.26	1.35	0.80	0.65	0.72
292939	Hs.35096	ESTs	0.95	0.59	0.93	0.70	0.92	0.91	0.73	0.70	1.05	0.81	0.52	1.28	1.21	0.88	1.32	1.07	1.36	1.91	1.19	0.68	0.57	0.91
137456	Hs.195850	keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types)	4.12	2.19	1.23	2.76	4.91	1.72	2.96	2.45	5.14	1.18	2.54	12.37	6.59	2.21	7.92	3.09	6.95	5.65	6.38	2.07	1.65	1.74
133180	Hs.172785	ESTs	3.47	3.46	1.08	2.18	4.28	5.87	1.77	2.03	1.32	1.40	3.97	2.54	1.07	0.73	1.79	1.28	2.42	1.95	2.97	1.66	1.72	2.12
130572	Hs.23389	ESTs	1.43	1.07	1.72	1.71	1.50	1.28	0.84	0.68	1.26	1.62	1.18	1.47	0.82	0.91	1.24	2.59	1.29	1.39	1.34	1.06	0.59	1.25
131316	Hs.23448	ESTs	2.19	1.40	1.41	1.78	1.23	0.91	4.07	0.77	1.03	2.61	1.00	1.36	0.66	0.51	1.34	0.36	1.12	1.83	4.55	0.91	0.44	1.30
131318	Hs.23449	ESTs, Highly similar to similar to insulin receptor substrate BAP2 [H.sapiens]	1.39	1.48	0.57	1.54	2.13	1.26	0.74	1.04	1.04	0.89	0.77	3.62	1.48	2.12	1.92	0.77	0.95	1.05	0.96	1.85	1.82	1.31
131050	Hs.28783	Homo sapiens mRNA; cDNA DKFZp564H122 (from clone DKFZp564H122)	1.14	0.84	0.76	0.54	1.12	0.76	0.69	0.77	1.05	1.17	1.22	0.98	0.55	0.43	1.50	0.85	1.13	0.79	1.14	1.12	0.65	0.53
233318	Hs.23754	ESTs	2.35	1.72	1.59	1.73	1.62	1.89	2.43	1.22	1.49	2.52	0.81	2.28	1.33	0.96	1.82	0.56	2.59	2.39	3.09	1.28	0.60	0.45
136772	Hs.23625	ESTs, Highly similar to cytokine-inducible SH2-containing protein [H.sapiens]	1.21	0.82	0.76	0.42	1.05	0.60	0.86	1.00	0.75	2.74	0.41	0.66	0.45	0.39	0.68	0.36	0.72	1.01	1.30	1.25	0.92	0.91
131563	Hs.23630	ESTs	0.80	0.98	0.37	0.43	1.06	0.39	0.49	1.24	0.77	0.80	0.63	0.33	0.26	0.22	0.40	0.81	0.35	0.84	0.52	0.25	0.75	0.91
143322	Hs.23635	ESTs	0.70	0.70	0.17	0.45	0.83	0.26	0.72	0.48	0.21	0.10	0.07	0.20	0.14	0.23	0.20	0.17	0.22	0.82	0.43	0.28	0.30	1.14
136317	Hs.180338	tumor necrosis factor receptor superfamily, member 12 (translocating chain-association m	2.02	0.92	4.98	2.80	7.20	2.41	3.34	3.28	3.38	50.04	3.74	3.40	0.99	1.48	2.72	2.57	3.00	4.39	4.58	2.40	0.97	0.41
139217	Hs.23294	ESTs, Weakly similar to weak similarity to HSP90 [C.elegans]	1.13	1.51	0.86	1.12	1.69	0.99	1.06	0.68	0.72	1.20	0.85	0.79	0.58	0.91	0.81	1.20	1.00	1.13	0.77	1.08	0.74	0.91
132285	Hs.218111	ESTs	0.83	1.20	1.23	1.55	1.90	0.92	1.67	0.70	1.25	2.02	1.75	0.97	0.77	0.57	0.99	0.95	0.82	1.11	1.54	0.89	0.70	1.56
133331	Hs.233602	KIAA0596 protein	3.57	2.94	3.59	2.79	4.58	1.96	2.83	2.67	4.37	11.25	2.80	3.36	2.29	3.40	3.75	1.52	3.19	3.37	2.08	2.10	2.19	0.91
133197	Hs.24083	KIAA0997 protein	1.24	1.30	1.46	1.69	1.77	1.16	0.44	0.57	1.24	0.86	1.42	1.46	1.73	0.84	1.04	1.05	0.51	1.21	0.76	0.87	1.10	1.09
133519	Hs.155972	KIAA0615 gene product	2.25	1.59	0.74	0.78	1.97	2.10	1.97	0.76	1.55	1.18	1.57	2.82	0.69	1.63	2.08	0.72	3.59	2.68	2.39	1.12	1.17	0.91
135240	Hs.126412	ESTs	1.23	2.00	0.49	0.79	2.79	1.31	0.56	1.27	1.36	1.30	0.82	1.75	1.31	0.93	1.39	0.49	1.11	1.48	1.01	0.83	1.50	0.91
133534	Hs.87013	ESTs	3.53	1.59	0.72	1.48	1.02	0.39	0.90	0.53	0.62	0.40	0.67	0.55	0.17	0.23	0.42	0.45	0.18	0.36	0.46	0.51	1.26	1.39
134495	Hs.24462	ESTs	1.13	1.23	0.74	1.15	0.98	1.00	0.96	1.65	1.62	1.30	0.70	0.87	0.99	1.16	1.06	0.30	1.61	1.20	1.75	1.52	1.34	0.91
135303	Hs.24371	ESTs	1.73	1.68	0.44	1.50	2.19	1.47	0.68	1.69	1.37	1.70	0.83	0.89	0.47	0.71	0.84	0.56	0.86	1.50	1.57	1.00	2.08	1.99
234376	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (from clone DKFZp564F112)	2.38	2.95	1.98	3.33	3.49	1.81	1.29	3.97	4.88	0.95	4.54	5.99	2.19	3.45	3.79	1.88	3.28	2.91	5.70	2.41	2.72	1.28
134829	Hs.15740	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	0.68	0.66	0.74	0.84	0.99	0.34	0.45	0.66	1.24	0.69	0.91	1.22	1.40	0.73	1.09	1.34	0.35	1.39	0.83	0.53	0.47	0.61
134439	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.39	3.62	1.81	2.90	2.93	2.55	1.20	2.18	2.24	2.58	3.84	1.65	1.82	1.20	2.10	0.89	1.91	1.57	1.60	1.30	1.77	0.91
138550	Hs.24545	ESTs, Moderately similar to NF2 protein [H.sapiens]	0.82	2.33	7.15	1.17	1.37	0.78	1.37	2.57	1.92	1.17	1.43	1.25	1.31	0.92	1.85	1.41	1.47	0.91	1.50	0.84	2.34	0.91
136301	Hs.24654	ESTs	1.04	1.29	0.98	1.66	1.83	1.19	0.51	0.94	1.13	1.51	0.97	1.00	0.76	0.80	0.99	0.69	0.81	0.91	0.88	0.76	1.02	0.91
136598	Hs.24870	ESTs	1.49	4.34	1.07	1.41	3.42	1.60	1.72	1.66	2.38	2.48	0.89	2.04	0.69	1.34	1.63	0.46	1.74	2.17	2.72	1.48	1.56	1.50
234150	Hs.141727	myotubularin related protein 4	1.73	2.43	1.75	3.86	2.45	2.30	2.72	3.84	2.61	3.48	4.84	2.86	2.72	2.90	2.67	2.37	2.06	1.42	1.64	1.23	1.79	1.68
136730	Hs.24846	ESTs	1.16	2.32	1.90	1.82	2.18	1.36	1.07	1.24	1.26	1.91	1.31	0.82	0.98	0.69	1.09	0.96	0.61	0.87	0.85	1.06	0.86	1.54
234617	Hs.24908	ESTs	2.04	9.94	1.67	4.09	5.93	2.18	2.20	2.79	1520.24	0.95	1.73	3.27	1.00	0.66	1.44	1.02	3.45	1.83	1.60	1.01	2.43	1.73
682555	Hs.239176	insulin-like growth factor 1 receptor	1.44	3.28	1.01	2.41	4.81	1.55	2.38	2.93	3.93	2.89	2.35	0.94	1.89	0.76	1.83	1.62	3.74	3.00	4.93	0.51	2.81	0.91
144762	Hs.25023	ESTs	1.13	1.48	0.49	0.87	1.16	0.81	0.42	1.03	1.22	1.04	0.91	0.66	0.43	0.49	0.73	0.37	0.67	0.89	0.83	1.17	0.98	1.56
137506	Hs.118640	dishevelled 2 (homologous to Drosophila dsh)	2.02	1.85	1.78	1.86	2.32	1.46	1.89	1.77	1.23	1.36	1.59	1.49	1.44	1.70	1.73	1.64	1.30	1.99	1.44	0.82	1.19	1.43
293599	Hs.25516	ESTs, Highly similar to ORF [H.sapiens]	1.13	1.11	0.56	0.97	1.71	1.01	0.99	0.85	0.91	0.69	1.00	1.33	1.27	1.03	1.55	1.08	1.49	1.47	1.13	0.95	2.53	0.91
234425	Hs.173542	ESTs	1.77	0.90	0.58	1.13	1.93	0.77	0.81	1.26	2.31	1.38	1.02	1.05	1.52	0.98	1.84	0.56	1.64	2.11	1.60	1.52	1.40	1.87
193381	Hs.25819	ESTs	0.90	1.86	0.80	1.58	2.32	1.38	1.64	1.01	1.04	1.65	1.78	2.24	1.16	1.20	1.97	1.75	0.87	1.25	1.07	0.70	1.68	0.91
138104	Hs.25978	ESTs	0.83	0.55	0.15	0.24	1.25	0.79	0.57	0.57	0.44	1.00	2.03	1.53	0.66	0.61	1.53	0.49	0.83	0.63	0.96	0.41	0.78	0.71
138141	Hs.108805	Homo sapiens mRNA from chromosome 5q21-22, clone:A3-A	0.82	0.53	0.75	0.86	0.97	0.68	0.37	0.31	1.37	0.50	0.59	1.18	2.27	1.03	1.28	1.97	0.62	1.17	0.54	1.13	0.43	0.79
233547	Hs.26169	ESTs	0.78	1.71	0.73	0.57	2.84	0.96	0.74	0.98	1.15	0.96	2.73	1.92	1.16	0.84	0.39	1.76	0.89	1.17	1.09	0.95	0.95	2.58
207850	Hs.26320	ESTs	1.33	1.30	0.54	0.58	2.31	1.55	2.78	0.84	0.92	1.38	1.43	1.40	0.79	0.87	1.61	0.62	1.37	2.04	2.00	1.04	0.91	0.91
154795	Hs.26438	ESTs	1.15	1.13	0.56	0.41	1.25	1.11	3.15	0.43	0.67	1.28	0.78	2.75	0.83	1.12	2.03	1.29	1.81	1.69	3.33	1.95	1.09	1.29
140852	Hs.43627	SRY (sex-determining region Y)-box 22	1.08	3.57	0.39	2.43	4.48	2.39	0.94	0.99	0.61	0.93	1.96	1.70	0.54	0.98	1.26	1.67	0.70	1.91	1.52	1.22	1.69	0.91
240938	Hs.26937	brain and nasopharyngeal carcinoma susceptibility protein	1.54	2.08	0.71	0.58	1.36	0.92	6.34	0.85	0.67	1.50	0.56	3.17	0.58	1.45	1.52	0.77	1.87	2.44	4.73	2.00	0.96	0.91
202514	Hs.26980	ESTs	3.48	1.94	2.78	2.95	2.62	2.75	7.16	0.69	1.19	3.25	1.47	3.55	1.26	2.74	2.28	2.22	4.43	3.13	6.02	1.78	1.77	0.85
121546	Hs.125078	Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	1.82	1.24	0.95	2.70	3.40	1.62	2.09	1.08	1.13	0.96	0.94	2.23	1.10	1.67	1.79	1.70	1.96	1.12	1.10	0.93	0.61	1.70
154138	Hs.27596	ESTs	1.12	1.45	1.19	1.07	2.52	0.84	1.21	1.24	1.66	1.54	1.37	0.83	0.85	0.53	0.88	1.14	1.04	1.20	1.35	0.90	0.70	0.91
198451	Hs.12420	ESTs	0.88	0.75	0.44	0.61	0.80	0.82	0.60	0.76	1.01	0.89	0.92	0.71	0.79	0.56	0.62	0.82	1.00	0.73	0.96	0.97	0.53	1.23
366966	Hs.27865	ESTs	0.67	0.61	1.22	0.92	0.74	0.30	0.52	0.60	0.63	0.93	0.46	0.51	0.45	0.43	0.68	0.04	0.33	1.13	1.23	0.79	0.49	0.33
139835	Hs.28309	UDP-glucose dehydrogenase	1.39	1.62	1.74	1.57	3.10	1.23	3.83	4.22	3.84	4.38	2.99	1.50	6.97	1.29	7.97	3.81	3.84	3.75	5.74	1.93	1.62	1.83
138579	Hs.108447	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	1.21	3.33	0.81	1.53	2.36	1.70	1.14	1.74	1.36	1.05	2.64	2.74	0.99	1.25	2.19	1.09	1.65	1.93	1.98	1.06	3.15	0.91
138672	Hs.28412	ESTs	1.90	0.92	1.14	1.24	1.31	0.72	1.45	0.63	3.71	3.65	1.31	2.62	1.33	1.02	1.85	3.90	2.02	2.15	2.48	1.41	1.22	0.78
139705	Hs.28465	ESTs	1.91	1.21	0.80	1.17	1.39	2.22	1.32	0.75	1.09	1.03	0.78	1.14	0.88	0.68	1.17	1.38	1.68	1.03	1.10	1.15	0.18	0.45
139957	Hs.28472	ESTs	2.55	1.67	0.45	0.74	3.28	1.92	3.01	2.05	1.06	1.12	1.20	2.35	2.52	2.21	1.78	1.00	1.76	1.81	2.28	2.00	1.15	0.91
139331	Hs.28436	ESTs, Weakly similar to coded for by C. elegans cDNA CEESW58F [C.elegans]	2.39	1.74	0.70	1.28	2.11	1.56	1.32	0.72	0.97	2.56	2.34	1.34	0.78	0.80	1.07	0.89	1.94	2.10	1.28	1.57	1.69	1.86
139689	Hs.28462	ESTs	0.66	0.65	1.74	0.83	0.77	0.77	0.78	0.61	0.98	0.82	1.03	1.06	0.34	0.43	0.82	1.65	0.52	1.30	1.08	1.00	0.08	0.91
139883	Hs.28501	ESTs	1.47	2.32	1.38	2.35	3.42	1.58	1.62	1.91	3.72	0.95	2.08	1.13	0.50	0.65	1.00	0.93	1.32	1.54	1.45	0.79	1.24	2.11
246292	Hs.28608	ESTs	0.64	1.93	0.92	1.15	2.24	1.12	1.27	1.77	1.58	1.58	1.53	1.59	0.83	0.81	1.45	2.86	1.22	1.57	1.53	0.96	0.97	1.89
140921	Hs.28752	ESTs	0.92	1.55	1.38	1.33	2.39	0.87	1.98	1.84	1.41	1.80	1.45	4.25	1.05	2.93	2.48	0.70	1.02	1.60	2.36	1.66	2.31	1.17
140966	Hs.28739	ESTs	0.40	0.64	0.49	0.61	1.05	0.28	0.46	0.41	0.55	0.44	0.51	0.99	0.30	0.36	0.44	0.26	0.20	0.68	0.46	0.32	0.30	0.48
140301	Hs.28792	ESTs	1.19	1.10	1.13	1.42	2.63	0.72	1.47	3.18	6.42	3.27	3.32	3.89	0.61	1.40	3.22	1.52	1.18	1.27	3.06	1.48	1.37	1.68
471372	Hs.28803	ESTs	1.81	1.32	1.22	1.27	1.01	1.15	1.32	0.55	2.04	2.28	0.91	2.21	0.87	0.87	2.11	1.50	2.26	1.90	2.52	1.37	0.93	1.10
138337	Hs.28838	ESTs	0.96	0.74	0.93	0.78	0.44	0.33	0.97	0.34	1.12	2.24	0.39	1.43	0.29	0.87	0.81	1.75	0.54	1.01	1.14	0.51	0.52	0.82
138477	Hs.28898	ESTs	1.94	1.94	0.60	1.82	2.01	1.19	1.13	2.60	2.17	1.60	1.70	2.89	1.45	1.84	2.05	1.15	1.47	1.68	1.92	1.92	1.98	1.59
141453	Hs.167812	ESTs	3.73	2.03	1.70	1.17	2.18	2.38	5.75	0.89	5.27	3.62	1.56	3.26	2.97	1.63	2.75	2.00	4.93	6.85	7.22	1.27	0.68	1.46

142442	Hs.29052	ESTs, Moderately similar to fetal globin inducing factor [M.musculus]	1.86	2.25	0.57	1.50	1.80	1.64	0.89	1.77	1.35	1.09	1.81	1.99	0.99	1.05	1.30	0.67	1.30	1.49	1.31	1.38	1.91	1.66
142532	Hs.29068	ESTs	1.31	1.87	1.24	1.09	1.97	1.50	1.11	0.94	1.45	0.94	1.28	1.79	0.63	1.20	1.39	1.16	0.58	1.01	2.72	0.76	0.86	0.84
143748	Hs.317	phospholipase C, gamma 1 (formerly subtype 148)	1.98	1.42	0.91	1.58	2.83	0.74	1.45	2.48	1.76	3.71	1.36	2.36	1.38	1.10	1.05	1.01	1.44	1.18	1.26	1.15	2.80	0.91
143962	Hs.29626	ESTs, Weakly similar to unknown [D.melanogaster]	1.20	1.13	0.64	1.33	1.90	1.14	0.96	1.26	1.05	1.33	1.03	2.19	2.11	1.86	1.71	0.52	1.00	1.51	1.00	0.85	0.99	0.91
241482	Hs.29189	KIAA1021 protein	1.52	0.79	0.77	0.52	1.31	1.34	0.61	0.26	1.29	1.79	0.27	0.86	0.42	0.78	0.66	0.52	0.38	1.09	0.48	0.87	0.52	0.91
144905	Hs.29494	SEC10 (S. cerevisiae)-like 1	1.56	1.65	1.59	1.42	1.10	0.94	1.14	0.89	1.29	1.27	1.14	1.03	0.60	0.59	0.85	0.66	1.43	1.04	1.09	1.25	1.22	0.64
248535	Hs.29667	ESTs	0.70	0.48	1.16	0.66	1.31	0.39	0.45	0.35	1.05	0.50	0.60	0.66	0.32	0.48	0.72	0.65	0.48	0.57	0.89	0.56	0.48	0.25
143887	Hs.154737	serine protease, umbilical endothelium	3.06	1.40	1.77	3.68	5.15	1.91	1.20	4.87	6.10	3.73	4.77	7.27	6.48	4.16	4.50	5.36	4.22	2.85	5.03	2.79	3.21	2.34
262920	Hs.174050	endothelial differentiation-related factor 1	1.02	0.61	0.81	1.42	1.12	1.28	0.61	0.56	1.09	1.11	1.27	0.66	2.44	0.87	2.24	1.24	1.14	1.03	0.65	1.18	0.47	0.89
154477	Hs.30120	ESTs	1.46	1.29	0.90	1.22	1.90	0.82	1.10	1.47	0.89	1.41	0.80	1.40	1.12	0.88	1.92	0.64	2.14	1.87	1.97	1.08	1.18	1.56
322759	Hs.30174	small nuclear RNA activating complex, polypeptide 5, 19kD	1.45	2.76	1.37	1.99	2.60	1.88	1.96	2.10	1.95	2.68	2.08	2.18	1.28	2.07	2.10	1.33	1.46	1.58	1.95	1.37	2.50	1.66
197775	Hs.32204	ESTs	0.80	1.63	0.71	0.73	2.34	1.10	0.95	1.54	1.13	1.27	1.05	2.09	1.04	0.54	2.43	1.12	1.66	2.31	2.18	0.97	1.34	1.13
139250	Hs.30821	ESTs	0.97	1.77	0.51	1.22	2.04	2.06	0.61	0.84	0.98	0.91	1.39	2.21	0.80	1.17	1.83	0.66	0.50	0.78	0.69	1.32	2.10	1.06
288658	Hs.30977	ESTs	0.53	1.25	0.93	0.73	1.63	1.11	0.72	0.32	1.19	0.77	0.48	0.92	1.24	0.78	1.14	1.60	0.69	1.38	1.08	0.88	0.95	0.60
295577	Hs.31542	ESTs	1.80	5.05	0.35	1.00	3.41	1.06	1.44	1.93	1.30	1.47	2.55	2.93	2.10	1.03	2.06	1.52	1.18	1.26	2.20	0.85	1.79	2.01
160485	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.90	6.18	4.40	2.46	5.34	4.24	7.96	4.26	6.02	1.23	2.05	4.55	1.22	2.92	3.83	2.13	4.39	6.02	4.98	1.97	5.93	3.10
209167	Hs.32391	ESTs	1.13	1.45	1.03	0.95	1.44	1.51	0.66	0.63	1.06	1.05	1.90	1.15	0.71	0.84	0.92	0.93	1.01	0.71	0.72	1.03	0.68	0.72
202740	Hs.32407	ESTs	0.99	0.94	0.48	0.54	1.23	0.68	0.41	0.92	1.12	1.27	0.89	1.34	0.54	0.58	1.09	0.49	0.85	1.29	1.44	1.06	0.97	0.91
204179	Hs.32922	ESTs	1.16	1.34	1.07	1.54	1.55	1.24	0.63	1.18	1.26	1.46	0.87	0.90	0.86	0.80	1.02	0.90	1.31	1.72	1.72	1.11	0.82	0.91
243294	Hs.6975	histone deacetylase 3	1.73	1.55	0.94	1.27	0.94	0.86	1.22	1.59	1.47	2.03	0.91	1.23	1.24	1.32	0.97	1.16	1.01	1.13	1.06	1.23	0.89	0.42
295229	Hs.33264	ESTs	2.02	2.67	3.55	3.14	0.68	1.80	3.04	4.00	1.90	4.00	1.96	2.45	1.07	0.84	1.84	0.99	2.78	2.16	2.88	1.18	1.11	1.53
193546	Hs.167526	ESTs	1.90	1.83	0.66	1.10	1.64	1.91	2.03	1.14	0.80	0.93	1.11	1.98	0.48	0.73	0.78	0.89	0.98	1.52	1.41	0.78	1.96	1.80
234380	Hs.33665	ESTs	1.97	2.86	1.13	1.12	3.27	1.21	4.19	1.40	1.27	2.18	2.02	2.88	1.24	1.43	2.07	2.47	1.98	2.02	3.81	1.40	1.19	1.56
293328	Hs.13472	Homo sapiens clone 24859 mRNA sequence	2.79	3.94	1.17	2.17	4.31	2.90	1.79	1.84	1.83	1.45	2.31	3.91	1.62	1.67	3.45	1.72	1.91	1.41	1.45	2.78	2.86	2.49
211758	Hs.3463	ribosomal protein S23	1.30	0.94	0.14	1.18	1.71	0.49	0.70	0.30	0.22	0.49	0.33	0.47	0.25	0.24	0.46	0.26	0.33	0.52	0.57	0.74	0.81	1.30
242687	Hs.173203	ESTs, Weakly similar to type II membrane protein [H.sapiens]	0.79	0.76	0.67	1.16	0.91	1.04	0.46	0.40	2.13	0.47	0.50	0.80	0.87	0.66	0.79	1.17	0.98	1.27	0.53	1.25	1.03	0.91
194965	Hs.34192	ESTs	0.66	3.25	0.80	1.75	1.66	1.74	0.46	1.07	2.20	0.95	1.29	1.64	0.29	0.54	1.12	0.86	1.34	0.76	0.71	0.52	0.64	1.28
195852	Hs.4082	lectin, galactoside-binding, soluble, 8 (galectin 8)	0.69	1.39	0.83	1.57	0.97	1.55	1.16	1.09	2.06	1.73	1.02	1.57	1.32	0.87	1.84	0.70	1.17	1.24	1.91	1.76	1.08	0.91
290054	Hs.34956	ESTs	1.92	4.49	3.97	2.52	2.85	1.12	2.58	1.83	2.81	3.30	1.35	2.11	0.81	0.93	1.52	1.61	1.33	2.10	2.20	1.25	1.08	2.12
243360	Hs.66881	ESTs, Moderately similar to cytoplasmic dynein intermediate chain 1 [H.sapiens]	1.03	1.37	1.22	1.49	1.07	0.78	1.66	1.75	4.31	3.09	1.27	2.04	0.79	0.86	1.56	0.76	1.49	1.14	1.61	1.08	1.14	0.91
196345	Hs.154103	LIM protein (similar to rat protein kinase C-binding enigma)	1.51	1.42	1.24	1.37	0.75	1.37	1.48	1.65	2.25	1.36	1.05	1.45	0.81	1.69	1.49	0.26	1.63	1.64	1.39	1.75	2.07	0.91
196849	Hs.173684	ESTs, Highly similar to NY-REN-37 antigen [H.sapiens]	0.79	0.62	0.90	1.13	1.19	0.64	0.75	0.26	1.11	1.24	1.35	1.16	1.00	0.75	1.14	0.43	0.86	1.22	1.25	0.58	0.69	0.63
199624	Hs.35586	ESTs	1.87	0.88	1.89	1.08	2.32	1.26	0.81	0.75	0.63	2.15	1.21	1.31	0.91	0.77	1.10	0.67	2.15	2.55	1.97	1.26	0.78	0.93
213969	Hs.35551	ESTs	1.92	0.69	2.10	0.54	0.94	0.33	3.56	0.50	1.36	0.95	0.15	1.41	0.50	0.81	1.31	0.91	2.67	3.58	0.79	1.32	0.36	1.42
198011	Hs.184721	ESTs	0.89	1.11	0.37	0.96	1.87	0.72	3.84	1.13	0.95	1.47	0.61	0.78	0.24	0.54	0.67	1.34	0.66	2.57	2.26	1.74	0.56	2.61
232837	Hs.9329	chromosome 20 open reading frame 1	2.27	1.00	1.26	1.63	1.24	1.53	2.50	0.82	1.25	0.66	0.50	1.08	1.98	1.18	1.36	1.39	0.85	0.38	0.97	2.00	0.77	1.65
359411	Hs.35947	methyl-CpG binding domain protein 4	1.85	2.21	1.07	1.81	2.42	1.76	1.02	1.27	2.01	1.62	1.79	1.43	0.54	1.09	1.03	0.94	0.90	1.18	1.49	0.86	1.63	1.61
207016	Hs.35976	ESTs	2.31	1.51	1.55	1.38	1.06	1.14	3.45	0.83	3.71	0.95	1.11	2.93	1.42	1.76	2.32	2.52	3.72	1.82	2.13	1.68	0.53	1.15
201393	Hs.36069	ESTs	1.12	1.38	1.00	1.10	1.97	2.64	1.13	1.01	1.15	1.02	3.28	2.10	0.76	1.00	1.25	0.77	1.08	0.93	0.90	1.05	1.12	0.91
200847	Hs.134428	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	0.89	1.11	0.35	0.45	1.90	0.45	0.53	0.88	0.64	0.90	1.34	0.79	0.64	0.43	0.87	0.69	0.87	1.37	1.28	0.84	0.97	1.60
109123	Hs.36475	ESTs	1.66	4.71	1.24	3.11	4.91	1.19	0.98	5.64	1.99	1.59	6.96	3.56	0.38	1.36	4.49	1.13	2.66	1.70	5.23	1.48	1.72	1.65
202931	Hs.36822	ESTs	1.63	1.38	0.39	1.11	1.20	0.14	2.12	1.97	0.92	0.82	1.30	2.37	0.52	0.86	1.46	0.43	1.37	2.64	2.52	0.91	1.65	0.91
244086	Hs.36958	ESTs	0.36	0.53	0.38	0.29	0.49	0.24	0.49	0.32	0.48	0.59	0.73	0.99	0.53	0.42	0.69	0.25	0.55	0.95	0.62	0.81	0.39	0.28
244310	Hs.37359	ESTs	0.32	0.50	0.53	0.80	0.95	0.39	0.16	0.78	0.64	0.20	0.53	1.42	1.84	1.66	3.60	1.08	0.39	1.16	0.45	0.59	0.53	0.24
204638	Hs.37380	ESTs	1.03	1.27	1.07	0.81	1.17	1.24	0.92	0.73	1.05	0.78	0.94	0.91	0.52	0.81	1.07	2.09	0.90	0.96	1.26	0.76	0.55	0.91
205490	Hs.108705	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform	2.96	2.59	1.91	1.37	1.83	1.58	0.99	1.38	1.33	1.30	2.09	2.66	1.16	1.57	1.88	1.11	0.81	1.29	0.88	1.09	1.21	0.91
294018	Hs.141232	ESTs	1.09	1.40	1.22	0.72	1.35	1.30	1.14	0.84	1.34	1.08	0.89	1.10	0.60	0.74	1.19	0.88	1.26	1.15	1.31	0.92	0.69	0.75
206683	Hs.37741	ESTs	1.44	1.43	0.40	1.23	2.09	0.93	1.32	1.49	1.22	1.90	1.10	2.77	0.59	0.74	2.06	0.45	1.29	2.09	2.93	0.85	1.51	1.35
296132	Hs.232076	A kinase (PRKA) anchor protein 11	0.95	0.94	0.99	0.89	0.86	1.09	1.03	0.79	1.54	0.83	0.33	0.70	0.55	0.55	1.02	0.55	0.98	1.12	0.99	0.87	0.53	0.36
208375	Hs.105695	ESTs	0.81	0.55	0.15	0.09	0.88	0.46	0.24	0.35	0.10	0.17	0.30	0.39	0.12	0.16	0.30	0.25	0.41	0.57	0.55	0.26	0.92	0.91
211747	Hs.38703	ESTs	1.40	1.60	0.67	0.55	1.67	1.10	2.38	0.53	0.86	1.65	0.22	1.43	0.62	1.16	1.31	0.48	1.60	2.11	2.74	0.90	1.38	1.74
244267	Hs.38891	ESTs	1.09	1.15	0.48	1.35	3.23	0.74	1.04	1.53	1.15	1.29	1.13	1.11	1.04	0.78	1.27	1.52	1.63	1.86	2.04	1.58	0.49	1.96
233719	Hs.39912	ESTs	1.09	1.46	0.58	0.72	2.11	1.37	1.50	0.83	0.90	1.33	1.66	1.67	0.64	1.05	1.21	1.46	1.83	1.96	1.98	0.84	0.72	0.91
240637	Hs.40094	Human DNA sequence from clone 167A19 on chromosome 1p32.1-33. Contains three gen	1.29	0.83	0.72	1.15	1.44	1.16	1.17	0.59	1.29	1.12	0.96	0.69	0.74	0.47	0.89	1.57	0.73	1.05	0.70	0.83	0.41	2.49
295992	Hs.40154	jumonji (mouse) homolog	0.56	1.09	0.70	0.94	1.91	1.38	1.14	1.20	1.20	0.86	0.77	1.78	0.68	0.94	1.29	2.06	0.91	1.26	1.51	1.22	0.68	2.18
292308	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (from clone DKFZp727C191)	2.63	0.56	2.58	2.03	1.07	0.80	1.93	0.44	5.96	3.70	1.83	3.22	1.55	1.66	2.14	1.32	2.23	2.47	2.88	1.55	0.48	1.04
240674	Hs.41380	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	0.80	0.69	1.99	1.71	1.25	0.91	2.14	0.55	1.79	3.02	1.61	2.20	1.46	1.65	2.32	1.09	1.53	1.28	1.69	1.26	0.55	0.87
243113	Hs.41974	ESTs	1.62	1.08	0.67	0.74	1.07	0.64	1.99	1.58	1.02	1.16	1.24	0.98	0.50	0.90	0.99	0.57	1.06	1.37	1.91	0.85	1.70	0.86
242087	Hs.41877	ESTs	1.76	2.50	0.98	2.52	3.30	1.87	1.61	3.29	2.11	4.07	1.69	2.54	1.07	1.38	1.97	0.78	2.42	3.53	3.30	1.54	2.26	1.80
230251	Hs.41895	ESTs	0.88	0.96	0.93	1.21	0.75	0.85	1.75	0.66	0.80	0.86	1.80	0.77	0.68	0.95	0.88	0.89	1.18	1.19	0.87	1.14	0.67	0.61
242780	Hs.193830	ESTs, Highly similar to KIAA0554 protein [H.sapiens]	1.68	2.39	2.01	1.41	2.06	1.47	2.23	2.14	3.84	3.98	1.59	3.48	1.06	1.82	2.36	1.19	2.34	2.13	3.27	1.52	0.51	1.46
242797	Hs.24341	DKFZP586I1419 protein	2.60	1.12	2.43	0.61	1.87	1.44	5.03	0.59	3.20	0.95	1.06	4.76	2.00	2.82	4.36	0.70	1.83	2.45	1.12	1.32	0.42	1.90
242698	Hs.41958	ESTs	1.49	1.60	0.33	0.70	1.61	0.72	2.17	0.57	0.88	1.10	0.53	0.58	0.26	0.44	0.57	0.47	0.51	2.16	0.89	1.27	1.31	1.16
243088	Hs.41972	ESTs	1.36	2.29	2.28	1.01	1.71	1.73	1.63	1.67	1.55	2.51	1.55	1.64	1.63	0.65	1.62	1.06	0.85	1.07	0.92	1.38	0.69	0.70
243230	Hs.41989	ESTs	2.21	0.72	1.80	0.55	1.13	0.96	1.55	0.64	1.18	0.95	0.57	1.75	1.01	1.04	1.35	1.60	2.21	2.43	2.46	1.25	0.78	1.39
244227	Hs.42179	ESTs	0.72	1.31	0.60	1.41	1.19	0.41	1.60	3.19	1.33	2.15	2.69	1.74	1.23	1.07	1.49	1.43	2.03	1.52	2.45	1.31	1.63	1.57
245409	Hs.188757	Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR prot	1.79	2.03	2.23	1.47	2.41	1.17	1.84	2.39	2.55	2.43	1.49	1.24	0.83	0.91	1.09	1.25	1.76	1.47	2.29	1.55	2.11	1.86
295140	Hs.42362	ESTs	1.23	0.75	1.59	1.51	0.89	0.81	0.88	0.81	0.79	1.64	1.74	0.86	0.53	0.58	0.87	0.56	0.73	1.36	1.01	0.77	0.54	0.76
366085	Hs.43905	ESTs	3.06	5.30	2.32	1.72	4.26	3.31	6.33	2.86	2.56	3.42	2.46	3.10	2.10	2.06	4.20	2.34	2.61	2.69	5.03	1.54	1.75	1.86
260619	Hs.42400	ubiquitin specific protease 12	1.40	1.48	1.03	1.44	1.65	1.43	1.14	0.96	1.12	0.75	0.90	1.33	1.24	0.82	1.59	0.93	1.42	1.97	1.28	1.92	1.31	1.61
282980	Hs.42640	ESTs	0.75	1.07	0.53	1.18	1.08	0.39	1.86	2.81	1.09	1.39	2.27	1.27	1.50	1.12	1.96	0.98	2.03	2.12	2.48	1.48	1.90	1.13
300972	Hs.42948	ESTs	1.04	0.62	0.75	1.14	1.55	0.69	0.66	0.40	0.73	1.10	0.68	0.87	0.41	0.70	1.00	0.55	0.65	1.12	1.32	0.49	0.59	0.52
309045	Hs.165169	Sarcolemmal-associated protein	0.93	0.90	0.79	0.97	1.67	0.90	0.35	0.86	1.13	0.44	0.96	1.20	1.32	0.75	1.27	0.74	0.69	1.11	0.81	0.84	1.21	1.71
308231	Hs.109805	Homo sapiens incomplete cDNA for a myosin class I, myh-1c	0.69	0.62	2.57	1.84	1.13	0.68	0.75	0.48	2.41	1.90	1.17	1.66	1.78	1.22	1.67	0.94	0.60	0.84	0.41	1.20	0.45	0.90
243878	Hs.44970	ESTs	1.75	0.67	1.44	0.77	0.69	0.88	1.43	0.43	2.01	1.97	0.65	1.44	0.59	0.74	0.95	0.55	1.38	1.24	1.41	1.25	0.49	1.33
243524	Hs.44526	ESTs	1.13	1.24	0.85	1.08	1.26	0.97	0.81	0.90	1.27	1.07	1.56	1.27	0.39	0.68	1.10	1.39	0.95	1.00	1.07	0.84	1.24	0.71
296180	Hs.44766	retinitis pigmentosa 2 (X-linked recessive)	2.04	0.68	1.76	0.80	0.55	0.69	1.25	0.45	2.80	32.30	0.44	3.11	1.66	1.81	1.91	1.18	1.88	1.78	2.46	1.32	0.47	1.52
243653	Hs.46981	ESTs	0.81	0.93	0.43	0.71	0.99	0.72	0.72	0.85	0.66	0.59	0.80	1.29	0.52	0.62	1.02	0.31	0.64	0.98	0.72	0.79	1.14	1.03
239708	Hs.46158	ESTs	1.92	2.27	0.97	3.23	3.65	2.44	4.29	2.82	4.93	4.37	1.22	2.26	1.32	1.46	2.07	0.92	3.51	2.45	3.43	1.73	3.02	1.72
213871	Hs.46853	ESTs	2.03	2.45	0.91	2.24	3.06	2.66	3.99	3.46	2.19	3.00	2.70	1.94	1.72	2.51	2.16	0.57	5.37	2.43	3.22	2.08	2.83	3.61
275176	Hs.46932	ESTs	1.37	2.40	0.56	1.38	3.23	0.97	3.17	2.86	1.40	2.82	0.83	2.02	0.75	0.82	1.35	0.66	2.61	1.64	2.27	0.76	2.17	0.91

243641	Hs.46933	ESTs	2.04	1.59	1.72	0.47	1.13	0.18	1.53	1.03	1.92	1.99	0.66	2.78	0.87	1.35	2.07	0.45	2.66	1.76	3.34	1.57	0.29	0.75
284341	Hs.47438	SH3-binding domain glutamic acid-rich protein	2.19	0.64	5.19	0.49	1.53	0.72	13.86	0.29	1.43	0.95	0.34	2.03	0.89	1.33	1.91	0.35	4.38	3.96	4.69	1.07	0.56	0.85
292364	Hs.48565	ESTs	1.02	1.76	1.10	1.56	1.44	1.04	1.04	1.94	1.77	0.95	0.78	1.20	0.68	0.68	1.27	1.15	1.26	1.30	1.26	1.06	1.83	1.24
292654	Hs.48604	DKFZP434B168 protein	2.13	2.72	1.71	2.77	1.18	1.45	1.23	1.02	2.01	1.89	1.02	1.45	0.77	0.96	1.35	1.20	1.53	1.03	1.23	1.08	1.60	2.50
293727	Hs.49738	ESTs	2.19	2.09	1.52	1.31	2.24	2.14	4.76	1.74	0.75	1.77	1.85	2.12	0.84	0.88	1.16	1.65	1.48	1.46	3.85	1.36	1.52	1.90
293500	Hs.49714	ESTs	0.55	0.90	1.19	1.76	1.40	0.37	1.74	0.56	0.77	0.40	0.82	0.57	0.26	0.54	0.56	0.65	0.21	1.44	0.65	0.76	1.84	0.98
295483	Hs.49853	ESTs	5.26	3.42	0.75	1.48	3.18	2.25	16.19	2.22	1.47	3.60	3.64	11.91	7.50	4.87	6.87	2.73	6.81	6.27	5.56	3.75	5.42	2.11
296597	Hs.11050	F-box protein Fbx9	0.82	2.49	1.28	1.28	1.26	1.01	1.24	1.05	1.29	1.51	0.75	1.24	1.30	0.93	1.30	1.30	1.56	1.67	1.68	1.14	1.08	1.82
811044	Hs.86958	interferon (alpha, beta and omega) receptor 2	2.65	5.27	4.09	3.32	3.43	1.42	1.88	3.20	0.63	1.55	1.37	3.13	0.98	2.20	3.22	0.70	2.31	1.89	2.73	1.07	1.87	2.06
754080	Hs.99995	intercellular adhesion molecule 3	1.12	1.80	1.98	2.13	2.34	3.02	1.29	2.71	4.47	4.58	2.30	1.86	1.66	1.40	1.52	2.49	1.91	1.32	2.09	1.37	2.47	1.26
469345	Hs.12337	kinase insert domain receptor (a type III receptor tyrosine kinase)	1.18	1.80	3.51	2.42	3.62	0.81	1.12	2.63	4.13	2.33	1.31	1.85	1.42	1.27	2.15	1.57	2.07	2.62	2.60	2.54	1.54	1.37
327676	Hs.74070	keratin 13	0.63	0.26	0.14	0.14	0.35	0.22	0.32	0.30	0.12	0.15	0.20	0.56	1.19	0.42	1.02	0.15	0.23	0.41	0.46	0.36	0.27	0.11
122428	Hs.198951	jun B proto-oncogene	1.40	0.93	0.51	0.64	0.86	0.44	0.45	0.40	1.07	0.36	0.64	1.05	0.21	0.58	0.76	0.58	0.50	1.24	0.69	0.55	0.42	0.34
810325	Hs.77510	isovaleryl Coenzyme A dehydrogenase	2.05	2.22	1.43	1.49	2.56	1.68	1.29	2.26	1.79	1.76	1.42	1.96	3.44	1.92	2.76	0.77	2.55	2.40	1.62	0.66	1.53	1.05
823696	Hs.20315	interferon-induced protein 56	5.10	12.97	17.67	9.54	5.78	1.51	3.54	11.21	30.30	49.58	6.56	4.07	5.16	2.28	8.60	3.01	8.58	3.04	7.13	1.32	4.30	3.63
727551	Hs.83795	interferon regulatory factor 2	1.65	1.60	1.99	1.76	1.80	2.13	0.84	1.92	2.18	2.19	1.94	1.74	1.23	1.82	2.69	1.95	1.68	1.55	1.45	1.15	1.39	1.46
180803	Hs.32309	inositol polyphosphate-1-phosphatase	0.89	1.84	1.00	2.60	1.26	0.64	0.45	0.79	0.94	1.03	0.64	1.18	0.55	2.32	0.77	0.79	0.54	0.55	0.44	0.44	0.79	0.78
276091	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	3.62	9.47	2.24	9.23	4.92	2.04	5.93	3.49	3.98	3.59	2.86	4.98	2.43	2.79	3.63	1.33	2.85	1.58	4.57	1.57	2.40	2.46
343072	Hs.256309	Human beta-1D integrin mRNA, cytoplasmic domain, partial cds	0.49	0.33	1.07	0.63	0.78	0.64	0.61	0.42	1.15	0.37	0.56	0.61	0.70	0.49	0.86	0.66	0.84	0.85	0.58	0.80	0.63	0.70
770859	Hs.149846	integrin, beta 5	1.08	0.78	0.77	1.52	1.03	0.60	1.10	1.11	2.36	1.02	0.97	0.92	0.52	2.09	1.11	1.31	0.83	1.19	1.61	1.20	0.65	0.57
811096	Hs.85266	integrin, beta 4	1.35	0.76	0.26	0.44	0.67	0.44	1.14	0.47	1.09	0.35	0.41	0.36	0.60	1.49	0.55	0.45	0.21	1.22	0.67	1.06	0.70	0.59
233721	Hs.162	insulin-like growth factor binding protein 2 (36kD)	3.35	3.90	1.72	4.04	14.44	2.12	7.73	8.67	9.08	15.53	12.44	8.98	21.00	5.04	13.45	4.32	4.98	2.37	7.14	1.97	3.97	5.83
148379	Hs.239176	insulin-like growth factor 1 receptor	1.68	2.78	1.30	2.62	3.94	1.33	3.15	2.60	2.87	2.66	3.07	1.33	2.62	1.03	2.95	1.68	4.42	3.16	5.12	0.61	1.78	1.66
240151	Hs.180919	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	0.78	2.42	1.42	1.42	2.31	1.01	0.81	1.08	1.59	1.32	1.34	1.58	0.38	1.18	0.97	1.08	1.67	0.94	0.77	1.32	1.17	1.08
47900	Hs.180866	interferon gamma receptor 1	0.75	1.43	0.98	0.95	1.33	1.32	1.10	1.01	1.12	1.25	1.04	0.84	0.43	0.75	0.88	0.51	1.01	1.73	1.38	1.36	1.46	1.01
740925	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	1.91	2.21	1.42	1.40	1.05	1.59	2.06	1.45	1.13	1.56	1.62	1.23	0.95	1.36	0.92	0.31	0.99	1.09	1.59	1.20	0.57	0.95
810504	Hs.77422	proteolipid protein 2 (colonic epithelium-enriched)	1.93	1.18	0.92	0.91	1.01	1.97	1.85	1.84	0.78	1.49	1.21	1.03	0.60	0.72	0.83	0.67	0.68	1.09	1.61	0.94	1.53	1.36
810213	Hs.82112	interleukin 1 receptor, type I	1.28	1.33	0.99	1.17	2.71	1.26	1.16	2.02	2.14	1.41	3.27	1.99	0.64	1.00	1.65	0.79	0.97	1.98	1.78	1.07	1.65	0.92
120106	Hs.2490	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)	2.46	4.18	2.21	2.52	1.80	2.04	1.00	2.54	2.44	2.47	2.42	2.26	0.69	1.25	1.31	0.94	1.87	1.32	1.70	1.05	1.11	1.69
346117	Hs.171862	guanylate binding protein 2, interferon-inducible	1.30	3.78	1.33	1.99	2.55	3.58	0.71	2.02	1.96	2.49	2.17	2.62	0.57	1.30	1.40	1.30	2.63	1.58	1.50	1.07	1.24	1.46
50754	Hs.149894	mitochondrial translational initiation factor 2	1.11	1.73	0.96	2.24	1.51	1.25	1.40	0.72	1.35	1.21	0.95	1.10	0.58	0.76	1.03	0.65	1.10	1.17	1.20	1.05	0.96	0.63
811108	Hs.119498	thyroid hormone receptor interactor 6	0.53	1.62	0.65	0.89	0.71	0.60	1.08	0.62	0.63	0.24	0.55	0.66	0.46	0.37	0.59	0.54	0.38	0.99	0.64	0.46	0.62	0.62
377320	Hs.236218	TAT-INTERACTIVE PROTEIN, 72-KD	1.52	5.90	0.97	1.24	2.03	0.93	1.26	1.29	1.99	2.02	1.13	0.72	0.43	0.51	0.59	0.55	0.69	1.29	1.69	0.61	1.40	1.14
39884	Hs.850	IMP (inosine monophosphate) dehydrogenase 1	0.55	1.11	0.60	0.95	1.22	1.24	0.62	0.90	0.97	0.92	1.54	1.58	1.78	1.18	0.67	1.15	0.91	0.81	1.19	0.47	1.27	1.26
23282	Hs.8024	RD element	0.69	0.88	0.59	0.83	0.67	0.75	0.59	0.69	0.83	0.89	1.10	0.65	0.74	0.63	0.87	0.87	0.82	0.70	0.88	0.57	0.55	0.92
183194	Hs.74122	caspase 4, apoptosis-related cysteine protease	1.48	3.09	1.55	1.70	0.61	1.17	0.82	1.68	1.54	3.10	1.06	2.97	0.89	1.42	2.40	0.65	1.01	1.42	1.60	0.68	0.79	1.03
126243	Hs.82609	hydroxymethylbilane synthase	1.78	4.09	2.04	1.66	1.63	1.62	1.92	1.62	1.56	2.39	1.49	3.13	1.36	1.37	1.27	1.17	0.89	1.19	1.78	0.54	1.42	0.55
188232	Hs.182965	Kruppel-like factor 4 (gut)	0.73	0.72	0.64	1.56	1.33	0.34	1.18	1.12	0.60	0.35	1.69	0.42	0.29	0.66	1.08	0.64	0.64	1.45	0.73	1.55	0.70	0.69
127677	Hs.119523	transformer-2 alpha (htra-2 alpha)	1.98	1.58	1.92	2.53	2.43	0.86	1.39	2.23	0.63	1.76	1.00	1.28	1.29	1.04	2.14	0.53	1.46	1.61	2.23	1.32	1.78	0.98
240367	Hs.57419	transcriptional repressor	1.47	1.32	1.51	1.54	1.58	1.04	1.24	1.40	1.93	1.70	1.24	0.89	0.55	0.83	1.15	1.12	1.16	0.91	1.48	0.85	1.04	0.99
45138	Hs.79141	vascular endothelial growth factor C	0.50	0.64	0.54	0.71	0.69	0.28	0.43	0.58	0.66	0.46	0.99	0.29	0.10	0.19	0.26	0.55	0.25	0.57	0.43	0.41	0.45	0.41
810600	Hs.174070	ubiquitin carrier protein	2.12	1.56	1.12	1.22	1.20	1.14	2.28	1.66	1.01	2.04	5.01	0.72	0.80	0.71	0.84	0.74	1.50	0.92	1.73	1.22	1.82	1.53
288896	Hs.79351	potassium channel, subfamily K, member 1 (TWIK-1)	0.53	0.88	0.41	0.94	1.34	0.82	1.90	1.30	1.48	0.70	1.28	0.37	0.97	0.68	0.79	0.68	0.38	0.64	0.41	1.02	0.80	1.14
341942	Hs.151777	Human translation initiation factor eIF-2alpha mRNA, 3'UTR	1.08	1.00	1.44	1.49	1.56	0.87	0.70	1.51	0.88	0.88	1.22	0.65	0.87	0.65	1.14	0.63	0.91	1.00	1.16	0.46	1.70	0.76
199945	Hs.8265	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	0.86	1.10	1.15	1.80	2.14	2.88	0.43	1.55	2.39	1.31	1.75	2.10	1.42	2.96	4.53	1.41	1.76	0.57	0.54	1.23	1.38	1.40
234736	Hs.50924	GATA-binding protein 6	1.16	1.33	1.67	2.66	1.02	0.74	1.34	0.91	1.26	1.70	0.81	1.34	0.60	1.12	0.98	0.63	0.85	1.04	0.97	0.87	0.51	1.01
110281	Hs.8906	syntaxin 7	1.16	3.04	1.16	2.06	2.83	3.62	1.35	2.05	2.06	2.37	2.01	2.05	1.17	1.76	1.91	1.07	2.55	1.24	1.18	1.75	2.02	1.45
346552	Hs.107019	Symplekin; Huntingtin interacting protein I	0.60	1.70	0.75	1.51	1.16	0.84	1.25	0.89	0.99	0.85	0.81	2.13	1.58	2.44	1.63	0.90	0.97	0.55	0.93	0.82	0.89	1.24
811843	Hs.16340	sulfite oxidase	1.44	2.69	1.08	2.14	1.65	2.01	1.06	1.42	1.83	1.36	2.15	1.19	0.85	1.00	1.17	1.25	1.43	0.97	1.28	1.25	1.86	1.88
727192	Hs.172674	nuclear factor of activated T-cells, cytoplasmic 3	2.06	1.50	1.45	1.44	2.17	1.52	2.34	1.40	1.83	1.61	1.78	2.95	1.98	2.33	3.28	1.25	2.08	1.41	1.99	1.00	1.80	1.25
725680	Hs.61796	transcription factor AP-2 gamma (activating enhancer-binding protein 2 gamma)	1.92	0.98	1.07	2.20	1.68	1.67	1.70	0.96	0.95	1.26	0.99	1.47	1.45	0.74	1.40	0.37	1.02	0.99	0.94	0.85	0.56	0.78
46786	Hs.5542	tetratricopeptide repeat domain 2	1.37	2.34	0.85	0.99	1.72	1.26	2.10	1.62	1.15	1.80	1.48	1.06	0.76	0.99	1.76	0.82	1.58	1.32	1.99	0.63	1.64	1.54
361171	Hs.6364	Tat interactive protein (60kD)	1.11	1.37	0.87	2.20	1.30	1.51	1.68	1.46	1.44	1.44	1.10	1.91	1.82	2.01	2.18	1.44	1.45	1.20	1.45	1.48	1.07	1.20
28469	Hs.177584	3-oxoacid CoA transferase	1.85	1.46	1.90	1.47	0.67	1.71	0.89	0.61	0.59	0.66	1.14	1.12	0.47	0.60	0.91	0.38	0.69	1.19	0.75	1.00	0.48	0.82
823590	Hs.107573	sialyltransferase	4.49	2.49	1.13	2.47	3.15	3.87	6.05	2.76	5.16	5.55	2.67	6.96	4.88	2.46	7.16	0.77	4.18	1.95	4.97	2.03	3.74	2.76
813419	Hs.171280	hydroxyacyl-Coenzyme A dehydrogenase, type II	1.64	3.69	2.13	1.29	1.75	1.70	2.28	1.09	1.56	2.50	1.36	1.87	1.02	0.97	1.37	1.54	1.22	0.90	2.07	1.17	2.03	2.27
813462	Hs.184081	seven in absentia (Drosophila) homolog 1	1.71	1.88	1.06	1.25	1.53	1.56	1.02	1.81	1.99	2.64	1.50	2.97	0.85	2.00	1.48	0.46	1.70	2.45	2.54	0.75	1.90	1.38
547247	Hs.25590	stanniocalcin	0.67	1.65	1.51	1.44	0.82	0.89	0.93	1.34	2.86	1.06	1.72	4.70	2.55	1.34	1.42	0.38	2.04	1.40	3.92	0.99	0.47	0.70
31866	Hs.77897	splicing factor 3a, subunit 3, 60kD	1.97	1.57	2.38	1.62	1.79	1.73	1.37	1.15	1.55	1.83	1.18	1.03	0.67	0.96	1.21	0.74	1.44	1.52	1.60	1.40	2.08	2.03
250667	Hs.28726	RAB9, member RAS oncogene family	1.66	1.60	1.02	1.08	2.74	1.12	0.98	0.87	0.80	0.86	1.25	0.94	0.51	0.64	0.79	0.86	0.72	0.87	0.99	1.35	1.03	1.07
292213	Hs.91299	postmeiotic segregation increased 2-like 12	1.45	2.13	1.81	1.41	1.52	0.98	2.02	1.55	1.58	1.55	1.95	1.16	1.49	0.98	1.08	1.65	1.07	1.90	1.98	1.48	1.78	0.85
324210	Hs.24447	sigma receptor (SR31747 binding protein 1)	2.34	2.26	0.79	2.07	1.25	1.15	2.20	1.12	0.74	0.83	1.11	0.71	0.75	0.69	0.83	0.70	0.53	1.12	1.44	1.33	0.92	1.02
197176	Hs.56845	GDP dissociation inhibitor 2	1.07	1.87	1.14	2.23	1.37	2.69	1.97	1.11	1.13	0.75	0.83	0.68	0.73	0.51	0.96	1.23	1.50	1.34	0.99	1.39	1.27	1.38
810331	Hs.77266	quiescin Q6	0.39	1.19	0.71	0.69	1.64	0.48	0.45	1.51	1.09	0.75	1.06	2.23	1.60	0.83	1.39	1.88	0.70	0.59	0.48	0.51	1.78	1.07
210887	Hs.119222	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting protein)	0.74	0.99	0.87	0.97	1.34	1.03	0.84	0.86	1.17	0.90	0.74	0.49	0.27	0.46	0.53	0.80	0.87	1.09	0.92	0.95	0.99	1.18
280666	Hs.79089	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytopla	2.27	10.28	2.28	4.97	3.83	3.80	3.61	4.01	4.23	4.83	4.71	9.40	3.89	4.47	8.05	0.59	2.93	2.90	3.07	1.74	2.22	3.66
813533	Hs.8180	syndecan binding protein (syntenin)	0.31	0.79	0.48	0.73	0.77	0.54	0.46	0.38	0.82	0.66	0.55	0.70	0.34	0.52	0.44	0.83	0.35	0.91	0.63	0.96	0.54	0.85
303048	Hs.161542	ESTs	0.93	2.08	0.83	0.99	1.16	0.38	1.10	0.76	0.38	0.35	0.59	0.95	0.44	0.29	1.02	0.42	0.36	1.23	0.73	0.41	0.68	0.86
187147	Hs.62349	Human ras inhibitor mRNA, 3' end	1.64	2.21	1.35	2.27	1.40	0.57	0.81	1.37	2.46	1.47	1.13	1.81	0.59	0.94	1.04	2.01	1.12	3.04	1.50	1.01	1.33	1.76
321529	Hs.6809	RAP2A, member of RAS oncogene family	2.06	3.48	2.42	3.70	2.29	2.05	0.97	1.20	1.66	1.50	1.19	3.94	2.51	2.31	0.74	0.80	1.39	1.61	0.80	2.14	1.33	2.02
142122	Hs.80306	Homo sapiens mRNA, clone:RES4-4	1.49	3.37	1.62	1.07	2.46	1.31	1.23	1.79	2.42	2.62	1.11	1.26	0.77	0.95	1.16	1.83	1.04	1.42	1.97	1.01	1.85	1.14
130916	Hs.204524	ESTs, Weakly similar to KIAA0747 protein [H.sapiens]	0.80	0.74	0.59	0.67	1.47	0.93	0.96	0.89	0.95	0.97	0.88	0.78	0.46	0.69	0.62	0.88	0.47	1.03	0.95	0.43	0.90	0.81
139818	Hs.52526	KIAA0669 gene product	1.72	0.99	1.60	0.98	1.59	0.85	1.64	0.77	1.40	1.56	0.71	2.13	0.80	1.52	1.47	0.70	0.76	1.01	1.14	1.10	0.78	0.63
244343	Hs.194125	ESTs	3.19	25.86	1.04	3.76	5.76	1.68	2.71	0.70	7.02	2.75	2.69	2.22	0.52	0.54	1.43	1.92	1.74	2.56	2.97	0.87	1.47	2.69
234468	Hs.56801	ESTs	1.67	0.79	0.85	0.95	1.23	1.60	1.05	0.86	0.71	0.78	1.26	0.48	0.75	0.64	0.76	1.00	0.61	1.30	1.27	0.87	1.08	1.02
345751	Hs.7910	Ring1 and YY1 binding protein	1.54	1.78	1.02	1.30	2.05	1.34	1.17	1.17	1.78	1.53	1.36	1.18	0.34	0.80	1.78	1.67	1.49	2.07	1.90	1.68	1.75	1.51
209381	Hs.57362	ESTs	2.12	4.12	1.08	1.34	1.86	2.07	3.39	1.35	1.65	1.93	3.36	4.99	3.92	2.17	5.69	1.22	3.71	4.41	8.20	2.12	1.36	0.91
591653	Hs.62675	ESTs, Highly similar to non-ocogenic Rho GTPase-specific GTP exchange factor [H.sapiens	1.45	2.56	1.46	1.95	3.80	2.39	2.31	1.76	2.62	1.76	1.22	3.20	0.72	1.50	1.69	2.98	1.82	2.24	1.49	1.48	2.50	2.71
200302	Hs.63609	ESTs, Weakly similar to protein Htf9C [M.musculus]	1.10	2.76	1.30	1.07	1.88	1.50	3.28	1.73	1.25	1.91	1.29	3.92	1.79	2.16	2.19	0.96	1.35	1.35	2.03	1.04	1.48	1.07
193182	Hs.173159	transforming, acidic coiled-coil containing protein 1	0.54	0.93	0.69	0.76	1.29	0.43	0.34	0.74	0.89	2.39	0.44	0.74	0.76	0.46	0.68	0.99	0.60	0.81	0.41	0.56	1.38	0.93
233274	Hs.64691	KIAA0483 protein	1.47	1.90	1.17	2.02	3.04	1.37	0.88	1.11	1.16	0.89	1.51	0.84	1.10	0.79	1.22	2.13	0.83	1.23	1.15	1.05	1.04	0.91

200307	Hs.68647	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	0.50	0.70	0.62	1.15	0.75	0.36	0.95	0.64	0.64	0.38	0.62	0.57	0.69	0.45	0.60	1.11	0.83	0.89	0.62	0.68	0.39	0.59
299815	Hs.72805	ESTs	1.73	2.72	0.74	0.85	2.18	2.04	1.16	1.06	0.72	1.04	0.91	0.78	0.56	1.16	1.68	0.68	1.22	0.70	1.72	0.96	1.07	1.51
814270	Hs.91728	polymyositis/scleroderma autoantigen 1 (75kD)	2.73	2.30	1.23	1.57	2.35	1.94	2.30	1.11	0.82	1.35	1.15	0.78	0.60	0.48	0.97	0.58	1.03	1.22	2.34	1.50	1.76	0.91
200402	Hs.70704	ESTs	1.52	0.89	0.66	1.03	1.36	0.34	1.93	0.92	0.62	1.54	0.77	0.31	0.47	0.60	0.45	0.70	0.39	0.48	0.93	0.96	0.41	0.79
244637	Hs.75847	chromosome 15 open reading frame 3	0.84	1.10	0.29	1.41	1.16	1.15	1.16	1.04	2.15	1.49	1.18	1.20	0.60	0.94	1.65	1.46	0.94	1.26	1.79	1.10	0.65	0.60
246546	Hs.77365	ESTs	0.80	0.93	1.26	1.02	1.15	1.04	1.13	0.98	1.16	1.33	1.33	1.93	1.54	1.55	1.31	1.19	0.85	1.04	1.30	1.24	0.85	1.08
126229	Hs.77677	ESTs, Highly similar to KIAA0445 protein [H.sapiens]	1.56	1.62	0.90	1.21	1.49	1.73	1.66	1.11	1.04	1.56	1.15	1.81	0.95	1.67	1.84	1.13	1.67	1.55	1.44	1.13	0.85	0.87
143310	Hs.7972	KIAA0871 protein	3.62	3.59	0.59	2.17	2.44	1.62	1.84	2.17	2.19	2.24	1.03	3.47	0.70	1.16	1.88	0.78	2.44	2.36	5.19	2.42	1.74	0.91
139278	Hs.155478	cyclin T2	1.07	1.96	1.10	1.15	3.80	1.22	1.56	1.34	1.28	1.24	1.58	2.84	0.73	1.16	1.92	1.65	1.77	1.45	2.05	1.47	0.69	0.51
324342	Hs.226046	ceramidase-like	4.14	7.99	0.95	3.24	4.00	3.61	1.43	2.47	3.96	1.68	3.32	3.45	1.16	2.15	1.32	2.99	2.61	2.84	3.88	0.77	3.47	2.72
203547	Hs.24594	ubiquitination factor E4B (homologous to yeast UFD2)	1.12	1.38	0.86	0.76	1.33	0.93	0.88	0.80	0.83	1.00	0.57	1.19	0.68	0.74	1.26	0.70	1.12	1.00	0.96	1.34	0.71	0.44
299093	Hs.79503	ESTs	1.40	1.76	1.23	1.04	1.87	1.65	2.25	1.43	0.85	1.28	0.79	2.65	1.89	1.35	2.09	1.20	1.04	1.42	1.96	1.16	0.97	1.13
246686	Hs.80021	ESTs, Weakly similar to 62D9.p [D.melanogaster]	1.17	1.02	0.77	0.89	1.22	0.89	1.16	1.09	0.87	1.22	0.69	0.76	0.82	0.72	0.86	0.86	1.00	0.76	1.07	0.97	0.60	1.05
233550	Hs.8661	Homo sapiens mRNA; cDNA DKFZp586H2223 (from clone DKFZp586H2223)	1.27	1.08	0.92	1.04	1.53	1.23	1.08	1.51	2.24	1.53	1.33	2.03	1.35	1.10	2.01	1.09	2.78	2.40	4.78	1.40	0.86	1.61
244277	Hs.82590	ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	1.40	2.52	1.61	1.53	2.38	1.16	2.51	3.16	3.18	2.48	2.55	2.24	1.05	1.67	3.01	1.23	1.73	1.43	3.05	1.65	1.81	1.59
126219	Hs.82184	ring finger protein 3	1.48	1.06	1.13	1.38	1.81	1.18	0.84	0.93	1.33	1.31	1.47	2.72	4.02	2.39	4.40	1.63	1.48	1.60	1.55	1.38	0.70	0.66
232670	Hs.82389	ESTs, Highly similar to CGI-118 protein [H.sapiens]	1.90	1.23	0.60	1.90	1.32	1.10	1.86	1.01	0.84	1.20	1.37	0.78	0.51	0.77	0.99	0.92	1.29	0.63	0.98	2.71	0.91	0.85
309583	Hs.82547	ESTs	1.61	5.86	0.03	0.44	3.33	5.87	0.23	0.28	0.16	0.09	0.26	0.87	0.25	0.49	0.53	0.63	0.20	0.21	0.17	0.62	0.51	0.95
296030	Hs.10362	ESTs	0.95	1.51	0.54	1.23	1.35	1.36	0.91	0.96	0.58	1.05	1.64	1.06	1.12	1.50	1.83	1.71	0.57	0.80	0.68	0.86	0.64	0.75
308163	Hs.84520	ESTs	1.38	0.55	0.51	0.72	1.29	0.81	0.58	0.58	0.77	0.46	0.56	0.43	0.33	0.34	0.55	1.45	0.42	0.98	0.52	0.76	0.44	1.28
357120	Hs.84640	ESTs, Weakly similar to proline-rich protein MP3 [M.musculus]	1.33	1.91	0.86	1.16	2.28	1.27	1.16	1.28	1.33	1.17	1.43	0.92	0.83	1.12	1.19	1.44	1.37	1.47	2.32	0.83	1.37	1.48
360885	Hs.89474	ADP-ribosylation factor 6	1.45	0.96	1.46	1.19	0.98	1.22	0.49	1.12	0.89	1.01	1.22	0.81	1.35	0.86	0.93	0.90	0.79	0.78	0.89	1.29	0.51	0.71
469952	Hs.77356	transferrin receptor (p90, CD71)	1.92	1.67	0.57	0.86	1.44	1.00	1.26	1.31	0.95	0.92	0.69	0.66	0.32	0.49	0.87	0.97	1.32	1.27	1.55	0.87	1.13	0.78
133236	Hs.90372	ESTs	1.87	3.18	1.02	2.34	4.23	3.51	3.41	1.17	1.56	1.39	1.49	2.30	1.16	1.02	2.43	1.74	1.23	1.78	1.04	1.04	1.10	2.97
130895	Hs.90790	ESTs	2.59	4.05	1.29	1.84	2.29	2.46	4.06	7.10	4.06	5.70	7.75	8.18	7.35	2.75	7.22	2.89	5.02	2.97	5.30	1.06	3.49	2.02
136560	Hs.194737	Homo sapiens mRNA for KIAA0453 protein, partial cds	1.61	1.28	0.77	0.88	1.22	1.37	0.78	0.65	0.82	0.96	0.84	1.59	0.90	1.48	1.46	1.27	0.96	1.32	1.18	1.00	1.32	0.39
301082	Hs.235089	ESTs	1.66	1.07	3.56	1.06	4.52	2.64	1.18	0.85	2.87	0.95	1.69	3.25	4.05	2.46	3.26	1.20	3.40	2.25	2.22	1.56	0.91	1.28
233071	Hs.171825	basic helix-loop-helix domain containing, class B, 2	1.16	1.29	2.02	2.27	3.70	2.21	2.63	2.26	17.47	1282.04	1.61	2.52	0.95	2.00	3.22	1.47	1.39	2.18	1.72	1.87	2.03	0.52
296616	Hs.194329	ESTs	0.97	0.65	0.97	0.47	1.23	0.40	0.78	0.95	3.24	1.08	0.62	0.39	0.36	0.23	0.50	0.74	2.08	1.73	2.09	0.74	0.64	0.55
241113	Hs.92200	KIAA0480 gene product	1.70	1.13	0.75	0.96	3.01	1.40	1.60	1.01	0.79	2.12	1.31	2.53	1.19	1.39	2.52	1.20	1.12	1.48	2.61	1.04	0.58	0.91
139376	Hs.91973	ESTs	1.99	0.86	1.34	1.01	2.51	1.00	1.33	1.60	1.00	2.01	2.21	1.16	3.21	1.96	2.08	1.42	1.44	1.70	1.21	2.20	2.53	0.91
138865	Hs.92145	ESTs	0.84	1.76	0.79	1.31	2.11	0.61	1.32	0.74	0.76	0.99	0.79	0.82	0.49	0.82	0.90	0.52	0.71	0.96	1.11	0.77	1.17	0.91
141192	Hs.92186	KIAA0989 protein	0.98	0.54	1.72	0.45	1.37	0.55	1.18	0.56	0.56	0.82	0.79	1.53	1.17	1.07	2.02	0.63	1.16	1.17	1.43	1.09	0.24	0.53
140655	Hs.28786	ESTs, Highly similar to proteasome [H.sapiens]	1.62	0.32	0.42	0.44	1.55	0.82	0.66	0.96	0.78	1.49	1.18	0.39	0.50	0.41	1.07	0.57	0.41	1.07	0.78	0.55	1.02	0.91
143756	Hs.251757	ESTs, Weakly similar to KIAA0681 protein [H.sapiens]	2.95	4.45	2.08	2.00	2.64	2.48	3.22	1.92	2.27	1.91	2.88	2.52	1.51	1.35	1.99	3.00	1.70	1.36	3.14	1.29	1.79	1.82
343737	Hs.92848	ESTs	1.22	1.98	0.90	1.05	1.86	2.46	1.27	1.25	1.62	0.85	2.08	1.09	0.48	0.87	1.36	1.30	0.92	1.86	2.08	1.41	1.28	2.13
753381	Hs.92962	Sec23 (S. cerevisiae) homolog A	1.28	1.11	2.87	1.26	1.68	1.35	0.82	0.63	2.43	0.77	1.31	0.63	0.30	1.41	0.92	2.38	0.78	1.07	1.18	0.83	0.65	0.91
232789	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	1.10	2.18	2.20	1.57	1.36	1.22	1.78	1.40	1.39	1.67	1.51	2.27	1.19	0.86	1.54	1.05	1.00	1.08	1.57	1.25	1.57	1.17
840404	Hs.172195	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	1.67	1.36	1.60	1.31	1.81	1.29	1.00	1.60	1.69	1.19	1.98	1.98	1.14	0.90	1.13	0.86	1.33	1.35	1.47	1.25	1.48	1.18
246194	Hs.125522	ESTs	1.08	1.29	1.28	0.77	1.63	1.12	1.30	0.78	0.83	0.63	0.96	0.95	0.53	0.85	0.93	0.92	1.17	1.28	1.09	1.45	1.52	1.26
292770	Hs.172084	ESTs	3.54	3.38	1.25	2.59	3.00	1.42	3.55	2.97	1.85	2.54	1.78	2.67	1.48	2.66	3.11	1.01	1.89	2.04	4.44	1.20	1.54	1.81
235008	Hs.182874	ESTs	2.14	1.94	1.62	1.86	2.97	2.57	3.66	1.96	1.67	1.54	1.11	1.52	1.53	0.93	1.72	1.99	3.19	2.29	2.68	1.91	3.22	2.35
296162	Hs.94300	amiloride-sensitive cation channel 2, neuronal	1.76	2.30	0.74	1.30	1.98	1.76	1.26	0.87	1.25	1.81	2.47	1.23	1.08	0.95	1.05	1.67	1.08	1.40	1.84	1.04	1.21	0.91
796198	Hs.30942	ephrin-B2	2.44	1.84	0.63	0.95	3.19	1.32	2.41	0.97	1.68	1.23	1.53	1.93	1.13	1.97	2.04	1.37	1.52	1.44	3.53	0.88	1.03	0.91
344352	Hs.94842	ESTs	1.43	1.57	1.06	0.98	1.39	1.10	1.08	0.62	0.77	0.93	1.00	0.89	0.41	0.62	0.86	1.00	0.58	0.92	0.95	0.97	0.70	0.36
125685	Hs.256551	ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]	1.20	1.23	0.73	0.65	1.50	1.10	0.78	1.14	1.59	1.36	1.32	2.31	1.39	1.25	1.80	1.56	1.11	1.03	1.37	1.01	0.63	0.86
140635	Hs.95893	ESTs	1.07	0.73	0.52	0.50	1.09	0.60	0.98	1.28	3.80	2.30	1.55	1.77	1.90	0.72	1.76	1.17	4.15	1.10	1.88	0.72	1.03	0.42
130835	Hs.96125	ESTs	1.07	3.08	0.36	0.57	1.82	1.44	0.33	1.49	1.97	10.41	1.50	3.06	2.48	0.91	2.02	0.98	0.81	1.30	1.80	0.65	1.25	0.91
774082	Hs.1619	achaete-scute complex (Drosophila) homolog-like 1	1.66	1.15	0.65	1.49	1.50	1.04	0.61	1.49	1.76	1.27	1.24	0.95	0.42	0.82	0.74	1.34	0.81	1.20	0.83	0.97	1.35	0.91
247081	Hs.98693	DKFZP586J0917 protein	1.00	1.17	0.64	0.59	2.18	1.04	0.51	1.28	1.15	1.26	0.96	2.17	0.88	1.06	1.72	1.34	1.12	1.48	1.22	0.86	0.65	1.33
161993	Hs.99029	CCAAT/enhancer binding protein (C/EBP), beta	1.54	2.04	1.14	0.93	2.44	1.42	2.42	1.49	1.03	1.41	1.07	0.80	0.48	0.66	0.53	0.89	1.01	1.65	1.44	1.33	1.67	1.25
470846	Hs.9605	pre-mRNA cleavage factor Im (25kD)	1.23	0.90	0.64	0.83	0.62	1.02	0.31	0.75	0.55	0.47	0.83	0.57	0.50	0.44	0.48	0.90	0.83	0.66	0.56	0.56	0.82	1.22
129071	Hs.240559	ESTs	1.27	1.83	1.36	1.24	1.47	1.58	1.28	1.72	1.62	0.93	0.75	1.08	0.83	1.04	1.14	2.03	1.12	1.75	1.32	1.05	1.15	0.91
825842	Hs.75744	S-adenosylmethionine decarboxylase 1	0.94	2.21	0.93	2.00	4.10	2.16	1.81	1.55	0.81	0.57	1.09	1.11	0.39	0.98	1.31	0.77	0.75	0.83	0.71	0.99	1.08	1.99
124271	Hs.17686	ESTs	1.50	2.70	0.25	0.78	1.80	2.22	2.36	1.73	1.42	3.20	1.32	2.65	2.65	1.57	3.60	2.16	1.22	1.73	2.65	1.37	2.19	1.89
130610	Hs.8752	putative type II membrane protein	1.44	1.10	1.50	1.00	0.52	1.01	2.93	0.84	0.85	1.58	1.17	1.54	1.48	1.43	1.44	3.32	1.90	1.11	1.83	1.80	0.54	0.72
208699	Hs.244452	EST	0.73	2.05	1.74	1.27	0.98	1.36	0.90	0.97	1.71	1.12	1.27	1.60	0.67	1.19	0.87	2.48	0.73	0.64	0.70	1.05	0.77	1.18
144870	Hs.101565	ESTs	1.39	2.37	0.69	1.21	1.87	1.44	1.10	0.92	1.53	1.15	0.99	1.08	0.39	0.59	0.91	1.25	0.88	1.49	1.61	0.89	0.88	1.51
172783	Hs.101750	ESTs, Weakly similar to PTB-ASSOCIATED SPLICING FACTOR [H.sapiens]	1.48	3.96	1.70	1.70	3.19	1.48	3.97	2.04	2.44	3.28	1.01	1.84	1.65	1.08	1.48	1.94	1.19	1.78	2.37	0.89	2.53	2.05
160573	Hs.101766	TGF beta receptor associated protein -1	1.35	1.08	0.86	0.85	1.40	1.18	2.10	0.43	1.69	0.95	1.05	2.73	1.28	1.47	2.14	1.49	2.06	1.42	1.35	1.10	1.18	2.88
232586	Hs.102219	EST	1.59	0.72	0.51	0.52	1.12	0.70	1.94	0.77	1.00	0.97	1.22	0.99	0.28	0.56	0.35	0.74	1.27	1.17	1.70	0.93	1.35	1.54
142586	Hs.102696	ESTs, Weakly similar to C11D2.4 [C.elegans]	0.97	0.85	0.73	0.57	1.27	0.78	0.66	0.98	0.97	0.84	0.96	0.39	0.51	0.44	0.58	1.11	0.93	0.72	1.36	1.33	0.75	1.00
234537	Hs.102480	ESTs	1.61	2.84	1.51	1.36	1.40	0.99	1.11	1.86	1.91	2.28	1.79	0.73	0.80	1.00	1.06	1.14	1.73	0.99	1.55	1.85	1.64	0.82
113300	Hs.102507	ESTs	1.06	0.91	2.37	1.25	1.27	1.09	1.55	1.93	1.57	2.36	0.45	1.19	1.26	1.07	1.19	1.62	1.14	0.94	0.52	1.01	0.56	1.11
143661	Hs.102541	ESTs	0.17	0.45	0.21	0.11	0.88	0.11	0.14	0.36	0.44	0.95	0.19	0.33	0.09	0.15	0.57	0.38	0.68	0.79	0.62	0.45	0.24	0.09
813410	Hs.150675	polymerase (RNA) II (DNA directed) polypeptide K (7.0kD)	1.27	1.32	1.68	1.91	1.45	1.58	0.89	1.74	1.86	2.96	1.23	0.71	1.36	0.76	1.29	1.40	2.17	1.02	0.86	1.88	1.03	2.15
240208	Hs.102669	DKFZP434O125 protein	1.47	1.05	0.89	1.16	1.04	1.01	1.36	0.82	0.99	0.95	0.50	0.94	1.04	0.72	1.03	0.76	0.73	0.87	0.74	0.97	0.85	1.01
769846	Hs.238030	secretory carrier membrane protein 2	1.07	0.87	0.40	0.71	0.98	0.99	0.78	1.08	0.98	0.88	0.87	1.79	1.10	1.70	1.27	1.12	0.71	0.89	0.97	0.76	1.32	0.93
229580	Hs.105255	ESTs, Weakly similar to hypothetical protein [H.sapiens]	1.62	1.76	0.63	1.60	1.59	1.98	1.17	1.26	1.36	1.43	1.06	1.50	1.33	1.07	1.17	1.28	1.60	1.09	1.41	0.81	1.50	0.84
143169	Hs.183576	ESTs	0.25	0.05	1.72	0.05	0.70	0.14	0.36	0.27	0.07	0.26	0.43	0.17	0.39	0.76	0.84	0.33	0.56	1.52	0.65	1.20	1.90	0.08
131887	Hs.103395	ESTs	3.66	3.00	1.21	1.18	5.67	1.32	4.53	3.36	3.71	2.85	1.73	16.61	2.79	6.56	6.51	1.76	2.59	4.03	13.40	2.68	5.11	1.40
132066	Hs.103808	ESTs, Weakly similar to RanBPM [H.sapiens]	1.25	1.06	1.19	1.14	1.16	1.72	1.68	1.39	1.45	2.27	1.66	1.25	1.69	1.08	1.81	0.93	3.07	0.94	1.03	1.04	0.93	0.66
121251	Hs.103834	ESTs	2.34	1.20	2.36	1.14	2.06	1.37	1.92	1.82	1.29	1.98	2.32	1.23	3.14	1.15	1.66	1.59	1.77	2.09	1.32	0.99	1.77	1.80
135220	Hs.104203	ESTs	1.12	0.80	0.78	1.20	2.06	1.12	1.49	0.55	1.36	1.41	0.88	1.57	2.15	1.19	1.99	1.38	1.77	1.16	1.16	0.70	0.68	0.67
811890	Hs.105751	Ste20-related serine/threonine kinase	0.59	1.24	0.58	1.60	1.91	0.83	0.56	0.98	1.06	0.92	1.44	0.88	0.62	0.35	0.79	0.35	0.66	0.90	1.32	0.63	1.23	0.74
130120	Hs.155489	NS1-associated protein 1	0.84	1.34	0.92	2.53	1.61	2.06	1.05	1.20	0.67	0.50	1.54	1.00	0.86	0.86	0.89	1.77	1.10	1.01	0.78	1.27	1.30	1.40
133972	Hs.78305	RAB2, member RAS oncogene family	1.23	0.99	1.06	0.83	1.66	1.13	0.91	0.86	1.56	1.70	1.16	0.75	0.69	0.79	1.12	1.21	1.08	1.50	1.15	1.61	1.40	1.25
347224	Hs.106728	ESTs	1.54	1.51	0.98	0.85	2.17	0.87	0.76	1.67	1.28	1.50	1.11	1.08	0.73	0.82	1.13	1.18	0.99	1.52	1.37	0.76	2.10	1.50
139680	Hs.106200	ESTs	2.16	3.34	1.53	1.57	3.67	1.18	7.07	1.99	2.44	0.95	3.50	9.31	2.81	3.67	10.07	1.46	6.92	1.75	10.87	1.59	1.28	1.12
141684	Hs.106243	ESTs	0.42	0.74	0.42	0.43	0.60	0.15	0.19	0.27	0.16	1.29	0.16	0.59	0.24	0.34	0.92	0.09	0.12	0.15	0.19	0.36	0.19	0.18
243546	Hs.106283	insulin-like growth factor binding protein 6	2.29	1.99	1.05	1.63	2.41	1.12	2.64	0.97	1.75	1.26	1.19	2.31	2.10	1.29	2.38	0.91	0.93	2.05	2.65	0.87	0.86	1.11

284592	Hs.74615	platelet-derived growth factor receptor, alpha polypeptide	1.03	4.21	1.87	2.58	4.47	1.76	4.00	1.40	1.26	0.88	1.04	0.84	0.56	1.18	0.70	1.22	0.75	1.30	1.10	1.45	0.99	3.60
136180	Hs.107057	ESTs	1.00	1.04	0.69	1.28	2.55	0.94	0.55	0.98	0.86	0.98	0.73	0.55	0.45	0.72	0.56	0.52	0.41	0.92	1.03	1.56	0.91	1.82
142067	Hs.182470	PTD010 protein	0.72	2.04	1.69	1.34	1.37	0.79	1.48	1.60	1.45	1.88	1.18	1.92	1.63	0.75	1.67	1.58	0.78	1.09	1.62	0.69	0.73	0.77
142851	Hs.107171	ESTs	0.80	1.85	0.88	1.29	1.88	0.79	0.89	1.17	1.84	2.13	0.69	1.67	4.35	2.19	2.05	1.20	1.49	1.23	0.72	1.26	1.17	1.75
212542	Hs.21851	Homo sapiens mRNA; cDNA DKFZp586J2118 (from clone DKFZp586J2118)	1.64	2.78	1.01	2.61	4.02	2.51	1.96	4.50	3.58	3.19	3.15	4.59	6.50	2.42	8.92	3.35	5.75	2.05	7.64	1.86	2.69	2.26
135688	Hs.760	GATA-binding protein 2	1.12	1.08	2.17	1.35	6.70	0.98	1.21	125.34	8.36	2.26	0.81	5.14	0.66	1.17	2.77	0.90	6.12	1.53	1.21	0.94	1.05	0.45
22074	Hs.724	thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene h	1.56	0.69	0.94	1.02	1.06	0.61	1.26	0.57	1.17	1.12	1.56	0.70	0.95	0.67	1.25	1.30	0.82	1.44	1.28	1.89	0.55	0.83
110503	Hs.4245	ESTs, Weakly similar to similar to S. cerevisiae hypothetical protein YKL166 [C.elegans]	0.66	0.78	0.46	1.57	1.11	0.40	1.21	0.83	0.41	0.54	0.52	0.93	0.24	1.30	1.58	0.38	0.43	0.54	0.98	1.00	1.21	0.91
141768	Hs.173664	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma deri	1.04	1.37	0.51	0.48	0.91	1.33	1.31	1.75	1.43	1.57	3.28	1.45	2.49	2.29	2.81	5.16	1.63	1.23	2.06	2.67	4.02	0.58
35236	Hs.73957	RAB5A, member RAS oncogene family	1.12	0.88	1.56	1.08	1.30	0.90	1.07	0.78	0.85	0.93	1.15	0.98	0.87	0.85	1.07	1.59	1.24	0.79	0.82	0.96	0.55	1.35
38763	Hs.250595	S-phase response (cyclin-related)	2.76	1.86	1.20	1.74	3.12	1.51	1.83	1.66	1.16	0.68	1.81	2.13	1.47	0.98	1.51	1.26	1.43	1.71	1.55	1.44	1.95	2.02
42076	Hs.250897	TRK-fused gene (NOTE: non-standard symbol and name)	1.20	1.42	0.76	0.68	1.42	1.54	1.53	0.73	1.30	0.72	0.79	0.40	0.61	0.95	0.69	1.30	1.01	0.82	0.93	1.00	1.04	1.68
42706	Hs.724	thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene h	0.77	2.12	1.22	1.33	1.84	1.06	1.33	1.04	0.73	0.97	1.51	4.69	2.23	2.96	0.72	1.99	0.77	1.19	2.60	0.83	0.73	0.89
207618	Hs.77183	v-raf murine sarcoma 3611 viral oncogene homolog 1	1.74	2.20	1.64	1.21	2.08	1.79	1.24	1.17	1.23	0.81	2.35	1.45	1.47	1.35	1.91	1.24	1.29	1.54	1.96	1.16	1.64	1.97
172440	Hs.5636	RAB6, member RAS oncogene family	1.24	0.84	0.57	1.85	0.99	1.43	0.45	0.61	1.12	1.68	2.10	1.66	3.32	1.49	2.19	1.34	1.17	0.78	0.41	2.54	0.43	0.94
180902	Hs.21247	ESTs	0.81	1.13	0.80	1.13	1.74	1.07	1.51	1.00	1.63	0.99	2.15	0.98	2.32	2.34	1.74	1.43	0.49	0.76	1.20	1.45	0.61	0.91
1035182	Hs.9610	purinergic receptor P2X, ligand-gated ion channel, 4	2.72	2.19	1.42	1.42	3.99	1.85	5.94	1.19	1.39	1.20	2.76	10.90	5.82	3.48	6.60	1.65	5.02	4.91	6.01	2.49	1.48	2.32
193913	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	0.99	3.48	2.27	1.40	3.52	1.67	1.33	1.30	1.59	0.93	2.24	2.18	0.66	1.76	1.06	1.52	0.96	1.27	0.98	1.20	1.39	2.48
244652	Hs.145279	SET translocation (myeloid leukemia-associated)	1.20	1.08	0.48	0.99	1.01	0.69	0.76	0.94	0.94	1.13	0.63	0.37	0.55	0.43	0.71	0.97	0.70	1.07	1.09	0.93	1.06	0.64
258589	Hs.44313	v-rel avian reticuloendotheliosis viral oncogene homolog	1.89	2.77	1.37	2.18	4.20	3.24	1.68	2.21	3.88	0.83	2.84	3.85	0.68	1.12	1.82	1.70	2.98	2.72	3.57	1.10	1.48	0.91
267431	Hs.169370	FYN oncogene related to SRC, FGR, YES	0.80	2.11	1.74	2.53	3.37	2.03	1.25	1.45	1.94	1.20	1.63	1.92	0.55	1.24	1.39	2.01	1.39	1.35	1.04	0.81	0.77	0.91
267634	Hs.85181	v-raf-1 murine leukemia viral oncogene homolog 1	1.46	1.13	1.04	1.04	1.45	1.04	1.00	0.95	0.87	1.08	1.28	1.11	0.62	0.87	0.78	1.28	1.50	1.19	1.20	0.76	1.03	1.38
273435	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	1.30	1.53	0.75	1.09	1.48	2.00	0.86	0.55	0.79	0.59	1.37	0.44	0.48	0.75	0.68	1.37	0.42	0.87	0.93	1.12	0.73	1.30
321189	Hs.156764	DKFZP586H0723 protein	0.68	0.79	1.57	1.44	1.40	1.27	0.69	1.02	1.71	0.66	0.99	0.68	0.61	0.71	0.81	1.43	1.36	1.32	1.22	1.57	1.34	1.73
322617	Hs.181309	proteasome (prosome, macropain) subunit, alpha type, 2	0.56	0.47	0.49	0.59	0.77	0.90	0.41	0.84	3.12	0.96	0.80	0.60	0.59	0.60	0.75	1.30	0.61	0.77	0.61	0.85	0.60	1.40
285226	Hs.2780	jun D proto-oncogene	1.12	3.62	1.25	1.50	1.62	1.36	1.11	1.62	2.18	2.46	1.32	2.29	1.49	1.43	2.44	1.25	1.98	2.23	1.90	0.93	1.60	1.00
293715	Hs.3642	DKFZP564B163 protein	0.81	0.59	0.69	1.25	0.95	0.97	0.92	0.76	1.25	0.85	0.74	0.61	0.54	0.67	0.80	0.95	1.04	0.87	0.69	1.02	0.72	1.11
302369	Hs.54589	NCK adaptor protein 1	2.12	0.95	0.70	1.68	1.66	1.18	1.69	0.87	1.13	1.59	0.87	0.68	0.65	0.49	0.66	1.26	0.71	0.94	0.67	0.86	0.80	1.47
309776	Hs.195175	CASP8 and FADD-like apoptosis regulator	1.07	1.49	0.49	1.58	3.33	2.01	1.85	1.34	1.57	1.07	1.83	1.09	0.70	1.33	1.00	1.41	1.95	2.39	1.19	1.52	1.39	0.91
309864	Hs.198951	jun B proto-oncogene	1.27	0.87	0.23	0.53	0.92	0.51	0.36	0.26	1.46	0.36	0.49	0.55	0.23	0.34	0.53	0.71	0.56	1.69	0.60	0.63	0.43	0.99
429574	Hs.74552	caspase 3, apoptosis-related cysteine protease	0.78	0.81	0.83	0.60	0.86	0.70	0.53	0.77	0.67	0.87	0.87	0.64	0.65	0.92	0.76	0.93	0.78	0.69	0.59	0.76	0.49	0.83
342069	Hs.78305	RAB2, member RAS oncogene family	1.29	0.85	1.19	0.83	1.39	1.05	0.92	0.84	1.17	0.78	1.02	1.21	0.94	1.20	1.47	1.02	0.86	1.03	0.76	1.51	1.63	1.36
343320	Hs.1976	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene ho	1.17	0.76	1.17	1.00	1.76	1.57	2.72	1.27	2.09	2.38	2.22	2.95	2.26	1.69	2.51	2.23	1.99	1.37	2.27	1.84	0.55	0.84
358531	Hs.78465	v-jun avian sarcoma virus 17 oncogene homolog	1.12	0.62	1.20	0.78	1.29	0.27	1.05	0.49	1.05	0.63	0.67	0.88	0.30	0.73	1.08	0.64	0.78	2.59	0.74	0.95	0.60	0.28
380620	Hs.25363	presenilin 2 (Alzheimer disease 4)	1.34	1.05	0.77	1.26	2.76	1.73	1.42	1.66	1.65	1.13	1.39	2.61	2.98	2.07	2.26	1.38	2.39	1.79	2.10	0.81	1.81	1.28
413633			0.46	0.95	1.39	1.05	1.48	0.47	0.72	0.52	0.69	0.33	0.62	0.79	0.26	0.67	0.82	0.81	0.46	1.05	0.72	0.63	1.00	0.50
416280			1.08	1.06	0.71	0.97	1.34	0.99	1.33	0.74	0.80	0.59	1.03	0.83	0.88	0.86	0.88	0.66	0.76	1.78	1.04	1.16	1.05	1.19
417226	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	0.59	1.11	0.43	1.37	0.63	0.63	1.47	0.42	0.36	0.25	0.40	0.12	0.62	0.22	0.40	0.29	0.29	1.95	0.70	0.83	0.14	1.62
586698	Hs.2942	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	0.70	1.22	0.32	0.52	1.23	1.18	1.53	0.96	0.31	0.65	1.50	0.79	0.47	0.90	1.13	0.68	0.15	0.84	3.08	1.12	0.47	0.91
783697	Hs.79428	BCL2/adenovirus E1B 19kD-interacting protein 3	0.67	0.97	1.38	0.86	1.22	1.24	1.80	1.74	0.67	0.47	2.23	0.58	0.83	0.79	0.53	0.87	0.77	1.29	0.94	1.52	1.45	1.52
240961	Hs.74316	desmoplakin (DPI, DPII)	2.22	0.64	0.21	1.50	0.68	1.27	1.49	0.78	0.79	1.21	1.00	0.29	1.07	0.58	0.69	0.36	1.27	0.49	1.38	1.57	1.07	1.42
136814	Hs.24462	ESTs	0.88	1.27	0.66	0.81	1.24	0.94	1.00	0.98	1.32	0.87	1.42	0.82	0.75	0.53	0.87	0.80	1.15	0.93	1.35	1.36	0.96	0.95
161583	Hs.229619	EST	1.18	2.12	0.97	1.61	2.23	2.48	0.92	2.10	2.59	1.55	2.58	2.07	0.55	1.23	1.75	2.07	2.25	1.82	3.14	1.34	2.26	0.80
232826	Hs.6895	actin related protein 2/3 complex, subunit 3 (21 kD)	0.73	0.71	0.36	0.55	0.65	0.75	0.68	0.68	1.05	0.81	0.71	0.79	0.72	0.58	0.58	0.91	0.78	0.67	0.90	0.69	0.72	1.34
154323	Hs.25897	ESTs	0.48	0.58	0.10	0.31	0.54	0.10	0.69	0.45	0.52	1.04	0.24	0.37	0.66	0.37	0.48	0.37	0.51	0.77	0.72	0.50	0.40	0.53
809776	Hs.82127	interleukin 16 (lymphocyte chemoattractant factor)	1.83	5.25	3.84	3.95	5.45	5.47	3.24	4.04	14.99	3.85	3.58	6.31	1.23	1.88	2.65	3.29	5.32	5.14	3.66	3.03	4.68	1.49
755054	Hs.159301	interleukin 18 receptor 1	1.55	2.56	1.33	3.08	2.13	0.38	2.00	10.08	0.63	2235.20	1.53	2.01	0.91	0.97	4.72	0.14	2.93	1.99	1.78	1.22	1.24	1.24
47681	Hs.30035	splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10	2.05	1.88	1.52	1.64	1.67	1.19	1.59	1.51	1.30	1.03	1.39	0.66	0.67	0.69	1.24	1.00	0.99	1.00	0.98	1.02	1.09	1.39
810452	Hs.76927	translocase of outer mitochondrial membrane 34	1.16	1.76	1.40	1.27	2.19	1.33	1.38	1.76	1.26	1.32	1.77	0.77	1.13	0.66	1.04	0.82	1.11	0.80	1.05	0.71	2.03	1.95
41658	Hs.27747	G protein-coupled receptor 37 (endothelin receptor type B-like)	2.76	1.66	0.93	1.77	2.35	1.24	1.10	1.94	2.22	1.98	1.41	1.25	1.73	1.45	3.20	1.16	1.11	1.74	1.60	2.27	2.06	1.14
242037	Hs.92374	Human putative cyclin G1 interacting protein mRNA, partial sequence	1.05	0.65	1.42	1.93	1.08	0.32	2.03	0.55	0.70	0.65	0.86	0.58	0.82	0.74	0.47	0.64	0.37	0.73	0.77	0.62	0.72	0.30
144816	Hs.24030	solute carrier family 31 (copper transporters), member 2	3.29	2.03	1.08	2.13	2.15	3.18	1.32	2.16	2.97	3.43	2.56	2.79	1.04	1.88	2.49	2.43	1.16	1.54	2.21	1.23	2.28	1.35
380797	Hs.182225	RNA binding motif protein 3	1.12	0.84	1.44	0.98	0.89	1.16	1.67	1.09	1.04	0.40	1.06	0.89	1.30	1.44	1.76	1.06	0.85	0.97	0.61	1.17	0.78	0.98
166934	Hs.173310	protocadherin 2 (cadherin-like 2)	2.09	3.02	2.94	2.17	3.38	1.51	0.94	2.11	1.03	1.44	1.76	3.48	3.18	2.69	2.89	2.12	1.31	1.63	0.98	1.17	2.02	1.65
809784	Hs.79361	kallikrein 6 (neurosin, zyme)	0.44	0.69	0.13	0.13	0.77	0.12	0.19	0.10	0.08	0.06	0.06	0.33	0.11	0.20	0.22	0.07	0.08	0.18	0.22	0.15	0.10	0.05
199403	Hs.4082	lectin, galactoside-binding, soluble, 8 (galectin 8)	1.37	2.92	1.45	1.93	2.61	2.18	1.36	2.03	1.59	1.31	2.67	2.08	1.49	1.20	1.42	1.76	1.96	1.95	2.70	2.45	2.43	1.90
771236	Hs.79769	protocadherin 1 (cadherin-like 1)	1.83	1.61	1.02	1.07	2.06	1.46	1.49	1.68	1.09	1.54	1.99	0.94	1.24	0.89	1.13	0.91	1.84	1.11	1.67	0.92	1.58	1.26
342378	Hs.2128	dual specificity phosphatase 5	0.41	0.46	0.35	1.37	0.70	0.52	0.51	0.55	0.73	0.99	0.56	1.50	0.63	1.00	1.85	0.49	0.82	0.98	0.92	0.79	0.47	0.36
146123	Hs.79005	protein tyrosine phosphatase, receptor type, K	0.42	0.97	0.49	0.84	1.46	1.65	0.55	0.73	0.70	0.91	0.59	0.90	0.30	0.76	0.44	0.46	0.87	0.56	0.31	0.28	1.30	1.46
42739	Hs.227777	protein tyrosine phosphatase type IVA, member 1	0.48	0.62	0.80	0.61	0.56	0.42	0.85	0.44	0.64	0.46	0.60	0.56	0.48	0.49	0.48	0.72	0.70	0.74	0.52	0.89	0.64	0.48
362853	Hs.82643	protein tyrosine kinase 9	0.46	0.64	0.61	1.47	1.06	0.85	0.43	0.46	0.88	0.51	0.76	0.87	1.16	0.49	0.78	0.54	0.83	0.65	0.58	0.47	0.89	1.27
484641	Hs.83974	solute carrier family 21 (prostaglandin transporter), member 2	0.61	1.53	0.92	1.44	2.07	1.44	1.17	1.97	2.85	1.53	2.66	1.56	0.62	1.26	1.18	1.83	0.82	1.36	1.32	1.44	1.68	0.91
753917	Hs.28757	transmembrane 9 superfamily member 2	1.96	1.68	0.67	0.85	1.24	0.97	0.90	0.79	1.27	1.09	0.84	0.81	0.54	0.63	1.39	0.95	1.65	0.87	1.03	1.31	0.90	0.68
296476	Hs.199061	p300/CBP-associated factor	1.44	2.22	1.26	1.43	1.06	2.62	0.77	1.59	1.57	2.83	1.55	3.62	1.13	1.35	2.51	0.49	1.87	1.66	1.50	0.92	1.34	1.69
682522	Hs.94376	proprotein convertase subtilisin/kexin type 5	0.36	2.00	0.46	0.88	1.39	0.59	0.39	0.76	0.66	0.76	0.98	0.99	0.29	0.37	0.72	0.76	0.36	0.47	0.57	0.54	0.86	0.80
52431	Hs.76329	tumor differentially expressed 1	0.79	0.40	0.75	0.66	1.18	1.84	0.37	0.93	1.23	1.20	0.87	0.54	1.43	0.57	0.78	1.03	1.02	0.80	0.67	0.96	1.42	0.74
230385	Hs.6335	phosphatidylinositol-4-phosphate 5-kinase, type II, beta	1.47	2.25	1.48	1.67	2.02	1.53	1.04	2.34	2.32	2.54	1.09	2.58	2.79	1.83	2.26	0.62	1.85	1.64	1.87	2.44	1.66	1.58
198372	Hs.25156	Human phosphatidylinositol (4,5) bisphosphate 5-phosphatase homolog mRNA, partial cds	2.17	1.89	1.30	1.47	1.38	1.80	1.11	1.08	0.88	2.61	1.14	3.09	2.48	1.57	1.98	1.22	1.08	1.14	1.43	1.04	0.65	0.68
511832	Hs.100724	peroxisome proliferative activated receptor, gamma	1.03	1.10	1.34	1.01	1.08	1.90	1.68	1.45	1.18	0.60	1.14	1.05	1.32	1.16	1.45	1.16	1.19	1.60	0.86	1.59	1.30	2.49
770080	Hs.102497	paxillin	0.17	0.39	0.26	0.23	0.37	0.34	0.43	0.48	0.73	0.35	0.47	0.56	0.38	0.65	0.47	0.45	0.30	0.39	0.45	0.56	0.30	0.19
754093	Hs.82733	nidogen 2	1.70	8.37	13.98	13.07	3.92	3.03	2.43	7.05	11.11	304.04	3.09	2.94	1.32	2.61	2.65	1.58	3.97	2.22	4.65	2.58	0.65	1.76
190887	Hs.82116	myeloid differentiation primary response gene (88)	1.11	1.67	1.25	1.86	2.25	1.83	0.94	1.68	1.65	1.32	1.37	1.75	1.75	1.66	1.63	1.96	1.08	0.81	0.94	1.13	1.17	0.72
48614	Hs.151139	E74-like factor 4 (ets domain transcription factor)	1.87	1.86	0.79	1.18	1.52	1.49	0.92	1.63	1.56	1.16	1.78	1.49	0.89	0.81	0.98	0.38	1.24	1.10	1.42	1.05	1.79	1.31
246786	Hs.23016	Human orphan G protein-coupled receptor (RDC1) mRNA, partial cds	1.18	4.43	4.84	1.88	3.98	1.12	2.02	4.42	5.07	3.36	3.86	4.32	1.25	1.79	3.09	1.14	1.59	243.70	2.56	1.79	2.19	1.51
221808	Hs.78103	nucleosome assembly protein 1-like 4	0.99	2.40	1.46	1.78	1.90	1.30	0.83	1.47	1.19	1.16	1.28	1.16	1.01	0.97	1.15	1.51	1.37	0.77	0.87	1.03	1.00	1.86
22918	Hs.74407	nucleolar protein p40	1.49	1.33	1.10	1.26	1.54	1.32	1.25	1.28	1.14	2.16	1.10	0.53	0.71	0.93	0.98	0.79	1.00	1.04	1.04	0.94	1.60	1.48
50614	Hs.79008	SKI-INTERACTING PROTEIN	0.73	0.81	1.05	1.29	0.87	0.70	0.96	0.67	0.77	1.66	0.67	0.84	0.62	0.56	0.92	0.69	0.76	0.76	1.10	0.88	0.68	0.50
206217	Hs.81336	nuclear receptor subfamily 1, group H, member 3	0.96	4.09	1.22	1.85	2.42	2.50	1.39	2.68	1.48	2.20	2.91	3.82	1.82	2.17	2.10	1.96	1.78	2.02	2.23	1.34	1.60	2.06
241826	Hs.181163	high-mobility group (nonhistone chromosomal) protein 17	2.17	1.06	2.72	1.31	0.81	1.88	1.37	1.40	1.23	0.97	1.43	1.33	1.57	1.44	1.88	1.15	1.77	1.21	1.92	1.73	0.96	0.71
31873	Hs.236774	high-mobility group (nonhistone chromosomal) protein 17-like 3	0.87	2.20	1.37	1.53	1.47	1.40	1.02	0.99	1.28	0.87	0.99	0.61	0.73	1.05	0.80	1.38	0.99	1.30	1.01	0.77	0.72	2.22
810743	Hs.79026	myeloid leukemia factor 2	1.19	2.48	1.13	1.85	1.65	1.25	2.87	1.43	1.62	2.03	1.29	1.76	1.33	2.01	1.79	1.07	1.33	0.86	1.03	0.57	1.31	1.70

232772	Hs.36102	ESTs, Highly similar to METALLOTHIONEIN-IB [H.sapiens]	2.00	0.92	1.33	1.13	0.83	0.85	1.72	1.57	1.46	2.98	1.44	1.26	1.16	1.35	1.49	1.06	1.46	1.02	1.47	1.79	1.18	0.64
122915	Hs.117242	meningioma expressed antigen 6 (coiled-coil proline-rich)	1.75	1.19	0.75	0.65	1.24	0.54	0.70	0.71	0.74	0.71	1.08	2.54	0.43	0.65	0.78	0.50	0.98	1.39	1.69	0.86	1.70	0.62
172765	Hs.150956	exostoses (multiple)-like 1	1.77	3.00	1.08	1.83	1.96	1.30	1.84	1.89	1.90	1.90	1.40	1.05	0.85	1.16	1.35	0.69	1.51	0.87	1.16	0.65	2.35	1.63
292212	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	2.03	2.60	3.11	2.24	2.98	1.09	2.71	4.80	5.51	10.83	3.01	5.35	3.07	1.33	5.41	1.75	4.13	1.64	2.47	1.77	1.74	2.56
134269	Hs.153880	polymerase (RNA) mitochondrial (DNA directed)	1.73	1.57	1.10	1.66	1.03	1.04	1.14	1.02	1.38	1.98	1.10	1.32	1.41	1.31	2.00	1.13	1.03	1.15	1.63	0.84	1.10	0.99
193106	Hs.429	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9) isoform 3	1.05	0.65	0.46	0.82	0.84	0.56	0.97	0.63	0.56	0.53	0.56	0.45	0.65	0.67	0.58	0.57	0.58	0.87	0.89	1.03	1.60	0.64
213890	Hs.81548	2,4-dienoyl CoA reductase 1, mitochondrial	0.65	0.69	0.73	0.66	0.38	0.25	0.33	0.42	0.25	0.21	0.47	0.22	0.32	0.34	0.49	0.39	0.23	0.54	0.46	0.54	0.68	0.28
810725	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD	1.81	1.72	1.68	1.83	1.00	1.30	2.37	1.84	1.73	3.76	1.91	1.88	2.48	2.12	2.24	1.56	1.68	1.06	1.52	1.72	1.64	0.85
50188	Hs.66394	ring finger protein 4	0.83	1.28	0.78	1.64	1.30	0.87	0.66	1.27	1.37	1.35	1.07	0.98	1.92	1.50	1.11	1.22	0.78	0.96	0.88	1.25	1.16	0.88
26314	Hs.8813	syntaxin binding protein 3	1.31	1.91	1.72	1.29	1.45	0.90	0.86	2.01	1.15	2.09	2.16	1.07	0.81	0.79	0.94	0.33	0.62	1.15	1.06	0.79	1.16	2.02
753914	Hs.238272	inositol 1,4,5-triphosphate receptor, type 2	2.61	0.67	3.97	2.44	0.62	0.82	5.10	1.01	14.26	0.95	1.22	2.07	1.97	1.27	3.03	0.88	2.20	4.16	1.92	0.79	0.64	2.03
730149	Hs.80598	transcription elongation factor A (SII), 2	0.45	0.96	1.69	0.59	0.76	0.49	0.75	0.74	0.97	1.09	0.52	0.76	1.20	0.56	0.64	0.72	1.50	0.74	1.32	0.61	0.45	0.36
246304	Hs.77311	BTG family, member 3	2.31	1.51	1.81	1.40	1.55	1.29	1.36	1.22	0.97	0.99	1.73	0.88	0.54	0.73	0.65	0.71	0.59	0.79	0.71	0.73	1.46	1.93
246120	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2	0.45	0.94	0.88	0.84	0.71	0.44	1.45	0.58	0.54	0.62	0.46	0.61	0.55	0.77	0.75	0.72	0.74	0.44	0.74	0.64	0.86	0.84
823598	Hs.4295	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	1.87	2.79	1.72	1.59	1.39	1.63	1.64	2.21	1.10	2.47	2.88	1.16	0.94	1.02	1.04	0.98	1.04	0.80	0.99	1.45	1.84	1.81
176606	Hs.79389	nel (chicken)-like 2	1.87	2.15	2.00	2.83	1.46	1.55	4.08	1.48	2.63	2.22	2.81	2.92	2.08	2.19	2.86	1.76	2.03	1.65	3.41	1.17	0.53	0.40
767049	Hs.79357	proteasome (prosome, macropain) 26S subunit, ATPase, 6	1.46	1.45	1.41	0.98	0.88	1.20	1.17	1.24	1.10	1.75	1.15	1.14	0.58	0.65	1.22	0.37	2.08	1.15	2.08	1.57	1.67	1.05
210405	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)	2.20	5.17	1.76	1.45	1.74	2.28	0.95	3.01	2.25	3.48	4.29	4.09	1.57	1.92	2.53	1.69	3.22	1.16	1.77	1.32	2.48	1.45
810124	Hs.6793	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)	2.39	2.45	1.59	1.67	1.59	0.77	2.96	1.65	1.69	5.12	1.27	2.89	1.50	2.33	2.70	1.20	1.90	0.91	4.62	1.49	1.32	1.09
33949	Hs.77498	phosphoribosyl pyrophosphate synthetase-associated protein 1	2.46	2.97	1.84	3.85	2.60	2.26	3.67	1.61	2.68	2.80	1.59	2.23	2.44	2.04	1.94	1.97	1.95	1.61	1.81	1.05	2.36	2.96
754601	Hs.153322	phospholipase C, epsilon	2.25	1.05	2.14	1.09	0.45	1.42	4.18	0.63	0.74	9.44	1.58	3.72	1.17	1.45	2.48	0.59	2.95	1.82	5.23	1.25	0.31	0.89
130884	Hs.226377	phosphate cytidylyltransferase 2, ethanolamine	2.23	3.68	0.95	1.54	2.07	2.14	3.32	1.56	1.76	2.70	1.53	2.82	2.73	2.06	1.85	1.59	1.75	1.68	2.77	1.41	2.88	1.83
202577	Hs.81182	histamine N-methyltransferase	1.54	13.19	8.74	15.76	4.98	4.49	1.75	6.53	17.45	3.28	4.58	5.29	3.17	3.13	5.76	4.04	4.77	2.46	5.15	1.62	2.48	2.19
823940	Hs.178137	transducer of ERBB2, 1	0.72	0.92	0.24	1.12	0.64	0.89	0.30	1.59	2.03	1.02	1.75	3.78	2.37	2.21	1.03	1.78	1.36	1.26	1.07	1.75	2.63	0.93
230100	Hs.199179	RAN binding protein 2	1.55	0.84	1.84	1.09	0.75	1.18	1.60	1.71	2.28	3.38	0.65	1.91	1.17	1.59	1.79	0.59	1.96	2.38	1.71	1.19	0.65	1.73
343443	Hs.80248	RNA-binding protein gene with multiple splicing	0.77	2.14	1.18	0.81	1.54	0.54	0.73	1.06	1.76	1.20	0.75	0.83	0.43	0.48	0.73	0.77	1.03	1.65	1.17	0.97	1.35	0.83
813673	Hs.89525	hepatoma-derived growth factor (high-mobility group protein 1-like)	1.12	3.84	0.61	1.71	1.73	1.08	2.08	1.29	0.83	0.97	0.85	0.66	0.55	0.72	0.88	1.08	0.93	0.57	1.14	1.15	0.86	1.83
47647	Hs.74566	dihydropyrimidinase-like 3	1.59	2.46	0.77	1.70	1.39	2.07	2.01	1.81	1.43	1.74	1.71	1.12	1.66	1.01	1.36	0.80	1.56	1.27	1.70	1.39	2.26	2.92
812196	Hs.152601	UDP-glucose ceramide glucosyltransferase	2.85	2.42	0.72	1.82	1.39	1.62	1.29	1.49	1.69	1.04	0.73	1.49	0.72	1.09	1.00	1.50	1.42	1.72	1.89	1.38	2.08	1.55
726779	Hs.21223	calponin 1, basic, smooth muscle	2.21	1.02	7.10	1.25	2.36	1.77	3.17	2.32	13.46	30.00	1.22	3.20	1.18	2.63	3.53	1.06	2.95	4.12	6.02	1.17	1.26	1.09
810612	Hs.256290	S100 calcium-binding protein A11 (calgizzarin)	1.42	1.09	0.85	0.47	1.20	0.87	1.64	1.05	0.83	0.79	0.62	1.22	0.33	0.79	0.56	0.76	0.52	0.60	0.72	0.97	0.91	1.01
31842	Hs.154073	UDP-galactose transporter related	0.93	1.57	1.42	1.85	1.24	1.19	1.68	3.93	1.80	1.98	3.14	2.81	1.98	2.76	2.60	1.84	2.00	0.84	1.27	1.17	1.89	1.09
281465	Hs.247118	phosphatidylinositol glycan, class B	0.94	1.17	1.18	1.04	1.42	0.83	0.87	1.23	2.84	1.74	1.27	1.14	0.67	0.90	1.48	0.79	0.73	1.23	1.62	0.59	0.94	0.67
364921	Hs.166011	catenin (cadherin-associated protein), delta 1	1.35	1.23	1.72	0.85	1.50	1.15	1.70	1.05	1.19	1.10	0.99	0.82	0.98	0.95	1.34	1.05	1.59	1.79	1.36	1.42	1.43	1.02
810010	Hs.170040	platelet-derived growth factor receptor-like	2.04	7.49	8.38	7.35	8.48	1.74	3.91	5.29	26.32	11.59	4.81	2.55	0.92	2.87	1.03	3.75	5.72	5.18	5.61	3.11	3.23	1.69
665658	Hs.89404	msh (Drosophila) homeo box homolog 2	0.67	0.87	1.73	1.58	1.19	0.30	0.46	1.68	1.92	1.78	1.80	2.88	1.42	0.70	2.16	1.04	1.02	0.87	1.39	0.60	0.59	0.48
23772	Hs.78788	leucine-zipper-like transcriptional regulator, 1	1.31	2.67	2.46	1.91	2.20	1.39	2.50	2.24	2.36	3.21	1.65	3.73	2.27	2.28	3.19	1.99	1.76	1.47	2.33	1.55	1.33	1.17
810551	Hs.89137	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor)	1.58	1.64	4.16	2.66	5.06	2.34	1.62	4.11	4.86	3.57	4.54	5.37	3.01	6.94	6.62	0.62	2.22	2.82	2.27	1.49	2.28	1.52
381166	Hs.27590	histone acetyltransferase	0.87	1.53	2.24	1.77	1.58	0.86	0.95	1.54	2.52	1.45	2.58	2.13	4.87	1.40	3.81	1.58	0.81	1.90	2.02	1.04	1.33	0.86
811029	Hs.190452	KIAA0365 gene product	2.31	3.10	1.41	2.16	2.60	1.59	3.17	1.98	1.56	3.02	1.87	2.71	1.76	1.45	2.15	1.39	1.81	2.15	3.82	1.07	2.06	1.71
244801	Hs.47822	KIAA0380 gene product; RhoA-specific guanine nucleotide exchange factor	1.47	1.57	1.92	1.86	1.95	1.17	2.35	1.73	2.06	2.11	5.17	2.12	1.17	1.88	1.59	1.56	1.42	1.46	2.74	1.27	0.87	1.47
233199	Hs.32556	Human mRNA for KIAA0379 gene, partial cds	1.36	2.51	0.84	1.27	3.23	0.85	1.51	1.57	1.18	1.67	2.65	1.53	0.72	0.62	1.30	0.86	1.68	1.27	1.74	0.84	1.59	1.83
32472	Hs.4791	KIAA0376 protein	1.90	4.43	4.47	1.86	3.54	1.98	2.84	2.73	3.03	3.15	3.61	3.65	3.39	2.28	2.77	1.57	2.00	2.51	2.04	1.81	2.39	1.63
666639	Hs.170098	KIAA0372 gene product	1.11	0.80	2.21	2.19	0.64	0.53	0.50	1.02	1.52	1.32	0.98	2.31	1.13	1.94	6.01	0.65	0.64	0.85	0.89	0.99	0.47	0.91
40844	Hs.89666	A kinase (PRKA) anchor protein 6	1.95	2.30	1.12	1.17	2.00	2.28	1.04	1.84	1.33	2.05	1.56	2.01	1.13	0.71	1.69	0.34	1.45	1.85	1.80	1.13	1.67	1.40
809944	Hs.5716	Human mRNA for KIAA0310 gene, complete cds	2.43	1.53	0.65	1.19	1.40	1.43	0.90	1.76	1.93	2.79	2.11	2.01	1.45	1.99	1.45	1.79	1.82	1.59	2.87	1.75	2.07	0.70
147630	Hs.10351	KIAA0308 protein	1.06	1.08	0.72	0.60	1.15	1.20	0.62	0.73	0.84	1.00	0.74	0.71	0.21	0.32	0.55	0.27	0.84	1.51	1.05	0.57	0.95	0.70
281904	Hs.15303	KIAA0349 protein	1.02	2.18	1.29	1.17	1.35	1.56	1.85	1.39	1.23	1.90	1.44	1.42	0.85	0.86	0.99	0.77	1.18	1.75	1.93	0.83	2.01	1.46
35271	Hs.7912	neuronal cell adhesion molecule	1.73	2.31	1.25	1.65	1.69	1.69	7.35	1.74	3.57	3.59	0.74	2.75	1.67	0.82	1.54	0.51	3.41	2.46	3.20	2.84	1.92	1.71
123061	Hs.179825	RAN binding protein 2-like 1	1.14	1.05	1.28	0.99	0.78	1.28	0.91	1.02	1.47	1.61	1.47	1.43	0.95	1.00	1.20	0.46	1.16	1.69	0.94	1.04	0.60	1.02
753770	Hs.29878	KIAA0335 gene product	1.40	2.15	0.67	0.97	0.92	0.89	1.27	1.34	1.10	1.57	1.00	1.52	0.64	0.79	1.19	0.23	1.15	2.11	2.27	0.70	1.12	1.05
296190	Hs.8663	KIAA0321 protein	1.36	1.75	2.30	1.51	1.19	1.27	2.11	2.41	2.05	2.30	1.92	2.11	0.99	1.40	1.56	0.65	1.63	1.60	2.38	0.99	0.86	1.04
726678	Hs.74583	KIAA0275 gene product	1.68	2.54	0.97	3.45	1.93	1.47	1.64	1.48	1.52	1.85	1.42	4.20	2.80	2.54	1.05	1.19	1.93	1.99	1.57	1.42	1.57	1.47
46154	Hs.106674	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	0.87	1.54	1.24	1.34	1.51	1.42	0.58	1.48	1.34	1.58	1.57	1.40	2.37	0.90	1.15	1.61	0.97	0.93	0.96	1.00	1.09	0.97
809541	Hs.75244	BCL2-like 2	1.55	1.86	0.79	0.74	1.45	0.95	0.81	0.90	1.27	1.69	0.90	2.29	2.02	1.72	2.62	0.53	1.14	1.64	1.35	1.02	1.08	0.85
768031	Hs.54985	KIAA0303 protein	1.05	1.15	0.43	0.64	1.37	0.85	0.57	0.94	1.31	1.56	0.96	3.83	1.25	1.27	2.67	1.25	1.17	0.96	3.19	0.87	0.80	0.38
184038	Hs.166151	Homo sapiens beta III spectrin (SPTBN2) mRNA, partial cds	2.49	2.09	0.46	1.03	1.90	1.89	1.85	1.43	0.65	2.06	2.18	1.13	0.48	0.92	0.87	0.62	0.37	0.80	0.71	1.77	1.77	1.19
233078	Hs.11711	KIAA0329 gene product	0.91	1.49	1.86	1.78	1.39	0.95	1.73	1.43	1.79	2.08	1.26	2.00	1.33	1.16	1.83	0.88	0.98	1.66	1.35	0.95	1.15	0.71
141763	Hs.251753	EST	1.05	2.45	1.17	1.18	1.53	1.15	0.99	1.31	1.67	1.68	1.26	2.65	1.52	3.02	0.88	1.10	1.50	1.61	1.63	1.20	1.46	1.06
756898	Hs.75400	KIAA0280 protein	1.70	2.06	1.91	3.63	2.26	1.92	1.21	1.41	3.22	4.83	1.46	3.61	1.98	1.69	3.36	1.54	1.48	1.80	0.98	0.76	1.08	1.23
175103	Hs.57652	EGF-like-domain, multiple 2	3.68	2.20	1.24	1.67	1.97	1.41	1.57	4.16	1.70	6.06	2.44	2.55	1.00	0.98	2.30	0.90	1.36	1.11	3.82	0.85	1.72	1.52
753420	Hs.240112	KIAA0276 protein	1.28	2.62	2.03	2.54	1.73	1.11	0.96	0.92	1.88	1.92	1.04	1.69	1.13	0.53	1.06	0.73	1.07	1.14	1.07	0.80	0.98	1.08
767769	Hs.10315	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	1.98	1.63	1.39	1.98	2.11	0.88	1.03	1.25	1.54	1.47	1.86	0.92	0.48	0.96	1.94	0.93	1.18	0.81	1.21	0.73	1.36	0.87
358344	Hs.78893	KIAA0244 protein	1.36	1.39	0.86	0.75	1.31	0.89	0.83	1.13	0.96	1.39	0.92	0.69	1.30	0.85	1.42	0.65	1.11	1.55	1.28	1.60	1.20	0.85
20115	Hs.62185	solute carrier family 9 (sodium/hydrogen exchanger), isoform 6	1.83	2.06	1.09	1.42	1.80	0.77	0.60	1.11	0.93	1.45	1.05	1.32	0.83	0.85	1.13	0.72	0.46	0.98	0.92	1.32	2.37	1.14
140716	Hs.192966	KIAA0265 protein	1.24	1.07	1.84	2.11	1.42	1.09	0.67	1.05	1.86	1.39	1.58	2.48	3.33	1.69	2.60	1.28	0.72	1.38	0.86	0.94	0.88	0.84
214448	Hs.5094	ring finger protein 10	0.89	1.15	0.73	1.49	0.98	1.14	1.02	1.40	1.09	1.07	1.26	1.01	1.26	0.96	1.17	1.27	1.07	1.18	1.20	1.09	1.56	1.01
301380	Hs.82635	KIAA0260 protein	1.80	1.40	1.56	1.64	1.16	1.00	1.45	0.92	1.52	1.28	1.52	1.07	0.59	0.65	1.31	1.09	1.22	1.31	1.72	0.76	0.55	1.15
200136	Hs.91417	topoisomerase (DNA) II binding protein	2.29	2.00	2.07	1.83	2.13	1.50	0.52	1.89	1.32	1.51	1.11	1.08	1.11	0.66	1.29	0.89	1.08	1.16	1.57	1.07	1.14	1.53
295255	Hs.76906	KIAA0254 gene product	1.81	1.21	1.19	1.32	1.30	0.97	1.00	0.98	1.18	0.81	1.29	0.67	0.81	0.85	1.24	1.13	0.70	1.10	0.97	0.95	1.01	0.57
199645	Hs.4788	KIAA0253 protein	0.86	1.50	0.60	0.98	2.09	0.85	1.11	1.33	0.95	0.77	0.89	0.69	1.14	1.21	0.99	1.16	0.87	0.80	1.65	0.88	1.52	1.28
110653	Hs.15087	KIAA0250 gene product	3.02	2.14	2.56	2.49	2.08	1.49	1.78	1.73	2.13	1.49	2.10	3.96	1.97	1.53	2.78	1.65	2.90	1.31	1.85	1.33	1.32	1.76
812042	Hs.79393	tuberous sclerosis 1	1.91	1.57	1.84	1.90	1.89	0.82	0.86	1.19	1.40	2.60	3.11	1.21	0.69	0.84	1.02	1.01	0.81	1.35	1.49	1.01	0.82	0.68
119914	Hs.193681	ESTs, Highly similar to CALCIUM-DEPENDENT GROUP X PHOSPHOLIPASE A2 PRECURSOR [	1.57	1.82	1.03	1.46	1.69	1.08	1.52	1.49	1.58	1.97	1.92	1.33	2.16	1.44	2.03	1.20	1.35	1.29	1.35	3.79	2.30	1.57
40567	Hs.75354	GCN1 (general control of amino-acid synthesis 1, yeast)-like 1	0.94	1.48	0.78	2.25	0.88	0.95	1.27	0.90	1.10	0.89	0.95	1.14	1.94	1.16	1.10	1.02	0.86	0.81	0.94	1.06	0.91	1.25
298118	Hs.17211	dedicator of cyto-kinesis 2	1.17	1.82	0.83	1.61	1.37	1.86	1.69	1.57	1.64	1.48	2.16	1.28	2.12	1.14	1.47	1.57	1.16	1.23	1.10	1.29	1.71	1.58
346995	Hs.77495	KIAA0242 protein	3.06	3.94	0.74	1.13	3.91	1.91	4.68	1.91	1.15	1.42	2.13	3.61	0.96	1.37	2.27	0.96	4.59	2.36	3.30	1.88	1.89	1.92
809779	Hs.9729	KIAA0239 protein	0.27	0.78	0.55	0.76	0.55	0.32	0.29	0.38	0.44	0.51	5.29	0.39	0.46	0.32	0.54	0.46	0.30	0.71	0.91	0.47	0.29	0.38
756657	Hs.80526	zinc finger protein 142 (clone pHZ-49)	1.28	2.81	0.99	1.61	3.02	1.91	2.40	1.66	1.39	1.78	2.46	3.09	2.85	2.28	2.42	1.46	2.01	1.68	1.70	1.31	1.70	1.80
755752	Hs.6151	Human mRNA for KIAA0235 gene, partial cds	1.50	0.73	1.46	1.37	0.45	1.13	1.33	0.69	1.41	1.76	0.63	1.22	0.84	1.23	1.50	0.95	1.39	1.57	1.67	1.37	0.71	1.26
254625	Hs.20060	KIAA0229 protein	1.26	0.73	1.21	2.32	0.75	0.63	1.45	0.66	1.06	1.36	0.57	2.71	0.91	1.35	1.64	0.57	0.78	1.73	1.21	1.19	0.33	1.16

809696	Hs.78054	KIAA0224 gene product	1.77	1.73	0.99	1.11	2.05	0.94	1.94	1.36	1.39	1.64	1.75	1.08	0.69	1.06	1.19	1.12	1.54	1.21	1.59	1.20	1.52	1.27
341317	Hs.48450	KIAA0222 gene product	1.30	1.29	1.29	2.20	1.22	0.82	1.29	1.16	1.33	1.42	1.03	1.10	1.48	1.49	1.57	1.00	1.50	1.05	1.35	1.34	0.56	1.12
195138	Hs.3610	KIAA0205 gene product	3.75	3.46	3.89	2.91	3.00	2.31	3.41	2.69	5.71	4.85	2.39	4.65	2.59	2.21	4.27	1.77	5.82	3.20	2.75	1.23	1.30	1.55
112131	Hs.178292	KIAA0180 protein	1.40	1.56	1.16	0.95	2.52	3.17	1.47	1.22	0.96	1.42	1.14	1.50	1.32	1.04	1.89	0.95	1.36	1.67	1.14	1.78	2.61	1.46
753987	Hs.77225	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)-like 1	0.87	2.54	1.27	1.68	1.58	1.47	1.32	1.35	1.34	1.21	1.11	1.09	0.55	0.75	0.84	0.62	1.02	1.11	1.69	2.48	0.68	0.98
34616	Hs.4935	KIAA0176 protein	1.96	2.69	1.20	1.70	3.16	4.12	2.23	1.65	2.47	2.70	2.29	2.12	3.11	2.01	3.06	1.30	1.88	1.82	1.52	1.59	1.94	1.80
302031	Hs.105751	Ste20-related serine/threonine kinase	0.97	1.08	0.51	0.91	0.85	0.85	0.34	0.64	0.72	0.57	0.89	0.76	0.72	0.35	0.64	0.41	0.46	0.97	0.54	0.62	1.15	0.89
23431	Hs.50421	KIAA0203 gene product	1.51	1.00	1.44	1.32	1.57	0.94	1.19	0.83	1.16	1.13	1.75	0.97	0.82	0.49	0.82	0.43	0.93	1.21	0.93	1.27	0.99	1.29
27104	Hs.76986	KIAA0200 gene product	1.10	1.45	1.08	1.56	1.72	1.20	0.95	1.24	1.20	1.12	1.16	1.29	1.29	1.23	1.37	1.19	1.05	1.49	1.51	1.28	1.25	1.34
40365	Hs.78442	SREBP CLEAVAGE-ACTIVATING PROTEIN	0.94	1.44	0.81	1.31	1.16	1.18	1.26	0.94	0.97	1.01	1.75	1.28	1.58	0.99	1.11	0.93	0.84	0.98	0.76	1.09	0.72	0.96
33299	Hs.22559	KIAA0197 protein	1.75	2.17	1.82	2.43	2.56	2.03	1.18	1.23	1.44	1.14	2.00	1.80	1.07	1.27	1.61	0.93	1.14	1.73	1.37	1.25	2.28	2.50
362729	Hs.75137	KIAA0193 gene product	1.06	1.64	1.07	0.85	1.38	2.00	1.03	1.02	1.54	0.93	2.04	0.77	1.82	1.20	0.88	1.13	1.86	0.52	0.34	1.54	1.12	0.98
43977	Hs.75909	KIAA0182 protein	0.92	1.20	0.42	0.53	0.89	0.91	1.03	1.06	0.71	2.50	1.24	1.04	0.75	1.10	0.77	1.20	0.89	0.98	1.97	1.28	1.41	0.47
812975	Hs.77546	KIAA0172 protein	1.16	2.06	0.34	0.54	0.83	0.24	1.28	0.32	0.21	1.60	0.25	0.29	0.18	0.23	0.45	0.23	0.20	0.87	0.42	0.57	0.43	0.57
245198	Hs.23106	KIAA0130 gene product	1.17	2.38	0.91	1.62	1.86	1.31	1.90	4.18	1.92	1.91	3.37	3.62	2.59	2.28	4.04	2.00	2.06	1.62	2.30	3.00	2.73	1.68
143966	Hs.90998	KIAA0128 protein; septin 2	1.75	2.39	1.11	2.26	1.81	1.89	1.37	1.42	1.71	2.00	1.60	2.93	1.65	1.54	1.43	2.05	2.08	1.64	2.24	1.10	1.40	1.45
823715	Hs.77293	KIAA0127 gene product	1.33	1.43	1.07	2.14	2.21	1.31	1.36	1.06	1.20	1.00	1.40	1.85	0.98	1.24	1.51	0.68	1.01	1.24	1.23	1.35	4.58	1.64
212704	Hs.169504	KIAA0170 gene product	1.97	5.66	2.57	2.02	3.76	2.18	2.37	2.74	2.52	2.30	2.48	2.35	1.65	1.71	2.30	1.67	1.31	2.11	3.20	1.39	2.49	2.66
30885	Hs.116875	KIAA0156 gene product	0.88	1.88	1.05	1.46	1.54	1.13	0.98	1.14	1.23	1.14	0.90	1.05	1.39	1.18	1.34	1.10	0.88	1.01	1.15	1.30	0.77	1.02
812167	Hs.87726	KIAA0154 protein	0.98	1.99	0.81	1.18	1.15	1.01	1.69	1.43	1.12	2.13	0.95	1.31	0.71	0.75	1.44	0.59	0.52	1.40	1.20	1.15	1.06	0.86
34106	Hs.82563	KIAA0153 protein	1.21	3.15	1.01	2.26	2.30	2.49	1.12	1.51	1.50	1.53	1.16	1.41	2.09	1.35	1.71	1.48	1.92	1.49	2.36	1.11	1.68	1.89
742007	Hs.250791	KIAA0146 protein	1.12	1.80	1.18	1.12	2.08	0.71	1.49	0.98	1.66	1.82	0.92	1.49	1.14	0.66	1.60	0.72	0.94	1.80	1.55	0.99	0.95	4.14
563451	Hs.18895	tousled-like kinase 1	0.93	2.04	1.15	1.45	1.50	1.18	1.32	2.04	1.81	1.59	2.47	1.86	1.35	0.85	1.24	1.24	1.65	1.70	1.08	1.99	2.43	0.94
51532	Hs.75249	KIAA0069 protein	2.14	1.35	1.77	1.50	0.90	0.66	2.21	1.67	1.03	1.08	1.57	1.23	1.79	1.24	1.54	1.24	1.38	1.51	1.78	1.03	1.33	1.37
753692	Hs.158203	actin-binding LIM protein	1.31	0.63	0.16	0.65	1.22	0.65	0.56	0.61	0.21	0.20	0.56	0.56	0.32	0.88	1.08	0.40	0.27	0.76	0.45	1.01	1.18	0.54
251135	Hs.89674	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	1.09	0.54	1.36	0.87	0.85	0.95	0.65	0.82	0.69	0.35	0.71	0.63	0.89	1.07	1.10	0.84	0.88	0.72	0.63	1.27	1.20	0.85
211206	Hs.124	gene predicted from cDNA with a complete coding sequence	0.83	1.18	0.90	1.43	1.36	0.79	1.57	1.35	1.07	1.11	1.27	0.68	1.13	1.06	1.48	0.93	0.73	0.77	1.21	0.73	1.15	0.99
768324	Hs.23488	KIAA0107 gene product	1.03	1.01	1.01	0.86	1.33	0.74	0.58	1.15	0.74	0.68	0.99	0.49	0.40	0.29	1.16	0.57	0.89	1.00	1.33	0.85	1.32	1.43
753313	Hs.79356	Lysosomal-associated multispanning membrane protein-5	3.95	11.41	17.21	8.79	8.50	6.18	3.63	7.90	35.55	9.38	9.04	15.10	9.45	8.07	5.75	3.81	7.00	4.64	6.87	3.39	3.26	4.01
713653	Hs.78871	KIAA0081 protein	1.31	1.39	1.50	1.21	1.52	0.90	1.29	0.94	1.18	0.77	1.34	2.00	0.37	1.25	1.21	1.10	1.03	0.78	1.00	0.85	1.10	1.36
563403	Hs.193725	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	2.31	1.47	1.14	1.55	1.61	0.90	0.89	1.26	1.54	1.86	1.86	0.78	0.74	1.26	1.99	1.14	0.55	0.95	1.14	1.46	1.69	1.30
823851	Hs.118397	AE-binding protein 1	4.69	14.60	20.15	4.26	16.92	7.91	9.52	5.84	5.71	11.46	11.42	19.29	8.02	3.43	12.61	7.50	4.67	5.33	10.05	3.56	5.68	5.59
813460	Hs.32978	proprotein convertase subtilisin/kexin type 7	1.39	1.84	1.72	0.82	1.61	0.70	1.21	1.19	1.03	1.66	0.90	1.34	0.40	0.87	0.85	0.35	0.86	1.56	1.19	0.94	1.29	1.33
823900	Hs.24340	centaurin beta2	2.74	1.52	1.68	2.25	1.01	1.11	0.90	1.06	1.61	1.26	0.82	1.44	1.28	0.84	1.16	0.74	1.15	1.08	1.58	0.47	0.56	1.74
203347	Hs.178710	clathrin, heavy polypeptide-like 2	1.84	1.65	1.27	1.81	2.06	1.01	0.84	5.22	1.68	4.75	5.07	4.04	1.37	1.95	3.08	1.37	2.12	1.51	1.85	1.48	2.03	1.70
687990	Hs.79307	PAK-interacting exchange factor alpha	1.89	5.13	5.88	3.32	5.00	7.03	4.20	4.99	7.98	3.47	2.80	10.28	6.89	4.34	7.72	2.76	8.61	3.91	4.03	2.25	2.65	2.11
666377	Hs.167558	zinc finger protein 161	1.05	2.69	2.08	2.30	2.24	1.11	1.07	3.52	2.89	2.25	3.92	5.79	4.76	6.79	1.91	1.77	1.14	0.78	1.00	1.22	1.47	1.72
119530	Hs.17287	potassium inwardly-rectifying channel, subfamily J, member 15	0.66	1.30	0.69	0.61	1.43	0.75	0.60	1.11	0.86	1.99	0.93	1.72	0.29	0.47	0.50	0.84	1.75	0.47	0.52	4.31	1.41	0.97
811920	Hs.64310	interleukin 11 receptor, alpha	1.92	1.67	1.26	1.87	2.22	1.50	1.69	1.64	1.65	1.50	1.43	1.38	1.19	1.28	1.32	1.47	1.25	1.28	1.34	1.29	2.05	1.07
120881	Hs.251531	proteasome (prosome, macropain) subunit, alpha type, 4	2.54	5.27	11.31	3.09	4.60	5.20	4.83	4.06	8.85	4.90	4.81	11.34	7.18	6.29	9.55	2.00	4.20	4.57	11.08	2.37	1.90	2.90
361565	Hs.77508	glutamate dehydrogenase 1	0.53	0.35	0.31	0.79	0.68	0.61	0.40	0.48	0.62	0.46	0.45	0.39	1.41	0.32	0.90	0.60	0.89	1.49	0.74	0.87	0.64	0.43
550355	Hs.69171	protein kinase C-like 2	1.23	2.04	1.01	1.63	3.18	1.48	0.67	0.99	1.08	0.76	1.42	0.91	0.41	0.57	0.82	0.96	0.91	0.83	0.73	0.79	0.99	1.66
361943	Hs.170177	Meis1 (mouse) homolog	1.87	3.35	2.87	2.30	3.01	1.70	1.23	2.65	2.53	3.59	1.73	1.83	0.67	1.36	2.00	0.57	1.51	2.92	1.76	1.32	2.25	1.49
325062	Hs.78452	solute carrier family 20 (phosphate transporter), member 1	0.60	1.60	0.84	1.01	1.07	0.80	0.62	0.77	0.68	0.56	2.02	2.65	2.85	1.43	1.86	0.97	1.06	0.76	0.52	0.89	0.89	0.83
345348	Hs.26719	PR domain containing 2, with ZNF domain	2.29	2.25	1.26	1.77	2.27	1.95	1.52	1.67	2.06	2.61	1.48	2.00	1.13	1.43	1.88	0.94	2.42	2.22	1.57	1.56	1.71	1.99
592359	Hs.66776	Ke4 gene, mouse, human homolog of	1.07	3.83	1.86	1.61	2.66	2.03	1.50	2.30	1.84	1.79	2.76	2.20	2.03	2.55	2.49	1.69	0.60	1.09	0.98	1.47	2.54	2.14
204148	Hs.173965	ribosomal protein S6 kinase, 90kD, polypeptide 3	1.18	2.01	1.71	1.48	1.77	1.23	0.97	0.80	1.33	1.64	0.97	1.12	0.99	0.87	0.84	1.25	0.97	1.54	0.54	0.79	0.75	0.68
45542	Hs.103391	Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA	5.33	25.74	16.15	17.80	18.81	5.69	15.38	5.73	12.58	19.60	20.92	25.92	12.50	16.77	42.35	7.22	8.26	5.33	10.69	3.62	3.22	1.73
810282	Hs.6453	inositol 1,3,4-triphosphate 5/6 kinase	0.31	0.75	0.43	0.58	0.63	0.43	0.59	0.89	0.52	1.00	0.90	1.08	0.65	0.69	0.83	1.09	0.57	0.83	0.75	0.62	0.61	0.36
136744	Hs.129951	speckle-type POZ protein	1.23	2.65	1.87	2.00	1.69	1.13	2.45	3.82	2.35	2.18	3.10	2.70	1.24	1.40	3.04	1.72	2.06	2.16	3.41	1.44	1.71	1.60
44975	Hs.76038	isopentenyl-diphosphate delta isomerase	0.96	2.28	0.95	4.06	1.51	5.57	1.69	1.52	1.55	1.63	1.25	1.07	1.17	0.79	0.94	1.45	2.07	0.99	1.06	2.20	2.02	1.66
160793	Hs.154294	discs, large (Drosophila) homolog 1	3.57	6.51	2.99	3.59	3.70	1.69	1.26	2.43	2.40	2.89	1.30	2.53	1.66	0.95	2.08	0.60	2.65	1.35	1.07	0.96	1.46	1.71
358457	Hs.245710	heterogeneous nuclear ribonucleoprotein H1 (H)	0.98	1.32	0.82	1.71	1.01	1.00	0.96	1.32	0.97	1.26	0.85	1.37	1.24	0.86	1.20	0.79	1.22	1.03	1.26	1.26	0.81	0.87
768562	Hs.155968	zinc finger protein homologous to Zfp103 in mouse	1.10	2.84	0.75	0.82	2.32	0.92	0.83	1.37	1.85	2.99	1.35	1.01	1.09	1.54	1.15	1.01	1.70	1.32	1.23	1.54	2.45	0.92
813149	Hs.2178	H2B histone family, member Q	3.56	8.63	8.54	3.79	3.67	1.93	4.40	3.56	4.71	11.18	2.79	4.88	3.76	2.69	4.62	4.64	2.75	1.85	6.10	1.18	2.13	2.73
769645	Hs.78473	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2	1.59	1.95	2.55	2.20	2.14	1.63	1.50	2.75	1.95	2.66	2.78	2.60	2.90	1.91	2.91	2.23	1.75	2.31	2.13	1.21	1.63	1.30
769676	Hs.26403	glutathione S-transferase zeta 1 (maleylacetoacetate isomerase)	1.30	0.76	0.76	0.84	1.47	0.55	0.85	2.01	0.77	0.69	2.19	1.33	0.98	1.01	1.22	0.67	0.40	0.99	1.82	0.66	2.27	0.54
809588	Hs.78619	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	2.45	1.08	2.28	2.67	1.95	0.56	1.02	1.21	0.57	0.67	1.31	0.15	0.39	0.61	0.71	0.51	0.82	0.50	0.76	1.86	1.53	1.34
134270	Hs.24385	Human hbc647 mRNA sequence	1.09	0.55	0.65	0.94	1.22	0.67	0.51	0.74	0.69	0.59	0.58	0.28	0.69	0.22	1.08	0.33	0.63	0.88	1.98	0.65	1.03	1.13
248531	Hs.5398	guanine-monophosphate synthetase	4.26	2.70	1.84	1.94	2.67	1.95	2.07	1.57	1.49	1.31	1.16	0.70	0.54	1.69	0.98	0.69	0.88	0.90	1.20	1.30	1.74	2.67
360168	Hs.90875	RAB interacting factor	1.79	1.97	2.07	2.36	2.48	1.49	1.47	2.14	3.94	3.38	1.78	2.13	1.55	1.74	2.35	1.41	1.40	0.95	1.88	1.73	1.54	1.75
234191	Hs.180029	Human guanine nucleotide exchange factor mRNA, complete cds	2.95	2.39	1.76	2.64	2.37	1.08	0.72	1.79	1.84	1.08	1.03	1.30	1.05	1.15	1.77	0.86	1.04	1.52	0.68	0.87	2.62	1.22
753285	Hs.174071	glycogenin	2.50	2.26	1.43	1.86	2.50	1.53	2.87	1.32	2.05	2.99	1.79	1.18	0.83	1.58	1.99	1.31	1.04	0.97	1.16	0.99	1.33	1.84
194364	Hs.173993	RNA binding motif protein 6	1.63	2.07	3.13	3.12	2.01	2.17	2.55	3.26	2.15	2.10	2.25	4.39	2.94	2.12	3.73	1.62	3.22	3.31	4.23	1.01	1.84	1.22
755975	Hs.76111	dystroglycan 1 (dystrophin-associated glycoprotein 1)	1.13	1.04	1.72	0.61	1.32	1.46	1.37	1.30	0.59	0.78	1.36	0.68	1.28	0.57	1.20	0.67	0.73	0.75	0.90	0.52	1.05	0.89
823663	Hs.52788	fragile X mental retardation, autosomal homolog 2	0.72	1.31	2.42	2.29	1.33	0.86	1.01	1.12	0.98	1.00	0.82	1.46	0.95	1.78	0.90	1.06	0.50	0.74	0.78	0.55	0.84	1.00
289551	Hs.82712	fragile X mental retardation, autosomal homolog 1	1.68	1.45	0.72	0.93	1.62	0.98	1.12	0.77	0.83	1.05	1.15	2.87	1.68	1.72	2.16	0.66	1.14	1.07	0.74	0.87	1.00	1.83
741139	Hs.29279	eyes absent (Drosophila) homolog 2	3.54	5.00	3.57	2.49	4.33	5.67	0.94	5.49	5.92	3.42	3.36	7.42	12.05	3.41	43.51	1.92	5.99	1.84	1.17	0.75	1.80	2.17
301122	Hs.81071	extracellular matrix protein 1	0.75	0.82	4.34	0.80	1.83	0.62	1.44	3.05	3.68	1.98	3.14	6.40	0.67	1.71	1.70	1.62	0.74	2.17	6.71	2.08	1.34	0.82
28098	Hs.7137	Human clones 23667 and 23775 zinc finger protein mRNA, complete cds	1.04	1.29	1.40	1.57	1.64	1.22	0.82	1.47	1.45	1.12	1.68	1.88	1.13	0.94	1.05	1.08	1.03	1.32	1.37	1.31	1.74	1.14
113298	Hs.169078	Human clone A9A2BRB6 (CAC)n/(GTG)n repeat-containing mRNA	1.01	4.00	1.38	1.57	1.96	1.12	0.81	2.05	1.38	1.53	1.93	2.51	1.38	0.89	1.79	0.70	0.93	1.53	1.78	1.21	2.12	0.99
249705	Hs.85215	Deleted in split-hand/split-foot 1 region	1.34	2.43	2.02	1.45	1.47	1.11	1.97	1.38	1.04	1.45	1.37	1.41	0.49	0.62	1.23	0.49	0.73	0.86	1.73	0.83	1.59	1.07
24032	Hs.155566	CASP2 and RIPK1 domain containing adaptor with death domain	0.88	0.97	0.61	0.84	2.01	2.69	1.00	1.22	1.69	1.77	1.44	0.95	1.83	1.09	1.06	0.67	0.60	1.51	0.77	0.69	1.43	1.09
768496	Hs.185705	cytokine receptor induced by latent Epstein-Barr virus infection	2.06	4.40	1.82	2.82	2.56	2.08	2.49	2.90	2.47	4.39	2.63	2.39	1.72	1.69	2.12	2.39	1.89	1.78	2.26	1.79	2.31	1.86
229579	Hs.78979	Golgi apparatus protein 1	1.87	1.69	1.59	1.36	3.24	1.63	1.52	1.17	1.85	1.78	1.20	1.08	0.35	0.97	0.86	0.63	1.37	1.11	1.29	1.11	2.25	1.81
30170	Hs.74552	caspase 3, apoptosis-related cysteine protease	0.86	1.47	1.51	1.24	1.47	1.29	0.42	0.99	1.05	1.81	1.71	0.96	0.88	1.02	0.89	1.41	1.68	0.63	0.69	0.76	1.36	1.03
769921	Hs.93002	ubiquitin carrier protein E2-C	3.21	2.12	1.98	1.48	1.70	2.77	6.60	2.14	0.72	3.00	2.19	1.49	1.20	0.67	0.89	0.96	1.21	0.76	3.58	1.77	2.26	1.95
767798	Hs.183373	ATX1 (antioxidant protein 1, yeast) homolog 1	0.50	1.79	1.09	0.94	0.93	0.87	0.72	1.17	1.16	1.53	1.28	1.06	1.07	1.40	0.94	1.32	0.92	0.83	1.52	0.88	0.96	0.84
771173	Hs.81281	Human clone 23732 mRNA, partial cds	1.26	2.53	1.66	1.47	1.86	1.20	2.81	1.71	0.98	1.20	0.79	1.46	0.58	0.83	1.12	0.89	0.64	0.73	1.50	0.95	1.08	1.48
248039	Hs.81360	Human clone 23722 mRNA sequence	1.61	1.28	1.41	1.29	1.61	1.05	1.31	1.17	1.43	0.98	1.24	0.88	0.74	1.13	0.67	0.95	1.34	1.90	1.47	1.34	1.63	0.97
666658	Hs.87150	Human clone A9A2BR11 (CAC)n/(GTG)n repeat-containing mRNA	2.62	1.77	3.51	2.97	2.23	1.59	1.94	1.38	1.81	1.52	1.51	4.07	2.72	1.77	3.45	0.54	1.61	2.11	1.02	1.79	1.40	1.62

204614	Hs.239483	Human clone 23933 mRNA sequence	0.65	1.29	0.97	1.02	1.25	0.90	0.76	0.97	0.69	0.48	0.95	0.54	1.22	1.13	0.70	1.08	0.68	0.88	0.47	0.61	0.68	1.13
126406	Hs.88051	Human clone 23907 mRNA sequence	0.76	2.33	1.01	2.79	2.10	2.02	0.60	1.79	1.08	2.09	1.76	2.73	1.11	1.63	2.66	1.58	1.71	1.17	0.75	1.53	1.63	1.45
563201	Hs.81897	Human clone 23865 mRNA sequence	1.09	2.96	1.44	2.86	2.30	1.09	0.76	1.66	2.22	0.95	0.99	2.94	2.14	2.12	2.52	1.15	1.49	1.14	0.99	1.06	1.62	1.80
767069	Hs.82845	Human clone 23815 mRNA sequence	2.72	5.12	2.55	6.36	3.24	3.50	1.14	2.65	5.50	0.95	2.91	2.59	2.10	1.97	3.00	3.18	3.39	2.64	1.76	1.28	2.63	1.81
201687	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (from clone DKFZp586F1822)	1.81	0.73	2.65	1.28	0.61	0.53	2.09	1.12	1.97	3.38	1.37	0.75	1.14	0.95	0.69	0.74	1.86	1.39	1.80	1.26	0.95	0.54
309032	Hs.83727	cleavage and polyadenylation specificity factor	5.51	4.46	7.68	4.24	5.22	3.11	0.92	3.21	2.87	1.69	3.78	2.29	4.03	1.38	0.16	2.43	0.86	2.60	1.07	1.62	3.57	2.21
41929	Hs.7885	Clathrin assembly lymphoid-myeloid leukemia gene	2.15	1.08	0.78	1.36	1.45	0.88	0.65	1.30	1.53	1.11	1.36	0.96	0.41	0.96	0.78	1.07	0.66	0.90	0.72	0.81	1.14	0.54
180244	Hs.240062	hypothetical protein	0.80	0.77	1.49	1.26	1.04	0.76	1.26	0.72	1.04	1.27	0.76	0.53	0.41	0.59	0.77	0.76	0.68	0.81	1.17	0.90	0.76	0.55
770884	Hs.12956	Tax interaction protein 1	1.02	0.54	0.78	0.53	1.07	0.53	0.56	0.89	1.08	0.44	0.79	0.62	0.53	0.89	0.69	1.08	0.38	0.56	0.51	0.89	0.76	0.58
669471	Hs.11506	Human clone 23589 mRNA sequence	2.37	2.63	4.03	3.16	2.92	1.47	1.72	2.24	2.78	4.36	1.87	2.59	1.82	0.98	2.01	1.45	2.73	2.02	1.84	1.90	2.76	2.14
73268	Hs.5057	carboxypeptidase D	0.87	0.68	0.90	0.81	0.81	0.48	0.60	0.87	0.83	0.90	1.12	0.67	1.62	0.98	1.22	0.70	0.84	0.88	0.67	2.21	1.66	0.48
292806	Hs.90073	chromosome segregation 1 (yeast homolog)-like	0.78	0.57	1.55	1.09	0.36	1.20	0.38	0.43	0.68	0.45	0.76	1.45	2.31	0.80	1.15	1.11	0.95	0.63	0.30	0.82	0.65	0.86
265680	Hs.79187	coxsackie virus and adenovirus receptor	4.86	2.51	0.85	2.72	3.47	3.39	1.26	2.37	3.19	1.61	3.49	4.22	2.33	1.93	0.71	1.85	0.89	2.20	1.33	1.00	2.71	2.37
756666	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	1.57	1.40	0.74	1.23	1.17	1.06	1.88	1.16	1.01	1.06	5.36	1.63	1.00	1.22	1.05	1.03	0.96	0.73	1.17	1.61	1.06	0.57
110467	Hs.139851	caveolin 2	0.37	0.11	0.20	0.13	0.26	0.19	0.20	0.12	0.14	0.11	0.15	0.15	0.08	0.12	0.13	0.12	0.12	0.35	0.21	0.23	0.30	0.15
230271	Hs.82837	Human chromosome 3p21.1 gene sequence	0.97	1.22	1.05	1.09	1.40	0.88	0.65	1.22	1.01	0.86	1.35	0.65	1.07	0.58	1.16	1.08	1.29	1.40	1.55	0.79	1.03	0.81
770377	Hs.118855	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory pro	0.56	1.07	0.92	0.62	0.80	0.61	1.01	0.93	1.50	2.37	0.65	0.95	0.99	1.18	1.04	0.92	1.06	0.73	0.96	0.52	0.70	0.36
188036	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	0.35	0.78	0.31	0.40	2.34	2.87	0.40	1.07	1.06	0.58	0.20	0.71	0.14	0.27	0.82	0.33	0.28	2.57	2.73	0.35	1.15	0.48
179276	Hs.83190	fatty acid synthase	0.63	1.38	0.92	0.65	2.20	0.61	0.84	1.05	1.15	0.93	0.92	0.95	0.75	0.61	0.81	0.88	0.90	2.05	2.04	1.53	0.58	0.58
510702	Hs.174170	carboxylesterase 2 (intestine, liver)	0.78	1.52	0.66	0.81	1.63	1.35	0.59	0.90	0.97	1.22	0.99	0.73	0.22	0.33	0.37	0.75	0.45	0.63	0.89	0.41	1.02	1.48
549073	Hs.75546	capping protein (actin filament) muscle Z-line, alpha 2	0.62	1.01	1.39	1.18	0.75	0.80	0.62	0.51	0.93	0.86	0.84	0.72	0.78	0.54	0.78	0.77	0.53	0.80	0.50	0.77	0.59	0.46
813426	Hs.155418	GS3955 protein	1.89	7.69	5.74	3.99	3.82	2.32	7.43	3.17	5.24	7.44	2.13	11.94	1.30	3.28	4.55	1.64	2.64	3.32	3.18	3.26	2.32	1.83
133178	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	1.80	2.03	1.22	1.46	1.48	2.14	0.88	0.72	0.85	0.77	1.22	0.74	0.77	0.84	0.90	0.50	0.83	1.17	1.54	1.30	0.91	1.21
753587	Hs.167741	butyrophilin, subfamily 3, member A3	2.62	10.27	3.25	3.62	3.85	5.11	2.63	4.70	5.40	3.99	5.12	5.76	0.94	3.24	3.28	3.06	5.21	3.58	4.20	2.56	3.45	2.14
233909	Hs.169963	butyrophilin, subfamily 2, member A1	0.89	2.77	1.93	1.35	1.66	1.65	1.33	1.45	1.43	1.22	2.11	1.98	1.58	1.72	1.89	1.66	1.31	1.56	1.25	1.01	0.92	1.00
204335	Hs.173996	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	1.14	0.81	0.09	1.89	1.62	4.86	0.31	0.52	1.94	0.31	0.33	1.07	0.58	0.50	0.83	0.95	1.64	0.43	0.24	1.02	1.74	1.39
204755	Hs.184571	splicing factor, arginine/serine-rich 11	1.96	4.02	1.58	2.28	1.57	1.70	1.91	0.82	1.29	1.69	0.81	3.70	1.12	1.32	2.58	1.05	0.80	1.32	1.60	0.96	2.04	1.83
77636	Hs.80756	betaine-homocysteine methyltransferase	0.49	0.86	3.42	0.35	0.86	0.34	1.53	0.49	1.63	9.12	0.22	4.41	1.71	2.74	3.32	0.22	1.07	0.94	2.29	0.62	0.46	0.87
376516	Hs.62354	cell division cycle 4-like	0.96	0.73	0.41	0.53	0.93	0.64	0.46	1.16	1.18	2.57	0.77	1.11	1.16	0.70	1.27	1.17	1.35	1.29	1.43	0.86	1.15	1.02
24642	Hs.174185	phosphodiesterase I/nucleotide pyrophosphatase 2 (autotaxin)	1.56	3.20	28.03	5.93	3.26	5.54	1.59	4.16	1056.27	1660.49	3.14	3.50	1.78	1.75	9.06	1.36	1.51	3.06	1.74	1.02	1.55	1.04
667598	Hs.82110	PC4 and SFRS1 interacting protein 1	2.71	4.13	2.39	3.55	2.55	1.72	1.48	1.74	1.55	2.13	1.32	1.12	0.86	0.80	1.06	0.75	1.42	1.44	1.41	0.65	1.17	1.99
470179	Hs.43509	ataxin 2 related protein	1.09	2.13	1.39	1.51	1.90	1.02	1.34	1.42	1.59	1.54	0.94	1.58	2.13	2.25	1.00	0.64	1.24	0.97	1.83	0.94	0.81	0.88
123802	Hs.61418	microfibrillar-associated protein 1	0.98	1.67	0.97	0.96	1.59	1.22	0.77	1.28	1.43	1.74	1.12	0.54	0.76	0.69	0.97	0.84	0.96	1.15	1.41	0.87	0.96	0.77
50413	Hs.171900	armadillo repeat gene deletes in velocardiofacial syndrome	0.98	2.74	2.14	1.54	2.37	1.37	1.95	3.50	3.06	7.29	2.13	7.15	4.28	3.27	5.16	1.48	1.61	1.58	1.51	1.32	2.43	0.96
183462	Hs.26232	mannosidase, alpha, class 2C, member 1	1.49	2.55	1.52	1.24	1.93	1.24	1.90	2.12	1.40	1.63	1.74	3.15	1.38	2.40	2.12	1.29	1.32	2.13	2.16	0.84	1.84	1.18
245422	Hs.183706	adducin 1 (alpha)	1.64	1.00	3.09	1.72	1.55	0.58	1.19	3.21	2.45	3.25	1.48	1.48	1.27	1.76	2.52	1.42	1.76	1.46	2.11	1.38	1.02	0.58
23831	Hs.155247	aldolase C, fructose-bisphosphate	0.77	1.19	1.24	0.53	0.85	0.42	0.79	0.96	0.63	1.20	0.97	0.31	1.20	0.82	0.58	0.68	0.40	1.01	0.65	0.69	0.99	0.52
135538	Hs.227630	RE1-silencing transcription factor	2.85	4.68	3.83	2.74	4.46	2.23	1.45	2.90	3.31	2.50	2.99	1.28	0.86	0.72	1.20	2.75	2.22	1.18	1.94	1.36	3.25	2.06
810506	Hs.166684	serine/threonine kinase 3 (Ste20, yeast homolog)	1.06	1.26	1.13	0.95	1.53	0.79	0.61	0.88	0.85	0.94	1.28	1.97	2.17	0.98	2.75	0.93	0.97	1.36	0.53	0.78	1.02	1.51
50680	Hs.171374	smg GDS-ASSOCIATED PROTEIN	1.07	1.16	1.82	1.61	0.92	0.86	0.88	1.10	1.89	1.32	4.26	1.94	0.55	0.85	1.25	0.87	1.08	0.77	1.78	0.90	0.50	0.95
509588	Hs.82037	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD	1.57	1.20	0.92	1.31	1.24	1.05	0.88	1.15	0.96	0.84	1.36	0.81	0.45	0.67	1.03	0.80	0.86	1.28	1.53	0.86	1.05	1.17
365930	Hs.155188	TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD	0.85	1.05	0.71	0.88	0.73	0.66	1.12	1.07	0.72	0.87	1.00	0.63	1.15	0.80	0.74	0.98	0.95	0.47	1.24	0.57	0.59	0.81
756488	Hs.326	TAR (HIV) RNA-binding protein 2	0.88	1.93	2.00	1.62	3.00	0.82	1.91	2.03	1.84	2.69	1.83	1.92	0.97	1.48	1.70	1.38	1.68	1.14	2.18	1.23	1.20	1.31
293576	Hs.193989	TAR DNA binding protein	2.60	1.72	1.37	1.72	1.74	1.46	2.11	1.57	1.47	1.30	1.61	1.12	0.77	1.05	1.46	1.41	1.61	1.70	2.17	1.55	1.80	1.74
26910	Hs.100391	T54 protein	1.71	1.49	2.00	1.55	2.74	1.72	2.59	1.42	1.62	1.84	5.01	1.62	1.23	1.50	1.47	1.36	1.14	0.93	1.33	1.06	0.89	2.16
360047	Hs.77069	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d,	0.93	2.22	3.57	5.84	2.10	0.97	3.31	1.56	0.91	5.30	1.41	1.93	1.50	1.42	2.95	1.80	1.74	2.43	2.38	1.15	0.77	0.79
567265	Hs.3248	mutS (E. coli) homolog 6	0.97	1.20	1.07	1.48	1.81	1.11	0.87	0.99	1.31	0.99	0.82	1.27	0.62	1.27	1.07	1.07	1.59	1.81	1.54	0.57	1.48	2.04
562983	Hs.75447	ralA binding protein 1	1.59	1.41	0.90	1.10	1.25	1.28	0.63	1.23	1.06	0.90	0.96	1.21	1.45	1.48	1.18	1.48	0.88	1.07	0.71	1.11	0.61	0.91
160838	Hs.236030	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c,	1.13	1.27	0.99	1.07	1.20	1.07	1.44	1.42	0.89	1.78	1.34	1.85	1.09	1.49	1.50	1.37	1.35	1.14	1.98	1.07	0.68	0.71
293325	Hs.58435	FYN-binding protein (FYB-120/130)	1.38	4.21	0.95	2.44	1.95	2.70	0.75	1.24	1.76	1.03	2.13	2.62	0.69	0.89	1.18	2.08	1.78	1.24	1.09	1.14	2.27	1.93
726637	Hs.75307	t-complex-associated-testis-expressed 1-like	1.40	1.38	0.93	1.26	1.55	0.95	0.40	3.31	1.68	1.21	1.00	1.35	0.96	0.87	1.17	1.15	1.14	1.41	1.07	1.19	1.66	1.42
25588	Hs.81248	CUG triplet repeat, RNA-binding protein 1	1.19	2.50	0.92	1.65	2.01	1.76	2.26	1.37	1.33	1.89	1.84	2.20	1.67	1.73	2.08	1.56	1.28	1.43	1.61	1.35	1.25	1.56
179804	Hs.79380	PWP2 (periodic tryptophan protein, yeast) homolog	1.26	0.98	0.92	1.04	1.04	1.51	0.93	0.65	1.69	2.65	0.52	3.53	3.53	3.25	2.95	0.32	1.32	1.08	0.82	0.96	0.47	1.30
131595	Hs.18048	melanoma antigen, family A, 10	1.95	3.91	1.71	2.23	3.29	1.52	2.00	1.75	2.77	2.85	2.14	3.89	1.63	2.22	3.24	1.89	3.22	2.00	2.44	1.15	1.68	1.83
360079	Hs.76228	amplified in osteosarcoma	1.02	0.94	1.42	0.86	1.36	0.95	0.86	1.44	1.84	1.29	1.26	1.09	0.99	1.62	1.16	1.64	1.89	1.05	0.96	0.96	1.07	0.89
28012	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptid	1.55	2.42	1.25	1.77	2.12	1.98	1.16	1.18	0.90	1.31	0.84	1.20	0.96	0.95	1.28	1.13	1.08	1.71	1.32	1.04	1.02	0.78
810316	Hs.75154	KIAA0631 protein	0.74	1.43	1.18	0.95	1.82	1.09	0.66	0.78	1.01	1.84	0.79	1.44	0.73	0.95	0.99	0.66	0.82	0.81	1.05	1.03	0.93	0.93
293859	Hs.71119	Putative prostate cancer tumor suppressor	1.33	1.69	0.57	0.82	1.10	0.41	0.70	0.93	0.74	0.93	0.66	0.92	0.22	0.40	0.44	0.38	1.13	1.06	1.00	0.69	0.94	0.81
292388	Hs.4187	Homo sapiens clone 24636 mRNA sequence	1.91	2.34	1.94	1.99	1.91	0.92	2.27	2.20	2.01	2.63	2.28	1.11	1.06	0.76	1.84	1.07	2.08	1.24	2.47	1.92	1.79	1.47
128783	Hs.115240	peroxisome biogenesis factor 13	1.79	1.14	0.96	1.75	1.96	1.10	0.99	1.68	1.74	1.05	0.86	0.85	0.76	1.26	1.38	0.59	1.08	0.98	1.08	1.40	3.21	1.50
811911	Hs.6106	RNA binding motif protein 4	1.47	1.41	1.00	1.76	1.58	0.95	1.61	1.45	1.26	1.00	1.38	0.99	1.27	1.72	1.48	1.47	1.08	0.70	0.75	1.27	1.29	0.91
282310	Hs.183648	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (l	3.08	1.35	1.60	1.91	1.67	1.41	1.81	0.81	1.68	0.95	1.27	3.02	1.94	1.98	2.78	1.42	2.11	1.47	1.96	2.75	0.84	1.03
245330	Hs.251664	insulin-like growth factor 2 (somatomedin A)	2.11	1.18	4.37	2.35	3.41	0.98	0.89	2.42	18.77	3.90	2.06	1.93	0.95	1.86	5.26	2.01	3.28	2.52	2.38	1.02	1.15	1.43
307553	Hs.184050	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog	2.44	3.96	3.60	3.06	5.82	1.48	1.95	3.79	6.58	4.57	1.70	1.91	1.38	2.05	3.13	0.74	2.38	1.50	1.97	1.50	2.65	2.04
201890	Hs.127799	apoptosis inhibitor 2	0.60	2.36	0.72	2.08	1.79	1.73	0.85	0.86	0.82	0.43	1.77	1.37	0.38	0.65	1.17	0.65	0.55	0.76	1.25	0.91	0.93	5.27
34852	Hs.75263	apoptosis inhibitor 1	1.67	1.54	0.74	1.20	1.67	1.29	0.76	0.85	1.00	0.58	0.82	0.51	0.63	0.49	0.97	0.65	0.62	0.96	0.75	0.84	1.34	3.64
345208	Hs.12379	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	1.64	1.92	1.60	1.99	1.30	1.33	1.48	0.93	1.37	0.96	1.53	0.52	1.21	1.27	0.93	1.46	0.85	0.98	0.78	1.22	1.11	1.52
209137	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, epsilon	2.11	0.42	0.56	0.44	2.16	1.59	0.45	1.83	0.16	0.40	0.64	0.35	0.12	1.43	0.27	0.81	0.15	0.43	0.61	0.39	0.76	0.47
823614	Hs.173824	thymine-DNA glycosylase	1.13	2.00	1.72	2.67	1.66	1.04	1.05	1.44	1.85	1.76	1.60	4.03	1.34	1.88	1.20	1.00	1.36	0.87	1.30	1.53	1.26	1.70
741815	Hs.216354	ring finger protein 5	1.79	1.74	2.35	2.26	1.16	0.91	1.99	1.51	1.65	1.71	1.79	2.07	1.52	1.92	3.38	1.45	1.19	1.26	2.74	1.03	1.25	0.91
293820	Hs.94479	transmembrane protein 1	1.59	2.09	0.69	1.73	1.75	1.01	1.37	1.27	1.17	1.68	1.47	1.46	1.21	0.87	1.48	1.29	1.40	1.36	1.40	1.15	1.60	1.48
563598	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	3.88	4.58	1.72	3.00	7.72	5.81	6.80	1.24	1.72	1.63	1.79	1.77	1.12	3.01	1.15	1.43	0.71	3.53	0.90	1.00	1.08	6.32
327150	Hs.82295	dedicator of cyto-kinesis 1	1.15	2.16	1.37	0.96	3.05	0.98	1.33	1.53	1.56	1.45	1.23	1.25	0.82	0.99	1.20	0.50	2.91	2.21	1.97	0.60	1.48	1.47
771206	Hs.74598	polymerase (DNA directed), delta 2, regulatory subunit (50kD)	2.25	2.12	1.17	1.42	2.30	1.72	2.08	1.58	1.00	1.62	1.81	0.84	1.30	0.82	1.02	1.09	2.21	1.17	2.05	1.23	2.56	1.32
300482	Hs.153636	far upstream element (FUSE) binding protein 3	1.18	1.34	1.13	1.05	1.06	0.76	0.58	1.11	1.28	1.64	1.18	0.82	0.85	1.91	0.92	0.76	0.72	1.01	1.07	1.32	0.68	0.85
123400	Hs.91142	KH-type splicing regulatory protein (FUSE-binding protein 2)	2.05	5.39	1.60	2.38	1.97	2.08	3.10	2.04	1.87	2.50	1.58	2.40	1.47	1.58	2.06	1.86	1.55	1.85	2.73	1.81	2.65	2.10
308588	Hs.173464	FK506-binding protein 8 (38kD)	1.47	1.44	0.74	1.05	0.93	1.52	0.81	0.75	1.29	0.64	0.90	1.44	2.40	2.31	1.48	1.46	0.76	0.73	0.66	0.83	0.75	1.37
361097	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5)	1.22	0.77	0.76	0.88	0.78	1.10	0.60	0.61	0.89	0.64	0.85	0.40	0.65	0.42	0.80	0.76	0.81	1.16	0.81	1.28	1.00	1.07
754538	Hs.118724	DR1-associated protein 1 (negative cofactor 2 alpha)	0.94	1.49	0.73	1.28	1.44	1.11	1.94	1.24	1.43	1.98	1.52	1.13	0.78	1.60	0.90	1.35	0.91	0.70	1.10	1.14	1.14	1.11
364329	Hs.23598	CREB binding protein (Rubinstein-Taybi syndrome)	0.76	2.95	1.47	1.21	1.99	0.82	1.95	1.33	1.66	2.15	1.10	1.49	0.87	1.30	1.35	1.37	1.24	1.17	1.30	0.87	0.96	0.79
813675	Hs.37616	Human D9 splice variant B mRNA, complete cds	2.78	3.02	0.97	1.94	2.37	1.55	4.87	2.20	2.92	4.69	2.76	7.22	6.31	5.24	8.80	2.47	2.47	2.05	3.29	2.17	3.40	2.56

280236	Hs.79877	myotubularin related protein 6	0.75	2.34	1.22	1.30	1.45	0.89	0.66	0.42	0.96	2.33	0.58	1.72	0.74	1.08	0.71	0.53	0.68	1.01	0.79	0.78	0.62	0.84
51737	Hs.29287	retinoblastoma-binding protein 8	1.57	1.40	0.90	1.35	1.08	1.15	0.69	0.62	0.52	0.53	0.67	2.65	0.98	0.94	1.61	0.32	0.53	1.69	1.64	0.56	0.94	0.86
754355	Hs.27621	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane do	2.39	2.73	1.25	1.97	2.50	1.65	4.20	2.23	3.26	5.45	2.72	4.39	5.05	3.01	3.66	3.24	2.26	1.70	2.13	1.56	2.76	2.38
204214	Hs.69563	CDC6 (cell division cycle 6, S. cerevisiae) homolog	1.56	3.12	2.26	2.52	2.18	2.20	2.42	5.05	1.82	3.25	6.00	3.08	1.45	1.59	2.22	1.13	1.57	0.88	1.36	1.96	5.07	2.06
109265	Hs.157169	ESTs	1.78	1.48	1.43	1.64	2.17	1.13	1.23	1.34	1.85	1.40	1.55	1.21	0.60	0.72	1.48	1.06	1.05	1.19	1.72	0.94	0.85	1.26
810974	Hs.3068	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	4.98	4.40	5.79	6.24	5.03	2.57	3.06	4.62	10.81	10.27	3.05	2.01	2.23	1.86	2.74	0.88	3.87	2.34	2.67	2.25	2.72	3.05
35077	Hs.21639	nuclear protein, marker for differentiated aortic smooth muscle and down-regulated with v	0.66	0.83	0.62	0.52	0.89	0.43	0.73	0.46	0.39	0.68	0.35	1.02	0.92	0.92	0.65	0.69	0.36	0.98	0.61	0.56	0.67	0.76
548957	Hs.169921	general transcription factor II, i, pseudogene 1	2.15	1.77	1.72	2.39	2.23	2.65	1.99	1.57	1.43	1.33	1.11	0.92	1.27	0.79	1.68	1.81	1.21	1.34	1.97	0.92	2.02	1.05
212198	Hs.44585	tumor protein p53-binding protein, 2	2.24	1.81	2.17	3.08	2.33	2.34	2.21	1.42	1.51	1.16	1.20	0.83	1.10	0.97	1.48	1.34	0.91	1.09	1.79	0.76	1.32	2.60
213136	Hs.75462	BTG family, member 2	1.27	2.02	1.15	2.50	2.58	1.69	0.66	2.24	1.52	1.64	1.66	7.28	5.85	1.67	9.87	1.61	3.26	3.87	2.03	0.63	1.77	1.33
46284	Hs.181304	putative gene product	1.60	1.41	2.41	2.27	2.63	1.32	2.15	1.80	3.01	2.11	1.65	2.64	1.36	1.39	2.66	1.89	3.24	3.85	2.91	2.05	1.40	1.12
175123	Hs.3080	mitogen-activated protein kinase 7	1.88	1.89	3.94	1.88	2.93	1.10	1.35	2.93	2.37	1.85	1.13	1.15	1.30	1.42	2.53	1.19	1.72	2.09	1.71	0.83	2.06	1.12
139540	Hs.197955	KIAA0704 protein	2.10	1.12	0.92	1.09	1.32	0.82	0.76	0.71	0.70	0.39	0.99	0.87	0.59	0.73	1.09	0.55	0.32	0.60	0.53	0.63	0.78	0.63
813184	Hs.76090	tumor necrosis factor, alpha-induced protein 1 (endothelial)	1.04	2.02	1.10	1.22	2.57	1.02	0.64	2.10	2.00	1.53	1.53	2.54	1.85	1.59	2.70	0.58	1.45	0.92	1.81	0.84	1.70	1.41
37234	Hs.82979	mitogen-activated protein kinase kinase kinase kinase 2	2.81	1.37	1.66	1.98	2.58	2.18	2.48	1.82	3.12	3.32	2.09	2.28	1.13	2.09	1.87	1.78	2.48	0.98	1.41	0.80	1.62	1.58
248454	Hs.93659	protein disulfide isomerase related protein (calcium-binding protein, intestinal-related)	0.78	1.72	2.18	1.38	2.01	1.34	2.25	1.38	1.28	1.29	2.43	1.48	0.82	1.46	1.07	1.61	1.39	0.96	1.15	1.76	2.76	2.34
564846	Hs.1540	nuclear matrix protein p84	2.01	3.62	1.68	2.47	2.85	2.42	1.34	1.61	1.46	2.27	2.28	1.48	1.16	1.06	1.46	0.95	1.20	1.63	2.79	1.18	2.13	2.31
813707	Hs.183601	regulator of G-protein signalling 16	4.24	10.78	2.52	4.88	7.67	4.70	13.81	7.60	10.33	3.45	8.58	30.74	8.81	7.95	21.78	2.49	6.92	5.81	13.71	3.71	2.98	2.81
127519	Hs.178761	26S proteasome-associated pad1 homolog	1.29	1.39	1.04	0.88	1.47	1.43	1.96	1.06	0.88	1.16	0.87	2.62	1.25	1.28	1.85	1.00	1.64	1.06	1.10	1.77	1.40	1.80
361048	Hs.79093	EBNA-2 co-activator (100kD)	0.69	0.83	0.74	1.17	0.79	0.71	1.14	0.51	0.75	0.49	0.67	0.99	0.62	1.15	0.83	0.74	0.44	0.67	0.62	1.16	0.57	0.81
810734	Hs.82520	Human 1.1 kb mRNA upregulated in retinoic acid treated HL-60 neutrophilic cells	0.76	0.56	0.29	0.43	0.77	0.62	0.98	1.08	1.05	1.29	1.13	0.75	0.76	0.46	1.00	0.80	1.31	1.12	1.46	1.09	0.90	0.30
296679	Hs.44898	ESTs, Moderately similar to cadherin 12 [H.sapiens]	2.11	3.09	3.01	2.40	3.08	2.91	1.37	2.57	3.90	3.14	2.03	2.28	1.10	1.48	1.51	0.99	3.11	2.84	4.66	1.00	2.15	1.15
135527	Hs.238030	secretory carrier membrane protein 2	1.80	1.87	0.97	1.56	2.73	1.69	0.83	1.73	1.66	1.50	1.59	1.53	1.53	1.73	1.18	1.55	1.06	1.19	0.98	0.96	1.64	1.73
49860	Hs.92261	pyruvate dehydrogenase kinase, isoenzyme 2	0.86	1.47	1.24	1.04	1.88	0.97	0.77	1.43	1.31	0.65	1.61	1.03	1.84	0.56	0.91	1.58	2.09	0.93	0.80	0.69	1.29	0.42
202535	Hs.173451	metallothionein 1G	1.53	0.71	0.50	0.42	0.80	0.42	2.10	0.67	0.68	0.65	0.69	0.60	0.30	0.78	0.53	0.47	0.91	1.92	1.41	1.33	1.62	1.17
327304	Hs.110707	H326	1.56	2.66	1.10	1.57	2.40	1.35	1.90	2.06	1.50	1.96	1.52	1.70	1.55	1.76	1.87	0.98	1.03	1.63	3.25	1.15	1.15	1.14
812105	Hs.75823	ALL1-fused gene from chromosome 1q	1.26	2.90	6.78	2.03	2.08	1.67	5.05	2.04	2.05	2.44	1.43	1.10	0.53	0.69	1.09	0.57	2.64	1.29	1.70	1.32	1.85	1.80
135773	Hs.194562	telomeric repeat binding factor (NIMA-interacting) 1	2.35	3.98	1.85	2.32	3.25	2.71	2.51	2.63	1.74	3.58	2.04	1.24	1.25	0.88	2.38	0.80	2.00	2.36	2.90	1.93	2.63	1.87
756847	Hs.6574	suppressin (nuclear deformed epidermal autoregulatory factor-1 (DEAF-1)-related)	1.57	2.04	1.56	1.74	2.23	1.93	1.25	1.06	1.12	1.29	1.66	1.43	1.17	0.99	0.45	1.23	1.39	1.50	1.57	1.26	1.23	1.57
193067	Hs.145696	splicing factor (CC1.3)	1.78	1.91	1.02	1.02	1.95	1.13	1.51	0.98	0.87	1.17	0.88	2.17	1.31	0.80	1.89	0.59	1.73	1.89	1.71	1.01	1.77	1.19
156045	Hs.200600	secretory carrier membrane protein 3	1.57	2.77	1.33	2.04	1.97	1.93	2.90	2.04	2.12	1.70	1.75	1.67	2.06	2.08	1.66	1.73	1.18	0.91	1.56	1.08	1.47	2.06
243321	Hs.91390	poly (ADP-ribose) glycohydrolase	1.45	1.87	1.18	1.77	2.37	1.20	0.86	1.36	1.49	1.10	1.11	1.65	1.35	1.02	1.48	1.13	0.84	1.48	1.55	1.24	1.99	2.02
46897	Hs.30954	phosphomevalonate kinase	2.36	2.09	1.14	1.83	1.99	1.30	2.61	2.31	1.17	1.77	1.71	1.39	1.46	1.42	1.87	1.75	1.56	1.27	2.71	1.07	1.51	0.99
41356	Hs.155079	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	2.23	1.88	1.12	2.21	2.24	2.10	1.03	1.17	1.86	1.58	1.69	2.65	2.09	1.64	2.45	1.57	1.73	1.53	3.38	1.45	1.36	0.47
26578	Hs.13501	pescadillo (zebrafish) homolog 1, containing BRCT domain	0.92	2.92	1.38	1.46	1.69	1.76	1.96	1.42	1.20	1.33	1.78	1.20	1.85	1.56	2.04	1.22	0.70	1.08	0.96	1.31	1.25	2.11
293104	Hs.172887	phytanoyl-CoA hydroxylase (Refsum disease)	1.33	2.24	2.00	2.50	1.63	2.68	1.53	0.54	0.97	1.43	0.72	0.92	1.25	0.82	0.81	0.98	1.75	1.37	1.22	0.90	1.54	1.08
124753	Hs.94395	ATP-binding cassette, sub-family D (ALD), member 4	1.32	2.44	1.95	1.99	2.46	1.45	0.94	1.90	1.83	2.19	1.86	2.14	1.97	1.50	2.16	0.89	1.72	1.90	2.49	1.67	1.79	0.99
347434	Hs.207251	nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein	1.50	4.84	3.97	2.16	5.64	1.43	2.40	3.67	7.90	7.12	2.24	2.85	2.76	2.18	2.37	2.28	3.77	1.79	2.98	1.14	2.25	3.30
85906	Hs.78146	platelet/endothelial cell adhesion molecule (CD31 antigen)	1.92	7.32	5.50	5.58	12.66	5.45	2.53	5.41	7.18	5.86	8.80	4.89	3.57	3.45	6.77	5.93	4.82	8.75	3.51	3.33	2.98	2.72
86017	Hs.168383	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	2.78	5.38	2.26	1.43	4.13	5.00	2.31	2.65	4.37	1.62	7.38	3.94	1.81	2.19	2.15	5.22	7.01	2.55	3.79	3.14	1.64	4.85
23464	Hs.75063	human immunodeficiency virus type I enhancer-binding protein 2	1.45	1.12	0.37	0.58	2.04	1.85	0.78	0.85	0.85	0.96	0.63	1.70	0.59	1.55	1.13	0.92	0.87	0.99	0.91	1.22	1.63	1.87
77577	Hs.155210	FOS-like antigen 2	1.07	1.53	2.18	0.85	1.50	1.16	0.77	1.32	1.56	0.66	1.26	1.21	0.41	0.95	0.31	1.15	0.83	1.23	0.80	0.81	1.03	1.08
81221	Hs.77424	Fc fragment of IgG, high affinity Ia, receptor for (CD64)	1.05	14.29	4.98	3.84	8.37	4.50	2.52	1.69	7.87	2.57	9.23	6.70	1.78	2.96	2.79	3.80	3.15	2.95	3.45	2.50	3.36	0.98
82991	Hs.11951	phosphodiesterase I/nucleotide pyrophosphatase 1 (homologous to mouse Ly-41 antigen	1.16	1.19	1.18	1.36	3.07	1.54	1.67	3.34	5.06	6.87	3.50	6.04	1.96	4.40	5.07	2.09	6.67	1.97	4.37	1.52	1.47	1.47
84730	Hs.154078	Untitled	1.69	1.35	0.86	1.31	1.40	1.34	0.81	1.00	0.99	0.73	1.56	1.05	0.85	0.77	0.91	0.65	0.96	1.39	0.98	0.76	0.99	1.11
115336	Hs.2554	sialyltransferase 1 (beta-galactoside alpha-2,6-sialytransferase)	1.11	1.13	1.05	1.23	1.30	1.90	1.46	1.00	1.09	1.24	1.98	1.03	0.63	0.64	0.85	0.82	1.40	1.36	1.26	0.89	0.84	1.42
110589	Hs.244613	signal transducer and activator of transcription 5B	1.10	1.68	1.29	1.01	2.57	3.20	1.04	1.36	2.25	1.88	0.95	1.18	1.12	1.12	1.33	2.03	1.40	2.14	1.82	1.19	1.46	0.91
112035	Hs.171680	pre-B-cell leukemia transcription factor 3	1.60	2.21	1.48	0.94	1.49	1.03	1.24	1.14	1.43	1.58	1.75	1.69	0.97	2.11	1.85	2.36	1.07	0.82	1.48	1.21	1.95	0.91
114116	Hs.1501	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	1.25	1.51	1.90	1.42	2.58	2.09	1.58	1.73	2.36	1.91	1.01	2.58	1.50	1.44	2.12	1.91	2.23	2.73	1.96	0.84	1.95	1.68
114648	Hs.83428	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	1.31	0.96	1.62	0.75	1.00	1.17	1.14	0.89	1.20	0.91	0.76	1.13	0.73	0.90	1.10	1.19	1.12	1.39	1.45	0.72	0.77	0.91
126379	Hs.19718	protein tyrosine phosphatase, receptor type, U	0.83	0.37	0.66	0.23	1.16	0.96	0.40	0.78	0.71	0.91	0.57	0.87	1.03	1.00	1.23	0.38	0.41	0.40	0.32	0.54	0.27	0.29
116713	Hs.77367	monokine induced by gamma interferon	0.92	1.23	0.72	0.91	1.47	0.99	0.95	1.12	0.93	1.70	0.75	0.81	0.52	0.39	0.78	1.30	1.36	1.18	1.34	1.07	1.62	0.91
121849	Hs.73828	T-cell acute lymphocytic leukemia 1	1.44	1.38	1.17	0.94	2.54	1.35	2.22	2.46	4.62	2.46	3.02	1.06	0.85	0.98	1.19	1.71	1.91	1.81	2.05	2.60	2.80	0.83
123586	Hs.82109	syndecan 1	2.00	3.82	0.72	0.84	3.37	2.58	2.60	2.82	5.76	3.52	2.28	2.56	1.27	0.85	1.96	3.78	1.17	2.14	3.45	2.37	1.88	1.60
123953	Hs.73931	major histocompatibility complex, class II, DQ beta 1	1.38	2.27	1.95	1.12	1.41	1.72	1.85	1.69	1.03	1.82	1.86	1.23	0.70	0.52	0.95	0.83	1.39	1.46	2.15	0.80	1.38	1.24
124554	Hs.173894	colony stimulating factor 1 (macrophage)	2.42	8.59	5.74	4.96	7.00	4.54	0.94	5.05	6.16	2.80	8.63	5.23	1.81	2.42	4.07	3.95	3.46	5.98	6.37	2.00	4.22	4.93
125187	Hs.99987	excision repair cross-complementing rodent repair deficiency, complementation group 2 (x	1.01	1.56	1.05	1.05	1.84	0.92	1.13	0.86	1.85	2.03	1.50	1.43	1.03	0.98	1.13	1.32	1.42	1.23	1.12	1.30	1.57	0.92
128100	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	0.78	0.48	0.14	0.21	0.60	0.49	0.48	0.42	0.61	0.90	0.38	0.81	1.09	0.21	0.56	0.48	1.04	0.66	0.98	0.82	0.64	0.29
26503	Hs.101047	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.74	2.02	1.16	1.91	1.44	2.05	0.97	1.98	1.34	1.43	1.09	0.86	0.86	0.72	1.03	1.29	0.86	1.22	0.91	0.88	1.89	1.79
26474	Hs.25647	v-fos FBJ murine osteosarcoma viral oncogene homolog	0.34	0.15	0.28	0.37	0.61	0.09	0.18	0.16	0.68	0.07	0.25	0.47	0.16	0.30	0.70	0.23	0.29	2.19	0.48	0.29	0.17	0.06
26167	Hs.86131	Fas (TNFRSF6)-associated via death domain	1.56	0.96	0.88	1.21	1.23	1.26	0.78	1.29	1.71	1.27	1.04	0.60	0.97	0.65	0.77	1.55	1.15	1.02	1.33	2.00	1.04	0.07
26811	Hs.150930	X-ray repair complementing defective repair in Chinese hamster cells 4	0.65	2.28	1.68	1.54	1.54	1.08	0.85	2.14	2.38	0.95	2.76	0.88	1.58	0.76	0.76	1.91	0.86	0.79	0.79	0.89	1.76	1.45
35516	Hs.79101	cyclin G1	0.12	0.28	0.31	0.44	0.34	0.27	0.34	0.24	0.24	0.18	0.28	0.16	0.22	0.17	0.45	0.22	0.16	0.33	0.27	0.23	0.30	0.29
31116	Hs.57301	mutL (E. coli) homolog 1 (colon cancer, nonpolyposis type 2)	1.90	1.72	1.36	2.22	2.25	1.30	1.58	1.65	1.92	1.49	2.01	1.59	0.97	1.08	1.32	1.93	1.14	1.57	2.12	1.11	1.18	0.85
32790	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1)	2.92	2.62	2.36	4.96	3.00	3.22	3.03	1.50	2.03	1.36	1.56	2.18	1.05	0.95	1.34	0.76	1.65	1.60	2.02	1.44	3.45	1.04
32983	Hs.22583	DKFZP434K2235 protein	1.73	0.86	2.29	2.13	2.00	1.64	1.26	1.44	2.01	1.51	2.60	2.68	1.40	1.79	2.37	1.97	1.30	1.49	1.91	1.23	0.95	1.50
34005	Hs.177559	interferon gamma receptor 2 (interferon gamma transducer 1)	1.17	1.59	1.20	1.78	1.66	1.32	1.18	1.29	1.82	1.27	1.80	2.08	1.60	2.24	1.71	2.24	1.10	1.35	1.71	1.43	1.62	1.80
36215	Hs.91640	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	1.85	3.02	10.43	4.88	4.91	5.59	2.92	4.75	10.17	8.75	3.94	5.92	6.36	4.90	7.15	5.20	3.63	3.76	7.75	2.92	0.61	2.52
138460	Hs.79069	cyclin G2	1.07	1.18	1.24	0.98	1.67	1.47	0.99	1.77	1.47	1.25	2.17	1.37	0.90	0.80	2.27	1.27	2.01	1.82	2.60	1.14	1.32	1.90
43129	Hs.317	phospholipase C, gamma 1 (formerly subtype 148)	0.72	0.86	0.71	0.95	1.02	0.63	0.85	0.94	0.89	0.93	1.06	0.68	0.58	0.75	0.66	0.76	0.77	0.65	1.15	0.93	1.03	0.62
131828	Hs.23800	ESTs, Moderately similar to HYA22 [H.sapiens]	1.29	1.60	0.84	1.47	1.58	1.67	1.85	1.45	0.94	1.24	1.10	1.56	1.40	0.94	2.01	1.41	1.26	1.82	2.24	1.05	1.33	1.28
132420	Hs.85146	v-ets avian erythroblastosis virus E26 oncogene homolog 2	2.25	6.29	4.44	2.52	8.32	4.79	3.28	4.37	6.35	5.86	3.06	7.34	2.13	6.30	5.04	5.07	3.25	4.57	5.40	2.67	2.47	1.90
135381	Hs.76556	growth arrest and DNA-damage-inducible 34	1.37	1.57	0.95	1.74	2.07	1.12	1.59	1.19	1.10	0.88	1.14	1.04	0.48	0.87	1.02	1.14	0.80	1.19	1.52	1.13	0.89	1.61
138604	Hs.82483	MAD (mothers against decapentaplegic, Drosophila) homolog 2	1.33	1.13	1.13	1.31	0.92	1.17	0.96	0.90	1.14	0.74	0.46	0.81	0.50	0.77	1.02	0.89	0.94	1.11	0.99	1.07	0.62	1.08
140827	Hs.75862	MAD (mothers against decapentaplegic, Drosophila) homolog 4	1.38	1.15	1.48	1.81	1.24	1.09	1.62	0.86	1.33	0.66	1.08	1.15	0.49	0.61	0.97	1.11	0.98	1.96	1.46	1.28	1.08	1.70
143751	Hs.56729	lymphocyte-specific protein 1	1.65	2.63	1.35	1.81	2.57	1.71	1.47	1.54	2.16	1.64	1.83	1.89	0.69	1.61	1.36	2.27	1.27	2.40	2.03	1.12	1.25	1.24
144944	Hs.89414	chemokine (C-X-C motif), receptor 4 (fusin)	3.76	16.68	7.11	8.57	8.00	8.74	17.17	7.23	7.40	5.11	9.08	13.08	1.71	2.83	4.94	6.99	7.07	5.32	15.60	3.37	6.35	4.64
144693	Hs.1103	transforming growth factor, beta 1	2.34	7.15	3.86	4.69	7.30	5.80	2.52	5.22	8.99	8.61	7.06	4.72	1.52	3.34	3.21	5.54	3.05	3.78	4.84	1.62	3.34	0.88
154472	Hs.748	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	1.38	1.07	2.83	2.26	2.47	0.86	5.98	3.51	5.77	13.09	3.02	5.53	3.77	1.41	2.17	2.20	3.78	1.55	1.89	1.31	1.74	0.37
154536	Hs.98493	X-ray repair complementing defective repair in Chinese hamster cells 1	1.34	1.72	1.40	1.20	1.69	1.43	0.96	1.38	1.53	2.13	1.69	0.88	0.72	1.22	1.14	1.37	1.10	0.94	1.25	0.80	1.22	1.93
162772	Hs.738	early growth response 1	1.12	6.11	0.45	4.20	7.73	2.67	1.91	3.26	2.80	2.27	7.00	5.19	0.75	1.30	3.97	3.03	0.84	2.95	1.78	2.24	3.37	1.55

48398	Hs.153752	cell division cycle 25B	0.98	0.54	1.55	1.42	1.15	1.15	0.94	0.71	0.46	0.52	0.76	1.88	2.40	2.51	1.51	1.35	0.53	0.75	0.63	1.61	1.72	0.63
49950	Hs.4756	flap structure-specific endonuclease 1	1.79	2.96	1.25	2.27	2.36	2.36	4.33	1.44	1.01	1.87	2.46	1.02	0.95	1.08	1.32	0.48	1.17	0.87	2.30	1.58	2.47	2.40
50576	Hs.180677	zinc finger protein 162	1.24	2.20	1.33	1.78	2.04	1.79	0.96	1.45	1.42	0.96	1.70	4.97	5.35	4.04	1.26	2.03	0.93	1.22	1.12	1.10	1.19	1.58
50503	Hs.83968	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrop	0.89	2.06	1.28	1.39	1.70	3.44	0.63	1.94	2.15	1.37	4.08	3.09	1.44	1.58	1.91	1.32	1.17	1.07	1.00	1.12	1.64	1.97
52489	Hs.111	fibroblast growth factor 9 (glia-activating factor)	1.87	3.23	1.98	1.88	5.45	2.00	2.93	2.16	3.18	4.11	1.93	2.80	0.93	0.66	2.34	2.82	3.36	1.50	1.99	1.89	3.18	1.64
201797	Hs.758	RAS p21 protein activator (GTPase activating protein) 1	0.90	0.92	0.69	0.82	1.79	1.16	0.48	0.94	1.07	0.71	0.49	1.65	0.79	0.57	0.89	1.18	0.85	1.67	1.48	0.66	0.98	1.11
52162	Hs.13471	ESTs	1.49	4.24	0.79	1.76	6.47	3.20	1.45	3.14	2.20	2.34	5.38	3.59	0.84	1.93	2.73	3.35	1.54	1.89	2.18	1.51	2.28	0.91
52681	Hs.858	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light p	1.02	7.27	1.21	2.01	6.18	3.37	1.19	2.52	3.98	2.08	4.70	3.95	0.72	1.57	2.02	3.20	0.86	1.94	1.46	1.67	2.85	5.17
179711	Hs.77810	nuclear factor of activated T-cells, cytoplasmic 4	2.38	4.41	10.80	1.83	6.90	1.67	1.62	2.66	4.42	9.28	9.72	3.80	2.74	2.75	6.71	3.33	2.54	3.44	4.94	1.01	2.85	0.91
183950	Hs.125359	Thy-1 cell surface antigen	4.08	8.51	14.59	7.79	13.45	6.83	8.26	7.61	9.60	10.06	13.81	11.26	4.75	4.09	9.58	6.16	6.49	4.45	11.56	3.79	7.12	4.10
187987	Hs.75545	interleukin 4 receptor	1.25	2.15	0.82	1.50	3.98	2.09	1.02	2.00	2.35	1.37	2.27	2.98	0.88	1.95	1.35	1.82	1.14	1.38	1.88	1.04	1.09	1.64
192694	Hs.182237	POU domain, class 2, transcription factor 1	1.72	3.12	1.57	1.44	3.09	2.28	1.66	2.88	1.92	2.89	2.21	2.79	1.08	1.60	3.24	1.62	1.86	1.82	2.63	1.25	3.13	1.51
201673	Hs.83795	interferon regulatory factor 2	1.67	2.26	1.49	1.87	2.63	2.78	0.89	1.91	2.67	1.75	2.21	3.24	1.69	2.22	2.49	2.69	1.85	1.53	1.19	1.45	1.91	1.75
221619	Hs.198253	major histocompatibility complex, class II, DQ alpha 1	2.77	17.65	6.20	7.95	7.62	8.52	7.85	5.70	9.07	12.01	16.24	15.28	7.53	5.37	6.79	4.72	4.11	5.43	10.31	3.15	9.70	8.24
223176	Hs.109012	MAX dimerization protein	1.48	2.47	1.11	2.02	2.99	2.19	1.09	1.67	2.37	1.18	3.10	2.05	1.40	2.10	1.32	2.12	1.52	1.55	1.43	1.47	2.21	1.94
230976	Hs.82380	menage a trois 1 (CAK assembly factor)	1.50	1.08	1.16	0.89	1.62	0.95	1.04	1.07	0.99	0.98	0.85	1.57	1.14	0.93	1.30	0.96	1.40	1.57	1.80	1.48	1.55	0.82
203132	Hs.83429	tumor necrosis factor (ligand) superfamily, member 10	5.56	12.30	1.30	5.19	3.57	6.43	1.55	7.86	10.02	2.49	12.51	4.01	0.76	2.35	3.35	5.36	4.33	4.81	4.14	1.82	5.69	5.36
203017	Hs.75254	interferon regulatory factor 3	1.02	1.66	0.80	0.85	2.10	0.92	1.08	1.59	1.38	1.35	1.16	2.05	0.88	1.29	1.08	1.26	1.25	1.15	1.90	1.58	1.32	0.54
204681	Hs.234799	breakpoint cluster region	0.94	2.94	0.76	1.42	2.33	1.78	3.46	1.83	1.78	1.71	2.42	1.42	1.88	1.46	1.55	1.83	1.00	1.17	1.14	1.71	2.93	1.83
209310	Hs.75569	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light	0.95	1.05	0.81	1.10	1.42	0.99	1.89	1.32	1.36	0.90	1.05	1.54	1.19	1.31	1.53	1.22	1.20	1.12	1.24	1.45	1.22	0.74
221690	Hs.41639	programmed cell death 2	0.78	0.99	0.60	1.16	0.94	1.19	1.11	0.94	0.92	0.92	1.81	0.97	0.78	0.94	0.94	1.23	0.76	1.13	0.81	1.93	1.09	0.77
231302	Hs.1189	E2F transcription factor 3	1.22	2.48	2.36	3.18	2.49	1.59	1.76	1.43	1.64	0.95	1.01	1.16	0.81	1.19	1.51	1.73	0.84	0.94	0.79	1.09	1.86	2.27
248032	Hs.156346	topoisomerase (DNA) II alpha (170kD)	2.31	3.24	3.25	2.62	1.41	2.61	3.10	5.73	1.43	2.03	7.38	0.30	0.64	0.45	0.69	0.78	1.65	0.78	3.92	1.55	3.91	2.70
248613	Hs.1334	v-myb avian myeloblastosis viral oncogene homolog	1.54	1.30	1.34	1.36	1.41	1.44	0.96	1.71	1.18	1.47	1.58	1.05	0.69	1.14	1.22	1.24	1.50	1.24	1.27	1.44	0.78	1.12
233194	Hs.74592	special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold-associating D	1.34	2.17	1.32	2.03	2.96	2.54	1.07	1.47	1.70	0.85	1.14	0.81	0.37	0.88	0.75	1.19	0.77	1.06	0.69	0.90	1.76	1.66
236338	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	1.53	3.59	1.24	1.54	1.80	1.15	1.29	1.87	1.96	1.04	1.23	0.99	0.83	0.89	0.94	2.37	0.73	1.12	0.55	0.85	2.05	5.39
238577	Hs.814	major histocompatibility complex, class II, DP beta 1	3.27	16.45	16.07	10.44	9.53	7.79	4.00	9.31	17.66	75.18	14.51	7.51	1.48	3.08	4.88	6.08	6.14	4.20	5.64	2.88	5.61	4.23
243159	Hs.171952	occludin	1.74	1.10	1.32	1.42	0.98	1.16	1.57	1.80	1.14	1.07	1.64	0.45	0.70	0.71	0.74	1.11	0.97	1.20	1.74	2.03	1.49	1.50
244355	Hs.84	interleukin 2 receptor, gamma (severe combined immunodeficiency)	1.28	2.34	1.34	2.13	2.12	2.22	2.14	5.41	2.42	2.09	6.92	1.74	1.07	1.08	2.07	2.18	2.11	1.20	2.00	3.24	3.31	2.52
267246	Hs.25363	presenilin 2 (Alzheimer disease 4)	1.37	0.96	1.04	1.26	1.69	1.55	1.16	1.77	1.66	1.39	1.86	1.05	0.99	0.81	1.09	1.52	1.28	1.04	1.68	1.29	1.80	1.66
267682	Hs.30692	p21 (CDKN1A)-activated kinase 2	2.72	2.35	1.30	1.98	7.82	2.77	1.12	1.49	1.61	1.13	2.30	1.71	1.91	1.42	1.96	1.73	1.62	1.54	1.08	1.31	1.18	2.45
257766	Hs.514	cyclin H	0.97	1.22	0.49	1.60	1.67	0.79	0.65	1.18	0.83	0.88	1.33	1.22	0.72	0.94	1.00	0.86	0.59	0.99	1.02	0.70	0.68	0.64
260052	Hs.14601	hematopoietic cell-specific Lyn substrate 1	1.77	3.83	3.69	1.76	4.63	2.92	1.18	2.20	2.96	2.03	3.05	3.49	1.28	1.80	2.38	2.40	1.93	1.80	1.61	1.54	1.51	2.25
262575	Hs.78006	DKFZP566A0946 protein	1.03	1.13	1.17	1.21	1.58	1.19	1.27	1.04	1.39	1.03	1.05	1.37	2.21	1.79	1.62	1.60	1.43	0.96	0.94	0.88	1.08	0.84
264606	Hs.40634	ESTs, Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "B FORM	1.05	1.47	0.72	0.98	1.32	1.45	0.78	0.85	0.98	1.26	0.81	0.71	1.03	0.72	0.73	0.55	1.08	0.89	0.94	0.85	1.65	1.36
281778	Hs.169300	transforming growth factor, beta 2	1.22	2.29	3.42	1.90	2.18	1.47	1.58	2.13	1.64	1.75	1.91	1.59	1.05	1.32	1.33	1.11	2.84	1.20	1.69	1.29	1.72	1.51
271662	Hs.155266	cell division cycle 2-like 5 (cholinesterase-related cell division controller)	0.97	0.92	0.97	1.02	1.26	1.20	1.04	1.43	1.00	1.27	1.43	0.89	0.68	0.59	0.94	0.87	1.48	0.97	1.41	0.75	1.21	1.70
272110	Hs.82143	new Ets-related factor	0.72	0.34	0.67	0.81	1.01	0.51	0.47	0.37	0.51	0.53	1.12	0.51	1.10	0.51	1.47	0.58	0.30	0.34	0.29	0.55	1.36	0.75
278409	Hs.75217	mitogen-activated protein kinase kinase 4	1.15	1.01	2.39	0.90	2.29	1.53	1.12	1.41	1.16	1.22	1.01	1.15	0.69	0.56	0.99	1.64	1.25	1.42	0.99	0.95	1.45	1.67
279482	Hs.108327	damage-specific DNA binding protein 1 (127kD)	1.90	3.81	1.15	2.26	5.91	2.04	1.22	3.39	6.01	4.01	1.93	2.87	1.17	1.53	3.50	1.61	1.00	2.45	4.89	1.50	3.88	1.44
293934	Hs.90073	chromosome segregation 1 (yeast homolog)-like	1.35	1.44	1.62	1.20	1.41	1.48	1.28	1.64	0.81	1.57	1.64	0.75	0.75	0.42	0.59	0.73	1.35	0.88	1.21	1.18	1.86	1.63
291057	Hs.4854	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.89	2.09	2.02	2.13	2.24	1.47	2.07	1.44	1.26	1.64	1.54	1.01	0.67	0.80	1.11	1.32	1.72	1.65	2.48	1.10	1.77	0.91
291736	Hs.82132	interferon regulatory factor 4	1.96	2.29	2.26	1.63	1.54	1.33	1.21	2.32	2.04	1.92	2.78	1.71	1.09	1.08	2.08	1.01	1.55	2.23	2.71	1.26	2.18	1.22
293274	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase)	1.23	2.38	4.40	2.23	4.37	2.49	1.28	2.80	4.83	2.44	2.79	1.66	0.98	1.12	1.61	2.24	1.31	2.84	2.78	1.10	2.64	2.05
299198	Hs.249217	Human CD1 R2 gene for MHC-related antigen	2.50	1.47	8.90	8.28	6.98	3.56	7.95	4.31	50.60	4.66	5.11	5.19	1.43	2.43	5.46	2.90	3.69	3.73	5.17	2.35	2.68	3.18
306134	Hs.26921	ESTs	1.20	0.77	0.66	0.87	1.46	0.88	0.26	0.79	1.25	0.77	0.67	0.46	0.26	0.69	0.44	0.73	0.60	0.98	0.49	0.78	1.20	0.56
307293	Hs.865	RAP1A, member of RAS oncogene family	1.28	1.31	1.46	1.44	1.44	1.27	0.72	1.97	1.69	1.12	1.98	1.02	0.37	0.57	0.93	1.15	0.96	0.92	0.69	0.94	0.62	1.25
299539	Hs.124752	fibroblast growth factor 12	3.04	8.68	11.26	5.63	6.82	4.23	7.00	7.00	8.00	7.20	7.11	5.47	1.83	3.16	5.73	3.58	3.47	4.33	5.23	2.69	3.98	3.47
300973	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.52	14.46	4.77	13.52	3.04	7.35	3.36	4.62	609.63	2.89	4.57	2.18	0.46	1.09	1.22	5.62	6.80	2.42	3.03	1.66	3.43	2.79
301723	Hs.214742	CDW52 antigen (CAMPATH-1 antigen)	2.35	4.93	1.83	3.63	3.29	4.60	1.67	3.12	2.96	2.95	4.57	5.09	0.48	3.10	1.90	4.26	3.48	1.82	2.03	1.82	3.51	2.38
302394	Hs.943	natural killer cell transcript 4	2.42	14.60	2.55	13.13	7.42	6.61	5.95	6.33	9.26	4.61	9.58	9.86	2.63	4.01	8.09	3.87	5.19	3.13	2.56	2.09	2.87	5.93
305455	Hs.1706	interferon-stimulated transcription factor 3, gamma (48kD)	3.71	7.03	3.02	4.34	2.87	5.18	1.70	5.03	5.30	6.89	6.10	2.58	2.81	3.93	0.72	3.43	5.18	2.04	3.48	2.91	4.62	2.08
306013	Hs.89751	membrane-spanning 4-domains, subfamily A, member 2	1.25	2.55	1.35	1.49	1.96	1.25	1.26	1.69	1.79	2.31	1.47	1.69	0.77	1.17	1.11	1.50	0.94	1.36	0.73	1.34	1.41	1.21
322604	Hs.211563	B-cell CLL/lymphoma 7A	1.57	1.68	0.95	1.29	1.73	1.50	2.03	1.82	1.14	1.54	1.32	2.34	1.43	1.27	1.96	1.78	1.49	1.75	1.72	1.93	1.79	1.51
323162	Hs.19192	cyclin-dependent kinase 2	1.12	1.07	1.54	1.19	1.39	0.63	1.29	0.71	1.09	0.88	0.98	1.05	0.58	0.72	1.11	0.64	0.66	1.38	1.44	1.19	0.55	0.58
323001	Hs.80645	interferon regulatory factor 1	1.30	0.95	0.39	1.05	0.98	0.70	0.96	0.99	0.40	0.46	0.98	0.41	0.36	0.51	0.83	0.62	0.62	1.65	0.74	0.54	0.96	0.65
310490	Hs.178658	RAD23 (S. cerevisiae) homolog B	1.84	2.28	0.90	1.35	1.58	0.85	2.57	1.54	1.68	1.80	1.15	0.76	1.00	0.85	1.48	1.31	1.01	1.46	2.46	1.49	2.35	1.53
310390	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, beta	0.78	0.85	0.72	0.57	0.50	0.48	1.10	0.58	0.60	0.52	0.46	0.63	0.42	0.48	0.65	0.49	0.64	0.72	1.13	0.68	0.73	0.58
310428	Hs.77313	cyclin-dependent kinase (CDC2-like) 10	2.64	1.69	1.26	1.45	3.68	0.96	1.65	1.88	0.69	1.17	1.06	1.71	1.09	1.35	3.49	1.71	1.02	2.26	2.29	0.76	1.84	0.94
323028	Hs.211578	MAD (mothers against decapentaplegic, Drosophila) homolog 3	1.10	1.35	1.24	1.14	0.95	0.96	1.13	0.52	1.06	0.93	0.70	1.58	1.38	1.75	1.82	3.81	1.05	1.07	0.86	1.10	0.53	0.78
327396	Hs.183418	cell division cycle 2-like 1 (PITSLRE proteins)	1.65	1.20	0.81	0.82	1.43	1.83	1.72	1.33	1.34	1.40	1.95	3.02	1.33	1.16	2.68	1.30	1.89	1.78	1.74	0.88	1.64	1.09
340644	Hs.184908	integrin, beta 8	1.80	1.14	0.96	1.10	1.93	2.24	1.23	1.08	1.02	0.76	0.96	0.79	0.51	0.54	0.53	1.23	1.37	1.44	2.16	1.08	1.35	1.95
323390	Hs.77929	excision repair cross-complementing rodent repair deficiency, complementation group 3 (x	2.22	1.94	0.91	1.29	2.97	1.94	1.47	0.93	1.10	1.23	1.48	1.00	1.17	1.07	1.04	1.60	1.41	1.35	1.40	1.07	1.30	1.56
323555	Hs.169370	FYN oncogene related to SRC, FGR, YES	0.76	1.17	1.94	2.23	2.30	1.61	1.04	1.39	1.76	1.30	1.40	1.05	0.39	1.16	0.94	1.92	1.08	1.21	0.92	1.09	0.86	0.69
323500	Hs.3280	caspase 6, apoptosis-related cysteine protease	1.70	2.24	1.43	1.46	3.64	2.20	1.49	1.29	1.53	1.09	2.73	1.53	0.93	0.94	1.91	2.13	1.66	1.75	1.90	0.83	2.89	2.26
324698	Hs.150423	cyclin-dependent kinase 9 (CDC2-related kinase)	1.89	1.54	0.67	0.88	1.57	1.60	1.37	1.11	1.41	1.96	1.25	2.54	1.10	1.70	2.19	1.75	1.61	2.09	2.86	1.26	1.27	0.86
324655	Hs.126256	interleukin 1, beta	1.39	1.45	1.28	1.24	1.50	1.72	1.09	0.54	1.75	1.08	0.97	0.77	1.23	1.10	0.88	0.91	1.31	1.52	1.16	1.46	0.74	1.04
340734	Hs.81328	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	1.41	1.17	1.39	1.18	1.06	1.29	2.17	0.48	1.13	1.55	0.50	1.14	0.89	1.28	1.25	0.74	1.28	1.32	1.66	1.39	0.48	0.88
346534	Hs.184572	cell division cycle 2, G1 to S and G2 to M	2.74	0.93	1.58	2.52	1.92	1.50	1.75	1.48	0.79	0.86	2.02	1.62	1.43	0.73	1.50	0.73	0.98	1.75	2.55	1.21	1.65	1.80
357309	Hs.320	xeroderma pigmentosum, complementation group C	0.98	0.70	1.23	1.02	1.11	1.61	0.92	2.05	3.29	2.16	2.00	1.62	0.91	1.60	0.97	1.61	1.09	1.23	1.90	1.42	0.67	0.53
357239	Hs.1608	replication protein A3 (14kD)	1.92	1.13	0.91	1.29	1.73	1.17	1.24	1.31	1.01	0.89	1.34	0.70	0.73	0.59	1.03	0.89	1.44	1.08	2.21	1.40	1.89	0.92
341130	Hs.79362	retinoblastoma-like 2 (p130)	1.31	1.12	0.89	1.07	1.02	1.03	1.24	0.88	0.74	0.78	1.22	0.47	0.55	0.61	0.79	1.00	1.02	1.34	1.49	1.80	1.08	1.01
340922	Hs.172674	nuclear factor of activated T-cells, cytoplasmic 3	0.96	1.02	1.08	0.99	0.62	0.84	0.98	0.83	0.96	0.63	0.77	0.49	0.52	0.64	0.68	0.83	0.69	1.13	0.89	1.33	0.75	0.51
340878	Hs.1852	acid phosphatase, prostate	1.12	1.01	0.70	0.77	0.82	0.74	0.96	0.88	0.93	0.65	0.80	0.49	0.44	0.55	0.72	0.91	0.80	1.43	1.16	1.65	1.07	0.69
343166	Hs.155218	E1B-55kDa-associated protein 5	1.17	2.03	1.10	1.23	1.19	0.89	1.23	1.14	0.94	1.07	0.87	0.70	0.54	0.77	0.78	1.03	1.12	0.90	0.95	1.19	0.98	0.86
343871	Hs.250870	mitogen-activated protein kinase kinase 5	1.45	1.15	0.58	1.05	1.45	1.31	0.86	0.89	1.08	1.62	0.81	0.96	0.48	0.64	0.98	1.18	1.03	1.29	1.32	1.07	1.16	1.17
344109	Hs.78996	proliferating cell nuclear antigen	1.45	0.88	0.85	0.93	0.78	1.30	1.05	0.70	0.47	0.69	0.77	0.49	0.44	0.41	0.50	1.10	0.76	0.63	1.35	1.72	1.27	0.91
345600	Hs.1087	serine/threonine kinase 2	1.62	1.39	1.85	1.91	3.40	1.18	2.89	1.23	2.23	1.31	1.19	1.35	0.78	0.90	1.55	1.61	1.31	1.73	1.31	1.56	1.45	1.71
345928	Hs.79067	MAD (mothers against decapentaplegic, Drosophila) homolog 1	1.28	1.25	0.86	1.02	1.46	1.96	1.04	1.05	1.93	2.35	1.15	1.38	0.89	1.20	1.09	1.44	1.18	1.48	1.24	1.52	0.69	0.66
357435	Hs.6289	growth factor receptor-bound protein 2	1.62	0.82	1.67	1.03	1.86	1.62	1.39	0.99	1.46	2.58	0.84	1.63	1.18	1.31	1.48	1.49	1.88	1.59	1.78	0.97	0.67	0.90
359769	Hs.90875	RAB interacting factor	0.67	0.66	0.39	0.49	0.86	0.66	0.38	0.62	0.59	0.49	0.69	1.87	0.68	0.50	0.52	0.90	0.61	1.24	0.96	0.42	0.79	0.37

360531	Hs.77183	v-raf murine sarcoma 3611 viral oncogene homolog 1	0.92	1.41	1.13	0.78	1.42	1.05	0.97	1.58	0.63	1.80	1.11	1.13	0.75	0.85	0.80	1.03	0.85	1.17	1.04	0.58	0.92	0.95
357442	Hs.82685	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	1.53	1.49	0.87	1.16	1.56	0.50	0.96	1.29	1.26	1.03	0.46	0.55	0.58	0.53	0.67	0.48	0.76	1.26	1.34	1.16	0.97	1.21
357909	Hs.154151	protein tyrosine phosphatase, receptor type, M	0.78	1.51	0.63	0.51	1.49	0.34	1.13	0.81	0.82	1.63	0.54	1.79	1.08	0.82	1.51	0.60	0.68	0.80	0.87	0.64	0.61	0.50
357807	Hs.9700	cyclin E1	0.39	0.80	0.26	0.34	0.56	0.19	0.34	0.50	0.63	0.36	0.29	0.45	0.25	0.32	0.42	0.42	0.37	0.64	0.62	0.55	0.25	0.53
358467	Hs.77572	BCL2/adenovirus E1B 19kD-interacting protein 1	0.85	1.10	1.78	1.14	1.47	1.20	2.18	2.42	1.01	2.13	0.77	1.16	0.74	1.03	1.39	0.69	1.18	1.29	1.42	1.07	0.69	0.53
358168	Hs.106127	Homo sapiens clone 25056 mRNA sequence	5.75	13.90	21.03	13.19	16.77	8.95	21.64	8.08	8.85	14.75	18.04	34.05	7.42	13.68	49.54	7.81	7.96	7.05	13.61	3.38	6.38	6.18
359171	Hs.182643	transcription elongation factor B (SIII), polypeptide 1-like	1.42	2.11	1.25	1.22	1.06	1.62	1.92	1.83	0.94	1.85	1.08	1.83	1.86	0.97	1.15	0.97	1.09	1.51	1.81	1.25	1.29	1.13
359051	Hs.2877	cadherin 3, P-cadherin (placental)	1.09	1.74	0.40	0.68	1.57	0.67	1.23	0.75	1.33	0.50	0.53	0.39	0.33	0.24	0.31	0.94	0.82	1.11	0.99	0.63	0.43	1.47
359412	Hs.75586	cyclin D2	0.52	0.23	1.67	0.64	0.91	1.35	0.69	1.37	2.08	1.53	1.75	2.17	1.36	1.62	0.86	1.72	0.87	1.13	1.26	1.02	0.49	0.70
365647	Hs.17483	CD4 antigen (p55)	5.75	5.94	2.33	1.91	4.15	3.53	17.83	3.98	2.88	3.64	6.66	18.35	10.40	3.57	10.22	2.62	7.39	5.78	6.14	3.68	1.98	2.29
366576	Hs.84665	titin immunoglobulin domain protein (myotilin)	1.12	1.01	0.58	0.86	1.84	0.73	1.08	1.19	0.94	0.94	1.17	1.94	0.49	0.56	1.27	0.89	0.81	1.19	1.44	0.84	1.26	1.01
362332	Hs.79194	cAMP responsive element binding protein 1	1.54	1.68	1.49	1.37	2.37	1.86	1.46	1.19	1.30	0.99	1.47	1.09	1.32	1.15	1.12	1.59	1.12	1.53	1.36	1.46	2.15	1.88
363799	Hs.2083	CDC-like kinase 1	0.72	0.37	0.37	0.42	0.81	0.31	0.42	0.46	0.60	0.39	0.43	0.50	0.31	0.40	0.66	0.43	0.63	2.37	1.07	0.61	0.50	0.21
364982	Hs.75216	protein tyrosine phosphatase, receptor type, F	2.51	2.57	0.69	1.02	2.21	1.41	2.70	1.75	1.19	1.50	1.60	1.16	1.12	1.29	1.22	1.46	1.62	1.63	2.06	1.51	2.63	1.26
364752	Hs.179735	ras homolog gene family, member C	0.83	0.93	1.10	0.56	0.59	0.37	0.91	1.84	1.52	1.39	2.68	0.99	0.88	1.10	1.01	1.16	0.60	0.97	0.94	0.80	0.47	0.68
364716	Hs.3248	mutS (E. coli) homolog 6	2.27	2.27	2.03	1.83	3.66	2.63	3.46	1.96	1.67	1.90	1.77	1.72	0.88	1.01	1.55	1.21	1.86	1.80	2.62	1.31	3.51	2.03
365147	Hs.173664	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma deri	1.22	1.54	0.77	0.89	1.10	1.19	1.40	2.75	2.13	1.91	3.19	1.47	1.54	1.89	2.15	4.39	1.99	1.24	2.39	3.31	4.67	0.70
366647	Hs.85155	butyrate response factor 1 (EGF-response factor 1)	3.02	2.51	3.64	2.81	1.25	2.50	4.08	1.28	1.13	1.03	1.03	1.00	1.31	2.02	1.30	1.53	1.08	0.99	2.07	1.91	1.44	1.41
380403	Hs.77273	ras homolog gene family, member A	0.99	0.86	1.10	0.88	0.93	1.07	1.21	0.93	0.91	0.55	1.08	0.53	0.72	0.43	1.11	1.21	1.16	1.40	1.05	1.37	0.81	0.80
415102	Hs.656	cell division cycle 25C	1.59	0.91	0.92	1.00	1.55	1.33	1.37	1.43	1.18	1.38	1.33	1.54	0.76	2.62	2.98	1.46	2.33	2.07	3.33	1.38	0.98	0.91
415731	Hs.86858	ribosomal protein S6 kinase, 70kD, polypeptide 1	1.63	2.11	1.02	1.62	1.61	2.52	2.08	5.20	2.17	4.38	4.40	2.90	1.21	1.58	2.62	1.95	1.94	1.49	2.21	0.85	1.49	1.31
366824	Hs.95577	cyclin-dependent kinase 4	2.98	2.84	2.73	2.44	1.73	2.19	4.10	1.29	0.93	1.12	2.01	1.06	1.06	1.04	1.20	1.64	1.72	1.33	2.51	2.00	1.74	2.22
366904	Hs.250871	non-metastatic cells 2, protein (NM23B) expressed in	1.38	1.33	0.67	1.30	0.54	0.67	1.86	1.77	0.85	0.71	1.31	1.94	0.81	1.49	0.71	1.06	0.91	1.25	2.12	1.34	0.63	0.91
375724	Hs.181243	activating transcription factor 4 (tax-responsive enhancer element B67)	0.59	0.78	0.43	0.53	0.56	0.92	1.14	0.58	0.53	0.60	0.62	0.47	0.46	0.60	0.88	1.09	0.92	1.01	1.06	1.42	0.86	0.51
375922	Hs.171834	PCTAIRE protein kinase 1	1.68	1.53	1.42	0.89	1.78	2.68	1.42	0.83	0.94	1.19	1.02	0.96	1.27	1.16	1.03	1.39	0.77	1.00	1.03	0.80	0.95	1.87
376362	Hs.149957	ribosomal protein S6 kinase, 90kD, polypeptide 1	1.05	2.08	0.95	1.33	1.87	1.77	1.36	1.20	1.91	2.81	1.84	1.71	1.65	1.12	1.41	1.65	1.32	1.57	1.77	1.24	1.86	1.79
376285	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	2.39	2.87	4.09	3.26	2.54	3.29	2.43	1.74	2.22	3.21	1.48	1.41	1.32	1.26	1.41	2.04	1.82	1.55	4.39	1.14	1.43	2.53
376649			1.22	2.08	1.89	1.19	1.65	1.08	1.40	1.50	1.53	1.26	1.18	1.03	0.81	1.11	0.94	1.59	1.19	1.85	1.53	1.16	1.13	0.84
417226	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	0.54	0.96	0.42	1.38	0.49	0.76	1.25	0.28	0.40	0.39	0.29	0.25	0.58	0.24	0.60	0.25	0.34	2.32	0.40	0.83	0.11	1.23
428248			1.12	0.77	0.49	0.85	1.56	0.54	1.03	0.46	1.56	0.39	0.73	0.74	0.25	0.52	0.63	0.50	0.91	2.07	0.48	1.39	0.40	0.36
429142	Hs.77271	protein kinase, cAMP-dependent, catalytic, alpha	2.54	1.98	1.20	1.79	1.81	1.91	2.07	1.37	1.42	1.68	1.15	1.54	1.09	1.01	1.58	1.90	1.29	1.64	1.81	1.04	1.57	1.10
417124	Hs.73722	APEX nuclease (multifunctional DNA repair enzyme)	1.37	1.01	1.03	1.04	0.89	1.03	0.95	0.94	0.95	0.77	1.11	0.44	0.66	0.77	0.72	0.90	1.02	1.21	1.23	1.71	1.18	1.64
417322	Hs.166994	FAT tumor suppressor (Drosophila) homolog	0.84	0.81	1.45	0.77	0.89	0.47	0.76	0.59	0.80	0.55	0.48	0.45	0.35	0.80	0.51	0.64	0.31	0.93	0.64	1.38	0.67	0.47
417357	Hs.171695	dual specificity phosphatase 1	0.27	0.13	0.16	0.16	0.41	0.07	0.16	0.19	0.66	0.08	0.26	0.38	0.07	0.40	0.22	0.29	0.45	1.75	0.34	0.42	0.26	0.09
417592	Hs.193852	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	0.27	0.22	0.09	0.07	0.32	0.08	0.25	0.11	0.07	0.12	0.09	0.27	0.11	0.19	0.18	0.11	0.16	0.21	0.23	0.22	0.32	0.10
470251	Hs.12503	interleukin 15 receptor, alpha	2.35	1.69	2.58	1.32	2.45	1.69	0.26	1.96	1.84	1.25	0.97	1.84	0.09	0.57	1.37	1.01	2.05	2.45	2.65	0.66	1.93	0.82
470621	Hs.184298	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	0.76	0.51	0.20	0.34	0.50	0.39	0.52	0.75	0.36	0.33	0.36	0.35	0.20	0.22	0.27	0.60	0.27	0.51	0.63	0.44	0.39	1.15
429926	Hs.75081	adenomatosis polyposis coli	0.73	0.94	0.90	1.38	1.50	0.80	0.64	1.03	1.23	0.95	0.62	0.85	0.27	0.50	0.83	0.32	0.68	1.14	1.25	0.78	0.50	0.82
469256	Hs.41714	BCL2-associated athanogene	1.10	0.58	0.25	0.69	0.79	0.72	0.65	0.68	0.94	0.36	0.39	0.32	0.34	0.34	0.63	0.56	0.56	0.74	1.03	0.69	0.41	0.44
469724	Hs.118962	far upstream element (FUSE) binding protein 1	1.24	1.42	1.10	0.79	0.87	1.18	1.16	1.24	0.89	1.06	0.98	0.51	0.32	0.44	0.77	0.84	0.86	1.14	1.05	1.14	0.94	0.86
470185	Hs.31472	transforming growth factor beta-activated kinase-binding protein 1	1.40	1.59	1.04	1.19	1.69	2.10	2.08	1.59	2.21	2.68	1.22	1.16	0.76	1.05	1.79	1.26	1.28	1.74	1.62	1.36	1.05	0.91
470196	Hs.48576	excision repair cross-complementing rodent repair deficiency, complementation group 5 (x	1.53	1.62	1.12	1.01	0.95	1.30	0.79	1.35	1.26	1.56	1.20	0.69	0.47	0.62	0.78	0.86	1.06	0.97	0.98	0.84	0.98	0.94
486161	Hs.1765	lymphocyte-specific protein tyrosine kinase	2.17	13.80	0.82	5.02	3.41	4.53	1.17	3.63	2.61	2.25	2.72	5.08	0.95	1.69	1.34	1.76	2.66	1.88	1.86	1.28	1.75	1.69
486074	Hs.3446	mitogen-activated protein kinase kinase 1	0.92	1.17	0.78	1.45	1.98	0.97	1.32	2.87	6.89	2.56	2.35	2.25	0.53	2.08	1.65	2.77	1.03	1.18	1.36	1.35	0.97	1.32
486716	Hs.861	mitogen-activated protein kinase 3	0.72	0.21	0.13	0.24	0.31	0.39	0.15	0.32	0.17	0.32	0.50	0.21	0.09	0.18	0.12	0.42	0.08	0.20	0.18	0.67	0.82	0.24
470730	Hs.740	PTK2 protein tyrosine kinase 2	0.91	3.61	1.97	0.94	2.59	1.12	1.89	1.37	0.92	1.65	1.45	0.85	1.23	0.64	1.56	1.04	0.56	1.10	1.11	1.09	1.09	1.25
470691	Hs.180455	RAD23 (S. cerevisiae) homolog A	2.01	2.15	0.98	1.34	1.87	1.83	4.49	1.48	1.25	2.25	1.32	0.96	0.94	0.87	1.32	1.34	1.00	1.12	1.62	1.30	1.93	1.32
471217	Hs.182741	TIA1 cytotoxic granule-associated RNA-binding protein-like 1	0.60	0.98	0.66	1.25	1.11	0.83	1.05	0.81	0.53	0.35	0.76	0.68	0.30	0.68	0.86	0.69	0.42	0.71	0.60	0.54	0.68	0.88
471620	Hs.76753	endoglin (Osler-Rendu-Weber syndrome 1)	1.22	0.90	1.02	1.15	2.07	0.90	1.35	1.34	1.16	1.07	1.26	1.72	0.67	0.73	1.24	1.38	0.96	1.59	1.85	1.72	1.74	0.93
471822	Hs.2340	junction plakoglobin	0.92	0.85	0.26	0.63	0.60	1.00	1.02	0.52	1.82	1.27	0.32	0.54	1.02	0.96	0.93	0.67	0.74	0.47	0.84	0.35	0.80	0.69
471918	Hs.83733	intercellular adhesion molecule 2	1.17	0.65	1.02	1.31	1.04	0.96	1.01	0.64	0.83	0.75	0.70	0.48	0.32	0.60	0.64	0.68	0.77	0.70	1.00	0.76	2.17	1.59
486510	Hs.63984	cadherin 13, H-cadherin (heart)	0.52	0.62	0.55	0.45	1.03	1.23	0.38	0.49	0.75	0.39	0.86	0.74	0.30	0.42	0.46	1.62	0.47	0.52	0.79	1.02	0.42	0.91
489194	Hs.178452	catenin (cadherin-associated protein), alpha 1 (102kD)	0.64	0.43	0.44	0.75	0.85	0.63	0.52	0.90	0.84	0.80	0.88	0.57	0.56	0.59	0.67	0.80	1.02	0.77	0.88	1.36	0.69	0.85
510130	Hs.89436	cadherin 17, LI cadherin (liver-intestine)	0.92	0.32	0.29	0.25	0.37	0.34	0.33	0.31	0.34	0.17	0.34	0.46	0.11	0.36	0.27	0.43	0.25	0.26	0.42	0.47	0.41	0.16
510258	Hs.111894	KIAA0108 gene product	2.56	1.74	0.86	1.11	1.74	0.90	2.24	1.92	1.12	1.52	1.80	2.06	1.05	0.95	3.55	1.66	2.08	2.73	3.76	1.27	1.50	1.01
487097	Hs.211595	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated pho	0.63	0.71	1.17	0.61	0.74	0.46	0.54	0.49	0.99	0.63	0.79	0.68	0.52	0.35	0.51	0.55	0.67	0.43	0.47	0.64	0.36	0.91
487777	Hs.75770	retinoblastoma 1 (including osteosarcoma)	0.82	1.20	1.31	0.88	1.42	0.94	1.49	1.27	1.09	0.92	1.03	0.89	0.58	0.59	1.25	1.00	0.84	1.56	1.69	1.35	1.15	1.53
487965	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	0.78	1.01	2.28	1.14	1.47	0.73	0.93	1.23	2.50	0.89	1.02	1.35	0.57	0.63	1.14	1.12	0.73	0.91	1.07	0.69	0.76	0.95
488891	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 homolog)	0.99	1.28	0.68	0.87	1.59	1.69	1.06	1.29	1.13	1.89	1.07	1.62	0.95	0.93	1.28	0.97	2.04	1.52	2.08	1.35	0.92	1.38
489327	Hs.85181	v-raf-1 murine leukemia viral oncogene homolog 1	1.44	1.38	1.57	1.00	1.92	1.12	1.30	1.35	0.86	1.40	1.46	1.46	0.58	0.91	0.98	1.20	1.57	1.18	1.61	0.82	0.92	1.18
489217	Hs.129548	heterogeneous nuclear ribonucleoprotein K	1.38	1.50	1.13	1.21	1.54	0.97	1.05	0.97	1.49	0.93	0.86	1.12	0.81	0.62	1.05	0.98	0.65	1.18	1.64	1.04	0.94	1.24
510467	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	1.58	1.05	0.75	1.19	1.01	1.51	1.55	0.84	1.28	0.90	0.92	1.31	0.93	0.95	1.18	1.28	1.19	1.23	1.56	1.20	0.97	0.71
124086	Hs.64310	interleukin 11 receptor, alpha	3.00	1.68	0.95	2.35	1.32	1.13	0.86	0.97	0.77	0.77	0.90	0.98	0.47	1.11	0.88	0.71	1.05	0.98	0.76	0.99	1.56	0.88
198205	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-like 2	2.73	1.83	1.50	1.88	2.10	3.61	4.49	1.61	1.17	1.82	1.85	1.66	1.71	0.84	0.73	1.32	1.76	0.98	2.03	1.53	1.55	1.87
322029	Hs.8325	mitogen-activated protein kinase 9	0.78	0.89	0.55	1.05	1.33	1.28	0.82	1.42	1.32	0.68	1.39	0.62	1.44	0.57	0.83	0.88	0.94	1.35	1.40	1.44	1.26	1.82
36809	Hs.210863	cell adhesion molecule with homology to L1CAM (close homologue of L1)	1.29	1.48	1.29	2.18	1.39	2.45	0.72	1.85	2.56	2.12	1.56	2.12	1.62	1.44	1.76	1.67	2.17	1.71	1.61	1.71	2.15	0.98
47559	Hs.73957	RAB5A, member RAS oncogene family	1.20	0.90	1.50	1.26	1.66	0.98	0.87	1.40	1.39	1.21	1.10	0.80	0.74	0.65	0.80	1.50	1.45	1.00	0.76	1.03	1.19	1.49
49576	Hs.121586	ESTs	1.40	1.79	1.56	2.62	2.18	1.97	1.41	1.85	3.28	2.52	1.43	1.65	1.21	1.18	1.41	2.37	1.55	1.38	0.78	1.20	1.51	1.76
151767	Hs.82359	tumor necrosis factor receptor superfamily, member 6	0.28	1.03	0.29	1.01	0.64	0.40	0.29	0.46	0.63	0.41	1.28	0.32	0.15	0.35	0.33	0.47	0.27	0.81	0.43	0.44	0.33	0.93
154420	Hs.170040	platelet-derived growth factor receptor-like	2.03	1.22	0.59	5.10	6.26	3.83	3.99	5.97	13.02	0.28	10.67	5.12	1.27	4.31	7.83	5.36	4.26	3.86	5.59	2.02	2.21	0.91
158970	Hs.2913	EphB3	3.06	1.72	3.30	2.41	3.45	0.74	4.09	1.57	2.14	2.54	1.11	1.71	0.85	1.09	1.42	1.19	1.30	2.01	0.82	1.10	1.20	4.14
158970	Hs.2913	EphB3	3.78	2.32	3.15	2.75	3.73	0.93	4.54	1.73	2.37	2.59	1.23	1.69	0.72	1.03	0.38	1.57	1.74	2.48	1.14	1.36	1.81	3.27
43504	Hs.724	thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene h	0.97	0.90	1.47	1.16	1.37	0.80	1.00	1.21	1.31	1.09	0.92	0.97	0.92	0.68	0.82	1.15	1.33	0.94	0.64	1.02	0.87	1.63
199381	Hs.37331	Homo sapiens vav 3 oncogene (VAV3) mRNA	3.46	1.47	1.73	2.02	2.52	3.65	1.17	5.63	7.64	6.22	8.75	3.43	2.85	3.61	4.62	3.73	5.82	3.69	4.27	2.54	2.02	1.64
241489	Hs.2551	adrenergic, beta-2-, receptor, surface	1.69	1.96	1.84	1.60	2.36	1.68	1.45	1.60	1.49	1.48	1.94	4.42	1.15	1.70	1.98	2.42	1.62	1.79	1.35	1.20	2.03	1.20
242134	Hs.155712	follistatin-like 1	1.22	1.75	0.82	1.06	2.04	1.49	0.76	1.30	1.07	2.15	1.12	1.40	0.96	1.56	1.08	1.61	1.50	1.33	1.40	0.95	0.96	1.32
213502	Hs.82212	CD53 antigen	2.60	6.53	6.21	2.98	8.88	9.90	4.08	6.52	10.11	5.09	2.11	5.22	1.86	1.32	5.22	5.26	9.02	4.54	5.16	2.70	3.81	4.38
236420	Hs.71891	discoidin domain receptor family, member 2	1.59	2.70	3.18	2.10	11.52	3.41	3.73	4.35	9.45	4.72	6.79	3.05	1.24	2.09	2.81	3.82	1.38	2.97	4.21	0.82	1.82	1.86
264576	Hs.6841	ESTs	1.49	2.21	3.51	3.72	5.00	2.29	7.03	3.60	4.37	3.85	3.62	1.75	1.10	2.04	1.78	2.33	1.89	2.38	1.82	1.49	4.77	2.95
264554	Hs.129953	Ewing sarcoma breakpoint region 1	0.88	1.10	0.98	1.31	1.08	1.56	0.85	1.12	1.49	0.58	1.45	0.90	0.95	1.95	0.90	1.65	0.95	1.20	0.93	1.06	1.18	1.42
268412	Hs.89543	MCF.2 cell line derived transforming sequence	1.30	1.85	0.62	0.85	1.74	0.84	1.19	1.93	1.58	3.10	2.04	1.51	1.28	1.03	1.72	1.46	1.70	1.48	1.83	1.14	1.64	1.04

254428	Hs.227730	integrin, alpha 6	0.74	0.37	0.26	0.65	0.57	0.15	1.10	0.22	0.29	0.15	0.15	0.32	0.31	0.37	0.32	0.24	0.21	0.81	0.45	0.81	0.30	0.48
258747	Hs.327	interleukin 10 receptor, alpha	2.33	2.28	1.81	2.48	2.66	2.05	1.60	1.57	2.05	3.13	2.26	2.07	0.91	1.82	2.33	2.26	1.33	1.43	1.80	1.51	1.41	0.48
259241	Hs.77522	major histocompatibility complex, class II, DM alpha	2.18	9.28	3.67	4.70	5.74	6.41	1.81	4.36	6.15	4.91	7.09	7.79	1.43	4.49	3.81	5.62	4.05	3.31	4.46	2.08	2.36	3.18
259291	Hs.149846	integrin, beta 5	1.30	1.39	1.06	0.77	2.87	0.99	1.13	2.12	3.64	2.62	1.68	4.01	1.56	1.67	2.89	2.48	2.06	1.69	2.62	1.38	1.82	0.65
262691	Hs.75772	nuclear receptor subfamily 3, group C, member 1	0.75	0.85	0.63	0.74	0.99	0.64	0.62	0.58	0.87	0.62	0.69	1.06	0.71	0.66	1.11	0.76	0.77	1.00	0.76	0.85	0.49	0.34
271198	Hs.75772	nuclear receptor subfamily 3, group C, member 1	0.55	0.78	0.57	0.63	0.82	0.65	0.19	0.40	0.62	0.95	0.39	0.51	0.72	0.46	0.68	0.61	0.56	1.07	0.42	0.52	0.35	1.68
290871	Hs.853	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	0.25	0.28	0.12	0.11	0.33	0.10	0.16	0.61	0.46	0.28	0.30	0.27	0.18	0.28	0.26	0.43	0.24	0.43	0.42	0.47	0.34	0.10
290724	Hs.90598	MHC class I polypeptide-related sequence A	0.47	0.84	0.35	0.62	0.78	0.63	0.50	0.83	0.81	0.84	0.63	0.93	1.27	0.95	0.97	0.91	0.65	0.68	0.44	0.53	0.77	0.57
280376	Hs.9625	putative serine-threonine protein kinase	0.98	1.52	1.01	1.12	1.32	1.08	0.82	1.70	1.72	1.69	1.10	1.26	0.95	1.06	1.08	1.70	1.19	1.40	1.25	1.25	1.69	1.32
280768	Hs.3337	transmembrane 4 superfamily member 1	3.22	1.02	0.73	2.65	2.71	3.92	1.92	0.43	2.43	0.08	0.40	0.83	0.47	2.01	1.16	0.42	0.49	0.71	0.34	0.75	0.63	2.20
284546	Hs.1447	glial fibrillary acidic protein	2.56	1.13	1.24	1.77	3.53	3.57	1.51	3.68	3.00	5.11	2.17	2.46	1.12	1.91	2.01	1.78	2.05	1.56	2.11	1.88	5.11	2.10
290493	Hs.25283	cyclin-dependent kinase 8	0.70	1.58	1.39	1.87	2.04	1.17	1.93	1.33	1.24	1.16	1.04	1.04	0.64	0.81	1.00	0.95	0.66	1.07	0.72	1.25	1.23	0.90
303109	Hs.189999	purinergic receptor (family A group 5)	1.29	1.23	3.36	1.22	4.02	1.18	1.20	1.98	2.09	1.88	1.41	2.50	1.32	1.95	2.61	1.35	1.21	2.74	3.29	1.67	0.58	1.15
306170	Hs.1244	CD9 antigen (p24)	1.01	0.63	0.41	1.11	0.81	0.90	1.72	1.20	1.21	1.23	1.08	0.64	1.16	0.77	1.41	1.38	1.33	0.99	0.78	0.69	1.07	0.70
297589	Hs.161002	absent in melanoma 1	0.83	0.73	0.72	1.21	1.17	0.82	0.77	0.48	1.10	0.77	0.49	1.42	0.74	1.68	0.93	0.64	0.80	0.58	0.58	0.93	0.56	0.70
298187	Hs.169760	BCL2-like 1	0.88	0.83	0.44	1.08	2.11	1.29	0.73	1.45	1.06	0.90	1.52	1.57	0.45	0.82	1.18	1.15	1.18	1.17	0.89	0.57	1.44	0.64
299626	Hs.250595	S-phase response (cyclin-related)	0.63	0.46	0.62	0.63	0.67	0.43	0.54	0.69	0.59	0.35	0.78	0.35	0.47	0.40	0.34	0.61	0.36	0.57	0.56	0.65	0.47	0.64
300051	Hs.75535	myosin, light polypeptide 2, regulatory, cardiac, slow	2.28	3.01	1.58	2.29	2.64	1.86	1.32	3.64	3.15	3.40	1.93	2.06	1.20	1.43	1.95	1.90	1.56	1.96	2.57	1.57	2.43	2.09
323648	Hs.84183	diptheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)	0.93	0.79	0.73	0.96	1.34	0.72	0.89	1.26	0.77	0.91	1.03	1.09	0.97	0.89	0.88	1.00	1.00	1.35	0.96	0.88	1.13	0.80
328330	Hs.89484	cadherin 4, R-cadherin (retinal)	1.85	1.29	0.59	0.76	2.73	1.25	2.06	1.55	1.31	1.47	1.63	3.06	1.02	1.23	2.86	2.36	1.31	1.84	2.37	1.04	2.12	0.70
320514	Hs.89839	EphA1	1.24	1.24	0.39	0.85	2.48	1.45	1.27	1.39	1.14	2.63	1.09	1.63	0.59	0.85	1.39	1.74	1.21	1.35	1.43	1.25	2.45	0.91
321246	Hs.156764	DKFZP586H0723 protein	0.65	0.87	1.60	1.46	1.85	1.05	0.84	0.99	1.87	0.74	1.21	0.88	0.75	0.79	0.99	1.34	1.20	0.86	1.01	1.26	1.27	0.94
321308	Hs.44585	tumor protein p53-binding protein, 2	1.75	3.18	1.28	1.31	2.83	2.27	2.42	2.00	1.62	4.71	2.91	2.16	1.14	0.88	1.56	1.63	3.24	1.54	2.80	1.21	1.94	1.76
322148	Hs.2281	chromogranin B (secretogranin 1)	2.01	1.73	0.46	1.39	1.99	2.43	0.55	0.89	1.10	0.66	0.71	1.06	0.69	1.20	1.09	1.03	0.88	1.05	0.75	0.87	2.13	1.50
323181	Hs.418	fibroblast activation protein, alpha; seprase	1.31	0.95	1.77	1.42	1.57	1.11	1.99	1.33	3.03	1.86	1.15	1.63	0.74	1.22	1.69	1.39	1.26	1.19	1.72	1.54	0.78	0.78
328467	Hs.122658	ESTs	2.92	2.31	1.26	1.71	3.10	1.63	1.76	1.27	2.05	1.29	1.27	1.83	0.63	1.14	1.02	1.45	1.29	1.16	1.32	1.19	1.53	1.23
346587	Hs.77266	quiescin Q6	0.86	1.68	0.76	0.82	2.56	0.69	0.72	2.07	1.24	1.00	1.22	4.25	1.22	0.85	1.99	1.82	1.17	1.12	1.13	0.82	2.32	1.39
346396	Hs.9651	related RAS viral (r-ras) oncogene homolog	0.85	0.77	0.44	0.50	0.81	0.81	0.88	0.29	0.36	1.95	0.33	0.42	0.43	0.46	0.77	0.34	0.65	1.27	0.90	1.10	0.68	0.76
346305	Hs.170263	tumor protein 53-binding protein, 1	1.81	1.29	0.59	1.07	1.68	1.31	1.42	1.36	1.39	1.52	1.23	0.99	0.67	0.94	1.40	1.24	1.32	1.91	2.32	1.08	1.29	2.29
341763	Hs.3257	caspase 5, apoptosis-related cysteine protease	1.08	1.34	1.50	1.04	1.83	1.09	1.32	1.60	2.38	1.35	1.55	1.77	1.09	1.24	1.98	1.63	1.35	1.34	1.61	1.33	1.37	0.92
342256	Hs.2003	T-cell receptor, beta cluster	1.93	1.82	1.80	1.64	2.44	1.59	2.19	2.28	2.27	2.19	1.76	1.48	0.76	1.16	1.41	1.43	1.32	1.81	1.04	1.71	2.24	1.48
343465	Hs.83468	gap junction protein, alpha 4, 37kD (connexin 37)	1.81	1.53	1.24	1.41	2.92	1.76	2.00	1.83	2.76	2.06	1.76	1.06	0.83	0.88	1.26	1.99	2.42	1.25	1.93	1.43	3.12	2.07
343311	Hs.1827	nerve growth factor receptor (TNFR superfamily, member 16)	1.70	2.29	2.46	1.85	3.32	1.57	1.65	1.98	2.14	1.97	1.69	1.22	1.05	0.99	1.48	1.67	2.31	2.26	3.97	1.83	3.10	1.33
343646	Hs.2969	v-ski avian sarcoma viral oncogene homolog	1.29	1.49	0.95	1.55	1.84	1.79	0.83	2.08	1.27	1.58	1.71	1.61	0.76	1.20	1.00	1.42	0.97	0.86	0.76	1.00	1.36	1.48
345645	Hs.1976	platelet-derived growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene ho	1.00	1.33	1.53	1.13	2.96	1.95	3.65	2.35	4.18	4.67	3.70	15.21	9.04	4.64	3.94	2.32	2.47	1.84	1.28	1.02	1.67	1.13
345722	Hs.150826	ESTs, Weakly similar to RAS-RELATED PROTEIN RAB-11A [H.sapiens]	1.28	1.06	1.79	2.88	1.10	1.06	2.12	0.51	1.68	1.65	0.61	1.67	1.09	1.47	1.54	0.79	1.97	1.34	2.28	1.63	1.15	1.14
347032	Hs.181309	proteasome (prosome, macropain) subunit, alpha type, 2	0.54	0.81	0.52	0.53	1.14	0.84	0.78	0.94	1.77	0.95	0.83	0.62	0.57	0.60	0.69	1.23	0.60	0.60	0.55	0.74	0.71	0.83
359465	Hs.83765	dihydrofolate reductase	2.35	1.18	0.53	1.59	0.66	1.20	1.37	1.53	1.45	1.37	1.35	0.73	0.58	0.86	0.96	0.91	1.35	2.17	1.52	2.05	0.57	0.91
359793	Hs.48145	ESTs	0.37	0.53	0.36	0.42	0.60	0.44	0.27	0.57	0.52	0.37	0.53	0.96	0.61	0.42	0.41	0.74	0.55	0.95	0.69	0.34	0.61	0.34
347751	Hs.1422	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	3.53	3.11	2.10	2.44	3.10	2.19	0.94	3.75	3.54	3.77	2.43	1.98	0.78	0.70	0.99	1.55	6.00	4.38	2.29	2.55	3.66	1.60
356890	Hs.75619	hyaluronoglucosaminidase 1	0.89	0.88	0.83	0.80	1.15	0.63	1.98	1.36	0.64	1.09	0.92	0.65	0.85	0.63	0.68	0.71	1.32	0.96	0.70	0.30	0.74	1.79
356964	Hs.146355	v-abl Abelson murine leukemia viral oncogene homolog 1	1.55	3.66	1.81	1.91	2.11	1.88	1.91	5.94	1.94	2.97	4.75	1.36	1.25	0.86	1.53	1.50	1.61	2.04	2.96	3.02	4.73	1.90
358848	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptid	1.08	1.11	1.01	0.80	1.14	0.82	0.49	1.09	0.92	0.78	0.81	0.53	0.32	0.56	0.57	0.70	0.73	0.90	0.78	1.24	1.20	0.79
359119	Hs.83758	CDC28 protein kinase 2	1.67	3.22	1.52	1.89	1.63	1.18	3.80	1.88	0.66	1.45	1.29	0.74	0.55	0.45	0.57	0.74	0.63	1.12	1.57	1.06	0.68	2.85
359077	Hs.149609	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	1.75	1.42	5.78	2.59	1.42	1.31	6.39	3.55	2.29	3.82	3.70	1.69	0.57	1.33	1.54	1.27	2.27	3.24	3.31	1.80	2.85	1.33
359466	Hs.110802	von Willebrand factor	2.70	0.78	3.77	1.44	12.02	3.98	1.65	1.25	10.10	2.85	3.92	6.85	1.08	5.71	9.33	1.73	5.05	2.11	6.68	1.75	1.63	3.83
366942	Hs.35937	myogenic factor 6 (herculin)	2.00	1.40	1.04	1.07	2.00	0.84	1.75	1.73	2.11	1.59	1.19	1.14	0.60	1.11	1.90	1.25	1.05	1.39	3.08	1.58	1.98	1.31
375620	Hs.169470	dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164,	0.77	1.01	0.41	0.57	1.04	0.43	0.85	0.72	0.58	0.43	0.62	0.66	0.18	0.51	0.71	0.64	0.46	1.16	1.87	0.88	0.53	0.27
375635	Hs.21704	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	0.97	0.69	0.38	0.41	1.05	0.90	1.47	0.60	0.90	0.44	0.53	0.62	0.70	0.53	0.72	0.66	0.59	1.37	1.00	0.44	0.98	0.80
361692	Hs.50984	sarcoma amplified sequence	1.31	1.09	1.20	1.03	2.26	1.22	1.67	2.27	2.76	2.22	2.18	1.92	1.90	1.92	2.20	0.62	2.63	2.18	1.65	1.26	1.84	1.30
363539	Hs.146580	enolase 2, (gamma, neuronal)	2.19	2.99	4.30	3.58	1.99	1.82	5.69	9.45	4.15	6.26	3.40	2.23	3.41	1.95	2.83	1.80	3.84	2.27	2.13	0.92	1.99	2.25
363805	Hs.129953	Ewing sarcoma breakpoint region 1	0.95	1.41	1.02	1.07	0.97	1.27	1.08	1.06	1.05	0.76	1.73	0.94	1.39	1.37	1.41	1.36	0.87	1.03	1.04	1.18	1.13	1.28
364975	Hs.12461	ESTs	2.81	3.41	0.99	1.52	8.82	2.87	1.95	1.98	1.72	4.49	1.42	1.42	1.08	2.25	1.89	1.35	1.72	2.29	2.32	1.64	3.44	2.41
366509	Hs.1288	actin, alpha 1, skeletal muscle	1.27	1.00	1.19	0.92	0.81	0.89	2.02	0.97	1.48	0.92	1.15	0.70	0.50	1.10	0.89	1.36	0.93	1.18	1.25	1.29	0.74	0.63
376110	Hs.76177	alpha-1-microglobulin/bikunin precursor	0.92	1.08	1.81	1.33	2.95	1.03	1.47	2.60	3.69	2.18	2.65	1.70	0.43	1.47	2.66	2.23	1.47	1.88	4.15	1.64	0.76	1.32
416184	Hs.194698	cyclin B2	1.87	1.99	1.74	1.27	1.41	1.61	1.23	1.30	1.45	0.99	1.75	1.10	0.47	0.70	1.34	1.66	0.98	0.92	1.33	1.13	1.13	1.78
376725	Hs.77899	tropomyosin 1 (alpha)	1.08	1.24	6.71	0.96	2.32	1.73	2.14	1.54	2.59	1.76	0.79	1.04	0.64	1.02	1.19	1.48	1.32	2.04	2.39	1.55	0.73	0.91
377275	Hs.82237	ataxia-telangiectasia group D-associated protein	0.94	0.12	0.11	0.26	0.44	0.16	0.43	0.14	0.13	0.07	0.12	0.12	0.05	0.15	0.13	0.13	0.13	0.27	0.19	0.14	0.15	0.07
377181	Hs.3144	Cas-Br-M (murine) ectropic retroviral transforming sequence b	1.10	1.43	0.65	0.73	0.78	1.74	1.26	1.58	0.83	1.52	0.77	1.69	0.45	0.98	1.28	1.66	1.42	1.20	1.69	1.15	1.21	0.91
415206	Hs.118836	myoglobin	1.58	1.26	1.60	1.68	1.28	1.55	2.29	1.96	1.51	1.41	2.07	0.75	1.12	1.01	1.03	1.40	1.49	1.53	1.68	1.51	1.59	1.60
417136	Hs.76228	amplified in osteosarcoma	0.94	1.17	1.61	0.94	1.73	1.05	1.05	1.46	2.21	1.65	1.92	1.40	0.75	1.20	1.31	1.75	1.54	0.94	1.30	1.09	1.44	0.84
428404	Hs.81170	pim-1 oncogene	2.12	0.88	0.60	0.86	1.82	1.06	1.06	0.78	0.98	0.50	0.80	1.48	0.42	0.64	0.81	1.18	0.77	1.85	1.04	0.87	0.90	1.29
428231	Hs.127799	apoptosis inhibitor 2	1.00	1.16	0.91	0.83	1.24	1.94	1.04	0.60	1.23	1.11	0.85	1.06	0.50	0.76	1.05	0.70	0.85	1.56	1.12	1.08	0.50	3.88
429135	Hs.119222	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-interacting protein)	1.03	0.97	0.84	0.94	1.27	1.14	0.86	0.84	0.98	0.85	0.73	0.71	0.30	0.54	0.79	1.02	0.98	1.57	1.39	1.08	0.93	2.06
418105	Hs.78305	RAB2, member RAS oncogene family	1.09	1.12	1.55	0.93	1.79	1.04	1.02	1.14	2.21	1.36	1.53	0.90	0.56	0.95	1.11	1.44	1.23	1.12	1.28	0.97	1.28	0.90
427943	Hs.171596	EphA2	0.53	0.38	0.29	0.26	0.57	0.39	0.38	0.34	0.33	0.27	0.40	0.68	0.31	0.39	0.49	0.35	0.25	0.68	0.41	0.61	0.34	0.40
427943	Hs.171596	EphA2	0.38	0.34	0.28	0.24	0.54	0.39	0.36	0.53	0.36	0.20	0.86	0.23	0.22	0.37	0.26	0.39	0.22	0.68	0.36	0.86	0.33	0.19
429539	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	1.31	1.56	0.92	1.70	2.17	2.49	3.38	2.29	1.40	0.95	1.64	1.37	0.93	0.82	1.28	1.52	1.57	1.02	1.23	0.59	2.19	2.61
471096	Hs.64639	glioma pathogenesis-related protein	0.76	0.61	2.43	1.13	1.63	1.05	0.99	1.31	2.87	2.39	0.86	1.06	0.53	0.74	0.83	1.08	1.07	1.38	1.12	0.59	0.95	0.51
429861	Hs.155421	alpha-fetoprotein	1.63	2.00	2.22	1.49	1.39	1.61	1.77	2.13	1.86	2.45	1.67	0.80	0.47	1.19	1.04	2.10	1.76	1.74	2.67	1.59	2.26	1.77
469272	Hs.77432	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene	0.72	0.52	0.57	0.83	1.03	0.84	0.67	0.62	1.83	1.66	0.44	0.36	0.28	0.39	0.37	0.68	0.46	0.62	0.39	0.18	0.84	1.92
469731	Hs.7788	ESTs	2.03	1.77	1.33	1.66	2.60	2.15	1.39	2.25	1.79	2.72	1.59	2.26	1.29	2.00	1.78	1.69	1.04	1.72	2.26	0.83	2.36	0.70
470602	Hs.110849	estrogen-related receptor alpha	0.63	0.95	0.87	0.67	0.83	0.52	0.52	1.22	1.54	1.43	0.85	0.68	0.29	1.14	0.69	1.04	0.99	1.34	1.41	1.59	1.96	0.44
470493	Hs.256278	tumor necrosis factor receptor superfamily, member 1B	1.59	1.04	1.27	1.93	1.88	2.51	7.88	2.04	2.93	2.13	2.11	1.09	0.39	0.84	0.91	1.70	1.43	0.72	1.43	0.37	1.21	1.61
470635	Hs.2894	placental growth factor, vascular endothelial growth factor-related protein	1.55	1.99	2.02	2.26	1.28	2.06	1.90	1.94	2.24	2.48	1.83	1.22	0.64	1.07	0.83	0.85	1.74	1.86	1.98	1.36	2.43	1.38
470610	Hs.83530	Homo sapiens mRNA in the region near the btk gene involved in a-gamma-globulinemia	1.60	0.69	1.19	1.11	1.28	1.06	1.48	1.21	1.92	1.37	0.73	1.02	1.03	0.82	1.19	1.20	1.49	1.41	1.81	1.26	0.82	0.85
486233	Hs.237955	RAB7, member RAS oncogene family	0.88	2.54	0.54	0.94	1.58	1.12	1.01	1.44	1.23	1.83	1.11	0.56	0.79	0.87	0.91	1.70	0.70	0.93	1.16	0.74	1.70	2.18
486086	Hs.166982	phosphatidylinositol glycan, class F	1.89	1.19	1.28	1.15	1.38	1.00	1.94	0.87	1.14	1.69	1.29	1.41	0.82	1.84	1.12	1.45	1.37	1.09	1.42	1.41	0.79	0.64
486785	Hs.81086	solute carrier family 22 (extraneuronal monoamine transporter), member 3	0.95	6.13	5.26	4.46	9.07	4.50	1.57	2.77	4.42	2.34	2.91	5.82	2.60	2.31	3.48	2.44	4.30	2.75	3.64	2.08	1.65	0.91
471715	Hs.89555	hemopoietic cell kinase	1.12	3.51	1.67	2.01	5.59	5.13	1.10	2.71	3.49	2.52	4.32	0.81	0.60	0.74	0.89	5.45	1.36	0.97	0.85	0.72	2.72	0.91
472067	Hs.151413	glia maturation factor, beta	5.04	0.38	1.72	1.19	1.51	1.07	3.16	1.61	1.04	0.30	1.11	2.39	2.34	1.93	2.58	0.77	3.16	2.62	2.57	2.15	1.85	1.23

484993	Hs.54457	CD81 antigen (target of antiproliferative antibody 1)	0.89	1.32	1.83	1.30	1.21	0.75	2.07	0.62	1.54	1.04	1.24	0.94	1.45	1.21	1.29	2.16	0.95	0.97	0.84	1.06	0.70	0.36
485690	Hs.146550	myosin, heavy polypeptide 9, non-muscle	0.96	1.87	1.92	1.26	2.39	1.56	0.95	1.99	2.43	1.81	1.38	0.53	1.10	0.66	0.93	1.88	0.59	1.22	0.47	1.23	1.99	1.81
486012	Hs.236494	ESTs, Highly similar to ras-related GTP-binding protein [H.sapiens]	0.60	1.20	0.94	1.22	0.96	1.45	1.00	0.56	1.35	0.81	0.96	0.86	1.23	0.84	0.85	1.10	0.79	0.73	0.77	0.70	0.49	0.90
486335	Hs.119000	actinin, alpha 1	1.06	3.10	1.99	1.38	2.63	1.71	1.33	1.89	1.74	1.91	1.57	1.63	1.20	1.53	1.37	1.53	1.39	1.58	1.35	1.37	2.39	2.49
486375	Hs.256309	Human beta-1D integrin mRNA, cytoplasmic domain, partial cds	1.17	1.01	1.59	0.96	1.14	0.58	1.35	0.69	0.55	0.76	0.88	2.32	0.88	1.20	1.63	0.78	1.11	1.31	1.01	1.18	0.98	0.42
486560	Hs.177543	antigen identified by monoclonal antibodies 12E7, F21 and O13	0.88	1.19	3.51	0.74	1.96	1.41	1.27	1.05	2.56	1.12	1.15	0.86	0.82	0.68	1.07	1.94	1.06	1.00	1.21	1.03	1.76	0.48
488801	Hs.44	pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	1.20	3.21	4.92	2.13	4.60	5.38	1.43	1.99	1.56	1.05	2.04	2.69	1.23	1.71	1.78	2.27	2.04	1.49	2.27	1.47	1.48	0.91
488989	Hs.16269	B-cell CLL/lymphoma 7B	1.31	1.62	0.98	1.46	1.40	2.03	0.88	1.00	1.42	1.16	1.27	1.30	0.66	1.79	0.48	1.53	0.85	1.39	1.13	1.50	1.02	0.50
489419	Hs.170133	forkhead box O1A (rhabdomyosarcoma)	1.09	0.42	0.32	0.56	0.98	0.90	0.71	0.45	0.77	0.45	1.16	4.94	2.03	3.62	4.08	0.84	5.39	1.95	2.34	1.52	0.55	0.41
486844	Hs.74471	gap junction protein, alpha 1, 43kD (connexin 43)	1.52	3.60	7.11	6.10	3.08	2.70	1.66	6.06	8.58	4.79	4.83	0.74	0.93	0.97	0.90	3.00	0.65	0.73	1.28	1.41	1.71	4.30
487417	Hs.75465	mitogen-activated protein kinase 6	1.14	0.98	0.70	0.63	1.23	1.58	0.85	0.69	1.20	0.83	2.48	0.60	0.56	0.78	0.74	2.29	0.60	0.62	0.60	1.10	1.11	0.91
487264			0.88	1.16	0.98	1.13	1.25	1.78	0.64	1.23	1.39	1.24	1.57	1.06	1.09	0.80	0.89	1.77	1.22	0.78	0.96	0.95	1.26	0.99
487386	Hs.239298	microtubule-associated protein 4	0.88	1.35	1.26	0.70	0.95	1.13	1.35	0.56	0.68	0.33	0.60	0.74	0.63	0.84	1.15	1.38	0.71	0.94	0.75	1.48	0.73	0.75
487878	Hs.111779	secreted protein, acidic, cysteine-rich (osteonectin)	1.31	12.91	17.70	7.31	5.83	4.87	2.75	7.44	6.50	6.14	13.08	2.04	0.97	1.65	2.02	6.44	2.66	2.88	3.59	1.91	4.81	6.66
488103	Hs.74561	alpha-2-macroglobulin	1.37	3.45	10.38	5.96	14.57	4.40	2.14	4.38	3.33	6.96	3.18	3.36	1.03	1.00	1.94	4.43	1.40	1.21	1.50	1.60	3.66	3.06
488596	Hs.25409	kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen	0.76	1.13	0.86	1.12	3.26	1.99	1.00	0.87	1.38	0.58	2.45	0.68	1.19	0.60	1.16	2.22	1.53	1.06	1.09	0.56	1.47	1.66
488373	Hs.82251	myosin IC	0.75	1.04	0.55	0.80	1.00	1.43	1.03	0.69	1.10	1.25	0.51	1.40	0.88	2.33	1.03	1.25	1.66	0.86	0.74	1.34	0.54	0.65
512458	Hs.103724	peripheral myelin protein 22	0.98	1.89	1.30	1.04	1.48	1.04	0.70	2.21	1.91	1.61	1.58	1.03	0.82	0.97	0.96	2.04	1.32	1.15	1.06	1.19	1.63	1.38
512472	Hs.111334	ferritin, light polypeptide	1.11	1.45	0.96	0.72	2.86	0.72	1.22	0.45	1.78	1.15	0.82	2.63	1.33	3.54	1.95	0.27	3.49	2.33	2.47	2.02	0.98	1.52
509710	Hs.78202	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	1.71	3.16	1.05	1.37	1.99	1.93	2.30	1.22	1.49	2.65	1.46	1.27	0.69	0.91	1.14	1.85	1.77	1.87	3.43	1.28	2.56	1.53
509731	Hs.84072	transmembrane 4 superfamily member 3	2.13	3.33	0.76	1.49	3.40	2.00	2.03	1.35	1.91	1.81	2.67	1.84	0.85	1.00	1.65	1.65	1.32	1.56	1.72	1.49	6.29	1.96
509820	Hs.77711	ets variant gene 4 (E1A enhancer-binding protein, E1AF)	0.90	1.91	0.61	1.68	1.99	1.85	0.65	1.40	1.50	0.80	1.35	0.59	1.05	0.79	0.97	1.39	0.90	1.30	0.67	1.24	1.78	2.34
510101	Hs.234489	lactate dehydrogenase B	0.94	0.95	0.89	0.92	1.01	1.03	1.58	0.66	1.19	1.04	1.09	1.52	0.81	0.80	1.54	1.09	1.02	1.17	0.91	1.49	0.74	0.71
510405	Hs.220529	carcinoembryonic antigen-related cell adhesion molecule 5	0.69	0.59	0.47	0.55	0.45	0.62	0.98	0.53	0.43	0.41	0.56	1.40	0.68	0.52	1.26	0.43	1.17	0.82	0.78	1.52	1.66	0.50
510595	Hs.2795	lactate dehydrogenase A	1.24	0.39	0.63	0.42	0.46	0.30	1.23	0.65	0.41	0.28	0.74	0.50	0.43	0.36	0.60	0.33	0.82	1.10	0.92	0.88	0.79	0.60
510245	Hs.57783	eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD)	0.92	1.18	0.67	1.71	1.22	1.39	0.98	1.35	1.75	1.25	1.38	0.51	0.69	0.58	0.61	1.35	0.65	0.79	0.56	0.78	1.49	0.79
512276	Hs.2064	vimentin	1.00	1.62	17.77	13.29	16.80	3.19	1.35	9.07	9.45	25.02	12.68	0.81	0.87	0.80	0.80	6.57	0.82	0.95	0.74	0.99	3.96	2.84
512244	Hs.75564	CD151 antigen	1.03	1.02	0.51	0.96	1.02	0.78	2.69	1.29	0.63	0.60	0.82	1.99	2.31	2.00	1.84	0.85	1.58	1.34	0.69	1.08	0.57	2.26
512429	Hs.162	insulin-like growth factor binding protein 2 (36kD)	1.95	0.51	0.96	0.62	1.03	0.52	0.72	0.53	0.27	0.31	0.41	2.07	1.98	1.69	2.31	0.49	1.62	1.61	1.21	0.97	0.67	0.87
135118	Hs.169946	GATA-binding protein 3	0.76	2.48	0.20	0.46	3.05	2.12	1.11	5.00	5.28	5.01	6.23	6.78	3.40	0.85	4.93	4.29	2.72	3.69	4.75	0.70	0.91	1.85
136769	Hs.1179	TATA box binding protein (TBP)-associated factor, RNA polymerase II, A, 250kD	0.43	0.95	1.06	1.23	1.64	0.88	1.22	2.46	3.19	4.13	2.68	4.29	3.66	0.93	5.00	1.69	3.33	2.74	3.55	0.89	0.34	1.37
154763	Hs.89633	promyelocytic leukemia	1.55	3.67	0.51	1.60	2.65	1.95	1.20	2.46	2.34	1.37	1.72	2.06	0.85	1.59	1.43	1.07	1.28	1.12	1.46	0.99	1.39	2.91
80549	Hs.93728	pre-B-cell leukemia transcription factor 2	1.39	1.38	1.31	0.24	2.23	0.96	2.22	1.75	1.29	0.89	0.92	1.53	1.32	1.38	1.97	1.23	1.56	1.70	2.01	1.36	2.71	1.36
129268	Hs.76362	general transcription factor IIA, 1 (37kD and 19kD subunits)	0.84	1.13	0.63	0.83	1.37	1.01	1.29	1.00	0.85	1.14	0.88	0.75	0.35	1.10	0.87	0.61	0.62	0.88	1.31	0.64	1.49	1.10
26503	Hs.101047	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.38	1.47	1.40	1.37	1.36	1.63	1.21	0.92	1.04	1.08	1.17	1.48	1.04	0.92	1.36	1.23	0.62	0.82	1.00	0.57	1.27	1.27
26599	Hs.21486	signal transducer and activator of transcription 1, 91kD	1.34	1.64	0.68	1.48	1.68	1.09	1.37	1.53	0.79	0.99	1.20	1.64	0.91	1.00	1.73	0.84	1.31	1.64	1.63	1.33	2.25	1.13
41959	Hs.2714	forkhead box G1B	0.92	1.30	0.79	0.88	1.86	1.03	1.68	0.87	1.03	1.71	1.24	2.77	1.83	1.95	3.12	1.28	1.50	1.31	1.33	1.00	0.73	0.91
162479	Hs.166096	E74-like factor 3 (ets domain transcription factor)	0.63	3.60	0.11	1.05	2.61	1.70	0.66	1.91	1.49	1.40	2.54	1.91	1.04	0.18	1.41	2.47	1.09	2.13	1.05	1.58	1.45	0.61
247869	Hs.765	GATA-binding protein 1 (globin transcription factor 1)	1.94	2.81	0.71	1.39	3.25	1.94	2.02	1.96	2.08	3.39	1.27	2.47	1.34	1.94	2.82	1.14	3.02	2.12	2.40	1.38	2.96	1.83
252185	Hs.153022	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kD	1.30	1.71	1.37	1.08	2.16	0.96	1.30	1.34	1.27	2.04	0.96	2.05	1.23	0.93	1.24	0.64	1.89	1.13	2.05	0.70	0.80	0.91
256323	Hs.142258	signal transducer and activator of transcription 3 (acute-phase response factor)	0.46	0.78	0.33	0.41	0.82	0.85	1.02	0.61	0.50	0.42	0.63	0.49	0.29	0.44	0.74	0.65	0.41	1.02	0.96	0.58	0.66	0.62
50576	Hs.180677	zinc finger protein 162	1.57	2.34	1.04	1.49	2.40	1.97	1.24	1.49	1.61	1.09	1.87	1.87	2.14	1.61	2.03	1.92	1.49	1.91	1.37	1.10	1.94	1.36
52681	Hs.858	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light p	2.14	2.20	0.79	0.91	1.81	0.76	3.05	1.24	1.47	1.07	1.98	3.75	2.44	2.27	2.66	1.87	3.36	2.04	3.40	0.93	1.24	0.93
190107	Hs.6975	histone deacetylase 3	1.51	2.51	1.29	0.95	2.66	1.46	1.25	1.52	1.58	1.26	0.85	1.70	0.85	0.55	1.87	1.19	1.90	1.84	2.36	1.40	1.82	1.80
192694	Hs.182237	POU domain, class 2, transcription factor 1	1.53	0.92	1.20	1.04	1.21	1.30	1.40	1.18	1.68	1.91	0.92	2.54	0.96	1.64	1.77	0.60	1.43	1.28	2.33	0.90	0.72	0.98
193901	Hs.1179	TATA box binding protein (TBP)-associated factor, RNA polymerase II, A, 250kD	1.62	1.96	0.81	1.24	3.58	2.84	1.97	1.86	2.21	2.63	2.02	1.87	1.11	1.41	2.26	2.37	1.89	2.49	2.37	1.48	2.93	0.91
209310	Hs.75569	v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light	0.84	0.81	0.89	1.03	1.15	0.86	1.61	1.05	1.01	0.79	0.65	1.87	1.11	0.81	1.21	0.86	1.17	1.05	1.04	0.81	0.60	0.57
222502	Hs.33102	transcription factor AP-2 beta (activating enhancer-binding protein 2 beta)	1.26	1.57	0.92	0.96	2.26	5.59	1.12	1.50	1.15	1.12	2.48	1.35	0.96	0.70	1.63	1.22	1.37	1.37	1.65	0.88	1.41	2.21
257458	Hs.78869	transcription elongation factor A (SII), 1	1.26	0.77	1.14	1.07	1.55	0.92	1.27	0.86	1.10	1.13	0.87	0.57	0.74	0.56	0.80	0.94	1.22	1.85	1.26	1.33	1.17	0.72
288650	Hs.234898	ESTs	1.32	1.36	1.14	1.54	1.66	2.26	1.79	1.40	3.40	2.35	1.65	2.10	1.01	1.73	1.88	1.78	3.13	1.50	1.26	1.06	1.01	1.63
290117	Hs.270	pleckstrin homology, Sec7, and coiled-coil domains protein-binding protein	1.67	3.98	1.07	4.49	5.99	6.54	2.02	4.48	2.38	1.93	7.39	2.79	1.06	2.01	1.48	3.94	4.30	2.85	2.41	0.90	3.90	2.53
260288	Hs.155005	TEA domain family member 1 (SV40 transcriptional enhancer factor)	3.42	3.64	4.03	3.63	8.49	2.43	5.36	7.68	7.36	7.14	11.51	2.30	3.30	1.03	1.97	3.91	3.88	3.48	5.52	2.11	4.47	3.57
264200	Hs.167503	signal transducer and activator of transcription 5A	0.95	0.83	1.05	0.35	1.57	1.25	2.82	0.50	1.54	2.74	1.49	2.14	1.28	1.16	1.42	0.81	0.97	1.79	1.39	1.34	0.65	0.91
271416	Hs.2021	Sp1 transcription factor	1.40	1.50	0.65	1.26	1.70	1.74	0.71	1.20	1.38	1.17	1.06	1.19	1.15	1.11	1.29	1.26	1.24	2.06	0.98	1.42	1.33	1.60
272110	Hs.82143	new Ets-related factor	0.84	0.57	0.67	0.44	0.68	0.52	0.40	0.34	0.52	0.98	0.32	0.84	0.31	0.37	0.43	0.27	0.34	0.47	0.35	0.96	0.56	0.33
280465	Hs.257325	ESTs	2.97	2.11	1.83	1.68	2.37	1.58	1.35	1.03	1.73	2.81	0.74	2.20	1.72	1.02	1.21	1.02	1.28	1.92	4.92	1.02	1.05	1.85
280735	Hs.1100	TATA box binding protein	1.56	2.32	1.48	1.34	1.72	1.77	1.81	1.84	1.10	1.85	1.95	1.23	0.89	0.55	1.10	0.95	1.55	1.35	2.14	1.34	2.13	1.85
282065	Hs.3763	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	1.40	1.05	0.91	1.15	2.55	1.62	0.97	1.44	2.27	2.89	1.36	1.69	0.87	1.13	1.77	1.31	2.81	1.56	2.39	1.13	1.18	0.58
291943	Hs.58593	general transcription factor IIF, polypeptide 2 (30kD subunit)	0.66	0.60	0.80	0.80	1.03	0.54	0.51	0.59	0.68	2.00	0.40	0.39	0.23	0.26	0.44	0.38	0.40	0.62	0.67	0.58	0.67	0.61
320538	Hs.97496	YY1 transcription factor	1.39	1.85	1.42	1.93	1.98	1.29	1.44	2.11	1.28	1.47	1.71	1.15	0.76	0.70	1.12	1.78	0.96	1.24	1.51	0.90	1.43	1.59
322000	Hs.154365	E74-like factor 1 (ets domain transcription factor)	0.96	0.81	1.13	1.19	0.97	1.15	1.14	1.33	1.63	1.02	0.34	3.25	1.94	3.14	3.67	0.64	1.21	0.99	0.93	0.24	0.31	1.41
327111	Hs.152292	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	2.21	2.68	8.73	5.09	2.68	1.89	3.52	4.98	6.74	10.53	2.96	1.19	3.38	1.22	1.96	1.45	7.15	3.33	3.10	2.44	2.72	0.91
293032	Hs.18387	transcription factor AP-2 alpha (activating enhancer-binding protein 2 alpha)	1.58	1.10	0.58	1.45	2.05	1.49	1.45	1.65	2.01	1.54	0.97	0.84	0.76	0.68	0.93	1.47	1.14	1.39	1.13	1.29	1.49	1.72
295093	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 related)	1.64	1.01	2.17	1.06	0.82	1.47	3.82	1.46	1.50	2.38	1.11	0.82	1.30	0.91	0.78	1.06	1.70	1.29	1.22	1.82	1.05	0.98
300071	Hs.197764	thyroid transcription factor 1	0.78	1.09	1.93	1.58	0.96	0.71	0.85	1.28	0.63	2.56	0.43	1.94	0.69	0.51	0.98	0.66	0.95	1.20	1.17	0.86	1.07	0.59
300960	Hs.14543	ESTs	2.17	1.17	1.81	1.45	1.45	1.73	1.63	1.56	1.99	1.49	1.30	1.28	0.74	0.80	1.13	1.30	1.44	1.46	1.63	1.62	1.53	1.60
304947	Hs.89633	promyelocytic leukemia	1.41	1.50	1.70	1.10	1.61	1.39	0.98	1.65	1.93	1.67	1.00	1.14	0.96	0.83	1.15	1.19	1.45	1.41	1.45	1.11	1.09	1.29
305455	Hs.1706	interferon-stimulated transcription factor 3, gamma (48kD)	3.74	5.96	2.14	3.29	2.37	4.93	2.91	3.86	4.57	5.54	4.52	4.17	6.51	6.04	7.87	4.67	5.43	2.72	3.36	2.42	3.43	2.22
309924	Hs.3352	histone deacetylase 2	0.76	1.47	1.17	1.95	2.07	2.58	1.27	1.28	1.06	0.79	0.88	0.71	0.33	0.82	0.68	0.77	1.12	0.55	0.50	0.72	2.33	1.35
361401	Hs.89578	general transcription factor IIH, polypeptide 1 (62kD subunit)	1.50	1.68	0.48	0.57	2.47	1.52	1.56	3.40	2.72	2.95	2.39	1.74	0.78	0.66	1.13	2.11	1.29	1.17	1.64	1.13	1.61	1.85
361815	Hs.15740	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	0.60	0.56	0.69	0.81	0.78	0.27	0.52	0.54	1.22	0.58	0.60	1.52	1.49	0.75	1.26	1.19	0.35	1.35	0.76	0.54	0.58	0.56
366981	Hs.154970	transcription factor CP2	1.32	2.25	0.77	1.25	2.58	0.94	1.46	1.82	1.65	1.70	0.68	2.10	0.54	1.33	1.74	0.66	1.73	1.35	1.98	1.14	1.75	1.98
344769	Hs.181368	U5 snRNP-specific protein (220 kD), ortholog of S. cerevisiae Prp8p	1.31	2.29	0.89	1.31	1.91	1.32	1.92	2.96	1.70	2.71	1.65	1.50	1.19	1.08	1.78	1.16	1.57	1.41	1.71	1.07	2.30	1.53
345527	Hs.96028	forkhead box D1	1.83	1.01	1.59	0.85	0.65	0.90	1.03	0.58	1.25	1.40	0.51	0.55	0.39	0.61	0.57	0.48	0.80	0.85	0.70	0.86	0.41	0.62
347573	Hs.64904	ADP-ribosylation factor-related protein 1	1.68	0.90	0.92	0.50	1.65	1.17	0.76	1.24	1.68	2.37	0.99	1.57	0.69	0.69	1.19	1.03	1.95	1.48	0.62	0.63	1.83	0.68
347685	Hs.179881	core-binding factor, beta subunit	1.91	1.02	1.08	1.23	1.15	0.98	1.01	0.89	1.51	0.96	0.70	0.96	0.38	0.81	0.77	0.96	1.00	0.96	1.64	1.12	0.91	0.96
357357	Hs.75133	transcription factor 6-like 1 (mitochondrial transcription factor 1-like)	1.70	2.34	0.65	0.90	2.24	1.39	2.06	1.30	1.41	1.59	1.23	1.11	0.76	0.66	1.46	0.84	1.89	1.89	2.45	0.91	1.88	0.91
358677	Hs.77100	general transcription factor IIE, polypeptide 2 (beta subunit, 34kD)	0.92	1.57	1.11	1.17	1.04	0.58	1.54	0.67	1.04	1.06	0.89	0.71	0.29	0.56	0.70	0.93	0.61	0.96	0.90	0.87	0.80	0.63
358538	Hs.737	immediate early protein	0.97	0.97	0.76	0.55	1.93	0.78	0.84	1.16	1.05	0.96	1.19	0.56	0.86	0.52	1.29	0.52	0.97	1.50	1.27	0.60	1.33	0.97
375635	Hs.21704	transcription factor 12 (HTF4, helix-loop-helix transcription factors 4)	0.83	0.94	0.55	0.67	0.91	3.49	1.04	0.54	0.83	0.55	0.38	0.96	0.63	0.64	0.70	0.58	0.53	0.82	0.98	0.55	0.30	0.43
418320	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (from clone DKFZp434E082)	1.66	1.56	0.48	0.94	1.35	2.24	1.06	1.36	1.13	1.07	1.03	1.12	0.85	0.83	1.01	1.83	1.68	1.70	2.22	1.31	1.54	1.81

428248			0.85	0.92	0.49	0.81	1.63	0.50	0.61	0.43	1.53	0.47	0.75	1.15	0.34	0.73	0.67	0.92	0.97	1.67	0.38	0.75	0.47	0.46
470792	Hs.258561	general transcription factor IIB	2.10	2.06	1.84	1.48	2.18	1.65	2.34	1.77	1.77	1.47	0.93	1.41	0.81	1.22	1.59	1.49	1.54	1.93	2.38	0.94	1.90	1.98
375724	Hs.181243	activating transcription factor 4 (tax-responsive enhancer element B67)	0.47	0.78	0.47	0.55	0.70	0.71	1.01	0.78	0.63	0.65	0.51	0.74	0.35	0.59	0.87	1.15	0.82	1.03	0.90	1.24	1.07	0.56
375843	Hs.168157	nuclear transcription factor Y, gamma	1.71	1.01	1.09	1.13	1.47	2.19	1.26	0.58	1.12	1.01	0.91	1.28	0.61	1.18	1.11	0.98	1.20	1.49	1.40	1.30	0.58	0.76
376294	Hs.57419	transcriptional repressor	1.58	2.08	1.13	1.19	2.49	1.53	1.47	1.46	1.93	1.82	1.93	1.22	0.49	0.52	1.08	1.94	1.79	1.47	3.13	1.04	1.52	1.59
376218	Hs.89633	promyelocytic leukemia	0.97	1.97	1.39	1.73	1.78	1.71	1.79	1.86	1.70	1.60	1.36	3.01	1.13	2.03	1.92	1.70	1.53	1.28	2.35	1.30	0.95	1.90
380738	Hs.75356	transcription factor 4	1.07	0.84	1.18	1.91	2.27	2.25	1.54	2.67	4.31	1.56	1.93	2.57	1.40	1.90	2.68	1.88	1.42	2.92	2.94	1.50	1.32	1.58
381219	Hs.505	ISL1 transcription factor, LIM/homeodomain, (islet-1)	0.60	0.96	0.39	0.62	1.22	0.77	0.98	0.90	0.66	0.73	1.14	0.73	0.40	0.34	1.07	0.81	1.23	1.33	2.03	0.39	0.85	1.57
417127	Hs.184771	nuclear factor I/C (CCAAT-binding transcription factor)	2.18	2.75	1.58	1.69	2.12	2.03	1.35	1.47	2.26	1.98	1.13	1.38	0.96	0.97	1.09	2.02	1.94	2.09	2.89	1.72	1.05	0.91
471218	Hs.232068	transcription factor 8 (represses interleukin 2 expression)	1.32	1.45	0.79	0.79	1.23	1.91	0.96	0.79	0.96	1.10	0.74	0.68	0.64	0.82	1.28	0.61	1.02	0.95	1.21	1.52	0.45	1.04
488904	Hs.79058	suppressor of Ty (S.cerevisiae) 4 homolog 1	1.79	1.84	1.01	1.60	1.45	1.27	1.77	5.04	1.90	3.38	3.97	2.16	1.47	1.59	2.66	1.53	1.75	1.29	1.67	1.02	1.54	1.40
509710	Hs.78202	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a,	0.83	2.40	0.95	1.35	1.37	1.75	1.69	1.23	1.45	1.99	1.01	1.60	0.87	1.12	1.30	1.62	1.26	0.79	1.40	1.30	1.29	1.52
509682	Hs.6975	histone deacetylase 3	0.75	0.90	0.95	0.91	1.83	0.72	1.11	1.44	1.85	1.58	1.08	5.43	1.61	2.70	7.78	1.81	1.53	2.32	3.91	2.23	1.21	0.98
471889	Hs.144630	nuclear receptor subfamily 2, group F, member 1	1.00	1.04	0.69	0.62	1.11	0.83	1.11	0.69	1.04	0.63	0.83	1.23	0.62	0.77	1.69	0.79	0.91	1.34	1.26	1.34	0.80	0.60
485192	Hs.74313	ESTs	2.30	2.94	1.23	2.29	2.54	1.72	2.90	2.27	1.83	1.72	1.68	2.16	0.83	1.17	1.98	1.88	1.98	2.01	4.00	1.57	2.31	1.79
486410	Hs.97496	YY1 transcription factor	1.45	1.82	0.66	1.16	1.78	1.23	1.81	1.12	1.09	0.76	1.01	1.14	0.62	0.80	0.63	1.49	1.21	1.42	1.04	1.21	1.13	2.02
487982	Hs.101025	basic transcription factor 3	0.60	0.38	0.39	0.49	0.58	0.48	0.92	0.73	0.60	0.50	0.62	0.57	0.38	0.52	0.81	0.58	0.50	1.13	1.37	0.71	0.44	0.52
488092	Hs.8383	bromodomain adjacent to zinc finger domain, 2B	2.06	1.24	1.20	1.73	2.59	1.48	1.07	2.61	4.61	2.01	2.02	4.86	1.00	2.67	3.72	2.15	3.48	3.15	2.30	2.16	2.23	1.28
488658	Hs.80598	transcription elongation factor A (SII), 2	0.67	1.36	1.14	0.63	1.12	0.68	1.04	0.93	1.03	1.31	0.65	1.64	0.93	0.78	1.02	0.79	1.43	0.74	1.30	0.81	0.57	0.45
509588	Hs.82037	TATA box binding protein (TBP)-associated factor, RNA polymerase II, J, 20kD	1.10	0.67	0.91	0.74	0.53	0.90	0.73	0.99	0.66	0.53	0.66	0.63	0.42	0.50	0.81	0.66	0.73	1.00	1.12	0.70	0.61	0.90
241412	Hs.154365	E74-like factor 1 (ets domain transcription factor)	1.06	1.44	0.64	1.02	1.13	1.33	1.44	1.31	1.20	1.34	0.90	0.91	0.48	0.74	0.87	1.02	1.16	1.45	1.56	1.31	1.00	0.91
248258	Hs.94100	EST	0.81	0.87	0.67	1.09	0.73	0.93	1.05	0.93	1.33	0.80	1.72	1.65	0.86	1.22	1.69	0.84	1.04	1.17	1.15	0.47	0.27	0.26
510381	Hs.4055	core promoter element binding protein	0.71	0.73	0.47	0.53	0.54	0.57	1.18	0.51	0.84	0.35	0.34	0.53	0.22	0.33	0.56	0.40	0.57	1.34	0.63	0.73	0.41	0.70
125555	Hs.181243	activating transcription factor 4 (tax-responsive enhancer element B67)	0.82	0.82	0.47	0.53	0.60	0.63	1.16	0.59	0.85	0.57	0.29	0.51	0.24	0.37	0.58	0.28	0.63	1.21	0.83	0.87	0.27	0.77
194384	Hs.101025	basic transcription factor 3	0.98	0.55	0.47	0.60	0.79	0.67	1.18	0.43	1.15	1.13	0.18	0.74	0.31	0.56	0.70	0.17	0.93	1.55	1.34	0.93	0.30	0.91
203184	Hs.163933	ESTs	0.62	0.68	0.67	0.77	0.53	0.82	1.02	0.73	1.52	0.67	0.17	0.64	0.62	0.55	0.80	0.18	0.75	1.07	0.92	0.60	0.23	0.91
22040	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase)	1.23	0.59	1.27	1.30	1.55	1.21	1.04	1.42	1.72	1.30	1.00	1.61	1.31	0.78	1.39	1.18	1.36	1.16	0.87	0.93	1.43	1.33
22230	Hs.146428	collagen, type V, alpha 1	1.84	1.47	1.97	2.03	1.97	1.33	2.59	1.30	1.39	1.67	1.09	1.26	0.88	1.22	1.62	1.54	1.13	0.99	1.10	1.10	1.21	1.64
22260	Hs.697	cytochrome c-1	0.41	0.67	0.62	0.40	1.14	0.75	0.64	0.54	0.61	0.36	1.18	1.73	0.62	1.04	0.36	0.53	0.31	0.32	0.38	0.42	1.01	1.50
21652	Hs.178452	catenin (cadherin-associated protein), alpha 1 (102kD)	0.13	0.25	0.20	0.37	0.42	0.44	0.37	0.53	0.65	0.32	0.68	0.41	0.67	0.76	0.60	0.72	0.53	0.37	0.49	0.38	0.35	0.66
21656	Hs.155188	TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 55kD	1.21	0.75	1.64	0.87	1.59	0.99	1.35	0.89	1.11	1.08	0.93	1.32	1.37	1.32	1.60	0.56	1.30	1.54	1.03	1.80	2.65	1.53
22012	Hs.119177	ADP-ribosylation factor 3	1.16	1.70	0.84	1.30	1.53	0.55	0.76	0.50	0.73	1.61	0.77	1.04	0.42	0.99	1.00	0.69	0.44	1.06	1.30	0.95	0.71	1.30
21810	Hs.177766	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase)	2.58	1.79	3.37	3.50	2.91	1.82	2.72	1.98	2.08	2.65	1.88	0.90	2.05	1.25	1.73	1.34	2.07	1.89	3.65	1.63	2.73	3.80
22611	Hs.82285	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phos	1.99	1.57	1.72	2.19	2.51	2.09	1.49	1.46	1.76	1.45	1.47	1.54	1.08	2.17	1.25	1.85	1.12	1.13	1.19	1.40	1.61	2.61
22798	Hs.184167	splicing factor, arginine/serine-rich 7 (35kD)	1.55	5.97	2.31	2.65	3.47	2.09	1.88	1.57	2.15	1.83	2.13	2.21	1.55	2.18	1.78	1.68	1.76	1.37	2.09	1.14	2.15	1.75
22379	Hs.119663	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16, EJ30, E	0.44	0.39	0.45	0.34	0.82	0.17	0.50	0.22	0.49	0.18	0.49	0.45	0.25	0.35	0.30	0.41	0.45	0.61	0.44	0.44	0.27	0.47
22493	Hs.91379	ribosomal protein L26	1.28	2.46	1.31	1.64	2.39	1.28	2.17	1.15	2.14	3.88	1.50	3.25	2.26	1.35	1.96	2.94	1.82	1.07	1.25	0.67	1.95	1.86
22568	Hs.75465	mitogen-activated protein kinase 6	1.07	1.07	1.01	1.50	1.41	1.18	1.22	0.83	1.15	0.75	1.12	0.80	0.55	1.15	0.82	0.97	0.63	1.09	1.13	1.07	0.94	1.34
22589	Hs.79356	Lysosomal-associated multispanning membrane protein-5	3.54	20.08	15.87	10.03	9.07	8.17	7.01	8.09	10.02	10.33	8.92	14.48	6.01	6.92	10.76	5.57	6.20	4.60	10.06	3.45	5.07	7.27
22589	Hs.79356	Lysosomal-associated multispanning membrane protein-5	3.69	16.10	9.71	3.72	15.06	8.79	4.77	6.96	10.74	9.82	10.87	22.56	7.55	9.36	12.70	7.37	5.97	2.16	9.81	2.86	5.18	3.66
23014	Hs.66151	mitogen-activated protein kinase 1	1.07	1.27	1.32	1.46	1.39	1.16	1.15	0.62	1.26	0.66	0.91	0.60	0.93	0.91	0.75	1.18	1.01	1.31	0.62	1.29	1.02	1.11
23831	Hs.155247	aldolase C, fructose-bisphosphate	0.63	1.57	1.05	0.77	0.95	1.45	0.62	1.06	0.95	0.97	1.92	0.71	1.06	0.79	0.65	1.02	0.76	0.72	0.56	0.79	1.77	0.99
23866	Hs.95577	cyclin-dependent kinase 4	1.77	2.02	2.00	1.73	1.88	1.62	3.18	2.04	1.59	1.92	1.10	0.96	1.44	1.27	1.24	1.48	1.34	1.57	1.40	1.48	2.27	2.60
23019	Hs.113368	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1	1.17	1.69	1.76	1.32	1.33	1.17	1.13	0.88	1.06	1.00	1.20	1.41	1.44	0.87	0.86	1.12	1.53	1.23	0.98	1.30	0.97	1.03
23073	Hs.56066	fibroblast growth factor 2 (basic)	0.68	0.72	0.78	0.69	1.63	0.46	0.73	0.60	0.75	0.47	0.66	0.53	0.36	0.55	0.58	0.73	0.57	0.89	0.84	0.96	0.37	0.46
23185	Hs.204133	hexabrachion (tenascin C, cytotactin)	3.20	1.68	2.92	3.06	6.76	5.94	3.03	5.76	8.60	2.52	4.06	3.40	1.28	3.87	3.39	4.26	1.58	4.96	6.93	1.92	2.00	2.71
23332	Hs.75437	putative protein	1.23	2.22	1.38	1.59	2.26	1.89	1.48	1.99	2.74	1.47	2.21	1.09	0.89	1.13	1.41	2.00	1.29	1.94	1.72	1.95	2.04	1.69
23346	Hs.111779	secreted protein, acidic, cysteine-rich (osteonectin)	5.65	22.33	8.51	14.47	19.25	10.41	18.27	4.78	3.78	13.89	21.72	32.70	18.12	5.20	22.78	8.59	4.94	5.95	8.39	3.70	6.72	5.90
23692	Hs.77183	v-raf murine sarcoma 3611 viral oncogene homolog 1	1.40	2.24	1.49	1.50	2.82	2.09	1.15	2.23	2.03	2.06	2.53	1.33	1.68	1.25	1.84	1.97	1.18	1.73	1.74	1.12	2.51	2.60
23731	Hs.83920	peptidylglycine alpha-amidating monooxygenase	0.52	0.78	0.71	0.65	1.33	0.28	0.51	0.84	1.72	0.37	0.79	0.95	0.37	0.67	0.69	0.92	0.39	0.50	0.48	0.58	0.55	1.28
24110	Hs.256278	tumor necrosis factor receptor superfamily, member 1B	1.63	1.37	1.31	1.41	1.00	1.18	0.68	0.95	1.40	0.89	0.99	0.96	0.74	1.47	0.90	1.28	1.07	1.40	1.01	1.19	1.83	2.24
24886	Hs.31551	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related	1.11	1.12	1.73	1.47	2.17	1.04	0.79	1.61	2.04	1.04	1.14	0.92	0.44	1.27	1.17	1.24	1.10	1.48	1.18	1.19	1.64	1.58
24899	Hs.76111	dystroglycan 1 (dystrophin-associated glycoprotein 1)	0.83	0.88	0.47	0.54	1.18	1.25	1.29	0.98	0.66	0.49	1.03	0.57	1.11	0.52	0.92	0.91	0.61	0.64	0.64	0.52	0.42	0.84
24927	Hs.77602	damage-specific DNA binding protein 2 (48kD)	1.17	0.97	0.94	0.95	1.06	0.85	0.97	1.12	0.96	0.98	0.90	0.68	0.74	0.69	0.77	0.85	0.89	1.16	1.09	0.77	1.55	1.19
24145	Hs.104125	adenylyl cyclase-associated protein	1.05	0.64	1.50	0.98	1.18	1.23	0.59	0.92	1.61	0.98	0.89	0.79	0.53	0.97	0.94	1.58	0.95	0.74	0.74	1.00	1.52	0.91
24269	Hs.183037	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)	0.96	1.36	1.39	1.01	0.72	1.07	0.50	0.93	1.64	1.08	1.09	0.67	2.75	1.29	1.00	1.59	1.25	1.34	0.53	1.36	0.79	1.02
24392	Hs.243960	HLA-B associated transcript-3	0.98	1.01	0.94	0.93	1.56	0.90	0.97	1.28	1.48	0.78	1.07	0.74	0.89	0.73	0.86	1.20	1.20	1.40	1.31	0.66	1.10	1.02
24588	Hs.242985	hemoglobin, gamma G	1.41	2.15	1.43	1.57	1.84	1.41	1.06	2.04	4.61	2.64	1.68	1.32	1.12	1.13	1.37	2.39	1.37	1.81	1.81	1.43	0.89	1.44
24638	Hs.865	RAP1A, member of RAS oncogene family	1.40	1.01	1.71	1.35	1.20	1.15	0.85	1.59	2.09	1.09	1.82	1.02	0.40	0.85	1.11	1.22	1.05	1.61	1.17	1.45	0.60	1.17
24642	Hs.174185	phosphodiesterase I/nucleotide pyrophosphatase 2 (autotaxin)	1.36	5.00	12.65	4.09	4.63	3.26	1.47	3.27	4.01	2.51	2.91	1.31	0.67	1.16	1.94	2.20	1.81	3.36	2.89	1.77	2.69	1.93
24652	Hs.85289	CD34 antigen	1.52	3.22	3.72	4.64	6.54	2.57	1.99	2.93	8.98	4.95	3.08	4.44	3.14	3.85	6.34	3.43	3.82	2.92	2.43	2.75	1.92	2.37
25169	Hs.234279	microtubule-associated protein, RP/EB family, member 1	1.13	0.78	1.06	0.99	1.14	0.95	1.11	0.92	1.01	0.89	0.95	0.71	1.13	1.01	0.90	1.20	1.14	0.89	0.85	1.29	1.44	1.09
25400	Hs.75356	transcription factor 4	1.39	1.32	1.08	2.87	3.49	2.18	1.30	3.16	4.27	2.08	3.84	4.04	1.37	1.99	3.19	2.11	1.71	2.91	2.73	1.85	1.80	1.48
25495	Hs.75935	KIAA0077 protein	1.64	1.36	2.38	2.60	2.38	1.53	1.43	1.40	1.61	1.09	1.17	1.87	0.99	2.11	2.37	0.82	1.47	1.72	1.53	1.57	2.13	2.29
25517	Hs.78885	biotinidase	1.58	1.39	1.19	1.47	1.93	1.31	1.45	1.15	1.50	1.99	1.20	1.15	0.95	1.26	1.64	1.86	1.30	1.23	1.20	0.93	1.10	1.37
25584	Hs.173554	ubiquinol-cytochrome c reductase core protein II	0.42	0.22	0.49	0.62	0.47	0.33	0.52	0.43	0.36	0.24	0.36	0.28	0.43	0.59	0.41	0.44	0.41	0.84	0.49	0.58	0.48	0.53
25725	Hs.48876	farnesyl-diphosphate farnesyltransferase 1	0.41	0.37	0.29	0.66	0.52	0.60	0.52	0.37	0.41	0.24	0.40	0.31	0.35	0.60	0.47	0.50	0.41	0.52	0.56	0.88	0.90	0.38
26082	Hs.73729	very low density lipoprotein receptor	1.25	1.95	1.12	1.61	2.04	1.58	1.58	1.15	1.09	0.80	1.09	0.77	0.69	1.32	0.94	1.27	0.97	1.05	1.01	1.06	0.92	0.94
26531	Hs.78869	transcription elongation factor A (SII), 1	1.25	1.16	1.04	1.33	1.35	0.94	1.26	0.98	0.94	0.82	1.37	0.59	0.58	0.95	0.73	0.98	1.06	1.57	1.07	1.21	1.63	1.18
26541	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like 1	1.35	1.65	1.35	1.38	1.67	1.85	2.65	1.17	0.76	1.03	2.41	0.67	0.82	0.65	0.80	1.09	0.71	0.65	1.28	1.49	1.78	2.53
26572	Hs.75607	myristoylated alanine-rich protein kinase C substrate (MARCKS, 80K-L)	1.32	3.11	3.91	2.64	4.08	2.08	1.61	2.17	3.36	2.55	2.42	2.11	0.62	3.28	2.71	2.34	2.32	1.49	2.03	2.08	3.78	2.36
26087	Hs.77490	glutathione S-transferase theta 1	1.76	5.34	1.71	2.14	2.77	2.56	1.35	1.63	3.18	2.01	2.10	0.77	0.65	0.62	0.97	2.37	1.24	1.55	1.45	1.17	2.21	2.42
26129	Hs.75285	inter-alpha (globulin) inhibitor, H2 polypeptide	1.62	1.16	0.69	0.95	1.87	1.28	1.05	0.60	1.01	0.67	0.61	1.09	0.93	1.22	1.20	0.91	1.15	1.23	1.14	1.11	0.70	1.35
26128	Hs.8375	TNF receptor-associated factor 4	1.68	1.62	0.80	1.20	1.73	1.41	1.33	1.00	0.61	1.24	1.10	1.07	1.18	1.00	1.55	1.47	1.51	1.51	1.54	1.29	1.49	1.88
26147	Hs.75510	annexin A11	1.59	1.33	0.85	1.08	1.96	1.43	1.12	0.91	1.62	1.00	1.48	1.12	1.06	1.22	1.33	1.55	1.21	1.48	1.52	1.10	0.92	1.29
26184	Hs.99910	phosphofructokinase, platelet	1.21	1.22	0.57	1.02	0.66	1.59	1.43	0.57	0.35	0.46	0.59	0.38	0.41	0.48	0.47	0.67	0.44	0.70	0.61	0.94	0.92	0.88
26286	Hs.75182	mannose receptor, C type 1	0.90	2.52	2.39	1.55	4.93	4.97	0.99	1.47	3.77	1.00	1.75	1.22	0.80	2.22	1.30	2.72	1.04	1.75	1.13	0.95	1.59	1.76
26366	Hs.110029	glucose regulated protein, 58kD	0.52	1.26	1.11	1.46	1.08	1.71	0.70	1.31	1.01	0.88	1.95	0.54	0.61	2.23	0.66	0.88	0.68	0.91	0.84	0.39	1.23	2.88
26483	Hs.180532	heat shock 90kD protein 1, alpha	1.12	1.49	0.96	1.24	1.88	1.26	0.74	1.20	1.25	1.24	1.38	1.15	0.96	1.22	1.07	1.61	1.50	1.08	1.31	0.94	1.48	1.28
27511	Hs.151791	KIAA0092 gene product	1.44	1.20	0.78	1.08	1.18	1.06	1.28	1.18	0.65	0.68	0.90	0.56	0.40	0.45	0.75	0.75	0.80	1.24	1.37	1.15	1.06	1.12
27549	Hs.249495	heterogeneous nuclear ribonucleoprotein A1	0.56	0.96	0.94	0.97	0.67	0.69	1.00	1.08	0.54	0.39	0.79	0.55	0.36	0.42	0.80	0.63	0.52	0.77	0.87	0.66	0.88	0.91

27624	Hs.75887	coatomer protein complex, subunit alpha	2.88	2.41	1.60	2.12	2.40	2.51	3.49	2.15	2.12	1.73	1.46	1.08	1.12	1.77	1.22	2.09	2.03	1.54	2.13	1.83	2.72	3.92
26593	Hs.1279	complement component 1, r subcomponent	2.39	10.41	6.78	7.00	10.49	5.69	8.48	7.32	8.69	4.81	8.86	8.83	1.79	3.68	6.15	4.42	4.72	4.90	7.19	2.80	4.37	5.92
26789	Hs.214982	laminin, gamma 1 (formerly LAMB2)	0.78	0.70	1.37	1.22	1.93	0.64	0.96	1.02	1.93	0.83	1.01	0.68	0.64	0.79	1.18	1.40	0.86	1.53	1.43	0.64	1.11	1.14
26922	Hs.79064	deoxyhypusine synthase	1.02	1.17	0.60	1.00	1.17	1.46	1.18	1.07	1.12	1.77	1.05	0.66	0.66	0.65	0.73	1.04	0.68	0.95	0.88	0.78	1.25	0.68
27230	Hs.179574	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), alpha isoform	0.70	1.07	0.83	1.11	0.98	0.78	0.81	0.76	1.29	0.54	1.10	0.66	0.45	0.76	0.88	1.02	0.78	0.71	0.59	0.79	0.94	0.74
27473	Hs.194660	ceroid-lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease)	0.68	1.19	0.48	1.01	1.06	1.31	0.74	1.18	1.26	1.44	1.03	0.91	2.97	2.01	1.31	1.33	0.89	0.97	1.04	0.76	0.45	0.78
28309	Hs.171625	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide	0.84	2.26	1.50	1.24	1.92	1.21	1.99	1.93	1.57	1.63	1.04	1.40	0.92	0.97	0.75	1.58	1.03	1.23	1.08	1.18	1.27	1.55
28410	Hs.82927	adenosine monophosphate deaminase 2 (isoform L)	1.33	1.28	1.64	1.24	1.70	1.03	1.21	1.14	1.54	1.33	0.69	1.07	0.91	1.04	1.40	0.85	0.92	0.81	1.25	0.56	1.16	1.40
27794	Hs.2853	poly(rC)-binding protein 1	1.55	2.57	1.73	1.84	1.22	1.55	1.68	1.28	1.87	1.40	1.36	0.70	0.84	0.89	0.97	2.00	1.29	1.64	1.34	1.65	0.93	1.25
27815	Hs.187958	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0.95	2.30	1.70	1.31	1.63	0.62	0.78	1.64	1.29	1.28	1.56	0.82	0.46	0.66	1.17	1.66	1.13	0.94	1.00	0.58	1.83	1.76
27818	Hs.82193	esterase D/formylglutathione hydrolase	0.91	1.33	0.47	0.88	0.95	0.59	0.42	0.76	0.92	0.48	0.66	0.39	0.51	0.39	0.51	0.83	0.38	1.12	0.78	0.75	0.54	0.62
27848	Hs.166160	acetyl-Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)	0.80	0.77	0.51	0.63	0.84	0.70	0.71	1.02	0.89	0.66	0.82	0.94	0.77	0.56	0.95	1.22	0.89	0.92	0.69	0.13	0.89	0.39
27927	Hs.75584	polymyositis/scleroderma autoantigen 2 (100kD)	1.07	0.94	0.85	1.15	1.05	1.27	1.40	1.09	1.08	0.75	1.00	0.92	0.82	1.12	1.21	1.33	0.80	0.79	0.76	0.98	0.78	1.52
28089	Hs.79404	neuron-specific protein	1.66	1.92	1.43	2.18	1.34	1.83	1.57	2.49	1.27	2.02	2.72	1.43	0.35	0.91	1.14	1.24	0.86	0.72	1.17	1.42	1.84	1.58
28116	Hs.159557	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	1.79	2.36	0.93	1.98	0.85	1.69	1.56	2.11	0.91	2.00	3.20	0.64	1.11	0.89	0.92	1.41	0.76	0.72	0.93	1.45	0.90	2.24
28573	Hs.21330	ATP-binding cassette, sub-family B (MDR/TAP), member 1	0.94	0.56	1.27	0.85	0.99	0.65	1.13	0.42	1.11	0.88	0.68	0.81	0.71	0.89	0.66	0.74	1.15	1.03	0.92	0.73	0.42	0.71
29627	Hs.1770	ligase I, DNA, ATP-dependent	1.62	1.71	1.18	1.55	1.66	1.18	1.39	1.36	0.88	0.99	1.02	1.27	1.24	1.17	1.27	1.13	1.26	1.58	1.54	1.61	1.58	1.69
29629	Hs.183105	nuclear autoantigen	0.93	0.93	0.81	1.01	0.91	0.57	1.04	0.61	0.89	0.80	0.70	0.85	0.79	0.92	0.94	0.73	0.85	0.81	1.13	1.60	0.71	0.46
29640	Hs.78466	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	1.66	0.84	0.70	0.79	0.86	2.42	1.10	0.87	0.79	0.74	0.71	0.54	0.95	1.24	0.75	1.01	1.20	0.53	0.83	0.73	1.40	1.12
28595	Hs.81118	leukotriene A4 hydrolase	0.69	0.70	1.02	0.94	0.88	0.84	0.70	0.80	0.84	0.43	0.89	0.90	0.66	1.13	1.00	0.79	0.76	1.39	0.93	0.71	1.00	0.59
28776	Hs.178710	clathrin, heavy polypeptide-like 2	1.15	0.86	1.10	1.37	0.81	0.94	1.69	2.45	1.41	1.93	4.54	0.83	0.80	1.39	1.46	1.44	1.07	0.71	0.86	0.99	1.07	0.66
28985	Hs.75372	N-acetylgalactosaminidase, alpha-	1.17	1.16	2.30	1.12	2.06	1.57	1.00	2.06	2.03	1.80	1.59	3.71	1.53	2.26	1.71	1.93	1.29	1.47	1.61	1.33	1.95	1.11
29054	Hs.153961	ARP1 (actin-related protein 1, yeast) homolog A (centractin alpha)	0.72	0.71	1.07	1.05	0.94	0.78	1.05	1.26	1.31	1.42	1.37	1.15	1.26	1.35	1.47	1.29	0.75	0.80	0.94	1.01	0.82	0.52
29204	Hs.177	phosphatidylinositol glycan, class H	1.27	1.46	1.33	1.43	1.91	1.15	1.11	1.68	1.19	1.59	1.23	1.04	1.05	1.00	0.88	1.36	0.82	1.05	1.43	1.54	1.97	1.28
29234	Hs.77854	regucalcin (senescence marker protein-30)	0.80	0.87	1.18	1.11	0.73	0.87	1.11	0.69	0.72	0.63	0.91	0.60	1.11	0.93	1.02	0.92	0.66	0.81	0.78	0.95	0.77	0.60
29435	Hs.73722	APEX nuclease (multifunctional DNA repair enzyme)	1.12	0.88	1.39	1.03	0.74	0.88	0.89	0.93	0.80	0.63	1.08	0.48	0.96	0.99	0.92	0.90	0.73	0.87	0.92	0.92	1.40	0.73
29438	Hs.98493	X-ray repair complementing defective repair in Chinese hamster cells 1	0.99	0.95	1.25	1.05	0.77	0.94	0.69	0.68	0.88	0.84	0.93	1.15	0.99	1.56	0.68	0.98	0.81	0.80	0.92	0.84	0.71	0.57
29799	Hs.77917	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	0.77	0.87	2.45	0.91	1.16	0.65	0.77	0.73	1.16	0.62	0.68	0.92	0.46	0.84	1.08	1.19	1.09	1.31	1.40	0.72	0.79	0.48
30622	Hs.250687	transient receptor potential channel 1	1.07	1.40	2.16	1.27	1.48	1.03	1.09	0.90	1.14	0.75	1.55	1.39	0.76	0.55	1.04	1.06	0.76	1.35	1.47	1.14	0.89	1.41
30664	Hs.207776	aspartylglucosaminidase	0.48	0.63	0.47	0.89	0.50	0.53	0.91	0.48	0.45	0.25	0.84	0.51	0.52	0.33	0.51	0.46	0.43	0.80	0.65	0.56	0.50	0.60
30012	Hs.75445	hevin	0.70	1.05	6.37	0.73	4.22	1.38	0.72	1.99	3.80	0.91	1.59	1.21	0.55	0.93	1.39	1.31	1.10	2.89	2.55	0.68	1.86	0.95
30149	Hs.250769	alkaline phosphatase, liver/bone/kidney	0.31	0.46	2.13	0.63	0.79	0.39	0.52	0.58	0.78	0.27	0.53	0.60	0.30	0.66	0.72	0.79	0.50	0.88	1.03	0.66	0.44	0.32
30272	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger), isoform 1 (antiporter, Na+/H+, amil	1.41	1.09	1.70	0.88	1.71	1.22	0.74	1.19	1.03	1.38	2.13	2.72	1.36	2.04	1.03	1.38	1.44	1.16	1.17	1.00	1.21	1.00
30543	Hs.158164	ATP-binding cassette, sub-family B (MDR/TAP), member 2	0.67	0.84	0.60	0.68	0.77	1.01	1.01	0.83	0.92	0.86	0.64	1.01	0.76	0.93	1.13	1.05	0.76	0.60	0.71	0.91	0.64	0.40
30573	Hs.273	galactosylceramidase (Krabbe disease)	1.05	1.75	1.65	1.70	2.75	2.01	0.97	0.99	1.96	1.50	2.07	1.63	1.92	1.10	1.51	1.74	1.82	1.85	2.35	1.44	1.55	1.44
30578	Hs.75485	ornithine aminotransferase (gyrate atrophy)	0.73	1.50	0.88	1.71	1.37	1.88	1.72	0.99	1.18	0.73	0.95	0.74	1.02	0.69	1.24	1.76	0.76	1.29	0.81	1.01	0.79	1.47
30588	Hs.75709	mannose-6-phosphate receptor (cation dependent)	1.13	2.15	0.94	1.60	1.41	1.51	1.87	1.04	1.17	0.96	1.50	1.26	1.07	1.07	1.31	1.43	1.29	1.73	1.24	1.18	1.50	2.20
30592	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein)	0.92	2.10	1.28	1.57	1.61	1.49	2.38	1.37	1.44	1.91	2.10	1.14	0.88	1.52	1.12	1.41	1.12	0.70	1.02	1.43	1.06	1.16
30691	Hs.180946	ribosomal protein L5	0.89	1.07	0.75	0.71	0.76	1.06	1.10	0.62	0.84	0.82	0.78	0.89	1.08	0.94	0.92	0.99	0.96	0.66	0.87	0.89	1.10	0.71
31143	Hs.73742	ribosomal protein, large, P0	0.37	0.66	0.59	1.01	0.59	0.34	0.94	0.68	0.44	0.35	0.52	0.55	0.54	0.41	0.53	0.51	0.42	0.75	0.55	0.31	0.63	0.64
30730	Hs.160786	argininosuccinate synthetase	0.47	0.30	0.22	0.21	0.39	0.30	0.41	0.34	0.08	0.14	0.38	0.21	0.20	0.57	0.26	0.26	0.36	0.39	0.50	0.62	0.44	0.50
30802	Hs.4888	seryl-tRNA synthetase	0.80	1.38	1.22	0.69	1.08	1.01	0.72	0.81	1.57	2.64	1.11	0.97	1.04	0.94	0.99	0.83	0.82	0.80	0.73	0.95	0.65	0.55
30852	Hs.74576	GDP dissociation inhibitor 1	2.06	3.23	1.22	1.07	1.72	1.49	1.56	2.21	2.64	3.41	1.98	2.85	3.02	1.84	2.28	2.01	1.90	1.44	1.68	1.46	2.04	0.94
30885	Hs.116875	KIAA0156 gene product	0.84	1.40	0.82	1.31	1.00	1.20	1.38	1.18	1.56	1.29	1.11	1.22	1.34	1.32	1.33	1.38	0.80	0.85	0.94	1.01	0.76	0.87
30970	Hs.80423	prostatic binding protein	1.33	3.78	0.71	2.24	0.94	1.11	1.06	1.25	1.69	1.54	1.00	0.82	0.84	1.26	0.77	1.59	1.04	1.89	1.34	1.29	1.77	1.41
30966	Hs.76152	decorin	1.84	3.09	1.31	11.75	15.80	7.34	0.71	7.91	7.86	22.55	14.49	10.46	3.87	5.41	7.16	8.21	6.71	3.44	2.34	2.26	3.60	4.98
31061	Hs.1432	protein kinase C substrate 80K-H	0.91	1.77	0.88	0.83	1.33	1.12	1.28	0.85	1.11	1.02	0.73	0.85	0.66	0.94	0.87	0.95	0.98	0.89	1.02	1.10	0.90	0.49
31155	Hs.77628	steroidogenic acute regulatory protein related	0.97	1.01	1.43	1.11	1.37	1.35	0.83	2.41	1.98	1.89	1.65	1.33	1.30	1.12	0.90	2.75	1.07	0.71	1.10	1.07	2.60	1.08
31456	Hs.76847	KIAA0088 protein	1.28	1.08	1.46	1.17	1.47	1.45	1.50	1.22	1.60	1.16	1.47	0.95	1.03	1.18	0.97	1.46	1.49	1.12	1.12	1.20	1.51	1.51
31863	Hs.92909	SON DNA binding protein	1.36	0.84	1.01	0.93	0.99	1.33	0.81	0.98	1.02	1.80	0.96	0.80	0.66	0.93	1.01	1.08	1.41	0.96	1.07	1.09	1.32	1.04
31154	Hs.80395	mal, T-cell differentiation protein	0.86	1.14	0.83	0.97	1.29	1.10	1.10	1.36	1.30	0.93	1.10	0.53	0.71	0.73	0.57	1.53	0.69	0.91	0.81	0.97	1.03	1.15
31169	Hs.75546	capping protein (actin filament) muscle Z-line, alpha 2	0.80	0.76	1.07	1.06	0.86	0.95	0.72	0.61	1.13	0.74	0.53	0.67	1.16	0.68	0.69	0.75	0.60	0.72	0.49	1.06	0.72	0.48
31164	Hs.89649	epoxide hydrolase 1, microsomal (xenobiotic)	1.09	0.95	1.00	1.15	1.42	1.39	0.70	0.82	1.41	0.89	0.95	1.00	0.88	0.94	1.08	1.19	0.67	1.09	0.64	0.83	0.61	1.13
31238	Hs.146354	thioredoxin-dependent peroxide reductase 1 (thiol-specific antioxidant 1, natural killer-enl	1.57	0.99	0.62	1.12	0.73	0.95	0.96	0.86	0.86	1.27	0.59	0.62	0.95	0.41	0.58	1.14	0.65	0.86	1.32	0.92	0.63	0.85
31242	Hs.80350	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	0.44	0.39	0.38	0.42	0.41	0.23	0.52	0.38	0.71	0.52	0.22	0.29	0.24	0.27	0.42	0.34	0.46	0.64	0.44	0.58	0.47	0.22
31355	Hs.75424	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	0.79	1.14	1.08	0.76	1.46	1.19	0.94	1.04	0.99	0.85	0.83	0.75	0.57	0.75	0.79	1.24	0.99	0.89	0.95	0.87	0.60	1.34
31454	Hs.183842	Human ubiquitin gene, complete cds	1.16	0.92	1.80	1.04	0.77	1.40	1.18	1.48	1.33	0.77	1.15	1.05	1.44	1.24	1.22	1.29	1.69	1.06	0.97	1.44	1.18	1.25
31852	Hs.118244	protein phosphatase 2, regulatory subunit B (B56), delta isoform	1.13	1.05	1.58	1.22	1.16	1.09	2.92	1.00	1.13	1.54	1.39	1.34	1.72	1.54	1.37	1.20	1.06	0.76	1.34	0.99	1.11	0.97
32438	Hs.78629	ATPase, Na+/K+ transporting, beta 1 polypeptide	1.34	2.56	0.84	1.59	1.89	1.10	0.55	1.75	1.11	1.17	1.09	1.13	1.28	1.38	1.58	1.12	1.50	0.82	0.96	0.67	2.52	1.62
32427	Hs.236963	protein phosphatase 2A, regulatory subunit B' (PR 53)	2.85	2.97	5.28	3.74	3.08	1.37	2.04	1.73	4.31	2.24	2.23	1.47	1.85	1.38	0.59	3.04	2.00	2.56	1.84	1.06	1.50	2.56
31855	Hs.154546	syntaxin 5A	1.46	1.61	1.22	1.24	1.92	1.73	2.70	1.55	1.37	1.25	1.56	2.42	1.64	1.83	1.71	1.62	1.54	1.07	1.47	1.41	2.27	1.38
31988	Hs.183994	protein phosphatase 1, catalytic subunit, alpha isoform	1.24	0.90	0.67	1.06	0.81	1.08	1.46	1.14	0.90	0.77	1.39	1.00	1.34	1.32	1.12	1.12	0.73	0.66	0.79	1.37	0.91	0.49
32141	Hs.138381	farnesyltransferase, CAAX box, alpha	0.69	1.35	0.56	1.10	1.03	0.93	0.86	0.73	0.73	0.95	0.68	0.79	0.73	0.83	0.68	0.74	0.64	0.70	0.81	1.09	1.49	0.99
32198	Hs.6551	ATPase, H+ transporting, lysosomal (vacuolar proton pump), subunit 1	1.08	1.30	0.80	0.80	1.13	1.09	0.90	1.10	1.42	1.56	1.33	1.94	3.73	1.59	1.96	1.85	1.44	0.81	0.87	1.02	0.96	0.46
32304	Hs.151301	Ca2+-dependent activator protein for secretion	1.05	0.84	1.11	1.07	1.65	1.00	1.05	1.25	0.92	0.80	0.96	1.40	1.16	0.86	1.09	1.26	0.94	1.20	0.81	0.77	1.14	1.32
32409	Hs.75725	transgelin 2	0.56	0.81	1.33	1.19	1.25	0.53	1.14	0.78	0.85	0.36	0.77	0.57	0.44	0.71	0.45	0.70	0.49	0.70	0.59	0.70	1.20	1.61
32407	Hs.196177	phosphorylase kinase, gamma 2 (testis)	0.71	0.91	1.47	1.20	1.30	0.82	1.19	0.81	1.41	1.84	1.64	1.16	0.94	1.22	1.27	1.29	1.12	1.04	1.33	0.71	0.71	0.72
32609	Hs.78672	laminin, alpha 4	0.77	0.88	0.66	1.00	0.87	0.95	1.41	0.85	1.16	1.00	0.98	0.59	0.76	1.14	0.97	1.82	0.49	0.67	0.74	0.83	0.77	0.57
32717	Hs.79391	huntingtin (Huntington disease)	1.60	1.97	3.94	2.01	3.22	1.93	1.14	2.37	2.31	3.24	3.30	2.05	1.18	1.30	1.55	2.32	1.58	1.32	2.33	0.94	2.10	2.15
32707	Hs.36587	protein phosphatase 1, regulatory subunit 7	0.86	1.43	0.52	0.87	1.21	1.00	0.92	0.81	0.94	0.76	1.00	1.48	1.17	2.23	1.89	1.23	0.51	0.83	1.06	1.00	0.58	0.77
32750	Hs.1898	paraoxonase 1	2.29	1.02	3.60	2.69	2.56	2.59	1.11	0.72	0.93	0.81	1.84	2.02	2.06	1.80	3.16	1.54	1.38	3.33	1.51	1.24	1.64	1.30
32615	Hs.179662	nucleosome assembly protein 1-like 1	1.13	1.12	1.11	1.65	1.42	0.97	1.22	0.99	1.26	1.28	1.20	0.69	0.65	0.76	1.06	0.94	1.23	1.52	1.13	1.01	1.44	1.23
32626	Hs.79358	testis-specific kinase 1	0.52	0.96	0.54	1.13	0.82	0.99	1.41	1.07	0.90	0.67	1.08	0.60	0.70	0.68	0.96	1.27	0.74	0.76	0.55	0.82	0.96	0.85
32649	Hs.77805	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPas	0.99	0.95	0.93	0.72	0.80	0.91	1.31	0.87	1.58	1.30	0.72	0.61	0.89	0.72	0.66	1.25	0.77	0.56	0.86	0.84	0.77	0.64
32644	Hs.80206	glucose-6-phosphate dehydrogenase	0.47	0.59	0.45	0.38	0.51	0.60	0.46	0.44	0.53	0.52	0.46	0.50	0.36	0.42	0.37	0.72	0.51	0.59	0.65	0.39	0.88	0.43
32658	Hs.75106	clusterin (complement lysis inhibitor, SP-40,40, sulfated glycoprotein 2, testosterone-repr	1.29	10.34	6.74	5.76	7.31	5.36	4.65	3.13	6.92	4.05	6.39	5.85	4.44	3.77	2.52	4.54	2.34	3.16	2.78	1.73	2.10	2.93
32682	Hs.2064	vimentin	2.06	6.77	4.12	4.77	5.22	3.40	2.34	3.28	3.87	4.04	5.72	2.24	2.64	3.46	1.84	4.36	2.55	2.36	2.42	1.78	2.67	4.82
32684	Hs.169793	ribosomal protein L32	1.58	2.04	4.06	1.88	2.24	1.39	2.55	1.82	2.39	1.72	2.22	1.93	0.94	1.91	1.64	1.90	1.57	1.47	1.79	1.54	0.82	1.54
32774	Hs.256340	homolog of mouse MAT-1 oncogene	0.87	1.14	0.87	1.24	1.27	1.49	1.37	0.77	1.28	0.83	1.01	0.69	1.21	0.93	1.11	1.20	0.87	0.99	1.21	1.02	0.90	0.74
33267	Hs.162	insulin-like growth factor binding protein 2 (36kD)	1.67	1.93	5.56	4.63	6.81	2.08	0.91	4.67	4.87	8.64	8.13	1.78	1.05	1.13	1.23	3.63	1.51	1.19	1.36	0.85	4.11	4.91
33274	Hs.76307	neuroblastoma candidate region, suppression of tumorigenicity 1	1.18	0.85	0.59	0.77	0.93	1.30	0.91	1.01	1.73	0.83	1.22	0.82	1.15	1.00	1.06	1.76	1.01	1.22	1.27	1.10	0.55	0.69

33415	Hs.172153	glutathione peroxidase 3 (plasma)	1.50	2.19	2.45	5.11	7.22	3.97	1.39	2.74	2.50	1.90	10.74	1.32	1.13	1.01	1.20	3.02	1.38	1.15	1.87	0.73	2.55	1.64
32790	Hs.78934	mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1)	1.25	1.36	1.14	2.52	1.36	1.97	1.28	1.04	1.32	0.79	1.14	0.49	0.57	0.56	0.71	0.82	0.93	1.19	0.96	0.99	2.98	1.98
32822	Hs.252979	G protein pathway suppressor 1	0.54	0.82	0.44	0.83	0.65	0.90	1.16	0.78	0.73	0.45	0.90	0.66	0.89	0.68	0.91	1.10	0.75	0.94	0.62	0.81	0.88	0.86
32875	Hs.159627	death associated protein 3	0.84	2.08	0.62	1.67	1.63	1.49	2.23	1.28	0.97	0.95	1.45	0.64	0.66	0.84	0.94	1.50	1.21	1.53	1.24	1.05	1.57	2.32
32898	Hs.76394	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	0.64	0.97	0.71	0.67	0.74	0.97	1.44	1.24	0.81	0.47	1.25	0.62	0.77	0.90	0.93	1.19	0.73	0.97	0.87	0.88	0.82	0.46
33008	Hs.75313	aldo-keto reductase family 1, member B1 (aldose reductase)	0.36	0.75	0.57	0.24	0.37	0.31	0.30	0.25	0.36	0.25	0.24	0.38	0.21	0.33	0.22	0.42	0.37	0.43	0.49	0.50	0.67	0.30
33045	Hs.169266	neuropeptide Y receptor Y1	1.48	3.24	2.42	2.47	2.49	3.26	1.62	3.31	4.48	3.60	3.69	2.09	2.43	1.58	1.46	2.93	2.93	2.05	2.09	1.54	1.57	1.63
33183	Hs.75722	ribophorin II	2.11	1.05	1.61	1.37	1.45	1.63	1.07	1.74	1.39	1.25	2.12	1.37	1.94	1.22	0.96	1.89	1.69	1.46	1.34	1.73	2.28	1.42
33176	Hs.76476	cathepsin H	1.07	1.93	2.50	1.78	1.39	2.67	0.63	1.58	1.76	2.46	2.15	1.90	0.75	1.18	1.11	2.08	1.16	0.72	0.87	1.14	1.15	2.29
33803	Hs.153820	hypothetical protein	1.60	1.80	1.61	1.76	1.79	1.56	1.10	1.41	1.82	1.44	1.40	0.79	0.70	0.82	0.99	1.43	1.09	2.01	1.47	1.23	1.67	1.35
33831	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9 (RNA helicase A, nuclear DNA helicase	1.17	1.59	1.03	1.83	1.07	1.10	1.08	1.13	1.21	0.78	0.85	0.77	0.86	0.83	1.08	1.20	0.94	1.13	1.16	0.83	1.28	0.89
33943	Hs.79222	galactosidase, beta 1	1.16	0.78	1.23	0.93	1.25	1.25	0.76	0.95	1.16	0.59	1.12	0.72	1.26	0.86	0.82	1.59	1.13	0.96	0.98	0.80	1.05	0.84
33477	Hs.75105	emopamil-binding protein (sterol isomerase)	1.10	0.84	0.36	0.75	0.67	1.32	1.08	1.03	0.54	0.59	0.78	0.36	0.47	0.48	0.59	0.70	0.64	1.05	0.76	0.94	0.65	1.33
33525	Hs.2186	eukaryotic translation elongation factor 1 gamma	0.59	0.75	0.54	0.73	0.56	0.70	1.07	0.65	0.46	0.26	0.63	0.38	0.58	0.51	0.70	0.63	0.59	0.78	0.49	0.77	0.74	0.94
33620	Hs.151761	KIAA0100 gene product	0.74	0.89	0.38	0.97	0.90	0.84	1.26	0.76	0.62	0.48	0.95	0.35	0.48	0.51	0.88	0.84	0.78	1.19	0.66	0.88	0.59	0.84
33632	Hs.597	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1)	0.74	0.79	0.57	0.86	0.59	0.69	0.93	0.88	0.64	0.50	0.68	0.53	0.75	0.53	0.73	0.61	0.75	1.05	0.75	1.04	0.73	0.47
33643	Hs.170808	glutamate decarboxylase 2 (pancreatic islets and brain, 65kD)	0.89	0.98	0.73	0.69	1.02	0.76	0.64	0.94	1.02	0.80	0.62	0.53	0.56	0.58	0.50	0.86	0.71	0.78	0.76	0.90	0.57	1.02
33690	Hs.64542	pre-mRNA cleavage factor Im (68kD)	1.31	1.27	1.13	1.26	1.00	1.34	0.89	2.10	2.19	2.60	1.44	0.93	1.40	0.86	1.04	1.37	1.05	1.07	0.97	1.16	1.16	0.91
33692	Hs.195432	aldehyde dehydrogenase 2, mitochondrial	4.58	4.83	3.40	5.59	3.30	5.91	0.99	3.19	4.77	4.06	5.15	4.40	5.03	3.47	0.63	3.84	3.88	3.60	3.14	2.53	3.56	3.52
33794	Hs.155433	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	0.62	1.18	0.46	1.35	0.57	1.50	1.27	0.65	0.53	0.26	0.40	0.42	0.46	0.45	0.49	0.61	0.85	0.61	0.68	0.77	1.18	0.81
34357	Hs.180952	actin, beta	1.30	1.20	1.43	0.96	1.32	1.10	1.31	0.86	1.18	0.89	1.20	0.51	0.46	0.88	0.85	1.45	0.90	1.56	1.13	0.99	0.92	0.97
34349	Hs.251064	high-mobility group (nonhistone chromosomal) protein 14	1.25	1.20	1.13	1.15	1.04	0.85	0.89	1.06	0.91	0.89	1.06	0.90	0.70	0.99	1.03	1.31	1.07	0.93	1.41	0.74	1.14	1.13
34355	Hs.182278	calmodulin 2 (phosphorylase kinase, delta)	2.59	1.27	1.62	3.31	2.30	2.38	1.86	1.45	2.25	1.25	1.65	1.09	1.08	1.16	1.81	1.88	1.62	1.58	1.75	1.31	3.68	2.15
34005	Hs.177559	interferon gamma receptor 2 (interferon gamma transducer 1)	1.26	1.42	1.21	1.53	1.55	1.28	1.25	1.31	1.93	1.42	1.77	1.59	1.49	1.95	1.58	2.05	1.11	1.32	1.82	1.52	1.17	1.63
34141	Hs.25911	HLA-B associated transcript-2	1.65	2.80	1.36	1.69	1.96	1.63	1.96	1.94	1.37	1.82	2.09	1.36	1.50	1.67	1.62	1.90	1.38	1.60	2.13	1.57	2.60	1.73
34247	Hs.183418	cell division cycle 2-like 1 (PITSLRE proteins)	1.95	2.24	1.01	1.37	1.78	1.15	1.01	1.45	1.02	1.51	1.13	1.51	1.21	2.02	1.58	1.18	0.97	1.34	1.19	1.08	1.83	1.14
34304	Hs.77100	general transcription factor IIE, polypeptide 2 (beta subunit, 34kD)	0.85	1.79	0.97	1.19	1.22	0.69	1.45	0.97	1.01	1.10	1.01	0.44	0.23	0.41	0.58	0.94	0.61	1.06	0.74	0.72	1.37	1.02
34327	Hs.25647	v-fos FBJ murine osteosarcoma viral oncogene homolog	0.63	0.78	1.31	0.90	0.75	0.39	0.61	0.41	0.99	0.50	0.64	0.69	0.33	0.72	0.59	0.64	0.40	1.35	0.68	0.39	0.50	0.39
34396	Hs.74335	heat shock 90kD protein 1, beta	0.79	1.77	1.31	1.19	1.39	1.04	2.26	1.20	1.28	1.21	2.11	1.33	1.55	1.34	1.64	1.48	1.18	1.05	1.22	1.28	0.99	1.42
34761	Hs.111894	KIAA0108 gene product	0.88	0.87	0.74	0.45	0.60	0.92	0.79	0.51	0.88	0.71	0.67	0.67	0.70	0.79	1.05	0.69	1.18	1.17	0.76	0.85	0.71	0.46
34945	Hs.12084	Tu translation elongation factor, mitochondrial	0.61	0.93	0.60	0.76	0.69	0.55	0.82	0.68	0.58	0.59	0.61	0.29	0.84	0.82	0.91	0.74	0.69	1.02	0.62	0.29	0.72	0.79
34537	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1	1.58	1.90	1.40	1.23	1.09	1.35	1.08	0.98	1.36	1.39	1.23	1.03	1.21	1.32	1.37	1.58	1.30	1.35	1.15	1.78	1.24	1.83
34555	Hs.83715	Sjogren syndrome antigen B (autoantigen La)	1.01	1.84	1.15	1.61	1.31	1.06	1.45	0.93	1.05	0.95	1.57	0.98	0.75	0.52	0.71	0.68	1.05	1.13	1.18	1.01	2.53	0.91
34606	Hs.181392	major histocompatibility complex, class I, E	1.34	4.19	1.38	1.97	1.98	2.47	1.32	1.96	1.80	1.05	3.29	3.14	0.69	2.23	2.37	2.86	2.79	2.45	2.38	1.12	1.91	1.66
34637	Hs.180841	tumor necrosis factor receptor superfamily, member 7	1.54	3.36	1.61	1.58	3.11	5.66	2.02	2.63	4.20	1.88	3.29	2.75	1.05	2.77	2.45	3.13	3.11	1.94	1.76	1.50	2.78	0.91
34647	Hs.118638	non-metastatic cells 1, protein (NM23A) expressed in	1.27	2.00	0.91	1.56	0.94	1.07	0.94	2.25	0.78	1.25	1.96	1.24	0.87	1.31	1.77	1.21	1.60	0.95	1.83	0.45	1.48	1.79
34662	Hs.75975	signal recognition particle 9kD	1.32	0.90	0.93	1.40	1.90	0.99	0.76	0.64	1.02	0.89	0.81	0.80	0.96	0.77	0.97	0.93	0.87	0.81	1.15	1.00	0.67	1.24
34660	Hs.57304	Ras-related GTP-binding protein	1.17	1.52	0.85	1.80	1.24	1.45	1.78	0.88	0.98	0.83	1.38	0.54	0.63	0.59	0.86	0.76	1.02	1.29	1.26	0.72	1.19	1.34
34671	Hs.75294	corticotropin releasing hormone	1.09	1.19	0.87	0.96	1.29	0.92	1.21	0.65	1.30	0.75	0.77	0.75	0.50	0.96	0.90	1.15	0.87	1.33	1.10	0.35	0.76	0.96
34974	Hs.77318	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD)	0.88	0.77	0.91	0.65	1.24	1.02	0.98	0.76	1.22	0.61	0.80	0.68	0.98	0.66	0.90	0.96	0.99	1.25	0.83	1.36	0.53	0.43
35110	Hs.69743	GM2 ganglioside activator protein	1.14	1.02	0.76	0.78	1.35	0.88	0.84	1.07	1.31	1.05	1.07	1.15	0.58	0.68	0.80	1.01	1.13	1.37	1.30	1.36	1.10	0.94
35284	Hs.75180	protein phosphatase 5, catalytic subunit	0.82	1.26	0.76	0.68	0.83	0.64	1.36	0.59	0.72	1.22	0.69	2.33	0.85	0.61	1.20	0.78	1.17	0.93	1.18	1.86	0.76	0.64
35297	Hs.7688	protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	0.86	1.21	0.77	0.96	1.21	1.07	0.92	1.21	1.15	1.03	1.11	0.59	0.52	0.52	0.56	0.91	1.01	0.94	1.11	0.95	1.63	1.15
35313	Hs.25	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	0.53	0.35	0.84	0.53	0.35	0.61	0.72	0.46	0.56	0.40	0.68	0.48	0.68	0.57	0.44	0.59	0.65	0.79	0.60	0.97	0.45	0.50
35320	Hs.25155	guanine nucleotide regulatory protein (oncogene)	1.49	2.20	0.56	2.29	1.66	1.68	2.18	1.40	1.73	1.09	1.45	1.18	1.38	0.94	1.72	1.37	1.63	1.61	1.17	1.50	1.67	1.32
35559	Hs.119503	methionine-tRNA synthetase	1.08	1.17	0.84	1.40	1.30	1.41	1.62	1.38	1.22	1.50	1.37	1.54	0.99	1.32	1.23	1.72	1.79	1.09	1.19	1.27	2.03	1.40
35609	Hs.118855	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory pr	0.78	1.09	0.43	0.55	1.26	0.93	1.17	0.67	1.26	1.31	1.02	0.84	0.98	1.10	0.96	1.06	1.13	1.22	0.97	1.07	0.49	0.51
35850	Hs.146580	enolase 2, (gamma, neuronal)	2.23	2.22	3.94	2.25	1.24	1.42	6.78	3.32	4.73	3.66	1.99	1.54	2.17	1.61	1.72	1.36	2.64	1.46	1.37	0.89	1.35	2.10
36393	Hs.4112	t-complex 1	0.98	1.07	1.77	1.43	1.16	2.11	1.63	1.28	1.34	1.34	0.98	0.71	0.54	0.90	0.79	1.00	1.11	1.25	1.07	1.22	1.86	0.93
36560	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	0.79	0.59	0.80	0.58	0.90	0.61	0.75	0.63	0.66	0.58	0.45	0.53	0.60	0.59	0.93	0.79	0.58	1.36	0.96	0.49	1.18	1.17
35865	Hs.118796	annexin A6	1.28	1.66	1.40	1.20	1.85	1.21	1.34	1.88	2.13	2.09	1.76	0.77	1.01	0.67	1.04	1.72	1.84	1.84	2.00	1.38	1.62	1.75
36007	Hs.78434	zinc finger protein 133 (clone pHZ-13)	0.95	1.05	0.78	0.69	1.30	0.67	0.68	1.36	1.02	1.22	0.80	0.78	1.22	0.88	1.02	0.86	0.94	1.08	0.97	0.82	1.48	0.80
36060	Hs.75348	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)	1.41	2.91	1.36	1.18	1.29	2.22	0.72	2.59	2.71	2.01	3.49	1.36	1.60	1.62	2.00	2.42	2.31	1.73	2.12	1.08	1.59	1.10
36109	Hs.75353	KIAA0123 protein	1.31	0.81	0.38	0.71	0.72	1.19	0.45	1.00	0.73	1.01	0.83	0.55	0.90	0.61	0.55	0.96	0.52	0.83	0.77	0.69	1.17	0.68
36191	Hs.118162	fibronectin 1	0.50	0.19	1.63	0.60	0.87	1.49	0.38	1.19	2.07	1.05	1.65	1.15	0.96	1.20	0.67	2.36	0.81	0.98	1.19	0.77	0.44	0.40
36202	Hs.183698	ribosomal protein L29	0.65	0.88	0.47	0.61	0.72	0.52	0.48	1.32	0.37	0.48	1.07	0.53	0.53	0.32	0.80	0.58	0.54	0.89	0.56	0.32	0.83	0.38
36593	Hs.78223	N-acylaminoacyl-peptide hydrolase	0.80	1.55	0.80	0.97	1.72	0.91	1.29	1.18	1.17	2.03	1.58	1.11	2.12	1.27	1.19	1.68	0.96	0.84	1.15	0.91	1.04	1.14
36904	Hs.119475	cold inducible RNA-binding protein	0.93	0.90	0.62	1.29	1.43	1.01	0.72	1.75	1.28	1.27	1.38	0.84	2.70	1.32	2.60	1.84	1.47	1.83	1.82	0.89	1.55	0.99
36916	Hs.77961	major histocompatibility complex, class I, B	2.13	7.46	2.38	4.74	3.83	6.91	2.25	3.54	4.20	2.58	10.95	8.13	3.92	6.69	6.22	6.48	5.16	2.86	4.00	1.80	2.83	3.76
36922	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD)	1.58	1.02	1.42	2.18	1.79	2.10	0.83	0.70	3.05	1.23	1.57	1.12	1.96	1.00	1.39	1.13	1.19	1.34	1.59	1.49	2.92	1.94
36676	Hs.180842	ribosomal protein L13	1.46	1.73	0.98	1.00	1.97	1.36	2.00	1.56	1.24	1.33	1.81	1.13	1.16	1.30	1.45	1.41	1.56	1.69	1.69	1.57	2.00	2.03
36681	Hs.179543	immunoglobulin heavy constant mu	2.51	4.06	2.17	1.85	4.58	5.58	3.69	2.95	3.05	3.99	3.96	2.26	0.89	0.53	1.95	4.00	2.96	2.29	3.62	2.20	2.59	1.37
36717	Hs.76090	tumor necrosis factor, alpha-induced protein 1 (endothelial)	1.13	1.20	0.95	1.17	1.20	1.18	1.02	1.37	1.70	1.33	1.71	1.15	1.02	1.60	1.55	1.29	1.56	0.93	1.44	1.36	1.05	0.87
36775	Hs.75860	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzy	1.07	1.06	0.88	0.84	1.07	1.17	0.96	0.71	0.68	0.56	0.88	0.66	0.38	0.67	0.76	1.03	0.88	1.15	0.87	0.95	0.86	0.84
36796	Hs.174071	glycogenin	1.66	1.35	1.72	1.14	1.51	1.43	1.57	0.87	1.45	1.31	1.31	1.07	1.11	1.65	1.10	1.47	0.95	1.20	0.96	0.83	0.86	1.66
36844	Hs.81134	interleukin 1 receptor antagonist	0.83	1.42	1.10	1.13	1.20	2.70	1.35	0.93	1.20	1.31	1.63	1.43	0.75	1.20	1.34	1.11	0.82	0.93	1.02	0.44	1.13	1.58
36927	Hs.177516	high density lipoprotein binding protein (vigilin)	1.46	1.79	1.33	1.09	1.88	1.15	1.98	1.20	1.51	1.48	1.66	2.18	1.43	2.99	2.03	1.24	0.98	1.54	1.33	1.66	0.97	1.17
37234	Hs.82979	mitogen-activated protein kinase kinase kinase kinase 2	0.95	1.74	0.92	1.40	2.02	1.62	1.01	1.10	1.89	1.35	1.76	0.89	0.87	0.91	0.78	1.44	0.92	0.72	0.92	0.69	1.54	1.28
37269	Hs.73947	peptidase D	1.27	1.23	1.15	0.99	1.50	1.27	1.04	0.96	1.23	0.92	1.45	2.31	0.85	1.67	1.69	1.37	1.59	0.82	1.22	0.49	1.16	1.30
36950	Hs.155455	phosphofructokinase, liver	1.93	2.18	1.98	1.78	2.34	4.67	6.00	1.42	1.88	1.70	2.35	1.64	1.31	1.32	1.96	1.89	2.41	1.78	4.36	2.41	2.15	2.08
36983	Hs.73799	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	1.22	1.29	1.58	1.67	0.86	1.38	1.08	1.01	1.25	0.76	1.63	0.86	0.56	0.99	0.83	0.94	0.66	0.70	0.67	1.26	0.57	1.29
37118	Hs.78504	inner membrane protein, mitochondrial (mitofilin)	1.16	1.11	0.56	1.54	1.17	1.83	1.37	0.76	0.80	0.87	1.80	0.62	0.53	0.59	0.78	0.95	1.03	1.25	1.25	0.61	1.52	1.09
37145	Hs.155101	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1, cardia	0.96	0.38	0.76	0.80	0.62	0.83	0.79	0.39	0.60	0.29	0.54	0.57	0.58	1.21	0.75	0.50	0.85	1.06	0.73	0.42	0.37	0.39
37196	Hs.181373	accessory proteins BAP31/BAP29	1.37	1.61	0.80	0.70	1.24	1.65	1.05	1.09	1.06	1.18	1.54	1.02	1.30	0.93	1.19	1.42	1.15	0.86	1.18	0.65	1.25	0.99
37230	Hs.154854	phospholipid transfer protein	1.41	2.10	3.98	1.27	4.02	2.20	1.34	2.02	2.11	1.62	3.40	1.09	1.10	2.09	1.01	2.16	1.43	1.43	1.44	1.07	1.40	1.72
37347	Hs.84298	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-	3.64	26.96	8.56	11.57	14.82	8.97	5.33	5.08	7.01	11.13	15.52	9.81	6.03	3.64	7.04	7.49	2.94	5.71	7.74	2.59	5.07	5.04
37513	Hs.77306	survival of motor neuron 1, telomeric	1.51	1.19	0.79	1.07	1.47	1.43	1.19	1.34	1.30	1.11	1.54	1.56	1.00	1.04	1.34	1.20	1.12	1.46	2.08	1.09	1.41	1.24
37622	Hs.155212	methylmalonyl Coenzyme A mutase	1.02	1.61	1.03	1.30	1.55	0.91	1.00	1.32	1.27	1.12	1.16	0.73	0.72	0.83	0.70	1.23	1.19	1.14	1.41	1.17	2.04	1.13
37366	Hs.179661	Homo sapiens clone 24703 beta-tubulin mRNA, complete cds	2.08	2.03	2.15	2.56	2.31	2.59	1.79	1.97	2.34	1.94	1.82	1.98	1.99	1.43	1.51	2.35	1.36	1.32	1.74	2.07	2.23	2.14
37380	Hs.172928	collagen, type I, alpha 1	1.02	3.54	7.22	6.82	7.71	4.51	2.03	6.32	6.27	8.01	7.55	1.82	1.96	1.89	1.56	4.78	1.63	1.67	1.53	1.74	2.91	3.35
37435	Hs.88778	carbonyl reductase 1	1.43	2.82	0.85	1.60	2.46	2.22	1.82	2.34	2.52	2.89	2.19	3.28	1.94	2.12	2.15	1.29	3.22	1.76	2.80	1.16	3.11	1.11

37433	Hs.151134	oxidase (cytochrome c) assembly 1-like	0.86	0.89	0.65	0.77	0.71	0.70	0.68	0.75	0.89	0.54	0.86	0.64	0.48	0.72	0.57	0.82	0.59	0.96	0.72	1.14	0.59	0.44
37451	Hs.173724	creatine kinase, brain	1.58	1.00	0.94	1.16	1.36	1.05	1.02	1.08	1.35	1.31	1.84	0.58	0.67	0.99	0.64	0.20	0.65	0.73	0.80	1.37	1.89	0.58
37477	Hs.254105	MYC promoter-binding protein 1	1.26	0.24	1.28	0.47	0.40	0.65	0.64	0.34	0.33	0.24	0.55	0.39	0.49	0.92	0.27	0.42	0.26	0.63	0.41	1.39	0.23	0.90
37485	Hs.75360	carboxypeptidase E	1.26	1.30	0.77	1.14	1.65	1.06	0.74	0.94	1.35	1.17	1.97	0.99	0.56	0.67	0.87	1.19	0.76	1.26	0.91	1.06	1.50	1.47
38393	Hs.75511	connective tissue growth factor	0.76	0.98	0.95	0.79	1.20	0.97	0.42	1.20	1.40	1.23	1.16	2.70	1.11	2.04	3.35	1.19	1.17	1.47	0.31	0.15	1.51	1.15
38500	Hs.62	protein tyrosine phosphatase, non-receptor type 12	1.42	1.57	1.04	1.47	1.74	1.57	1.51	1.33	1.66	1.46	1.30	1.38	0.69	0.87	1.16	1.08	1.02	1.36	1.54	1.23	1.51	1.06
37760	Hs.155314	KIAA0095 gene product	1.84	1.93	1.30	1.46	1.54	1.46	1.23	1.14	1.40	1.31	0.98	0.90	0.87	1.01	0.78	1.25	1.15	0.92	1.13	1.35	1.94	1.81
37797	Hs.183704	ubiquitin C	1.05	0.77	1.68	0.65	0.81	0.55	1.52	1.38	1.42	1.01	1.55	0.64	1.57	0.82	0.65	1.22	0.89	1.38	1.56	1.30	0.94	1.07
37892	Hs.26886	unknown prepropeptide specific to rod photoreceptor;	0.93	1.08	1.21	0.80	0.85	0.73	0.72	1.29	0.67	0.95	0.90	0.77	1.11	0.79	0.82	1.01	1.33	1.04	1.13	0.65	1.24	1.14
37964	Hs.1540	nuclear matrix protein p84	1.20	1.52	1.52	1.33	1.89	1.24	0.84	1.18	1.38	1.73	0.87	0.72	1.19	0.75	1.12	0.84	1.37	1.01	1.85	1.04	1.67	1.69
38397	Hs.78713	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	0.49	0.34	0.28	0.31	0.44	0.43	0.30	0.37	0.54	0.36	0.26	0.30	0.37	0.34	0.39	0.49	0.44	0.48	0.41	0.70	0.36	0.33
38829	Hs.198288	protein tyrosine phosphatase, receptor type, R	1.82	1.73	1.28	2.11	2.61	1.87	1.68	2.55	2.57	1.96	2.44	2.09	1.93	2.00	2.24	2.19	1.98	1.82	2.11	1.54	4.01	2.14
38840	Hs.78501	growth arrest-specific 6	1.13	1.83	1.14	1.18	2.00	1.59	0.81	1.15	0.94	1.26	1.11	1.05	0.96	1.40	0.64	1.43	1.02	1.04	1.42	1.13	1.83	1.84
39093	Hs.78935	methionine aminopeptidase; eIF-2-associated p67	0.39	0.58	0.72	1.07	0.97	0.62	0.39	0.48	0.88	0.57	0.95	0.37	0.40	0.39	0.45	0.66	0.83	0.37	0.51	0.65	0.75	0.96
39380	Hs.12409	somatostatin	1.20	1.38	0.92	0.70	3.12	1.22	1.70	1.20	0.86	1.26	3.79	1.34	2.33	1.36	1.19	1.29	1.09	1.28	1.70	0.93	0.94	1.26
39148	Hs.230	fibromodulin	2.37	1.77	4.09	2.63	5.22	2.97	2.67	3.73	5.88	2.68	3.98	10.44	1.88	4.37	4.38	2.76	4.17	4.38	1.42	5.29	2.38	2.17
39159	Hs.181013	phosphoglycerate mutase 1 (brain)	0.86	1.03	1.29	0.91	2.60	0.93	1.14	1.28	2.27	1.06	1.04	1.77	0.95	2.24	1.50	1.90	1.17	1.06	1.47	1.12	1.19	1.23
39169	Hs.54457	CD81 antigen (target of antiproliferative antibody 1)	1.21	2.37	1.62	1.33	1.94	1.02	1.25	1.60	1.84	1.36	1.46	0.69	0.97	0.90	0.66	2.23	1.16	1.81	1.07	1.12	1.47	1.02
39173	Hs.2491	DiGeorge syndrome critical region gene 2	0.88	1.62	0.89	1.16	2.43	1.04	1.44	1.31	1.30	1.06	1.60	1.01	1.23	1.49	1.15	1.90	0.76	0.87	0.91	1.21	1.10	1.12
39195	Hs.16269	B-cell CLL/lymphoma 7B	1.54	1.73	1.14	1.65	2.88	2.12	1.72	1.57	1.38	1.68	1.42	1.38	1.25	1.47	1.37	1.28	1.03	1.29	1.60	1.22	1.34	0.77
39205	Hs.101047	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0.89	1.47	0.92	1.18	2.12	1.74	1.46	1.56	1.50	0.94	1.08	1.15	1.14	3.30	1.27	1.60	0.78	0.79	1.14	1.21	1.62	1.63
39270	Hs.234799	breakpoint cluster region	1.11	2.68	1.03	1.89	2.93	2.61	2.87	2.25	2.51	2.14	1.92	1.57	1.85	1.74	1.88	1.47	1.09	1.56	1.36	1.41	2.76	2.87
39285	Hs.77508	glutamate dehydrogenase 1	0.44	0.41	0.32	0.68	0.50	0.28	0.48	0.44	0.59	0.59	0.37	0.36	0.78	0.31	0.62	0.59	0.67	0.79	0.70	0.57	0.40	0.21
39965	Hs.75777	transgelin	3.32	2.77	4.77	3.76	8.19	3.72	9.33	4.58	5.26	7.10	8.34	8.23	1.82	4.95	7.25	5.65	3.94	5.12	7.31	2.34	3.95	3.83
39993	Hs.75428	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	0.85	0.69	0.69	0.73	0.58	0.71	1.03	0.93	0.92	1.51	0.83	1.13	0.90	0.87	1.25	0.94	1.59	0.75	1.14	0.53	1.19	1.02
39728	Hs.155291	KIAA0005 gene product	0.38	0.38	0.46	0.60	0.94	0.50	0.50	0.60	0.71	1.12	0.81	0.47	0.58	0.52	0.55	0.64	1.20	0.67	0.82	0.92	0.84	0.66
39781	Hs.76294	CD63 antigen (melanoma 1 antigen)	0.42	0.59	1.45	0.60	0.83	0.63	0.84	1.20	1.57	1.16	1.13	1.35	0.96	1.56	1.52	1.27	0.96	0.70	1.07	0.96	0.64	0.59
39796	Hs.831	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	1.37	1.18	0.96	1.03	2.56	1.26	1.42	1.26	1.80	1.27	1.25	1.23	1.26	2.82	1.94	1.46	1.60	2.39	2.26	1.79	1.69	1.42
39827	Hs.7957	adenosine deaminase, RNA-specific	1.78	2.72	1.50	2.34	3.23	2.17	2.72	2.60	2.70	1.69	2.18	1.62	1.98	2.68	2.88	3.17	2.16	1.83	2.23	1.77	2.40	2.79
39861	Hs.75108	ribonuclease/angiogenin inhibitor	1.42	0.69	0.77	1.45	1.43	1.10	1.41	1.87	1.92	1.10	1.33	1.84	0.76	2.02	1.64	1.51	1.32	1.37	2.22	1.21	1.06	0.99
39876	Hs.112028	cholinergic receptor, nicotinic, epsilon polypeptide	0.94	1.18	0.74	0.79	0.99	0.99	0.90	0.96	1.13	1.27	0.98	0.89	0.84	0.96	1.02	1.15	0.70	0.74	0.95	1.09	1.20	0.80
39903	Hs.169902	solute carrier family 2 (facilitated glucose transporter), member 1	0.91	0.42	0.90	0.63	0.44	0.37	0.36	0.30	0.98	0.44	0.43	0.42	1.29	0.34	0.35	0.31	0.49	0.25	0.32	0.65	0.53	0.32
40440	Hs.78546	ATPase, Ca++ transporting, plasma membrane 1	0.86	0.83	1.77	1.68	1.63	1.05	1.15	1.43	2.26	1.43	0.94	1.60	0.73	0.83	1.10	0.86	1.24	1.14	1.07	1.01	1.53	0.78
40442	Hs.108327	damage-specific DNA binding protein 1 (127kD)	0.84	1.03	0.22	0.64	1.99	1.14	1.28	0.79	1.19	0.81	1.55	0.64	1.27	1.11	1.06	1.52	1.17	1.08	0.90	1.21	0.46	0.91
40110	Hs.194366	transthyretin (prealbumin, amyloidosis type I)	1.20	1.59	2.12	2.17	1.77	1.71	2.14	2.51	2.79	2.46	2.20	1.13	1.42	1.63	1.23	1.67	1.46	1.18	1.35	1.61	1.10	1.87
40111	Hs.232068	transcription factor 8 (represses interleukin 2 expression)	1.86	1.45	1.25	1.45	5.41	0.57	1.87	1.83	2.06	1.05	1.16	3.74	0.65	8.07	7.37	1.63	4.26	5.96	7.94	3.38	1.97	1.42
40151	Hs.75736	apolipoprotein D	1.33	2.96	10.22	7.40	19.12	1.61	4.59	6.36	8.60	6.98	5.20	5.18	8.82	11.20	13.10	7.86	5.69	6.95	9.31	3.54	5.53	8.26
40205	Hs.249982	cathepsin B	1.12	0.85	0.87	1.08	1.13	2.10	0.91	1.65	2.14	1.17	2.09	1.17	0.86	1.79	0.68	1.58	1.13	0.61	0.74	0.85	1.17	1.08
40276	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 homolog)	1.01	1.10	1.68	0.92	1.18	0.97	0.42	1.08	1.37	1.13	0.79	0.91	1.21	0.86	0.95	1.29	0.93	0.83	0.80	0.90	0.80	0.74
40304	Hs.469	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.61	0.97	1.23	1.13	1.14	1.14	0.84	0.99	1.07	0.76	0.80	0.57	0.72	0.74	0.68	2.29	0.94	1.25	0.95	1.53	1.65	1.18
40360	Hs.2437	eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)	1.62	1.41	1.11	0.88	1.11	0.72	1.45	1.50	1.45	1.65	0.84	1.88	0.91	0.91	1.82	1.52	1.74	1.12	1.61	1.19	0.92	0.76
40959	Hs.79172	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	0.98	0.46	0.47	0.59	0.66	0.67	0.61	0.62	0.43	0.25	0.69	0.30	0.84	0.41	0.50	0.89	0.47	0.67	0.64	1.17	1.08	0.64
40991	Hs.78465	v-jun avian sarcoma virus 17 oncogene homolog	2.03	1.03	2.69	1.96	1.45	1.91	1.16	1.19	2.11	2.02	1.29	0.86	1.49	0.83	1.34	1.25	2.44	1.50	1.69	2.05	1.47	0.66
40562	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated glycoprotein)	1.58	1.59	2.92	1.94	2.00	1.28	1.17	1.90	1.78	1.42	1.52	0.79	0.58	1.00	0.88	0.79	0.87	1.14	0.86	0.93	1.45	1.21
40764	Hs.76930	synuclein, alpha (non A4 component of amyloid precursor)	2.34	5.99	6.13	6.10	6.20	5.20	3.00	5.78	7.52	5.50	8.11	9.27	3.99	7.42	4.45	2.71	4.64	4.54	4.86	2.71	3.66	3.21
40765	Hs.76807	Human HLA-DR alpha-chain mRNA	1.84	7.09	5.94	3.92	5.19	5.88	2.77	4.72	6.84	4.74	7.85	5.92	2.67	5.78	3.66	3.73	4.87	2.71	3.64	2.88	3.37	3.53
40874	Hs.21635	tubulin, gamma 1	1.35	1.53	1.12	1.10	1.18	1.53	1.47	0.98	1.28	1.42	1.19	1.02	2.19	1.39	1.35	1.12	1.04	0.92	1.21	0.90	1.45	1.40
40911	Hs.119192	H2A histone family, member Z	1.07	0.82	1.21	1.10	0.61	0.72	1.55	0.87	0.60	1.04	1.10	0.36	0.65	0.72	0.77	0.77	0.58	0.52	1.13	1.40	0.55	0.82
41208	Hs.1274	bone morphogenetic protein 1	0.36	0.65	0.83	0.95	1.22	0.46	0.43	0.85	1.69	0.73	1.38	1.13	0.49	0.92	0.70	1.08	0.48	0.47	0.51	0.55	0.45	0.33
41796	Hs.155017	nuclear receptor interacting protein 1	0.63	0.99	0.73	0.75	1.74	1.27	0.61	1.25	1.83	1.94	2.29	0.81	0.88	0.89	0.99	1.62	1.30	1.27	3.05	1.29	1.44	3.22
41356	Hs.155079	protein phosphatase 2, regulatory subunit B (B56), alpha isoform	1.80	2.05	1.22	2.07	3.47	2.12	0.86	1.51	2.37	2.02	1.84	2.16	2.21	1.68	2.19	2.00	1.82	1.18	2.78	1.37	2.19	1.87
41392	Hs.169370	FYN oncogene related to SRC, FGR, YES	2.57	1.89	1.64	2.15	2.58	2.26	1.72	2.09	2.97	2.44	2.47	2.22	2.68	2.15	2.54	2.07	2.28	1.86	1.71	1.83	2.15	1.78
41439	Hs.180370	cofilin 1 (non-muscle)	0.61	1.01	1.52	1.42	1.75	1.24	1.94	1.34	1.56	1.04	1.67	0.91	1.01	1.16	0.95	1.80	0.86	0.48	0.80	1.51	1.23	1.05
41452	Hs.28491	spermidine/spermine N1-acetyltransferase	0.42	0.80	0.83	0.57	0.98	0.52	0.41	0.70	0.63	0.62	0.78	0.93	0.28	1.08	0.57	0.71	0.46	0.54	0.61	1.31	1.27	0.66
41511	Hs.12163	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)	0.76	1.10	0.63	1.13	1.54	0.93	1.10	0.71	0.82	0.86	0.97	0.57	0.53	0.62	0.70	0.76	0.65	0.52	0.66	0.91	1.67	1.29
41559	Hs.76480	ubiquitin-like 4	1.57	1.66	1.24	1.25	1.48	1.91	1.26	1.45	1.45	1.25	1.90	0.96	1.87	0.96	0.87	1.33	1.11	1.02	1.06	1.84	1.92	1.62
41773	Hs.99908	nuclear receptor coactivator 4	0.90	1.40	1.12	1.15	2.12	1.06	1.82	0.96	1.57	1.79	0.90	1.94	0.95	1.04	1.60	2.34	0.90	1.00	1.12	1.17	0.94	0.77
41857	Hs.151734	nuclear transport factor 2 (placental protein 15)	0.65	1.32	1.09	0.62	1.42	0.78	0.85	0.86	1.03	0.96	1.02	1.16	0.60	1.33	0.73	0.92	0.54	0.39	0.58	0.57	0.58	0.95
42284	Hs.75102	alanyl-tRNA synthetase	1.61	1.48	0.88	1.36	1.72	1.34	2.45	1.12	1.86	1.03	1.31	0.78	0.71	1.29	0.67	1.29	1.74	0.78	1.16	1.41	1.70	1.30
41918	Hs.1861	membrane protein, palmitoylated 1 (55kD)	1.05	1.56	1.14	1.44	1.89	1.69	0.75	1.43	1.73	1.26	1.78	1.28	1.01	1.52	0.91	1.55	1.36	1.35	0.98	0.95	1.59	1.44
42020	Hs.148027	polymerase (RNA) II (DNA directed) polypeptide B (140kD)	1.35	2.24	1.63	1.95	2.49	1.90	1.22	1.97	2.41	1.93	1.88	1.55	1.16	1.39	1.56	1.95	1.13	1.23	1.53	1.43	1.86	1.74
42058	Hs.6289	growth factor receptor-bound protein 2	2.74	2.46	1.50	2.38	2.17	2.44	1.82	2.27	3.96	3.76	2.36	2.98	3.71	2.37	2.83	3.44	2.72	2.06	1.28	1.44	2.40	3.52
42059	Hs.74635	dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-	0.30	0.82	0.60	0.93	0.78	0.84	0.42	0.38	0.55	0.34	0.66	0.46	0.52	0.61	0.55	0.58	0.34	0.51	0.38	0.65	0.85	0.88
42088	Hs.15196	putative receptor protein	1.06	1.10	1.09	1.02	1.43	1.05	1.31	1.18	1.10	1.04	1.01	1.35	1.18	1.76	1.17	1.05	1.08	0.98	0.97	1.33	1.87	1.16
42096	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	0.93	2.27	0.65	1.58	1.36	1.42	2.27	1.35	0.90	1.11	1.31	0.65	0.60	1.13	1.16	1.40	0.77	0.83	1.34	1.17	1.46	1.85
42130	Hs.78614	complement component 1, q subcomponent binding protein	1.82	0.92	0.79	1.16	1.40	2.02	0.72	0.77	1.23	1.19	0.35	1.01	1.01	1.20	0.90	1.25	0.94	1.11	1.08	1.09	1.41	1.76
42777	Hs.2707	G1 to S phase transition 1	0.64	0.85	0.57	0.81	1.77	1.21	1.40	1.25	0.79	0.95	1.53	0.58	0.52	0.58	0.66	1.11	1.42	1.26	0.82	1.07	0.51	1.41
42844	Hs.158084	peroxisome receptor 1	0.82	0.68	1.13	1.68	1.41	1.07	1.69	1.16	1.37	2.19	0.28	0.90	1.16	1.20	2.43	0.62	1.61	1.68	0.78	0.56	0.99	1.36
42888	Hs.75117	interleukin enhancer binding factor 2, 45kD	2.58	2.02	2.06	2.64	2.28	2.90	2.36	1.41	1.17	0.91	1.21	0.54	0.76	1.55	1.05	1.56	1.35	1.34	1.77	1.49	1.04	3.13
42576	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing	0.81	1.13	0.79	0.71	1.38	0.97	1.01	1.18	0.81	0.93	0.86	1.06	0.79	1.35	1.34	1.35	0.74	0.85	0.88	0.85	0.69	2.13
42648	Hs.89643	transketolase (Wernicke-Korsakoff syndrome)	0.20	0.26	0.11	0.17	0.31	0.27	0.15	1.05	0.15	0.15	0.26	0.15	0.32	0.22	0.18	0.38	0.26	0.22	0.17	0.25	0.16	0.18
42677	Hs.76894	dCMP deaminase	0.85	0.98	0.66	0.86	0.97	0.64	0.35	0.79	1.16	1.01	0.59	0.59	0.98	0.94	0.76	1.06	0.82	1.03	0.58	0.49	1.51	1.08
42894	Hs.172589	nuclear phosphoprotein similar to S. cerevisiae PWP1	0.91	1.31	1.32	1.68	1.23	0.95	3.34	0.96	1.32	0.99	0.88	1.87	1.03	1.36	1.58	0.95	1.32	0.70	0.88	0.66	0.90	0.89
43129	Hs.317	phospholipase C, gamma 1 (formerly subtype 148)	1.19	0.79	0.57	1.03	1.30	0.86	1.05	1.03	0.87	0.95	1.40	0.70	0.81	0.76	0.84	0.76	0.96	1.08	1.32	1.07	1.28	0.91
43229	Hs.78996	proliferating cell nuclear antigen	1.30	0.64	0.74	0.90	1.01	1.24	0.85	0.75	0.56	0.47	0.94	0.59	0.69	0.53	0.70	0.86	0.72	0.80	1.09	0.74	1.50	0.93
43021	Hs.239817	histidyl-tRNA synthetase	0.71	0.71	0.43	0.58	0.81	0.55	0.80	0.91	0.68	0.90	0.79	0.78	0.72	1.21	0.96	0.86	0.71	0.75	0.94	0.66	1.08	0.94
43060	Hs.76989	KIAA0097 gene product	1.18	1.73	1.00	1.47	1.15	1.73	3.03	0.97	1.09	1.48	1.24	0.90	1.11	0.90	1.13	1.35	1.02	0.77	1.55	0.78	1.33	1.76
43092	Hs.177543	antigen identified by monoclonal antibodies 12E7, F21 and O13	0.43	0.39	0.81	0.41	0.59	0.35	0.65	0.64	0.31	0.26	0.76	0.29	0.34	0.37	0.36	0.33	0.35	0.58	0.66	1.03	0.85	0.70
43110	Hs.82689	tumor rejection antigen (gp96) 1	0.74	1.18	2.00	1.19	1.13	0.92	1.38	0.86	1.29	0.86	1.28	0.58	0.61	0.73	0.66	0.80	1.13	0.99	0.86	1.28	1.05	1.63
43231	Hs.74619	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2	1.57	1.21	1.09	1.09	1.02	1.12	1.66	0.93	1.27	1.25	0.76	0.78	1.11	0.85	1.00	1.30	1.24	0.62	0.81	1.14	0.70	1.09
43631	Hs.84981	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-bre	1.11	0.87	0.78	1.46	1.36	1.04	1.06	1.02	0.95	0.84	1.30	0.55	0.64	0.89	0.92	1.22	1.15	1.41	1.22	1.09	1.25	1.60

43338	Hs.182447	heterogeneous nuclear ribonucleoprotein C (C1/C2)	1.51	1.65	1.14	1.27	1.11	1.27	1.41	0.84	0.91	0.98	0.97	1.58	1.08	1.01	1.84	1.16	1.14	1.43	1.47	1.29	1.16	1.22
43241	Hs.173912	eukaryotic translation initiation factor 4A, isoform 2	1.49	1.62	0.83	1.33	0.99	1.57	1.10	0.95	1.13	0.97	1.00	0.92	1.22	1.26	1.44	1.24	1.09	1.02	1.39	1.14	0.71	0.92
43409	Hs.30942	ephrin-B2	1.25	1.34	0.57	0.97	1.93	1.39	0.62	0.56	0.94	0.66	1.17	1.91	0.53	0.84	1.64	1.44	0.74	0.79	0.51	0.63	0.83	2.35
43504	Hs.724	thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene h	1.26	0.84	0.90	1.04	1.11	0.85	0.70	0.78	1.31	0.94	1.11	0.64	0.85	0.66	0.92	1.19	0.79	1.00	0.82	1.04	1.00	0.73
43541	Hs.20313	protein tyrosine kinase 2 beta	0.43	0.64	0.17	0.39	0.75	0.98	0.34	1.73	0.28	0.32	0.64	0.59	0.24	0.67	0.46	0.86	0.32	0.47	0.39	0.46	0.40	0.23
43549	Hs.198281	pyruvate kinase, muscle	0.39	0.36	0.67	0.27	0.30	0.29	0.57	0.37	0.40	0.28	0.35	0.56	0.28	0.53	0.30	0.63	0.45	0.43	0.57	0.72	0.25	0.53
43550	Hs.2795	lactate dehydrogenase A	0.53	0.32	0.55	0.32	0.43	0.23	0.56	0.42	0.27	0.19	0.47	0.45	0.43	0.51	0.33	0.22	0.33	0.80	0.69	1.11	0.53	0.54
43563	Hs.82568	cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthoma	1.21	1.03	0.89	0.88	1.26	1.95	2.25	1.23	1.10	1.11	1.34	0.80	1.12	2.04	1.36	1.33	1.28	1.07	1.01	1.36	0.80	2.17
43711	Hs.552	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydroge	1.69	1.34	2.82	2.52	4.34	2.33	2.99	1.95	2.67	1.48	1.98	1.84	1.48	2.05	2.07	2.73	2.12	2.56	2.47	1.32	1.49	1.55
44159	Hs.75061	MARCKS-like protein	3.72	8.06	5.15	4.36	6.57	3.69	3.59	3.72	5.44	5.22	3.59	3.16	3.81	2.31	4.25	5.22	4.23	2.96	3.98	2.48	4.67	5.21
44173	Hs.16003	retinoblastoma-binding protein 4	2.62	1.46	1.61	1.62	0.94	1.23	1.34	0.89	1.61	0.77	0.85	1.80	1.98	1.52	2.23	1.62	1.94	1.74	1.68	2.00	1.07	1.81
44180	Hs.74561	alpha-2-macroglobulin	0.87	0.74	0.53	0.65	0.87	1.20	0.56	0.95	1.27	0.90	1.39	0.88	1.44	0.95	1.27	1.19	1.69	1.51	1.58	1.19	1.65	0.94
43719	Hs.91773	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	1.37	1.44	1.82	1.50	2.59	1.31	1.67	1.52	2.03	1.17	1.28	1.06	0.86	1.05	1.24	1.79	1.43	2.23	2.10	1.50	1.26	1.47
43826	Hs.86905	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42kD; Vacuolar proton-ATPas	1.30	0.93	1.07	1.08	0.88	1.54	0.81	0.81	1.46	1.62	1.22	0.75	1.68	0.70	1.28	0.83	1.29	1.19	0.66	1.27	0.66	1.23
43858	Hs.71891	discoidin domain receptor family, member 2	1.50	2.74	2.69	5.33	4.50	2.10	4.24	3.34	6.03	2.66	3.24	3.11	1.16	1.78	2.88	2.99	2.05	3.37	3.52	1.57	2.60	2.21
43885	Hs.172801	isoleucine-tRNA synthetase	1.21	1.98	0.79	1.95	1.27	0.98	1.39	0.87	1.14	0.86	0.76	0.60	0.61	0.54	0.64	0.85	0.64	1.10	0.79	1.45	0.80	1.85
43960	Hs.75551	Ras suppressor protein 1	1.92	2.69	2.22	1.66	1.91	2.35	1.63	1.51	1.94	1.59	1.56	0.93	0.65	1.03	0.88	1.79	1.35	1.43	1.17	1.08	1.68	2.71
44014	Hs.752	FK506-binding protein 1A (12kD)	0.50	0.81	1.13	0.54	0.55	0.44	0.60	0.45	0.62	0.48	0.39	0.48	0.35	0.50	0.45	1.70	0.50	0.73	0.49	0.97	0.54	0.55
44050	Hs.75080	LIM and SH3 protein 1	0.91	0.57	0.62	0.58	0.66	0.85	0.56	0.70	1.72	1.26	0.56	0.89	0.98	1.24	1.29	1.33	1.62	0.90	1.09	2.36	1.28	0.50
44105	Hs.81964	SEC24 (S. cerevisiae) related gene family, member C	0.88	0.74	0.57	0.69	0.87	0.78	0.85	0.70	0.85	0.64	0.82	0.73	1.06	0.80	0.89	0.93	0.98	1.03	0.89	1.20	0.88	0.67
44178	Hs.74637	testis enhanced gene transcript	2.55	2.49	13.02	9.72	13.61	6.39	9.21	7.09	9.15	6.25	7.03	8.39	2.91	4.82	7.65	5.75	5.67	4.37	9.47	3.14	4.84	3.94
44414	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	1.61	1.80	0.93	0.93	1.44	1.19	1.19	1.50	1.84	1.42	1.13	1.18	1.33	1.38	1.23	1.42	1.60	1.45	1.36	1.47	1.35	1.90
44477	Hs.109225	vascular cell adhesion molecule 1	2.80	23.62	19.06	10.11	5.07	5.72	2.19	6.32	10.32	0.95	4.92	4.23	1.85	1.97	3.11	3.50	3.70	2.37	2.06	2.24	3.66	4.20
44193	Hs.75350	vinculin	1.06	0.85	2.00	1.20	1.66	0.89	1.03	1.53	2.16	0.99	1.07	1.14	0.66	0.87	1.04	1.66	0.93	1.61	1.52	1.13	0.92	0.88
44218	Hs.79322	glutaminyl-tRNA synthetase	0.64	0.60	0.55	0.50	0.67	0.60	0.78	0.99	0.46	0.50	0.70	0.55	0.65	0.55	0.78	0.67	0.56	0.96	0.79	0.38	0.61	0.36
44255	Hs.79086	ribosomal protein, mitochondrial, L3	1.45	0.85	1.02	1.09	1.46	1.11	1.25	1.34	1.53	1.38	1.03	0.82	0.88	0.92	0.53	1.13	1.19	1.55	1.78	1.42	0.84	1.45
44266	Hs.74077	proteasome (prosome, macropain) subunit, alpha type, 6	1.12	1.02	0.95	0.86	0.64	0.80	0.75	0.93	1.20	1.12	0.85	0.82	1.11	1.03	1.03	0.89	1.34	0.78	0.92	1.09	0.90	0.86
44302	Hs.8997	heat shock 70kD protein 1	1.39	2.19	1.13	1.24	1.94	1.69	2.00	2.26	2.53	2.05	2.77	2.52	1.16	1.15	2.47	1.97	1.85	1.65	2.60	1.56	1.42	3.36
44307	Hs.2178	H2B histone family, member Q	3.01	4.10	6.16	2.52	2.45	1.56	2.16	3.08	4.72	8.24	1.55	1.75	1.37	1.27	2.00	3.32	1.80	1.85	3.87	0.72	1.76	2.49
44311	Hs.211579	melanoma adhesion molecule	2.92	2.18	2.79	2.12	2.71	1.70	2.43	1.64	2.74	5.00	2.72	2.33	1.27	2.04	2.28	2.04	2.00	1.57	1.78	1.90	2.71	1.72
44367	Hs.3100	lysyl-tRNA synthetase	0.71	0.54	0.54	0.47	0.94	0.68	0.85	0.53	0.77	0.53	0.52	0.33	0.28	0.34	0.35	0.56	0.67	0.48	0.53	0.80	0.99	0.87
44721	Hs.78596	proteasome (prosome, macropain) subunit, beta type, 5	1.20	1.15	1.20	0.73	0.88	0.76	1.15	1.09	0.86	1.19	1.14	0.74	1.10	1.27	1.27	1.08	1.51	0.84	1.12	1.14	1.52	0.88
44722	Hs.79889	monocyte to macrophage differentiation-associated	1.89	1.59	3.29	3.04	2.81	3.02	2.85	5.35	5.78	4.50	6.79	3.94	1.43	2.05	2.80	2.72	2.15	1.73	2.57	1.80	1.29	3.51
44537	Hs.83753	small nuclear ribonucleoprotein polypeptides B and B1	1.10	1.04	1.00	1.03	1.02	1.11	1.30	1.39	0.79	0.85	1.23	1.03	1.26	1.21	0.96	2.16	0.80	0.95	1.20	1.10	2.59	0.68
44563	Hs.79000	growth associated protein 43	1.00	1.01	1.06	0.96	0.87	0.95	1.35	1.13	0.86	0.73	1.06	0.97	1.02	1.32	0.87	1.67	0.78	0.86	1.19	0.99	1.46	0.46
44584	Hs.4909	regulated in glioma	1.33	0.49	2.05	0.72	1.43	1.21	1.09	1.56	2.73	1.24	1.34	1.35	0.72	1.03	1.15	1.48	0.88	1.82	1.76	0.90	1.33	1.16
44605	Hs.107979	small membrane protein 1	0.61	0.55	0.98	0.52	0.70	0.75	0.45	0.62	1.16	0.67	0.59	0.56	0.58	0.86	0.56	0.91	0.49	0.58	0.60	0.47	0.53	0.54
44666	Hs.197345	thyroid autoantigen 70kD (Ku antigen)	1.01	0.91	1.39	1.25	1.32	1.75	1.02	0.81	0.90	0.90	1.01	0.67	0.62	0.81	0.98	1.27	1.02	1.12	1.23	1.03	1.31	1.84
44689	Hs.31314	retinoblastoma-binding protein 7	1.85	1.66	1.90	1.69	1.73	0.83	1.27	1.05	1.17	1.01	1.18	0.66	0.99	0.62	1.42	1.26	1.22	1.37	1.24	0.91	1.01	1.37
44699	Hs.7476	ATPase, H+ transporting, lysosomal (vacuolar proton pump) 21kD	1.13	2.43	1.86	1.39	2.23	1.67	2.37	2.67	2.13	4.27	2.83	1.91	2.23	1.98	2.36	1.70	2.00	1.20	2.37	1.67	2.00	1.04
45222	Hs.155191	villin 2 (ezrin)	0.77	0.69	0.84	0.80	0.78	2.38	0.87	0.80	1.47	0.77	0.99	1.06	1.10	1.17	1.14	1.02	0.82	0.68	0.72	1.18	0.76	0.40
45658	Hs.170198	KIAA0009 gene product	1.56	1.34	1.03	1.73	1.34	1.75	0.97	0.80	1.01	0.65	1.84	0.91	1.36	1.07	1.08	1.33	1.33	1.37	1.03	1.75	1.44	2.61
45794	Hs.78853	uracil-DNA glycosylase	1.21	2.41	0.93	1.75	1.39	1.30	2.04	1.05	1.71	1.80	1.46	0.98	1.14	0.85	0.96	1.35	0.98	1.20	0.93	0.77	0.93	1.24
45851	Hs.78409	collagen, type XVIII, alpha 1	1.39	2.85	3.53	2.14	3.50	3.10	6.12	2.57	3.87	1.58	3.60	1.15	0.95	1.42	2.21	2.48	2.64	3.13	4.78	2.18	1.60	0.91
45233	Hs.82916	chaperonin containing TCP1, subunit 6A (zeta 1)	1.70	1.42	1.10	1.69	1.62	1.88	1.13	0.92	0.78	0.88	1.62	0.77	0.67	0.68	0.83	0.91	1.00	1.11	1.05	1.50	2.16	1.80
45291	Hs.169488	dentatorubral-pallidoluysian atrophy (atrophin-1)	1.17	1.42	1.02	1.39	1.48	4.57	1.30	0.70	0.65	0.82	1.35	0.67	0.80	1.03	0.93	1.72	0.72	0.76	0.95	1.33	0.48	0.87
45376	Hs.32500	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase)	1.12	0.46	0.73	0.61	0.70	1.19	0.72	0.40	0.49	0.41	0.79	0.59	0.37	0.73	0.59	0.60	0.67	0.82	0.75	0.70	0.72	0.72
45421	Hs.118787	transforming growth factor, beta-induced, 68kD	0.23	0.16	0.99	0.20	0.26	0.30	0.25	0.30	0.56	0.19	0.28	0.43	0.41	0.38	0.21	0.38	0.23	0.24	0.26	0.29	0.17	0.15
45564	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.16)	1.30	0.65	1.05	0.74	1.67	1.23	0.66	0.69	1.64	1.37	1.01	0.83	1.99	0.84	1.53	1.34	1.67	1.69	2.09	0.81	1.10	1.16
45568	Hs.76359	catalase	0.95	1.12	1.84	1.02	1.25	1.20	1.07	1.33	2.78	1.04	0.96	0.96	1.06	1.39	1.11	1.15	1.27	1.72	1.46	1.38	0.79	0.79
45604	Hs.211563	B-cell CLL/lymphoma 7A	1.04	1.02	0.81	0.74	1.06	2.13	1.47	0.85	1.09	0.92	0.94	0.49	1.55	0.92	0.70	1.06	1.18	1.63	1.40	1.04	0.62	0.91
45643	Hs.51043	hexosaminidase B (beta polypeptide)	0.81	0.88	0.89	0.69	1.04	0.99	0.68	0.69	0.81	0.54	2.65	0.72	0.66	0.90	0.85	0.99	0.85	0.81	0.78	1.15	0.44	1.03
45840	Hs.76122	splicing factor, arginine/serine-rich 4	1.79	1.63	1.63	1.40	1.10	1.77	1.35	1.04	1.19	1.02	0.89	1.21	0.74	1.05	1.15	1.39	1.34	1.42	1.40	1.09	0.91	1.11
46339	Hs.85181	v-raf-1 murine leukemia viral oncogene homolog 1	1.56	1.19	1.47	1.01	1.41	0.88	1.06	1.02	0.79	0.99	1.05	1.18	0.68	0.90	0.94	1.33	1.57	1.21	1.37	1.05	0.92	1.00
46354	Hs.20894	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1.50	1.76	2.41	1.57	2.35	2.09	1.63	2.30	3.69	1.52	2.39	1.23	1.70	1.89	1.26	2.78	1.97	2.64	1.79	0.98	1.04	1.67
46419	Hs.286	ribosomal protein L4	0.51	0.85	0.45	0.83	0.53	0.47	0.77	0.55	0.43	0.33	0.79	0.81	0.50	0.70	0.85	0.45	0.37	0.80	0.63	0.59	0.54	0.69
45941	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	1.58	4.96	1.62	3.03	2.69	2.84	1.45	1.61	1.89	2.20	1.61	0.95	0.92	0.83	0.93	2.04	0.94	1.45	1.42	1.42	2.46	2.46
46019	Hs.77152	minichromosome maintenance deficient (S. cerevisiae) 7	1.19	3.35	1.94	2.25	1.66	2.30	1.47	1.13	0.81	0.81	1.27	0.81	0.79	1.00	0.76	1.03	0.54	1.13	1.40	1.17	0.84	1.16
46042	Hs.75199	protein phosphatase 2, regulatory subunit B (B56), beta isoform	1.40	2.38	1.60	1.93	2.07	1.69	1.92	1.85	1.16	2.06	1.69	1.63	1.51	1.51	1.39	2.07	1.52	1.58	1.71	1.37	1.79	1.62
46171	Hs.129673	eukaryotic translation initiation factor 4A, isoform 1	0.68	0.76	1.61	0.78	0.97	0.79	0.98	1.15	0.67	0.51	1.05	0.87	1.07	0.92	0.76	0.98	0.68	1.09	0.86	0.77	0.73	0.93
46213	Hs.110713	DEK oncogene (DNA binding)	0.87	0.84	1.15	0.49	1.04	0.60	0.86	0.90	0.62	0.63	0.60	0.61	0.63	0.61	0.70	0.94	0.69	1.36	0.98	0.67	0.84	0.69
46302	Hs.183760	aldolase A, fructose-bisphosphate	0.35	0.49	1.27	0.29	0.38	0.25	0.57	0.46	0.43	0.79	0.38	0.37	1.79	0.74	0.48	0.52	0.70	0.86	0.75	0.72	0.37	0.63
46303	Hs.119252	tumor protein, translationally-controlled 1	0.64	0.76	0.91	0.44	0.43	0.59	0.64	0.67	0.72	0.82	0.70	0.29	1.53	0.84	0.54	0.81	1.02	1.30	0.96	0.75	0.58	0.42
46329	Hs.76368	capping protein (actin filament) muscle Z-line, beta	1.48	1.12	1.15	1.06	0.84	1.70	0.94	0.87	1.89	0.88	0.98	1.07	1.05	1.20	1.04	2.01	1.54	1.37	1.07	1.41	0.75	0.93
47125	Hs.79572	cathepsin D (lysosomal aspartyl protease)	1.20	2.00	1.14	1.61	1.34	1.33	1.21	1.59	1.74	0.87	1.20	0.61	0.53	0.65	0.79	1.50	1.18	1.03	1.28	0.89	1.34	0.85
47202	Hs.74571	ADP-ribosylation factor 1	2.46	1.68	1.05	1.36	1.71	1.44	2.16	1.85	1.60	0.78	1.23	1.78	3.13	1.72	1.76	1.78	1.68	1.10	1.50	1.48	1.85	1.96
46548	Hs.138860	Rho GTPase activating protein 1	1.86	1.45	1.09	0.84	1.76	1.54	1.94	1.13	1.62	1.28	1.18	1.47	1.67	1.50	1.66	2.11	1.67	1.85	1.29	0.91	2.15	1.47
46574	Hs.77269	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	1.09	1.45	1.45	1.17	1.84	1.39	1.42	1.76	1.83	1.31	1.75	1.69	1.16	1.20	1.30	1.90	1.39	1.38	1.35	1.15	1.35	1.43
46711	Hs.77608	splicing factor, arginine/serine-rich 9	0.76	0.72	0.81	0.63	0.81	0.76	0.91	1.00	0.83	0.43	0.66	0.71	0.67	0.44	0.77	0.87	0.79	1.14	0.82	0.79	0.90	0.58
46777	Hs.75344	ribosomal protein S4, X-linked	0.86	0.79	0.30	0.49	1.09	0.91	0.82	0.90	0.49	0.45	0.75	0.70	0.20	0.39	0.73	0.79	0.45	1.25	0.90	0.40	0.86	0.73
46920	Hs.79081	protein phosphatase 1, catalytic subunit, gamma isoform	0.58	0.83	0.63	1.38	0.61	0.70	0.73	0.57	0.94	0.43	0.59	0.42	0.72	0.32	0.63	0.68	0.65	0.91	0.60	0.66	0.72	0.91
46936	Hs.404	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated	1.34	1.19	1.05	1.47	1.24	1.16	1.35	1.12	1.10	1.04	1.16	0.84	0.67	0.71	1.05	1.11	1.18	1.59	1.25	0.97	1.44	1.01
47038	Hs.119	gene predicted from cDNA with a complete coding sequence	0.76	0.69	1.14	1.13	0.89	1.04	0.64	0.65	1.09	0.54	0.70	0.47	0.36	0.55	0.50	0.99	0.77	1.17	0.48	0.58	0.98	1.10
47631	Hs.75160	phosphofructokinase, muscle	0.44	1.14	0.95	0.75	0.94	0.34	0.74	0.62	0.81	0.73	0.82	0.50	0.55	0.65	0.93	1.19	0.86	1.07	0.77	0.57	1.05	1.00
47384	Hs.172665	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolat	1.75	0.91	1.13	1.25	0.92	1.11	1.13	0.66	0.46	0.59	0.93	0.64	0.82	0.43	1.08	0.82	0.84	1.19	1.65	1.03	1.26	1.50
47386	Hs.234726	alpha-1-antichymotrypsin	1.33	4.98	0.52	2.57	7.07	0.24	3.02	2.26	2.48	2.80	1.13	1.55	7.46	1.74	6.43	2.02	2.76	2.14	4.23	0.22	0.38	3.57
47463	Hs.173288	KIAA0155 gene product	1.02	1.34	0.49	1.38	1.91	1.15	1.02	1.19	1.52	0.91	1.05	1.07	1.03	0.89	1.29	0.86	0.86	1.24	1.50	0.76	1.53	1.68
48234	Hs.190703	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0.48	0.27	0.32	0.34	0.40	0.32	0.38	0.27	0.35	0.19	0.49	0.23	0.20	0.40	0.36	0.31	0.29	0.30	0.34	0.84	0.30	0.30
48406	Hs.75441	hydroxysteroid (17-beta) dehydrogenase 4	0.71	0.85	0.44	0.62	1.01	0.53	0.42	0.72	1.27	1.01	0.72	0.88	0.52	0.85	1.16	0.86	0.87	0.90	1.30	0.46	0.80	0.97
47679	Hs.75627	CD14 antigen	1.46	1.77	2.85	1.51	2.65	2.50	0.71	1.72	2.47	1.11	3.02	1.72	1.62	1.17	1.87	2.00	1.41	1.96	1.38	1.13	1.66	2.39
47727	Hs.75658	phosphorylase, glycogen; brain	0.33	0.14	0.21	0.23	0.25	0.20	0.27	0.21	0.16	0.12	0.16	0.25	0.20	0.36	0.19	0.20	0.18	0.40	0.30	0.50	0.25	0.23

47838	Hs.75432	IMP (inosine monophosphate) dehydrogenase 2	0.41	0.38	0.38	0.55	0.49	1.43	1.45	1.06	0.25	0.28	1.91	0.35	0.87	0.23	0.82	0.50	0.56	1.73	0.96	0.66	0.38	0.49
47833	Hs.248323	Tubulin, alpha, brain-specific	1.61	1.17	2.03	1.75	1.13	1.58	2.49	1.56	1.95	1.14	2.39	1.07	1.95	1.40	0.86	1.61	1.53	1.61	1.48	1.68	0.75	1.21
47884	Hs.73798	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	4.11	4.14	8.88	3.19	7.01	4.62	2.30	2.58	3.66	1.76	2.85	2.60	1.55	2.21	2.31	3.76	2.46	1.73	2.28	1.65	2.49	2.24
48077	Hs.76893	3-hydroxybutyrate dehydrogenase (heart, mitochondrial)	2.83	3.45	0.81	1.24	2.37	1.81	0.64	1.45	0.53	0.95	0.95	1.93	3.65	1.58	1.46	1.87	1.82	1.36	2.45	2.12	1.70	0.91
48085	Hs.85155	butyrate response factor 1 (EGF-response factor 1)	1.25	2.49	0.57	1.51	1.44	1.06	3.00	1.10	1.09	2.18	1.61	1.15	1.32	1.73	1.18	1.94	0.98	0.35	0.95	1.15	1.70	1.96
48452	Hs.77813	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)	0.63	0.77	0.74	0.83	1.15	0.69	0.63	0.42	1.84	0.66	0.97	1.09	1.18	0.97	0.92	1.65	0.77	0.96	0.93	0.85	0.82	1.25
49243	Hs.155595	neural precursor cell expressed, developmentally down-regulated 5	0.62	1.41	0.65	0.91	1.28	0.88	0.77	0.78	1.61	0.66	0.75	0.83	0.56	0.83	1.12	1.29	0.65	1.10	0.90	1.02	0.69	1.16
48458	Hs.110587	melanoma-associated antigen recognised by T lymphocytes	1.02	1.27	0.57	0.66	1.35	0.96	1.36	1.65	0.88	1.08	1.44	1.24	1.08	0.89	1.35	1.06	1.21	1.40	1.30	0.85	1.07	0.91
48503	Hs.75317	solute carrier family 16 (monocarboxylic acid transporters), member 2 (putative transpor	0.70	0.94	0.57	0.81	1.04	0.71	0.98	0.96	1.50	1.17	0.83	0.71	0.92	1.05	0.93	0.97	0.98	0.95	0.75	1.14	0.82	0.62
48629	Hs.180107	polymerase (DNA directed), beta	0.88	1.80	0.55	1.31	1.71	1.38	1.70	1.24	1.97	4.34	1.23	1.06	0.87	0.87	1.45	1.97	1.55	1.49	1.67	1.70	2.08	1.24
48717	Hs.57419	transcriptional repressor	1.70	1.63	1.15	1.44	1.93	1.37	1.12	1.35	2.04	1.41	1.84	0.85	0.89	0.69	1.21	1.79	1.72	1.77	2.02	1.54	1.75	1.33
48713	Hs.2210	thyroid hormone receptor interactor 3	0.72	0.71	0.48	0.80	0.76	0.94	0.56	0.72	0.99	0.54	1.42	0.49	0.48	1.12	0.50	0.96	0.58	0.60	0.58	0.77	0.45	0.83
48803	Hs.159223	NGFI-A binding protein 2 (ERG1 binding protein 2)	1.57	2.28	2.06	1.56	2.48	1.46	2.13	2.38	2.82	1.92	2.33	2.97	0.91	1.07	1.85	1.66	1.59	1.36	1.70	1.54	1.40	1.93
49277	Hs.142827	P311 protein	2.98	1.30	7.88	3.41	3.85	1.90	0.60	2.97	5.72	1.91	4.25	2.12	0.95	2.06	2.57	3.27	1.91	1.43	1.88	1.38	2.06	1.55
49666	Hs.157145	tetracycline transporter-like protein	0.67	1.19	0.62	0.71	1.57	0.97	1.46	2.11	1.86	1.99	1.31	1.02	0.19	0.59	0.98	1.39	1.54	1.88	3.33	0.91	1.89	0.75
49691	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler-Scheinker syndrom	0.57	0.85	0.57	0.83	1.03	0.54	0.59	0.54	1.03	0.42	0.40	0.63	0.48	0.61	0.78	1.00	0.35	0.77	0.43	0.51	0.29	0.73
49322	Hs.78436	KIAA0064 gene product	0.84	1.39	0.83	0.86	0.86	0.83	0.98	1.09	1.17	0.95	0.78	0.63	0.77	0.96	0.83	1.11	1.08	0.87	0.82	1.03	2.48	0.75
49383	Hs.76297	G protein-coupled receptor kinase 6	1.41	1.30	0.97	1.52	1.48	2.15	1.31	1.92	1.13	1.85	1.63	2.45	1.85	1.58	2.50	1.36	1.08	1.16	0.49	1.50	1.74	1.38
49403	Hs.146763	nascent-polypeptide-associated complex alpha polypeptide	0.64	0.61	0.74	0.57	0.60	0.66	0.95	0.91	0.53	0.47	0.76	0.90	0.79	0.62	0.80	0.56	0.78	1.11	0.94	0.62	0.83	0.82
49584	Hs.85226	lipase A, lysosomal acid, cholesterol esterase (Wolman disease)	0.47	0.65	0.52	1.24	1.00	1.35	0.36	0.78	1.65	0.48	1.16	0.81	0.72	1.21	0.77	2.20	0.67	0.68	0.40	0.73	1.05	0.96
49608	Hs.81634	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1	0.57	0.88	0.45	0.70	0.76	1.12	0.43	1.25	0.49	0.45	1.95	0.26	0.28	0.32	0.44	0.80	0.44	0.60	0.42	0.67	1.09	0.56
49665	Hs.82002	endothelin receptor type B	1.77	2.94	2.44	1.97	5.15	1.88	2.59	2.21	2.28	5.74	1.61	2.92	0.80	0.73	1.84	2.77	2.26	1.70	1.76	1.59	3.00	1.32
50038	Hs.78771	phosphoglycerate kinase 1	0.44	0.34	0.81	0.53	0.47	0.87	0.26	0.77	0.43	0.24	1.15	0.34	1.04	0.61	1.36	0.80	0.39	0.30	0.26	1.09	0.59	0.70
49777	Hs.125078	Human mRNA for ornithine decarboxylase antizyme, ORF 1 and ORF 2	1.08	0.91	0.76	0.80	0.90	1.15	0.64	1.31	1.32	1.03	1.90	0.66	1.50	1.31	1.13	1.49	1.56	0.98	1.20	0.99	1.38	0.97
49788	Hs.12068	carnitine acetyltransferase	0.71	0.95	0.78	0.86	0.76	0.75	0.76	1.78	1.03	0.93	1.40	0.94	1.40	1.58	1.01	1.63	1.29	0.99	1.05	0.79	1.05	0.58
49888	Hs.183153	ADP-ribosylation factor 4-like	0.77	0.56	0.38	0.69	0.63	0.25	0.51	0.55	0.69	0.48	0.63	0.74	1.22	1.19	1.04	0.59	0.77	0.61	0.57	0.47	0.69	0.20
50117	Hs.195188	glyceraldehyde-3-phosphate dehydrogenase	0.28	0.53	0.53	0.62	0.42	0.59	0.92	0.43	0.36	0.36	0.70	0.68	0.84	1.07	0.57	0.45	0.25	0.34	0.31	0.26	0.43	0.62
50363	Hs.77196	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	1.38	1.16	0.64	1.27	1.52	1.57	0.68	0.86	1.30	1.37	1.15	1.33	0.89	1.13	1.30	1.67	0.60	0.77	0.81	0.85	0.85	0.87
50106	Hs.75514	nucleoside phosphorylase	2.84	2.15	0.94	1.47	1.13	3.11	1.06	0.84	0.68	0.65	2.63	0.93	0.53	1.50	0.88	0.80	0.75	1.15	1.53	1.72	1.56	1.09
50232	Hs.82911	protein tyrosine phosphatase type IVA, member 2	0.98	1.21	1.63	1.29	1.56	1.49	1.01	1.27	1.86	0.82	1.45	1.22	1.12	0.92	2.36	1.90	1.34	1.32	1.70	1.09	1.15	1.73
50271	Hs.78950	branched chain keto acid dehydrogenase E1, alpha polypeptide (maple syrup urine disea	1.18	1.12	0.99	1.15	1.98	1.35	0.72	1.15	1.58	1.31	3.71	1.25	1.92	1.31	1.26	1.47	1.69	0.71	0.75	0.87	1.03	1.08
50308	Hs.79339	lectin, galactoside-binding, soluble, 3 binding protein (galectin 6 binding protein)	1.18	3.18	0.90	1.83	1.47	2.15	2.43	1.53	1.31	1.86	1.92	0.76	0.51	0.71	0.86	1.62	1.15	0.99	0.96	0.79	1.96	2.61
50322	Hs.180909	proliferation-associated gene A (natural killer-enhancing factor A)	0.88	0.93	1.07	0.91	1.01	1.26	0.93	0.72	0.81	1.68	0.99	0.91	0.60	0.93	1.30	1.04	0.98	0.43	0.77	0.93	1.13	1.00
50555	Hs.119598	ribosomal protein L3	0.47	0.79	0.57	0.35	0.64	0.33	0.95	0.41	0.42	0.41	0.47	1.22	0.79	0.65	0.73	0.58	0.57	1.48	0.82	0.40	0.52	0.73
51018	Hs.217493	annexin A2	0.41	0.24	0.44	0.29	0.40	0.51	0.39	0.31	0.56	0.23	0.34	0.24	0.31	0.55	0.31	0.45	0.39	0.36	0.46	0.54	0.15	0.52
51209	Hs.21537	protein phosphatase 1, catalytic subunit, beta isoform	1.79	2.54	1.29	1.13	2.36	1.48	1.25	0.69	0.93	0.73	0.71	0.62	0.38	0.81	0.73	1.17	1.12	1.21	0.80	1.23	3.04	1.36
50561	Hs.77202	protein kinase C, beta 1	0.76	0.73	0.57	0.72	0.68	0.60	0.68	0.97	0.72	0.51	0.79	0.42	0.51	0.41	0.71	1.41	0.59	0.90	0.91	0.87	0.92	0.61
50576	Hs.180677	zinc finger protein 162	0.83	1.20	0.80	1.19	1.03	1.38	1.21	0.96	1.56	0.68	1.23	0.68	0.78	0.51	0.67	1.62	0.92	1.14	0.92	1.28	0.69	0.93
50609	Hs.79110	nucleolin	1.44	2.34	0.61	1.29	1.88	1.26	1.93	1.65	1.06	1.58	1.63	1.17	0.78	0.65	1.24	1.27	1.09	1.93	1.80	1.89	1.49	1.87
50603	Hs.223241	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0.76	1.01	0.70	0.55	0.99	0.68	0.88	1.29	0.56	0.50	1.74	0.86	1.05	0.80	2.26	0.67	0.34	0.60	0.56	0.95	0.70	0.50
50666	Hs.89674	dolichyl-diphosphooligosaccharide-protein glycosyltransferase	0.94	0.63	0.85	0.88	0.94	1.03	0.63	1.49	0.86	0.47	0.72	0.62	0.75	1.13	0.80	0.93	0.79	0.70	0.61	1.10	0.90	0.98
50816	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiesterase	0.88	4.48	1.50	1.67	1.90	2.05	1.39	1.78	1.98	3.07	1.63	1.16	1.16	2.04	1.50	2.57	0.97	0.72	1.22	0.92	2.29	1.97
50888	Hs.75454	antioxidant protein 1	0.79	1.15	0.91	1.59	1.48	1.03	1.17	1.23	1.37	0.84	1.40	1.27	1.13	0.71	1.35	1.37	1.30	1.90	1.16	0.99	1.64	1.44
50941	Hs.63984	cadherin 13, H-cadherin (heart)	0.45	0.71	0.49	0.33	0.86	0.28	0.29	0.37	0.81	0.44	0.90	1.05	0.82	0.92	0.96	0.90	0.32	0.42	0.48	0.76	0.55	0.43
51219	Hs.43910	Sialomucin CD164	0.69	0.82	0.80	1.38	1.56	2.37	0.34	1.11	1.65	0.53	1.25	0.75	0.45	1.19	0.97	1.28	1.53	1.44	1.00	1.21	2.09	1.01
51454	Hs.215595	guanine nucleotide binding protein (G protein), beta polypeptide 1	1.42	1.76	1.01	1.07	1.01	1.19	0.71	1.21	1.32	0.98	1.23	0.55	1.01	0.94	0.74	1.28	1.00	1.26	0.75	1.71	1.95	1.07
51461	Hs.180877	H3 histone, family 3B (H3.3B)	1.41	1.90	0.93	1.33	1.33	1.14	1.53	1.49	2.50	1.62	1.85	1.30	1.98	1.02	1.51	2.01	0.84	1.31	1.11	0.98	0.87	1.77
51504	Hs.99858	ribosomal protein L7a	1.37	0.94	0.44	0.70	0.92	0.71	0.52	1.20	0.68	0.99	1.15	0.65	0.62	0.32	0.55	0.88	0.54	1.10	0.89	0.94	2.71	0.54
51241	Hs.78902	voltage-dependent anion channel 2	0.55	0.39	0.43	0.64	0.59	0.59	0.64	0.84	0.46	0.40	0.58	0.37	0.54	0.39	0.58	0.73	0.49	0.72	0.65	0.57	0.56	0.69
51302	Hs.77273	ras homolog gene family, member A	0.71	0.59	0.91	0.84	0.70	1.06	0.85	0.86	1.02	0.36	1.02	0.67	1.24	0.48	0.57	1.24	0.99	0.99	0.66	1.32	0.65	0.41
51293	Hs.79	aminoacylase 1	1.25	2.30	1.10	1.27	3.48	0.91	1.53	1.77	1.71	3.74	1.13	1.73	0.62	0.52	1.08	1.84	1.88	2.02	1.56	1.46	2.79	1.42
51318	Hs.118625	hexokinase 1	1.07	0.60	0.43	0.55	0.76	0.52	0.95	0.72	0.64	0.63	0.62	1.66	0.71	1.11	1.13	0.85	1.11	0.93	0.91	0.90	0.91	0.72
51432	Hs.180455	RAD23 (S. cerevisiae) homolog A	1.47	1.63	0.70	1.03	0.90	1.30	1.00	0.69	0.93	1.15	0.66	1.22	1.19	0.83	1.31	0.97	0.79	0.64	0.71	0.74	0.59	1.16
51785	Hs.82159	proteasome (prosome, macropain) subunit, alpha type, 1	2.29	0.99	0.56	0.75	1.21	0.67	2.21	0.83	0.91	0.54	0.81	1.49	2.72	1.91	1.88	1.00	1.45	1.33	1.58	1.11	1.16	1.15
51814	Hs.695	cystatin B (stefin B)	1.14	1.78	1.01	1.34	1.20	1.46	1.36	0.91	0.90	1.18	0.91	1.29	0.92	1.04	1.31	1.20	1.05	1.19	2.14	1.20	0.93	1.52
51666	Hs.77929	excision repair cross-complementing rodent repair deficiency, complementation group 3 (x	1.19	1.09	1.04	1.09	1.05	1.01	1.69	0.43	1.79	1.04	0.94	0.73	0.93	1.00	0.71	1.36	0.95	1.47	1.01	1.10	0.51	0.71
51685	Hs.172182	poly(A)-binding protein-like 1	1.41	0.94	1.18	1.15	1.11	1.08	2.75	0.73	0.42	0.62	0.98	2.04	0.83	1.50	1.76	0.80	1.16	1.81	1.79	1.39	0.85	1.36
51687	Hs.228059	KRAB-associated protein 1	1.25	0.80	0.66	0.78	0.74	0.44	0.86	0.44	0.79	0.50	0.41	1.17	0.58	1.50	1.18	0.82	0.84	0.87	0.79	1.09	0.80	0.50
51699	Hs.79070	v-myc avian myelocytomatosis viral oncogene homolog	2.78	0.91	0.40	1.40	0.68	0.83	2.86	0.29	0.30	0.18	0.36	1.33	0.82	0.66	1.41	0.28	1.58	1.11	2.11	1.54	0.36	2.03
51740	Hs.146812	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzy	1.31	1.73	1.04	1.01	1.54	0.96	1.01	0.74	1.21	1.41	0.75	0.66	0.56	0.60	0.92	1.17	0.91	0.89	1.21	0.64	1.11	0.67
51961	Hs.119251	ubiquinol-cytochrome c reductase core protein I	0.96	0.72	0.52	0.97	1.42	0.98	0.78	0.83	0.65	0.38	0.69	1.26	0.53	0.99	1.03	0.55	0.83	0.72	1.34	0.90	0.65	0.91
52650	Hs.85146	v-ets avian erythroblastosis virus E26 oncogene homolog 2	1.31	1.67	0.82	1.09	1.25	2.96	2.09	0.43	0.75	0.42	0.68	1.63	1.52	1.45	1.62	0.90	0.99	1.07	1.55	0.86	0.58	0.98
52222	Hs.251664	insulin-like growth factor 2 (somatomedin A)	0.85	0.73	0.56	0.52	1.98	1.37	1.22	1.23	2.01	0.97	1.58	0.80	0.61	1.02	0.70	1.83	0.43	0.66	1.03	1.30	1.07	0.91
52342	Hs.76084	lamin B2	0.78	0.96	0.88	1.24	0.87	1.14	1.12	1.01	0.90	0.74	1.16	2.79	0.79	1.28	2.35	1.07	1.96	1.99	2.76	1.33	1.38	1.10
52338	Hs.26014	activin A receptor, type II	0.54	1.14	0.88	0.90	1.13	0.79	1.12	0.43	1.27	1.32	0.34	0.47	0.36	0.81	0.67	2.37	0.62	0.59	0.50	1.05	0.60	0.62
52415	Hs.151242	complement component 1 inhibitor (angioedema, hereditary)	4.76	7.33	6.73	4.35	5.13	4.77	19.17	5.62	6.31	2.74	4.32	31.10	14.20	5.88	22.94	4.97	6.92	6.25	13.00	3.92	2.66	3.95
52587	Hs.82030	tryptophanyl-tRNA synthetase	0.80	5.20	1.09	2.96	2.08	6.27	1.16	1.36	1.90	0.67	2.54	1.09	0.68	2.07	1.44	2.57	0.45	0.70	0.73	1.29	0.91	1.53
53107	Hs.141011	calmodulin 3 (phosphorylase kinase, delta)	1.06	0.97	0.81	0.67	0.91	0.84	1.22	0.74	0.85	0.83	1.02	0.85	0.31	0.58	1.24	1.14	1.05	1.94	2.64	1.96	1.04	1.09
52773	Hs.75216	protein tyrosine phosphatase, receptor type, F	0.89	3.72	0.80	1.59	3.20	1.85	1.40	1.35	2.11	2.53	1.60	2.08	0.73	1.54	0.52	1.77	1.41	1.13	1.43	1.22	2.57	2.22
52896	Hs.180612	peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	3.44	1.25	0.60	1.23	0.80	0.66	0.73	0.97	0.91	0.77	1.28	0.90	0.77	1.42	0.87	1.20	1.09	0.93	0.55	0.91	1.51	0.89
52931	Hs.75113	general transcription factor IIIA	2.45	0.85	1.24	1.13	1.36	1.38	0.95	0.35	1.14	1.21	1.31	0.91	0.71	1.25	1.04	1.65	1.23	0.99	0.93	1.36	0.73	0.81
53068	Hs.75875	ubiquitin-conjugating enzyme E2 variant 1	0.38	0.56	0.75	0.49	0.63	0.83	1.10	0.66	0.75	0.95	0.58	0.38	0.36	1.37	0.37	0.64	0.48	0.37	0.53	0.90	0.84	0.51
53084	Hs.64797	amyloid beta (A4) precursor-like protein 2	2.30	0.73	0.66	0.90	0.61	0.99	1.30	0.67	0.70	0.28	0.76	1.05	0.74	1.05	1.45	0.89	1.59	1.46	1.56	1.39	0.96	0.43